UNIVERSITY OF SOUTHERN QUEENSLAND

Crown Rot (*Fusarium pseudograminearum*) Symptom Development and Pathogen Spread in Wheat Genotypes with Varying Disease Resistance.

A Thesis submitted by
Cassandra D Malligan, BSc (Hons)

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Abstract

Crown rot, caused by *Fusarium pseudograminearum* (*Fpg*), is an important soilborne disease of wheat and barley. The degree of crop damage depends on seasonal conditions. Typically, high moisture conditions early in the season encourage seedling infection from stubble residues. Moisture stress later in the season leads to the production of unfilled "whiteheads". Current control relies on cultural practices and sowing of partially resistant varieties. In order to understand the nature of partial resistance, I have examined the patterns of disease symptom development and pathogen spread in susceptible and partially resistant tissues of both pot-grown wheat, barley and oat seedlings and field-grown inoculated wheat trials. Further research was conducted to determine whether differences in pathogenicity occur amongst a small subset of Australian *Fpg* isolates.

Seedling experiments confirmed that differences in disease ratings between susceptible and partially resistant genotypes are detected in younger leaf sheaths of older seedlings. At later harvest times differences between these genotypes are not significant in older leaf sheaths. Re-isolation of *Fpg* from inoculated seedlings has shown that each tissue was infected later in partially resistant genotypes compared to susceptible ones with a significantly lower number of isolations recorded at each harvest time in 42 day old seedlings. Barley cultivars were rapidly infected by the pathogen and exhibited high levels of disease symptoms. By comparison levels of infection in oats were low compared to all other genotypes. No significant differences between genotypes were observed in coleoptile tissues, either in fungal colonisation or development of disease symptoms. Disease development in the subcrown internode varied between lines/cultivars but was not representative of the relative susceptibility of each genotype. The pathogen did not appear to invade plant tissue via the vascular system but rather spread directly across the stem from leaf sheath to leaf sheath.

Field trials were designed to study disease symptom development and localisation of *Fpg* hyphae in all expanded tissues (excluding head and roots) in wheat genotypes of known susceptibility to crown rot. Plants were harvested at approximately fortnightly intervals throughout the growing season. The main effects and interactions of harvest, genotype and tiller on each plant part were examined with a detailed statistical analysis of differences seen in these factors between susceptible and partially resistant wheat genotypes, in two inoculated field trials. While differences between genotypes were mostly not significant at each harvest when disease rating or isolations from leaf sheath tissues were examined, important differences between susceptible and resistant genotypes were seen in disease developments and *Fpg* infections of stem tissue in field trials. Restriction of pathogen growth and symptom development was more pronounced in the tissues of 2-49 (possesses seedling resistance) than in the field resistant Sunco. At present, the mechanisms that lead to these resistance responses are unknown.

The pathogenicity study aimed to determine whether 7 *Fpg* isolates and a mixed inoculum differed in ability to cause crown rot in 9 wheat genotypes ranging in susceptibility to this disease. Although a genotype*inoculum interaction was significant, there is no evidence of stable pathogenic races in the isolates examined in these experiments. The growth of all isolates was partially inhibited in a consistent manner on resistant genotypes when compared to very susceptible genotypes. These results confirm significant differences in the aggressiveness of *Fpg* isolates on wheat, evidenced by variation in mean disease severity between isolates growing on a range of host genotypes.

Certification of Thesis

I certify that the experimental work, results, analyses and conclusions reported in this thesis are entirely my own effort, except where otherwise acknowledged. I also certify that the work is original and not been previously submitted for any other award, except where otherwise acknowledged.

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Signature of Candidate Date

ENDORSEMENT:

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Signature of Supervisor Date

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Glossary of Abbreviations

AFLP:	Amplified Fragment Length Polymorphism
CAE:	Cellulose-acetate electrophoresis
COL:	Coleoptile
CZA^{++}:	Czapec Dox Agar plus antibiotics plus Allisan
DAP:	Days after planting
DH:	Doubled Haploid
DPI&F:	Department of Primary Industries and Fisheries
Fg G1:	*Fusarium graminearum* Group 1
Fg G2:	*Fusarium graminearum* Group 2
FHB:	Fusarium Head Blight
Fpg:	*Fusarium pseudograminearum*
I/'s:	Internode/'s
LRC:	Leslie Research Centre
LS/'s:	Leaf sheath/'s
MAT:	Mating type identification
PCR:	Polymerase Chain Reaction
PDA:	Potato Dextrose Agar
QTL:	Quantitative Trait Loci
QWRI:	Queensland Wheat Research Institute
RAPD:	Random Amplified Polymorphic DNA
rDNA:	ribosomal DNA
RFLP:	Restriction Fragment Length Polymorphism
SCI:	Sub crown internode
WAP:	Weeks after planting

Chapter 1: Introduction and Literature Review

1.0 General Introduction

Wheat has been in production in Australia since 1788, and is today grown in all Australian states. The area known as the wheat belt forms a narrow, discontinuous curve stretching through Queensland, New South Wales and Victoria, parts of southern South Australia and the south west of Western Australia (AWB, 2003).

Wheat is the most important grain crop in Australia accounting for approximately 90% of the total value of Australian grain production (AWB, 2003). The remaining 10% is made up from barley, oats, sorghum, lupins, rice, field peas, triticale, maize, peanuts, sunflower seed, soybeans, cottonseed and other oilseeds.

During the last 20 years the average Australian wheat production was 17.5 million tonnes a year with a total annual value between $AUS6-7 billion. Approximately 4.9 million tonnes of wheat is consumed annually by the domestic market with the remaining production exported. In Australia an average of 2.2 million tonnes of wheat is used for industrial and human consumption, 2.2 million tonnes for stock feed and 0.5 million tonnes as seed (Grains Council of Australia, 2004). Internationally a great diversity of products are made from Australian wheats. Most exports are to Asian countries for production of various noodle types and to the Middle East for production of different Arabic flat and pocket breads. Other products such as Chinese steamed breads and conventional pan breads are also important export uses (O'Brien et al., 2001).

1.1 Origin of Wheat

The origin of wheat has been traced back to the Middle East region, particularly an area now part of Iraq. Wheat belongs to the genus *Triticum*, which contains several species and sub species. The genus is characterised by a variation in ploidy between species. One group has two sets of chromosomes (diploid, haploid n=7), one group has four sets (tetraploid n=14, e.g. 7A + 7B chromosomes) and a third group has six sets of chromosomes (hexaploid n=21, 7A + 7B + 7D). This third group of wheats includes the most important common (bread) wheats (*Triticum aestivum*). Durum wheats (*Triticum durum*) are tetraploid and are also cultivated in Australia and elsewhere. No diploid wheats are grown commercially today (Cook and Veseth, 1991). Bread wheats emerged as a crop 10, 000 years ago through the hybridisation of *Triticum dicoccum* (tetraploid A & B genomes) with *Aegilops tauchii* (diploid donor of the D genome) (Worland and Snape, 2001).

1.1.1 Wheat development

A wheat seedling consists of a coleoptile, sub-crown internode, crown, leaves (consisting of a leaf blade and sheathing leaf base) and seminal or primary roots. The coleoptile and seminal roots emerge first from the wheat seed. The crown consisting of unexpanded nodes is formed just below the soil surface. These unexpanded nodes will form all leaves, roots and tillers of the plant. The crown is normally separated from the seed by a sub-crown internode. Wheat development occurs in a definite pattern in an unstressed wheat plant and can be divided into tillering, stem extension, heading and ripening (Wiese, 1987).

During tillering the seedling forms one or more tillers depending on the variety and growing conditions. Secondary tillers may also develop from primary tillers. Each tiller potentially gives rise to a fertile seed head whose development is initiated during tillering (Simmons et al., 1995).

The stem is telescoped at the crown and during stem extension the internodes begin to expand, separating the individual nodes (Cook and Veseth, 1991). Each of these nodes gives rise to alternating leaves. During heading the head emerges from the sheath of the final leaf (flag leaf) and flowering begins. The wheat head consists of two rows of spikelets arranged on alternate sides of the rachis. The number of spikelets formed on each head is genotypically dependent with more spikelets produced on the main stem then on the other tillers. Eight to 12 florets are initiated by each spikelet, however only four to five will remain fertile at flowering. During flowering green anthers are extruded from each floret (anthesis). Florets in the central spikelets mature first, followed by extrusion of anthers up and down the head.

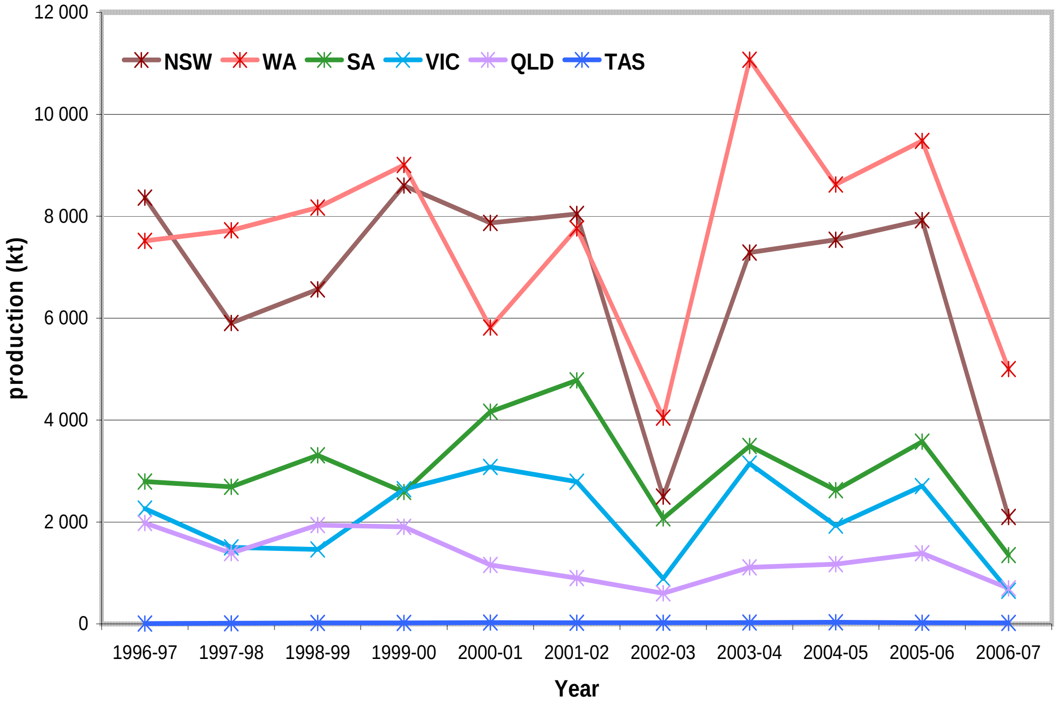
Pollination occurs shortly after heading when the anthers turn yellow or grey and usually occurs over about 4 days (Simmons et al., 1995).

Under typical conditions kernel growth and ripening takes approximately 4 weeks and is divided into 3 phases. During the milk stage the major starch and protein storage portion of the kernel is established. The soft dough stage occurs 1-2 weeks after pollination and kernel weight increases rapidly (60-80 % of final weight). During the final stage kernel-fill decreases and its consistency becomes hard dough. The percentage of moisture in the kernel decreases throughout grain fill to between 30 and 40 % at physiological maturity (Simmons et al., 1995, Cook and Veseth, 1991). Grain is subsequently harvested when grain moisture levels fall below 15%.

1.1.2 Wheat production in Australia

Grain production in Australia occurs over a latitude range from tropical to temperate resulting in a great variation in rainfall distribution across the wheat growing regions (O'Brien et al., 2001). Three regions are distinct within the Australian wheat belt. The southern region accounts for approximately 70% of Australia's cereals and includes Western Australia, South Australia, western Victoria and south-western New South Wales. Most rainfall is received between June and September during winter in this area. The northern region extends from central New South Wales to Queensland and is dominated by summer rainfall. This region accounts for about 25% of cereal production and often relies on stored soil moisture. The remaining 5% of cereals are produced in the south-eastern regions of NSW, Tasmania and eastern Victoria which receive both summer and winter rainfall (Cramb et al., 1991). Area sown to wheat and subsequent production proportions change from year to year in line with economic and environmental conditions particularly rainfall (as discussed below 1.1.3). Generally wheat production is highest in WA and NSW and lowest in Tasmania (Figure 1.1).

Figure 1.1 Wheat production (kt) in each state of Australia over the last 10 years (1996/97-2006/07) (adapted from ABARE 2007). NB: Lines in chart are for illustration purposes only they do not represent between year measurements



In Australia most wheat varieties are spring wheats, planted in late autumn (April-June) and maturing from late spring to mid-summer (October-January). Winter wheats are also grown in small acreages particularly in areas prone to frost damage. These wheats can be sown early if conditions are favourable and will remain in the vegetative phase until vernalisation requirements are met (Simmonds, 1989).

Wheat is divided into red and white wheats, classified on the presence or absence of a red to brown pigmentation of the seed coat. White grained wheats are the focus of Australian wheat production with virtually no red wheats grown (Simmonds, 1989).

In Australia wheat was usually grown as a monoculture up to the 1940's. This may have been with a fallow year to aid moisture retention or as continuous cropping. Limited rotation was employed and it would usually involve other cereals such as barley and oats. After this time wheat -ley rotations were introduced to improve the rapidly declining soil fertility and structure and to limit disease epidemics. However cropping in some parts of the wheat belt still do not employ ley or other non-cereal crops as part of rotations, particularly in Queensland. The main non-cereal rotation crops used in Australia are legumes with lupins grown mainly in WA, chickpeas, in northern NSW and Qld and field peas and faba beans mainly in SA and Vic. The oilseed crop Canola is also grown in NSW and Vic as a suitable disease break (Hamblin and Kyneur, 1993).

1.1.3 Factors limiting wheat production

The primary constraint to wheat production and quality in Australia is water, followed in importance by soil fertility and disease.

1.1.3.1 Rainfall and seasonal conditions.

Variations in rainfall and climatic conditions have a direct impact on the success of wheat production in Australia. Production is largely confined to areas receiving 300 to 650mm of rain each year. Fallowing is also used in low-rainfall areas to provide stored soil moisture for subsequent crops (Hamblin and Kyneur, 1993).

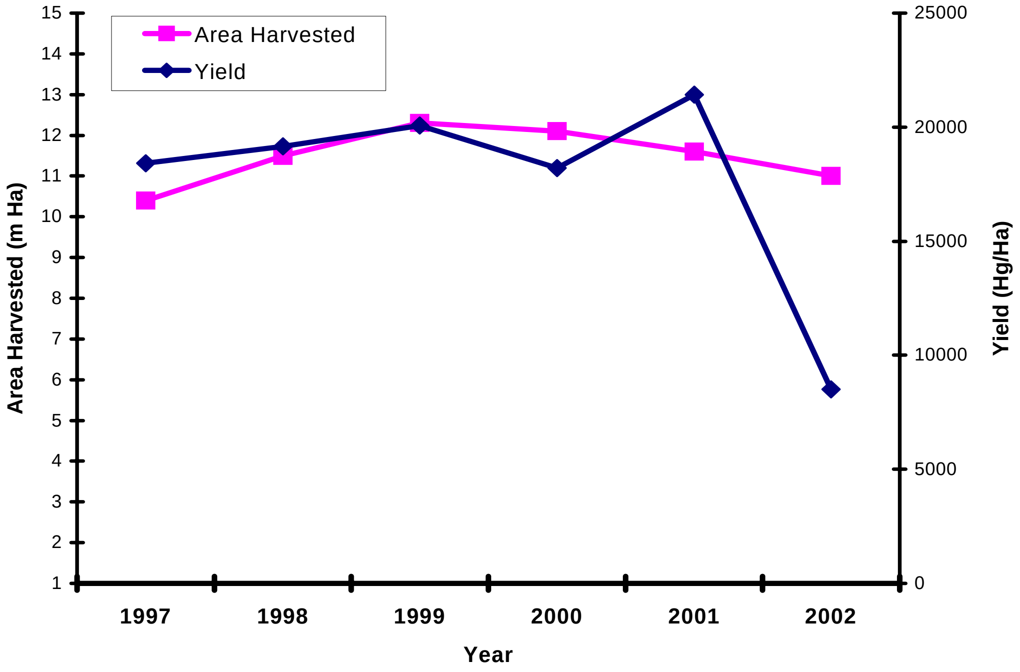
Drought conditions saw grain production fall from 39.7 (Mt) in 2001-2002 to 15.4 (Mt) in 2002-2003, while area sown to grain only fell from 21 to 18 m ha (Hooper et al., 2003). Figure 1.2 below shows the relationship between area of wheat harvested and yield from 1997 to 2002. A sharp decline in yield was seen in the 2002-2003 season associated with these low rainfall conditions.

1.1.3.2 Soil types-nutritional requirements

In Australia wheat is grown on a range of soils varying considerably in structure and fertility across the wheat belt. From the red brown earths utilised in SA, northern Vic and as far north as the Liverpool Plains of NSW, to the high yielding black earths of the Darling Downs in Qld and poorly fertile sandy yellow and red earths in large areas of WA (McGarity, 1975).

Today most Australian soils are old, weathered and low in organic matter. Of particular importance to wheat nutrition are the deficiencies of phosphorus and nitrogen (Hamblin and Kyneur, 1993). Phosphorus deficiency in wheat was first

Figure 1.2 Area harvested and yield of wheat crops grown from 1997 to 2002 in Australia (adapted from (FAOSTAT, 2003).



recognised in SA in 1882 and led to the standard application of phosphate fertilisers in wheat production from that time (Storrier, 1975). Nitrogen is also low in Australian wheat soils and inorganic fertilisers, leguminous pasture ley rotations and fallowing (promoting the mineralisation of organic nitrogen) have been utilised as a source of nitrogen for wheat crops (Hamblin and Kyneur, 1993, Storrier, 1975).

1.1.3.3 Wheat disease

Wheat may be attacked by various organisms causing diseases of the leaves, stems, heads or roots of the plant. Pathogenic organisms that complete a significant proportion of their lifecycle in the soil are defined as soilborne plant pathogens. These pathogens are most often associated with diseases of the roots and stem bases of the plant, and their overwintering and dispersal stages are usually confined to the soil. Soilborne plant pathogens can prove to be highly destructive and include various species of bacteria, fungi, viruses and nematodes (Hillocks and Waller, 1997).

The major soilborne diseases impacting wheat production in Australia are the fungal diseases take-all (*Gaeumannomyces graminis* var. *tritici* Walker), crown rot (*Fusarium pseudograminearum*), Rhizoctonia barepatch (*Rhizoctonia solani* Kühn), common root rot (*Bipolaris sorokiniana*), and disease caused by cereal cyst nematode (*Heterodera avenae*), and root-lesion nematode (*Pratylenchus* spp.).

1.2 Crown Rot: The Disease

Crown rot was first recorded in Australia in 1951 by Mc Knight, on the Darling Downs in Queensland. Symptoms similar to crown rot were reported as early as 1940 however the cause was unknown (McKnight and Hart, 1966). The disease has since been recorded in all wheat growing regions of Australia, including New South Wales (Magee, 1957, cited in Burgess et al., 1981), Victoria (Chambers, 1972), South Australia (Grewal et al., 1996) and Western Australia (Chambers, 1960, cited in Burgess et al., 2001). Crown rot is also emerging as an important disease internationally, and has now been reported in the Pacific Northwest of the USA (Smiley and Patterson, 1996), South Africa (Van Wyk et al., 1987), Italy (Balmas, 1994, cited in Burgess et al., 2001), Egypt and Syria (Burgess et al., 2001), Turkey (Bentley et al., 2004), west Asia and north Africa (Mitter et al., 2006a) and has in recent years been isolated from the cereal growing regions of western Canada (Mishra et al., 2006).

1.2.1 Economic losses

In Australia crown rot of wheat and barley is an economically important disease, particularly in northern New South Wales and southern Queensland. While it is difficult to put a cost on damage incurred by one disease in the field, it was reported in the 1995 – 1996 growing season that losses in wheat due to crown rot were estimated at $21.3 million in the northern wheat belt (ABARE, 1996). More recent reports suggest that nationally losses due to crown rot are $56.3 million annually, with a potential cost of $160.4 million in a single season (Brennan & Murray, 1998, cited in Ritter, 2001). Where crown rot has built up to significant levels in a field, losses in grain have been reported at 50% or higher (Klein et al., 1991).

1.2.2 Disease symptoms

Crown rot is a soilborne disease that infects the base and crown of the plant from the surrounding soil or organic matter. A pre-emergence rotting and seedling blight have been observed in the field and in the laboratory in severe infections of highly susceptible materials (Butler, 1961, cited in McKnight and Hart, 1966). In emerged seedlings the first symptom of disease is a discolouration or development of lesions on the basal parts of the susceptible plant, including the coleoptile, subcrown internode, and leaf sheaths.

Plants with severely infected crowns can suffer a complete collapse of the root system (Purss, 1966). Roots infected with the disease exhibit external discolouration of tissue. Brown lesions may be observed on seminal and secondary roots. Purss (1966) reported two types of infection on roots. One was directly associated with disease of adjacent crown or subcrown internode tissue and the other with discrete lesions on both seminal and secondary roots. Infection of stem bases via the roots is considered to be infrequent, however crown roots may become colonised from crown or stem tissue (Burgess et al., 2001).

A honey brown discolouration of the stem may be seen as high as the sixth internode of a tiller (Purss, 1966), but infection of the head via the stem is rare (Burgess et al., 1981). The basal discolouration on internodes and leaf sheaths may develop in a streak-like pattern and it may be confined to one side of the stem (Butler, 1961, cited in McKnight and Hart, 1966).

Ultimately the disease leads to the formation of white heads (or deadheads), which contain no grain, and heads with varying degrees of shrivelled grain. It is believed that this results from a disruption to the translocation system, causing premature ripening of the plant (Burgess et al., 1981). Under wet conditions whiteheads become dark and discoloured due to the activity of saprophytes (Butler, 1961, cited in McKnight and Hart, 1966). A recent paper has reported for the first time an increase in protein content associated with increasing crown rot, resulting in reduced grain quality for growers in the Pacific Northwest states of America. Wheat production in this region is focussed on low-protein soft-white wheats (Smiley et al., 2005).

The processes that occur in the plant/fungal interaction leading up to whitehead formation have not been reported for this disease. Descriptions of disease developments are from the results of systemic isolations from various parts of plants sampled at intervals, not from extensive histological exploration. Apart from a limited microscopic examination on wheat seedlings carried out during my Honours year (Lusted, 1998) no such histological investigations have been published with respect to the examination of crown rot infection of wheat. If the formation of whiteheads does result from a disruption to the translocation system, the events that lead up to this are unknown.

1.2.3 Identification of the crown rot causing organism

Since crown rot in Australia was first described in 1951, several studies have looked at identification of the pathogen(s) responsible. DNA technologies applied over the past decade have further enhanced the characterisation of the fungal species involved.

During the 1960's the pathogen associated with crown rot was described as *Fusarium graminearum* Schwabe. The perfect stage (or teleomorph) of this fungus *Gibberella zeae* (Schw) has been widely described as a plant pathogen responsible for diseases such as head blight in wheat (scab), stalk and cob rot in maize and crown rot of several grass species (McKnight and Hart, 1966, Purss, 1966).

In 1969 Purss proposed that pathogenic races of *G. zeae* occurred in Queensland. In assessing pathogenicity of *F. graminearum* isolates from various gramineous hosts in Queensland he found that isolates of *G. zeae* from stalk and cob rot of maize were incapable of causing crown rot in wheat. These isolates also formed the perfect stage of the fungus much more readily then those isolated from wheat and other grasses (Purss, 1969). In examining this relationship, Purss conducted further experiments in Queensland as well as travelling to the USA to conduct trials in Minnesota. In these tests he examined the capability of cultures from plants affected by crown rot of wheat (Qld, 4 isolates), stalk rot of maize (Qld, 2; USA, 3 isolates), and head blight of wheat (USA, 2 isolates) to cause the above mentioned diseases. These experiments indicated that all isolates were capable of causing head blight in wheat and stalk rot in maize and therefore no definite pathogenic specialisation was associated with these diseases. Once again pathogenic specialisation was reported in which cultures of *F. graminearum* from maize, while causing disease in that host were unable to produce crown rot in wheat. Purss concluded that the severe crown rot syndrome in Queensland was caused by a distinct pathogenic race (Purss, 1971b).

Burgess et al. (1975) noted different morphological types within the species *F. graminearum* Schwabe when conducting surveys of Fusaria associated with crown rot of wheat across Eastern Australia. Francis and Burgess (1977) investigated isolates of *F. graminearum* Schwabe causing stalk rot in maize and crown rot in wheat and concluded that two distinct populations of *F. graminearum* Schwabe exist. They assigned them to two groups. Group 1 causing crown rot in wheat and Group 2 causing stalk rot of maize and head blight of wheat. An important characteristic in the distinction was perithecial formation. *Fusarium graminearum* Group 2 isolates readily formed fertile perithecia on carnation leaf agar, potato dextrose agar and several other substrates. Perithecia were also easily isolated from host tissue. Isolates of *Fusarium graminearum* Group 1 were grown on a range of media and failed to produce perithecia in culture (Burgess et al., 1975, Francis and Burgess, 1977). Perithecial production by *Fusarium graminearum* Group 1 has rarely been reported in the field. Under standard light and temperature conditions the two groups could also be distinguished on the basis of colony growth and morphology, conidial dimensions and intensity of sporulation. However these characteristics can vary under different conditions and the ability or inability of the isolate to produce perithecia remained the most distinguishing characteristic (Francis and Burgess, 1977). From this time the pathogen associated with crown rot was identified as *Fusarium graminearum* Group1 (*Fg* G1) and that associated with stalk rot of maize and head blight of wheat *Fusarium graminearum* Group 2 (*Fg* G2).

Benyon et al. (1995) used a genetic approach based on Restriction Fragment Length Polymorphism (RFLP) data collection to analyse differences between several Fusarium species. Results confirmed that distinct subspecific groups existed within the species *F. graminearum.*

Aoki and O'Donnell (1999a) examined morphological characters and DNA sequences from 17 Group 1 and 15 Group 2 strains from different geographical regions to determine whether clear phenotypic and genotypic characters could be found that differentiate the two *Fusarium graminearum* groups.

The phenotypic comparisons included colony radial growth rates on various media, colony morphology, colour and odour comparisons, microscopic observations, production of chlamydospores, and conidial dimensions (grouped on the basis of number of septae). They found that all strains of G2 formed perithecia, where G1 strains did not. Colony growth rates of G1 strains were consistently lower than G2. No distinct differences in colony characteristics were observed; in fact they reported more variation among strains within the groups than between the groups and chlamydospore production was not found to be a distinguishing characteristic. Size of conidia of each Group yielded very similar values. However, they found that conidial morphology could be used to separate the two groups. Macro-conidia of *Fg* G2 strains are most frequently widest one-third to two-fifths from the apex eg between the first and second septum for 3-septate conidia. In contrast the widest position of conidia of *Fg* G1 strains is at the middle septum. Francis and Burgess (1977) also noted the conidia from cultures of *F*g G1 were greater in length and breadth then those produced by *Fg* G2.

Aoki and O'Donnell (1999a) concluded that the Group 1 isolates represent a distinct species that they named *Fusarium pseudograminearum* sp. nov. (*Fpg*).

Aoki and O'Donnell (1999b) then went on to explore the production of the perfect stage of *Fpg* in culture. They conducted mating experiments with 18 strains of *Fpg* to examine their ability to produce a teleomorph (fertile perithecia). Isolates were paired in all combinations and out of the 153 possible pairings 8 combinations resulted in the heterothallic production of perithecia and 7 of those contained viable ascospores. The authors compared these cultures with the teleomorph of *Fg* (*G. zeae*) and found that the ascospores of *Fpg* were longer than ascospores from the *Fg* isolates and differences also occurred in colony morphology. They concluded that the *Fpg* teleomorph was a distinct species, which they named *Gibberella coronicola.*

1.2.3.1 Genetic identification of *Fpg*

Further studies have supported this taxonomic split and several research groups have employed genomic technologies to assist in the identification and discrimination of different Fusaria.

Genomic comparisons in the study of Aoki and O'Donnell (1999a) involved polymerase chain reaction (PCR) amplification and sequencing of the β-tubulin gene. Analysis of DNA sequence data showed that maximum parsimony analysis of β-tubulin gene intron and exon sequences yielded a single most parsimonious tree in which all 17 strains of *Fpg* formed an exclusive group.

Aoki and O'Donnell (1999a) employed aligned translation elongation factor EF-1α gene sequences to design a *Fpg*-specific PCR primer pair (Fp1-1/Fp1-2). PCR experiments conducted on genomic DNA demonstrated that the primer pair was able to specifically amplify a PCR product of 523 bp only from strains of *Fpg*.

Laday et al. (2000), used cellulose-acetate electrophoresis (CAE) to conduct isozyme analysis on 34 *Fg* and *Fpg* strains. They found from the 33 enzyme bands evaluated that five were specific to *Fg* and five were specific to *Fpg*. Based on cluster and principal co-ordinate analysis this same study reported that *Fg* had a greater affinity with *F. crookwellense* and *F. culmorum* than to *Fpg*.

In an examination of the genetic relationship of 56 isolates of *Fusarium* using Restriction Fragment Length Polymorphism (RFLP) analysis, Benyon et al. (2000) also reported that *Fg* had a strong genetic relationship with *F. crookwellense* and *F. culmorum*, while *Fpg* only shared 40 % of genomic DNA RFLP bands with this group. However in this study *Fg* and *Fpg* isolates shared the greatest similarity in mitochondrial DNA RFLP patterns.

Williams et al. (2002) developed PCR-based assays to assist in the detection and identification of Fusarium species associated with crown rot of durum wheat in South Australia. Random Amplified Polymorphic DNA's (RAPD)'s were successfully employed to identify unique bands and specific primers were designed that separated *Fpg* and *F. acuminatum* from each other and from *Fg*, *F. culmorum*, *F. crookwellense* and *F. avenaceum*. In another study *Fpg* was effectively separated from *Fg*, *F. culmorum* and *F. cerealis* using rDNA internal transcribed spacer sequences (Tan and Niessen, 2003).

1.2.3.2 Genetic diversity of *Fpg*

Several studies have recently emerged exploring the diversity within *Fpg* populations. A high level of genetic diversity was reported in *Fpg* populations collected from south, east and western Australia (Bentley et al., 2005a). Amplified Fragment Length Polymorphism (AFLP) analysis indicated that genetic diversity was spread over these regions with no clustering or sub grouping according to location or host origin of isolate, except for a lower level of diversity observed in the west Australian populations. Scott et al. (2005) distinguished 5 haplotypes within *Fpg* populations isolated from Australia, USA and Canada.

Bentley et al. (2005b) also looked at the contribution of sexual recombination in *Gibberella coronicola* to genetic diversity in Australian field populations. Results suggest that sexual reproduction in the field occurs frequently and that a single recombination event results in a high level of genetic variation, significantly contributing to genetic diversity in *Fpg* populations. Akinsanmi et al. (2006a) also reported that sexual recombination in *Fpg* field populations occurs frequently; however they concluded that its contribution to the significant genotypic diversity reported in *Fpg*, using AFLP markers, was limited. Only 4% of the diversity within Australian *Fpg* was associated with geographic distribution in this study.

In contrast, a phylogenetic study using AFLP analysis of *Fpg* isolates in New Zealand found that groups of isolates were separated according to geographic location and host origin (Monds et al., 2005).

1.2.4 Classification of the genus *Fusarium*

The genus *Fusarium* belongs to the Hyphomycetes in the subdivision Deuteromycotina or imperfect fungi. They produce hyaline, septate macroconidia with a foot-shaped basal cell (Burgess et al., 1994). These fungi reproduce by asexual means and may also produce a teleomorph or sexual stage. The majority of *Fusarium* species have a teleomorph belonging to *Gibberella* (Summerell et al., 2001). These fungi belong to the phylum Ascomycota, characterised by their formation of asci, which are sac-like cells containing typically 8 ascospores (Alexopoulos et al., 1996). The genus *Gibberella* is within the group of filamentous ascomycetes, and form deep blue or purple perithecia, which enclose the asci (Alexopoulos et al., 1996).

1.2.4.1 *Fusarium pseudograminearum* Schwabe Characteristics

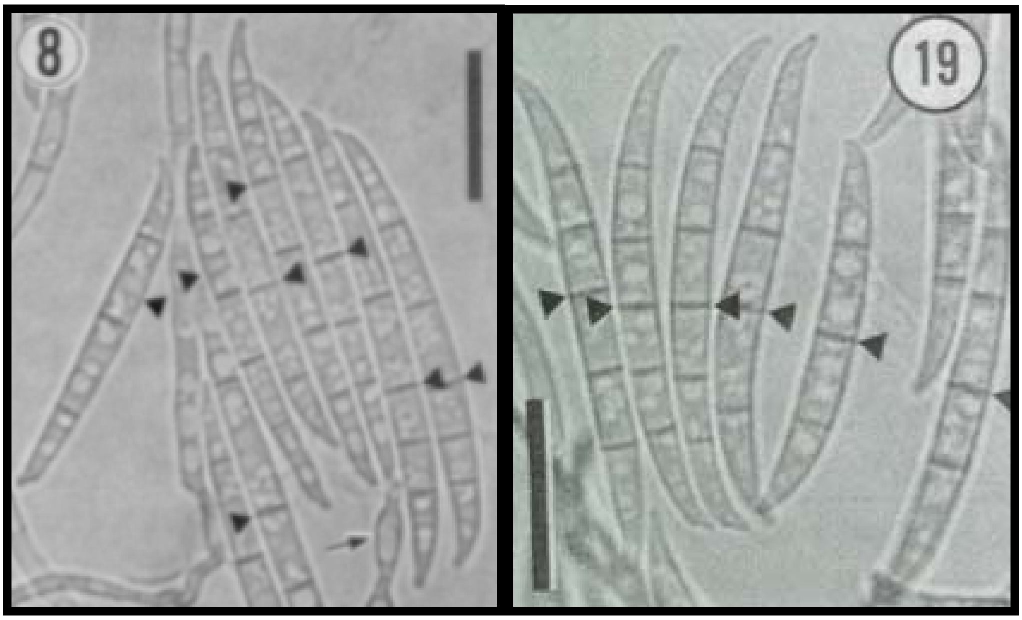
Deuteromycetes typically produce well developed, branched, septate hyphae, the same as that produced by the sexual stage. *Fpg* colony colour on Potatoe Dextose Agar (PDA) is red, reddish white, greyish brown, brownish orange, brownish yellow to white. Generally abundant aerial mycelium is produced however, in some isolates it is sparsely developed. It is loosely to densely floccose (Aoki and O'Donnell, 1999a).

The Deuteromycetes reproduce by means of asexual spores termed conidia (microconidia and/or macroconidia). These spores are produced at the sides or tips of modified hyphae, called conidiophores (Alexopoulos et al., 1996). *Fpg* does not produce microconidia (Toussoun & Nelson, 1976). The macroconidia are produced from conidiophores aggregated in sporodochia (cushion shaped structures made up of tightly grouped conidiophores) or formed directly on aerial hyphae. Conidiophores may be branched verticillately or unbranched forming simple monophialides (Aoki and O'Donnell, 1999a).

The morphology of the macroconidium is the main distinguishing characteristic of the species (Booth, 1977). The number of septae in the spore varies from 3 to 7, depending on its size. The spores are long and thin, generally with an elongated apical cell, which narrows gradually to a point. They also have a well-marked foot cell, which is often distinguishably bent (Booth, 1971). *Fpg* macroconidia are falcate to fusiform but some are almost cylindrical and gently curved. The morphological characteristic which finally separated Group 1 and Group 2 strains as separate species was that the *Fpg* macroconidium is widest at the middle septum or mid region of the spore, whereas Group 2 isolates are widest 1/3 to 2/5 from the apex (Figure 1.3) (Aoki and O'Donnell, 1999a).

Chlamydospores, which are resting spores, are rarely produced. When they are produced they are hyaline to pale, yellowish-grey or pale-yellow with a smooth or slightly roughened outer wall, measuring 10-16.5 x 7.5-14 µm (Aoki and O'Donnell, 1999a).

Figure 1.3 *F. graminearum* (8) and *F. pseudograminearum* (19) macroconidia. Triangles indicate widest position of each conidium. Scale bars = 20 µm. (Figures scanned with permission directly from (Aoki and O'Donnell, 1999a)).



Perithecia of *Fpg* were first described in detail by Aoki and O'Donnell (1999b). They are subglobose to ovoid, 120-370 µm in diameter, 140-400 µm high, produced solitarily or in groups. They are nonpapillate to slightly papillate, brownish-grey, greyish-brown to black in aerial view under low magnification. The wall of the perithecia is nearly smooth to slightly warted 25-87.5 µm thick. The asci are thin walled, unitunicate, clavate, 79.5-106.5 x 10.5-17.5 µm, containing 8 ascospores.

Ascospores are hyaline to pale 1-3 septate, becoming pale brown after discharge. A more complete description is provided by (Aoki and O'Donnell, 1999b).

1.2.4.2 The elusive sexual form of *F. pseudograminearum*

Prior to 1999 there was limited evidence for the production of fertile perithecia by *Fpg*. Purss (1969) reported perithecia in the field on wheat, *Agropyron scabrum*, canary grass and wild oats on the Darling Downs in 1964. He observed that amongst the fertile perithecia there was a great deal of rudimentary perithecia and that in some wheat specimens it was difficult to find any fertile perithecia. He also reported occasional perithecia on wheat approaching maturity after heavy rain in 1966. He examined the ability of cultures from various hosts to form perithecia in the glasshouse and found that maize isolates produced abundant perithecia, a few rudimentary perithecia were produced from one wheat culture and no perithecia were recorded from the grass hosts. Fertile perithecia from *Fpg* cultures were produced in two crosses by Francis and Burgess (1977). However, pairing of the same cultures six months later was unsuccessful. It was concluded, as reported by Butler (1961) that while *G. zeae* from *Fg* was considered to be homothallic, *Fpg* was considered to be heterothallic, poorly fertile or unfertile (Francis and Burgess, 1977). Aoki and O'Donnell (1999b) were the first to report consistent production of *Fpg* perithecia in culture where 153 possible pairings from 18 strains resulted in the heterothallic production of perithecia containing viable ascospores in 7 strain combinations (as described above in section 1.2.3). Subsequently Summerell et al (2001) collected, identified and compared perithecia naturally occurring on wheat plants in the Moree district of Australia with previously published reports. Since this time Bentley et al. (2005b) has reported genetic studies on both field collected and *in vitro G. coronicola* isolates in which 17 fertile laboratory crosses were made from 10 MAT1-1 (mating type identification) and 10 MAT1-2 isolates.

1.2.5 Fusaria associated with Crown Rot in Australia

Butler (1961) described several *Fusarium* species associated with a foot or root rot of wheat in Australia. Of particular pathogenic importance was *F. culmorum* and *F. graminearum*, whereas the others were dismissed as secondary pathogens. The first reports by McKnight and Hart (1966) and Purss (1966) referred to *F. graminearum* as the principal crown rot causing pathogen in Queensland whereas early surveys of Victoria had reported *F. culmorum* as the pre-dominate pathogen causing foot and root rot in wheat (Geach, 1932, cited in Chambers, 1972).

These early surveys in Victoria relied on macroscopic identification of species and Chambers (1972) conducted surveys of Victorian wheat crops in 1970 and 1971 to re-determine *Fusarium* species associated with these wheat crops. 13 different *Fusarium* species were recovered from wheat across Victoria. *F. culmorum* was prevalent only in the Southern areas of Victoria and *Fpg* was only occasionally isolated. The remaining Fusaria isolated were considered to be weakly or only moderately pathogenic. The most commonly isolated species were *F. avenaceum*, *F. equiseti* and *F. oxysporum*. The author concluded that *Fusarium* root diseases are of less importance in Victoria. However isolations in this study were only made from root tissue and it is likely that if samples had also been taken from crown tissue, *Fpg* would have been isolated more frequently.

Burgess et al. (1975) reported on surveys of Fusaria associated with crown rot of wheat across the eastern wheat belt of Australia (SE Qld, NSW and Victoria) in 1972, 1973 and 1974. Samples were collected from the basal sections of tillers affected by crown rot. *Fpg* was the predominant pathogen isolated. *F. culmorum* and *F. avenaceum* were infrequently found along with several other non-pathogenic Fusaria across the three sampling years. Wearing and Burgess (1977) also isolated *Fpg* from most areas of the wheat belt and failed to recover *F. culmorum* and *F. avenaceum* when soil samples were examined.

Hollaway et al. (1999) conducted surveys of western Victoria, breaking the study area up into three zones characterised on rainfall patterns. Results suggested that crown rot was a serious problem in Western Victoria and that overall *Fpg* was the predominant pathogen. However *F. culmorum* was found to be the predominant fungus isolated from crowns from crops in the high rainfall areas. It was not detected in the lower rainfall areas where previous surveys had been conducted.

Backhouse and Burgess (2002) analysed the distribution of *Fpg*, *Fg* and *F. culmorum* in relation to climate across the cereal growing regions of Australia. These analyses found that *Fpg* was predominant throughout the main cereal growing regions of Australia and that's it's occurrence was not limited by climate. *F. culmorum* was reported extensively in western Victoria and eastern South Australia. The distribution of *Fg* was linked to areas where maize is grown, i.e. the temperate to subtropical areas with moderate to high summer rainfall (Backhouse and Burgess, 2002).

In a more recent study on the distribution of *Fusarium* species associated with wheat in Qld and Northern NSW Akinsanmi et al. (2004) isolated 20 different *Fusarium* species from 650 samples collected from stubble, head, crown and flag leaf tissue. *Fpg* was the species most frequently isolated from the crowns of wheat in all regions examined except around Inverell, NSW. *Fg* was also frequently recovered, particularly in northern NSW and one site in Qld (Goondiwindi). Almost 70% of these isolates came from wheat heads showing symptoms of FHB. Of the remaining *Fusarium* species *F. crookwellense* constituted 8%, *F. avenaceum* 4 % while all others combined constituted ≤ 2% of isolates.

In further experiments in this study 76 isolates from 10 Fusarium species (including *Fg*) caused crown rot symptoms on the cultivar Kennedy. Symptoms ranged from very faint lesions on the outer leaf sheath to very severe lesioning of stem tissue with differences in aggressiveness being reported between and within Fusarium species for both crown rot and FHB (Akinsanmi et al., 2004).

The principal pathogen associated with crown rot of wheat and barley in Eastern Australia was extensively examined during the 1996 to 1999 seasons (Backhouse et al., 2004). *Fpg* was the most common Fusarium species detected in all areas except South East South Australia and the Victorian high rainfall region. In these areas *F.culmorum* was the dominant pathogen isolated. *Fg*, *F. crookwellense* and *F. avenaceum* were found to be insignificant causes of crown rot in Eastern Australia.

Fusarium pseudograminearum (*Fpg*) is the principal pathogen associated with crown rot in Australia and will be the focus of this thesis.

1.2.6 *Fpg* lifecycle and plant infection

Crown rot inoculum originates in stubble remaining on or in the soil, and contacts potential hosts around the roots and crown (Cook, 1981, cited in Miedaner, 1997). It is unknown how far the fungus can grow through the soil and it is presumed that direct contact between host and stubble fragments is required to initiate infection (Burgess et al., 2001, David Backhouse, 2006, 'pers comm'). Purss (1966) isolated the pathogen from plant tissue at intervals prior to maturity (38 – 163 days) and concluded that the subcrown tissues were important primary sites of infection, where the coleoptile, subcrown internode, and the remains of the scutellum are encountered first by the pathogen. However, the site of penetration depends on the distribution of inoculum in soil. In minimum tillage and no tillage systems (as is commonly practiced today) the inoculum is at or above the soil surface and penetration occurs at the crown and lower stem bases. When stubble is incorporated (as was common practice), penetration of the subcrown internode is more important (Summerell et al., 1990).

In seedlings, the soft tissue of the leaf bases become infected via the coleoptile, and invasion of the tillers or stems proceeds inwards from these tissues (Purss, 1966). While the roots of the plant may become infected, Purss (1966) concluded that these tissues do not play an important role as sites for primary infection. Balmas et al. (1995) isolated *F .graminearum* Schwabe Group 1 from 100% of stem bases, 99.4% of crowns, and only 41.7% of roots in 90-day-old infected wheat plants.

The infection process is progressive throughout the life of the plant and is not restricted to any particular stage of development (Purss, 1966). The fungus progresses up the plant from each infected stem base. Mycelium has been found in the internode below the head, however, the pathogen rarely colonised past the third internode above the crown (Purss, 1966). At 70 days Balmas et al. (1995) isolated the pathogen from 93.2% of sections taken from the stem 0cm above the crown, only 4.5% from sections 10cm higher, and no isolations were made from sections 20cms above the crown.

Spread of the disease through the tiller is associated with dense white mycelium in the lumen of the colonised region of the stem. This mycelium may develop extensively on the outside of the crown region of the plant, together with salmon pink spore masses, when moist conditions prevail. These conidial spore masses can also be found associated with the nodes of the stem (Burgess et al., 1981). However their role in the infection process has not been demonstrated.

Reproductive structures of *Fpg* have been found in the soil, but their role as overwintering structures appears to be limited. (See also section 1.2.4.1 above). Wearing and Burgess (1977) observed the presence of modified macroconidia in the soil, but the spores declined rapidly over time, particularly in warmer temperatures such as those that would occur over the summer months (Wearing, 1976, cited in Wearing and Burgess, 1977). Chlamydospores have been found in soil samples, but these spores also exhibit sensitivity to heat and rapid drying (Sitton and Cook, 1981, cited in Cook, 1981), and would be unlikely to survive for long periods of time.

Burgess (1978) reported that the pathogen does not grow in the soil, is rarely carried on seed and does not spread in the air from plant to plant. However in very moist conditions splash dispersal of conidia may occur (Burgess et al., 2001). *Fpg* survives and overwinters as hyphae in infected stubble residues. Depending on the degree to which stubble is broken down in the soil *Fpg* inoculum may persist for more than 2 years (Wallwork, 1996).

1.2.7 Host range

Crown rot is most economically important in the bread and durum wheats, barley and triticale. However the host range includes many temperate cereals and grasses (Burgess et al., 2001). It is therefore important to control grass weeds in rotations and fallows. There have been no reports of *Fpg* causing crown rot in dicotyledonous plants (Burgess et al., 2001).

Bentley et al. (2004) have demonstrated that Plains Grass (*Austrostipa aristiglumis*) is a host of many pathogenic and saprophytic *Fusarium* species. *Fpg* was isolated from symptomless plants at all sites sampled in the Liverpool Plains area of northwest NSW, where Plains Grass is the dominant species in native grasslands. The role of native and introduced grasses as intermediate hosts of *Fpg* in wheat cropping regions warrants further investigation. Recently, *Fpg* has also been isolated from finger millet in Kenya (Amata et al., 2004).

All small grain cereals can be infected with crown rot although levels of partial resistance (or tolerance) occur in bread wheats. Durum wheats are considered the most susceptible of the cereals.

Barley varieties also show levels of stem browning similar to the more susceptible wheat varieties. However, the impact on yield is generally less severe perhaps because barley matures early avoiding the late season moisture stress that contributes to severe whitehead formation (Backhouse et al., 1997). Denis and Wallwork, unpublished, cited in Wallwork et al. (2004) observed low yield losses in barley with severely lesioned crown tissues and suggested that this reaction indicates that barley is relatively tolerant to crown rot infection. Conversely a recent study in the USA by Smiley et al. (2005) recorded a 13% reduction in the yield of inoculated barley plots compared with uninoculated (natural infection) plots, with no significant increase in disease incidence or severity parameters. Oat varieties have been described as symptomless hosts (Nelson and Burgess, 1994) however limited results from my Honours work suggest that oats is much less susceptible to extensive infection by *Fpg* than wheat (Lusted, 1998).

1.3 Environmental and Field Conditions Affecting Crown Rot

Extensive research has been carried out since the discovery of crown rot on the role of environmental factors on the severity of disease symptom development in the field. This has included investigations into the effects of soil type, soil moisture, topography, farming practices and time of planting on the incidence and extent of *Fpg* infection in wheat and barley fields.

1.3.1 Time of planting

The incidence of disease is lower when plants are sown later in the growing season. Klein et al. (1989) examined the incidence of crown rot in bread wheat, durum wheat, triticale and barley when sown on two dates in fields with a history of high crown rot levels. Results suggested that incidence of infected plants and the number of plants with basal browning was less in plants sown in July than in plants sown in May. However, the mean loss in potential yield was not significantly different between the two sowing dates. Purss, (1971a) also examined the effect of time of planting on crown rot infection, sowing uninoculated seed in May, June, July and August, in fields where crown rot-infected wheat had been grown in the previous year. He too reported a higher incidence of disease in plants that were sown earlier, and found that the plants expressed more severe disease symptoms. The author noted that infections occurred throughout the life of the plant and seemed to be most severe between the rosette and late flowering stage. This stage is shortened in plants sown later in the season.

1.3.2 Soil type

Crown rot can occur on all soil types but is more prevalent on heavier soils. Damage is more severe in soils that are poorly drained (Wallwork, 1996). McKnight and Hart (1966) noted an absence of crown rot on the Wandoan soils in a 1959 survey of the western Darling Downs. These soils are lighter in texture compared to other soils of this region in which crown rot was recorded.

1.3.3 Field topography

In any single location where crown rot occurs, a higher incidence and severity is associated with higher levels of soil moisture in low-lying sections of planted fields. McKnight and Hart (1966) observed that all areas of high incidence of disease were associated with soil depressions. Burgess et al. (1975) and Klein et al. (1991) also reported that the incidence of crown rot was greater in low-lying areas of fields and plains compared to slopes. These authors concluded that these greater levels of disease incidence were due to the higher soil moisture in low-lying areas. While the high soil moisture favours plant growth and development, it also favours the growth and colonisation of the plant by the fungus. Plants that are grown at optimal soil moisture conditions may become infected by the pathogen without showing symptoms of disease. However, if these plants suffer water stress late in the growing season, when they are requiring large amounts of water to carry out grain fill, symptoms of disease may become more obvious, such as patches of whiteheads in the field.

1.3.4 Moisture

Crown rot is generally found in regions where wheat matures under hot dry conditions (Burgess et al., 2001). This was seen in the increased severity of crown rot damage in cereal crops, particularly durum wheat, in the 2002 drought conditions in South Australia (Dennis and Wallwork, 2003).

It has been well demonstrated that soil moisture is critical in the incidence and severity of crown rot infection in the field. McKnight and Hart (1966) observed several seasons that were characterised by below average rainfall and which resulted in a higher incidence of crown rot. During a survey from 1972 to 1974, 33% of crops sampled in north eastern NSW and south eastern Qld were affected by crown rot with many of these sites experiencing dry conditions late in the growing season. Crown rot was only detected in 4% of crops in south eastern NSW and northern Victoria, regions characterised by high soil moisture throughout the same season (Burgess et al., 1975).

Crown rot is particularly important in limiting yield in central and northern regions of the eastern Australian grain belt where wheat is commonly grown on stored subsoil moisture. The surface soil may remain air-dry for extended periods in these regions (Swan et al., 2000). Detailed laboratory and glasshouse experiments have demonstrated that moist surface soil is required for infection (eg. Liddell and Burgess, 1985, Liddell and Burgess, 1987, Liddell and Burgess, 1988). These authors determined the optimum water potential for infection of wheat seedlings in natural soils is between -0.3 MPa and -0.7 MPa, with negligible infection below -1.5 MPa.

Beddis and Burgess (1992) conducted seedling trials using wax partitioning of the soil profile to determine the effects of seedling water potential on incidence of *Fpg* infection. They reported that plant water stress corresponded with an increase in colonisation of wheat seedlings in glasshouse trials of both tolerant and non-tolerant wheat seedlings.

Field investigations have measured total available soil water in relation to crown rot incidence and severity. Wildermuth et al. 1997b) measured available soil moisture (depth 1.2m) at sowing and anthesis during field trials examining stubble treatments. These trials found the incidence of whiteheads was highest in treatments which had the lowest available soil water at anthesis and the incidence of whiteheads was lowest in treatments with the highest soil moisture at anthesis. Felton et al. (1998) found that the incidence of crown rot declined with increasing soil moisture, based on analysis of previously collected data sets.

Swan et al. (2000) verified the relationship between surface soil moisture and the incidence of infection of wheat through the growing season under field conditions. Data from this study suggest that in-crop rainfall is important for initiating infection throughout the growing season. However in determining incidence of infection they only measured presence or absence of *Fpg* in the sub crown internode and stem of the primary tiller. A true indication of incidence would require examination of outer leaf sheaths that would be exposed to potential inoculum. It is possible that under dry surface soil conditions the growth of the fungus through the leaf sheaths across to stem tissue may be slowed. Therefore detection of infection in the stem would be delayed. These trials also showed that incidence of crown rot infection increased following rainfall events in the field which raised soil moisture above -1.5Mpa water potential. They concluded that the relationship between soil moisture available to the plant and at the infection court, with incidence of infection and yield loss still needs further clarification.

A common trend has become apparent over the years in relation to rainfall and the progress of crown rot infection. While soil moisture is important for initiation of infection, if high moisture is retained throughout the growing season, particularly at anthesis, then symptoms of disease become less obvious. Water stress is required for whitehead production and several authors have noted an absence or decline of basal browning and dead head production under wet field conditions (eg Wildermuth et al., 1997b, Felton et al., 1998). Hence in wet years an estimation of disease severity may be a poor predictor of damage in a subsequent crop. Under these circumstances the incidence of infection would be a better estimator of inoculum carry-over. (Backhouse et al., 1997).

An interesting result regarding the effect of in crop precipitation on the severity of crown rot has emerged from field trials conducted in the Pacific Northwest of the USA (Smiley et al., 2005). While crown rot severity and associated yield reductions were highest in years of drought, two out of three years characterised by high rainfall had significant yield losses (up to 19%) associated with crown rot infections. Inoculation with *Fpg* reduced yield by up to 12% compared with native crown rot flora, with no apparent increase in whitehead formation in two years characterised by higher precipitation in these trials. The authors concluded that in higher precipitation zones, a low number of whiteheads in the field, is not an adequate indicator of yield loss severity.

1.3.5 Crop nutrition

The effect of the nutrients Nitrogen and Zinc on crown rot incidence and severity has been examined in wheat. The association of other nutrients on crown rot severity still needs to be explored.

Field experiments at Tamworth NSW were developed to examine the effects of varying nitrogen (N) concentrations and watering regimes on the incidence and severity of crown rot in wheat (Verrell et al., 2003). Differences in the recovery of *Fpg* from crowns at tillering were not seen between any of the treatments. At maturity incidence of crown rot increased in all treatments, but to a lesser extent in the high water treatment. A high correlation was established between incidence and severity of crown rot under low water, however under high water severity was substantially lower compared to incidence. This may be due to higher soil plant available water at flowering and grain fill. The results also indicated that water was more important than N in limiting the disease. High N treatments actually led to higher incidence and severity of crown rot (but not significantly) (Verrell et al., 2003).

Wildermuth et al. (1997a) found significant increases in crown rot severity with applied nitrogen fertilisers in the field. This trial was conducted with or without the application of basal nutrients (phosphorus, potassium, sulfur and zinc). Incidence of disease was similar in the presence or absence of the basal nutrients and increased significantly with all concentrations of nitrogen applied.

Cook (1973) indicated that plants with high nitrogen grow more luxuriantly early in the season consuming the limited water supply more rapidly. This leads to the development of a low leaf osmotic potential by the dough stage leading to severe development of disease in these plants. Therefore the nitrogen in the soil is not responsible for increased disease, but the plant response to high nitrogen leads to water stress in relation to soilborne diseases.

Crown rot is more severe in zinc deficient plants (Sparrow and Graham, 1988). The extent of crown rot infection in wheat plants differing in zinc- efficiency was compared (Grewal et al., 1996). Basal browning significantly decreased with increasing rates of zinc application. The zinc-efficient cultivar Excaliber showed lower levels of disease and produced more shoot and root dry matter than the less zinc-efficient cultivars. Where crown rot is a problem the authors recommend that zinc-efficient cultivars are grown along with zinc fertilisers to reduce the severity of disease.

1.4 Crown Rot Control

Current control of crown rot relies on cultural practices and sowing of partially resistant varieties. Burning of severely infested stubble has been recommended, but with soil erosion issues more emphasis has been placed on stubble retention and incorporation. In the last decade the importance of crop rotations in cropping systems has become apparent and extensive research into identifying non-hosts that can be used in a suitable rotation pattern with the susceptible wheat and barley cultivars has been conducted. Pulses, canola, sorghum and sunflowers are considered non hosts of crown rot and therefore suitable rotation crops (Wallwork, 1996).

1.4.1 Stubble management

Cropping practices have moved from stubble burning to stubble retention, along with reduced to no tillage to reduce soil erosion and aid in soil moisture retention during fallows (Wildermuth et al., 1997b). However *Fpg* survives as hyphae in stubble remains and these practices have led to an increase in the density of crown rot inoculum and a movement of inoculum up the soil profile. Summerell et al. (1990) reported that when stubble was incorporated or burnt and the remains incorporated infection by *Fpg* was initiated through the scutellum, sub-crown internode and lower crown regions. When stubble was retained on the surface penetration occurred mainly through the crown and lower stem regions with little infection of the sub-crown internode and scutellum. However they concluded that the site of penetration did not appear to be important in the degree of host colonisation as infection in each treatment was similar at maturity.

The incidence of plants infected with *Fpg* is significantly reduced when stubble is burnt after harvest (Dodman and Wildermuth, 1989, Wildermuth et al., 1997b, Klein et al., 1988, Summerell et al., 1989, Simpfendorfer et al., 2005b). However this does not eliminate the pathogen, which survives in stubble residues below the soil surface. A lower incidence of disease is also achieved when stubble is retained but incorporated into the soil which, leads to an increase in the rate of stubble breakdown (Dodman and Wildermuth, 1989, Summerell et al., 1989). Current research on this issue is focussed on developing stubble management practices which will both reduce inoculum at planting and maintain soil moisture and structure (Wildermuth et al., 1997b).

A range of fallow management strategies were considered for crown rot incidence in a wheat monoculture system (Simpfendorfer et al., 2003). Lowest levels of crown rot were recorded in an early burn - cultivated treatment and highest levels recorded under a zero-till treatment. Survival of the pathogen under zero till was significantly higher after a short fallow than after a long fallow prior to sowing in the following season.

In a trial investigating the effects of 3 different stubble management practices on the incidence of *Fpg* infection in wheat (Burgess et al., 1993), incidence was measured between late dough development and harvest, by isolation from the basal 2cm of the crown and sub crown-internode. In contrast to earlier reports (Dodman and Wildermuth, 1989, Summerell et al., 1989) no significant difference was found between stubble retained or stubble incorporation regimes suggesting that survival of *Fpg* in stubble is not reduced by incorporation. This may be because while stubble incorporation increases decomposition of the stubble it may also aid in dispersal of the infected residue. Hence contact between the host and pathogen may be increased (Backhouse et al., 1997).

A GRDC research program funded by three projects over a twelve year period (1991-2002) reported that as frequency of stubble burning increased, crown rot severity decreased to very low levels during a high intensity cereal cropping regime. It was however not eliminated after burning in 7 of 9 wheat crops (Verrell, 2003). Under these high burning regimes common root rot, (*Bipolaris sorokiniana*) was given a competitive advantage and rose to levels of 60% severity.

Recently the impact of inter-row sowing on crown rot severity has been investigated in winter cereals (Simpfendorfer et al., 2006, Simpfendorfer et al., 2005a, Verrell et al., 2006). In a no-till farming system planting between the rows limited the incidence and severity of crown rot and resulted in increasing yields even under high disease pressure. In 2005 trials 25 wheat, 14 barley and 5 durum wheat paddocks were evaluated. Inter-row sowing reduced incidence and severity by an average of 45% in barley and 55% in the bread and durum wheat paddocks (Simpfendorfer et al., 2006). Inter-row sowing is not considered a crown rot control method but rather may be used as part of an integrated control along with crop rotations and stubble management to assist in reducing levels of *Fpg* inoculum in the field.

1.4.2 Crop rotation

A long fallow (> 18 months) causes a substantial decline in the level of inoculum in the soil (Burgess, 1978). However fallows are not suitable in many situations as they result in a loss of potential income. Rotations allow continual cropping of land while reducing inoculum levels in the field by growing a non-host and allowing a prolonged period for natural microbial decomposition of infested stubble residues (Verrell, 2003). At least two years between susceptible varieties is required to substantially reduce crown rot inoculum (Dennis and Wallwork, 2003). Bhathal and Loughman (1999) examined wheat stubble retention in a rotation system with lupin while examining carry over of *Septoria nodorum* blotch and yellow spot. Six months after germination of the rotation crop 47-73% of stubble remained from the previous wheat crop. After establishment of the returning wheat crop (18 month old stubble) only 3-7% of stubble remained.

In crown rot studies sorghum has proved to be effective in maintaining low levels of inoculum through wheat-sorghum rotations, however it was unsuccessful in eliminating the pathogen even after 30 months between wheat crops (Burgess et al., 1996). Sorghum is resistant to crown rot infections however, as with all rotations, control of weeds is very important. For example Barnyard grass (*Echinocloa crus-galli*), a common weed in sorghum fallows, is very susceptible to *Fpg*. One result from a rotation trial at Goondiwindi saw crown rot levels rise from 8% to 32% in wheat following two years of sorghum. It was presumed that the survival and build up of *Fpg* on Barnyard grass was the cause (Burgess et al., 2005).

Reduced crown rot infection was also observed in wheat following Chickpea compared to wheat on wheat (Felton et al., 1998). Increased yields in the subsequent wheat crop have been observed in all of these rotational studies.

In field trials carried out in Victoria and northern NSW Kirkegaard et al. (2004) found a significant effect of previous crop on the incidence of crown rot infection in wheat. In examining rotational effects of Brassica, chickpea, wheat and barley crops on yield and crown rot incidence in the following season, they found that yield was highest after mustard, intermediate after canola and chickpea, and lowest after the cereals. In most cases these yield trends were shown to be associated to the level of crown rot infection at harvest in both susceptible Durum wheat (Yallaroi) and to a lesser extent in the partially resistant bread wheat (Sunco). It was suggested that the significant difference observed in the Brassica rotation over chickpea was related to an increased breakdown of stubble and hence reduced levels of crown rot inoculum under the denser Brassica canopy. *Fpg* severity may also have been enhanced after chickpea due to the effect of higher Nitrogen as described in section 1.3.5 above. Another plausible contributing factor may have been related to the soil microfauna, where *Trichoderma* spp. (see section 1.4.3 below) were isolated at much higher levels from wheat following a Brassica crop than from wheat following cereals or chickpea.

Moore et al. (2003) determined that canola, chickpea, faba bean and sorghum all proved effective as winter break crops encouraging breakdown of the previous crop residue. Following rotation with each alternative crop, remaining wheat residue (measured as stubble ground cover) was 15% (after sorghum), 28% (faba bean), 30% (canola) and 41% chickpea compared with 88% for continuous zero-till wheat. The recovery of *Fpg* from stubble following these crops was 10-15% compared to 49% for continuous zero till wheat.

1.4.3 Biocontrol

Biocontrol of *Fpg* by the bacterial species *Burkholderia cepacia* was investigated in laboratory, glasshouse and field trials (Huang and Wong, 1998). In the laboratory a pronounced inhibition zone was formed between *Fpg* and *B. cepacia*. Microscopic observation of the fungal hyphae closest to the bacteria revealed that cells were extensively lysed. It is believed that antibiotics produced by *B. cepacia* may be highly inhibitory to *Fpg*. *B. cepacia* proved to be effective at reducing crown rot in both field and glasshouse trials in three soil types. In the glasshouse while both treatments proved effective a soil drenching gave more significant reduction in disease severity then seed dressing (Huang and Wong, 1998). Wong et al. (1999) found that *Fpg* was completely eliminated from buried straws in the presence of *Trichoderma* spp. after 6 months in moist (-0.3Mpa) soil at 25^0C, compared to 40% of the stubble still infected in the absence of *Trichoderma*. No further studies on biocontrol have been found since these reports and the role of *Trichoderma* spp. as an effective control against crown rot warrants further investigation.

1.5 Resistance to Crown Rot

Research is being undertaken across Australia in search of suitable crown rot resistance in cereals. This research largely involves rating mature plants for levels of disease (degree of stem browning/number of whiteheads), which have been sown in crown rot infested soils (eg. Klein et al., 1989, Wildermuth and McNamara, 1994). In measuring resistance in the field the grain yield of susceptible wheat genotypes was closely related to the level of infection in the tillers ($r^2 = 0.6$) (Kirkegaard et al., 2004). However, this was not found in "tolerant" varieties. While field assessment is still the most effective screening tool, less resource-intensive seedling tests have also been developed. These tests enable the screening of numerous varieties of wheat and barley for resistance to crown rot prior to their examination in the field and have greatly enhanced the efficiency of screening programs.

1.5.1 Development of measures for crown rot infection

In researching crown rot an efficient method for assessing differences in susceptibility between genotypes is required. It is also important to have an indication of levels of crown rot inoculum in the field that may carry over to infect subsequent susceptible crops. For these reasons research has been devoted to measuring crown rot infection and standardising screening for resistance in wheat.

To examine large numbers of genotypes for crown rot resistance, methods of inducing crown rot infection have been assessed. Purss, (1966) used seed inoculations to examine crown rot characteristics in field and seedling trials. He also investigated a pot test with an inoculated cornmeal/sand medium. Seed inoculations with a spore suspension significantly increased expression of disease providing a satisfactory method for inducing crown rot infection in the field. The tolerance of the hexaploid variety Gala could be distinguished from other varieties by measuring total levels of disease and clear differences were seen between varieties in the production of whiteheads. However, high levels of variability within treatments for both measurements were recorded. In the seedling tests emergence, seedling blight, extent of root rot and a measure of the length of the longest leaf sheath showed no significant correlation to field reaction to crown rot.

Liddell et al. (1986) assessed methods by which plants could be grown in the glasshouse for disease assessment. They experimented with three quantities of inoculum and found that satisfactory levels of disease could be achieved with relatively small amounts of inoculum. Plants were harvested at 130 days and the authors concluded that symptoms of disease and yield losses were similar to those observed in plants grown in the field. A range of inoculation methods for measuring resistance to crown rot in wheat were examined in both glasshouse and field trials by (Dodman and Wildermuth, 1987). Resistance was most clearly demonstrated where inoculum was placed onto or into the soil rather than directly onto the plants.

These screening methods outlined above rely on growing plants through to an adult stage, which is time consuming and costly. A seedling trial which correlated disease development with field reaction to crown rot would greatly reduce the time and cost of screening genotypes for resistance.

Wildermuth and McNamara (1994) assessed methods by which seedlings could be rated for disease. They found that a rating predictive of field performance could be achieved in 21 day old seedlings infected by a band of inoculum chaff placed below the soil surface. A delayed watering reduces the risk of seedling blight. The first 3 leaf sheaths of each plant are rated on a scale of 0-4, where 0 = completely healthy and 4 = greater than 75% of the tissue is necrotic. The values for each leaf sheath are added together as a disease score. This method allows more efficient screening of cultivars for resistance to crown rot and is currently used to screen for new sources of resistance at the Leslie Research Centre, QDPI&F, Toowoomba, Qld.

Wallwork et al. (2004) have found that screening in the field in South Australia was relatively unreliable due to contamination with other pathogens, adverse weather conditions resulting in poor disease expression and an uneven distribution of natural inoculum. They set out to develop a large scale crown rot screening method which would enhance the identification of partial sources of resistance in adult plants. This method involves growing plants in open ended tubes containing potting mixture with inoculum chaff dispersed in the top layer of soil. These tubes were placed in crates and embedded into outdoor terraces of freshly cultivated sand so that roots may grow through. Terraces were watered daily from overhead irrigators. Plants were harvested at maturity and the 1st internode of the main stem was rated for lesion development using a scale from 0-5, where 0 = no stem browning and 5 = >75% of the stem lesioned. This system enables a large number of plants to be screened at a low cost and has reduced the reliability problems associated with screening for crown rot in the field in South Australia. Sources of resistance such as the genotypes 2-49 and Sunco are detected in these trials as are the susceptible check cultivars Puseas and Yallaroi (durum). However a high variability in overall cultivar reaction can be observed in successive years and the high susceptibility of durum wheats is not always detected.

A method of inoculating individual wheat seedlings has been reported by Akinsanmi et al. (2004) to examine differences in crown rot infection caused by a range of *Fusarium* isolates. Wheat seedlings were grown singly in autoclaved potting mixture in a controlled environment facility at the CSIRO Plant Industry Brisbane laboratories with 25/15°C day/night temperature, 65% relative humidity and 12 hr photoperiod. Plant stems were inoculated with a 700µL spore suspension poured onto absorbent cotton which was secured to tillers by a plastic sleeve placed 1cm above soil surface. 35 days after inoculation (dai) a crown rot severity index was calculated by multiplying the proportion of stem length discoloured with the number of leaf sheath layers discoloured. The experiment was standardised using a single wheat genotype (Kennedy).

This method appears to have been refined in a publication by Mitter et al. (2006a), where seedlings are grown under glasshouse conditions after stem inoculation with a spore suspension of a single isolate. 10 days after emergence seedling punnets are laid on their sides and a 10uL drop of a 10^6 macroconidia/mL^{-1} suspension is placed onto the stem 0.5cm away from the soil surface. Seedlings were incubated for 48hrs in the dark at near-saturated relative humidity and then placed upright on seedling trays until rated for disease 35 dai as described above.

1.5.1.1 Measuring end of season inoculum carry over

While the incidence of infection at the end of the season is the most useful indicator of levels of inoculum available to be carried over, Swan et al. (2000) showed that monitoring infection over the entire growing season gave a better indication of the amount of disease present and the potential losses that could be expected from the disease.

Backhouse (2006) explored the usefulness of a variety of environmental variables and disease parameters measured in two no till, stubble retained, continuous wheat, long term crown rot trials, to determine the risk of crown rot in successive wheat crops. He found that under these conditions the incidence of crown rot in the next season could be predicted and that crown rot risk could be placed into high, medium or low categories based on an index calculated from disease incidence and either in-crop rainfall or yield. While other factors measured (e.g. soil moisture at sowing and temperature) did little to improve the accuracy of predicting crown rot severity, a simple model using disease incidence and either in-crop rainfall or yield is recommended to calculate risk with modifications depending on these other factors if doubt still remains.

1.5.2 Screening for resistance

Differences in the susceptibility of wheat varieties to crown rot were observed soon after its discovery. The first report of resistance to crown rot was made by McKnight and Hart (1966) where Gala was described as consistently showing a lower incidence of dead heads than any other variety. Purss (1966) also reported levels of partial resistance in Gala and to a lesser extent in the cultivar Mengavi. He suggested that this resistance was related to the rate of development of disease.

Following these reports an intensive programme screening for crown rot resistance was established at the then Queensland Wheat Research Institute (QWRI) (now the Leslie Research Centre, QDPI&F) (Wildermuth and Purss, 1967) and is today still evaluating germplasm for resistance to crown rot. Early in this programme, considerable difficulties were encountered due to variations in cultivar reaction observed between seasons. After screening over 100 varieties in a single year no complete resistance was observed, although Gala was considered more resistant than any other cultivar (Wildermuth and Purss, 1967).

In subsequent screening trials of approximately 400 cultivars, several lines with partial resistance to crown rot were identified, including Gluyas Early and two overseas cultivars Reliance and Mexico 234 (Wildermuth and Purss, 1971). Gala was still considered the most consistently resistant and it was noticed that this resistance was greater than that observed in either of its parents (Gabo and Lawrence). Along with continued screening for crown rot resistance in bread wheat, selection of lines from other Triticum spp with varying levels of partial resistance to crown rot began, for inclusion in a hybridisation program aimed at increasing crown rot resistance in wheat. These screenings included lines of *Triticum aestivum*, *T. monococcum*, *T. durum* and *T. dicoccum*. Recommended for inclusion were some lines from the 1965 International Spring Wheat Rust Nursery IRN 497, IRN 527 & IRN 538 (Wildermuth and Purss, 1971). Other partially resistant lines were identified through University of Sydney trials which indicated that the varieties Timgalen, Gatcher, Shortim and Eagle were relatively tolerant under field conditions (Burgess, 1978).

During the late 1970's - early 1980's crown rot screening continued and the varieties identified by the QWRI as least susceptible to crown rot included Kite, Cook, Suneca, Bass, Timgalen, Shortim, QT2338-9 and Hibrid Titan as well as some lines with resistances similar to Gala, from a cross between Gala and Kite (Dodman et al., 1980, Dodman et al., 1982, Wildermuth and McNamara, 1986 - QWRI – biennial reports). Two lines from a cross between Gala and Gluyas Early were found to have levels of resistance higher than either parent, one of which was the line 2-49, and were recommended for inclusion in the resistance breeding programme (Dodman et al., 1980). Subsequently glasshouse screening trials suggested partial resistance to crown rot in Cook, Banks, Kite and SUN 69A (Klein et al., 1985). In contrast several reports have considered Banks to be highly susceptible to crown rot (e.g. Dodman and Wildermuth, 1987, Dodman et al., 1980, Wildermuth and McNamara, 1994).

Subsequent trials employing the new seedling based testing method (Wildermuth and McNamara, 1994) identified the line 2-49, progeny of a cross between Gala and Gluyas Early, as a superior source of resistance to crown rot. Since then it has been used as a partially resistant reference line in screening programmes across Australia.

Sources of resistance have also been identified in several synthetic hexaploid bread wheat lines, derived from crosses between *T. durum* and *Aegilops tauschii*. Further testing has demonstrated that the high level of resistance in these lines is derived from the *A. tauschii* parent of these crosses (Wildermuth et al., 2003).

Sunco has a relatively high level of partial field resistance to crown rot (Wildermuth and McNamara, 1994, Wildermuth et al., 2001). However it appears to be less resistant in seedling trials (as discussed below section 1.5.2.1). It is interesting to note that Sunco possesses a *T. timopheevii* introgression also found in several other partially resistant genotypes including Timgalen, Cook, Mengavi, Mendos and Lang. Research currently being conducted at USQ indicates that this introgression contributes to crown rot resistance in several of these genotypes (Bovill et al., 2006). In 1997 only 2 of 13 cultivars available for growing in Queensland were reported to have partial resistance to crown rot (Wildermuth et al., 1997b), and in years of high inoculum pressure yield losses still occur in these partially resistant varieties.

Of the 21 wheat varieties recommended for Queensland by the QDPI & F in 2006, two (Sunco and EGA Wylie) have crown rot resistance ratings of 6: indicating medium resistance with some yield loss in crown rot favourable conditions, two varieties (Lang and Baxter) have slightly lower resistance ratings of 5 with the remainder ranked at 4 or below using a scale of 1-9 (1 = highly susceptible, 9 = highly resistant.). All four durum wheats were ranked as 1 or 2. Of all the important diseases in Qld, crown rot is still the only one where breeding has not been able to produce a variety with a resistance rating of 7 or more (QDPI&F, 2006).

Mitter et al. (2006a) reported the screening of over 1400 wheat genotypes for crown rot resistance using the CR bioassay as described above (section 1.5.1). Putative crown rot resistance comparable to that of 2-49 has been identified in 14 genotypes and is currently being verified in field tests (Mitter et al., 2006a, Chakraborty et al., 2006, Liu et al., 2004).

Extensive screening (> 15 000 genotypes) of both spring and winter wheat cultivars and lines for root rots is also being carried out in field and laboratory disease nurseries by CIMMYT in collaboration with the Turkish Ministry of Agriculture and Rural Affairs. These screenings have identified a number of lines with crown rot resistances superior to that seen in 2-49 and Sunco. Some of the crosses carried out are providing material with not only high resistance but also improved yield up to 20 % higher than the parents (e. g. Sunco/ Pastor) ((Nicol et al., 2004; Nicol *et al*, 2007, cited in Chakraborty et al., 2006).

1.5.2.1 Different sources of resistance

Only partial resistance to crown rot has been identified and the mechanisms by which this resistance is expressed by the host are unknown. Dr Graham Wildermuth and his colleagues at the Leslie Research Centre (LRC) have proposed that there is possibly more than one type of partial resistance acting in current wheat cultivars/lines. One type of partial resistance, exhibited by some older varieties such as Gluyas-Early and Gala and the derived breeding line 2-49 is detectable in the field and in a seedling test. The other source of partial resistance, which is seen in the commercial wheat variety Sunco, is not detected in the seedling test but is exhibited as adult plant resistance in the field (Wildermuth et al., 1999b).

Wildermuth et al. (2001) examined whether partial resistance to crown rot is related to crown depth. Partial resistance was inversely related to crown depth in seedlings and mature plants. Genotypes with deeper crown formation were more susceptible to crown rot than those with shallow crowns with the exception of Sunco and Pelsart. A greater exposure of leaf sheath tissue results from crowns formed deeper in the soil, with the shallow crown formation of the more resistant lines such as 2-49 escaping more severe infection. The reactions of Sunco and Pelsart which form deeper crowns and are susceptible as seedlings while showing partial field resistance further support the suggestion that more than one type of partial resistance may exist.

1.5.3 Molecular markers in crown rot resistance screening

Phenotypic evaluation of crown rot resistance has relied on traditional breeding practices in the field and on seedling selection as described above (section 1.5.1 and 1.5.2). Molecular markers are regions of DNA that can be used to identify the presence or absence of particular genes that correspond to a trait of interest (Varshney et al., 2004). While selection of desirable traits may still take many cycles of traditional plant breeding, the use of molecular markers linked to genetic loci conferring crown rot resistance may greatly reduce the time and resources needed for selection of resistant genotypes.

Molecular marker research is being undertaken at the University of Southern Queensland in cooperation with the LRC, to identify molecular markers, in doubled haploid (DH) wheat and barley populations, which are linked to resistance against crown rot. A number of DH populations have been developed which segregate for crown rot resistance and these are currently being mapped to identify areas of chromosomes which contribute to crown rot resistance. A framework map consisting of 165 markers has been developed for the DH wheat population derived from 2-49 (partial resistance) x Janz (susceptible) (Collard et al., 2005). Simple and composite interval mapping identified six regions associated with crown rot resistance. A highly significant quantitative trait loci (QTL) was identified on 1D explaining 21% of the phenotypic variation. The combined effect of 5 QTL's explained 40.6% of the phenotypic variance (Collard et al., 2005). Confirmation and validation of these markers in different breeding lines was recently undertaken (Collard et al., 2006). The major QTL on 1DL (long arm of chromosome) and the minor QTL on 2BS (short arm of chromosome) was confirmed in the independent DH population Gluyas Early (parent of 2-49) x Janz. It was found that the 1D QTL is inherited from Gluyas Early and the 2B QTL inherited from Janz. The three other QTL’s identified in the initial study were inherited by 2-49 from its other parent Gala and therefore unable to be confirmed in this study (this work is currently in progress). While further confirmation is still being undertaken 2 markers linked to the 1D QTL have so far shown to be absent in other genetic material and therefore useful for marker assisted selection in 2-49 derived populations.

Important QTL's have also been identified in a second DH wheat population from a cross of W21MMT70 (partial seedling and field resistance) x Mendos (partial field resistance/seedling susceptible). Of the 8 QTL’s identified across the 3 seedling trials, 3 were consistently linked to crown rot resistance in all seedling trials. The QTL’s located on 5D and 2D were inherited from W21MMT70 while the other important QTL located on 5B was inherited from Mendos. DH lines which contained all 3 of these QTL’s had mean crown rot disease ratings 28.4% lower than the population mean (Bovill et al., 2006).

Phenotypic data from both the W21 x Mendos and 2-49 x Janz populations indicate that resistance is a quantitatively inherited trait (controlled by multiple genes), and as the location of high levels of resistance within a single cultivar is proving continually difficult, upon identification of resistance loci, gene pyramiding may be an option to provide more complete crown rot resistance (Collard et al., 2005); (Bovill et al., 2006).

1.6 Thesis Rationale

While we know that infection of the host occurs as early in the growth cycle as soon after germination in an emerging seedling, the spread of the pathogen within host tissues from this time until yield is compromised at host maturity is poorly understood. Previous work conducted in my Honours research has revealed that spread of the pathogen is slower in seedlings of partially resistant wheat compared to highly susceptible material. Furthermore, while coleoptile material of all genotypes tested was readily colonised, the rate and extent of infection of the leaf sheaths in seedlings varies with host genotypes (Lusted, 1998). These results were from a single trial and were therefore considered preliminary, warranting further investigation. Hence the first aim of this PhD study was to extend the initial observations of disease spread in seedling pot trials over a more extended period.

An examination of crown rot infection and disease development of 10 different wheat genotypes was conducted by (Purss, 1966). His examinations reported varietal differences expressed in both glasshouse and field trials. In Purss’s trials the majority of the field observations and measurements of individual genotypes were conducted between heading and maturity. He also reports on differences seen in the number of isolations from diseased tissues of either individual genotypes (ie plant parts combined) or individual plant parts (irrespective of genotype) at up to 5 sampling times (approximately monthly) throughout the season. (Purss, 1966) concluded that the rate of disease development was slowed in the more tolerant genotypes (such as Gala).

However a concise time course of fungal spread, which examines the differences seen between susceptible and partially resistant genotypes during the infection process had not been investigated. In the current project field trials were conducted to extend the findings of the seedling experiments and provide a more complete picture regarding the extent of infection and expression of disease symptoms throughout the growing season in both susceptible and partially resistant genotypes.

Only partial resistance to crown rot has been identified and the mechanisms by which this resistance is expressed by the host are unknown. From preliminary evidence, it appears that there may be at least two types of partial resistance. One type is detected in both seedling and field trials, as seen in the line 2-49, while a second type of partial resistance is observed in adult plants in the field, such as that observed in the variety Sunco (Wildermuth et al., 1999b). Partial resistance similar to levels seen in 2-49 has also been observed in synthetic hexaploid wheats and a few other bread wheat lines. Marker analysis of different resistance sources indicates the groups of QTL detected in 2-49, Sunco, W21MMT70 and IRN497 are different but overlapping (Collard et al., 2005, Collard et al., 2006, Bovill et al., 2006); Bovill *unpublished*, 2007), with some QTL being apparent in more than one of these sources.

In this study, the partial resistances of 2-49, Sunco and that seen in the synthetic hexaploid wheat CPI133814 were compared to determine whether these partial resistances act in the same fashion. The detailed time course of fungal spread and development of disease symptoms in field trials will enable the identification of when and in what tissues these differences in partial resistance are expressed.

To date no research has been published with regard to differences that may occur in the pathogenicity of *Fusarium pseudograminearum* isolates. To overcome any differences that may occur in aggressiveness of isolates several are combined in the production of inoculum (at LRC a mixture of three aggressive isolates is used.). This study has compared the aggressiveness of *Fpg* isolates collected from across Australia, against a range of wheat genotypes differing in susceptibility to crown rot to determine whether any pathogenic races occur within this pathogen population.

This study began with five main objectives, aimed at identifying critical differences in crown rot infection seen between susceptible and resistant cereal genotypes and between different types of resistance.

1. To compare disease symptoms between and within a range of genotypes differing in field and seedling reactions to the crown rot pathogen.
2. To study different sources of resistance to crown rot in seedling and field trials to determine whether they act in a similar fashion.
3. To compare the spread of the disease organism within the plant, under field conditions, at different stages of the growth cycle.
4. To determine whether differences occur in pathogenicity of *Fusarium pseudograminearum* isolates when inoculated onto a range of partially resistant host genotypes.
5. To conduct novel microscopic examinations in this host pathogen relationship.

Subsequently, the final aim was set aside, partly as a result of initial difficulties in initiating point inoculations in the laboratory, but several staining techniques were established. This work was then passed to another PhD student to pursue, due to the extent of data collection and analysis required by the other goals in the project. This issue will be touched on again in Chapter 5.

Chapter 2: Disease Development and Localisation of *Fusarium pseudograminearum* in Seedlings.

2.0 Introduction

Complete resistance to crown rot has not been observed in any wheat variety. Rather, differences in susceptibility to infection are seen between genotypes. These differences can be measured in the development of lesions on plant tissues in seedlings and/or mature plants (as described in section 1.5 Resistance to crown rot). A screening method developed at the LRC has clearly distinguished susceptibility to crown rot between wheat genotypes at 21 days after planting (Wildermuth and McNamara, 1994).

Experiments conducted during my Honours year examined initial lesion development in seedling plant parts at intervals up to 21 days. These results indicated that no significant differences were seen in the development of lesions on coleoptile tissue between susceptible and partially resistant wheat, barley and oat seedlings. Differences were seen in disease symptoms of the sub-crown internode. However these differences did not correspond to relative field susceptibility of the genotype (Lusted, 1998, Wildermuth and McNamara, 1994).

Significant differences corresponding to field susceptibility are seen between susceptible and partially resistant genotypes in the development of lesions on the first three leaf sheaths of seedlings up to 21 days after planting (Wildermuth and McNamara, 1994). These differences were most clearly seen early in the infection of each leaf sheath (e.g. 5 days after inoculation in the 1st leaf sheath). At later harvest times in these same tissues the differences in development of disease symptoms were not as clear, where disease scores of partially resistant tissue approached those recorded in susceptible tissues (Lusted, 1998).

By re-isolating the fungus from infected plant tissue, preliminary experiments (Lusted, 1998) measured the number of colonies of *F. pseudograminearum* (*Fpg*) isolated from plant tissues. After activation (watering) of inoculum at 7DAP, *Fpg* was reisolated from the 1st LS of susceptible genotypes sooner than from LS1 of partially resistant genotypes. These isolation experiments were further developed in the experiments of this chapter to follow the growth of the fungus through each tissue of the plant up to 42 DAP.

This chapter reports on the results of two inoculated seedling trials examining disease development and growth of *Fpg* through the leaf sheaths and internodes of three winter cereals (wheat, barley and oats) at intervals up to 42 DAP. The first experiment was conducted during my honours year in 1998 and preliminary results were presented unanalysed in that thesis. This experiment warranted repeating and this was completed in the first year of my PhD candidature. Results of both experiments were combined for statistical analysis and are presented together here.

These experiments were designed to examine the timing and extent of differences in crown rot symptoms between susceptible and partially resistant genotypes in developing tissues of older seedlings. These experiments also assess whether differences seen between cereal species and between wheat genotypes in disease symptom development are reflected in the extent of fungal colonisation at the seedling stage.

The Australian cultivar Puseas was identified as very susceptible to crown rot in early screening of varietal resistance (McKnight and Hart, 1966, Purss, 1966) and has since been commonly used as a susceptible standard in crown rot trials (eg Dodman and Wildermuth, 1987, Wildermuth and McNamara, 1994, Wildermuth et al., 2001, Wildermuth and Purss, 1971). The line 2-49 is one of the best sources of partial resistance identified in bread wheats and these two genotypes are commonly used as extreme standards in screening trials (e.g Wildermuth and McNamara, 1994, Wildermuth et al., 2001). Partial resistance has also been observed in synthetic hexaploid wheat. The line CPI 133814 is one that has exhibited partial resistance as good as 2-49 in both seedling and field trials (Wildermuth et al., 2003). Barley is usually considered susceptible to crown rot when rated for lesion development (Klein et al., 1989, Nelson and Burgess, 1994), however barley is also considered tolerant when yield loss is assessed (Denis and Wallwork, unpublished, cited in Wallwork et al., 2004, Backhouse et al., 1997, Hekimhan et al., 2004). Oat varieties show limited symptom development and have been described as partially resistant to resistant (Wildermuth and Purss, 1971, Nelson and Burgess, 1994) to crown rot infection.

2.1 Methods

Seedling trials were conducted using a layered pot design (Appendix 2A), adapted from that used for crown rot resistance screening at the Leslie Research Centre, DPI, Toowoomba, Qld (LRC) (Wildermuth and McNamara, 1994). The first experiment was conducted in 1998 at the LRC in a growth room (Experiment 2.1). The second experiment was conducted in 2000 at USQ in a controlled environment cabinet (Experiment 2.2).

The Soilborne Disease Section at LRC supplied inoculum and pasteurised soil used in the seedling trials. Inoculum production was carried out by me for the experiments in Chapter 4 using the same procedures, and details of these are outlined in the Chapter 4 methods. 3 aggressive *Fpg* isolates collected on the Darling Downs, Queensland were used to inoculate wheat/barley grain. Colonised grain was air dried and milled to pass through a 2mm sieve with the resulting inoculated chaff used in a layered pot design as outlined below.

2.1.1 Genotypes

The genotypes examined in these experiments were selected based on known susceptibilities to crown rot disease and included:

Puseas – bread wheat (susceptible)
2-49 – bread wheat (partially resistant)
CPI 133814 – synthetic hexaploid wheat (partially resistant)
Tallon – barley variety (susceptible/tolerant)
Cleanleaf – oat variety (partially resistant/resistant)

2.1.2 Pot design

Pots of each genotype were prepared following the methods of (Wildermuth and McNamara, 1994). 295g of dry coarse soil was weighed into each plastic pot (500 cm^3) and the surface levelled. 80mls of distilled H_2O was added and seeds were lightly pressed into the surface. Another 5mls of distilled H_2O was pippetted onto the seeds bringing the soil to field capacity. In Experiment 2.1, five or six seeds of each genotype were planted, while 13 seeds were planted per pot in Experiment 2.2. Seed was covered with 160g of fine (sieved through a 6.25mm screen) dry soil and the surface levelled. 0.45g of inoculum chaff was evenly sprinkled over the soil surface and another 40g of fine soil covered the inoculum layer. Two pots were set up for each genotype for each harvest time.

2.1.3 Growth conditions

Pots were placed randomly in a growth cabinet/room and after 7 days incubation watered daily to field capacity. Any late emerging plants were removed after the first watering. In both experiments plants were incubated at 25^0C with a 12 hour day/night cycle for 42 days. The growth room in Experiment 2.1 provided higher light intensity (459 umol s^{-1} m^{-2}) than the growth cabinet used in Experiment 2.2 (267 umol s^{-1} m^{-2}). By 28 days secondary tillers had begun to develop and some genotypes were pot-bound in Experiment 2.1. Remaining plants were re-potted in larger pots with 800g more soil.

In each experiment two pots of each genotype were harvested at 7 day intervals from 14 to 42 days after planting (DAP). Excess soil was washed from roots and the lower crown region. Plants were stored in their original pot with a small amount of water until rated for disease and plated on to media the same day.

2.1.4 Disease ratings

In experiment 2.1 up to 5 plants and in Experiment 2.2 up to 10 plants from each replicate were examined for lesion development at each harvest. The mean disease rating was calculated for each plant part. The leaf sheaths and internodes of primary and secondary tillers (Experiment 1) were rated for disease using the following scale (Figure 2.1).

0 = no lesions

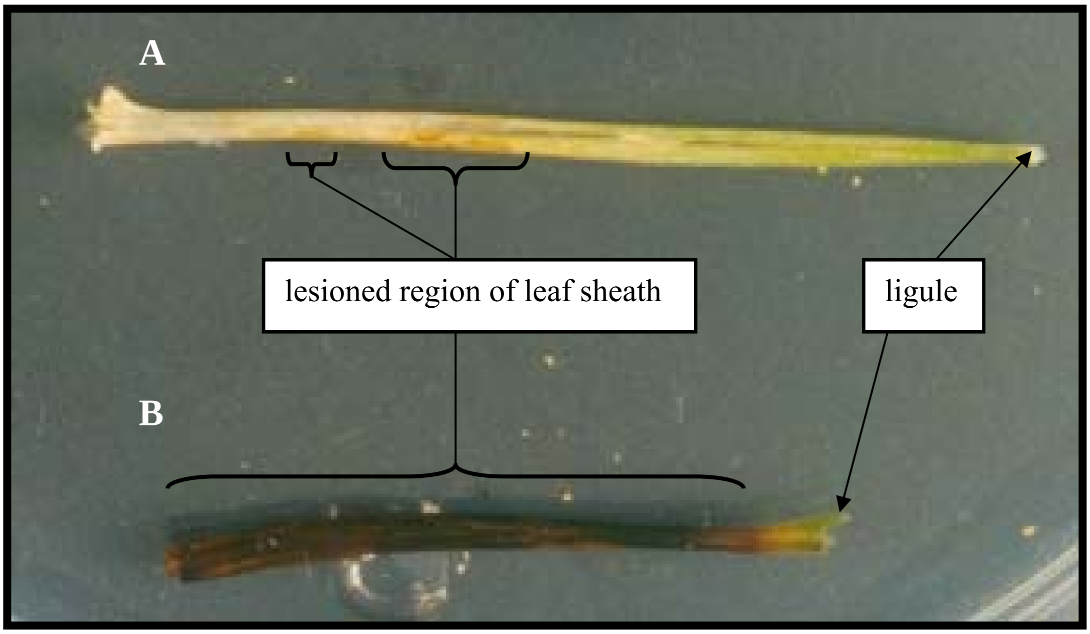
1 = 1-25% of tissue lesioned

2 = 26-50% of tissue lesioned

3 = 51-75% of tissue lesioned

4 = >76% of tissue lesioned.

Figure 2.1 Lesioned Puseas leaf sheath tissue. Disease rating of A) = 1, B) = 4.



2.1.5 Pathogen re-isolation

In experiment 2.1 the five plants from replicate one, and in experiment 2.2 the first five plants rated for disease from both replicates were examined for pathogen re-isolation. Once given a disease rating each plant part was surface sterilised in 2% sodium hypochlorite for one minute, rinsed twice in deionised water and air-dried on sterile blotting paper. Each plant part was plated onto Czapek Dox Agar (CZA_{10}^{++}) containing antibiotics and a fungicide (Appendix 2B). Plates were incubated at 25^0C in the dark and checked daily with the naked eye for three days. Each day sites of fungal colony emergence were marked with ink on the back of each plate. After one week of incubation colonies of *F. pseudograminearum* were identified from pink coloration of mycelium and the number of colonies per plant part counted. To examine the localisation of *Fpg* within each tissue each plant part was divided into quarters and the number of colonies per quarter was also recorded.

2.1.6 Data analysis

Treatments within the two experiments were arranged in a randomised block design. Data was analysed with the assistance of Kerry Bell (biometrician from the QDPI & F, Toowoomba), using the Genstat 6th Edition software package (Laws Agricultural Trust, Rothamsted Experimental Station, VSN International Ltd, UK). Disease rating data and square root transformed isolation counts were analysed using the Restricted Maximum Likelihood (REML) Variance Components Analysis, except for the isolation counts for leaf sheath 1 where the data would not converge and an ANOVA was used in this instance. REML was used to generate Chi- square probabilities to determine significance of the fixed factors experiment, harvest, genotype and the corresponding two and three way interactions. Standard error of difference (SED) values were multiplied by t and divided by the $\sqrt{2}$ to give a 95% confidence interval (CI) of error. This value was used to determine where individual means were significantly different.

A large volume of isolation data was generated by counting the number of colonies per quarter in each plant tissue and a suitable analysis procedure was not available to include these data sets. Therefore, only the total isolation scores from all four quarters for each plant tissue were included in the analysis.

95% confidence intervals for isolation counts

As the isolation data was square root transformed it was more difficult to obtain 95% CI of error. These values were calculated by adding/and subtracting the SED ($*t/\sqrt{2}$) for each plant part to each transformed mean to obtain a lower and upper limit. The three values (mean, upper limit, lower limit) were then squared to back transform. The differences between the mean and the upper and lower limits were then obtained and used as error bars for each mean.

2.1.6.1 Correlation of disease rating and isolation data

Raw disease rating scores and total isolation counts were correlated using SPSS 14.0 for Windows. Pearsons correlations coefficients were used to calculate the coefficient of determination (r^2) and correlation strength was estimated according to (Fowler et al., 1998) pg 132. As the disease rating data is a ranked score and the relationship between the variables is not always linear, the non parametric Spearman Rank Correlation Coefficient (r_S) was also determined. Correlations were performed on all data and according to experiment, genotype, plant part and harvest.

2.2 Results

Differences were seen in the growth patterns of seedlings between the two trials. In Experiment 2.1 (Exp 2.1) at 42 days after planting (DAP), seedlings had developed up to 8 leaf sheaths and two tillers had begun to expand. In experiment 2.2 (Exp 2.2) up to 7 leaf sheaths and 4 internodes had developed on the primary tiller at 42 DAP with minimal secondary tiller development. As the data for secondary tillers was quite limited and will be covered extensively in the following chapter on field trials, results have been presented here for leaf sheaths and internodes of the primary tiller only. All raw data is presented in Appendix 2C.

2.2.1 Data presentation

The nature of the data analysis procedures resulted in some data being excluded from the final analysis. The main reason for exclusion was limited variance, which resulted when the data contained too many values that were the same. This was particularly seen in uninfected tissue with many individual scores of 0 and in highly diseased tissues where scores were typically rated at the maximum of 4. Also as plants developed at different rates, particularly between genotypes, not all plants had the same number of plant parts at each harvest time or between harvests. Consequently data was also excluded, when insufficient numbers of seedlings had developed a particular plant part.

Infected tissues consistently scoring 0 across most or all replicates are important to this research because 0 indicated no lesions or no isolations of *Fpg*, and therefore resistance of particular tissues when compared to tissues with values >0. As much of this important data was excluded from the statistical analysis process, data has been presented here in charts including both analysed and non-analysed results.

Information regarding plant parts that had expanded at each harvest and which data points were included or excluded for the analysis is summarised in Table 2.1. Reasons for data exclusion are presented in the legend below the table.

The analysis output for both seedling trials is presented in Appendix 2D. The harvest/genotype/experiment interaction was highly significant ($P<0.01$) in the disease rating of LS's 1, 2 and 3, as was the experiment/genotype interaction in LS4 (Appendix 2D). Also only the isolation data for Exp 2.2 was included in the analysis. For these reasons the results for each experiment have been separated on each chart in this chapter. All data is presented in charts as means ± error for each harvest time. Where data has been included in the analysis the error bar represents the 95% CI of error for that plant part and is the same for that plant part across harvests (charts). Where data was not included in the analysis (shown on charts with a bold outline) bars are means ± standard error. Only data with 2 or more values for a particular reading is included in the presented results.

Presented with each chart is a table for that harvest recording the number of plants in which that plant part had expanded (bold). Below this value is the number of plants that gave a score >0 (incidence). These tables indicate whether the absence of a score for a particular plant part at each harvest is due to a score of 0 or whether the plant part was yet to expand in each genotype.

Table 2.1 Expanded plant parts included in the analysis of seedling experiments.

	Harvests (days after planting)				
Plant Part	**14**	**21**	**28**	**35**	**42**
leaf sheath 1	🟩□	🟩□	🟩□	🟩□	🟩□
leaf sheath 2	🟩□	🟩□	🟩□	🟩□	🟩□
leaf sheath 3	0's	🟩□	🟩□	🟩□	🟩□
leaf sheath 4	***	0's	🟩	🟩	🟩
leaf sheath 5	***	0's	?	?	?
leaf sheath 6	***	***	0's	0's	0's
leaf sheath 7	***	***	NE	NE	NE/0's
leaf sheath 8	***	***	***	***	NE
leaf sheath 9	***	***	***	***	NE
internode 1	Internodes not analysed				
internode 2	as too many zero's or data too sparse				
internode 3					
internode 4					
internode 5					

	Table Legend
🟩 Disease rating	Analysed (Exp 1&2)
□ Isolation counts	Analysed (Exp 2)
***	tissue not developed or not collected
0's	data contains too many zero's
NE	data for that tissue too sparse
?	Many O's- but Tallon and Puseas diseased

2.2.2 Disease ratings

Figures and Tables displaying results at 14, 21, 28, 35, and 42 DAP are presented sequentially at the end of each subsection. At 14 DAP 3 leaf sheaths (LSs) had expanded in Exp 2.1 and 2 LSs in Exp 2.2. All plants had lesions on leaf sheath 1 (LS1) in Puseas, Tallon and 2-49. Lesions were recorded on 22 out of 28 CPI 133814, and only 6 out of 30 Cleanleaf LS1's at 14 DAP (Table 2.2). The mean disease ratings of 2-49, CPI 133814 and Cleanleaf LS1's were significantly lower than Puseas and Vasco in Exp 2.1 with the 2-49 error bars only just overlapping Puseas and Tallon in Exp 2.2 (Figure 2.2). Cleanleaf had a mean rating of below 0.5 and was also significantly lower than 2-49. Almost all Puseas and Tallon LS2's had lesions. While only 8 plants in 2-49 and 3 in CPI 133814 recorded lesions on LS2 in

Exp 2.2. No lesions were seen on LS2 in Cleanleaf. Lesions were not observed on LS3 in any genotype at 14 WAP (Figure 2.2, Table 2.2).

At 21 DAP CPI 133814 and Cleanleaf in Exp 2.1 and only Cleanleaf in Exp 2.2 had mean disease ratings for LS1 significantly lower than the other genotypes (Figure 2.3). Less than half of Cleanleaf LS2's displayed lesions and the mean disease rating of 2-49, CPI 133814 and Cleanleaf was significantly lower than Puseas and Tallon in this tisssue. Lesions were also recorded on several Puseas and Tallon LS's 4 and 5. (Figure 2.3, Table 2.3).

At 28 days all disease ratings in Cleanleaf LS's were significantly lower than the other genotypes. No significant differences were seen between Puseas, Tallon, CPI133814 and 2-49 in the mean disease rating of LS1. CPI133814 had disease ratings of the 2nd LS significantly lower than the susceptible Puseas and Tallon in both experiments and also lower than 2-49 in Exp 2.1. In Exp 2.1 Puseas and Tallon had mean disease ratings for LS4 greater then 2 (Figure 2.4) and only a few 2-49 and CPI 133814 plants had small lesions on LS4 at 28 days. Puseas also had lesions on LS's 5 and 6, with symptoms of disease recorded on 5 out of the 7 Tallon LS5's.

In Exp 2.2 the mean disease rating of LS3 was significantly lower in CPI 133814 and 2-49 than in Puseas and Tallon. Only one out of the 30 Cleanleaf 3rd LS's examined had a small lesion at 28 DAP (Table 2.4). In Exp 2.2 all LS 3's were highly diseased at 28 days in Puseas and Tallon, and the majority of these plants had stopped growing. The internodes (I) of the remaining plants had begun to expand and while only 1 out of 5 Puseas LS4's were diseased, the internodes below this leaf sheath were highly diseased (Figure 2.4). 4 out of the 5 Tallon LS4's were diseased and only 1 LS5 had expanded. The internodes below these leaf sheaths had also developed lesions. In 2-49 the internodes had not begun to expand and small lesions were seen in only 2 LS 4's and on 1 LS 5. No lesions were recorded on the 4th and 5th LS's of CPI 133814 and Cleanleaf but small lesions had begun to develop on the lower internodes of these plants (Figure 2.4).

The results of the first 4 leaf sheaths at 35 DAP was similar in all genotypes to that seen at the previous harvest. However, the difference between the mean disease ratings of LS3 and LS4 between the partially resistant lines 2-49 and CPI 133814 and the susceptible Tallon and Puseas had reduced in Exp 2.2 (Figure 2.5). From 28 expanded plant parts across both experiments only 9 LS 2's and 1 LS 3 had symptoms of disease in Cleanleaf.

In Exp 2.1 high disease ratings were seen in LS's 5, 6 and 7 in Tallon at 35 days. Puseas also had high disease ratings up to LS 5 and no symptoms were seen on these inner leaf sheaths of the partially resistant genotypes (Figure 2.5).

In Exp 2.2 no disease rating is recorded for Tallon on LS 5 at 35 DAP however only 1 had expanded in the plants harvested at this time. One Puseas, three 2-49 and no CPI 133814 or Cleanleaf LS 5's had disease ratings. All genotypes recorded mean disease ratings of the 1st internode at 35 days. However, Cleanleaf was significantly lower than the other genotypes. Internode 2 had disease symptoms in Tallon, Puseas and 1 CPI 133814 plant. High standard errors are seen on the Tallon internodes, as only 2 plants had internodes expanded and one of these was diseased while the other was not (Figure 2.5, Table 2.5).

In both experiments differences between the susceptible and partially resistant genotypes in LS 3 and LS 4 were mostly still significant at 42 DAP. In Exp 2.1 large lesions continued to develop on the inner leaf sheaths of Puseas and Tallon (Figure 2.6). In Exp 2.2 LS’s 5, 6 and 7 had not developed in Tallon and only 1 Puseas LS 5 had expanded at 42 DAP (Table 2.6). Limited disease symptoms were seen on the inner leaf sheaths of a few plants in the partially resistant genotypes (Figure 2.6). At the 42 DAP harvest only 1 Puseas and no 2-49 plants had developed internodes. Tallon had 4 plants that had developed internodes and the disease rating of these plant parts was high. There was limited lesion development on the CPI 133814 and Cleanleaf internodes.

2.2.3 Pathogen re-isolation

At 14 DAP *Fpg* was re-isolated from the 1st LS of all genotypes in both experiments. In Exp 2.1 isolations from this LS were significantly higher in Puseas. In Exp 2.2 almost twice as many isolations were recorded in Puseas and Tallon than in 2-49,

Figure 2.2 Mean disease rating of primary tiller leaf sheaths (LS) 14 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE

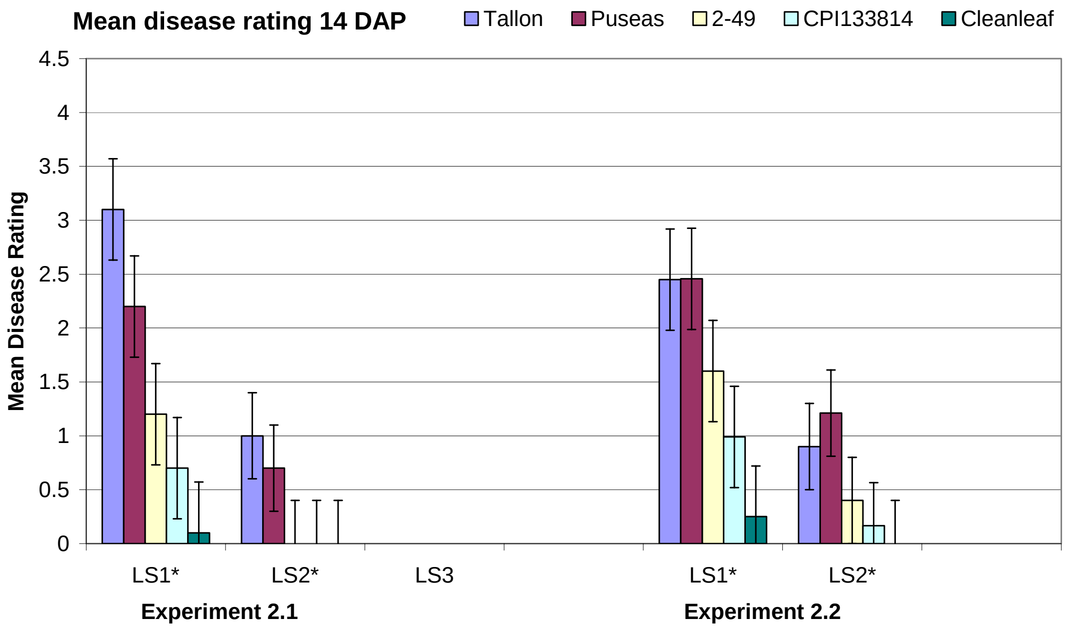


Table 2.2 Number of plants rated for each plant part (bolded) and the total number of those plants diseased (ie disease rating > 0) at 14 days after planting.

14 DAP	**Experiment 2.1 (max 10)**			**Experiment 2.2 (max 20)**	
	LS1	LS2	LS3	LS1	LS2
Tallon	**10**	**10**	**10**	**20**	**20**
	10	10	0	20	16
Puseas	**10**	**10**	**10**	**19**	**19**
	10	7	0	19	18
2-49	**10**	**10**	**10**	**20**	**20**
	10	0	0	20	8
CPI133814	**10**	**10**	**10**	**18**	**18**
	7	0	0	15	3
Cleanleaf	**10**	**10**	**10**	**20**	**20**
	1	0	0	5	0

Figure 2.3 Mean disease rating of primary tiller leaf sheaths (LS) 21 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE

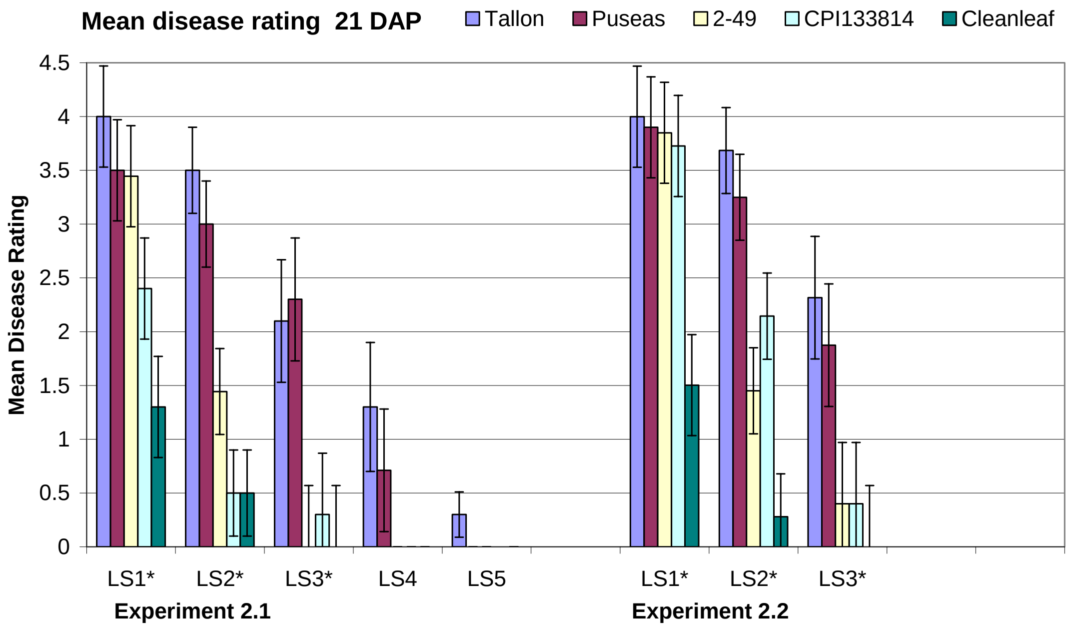


Table 2.3 Number of plants rated for each plant part (bolded) and the total number of those plants diseased (ie disease rating > 0) at 21 days after planting.

21 DAP	**Experiment 2.1 (max 10)**					**Experiment 2.2 (max 20)**		
	LS1	LS2	LS3	LS4	LS5	LS1	LS2	LS3
Tallon	**10**	**10**	**10**	**10**	**10**	**20**	**20**	**20**
	10	10	8	4	2	20	20	20
Puseas	**10**	**10**	**10**	**7**	**5**	**20**	**20**	**16**
	10	10	8	2	0	20	20	12
2-49	**9**	**9**	**9**	**9**	**8**	**20**	**20**	**20**
	9	9	0	0	0	20	19	8
CPI133814	**10**	**10**	**10**	**10**	**---**	**14**	**14**	**10**
	10	4	1	0		14	11	3
Cleanleaf	**10**	**10**	**10**	**10**	**8**	**18**	**18**	**17**
	8	5	0	0	0	16	5	0

Figure 2.4 Mean disease rating of primary tiller leaf sheaths (LS) and internodes (I) 28 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.

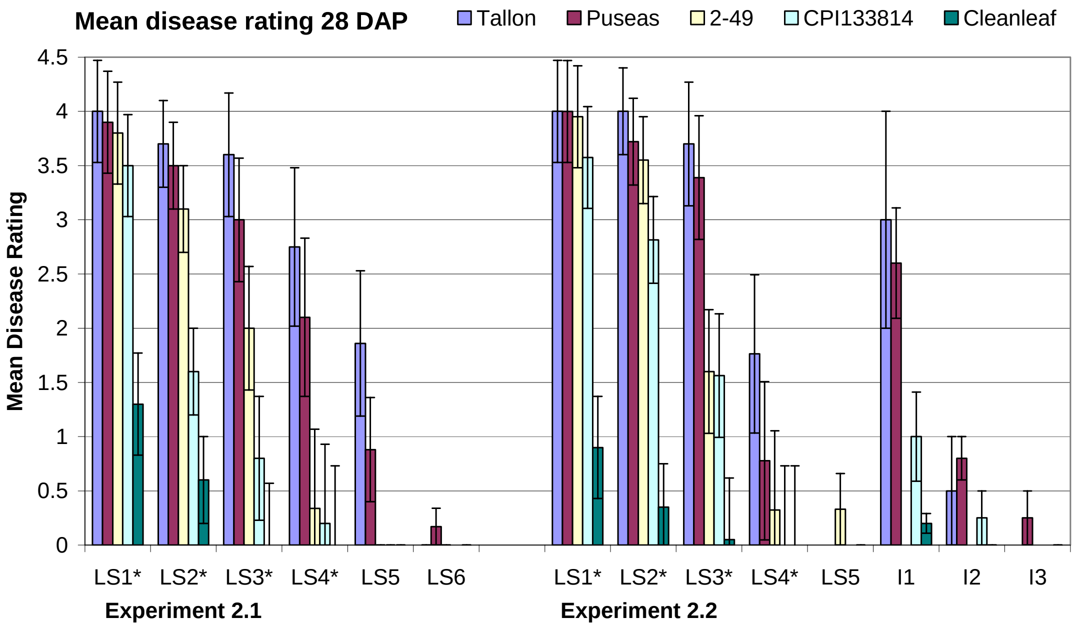


Table 2.4 Number of plants rated for each plant part (bolded) and the total number of those plants diseased (ie disease rating > 0) at 28 days after planting.

28 DAP	**Experiment 2.1 (max 10)**						**Experiment 2.2 (max 20)**								
	LS1	LS2	LS3	LS4	LS5	LS6	LS1	LS2	LS3	LS4	LS5	I1	I2	I3	I4
Tallon	**10**	**10**	**10**	**8**	**7**	**3**	**20**	**20**	**20**	**5**	**1**	**2**	**2**	**1**	**1**
	10	10	9	7	5	0	20	20	20	4	0	2	1	0	0
Puseas	**10**	**10**	**10**	**10**	**8**	**6**	**18**	**18**	**18**	**5**	**2**	**5**	**5**	**4**	**2**
	10	10	10	9	4	1	18	18	18	1	0	5	4	1	0
2-49	**10**	**10**	**10**	**9**	**9**	**8**	**20**	**20**	**20**	**9**	**3**	**---**	**---**	**---**	**---**
	10	10	10	3	0	0	20	20	20	2	1				
CPI133814	**10**	**10**	**10**	**10**	**9**	**---**	**16**	**16**	**16**	**7**	**1**	**4**	**4**	**1**	**---**
	10	10	7	2	0		16	16	15	0	0	3	1	0	
Cleanleaf	**10**	**10**	**10**	**10**	**8**	**5**	**20**	**20**	**20**	**13**	**5**	**20**	**20**	**17**	**9**
	9	6	0	0	0	0	15	7	1	0	0	4	0	0	0

Figure 2.5 Mean disease rating of primary tiller leaf sheaths (LS) and internodes (I) 35 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE

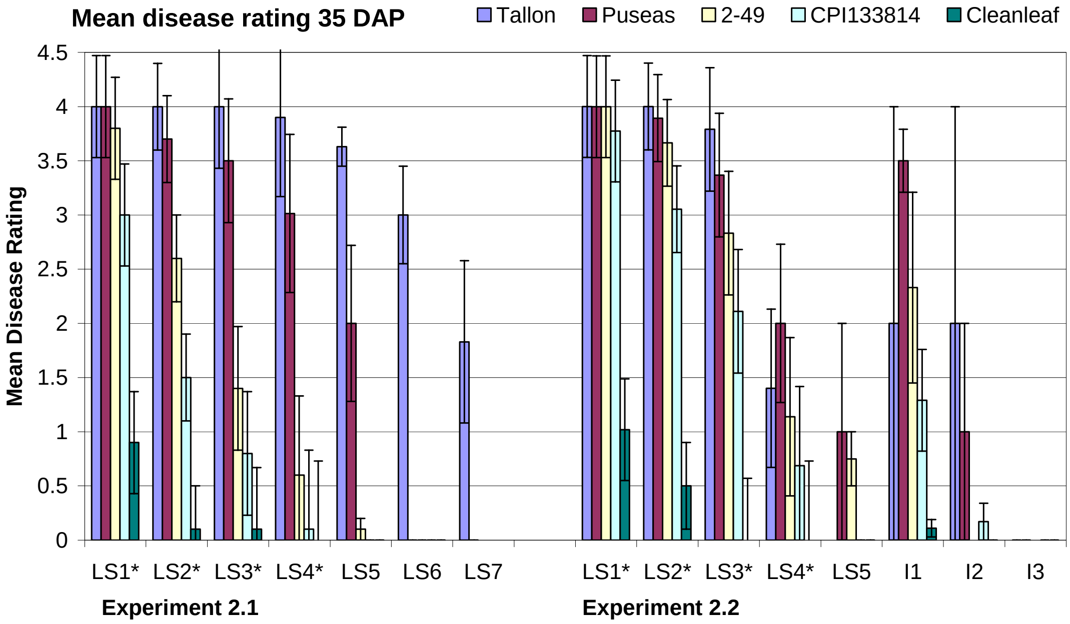
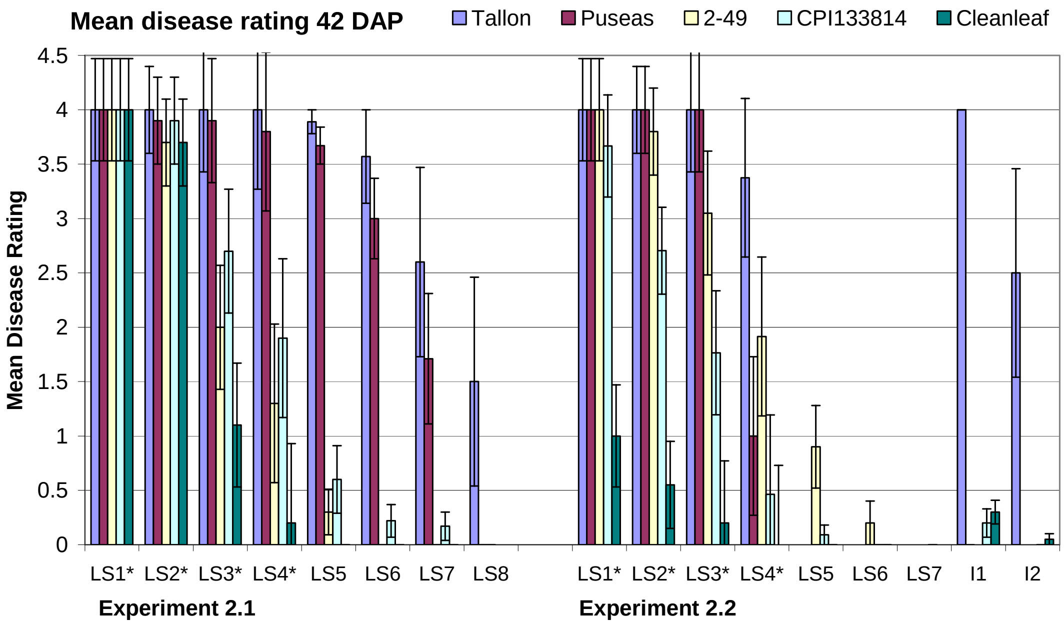


Table 2.5 Number of plants rated for each plant part (bolded) and the total number of those plants diseased (ie disease rating > 0) at 35 days after planting.

35 DAP	**Experiment 2.1 (max 10)**							**Experiment 2.2 (max 20)**								
	LS1	LS2	LS3	LS4	LS5	LS6	LS7	LS1	LS2	LS3	LS4	LS5	I1	I2	I3	I4
Tallon	**10**	**10**	**10**	**10**	**8**	**7**	**6**	**19**	**19**	**19**	**3**	**1**	**2**	**2**	**2**	**---**
	10	10	10	10	8	7	4	19	19	19	1	0	1	1	0	
Puseas	**10**	**10**	**10**	**9**	**7**	**4**	**4**	**19**	**19**	**19**	**6**	**4**	**4**	**4**	**3**	**3**
	10	10	10	9	5	0	0	19	19	16	3	1	4	1	0	0
2-49	**10**	**10**	**10**	**10**	**10**	**10**	**---**	**18**	**18**	**18**	**6**	**4**	**3**	**1**	**---**	**---**
	10	10	10	4	1	0		18	18	18	6	3	3	1		
CPI133814	**10**	**10**	**10**	**10**	**10**	**2**	**---**	**18**	**18**	**18**	**13**	**5**	**7**	**6**	**3**	**---**
	10	7	5	1	0	0		18	18	15	7	0	6	1	0	
Cleanleaf	**10**	**10**	**10**	**10**	**10**	**7**	**---**	**18**	**18**	**18**	**18**	**6**	**18**	**18**	**18**	**6**
	7	1	1	0	0	0		16	8	0	0	0	2	0	0	0

Figure 2.6 Mean disease rating of primary tiller leaf sheaths (LS) and internodes (I) 42 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.



Tables 2.6 Number of plants rated for each plant part (bolded) and the total number of those plants diseased (ie disease rating > 0) at 42 days after planting (DAP).

42 DAP	**Experiment 2.1 (max 10)**								**Experiment 2.2 (max 20)**										
	LS1	LS2	LS3	LS4	LS5	LS6	LS7	LS8	LS1	LS2	LS3	LS4	LS5	LS6	LS7	I1	I2	I3	I4
Tallon	**10**	**10**	**10**	**10**	**9**	**7**	**5**	**4**	**20**	**20**	**20**	**8**	**---**	**---**	**---**	**4**	**4**	**1**	**---**
	10	10	10	10	9	7	4	2	20	20	20	8				4	3	1	
Puseas	**10**	**10**	**10**	**10**	**9**	**7**	**7**	**5**	**20**	**20**	**20**	**1**	**1**	**---**	**---**	**1**	**1**	**1**	**---**
	10	10	10	10	9	7	4	0	20	20	20	1	0			1	0	0	
2-49	**10**	**10**	**10**	**10**	**10**	**10**	**10**	**7**	**20**	**20**	**20**	**13**	**10**	**5**	**1**	**---**	**---**	**---**	**---**
	10	10	10	8	2	0	0	0	20	20	20	13	6	2	0				
CPI133814	**10**	**10**	**10**	**10**	**10**	**8**	**6**	**---**	**17**	**17**	**17**	**13**	**11**	**5**	**2**	**10**	**9**	**3**	**1**
	10	10	10	9	4	2	1		17	16	13	4	1	0	0	2	0	0	0
Cleanleaf	**10**	**10**	**10**	**10**	**10**	**10**	**4**	**---**	**20**	**20**	**20**	**18**	**11**	**2**	**---**	**20**	**20**	**19**	**12**
	10	10	7	2	0	0	0		14	10	3	0	0	0		6	1	0	0

CPI133814 and Cleanleaf, however differences were not statistically significant (Figure 2.7). In Exp 2.1 isolations were made from all 5 Puseas, 4 Tallon and 3 2-49 2nd LS's with 1 Tallon 3rd LS infected at 14 DAP (Table 2.7). In Exp 2.2 a small number of isolations were made from 9 Tallon, 6 Puseas, 5 2-49 and 3 CPI133814 2nd LS's.

At 21 DAP only Cleanleaf had isolations significantly lower than the susceptible genotypes in LS 1. Isolations from LS 2 and LS 3 were significantly lower in the partially resistant genotypes in both experiments (Figure 2.8). In Exp 2.1 isolations were made from both Tallon and Puseas LS 4's and 2 of 5 Tallon LS 5's recorded isolations. LS's 4 and 5 were yet to expand in Exp 2.2 (Table 2.8).

In LS 1 the differences seen between genotypes were less distinct at 28 DAP except in Cleanleaf where a small number of isolations were still confined to the 1st two LS's in both experiments. Cleanleaf isolations were significantly lower than all other genotypes. Tallon consistently had the largest number of isolations from all other expanded LS's and along with Puseas these were significantly higher than isolations made from 2-49 and CPI133814 at 28 DAP in both Exp 2.1 and Exp 2.2 (Figure 2.9). As noted above (Section 2.2.2) at 28 DAP, the majority of Puseas and Tallon plants had stopped expanding and most plants in each pot showed severe necrosis in Exp 2.2. Only 2 Tallon and 1 Puseas plant had developed a 4th LS at this time (Table 2.9). In Exp 2.2 internodes had begun to expand in all genotypes except 2-49 at 28 DAP (Table 2.9).

A similar result was observed at 35 DAP where Puseas and Tallon had a higher number of isolations than the partially resistant genotypes in all expanded LS's (Figure 2.10). In Exp 2.1 the differences between these genotypes were highly significant; however, in Exp 2.2 differences particularly between 2-49 and Puseas were not significant. Cleanleaf only had isolations from the 1st LS in Exp 2.1 and small isolations from the 1st three LS's in Exp 2.2 (Figure 2.10). In Exp 2.2 only one Puseas and one Tallon plant had internodes expanded and these were infected (Table 2.10). Isolations were not recorded from CPI133814 internodes and while 2-49 only had two 1st internodes expanded one was infected and the other was not. Isolations were also recorded on 3 out of 10 Cleanleaf 1st internodes (Figure 2.10, Table 2.10).

Figure 2.7 Mean number of isolations from primary tiller leaf sheaths (LS) 14 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.

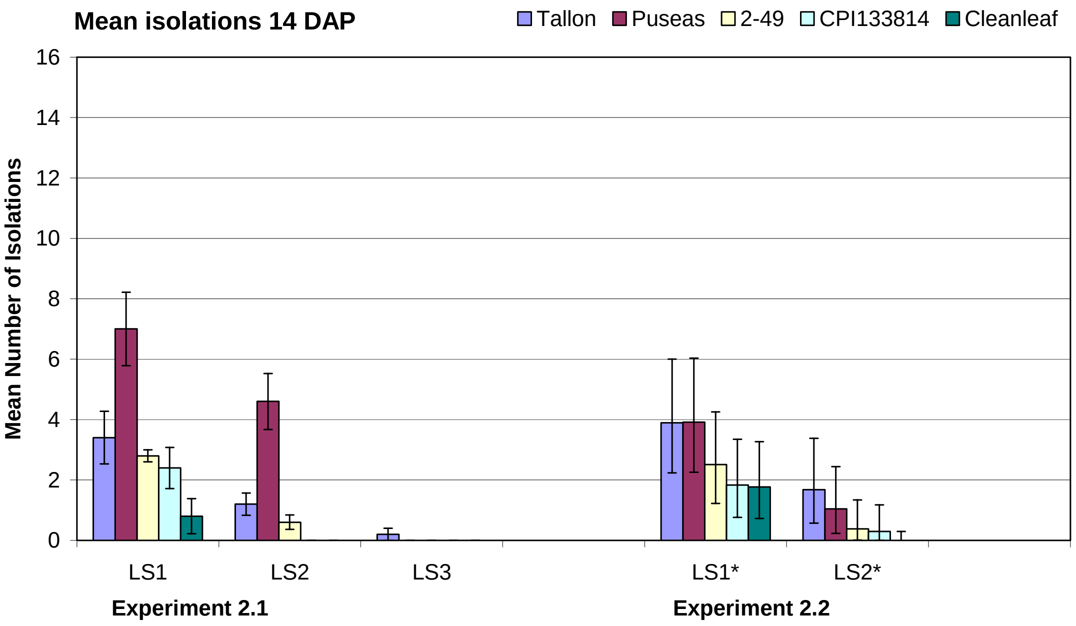


Table 2.7 Number of plants isolated from for each plant part (bolded) and the total number of those plants infected (ie isolations > 0) at 14 days after planting.

14 DAP	Experiment 2.1 (max 5)			Experiment 2.2 (max 10)	
	LS1	LS2	LS3	LS1	LS2
Tallon	**5**	**5**	**5**	**10**	**10**
	5	4	1	10	9
Puseas	**5**	**5**	**5**	**10**	**10**
	5	5	0	10	6
2-49	**5**	**5**	**5**	**10**	**10**
	5	3	0	10	5
CPI133814	**5**	**5**	**5**	**10**	**10**
	4	0	0	9	3
Cleanleaf	**5**	**5**	**5**	**10**	**10**
	2	0	0	9	0

Figure 2.8 Mean number of isolations from primary tiller leaf sheaths (LS) 21 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.

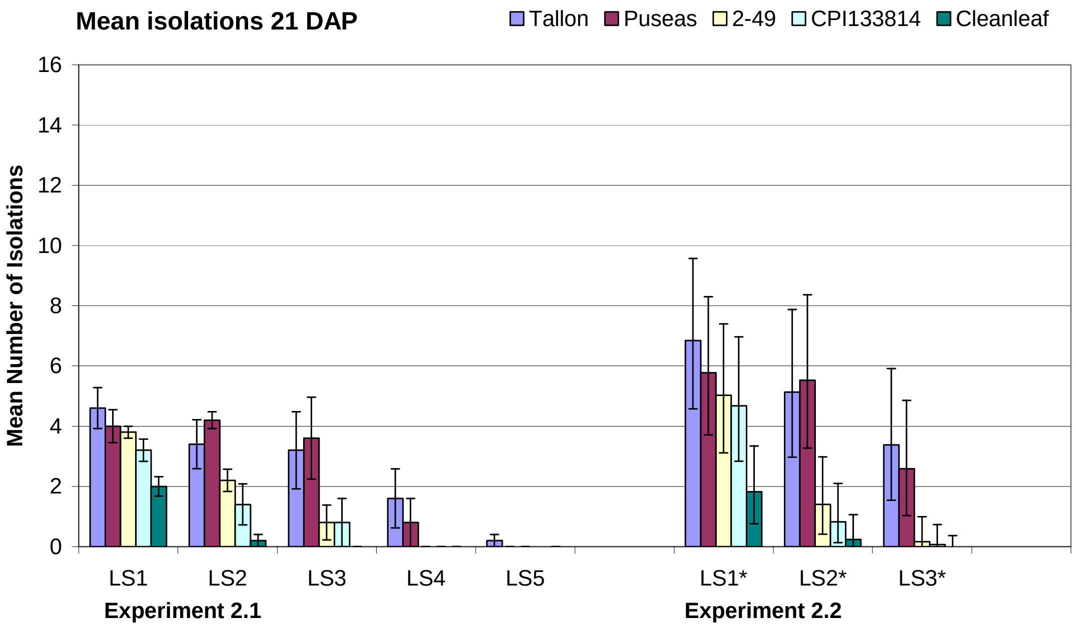


Table 2.8 Number of plants isolated from for each plant part (bolded) and the total number of those plants infected (ie isolations > 0) at 21 days after planting.

21 DAP	**Experiment 2.1 (max 5)**					**Experiment 2.2 (max 10)**		
	LS1	LS2	LS3	LS4	LS5	LS1	LS2	LS3
Tallon	**5**	**5**	**5**	**5**	**5**	**10**	**10**	**10**
	5	5	4	2	0	10	10	9
Puseas	**5**	**5**	**5**	**5**	**3**	**10**	**10**	**9**
	5	5	4	1	0	10	10	6
2-49	**5**	**5**	**5**	**5**	**5**	**10**	**10**	**10**
	5	5	2	0	0	10	7	3
CPI133814	**5**	**5**	**5**	**5**	**---**	**10**	**10**	**8**
	5	4	1	0		10	5	1
Cleanleaf	**5**	**5**	**5**	**5**	**4**	**9**	**10**	**9**
	5	1	0	0	0	7	3	0

Figure 2.9 Mean number of isolations from primary tiller leaf sheaths (LS) and internodes (I) 28 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.

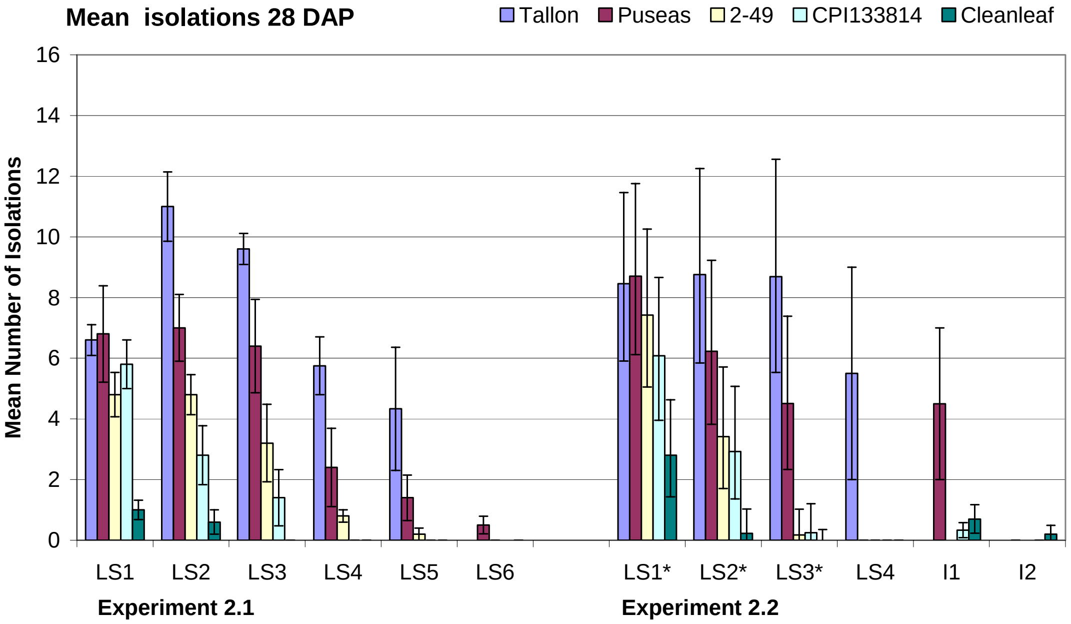


Table 2.9 Number of plants isolated from for each plant part (bolded) and the total number of those plants infected (ie isolations > 0) at 28 days after planting.

28 DAP	**Experiment 2.1 (max 5)**						**Experiment 2.2 (max 10)**							
	LS1	LS2	LS3	LS4	LS5	LS6	LS1	LS2	LS3	LS4	LS5	I1	I2	I3
Tallon	**5**	**5**	**5**	**4**	**3**	**1**	**10**	**10**	**10**	**2**	**---**	**1**	**1**	**---**
	5	5	5	4	3	0	10	10	10	2		1	1	
Puseas	**5**	**5**	**5**	**5**	**5**	**4**	**10**	**10**	**9**	**1**	**1**	**2**	**2**	**1**
	5	5	5	3	3	2	10	10	8	0	0	2	0	0
2-49	**5**	**5**	**5**	**5**	**5**	**4**	**10**	**10**	**10**	**7**	**1**	**---**	**---**	**---**
	5	5	4	4	1	0	10	10	3	0	0			
CPI133814	**5**	**5**	**5**	**5**	**4**	**---**	**10**	**10**	**10**	**5**	**1**	**3**	**3**	**---**
	5	5	3	0	0		10	8	3	0	0	1	0	
Cleanleaf	**5**	**5**	**5**	**5**	**4**	**3**	**10**	**10**	**10**	**4**	**1**	**10**	**10**	**7**
	4	2	0	0	0	0	7	3	0	0	0	2	1	0

Figure 2.10 Mean number of isolations from primary tiller leaf sheaths (LS) and internodes (I) 35 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.

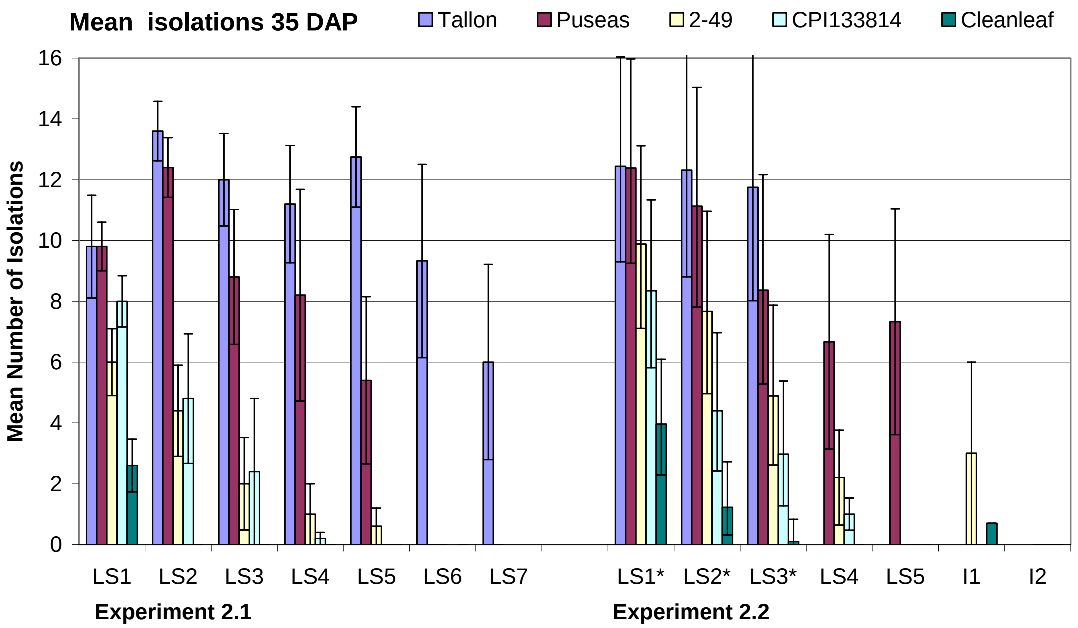


Table 2.10 Number of plants isolated from for each plant part (bolded) and the total number of those plants infected (ie isolations > 0) at 35 days after planting.

35 DAP	**Experiment 2.1 (max 5)**							**Experiment 2.2 (max 10)**								
	LS1	LS2	LS3	LS4	LS5	LS6	LS7	LS1	LS2	LS3	LS4	LS5	I1	I2	I3	I4
Tallon	**5**	**5**	**5**	**5**	**4**	**3**	**3**	**10**	**10**	**10**	**1**	**---**	**1**	**1**	**1**	**---**
	5	5	5	5	4	3	2	10	10	10	1		1	1	0	
Puseas	**5**	**5**	**5**	**5**	**5**	**3**	**3**	**10**	**10**	**10**	**3**	**3**	**1**	**1**	**1**	**1**
	5	5	5	4	3	0	0	10	10	9	2	2	1	0	0	0
2-49	**5**	**5**	**5**	**5**	**5**	**5**	**---**	**10**	**10**	**10**	**5**	**3**	**2**	**2**	**---**	**---**
	5	5	3	1	1	0		10	10	9	2	0	1	0		
CPI133814	**5**	**5**	**5**	**5**	**5**	**---**	**---**	**10**	**10**	**10**	**9**	**3**	**4**	**4**	**2**	**---**
	5	4	1	1	0			10	8	7	3	0	0	0	0	
Cleanleaf	**5**	**5**	**5**	**5**	**5**	**2**	**---**	**10**	**10**	**10**	**10**	**3**	**10**	**10**	**8**	**3**
	4	0	0	0	0	0		10	6	2	0	0	3	0	0	0

Figure 2.11 Mean number of isolations from primary tiller leaf sheaths (LS) and internodes (I) 42 days after planting (DAP). * = Plant part included in the analysis and represents analysed data ± 95% CI of error, unanalysed data is presented as means ± SE.

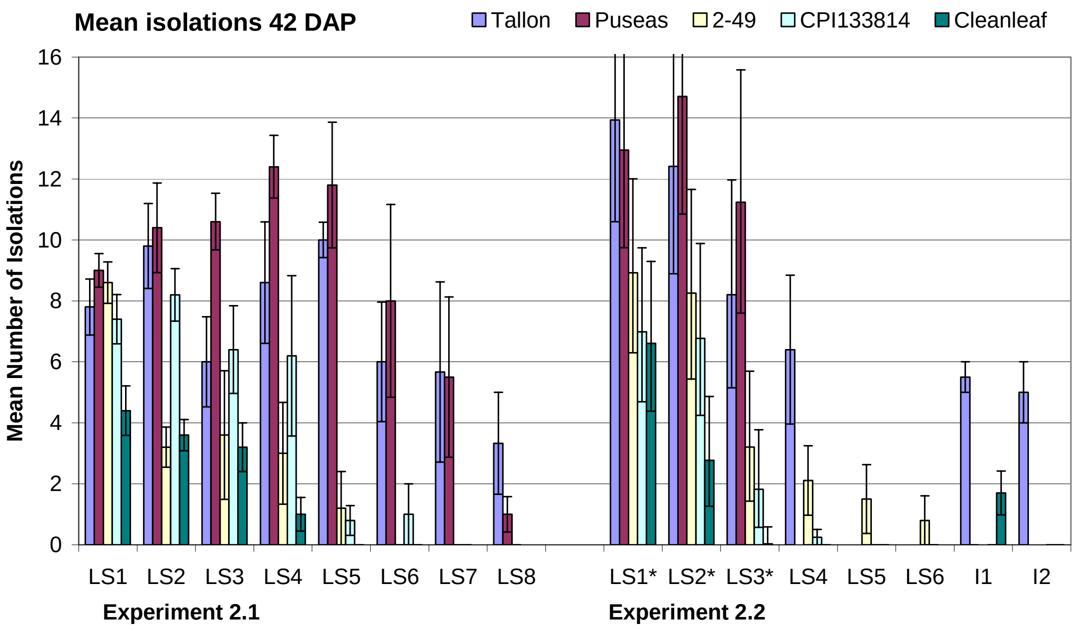


Table 2.11 Number of plants isolated from for each plant part (bolded) and the total number of those plants infected (ie isolations > 0) at 42 days after planting.

42 DAP	**Experiment 2.1 (max 5)**								**Experiment 2.2 (max 10)**								
	LS1	LS2	LS3	LS4	LS5	LS6	LS7	LS8	LS1	LS2	LS3	LS4	LS5	LS6	I1	I2	I3
Tallon	**5**	**5**	**5**	**5**	**4**	**4**	**3**	**3**	**10**	**10**	**10**	**5**	**---**	**---**	**2**	**2**	**1**
	5	5	5	5	4	4	2	2	10	10	10	4			2	2	1
Puseas	**5**	**5**	**5**	**5**	**5**	**4**	**4**	**3**	**10**	**10**	**10**	**1**	**1**	**---**	**1**	**1**	**1**
	5	5	5	5	5	4	4	2	10	10	10	0	0		1	0	0
2-49	**5**	**5**	**5**	**5**	**5**	**5**	**5**	**2**	**10**	**10**	**10**	**9**	**8**	**4**	**---**	**---**	**---**
	5	5	5	3	1	0	0	0	10	10	9	4	2	1			
CPI133814	**5**	**5**	**5**	**5**	**5**	**4**	**3**	**---**	**10**	**10**	**10**	**8**	**7**	**3**	**8**	**7**	**1**
	5	5	5	4	2	1	0		9	8	7	1	0	0	0	0	0
Cleanleaf	**5**	**5**	**5**	**5**	**5**	**5**	**---**	**---**	**10**	**10**	**10**	**8**	**4**	**---**	**10**	**10**	**9**
	5	5	5	3	0	0			10	8	1	0	0		4	0	0

In Exp 2.1 up to eight LS's had expanded at 42 DAP and Tallon and Puseas recorded isolations from all these plant parts. Isolations were recorded from the 1st 4 LS's in all genotypes in this experiment, with a small number recorded from the 5th LS in 2-49 and the 5th and 6th LS in CPI133814 at this harvest time (Figure 2.11). In Exp 2.2 isolations were recorded in the 1st three LS's for all genotypes at 42 DAP and isolation from Puseas and Tallon were higher than the other genotypes in all these LS's. Puseas was significantly higher than CPI133814 in LS1 and LS2 and significantly higher than 2-49 and CPI133814 in LS3. Tallon had a greater number of isolations than 2-49 and CPI133814 in LS 4 with only one Puseas LS 4 expanded at this harvest. Isolations were recorded from two out of eight 5th LS's and one out of four LS 6 in 2-49 at 42 DAP (Table 2.11). Isolations were recorded from all expanded internodes in Tallon and 4 out 10 Cleanleaf 1st internodes were infected at 42 DAP (Figure 2.11, Table 2.11).

2.2.3.1 Re-isolation from individual quarters

Data for the re-isolation of *Fpg* from individual quarters of each leaf sheath was not included in the analysis and raw data is presented in Appendix 2C. To give an indication of localisation of the pathogen within leaf sheath tissues, charts for a selection of these harvests have been presented here (Figure 2.12). At 14 DAP *Fpg* was more commonly isolated from lower quarters (closest to the crown). This is more obvious in Experiment 2.1 where the fungus is confined to the lower half of LS1 in CPI133814 and 2-49. At 21 DAP isolations are made from all 4 quarters of the 1st 3 or 4 LS’s in Puseas and Tallon in both experiments, while still confined to the lower 3 quarters in Exp 2.1 in the partially resistant genotypes. At 42 DAP isolations are made from all four quarters of all leaf sheaths in the susceptible genotypes Puseas and Tallon. In the partially resistant genotypes the pathogen is recovered from all four quarters of the older leaf sheaths; however isolations are confined to the lower quarters of the younger leaf sheaths at this time (Figure 2.12).

Figure 2.12: Mean isolations from each quarter of each leaf sheath at 14, 21 and 42 days after planting. Number of expanded leaf sheaths of each genotype is represented on the x-axis for experiment 2.1 and 2.2.

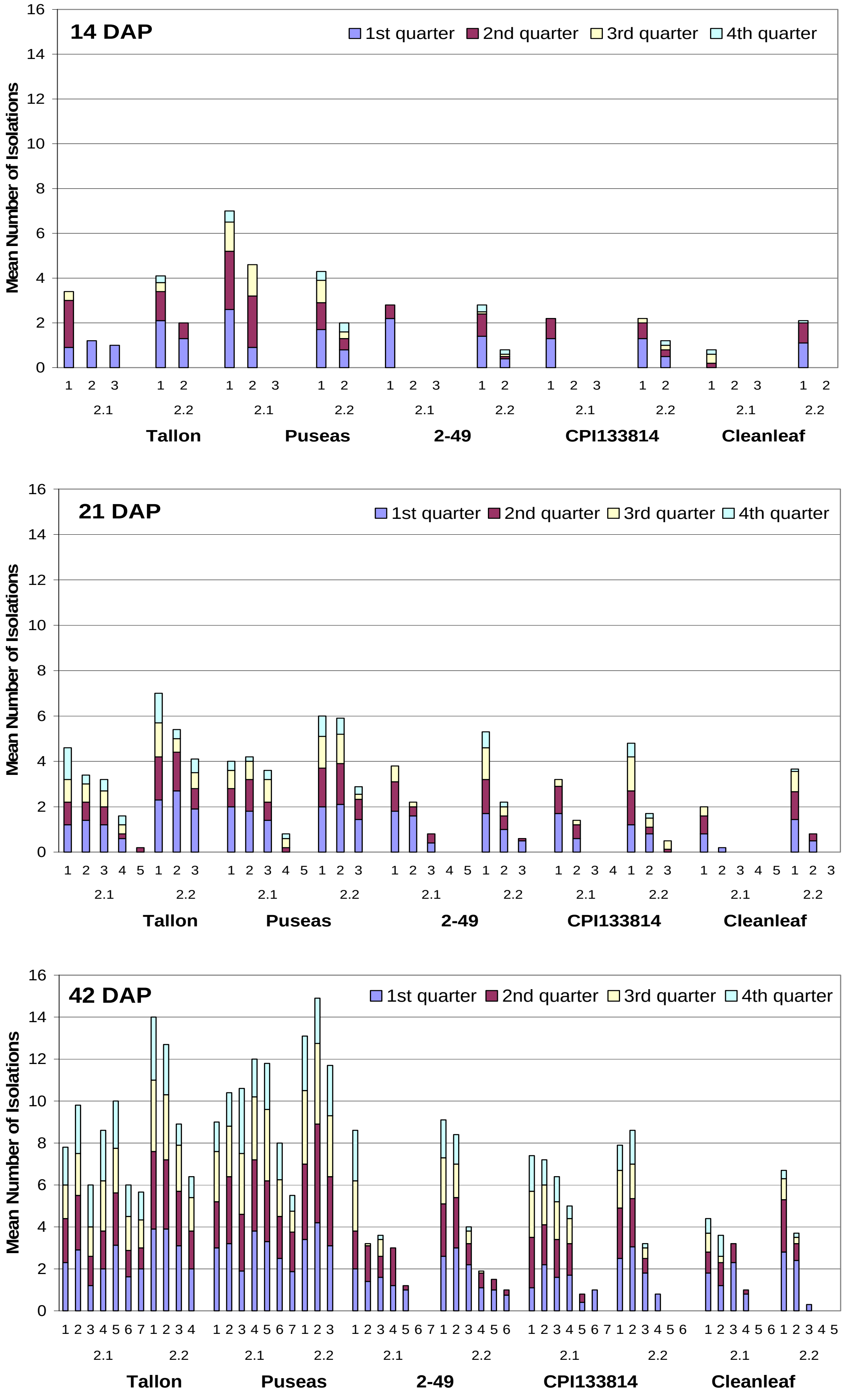


Figure 2.13 X-Y scatter plot of disease rating and isolation data with trend-lines for all data (Exp), Exp 2.1 and Exp 2.2. Data points have been jittered on both axis to allow visual observation.

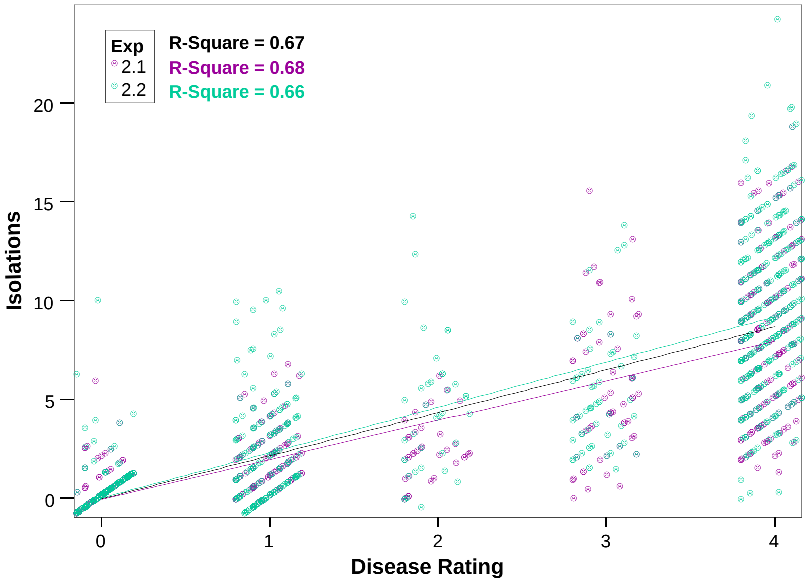


Table 2.12 Correlations of disease rating and isolation data. Pearson correlation coefficients (r) were used to calculate r^2 values. Correlation strength presented according to (Fowler et al., 1998) pg 132. The non parametric Spearman coefficients are also presented.

variables		coefficient of determination (r^2)	correlation coefficient (r)	correlation strength	Spearman's rho (rs)
Experiment	All Data	0.6676	0.8171	strong	0.876
	2.1	0.6820	0.8258	strong	0.895
	2.2	0.6600	0.8124	strong	0.861
Plant part	Leaf Sheath 1	0.4623	0.6799	modest	0.737
	Leaf Sheath 2	0.6001	0.7747	strong	0.844
	Leaf Sheath 3	0.7531	0.8678	strong	0.886
	Leaf Sheath 4	0.7245	0.8512	strong	0.811
	Leaf Sheath 5	0.8447	0.9191	very strong	0.874
	Internode 1	0.4634	0.6807	modest	0.714
Harvest	14 DAP	0.5085	0.7131	strong	0.751
	21 DAP	0.7149	0.8455	strong	0.888
	28 DAP	0.7202	0.8486	strong	0.883
	35 DAP	0.7847	0.8858	strong	0.896
	42 DAP	0.6294	0.7933	strong	0.858
Genotype	Puseas	0.6398	0.7999	strong	0.828
	Tallon	0.4871	0.6979	modest	0.718
	2-49	0.6676	0.8171	strong	0.848
	CPI133814	0.6655	0.8158	strong	0.852
	Cleanleaf	0.3064	0.5535	modest	0.739

2.2.4 Correlation of disease rating and isolation data

Correlations between disease rating and fungal isolation data were highly significant (P<0.01) (Appendix 2E). Correlation coefficients (r) were strong for most treatments in both 42 day seedling experiments (Table 2.12, Figure 2.13). When data was correlated according to plant part a modest correlation was observed in LS1 and I1 with a very strong correlation ($r = 0.9191$) in LS5. A strong correlation was seen for all harvests with between 50 – 78 % of the variance shared between disease rating and isolation data. A modest correlation was seen in Tallon and Cleanleaf compared to strong correlations in Puseas, 2-49 and CPI133814 data (Table 2.12). The non parametric Spearman's coefficient's were similar to the values obtained using Pearson's correlation. However, the range for plant part correlations was reduced compared to the parametric Pearson's coefficients. SPSS output of correlation results is presented in Appendix 2E.

2.3 Discussion

The crown rot screening methods developed at the LRC (Wildermuth and McNamara, 1994) have provided a useful tool to study the differences in *Fpg* colonisation and disease symptom development between partially resistant and susceptible wheat, barley and oat seedlings. *Fpg* was recovered from plants of all genotypes in both seedling trials however significant differences were observed amongst cultivars at each harvest time.

Differences in plant development were seen between the two trials conducted in different growth chambers at different locations. At the final harvest (42 DAP) seedlings had developed up to 8 leaf sheaths and two tillers had begun to expand in Exp 2.1. In Exp 2.2 up to 7 leaf sheaths and 4 internodes had developed on the primary tiller at 42 DAP with minimal secondary tiller development. This may be a result from differences in light intensity and soil space provided to the seedlings of the two trials. In Exp 2.1 we halved the amount of seeds (to 6) usually planted into each pot (12) (Wildermuth and McNamara, 1994) to allow for the longer experiment duration. However the plants had to be re-potted 28 DAP and we therefore increased plant density back to 10 plants per pot in Exp 2.2. The growth room in Exp 2.1 also provided 40% greater light intensity than the growth cabinet used in Exp 2.2. The lower light levels stimulating elongated plants with few secondary tillers. Overall greater differences were seen between genotypes in Exp 2.1 and while a wide range of symptoms were seen in both experiments the results for the two trials were presented separately.

The two bread wheats, Puseas and 2-49 produced disease ratings consistent with the results obtained by Wildermuth and McNamara (1994), where Puseas showed a susceptible reaction to crown rot and 2-49 showed partial resistance. McKnight and Hart (1966) assessed 18 wheat cultivars for white-head formation at maturity and found Puseas to be the most susceptible cultivar tested for crown rot severity. 2-49 is one of the best sources of partial resistance to crown rot and is used extensively as a standard in screening trials by different organisations across Australia (e.g (Wallwork et al., 2004, Wildermuth et al., 2001, Liu et al., 2004).

Studies on the genetic resistance to crown rot have shown that the resistance expressed in several synthetic hexaploid lines is as good as or superior to that of 2-49. This resistance is assumed to be derived exclusively from the *Aegilops taushii* parent not from the durum parent of the cross (Wildermuth et al., 2003). This is not surprising considering the high level of susceptibility exhibited in durum cultivars. The synthetic hexaploid wheat CPI133814 showed partial resistance to crown rot as good as and usually better than that of 2-49 in these seedling trials.

The barley cultivar Tallon exhibited high levels of disease in both experiments similar to or greater than the more susceptible wheat cultivar Puseas. Barley cultivars have continually been reported to show high levels of crown tissue lesioning and stem browning similar to or greater than the more susceptible wheat genotypes in both glasshouse and field trials (Wildermuth and Purss, 1971, Klein et al., 1989, Nelson and Burgess, 1994). However, Denis and Wallwork, unpublished, cited in Wallwork et al. (2004) reported low yield losses in barley with severely lesioned crown tissues suggesting that barley may be relatively tolerant to crown rot infection. Backhouse et al. (1997) also suggested the impact on barley yield is generally less severe perhaps because barley matures early, avoiding the late season moisture stress that contributes to severe whitehead formation. When whitehead formation and yield loss were measured in 4 cereal genotypes inoculated with a mixture of *Bipolaris sorokiniana*, *F.culmorum* and *F. pseudograminearum*, barley genotypes generally showed the highest level of tolerance followed by triticale, bread wheat, and durum wheat (Hekimhan et al., 2004).

In the current experiments disease symptoms were recorded on plant tissues in oat seedlings, however they were low compared to all other genotypes. Wildermuth and Purss (1971) reported that levels of disease in five mature oat cultivars were similar to that of the partially resistant variety Gala. Nelson and Burgess (1994) described Oat varieties as symptomless hosts after they failed to detect lesioning on inoculated 6 week old seedlings. A scale of 0-4 was used in these trials and disease scores were quite low with bread wheat scores of 0.52 and 0.66 and barley varieties between 1.57 – 1.97, suggesting the possibility of low disease pressure. However, they subsequently reisolated the pathogen from up to 32 % of subcrown internodes from these oat varieties. On the other hand the seedling trials conducted here would represent a high inoculum pressure compared to what may be experienced early in the infection process under field conditions.

2.3.1 Disease symptom development in seedlings over time

While each cultivar displayed levels of disease consistent with reports in the literature the differences observed between genotypes varied at different harvest times. The oat variety Cleanleaf had statistically significantly lower disease ratings than the other genotypes in almost all LS and internode readings in both experiments at each harvest time. When this was not the case, Cleanleaf expressed the equal lowest disease ratings. Puseas and Tallon exhibited the highest levels of disease in both trials. However differences observed between these susceptible genotypes and the partially resistant genotypes 2-49 and CPI133814 were not consistent.

At 14 DAP differences between the susceptible Puseas and Tallon and the partially resistant 2-49 and CPI133814 were clearly seen in LS's 1 and 2 in both experiments (Figure 2.2). This difference was lower in the 1st LS by 21 DAP, and no significant difference was seen at 28 DAP in this tissue. Differences were however seen in the 2nd and 3rd LS's at these times (Figures 2.3 and 2.4). By 42 DAP differences seen in

LS 2 were insignificant in Exp 2.1 and only significant in CPI 133814 in Exp 2.2 (Figure 2.6). However significant differences were seen in the younger leaf sheaths at these later harvest times.

In Exp 2.1 strong differences between susceptible and partially resistant genotypes were observed in the inner leaf sheaths at later harvest times. At 42 DAP (Figure 2.6, Table 2.6) disease symptoms were recorded on all Puseas and Tallon LS's 5 and 6. Only a few of the 2-49 and CPI133814 plants showed disease on these tissues and the overall mean disease rating of these were significantly lower than the susceptible genotypes.

These results suggest that in partially resistant seedlings disease symptom development is initially slowed in each tissue. As the infection progresses however, each tissue may become as infected as the tissues of susceptible genotypes only at a later time. This concept of disease catch up is clearly shown for LS's 1, 2 and 3 below (Figure 2.14).

The later development of disease symptoms in partially resistant tissue in these experiments seems to be similar to the Type II resistance (resistance to spread) seen in wheat to Fusarium Head Blight (*F. graminearum,* other *F.* species and *Microdochium nivale*). Ribichich et al. (2000) described a similar response in inoculated spikelets of the spring wheat cultivars Pro INTA Oasis (susceptible) and Sumai 3 (Type II resistance) whereby the same symptoms of disease occurred in each spikelet but at a later harvest time in Sumai 3. Muthomi et al. (2002) assessed disease severity (% of bleached spikelets) every five days from the initial development of symptoms after inoculation until ripening in 15 Kenyan wheat varieties. Severity was always lower in the partially resistant varieties compared to highly susceptible varieties; however the number of diseased spikelets did continue to increase at each assessment in the partially resistant varieties but at a slower rate than the susceptible ones.

The disease rating results in these experiments emphasise the importance of timing of measurements in determining susceptibility to crown rot in seedling trials. Differences between genotypes need to be assessed in younger newly expanded leaf sheaths, as at later harvest times in older tissues differences between genotypes are not as clear. Timing of inoculation and measurements of resistance response has also been shown to be important in Foliar blight of wheat (*Alternaria triticania* and *Bipolaris sorokiniana*). Screening trials in India demonstrated that 95% of CIMMYT lines tested were disease free at growth stage (GS) 47, 80% at GS 57, 46% at GS 69 and only 4.23 % showed resistance at milk development (GS 77) (Chaurasia et al., 1999).

2.3.2 *Fpg* isolation in seedlings over time

These experiments (reported here and in my Honours thesis) are the first time course studies of *Fpg* infection in seedling leaf sheath tissues. Systemic isolations have been made from the crown and stem tissues in more mature plants particularly as a means of identifying the disease causing organism (e.g. Balmas et al., 1995, Purss, 1966). These studies will be considered in Chapter 3 which deals with disease development and fungal spread up to maturity in field trials.

Fpg was isolated from all genotypes in both experiments at all harvest times. However, consistent with the disease rating results, differences were seen between genotypes. Overall a smaller number of isolations were made from each leaf sheath of the partially resistant genotypes compared with the susceptible ones. Also, the fungus progressed through to each younger leaf sheath at a faster rate in the susceptible tissue, than seen in the partially resistant tissue (Figure 2.14 below).

Infection and subsequent movement of *Fpg* occurred through 2-49 and CPI133814 tissue at a similar rate. Most isolation counts for these 2 genotypes were not significantly different. This suggests that partial resistance in these 2 genotypes may act in a similar fashion. However QTL analysis has shown that markers across the whole genome contribute to resistance in 2-49, while the resistance in the synthetic hexaploid wheat, has been shown to come from the *A. tauschii* parent of these crosses or the D genome (Collard et al., 2005, Bovill et al., 2006, Wildermuth et al., 2003). Puseas and Tallon also had similar isolation counts representing the increased susceptibility to pathogen spread through leaf sheath tissues in this susceptible bread wheat and barley cultivar. The isolation counts for Cleanleaf were usually much lower than the wheat and barley counts. Infections did occur in each tissue but at an even slower rate than in CPI133814 and 2-49. This is clearly demonstrated in the virtual absence of *Fpg* in Cleanleaf LS 3's even at later harvest times (Figures 2.9, 2.10 and 2.11). It is possible that the resistance mechanisms in Cleanleaf are the same as 2-49 and CPI133814, only stronger, or there may be other resistance mechanisms operating. Further examination of this response is required. Oats has been shown to offer strong FHB resistance (Langevin et al., 2004). However this has been attributed to the structural characteristic of large spacings between florets.

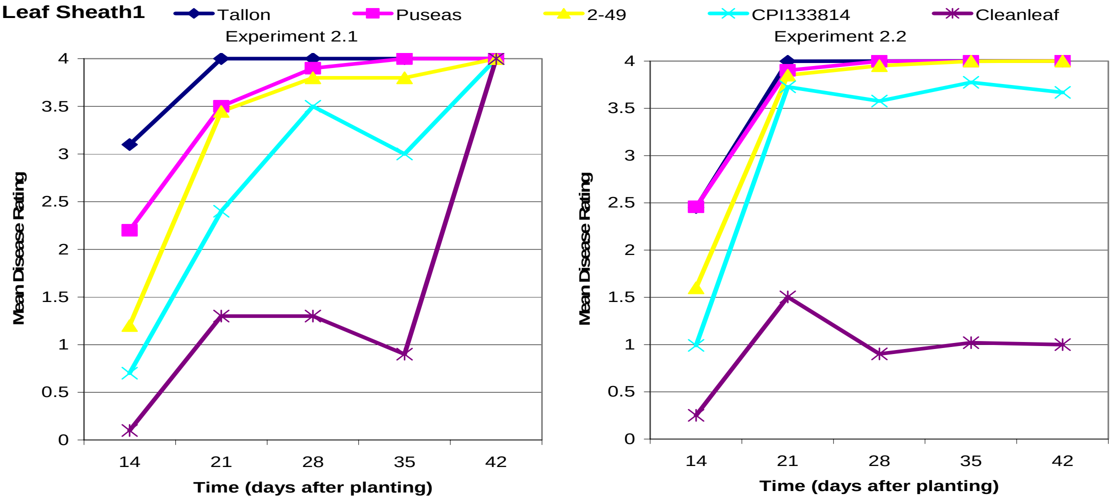
These seedling experiments have confirmed that early in the infection process isolations are made more readily from the lower quarters (closest to the crown) of the 1st leaf sheath. As the infection progresses the pathogen moves up the infected leaf sheath and across into each new inner leaf sheath. In the more susceptible genotypes the pathogen moves more quickly through each tissue and later leaf sheaths may become infected as they expand rather then being infected through the base first and the pathogen then growing up these tissues. This is represented by isolations being made from all four quarters of later leaf sheaths as soon as they have expanded (Figure 2.12).

In the partially resistant genotypes the pathogen moves more slowly through each tissue and as a result each subsequent leaf sheath is usually expanded completely prior to infection. As the pathogen moves inwards in these genotypes the lower quarters are infected with isolations not seen from the higher quarters until later harvest times, if at all. This in turn also slows infections of each inner leaf sheath in the partially resistant tissue compared to the susceptible infection process. It appears that if the fungus has not colonised up the entire leaf sheath prior to it coming away from the main stem then it may not, with a preference to move inwards to the next leaf sheath.

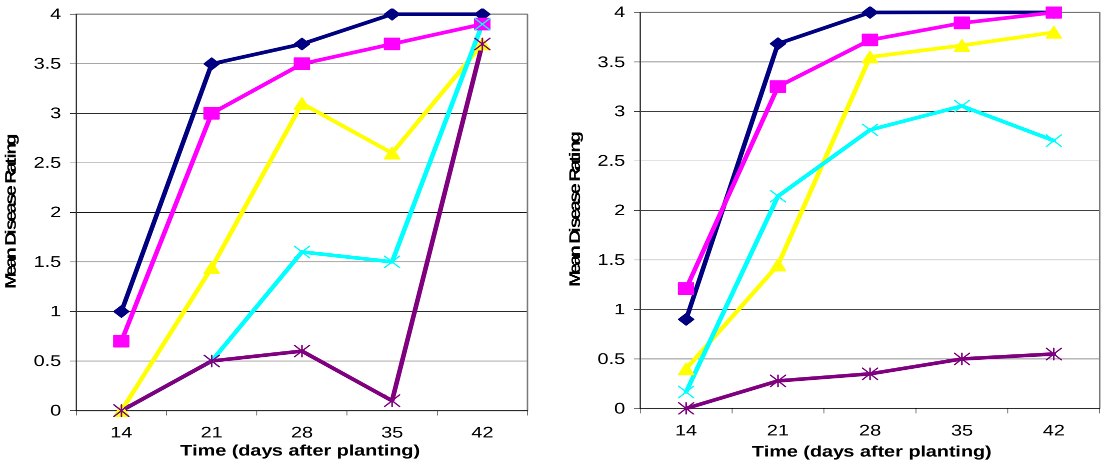
It is interesting that the number of isolations made from leaf sheaths at later harvest times is often lower than previous harvests. This is particularly obvious in older infections of susceptible genotypes. For example the mean number of isolations from Tallon LS 3 was significantly lower at 42 days than at 35 DAP (Figure 2.15 above). Purss (1966) reported a similar phenomenon in stem tissue in field trials

Figure 2.14 Mean disease rating of Leaf sheaths 1, 2 and 3 14 to 42 days after planting for experiments 2.1 (left) and 2.2 (right). NB: Lines in chart are for illustration purposes only they do not represent between time measurements

Leaf Sheath1



Leaf Sheath 2



Leaf Sheath 3

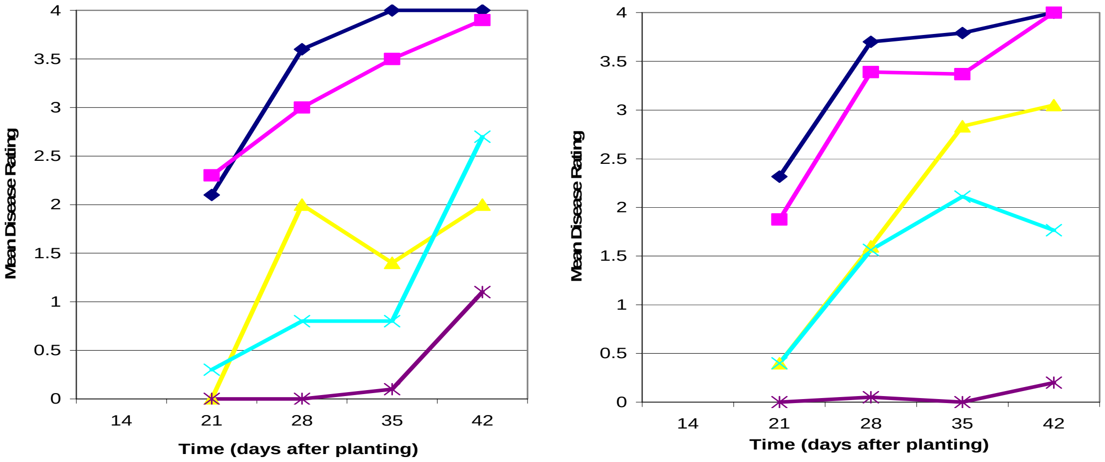
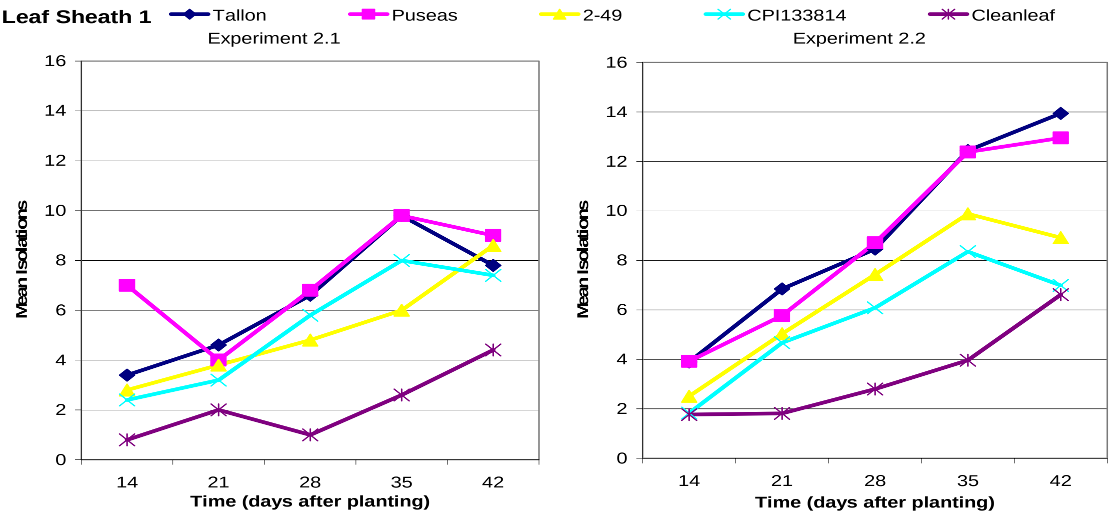
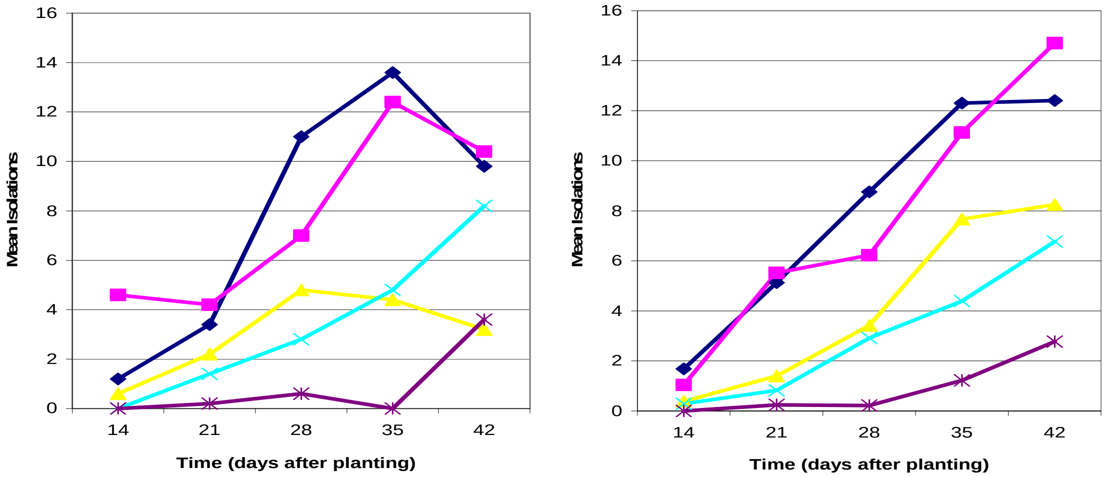


Figure 2.15 Mean number of isolations from Leaf Sheaths 1, 2 and 3, 14 – 42 days after planting for Experiments 2.1 (left) and 2.2 (right). NB: Lines in chart are for illustration purposes only they do not represent between time measurements

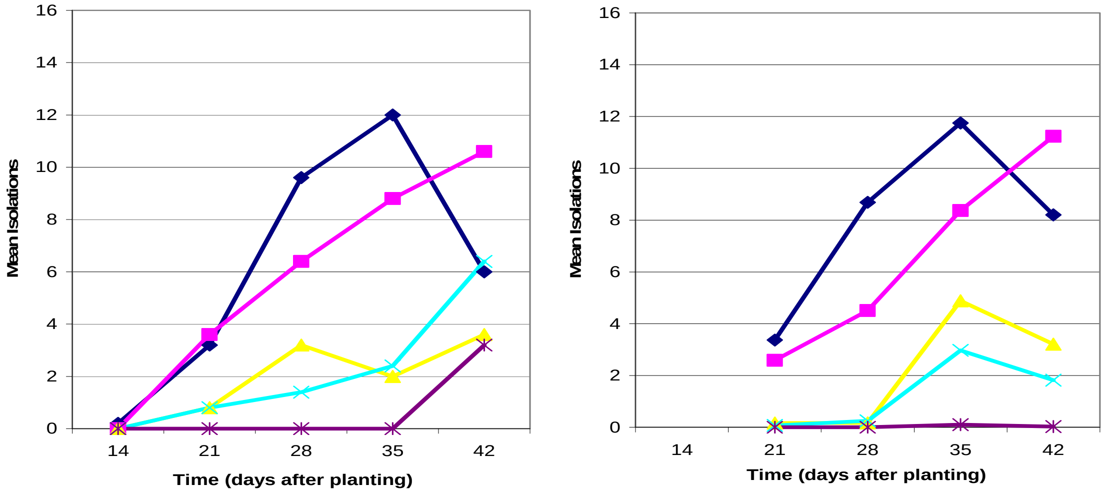
Leaf Sheath 1



Leaf Sheath 2



Leaf Sheath 3



where a lower number of isolations were made from the 1st internode compared with the 2nd internode in mature wheat plants. He concluded that the lower internodes were badly decayed and may be more difficult to isolate from. There was also a possibility of 2nd internode infections originating directly from leaf base infections. The results of these seedling trials support the first explanation given that the older tissues with lower isolations were also showing signs of severe necrosis. Recovery of pathogens from very necrotic tissues may also be inhibited by toxic metabolites and the presence of saprophytes (Royal Botanic Gardens, 2008).

Another interesting result obvious particularly when the data has been presented as line charts over time (Figure 2.15 above) is the lower number of isolations consistently recorded in partially resistant tissues at later harvest times. While the concept of disease catch up was put forward above in relation to disease symptom development in partially resistant leaf sheaths, this does not seem to be the case with the actual amount of fungus in these seedling tissues. Only in LS 1 Exp 2.1 at 42 days are the differences in mean number of isolations not significant between the susceptible and partially resistant genotypes. In all other cases at 35 and 42 DAP, 2-49 and CPI133814 have a lower number of isolations from leaf sheath tissue than Puseas and Tallon, ie while the disease expression catches up at later harvests in older tissues this is not as a result of a higher amount of *Fpg* in these tissues.

2.3.2 Correlation of disease rating and isolation scores

Correlations between disease rating and isolation scores from the seedling trials were all highly significant. Whether plants were separated by plant part, experiment or harvest, correlations were usually strong with the exception of LS1 and I1. Correlation of seedling results showed that 48.71 % of the variance was shared between disease rating and isolation data for Tallon and 30.6 % for Cleanleaf compared to the three wheat genotypes which were above 60%. This may reflect the different nature of the disease and infection responses detected in wheat genotypes compared to that expressed in the barley and oat varieties.

2.3.3 Infection of seedlings internodes

The inconsistent development of internodes made it difficult to distinguish between susceptible and partially resistant genotypes in these tissues in this seedling trial. Particularly in Puseas and Tallon only one or two plants per pot had developed internodes. The internodes and leaf sheaths of these plants often had low disease ratings and pathogen isolations compared to the others plants in the pot (data not shown here-see Appendix 2C for individual plants scores). This indicates that in the susceptible genotypes these individual plants may have escaped early infection compared to the other plants in the same pot and also that internode expansion may have been restrained in highly diseased plants. The differential expansion of internodes between genotypes may be more important in explaining disease reaction then the susceptibility of the genotype when rating internodes in this seedling trial. For example Cleanleaf consistently had isolations for the internodes in the last three harvests. However it was the first genotype to develop internodes and it had more plants per pot with internodes than other genotypes at all of these harvest times. Therefore these Cleanleaf internodes may have been exposed to the crown rot inoculum for a longer period of time than the other genotypes.

These experiments have confirmed that differences in disease ratings between susceptible and partially resistant genotypes are detected in younger leaf sheaths of older seedlings. At later harvest times differences between susceptible and partially resistant genotypes are not significant in older leaf sheaths. Re-isolation of *Fpg* from inoculated seedlings has shown that each tissue is infected later in partially resistant genotypes compared to susceptible ones with a significantly lower number of isolations recorded at each harvest time in 42 day old seedlings.

The question arises - Does this slowing of disease symptom development and restriction of *Fpg* hyphae spread through partially resistant tissue continue through out the growing season and into each leaf sheath, internode and even into newer tillers of more mature plants? This question is addressed in the following chapter which examines disease development and *Fpg* infection of each tissue of developing wheat plants up to maturity in inoculated field trials.

Chapter 3: Differences in Disease Development and Pathogen Growth Between Wheat Genotypes in Inoculated Field Trials

3.0 Introduction

When *Fpg* infects germinating wheat seedlings through contact with the coleoptile and/or the subcrown internode, lesions subsequently develop on coleoptile, sub-crown internode and leaf sheath tissues. Susceptibility to crown rot can be distinguished in wheat genotypes at this stage under glasshouse or growth cabinet conditions by rating the extent of lesion development on leaf sheaths (Chapter 2, (Wildermuth and McNamara, 1994, Wildermuth et al., 2001).

In the field, differences in the level of tiller base browning and whitehead formation at maturity have been used to estimate relative susceptibility. Genotypes have also been distinguished by the percentage of diseased tillers or plants in both field and container grown plants at maturity (eg. Wildermuth and Purss, 1971, Nelson and Burgess, 1994, Purss, 1966, Dodman and Wildermuth, 1987). Incidence of infection by *Fpg* is commonly found to be similar amongst varieties differing in the expression of disease symptoms. However most of these measurements are conducted at maturity. The process of infection and subsequent disease development has not been extensively studied throughout the growing season (Dodman and Wildermuth, 1987).

Purss (1966) reported on the progress of crown rot infection and disease development in wheat genotypes. Percentage infection of each variety in the field was determined by isolation at five harvest times from 38 days to maturity. This study also recorded isolations from each plant tissue of different varieties at maturity. Purss (1966) concluded that the rate of disease development was slowed in the more tolerant genotypes (such as Gala).

The majority of studies on cultivar reaction to crown rot from the 1960’s through to the late 1990’s were focussed on developing techniques to screen wheat varieties for resistance to crown rot (eg Liddell and Burgess, 1987, Purss, 1966, Purss, 1971a, Liddell and Burgess, 1985, Wildermuth and McNamara, 1994, Dodman and Wildermuth, 1987, Klein et al., 1985) and reasons for differences in symptom development between genotypes and the processes of resistance are still unknown. The timing of differences in symptom expression (lesioning of plant tissue) in the field has not been determined and the movement of *Fpg* through plant tissue of different genotypes is also unclear.

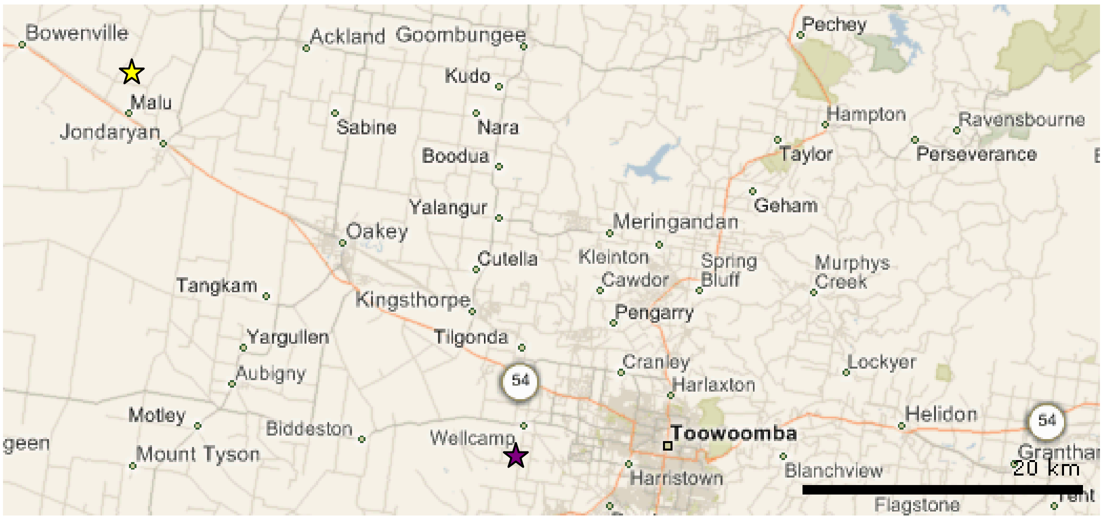
The current inoculated field trials were designed to move beyond the early studies of Purss by studying disease symptom development and localisation of *Fpg* hyphae in all expanded tissues (excluding head and roots) in wheat genotypes of known susceptibility to crown rot. Plants were harvested at approximately fortnightly intervals throughout the growing season. The main effects and interactions of harvest, genotype and tiller on each plant part were examined with a detailed statistical analysis of differences seen in these factors between susceptible and partially resistant wheat genotypes, in two inoculated field trials located on the Darling Downs of Queensland.

3.1 Methods

Inoculated field trials were conducted in 2000 and 2001. The 2000 trial was carried out on T. Kummerow's property located at Malu close to Jondaryan, 50kms west of Toowoomba (Jondaryan Trial). The second trial (2001) was conducted at the LRC Experimental Farm at Wellcamp, 9kms west of Toowoomba (Wellcamp Trial) (Figure 3.1).

Three replicates of five wheat genotypes were planted using a randomised block design. All seed and inoculum were provided by Dr Graham Wildermuth from the LRC, QDPI & F, Tooowoomba, Qld. Seed (dusted with benomyl) was planted in a furrow at a rate of 6gm per row in 2.7 metre rows. Inoculum was placed in a band lying above the seed at sowing, at a rate of 2gm per metre. Methods of inoculum production were as summarised in Chapter 2 and can be found in detail in Chapter 4, however for these field trials the chaff was only coarsely ground to pass through a 5mm sieve.

Figure 3.1 Field trial locations ☆Jondaryan Trial ★Wellcamp Trial (source: http://live.com/PrintableMap.aspx?mkt=en-au&a=false ©2006 Microsoft Corporation © AND © 2006 MapData Sciences Pty Ltd).



3.1.1 Site characteristics

Minimum and maximum temperatures and rainfall data were collected throughout both trials. For the Jondaryan site this data was downloaded from the Bureau of Meteorology (http://www.bom.gov.au/cgi-bin/wrap_fwo.pl?IDO31Q01.html) daily except for a period between the 20/10/00 and the 25/10/00 when I was unable to access the internet. Data for this trial was obtained for Oakey, the closest weather station to the trial (approx 15 kms). Data for the Wellcamp trial was recorded on site and obtained from the QDPI&F records.

Soil cores were taken from both sites after the final harvest to a depth of 90cm for physical and chemical analysis. These analyses were conducted by the Analytical chemistry laboratory at the LRC, DPI & F, Toowoomba, Qld. Tests conducted for both sites included pH, electrical conductivity, concentrations of chloride, nitrate, ammonium, total nitrogen, organic carbon, bicarbonate extractable P and DTPA extractable zinc. Samples from 1-10, 10-30, 30-60 and 60-90 cm into the soil profile were examined. At the Jondaryan site exchangeable cations (Mg, Ca, Na, K), CEC and percentage of exchangeable sodium were also obtained, along with percentages of sand, silt and clay for each soil depth. An intensive analysis of the soils at the Wellcamp Research Farm was carried out by QDPI&F Land Resources Branch

(Powell and Christianos, 1985) and data on physical properties and structure of these soils were obtained from this report.

3.1.2 Genotypes

The genotypes used in both field trials included the crown rot susceptible bread wheat variety Puseas, the partially resistant breeding line 2-49 and the synthetic hexaploid wheat CPI 133814. More detailed descriptions of these genotypes are presented in Chapter 2 (2.1.1). The bread wheat varieties Vasco and Sunco were also included in these field trials. Vasco is susceptible to crown rot, exhibiting high disease ratings both in seedling trials and in the field (Wildermuth and McNamara, 1994, Wildermuth et al., 2001). Sunco has offered the greatest level of field resistance to crown rot in any commercial cultivar for many years, however it’s field resistance is inferior to that of some experimental lines such as 2-49 and CPI133814 and it has been shown to be rated with more susceptible genotypes such as Vasco in seedling trials (Wildermuth and McNamara, 1994, Wildermuth et al., 2001, QDPI&F, 2007).

Zadoks scale (Zadoks et al., 1974) was used to identify major developmental phases of plants in both field trials. A comprehensive comparison with the scale was not used as each genotype differed slightly in their rate of development. However a general indication of plant stages at each harvest has been presented.

3.1.3 Measurement of disease severity and re-isolation of *Fpg*

Five plants from each of three replicate rows were harvested at two to three week intervals and all plant parts (excluding heads and roots) from each tiller were rated for disease. Each plant part from the first two replicates of each trial was then surface sterilised and plated onto nutrient media to localise *Fpg* in these tissues. Methods used for disease rating and re-isolation of the fungus from infected plant tissues are as outlined in Chapter 2.

In the Wellcamp trial data was collected for all tillers up to and including harvest 6 (16 WAP) at which point the volume of plant material being collected was becoming too large to be processed in a reasonable time. From harvest 7 onwards only the first 5 tillers of each plant were examined. Only 5 tillers for each plant for all harvests were included in the analysis and in this report.

3.1.3.1 Head condition

In the Wellcamp trial the condition of the head and grain for each tiller of the 5 plants from each of the 3 replicates was recorded at the final three harvests. Frequently diseased tillers did not complete development resulting in the absence of any head. This data was recorded. Heads that contained grain that was slightly shrivelled together with sterile heads containing no grain (deadheads) were recorded as pinched grain. At each harvest a % of healthy heads was obtained for each genotype by calculating: ((tiller number - (tillers with no heads + tillers with pinched grain)) / tiller number)*100.

3.1.4 Data analysis

Data for each plant part from each trial was analysed separately with the assistance of Kerry Bell (biometrician from the QDPI&F, Toowoomba) using the Genstat 6th Edition software package (Laws Agricultural Trust, Rothamsted Experimental Station, VSN International Ltd, UK). Advice on data interpretation and presentation was also provided by Dr Ashley Plank (Department of Maths and Computing, USQ). As described for the seedling trial data in Chapter 2 suitable analysis procedures were not available to deal with the isolation data where each plant tissue was divided into quarters and therefore only the total isolation scores for each plant part were included in the analysis.

Disease rating data were analysed untransformed and the isolation counts were given a square-root transformation prior to analysis and then presented in the results as back-transformed means. Treatments within the two experiments were arranged in a randomised block design. Restricted Maximum Likelihood (REML) Variance Components Analysis was used to generate probabilities to determine significance of the fixed factors harvest, genotype, tiller and the corresponding two and three way interactions. Standard error of difference (SED) values were multiplied by *t* (in most cases 2 was used) and divided by the √2 to give a 95% confidence interval of error. This value was used to determine where individual means were significantly different.

95% confidence intervals for isolation counts

As the isolation data was square root transformed it was more difficult to obtain a 95% confidence interval of error. These values were calculated by adding/and subtracting the SED (*t/√2) for each plant part to each transformed mean to get a lower and upper limit. The three values (mean, upper limit, lower limit) were then squared to back transform. The differences between the mean and the upper and lower limits were then obtained and used as error bars for each mean.

As an example if the transformed mean = 2 and SED (*t/√2) = 0.5.

The lower limit would be 1.5, the upper limit 2.5.

Squaring all these values we get a mean of 4 an upper limit of 6.25 and a lower limit of 2.25. After calculating the differences, the mean = 4, +2.25 and –1.75.

3.1.5 Correlation of disease rating and isolation data

Correlations of disease rating and isolations were performed for all plant parts of each trial using SPSS 14.0 for Windows. Pearsons correlations coefficients were used to calculate the coefficient of determination (r^2) and correlation strength was estimated according to (Fowler et al., 1998, pg 132).

3.2 Results

3.2.1 Site characteristics

Charts of weather data for both trials are presented in Figures 3.2a) Jondaryan and 3.2b) Wellcamp. The temperature range of each trial was very similar with the maximum temperature of 35° and a minimum temperature of -5° observed for both trials. However the Jondaryan trial had twice as many days (30 days) under 0° compared with the Wellcamp trial (15 days) (Figure 3.2). Oakey generally has minimum temperatures during winter a couple of degrees lower than those experienced in Toowoomba (Bureau of Meteorology, 2007 http://www.bom.gov.au).

Large differences were seen in the moisture available to both trials. While the frequency of rainfall events was similar the amount of overall precipitation at each trial was different. The Jondaryan trial was very dry with the greatest precipitation at any one time recorded as 7mm on 11th of July and again on the 14th of October (Figure 3.2a). The Wellcamp trial on the other hand received three rainfall events above 30mm in October and November and one above 20mm at the seedling growth/tillering stage in July (Figure 3.2b). Both trials received supplementary watering to a depth of 1 inch to ensure initiation of infection. The Wellcamp trial was irrigated on the 17th of July after I had conducted the 1st harvest. The Jondaryan trial was irrigated on the 1st of August, a couple of days prior to the 2nd harvest. However when this 2nd harvest at 6 weeks after planting (WAP) was conducted it was noted that the surface was very dry. The days surrounding the irrigation were very windy and it is thought that very little moisture was retained.

The soils at both trials have an Australian Soils Classification of "Self Mulching Black Vertisol" (Powell and Christianos, 1985, pers comm. with Boyd Mc Namara). The analysis conducted by LRC revealed that there was good soil consistency between the replicate cores taken at each trial (Table 3.1). Most tests revealed very similar results with the only exception observed in the third replicate of the Jondaryan trial whereby the level of ammonium (NH_4-N) in the top 0-10cm of the profile was 5 times higher than that seen in the soils for the other replicates. There were also similar results between soils of the two trials although the Jondaryan soils had an overall higher level of EC, chloride, nitrate and ammonium at the end of the growing season (Table 3.1a) while the Wellcamp soil was higher in the exchangeable cations calcium and magnesium (Table 3.1b).

Figure 3.2 Daily rainfall and temperature data for the Jondaryan Field Trial, Queensland, 2000 (data collected at Oakey).

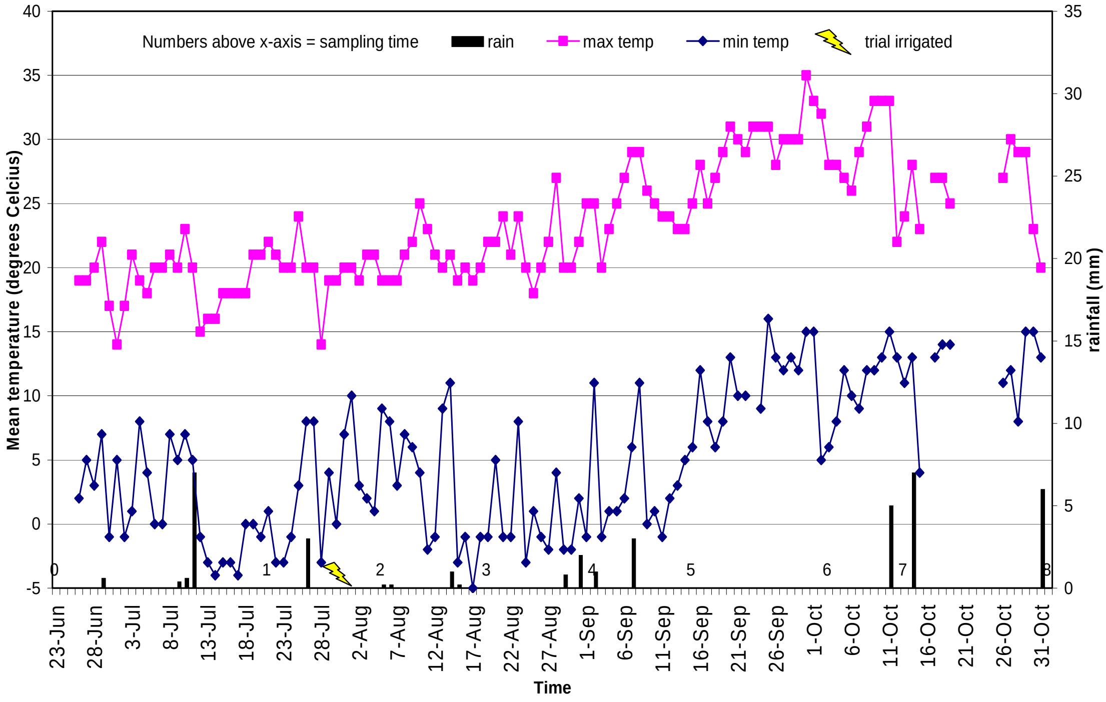


Figure 3.3 Daily rainfall and temperature data for the Wellcamp Field Trial, Queensland, 2001 (data collected on site).

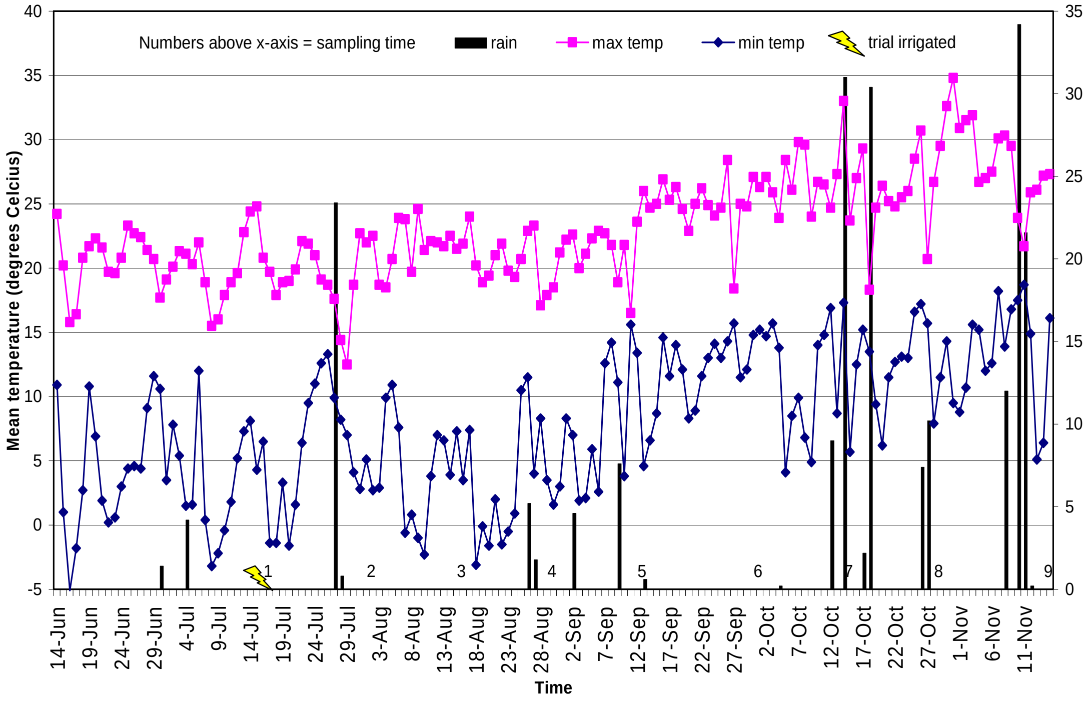


Table 3.1 Soil analysis of the Jondaryan and Wellcamp trials

a) analysis of soils for each replicate in each trial (conducted by LRC)

Site/ Replicate	Soil depth (cm)	pH	EC (mS/cm)	Chloride (mg/kg)	NO3-N (mg/kg	NH4-N (mg/kg)	Total N (%)	Organic carbon (%)	Bicarb. extractable P (mg/kg)	DTPA extractable Zn (mg/kg)
Jondaryan Rep I	0 - 10	7.27	0.453	130	150.8	7.5	0.157	1.54	24.9	0.343
	10 - 30	8.22	0.390	210	50.8	3.2				
	30 - 60	8.3	1.030	1040	13.6	2.3				
	60 - 90	7.64	4.500	1920	3.3	2.1				
Jondaryan Rep II	0 - 10	7.18	0.566	190	185.0	7.4	0.146	1.47	31.0	0.36
	10 - 30	8.29	0.434	180	55.5	3.2				
	30 - 60	8.37	1.025	930	18.1	2.7				
	60 - 90	7.7	4.330	1660	6.2	1.7				
Jondaryan Rep III	0 - 10	6.87	0.520	200	147.9	39.5	0.172	1.69	29.4	0.425
	10 - 30	7.97	0.560	310	46.8	4.0				
	30 - 60	8.26	1.070	1060	13.1	3.1				
	60 - 90	7.69	4.160	1470	3.3	2.0				
Wellcamp Rep I	0 - 10	8.53	0.165	26	19.1	1.3	0.162	1.76	35.2	2.14
	10 - 30	8.39	0.235	64	30.1	1.8	0.149	1.61	9.2	0.48
	30 - 60	8.18	0.285	114	34.9	1.7	0.121	1.56	6.0	0.46
	60 - 90	8.37	0.298	126	23.5	1.0	0.098	1.28	5.2	0.41
Wellcamp Rep II	0 - 10	8.51	0.187	26	23.8	0.9	0.142	1.67	37.2	2.47
	10 - 30	8.38	0.260	62	42.1	1.7	0.105	1.25	8.0	0.66
	30 - 60	8.42	0.272	102	38.3	1.7	0.056	0.68	1.5	0.48
	60 - 90	8.47	0.262	123	24.3	0.8	0.049	0.62	1.0	0.25
Wellcamp Rep III	0 - 10	8.49	0.174	29	20.5	1.7	0.152	1.66	35.0	1.97
	10 - 30	8.29	0.251	88	31.0	1.7	0.146	1.60	10.8	0.52
	30 - 60	8.23	0.292	138	31.2	1.5	0.129	1.61	5.0	0.59
	60 - 90	8.21	0.290	160	20.3	1.5	0.096	1.43	4.0	0.35

b) composite soil analysis for each trial

Trial Site	Soil depth (cm)	pH	Total N (%)	Organic C (%)	Bicarbonate extractable P	DTPA extractable Zn (mg/kg)	Exchangeable cations and CEC (m.equiv./100g)					Exchangable Na (%)
							Ca	Mg	Na	K	CEC	
Jondaryan LRC analysis (2000)	0 - 10	7.06	0.167	1.65	28.3 mg/kg	1.873	35	16	3.1	1.1	60	5
	10 - 30	8.15	0.135	1.56	8.4 mg/kg	0.442	34	17	6.4	0.6	64	10
	30 - 60	8.25	0.098	1.37	7.9 mg/kg	0.623	32	20	8.7	0.6	63	14
	60 - 90	7.74	0.034	0.53	8.7 mg/kg	0.310	27	18	7.9	0.7	53	15
Wellcamp Powell & Christianos (1985)	0 - 10	8.7	0.150	1.60	10 ppm	0.3 ppm	60	25	0.4	1.7	85	
	20 - 30	8.4					57	33	0.4	1.1	97	
	50 - 60	8.7					43	43	0.8	0.7	89	
	80 - 90	8.8										

Trial Site	Soil depth (cm)	Sand (%) Fine/Coarse		Silt (%)	Clay (%)
Jondaryan LRC analysis (2000)	0 - 10		25.4	16.0	58.6
	10 - 30		17.5	17.1	65.4
	30 - 60		20.0	16.3	63.7
	60 - 90		19.9*	73.0*	7.1*
Wellcamp Powell & Christianos (1985)	0 - 10	9.0	3.0	17.0	74
	20 - 30	7.0	1.0	14.0	82
	50 - 60	8.0	3.0	12.0	76
	80 - 90	8.0	3.0	12.0	79

* Aggregation due to gypsum
(sulphate revealed by testing with barium chloride)

Table 3.2 Plant age and development at each harvest for a) Jondaryan trial and b) Wellcamp trial, with a general outline of Zadoks growth stages (Zadoks et al., 1974).

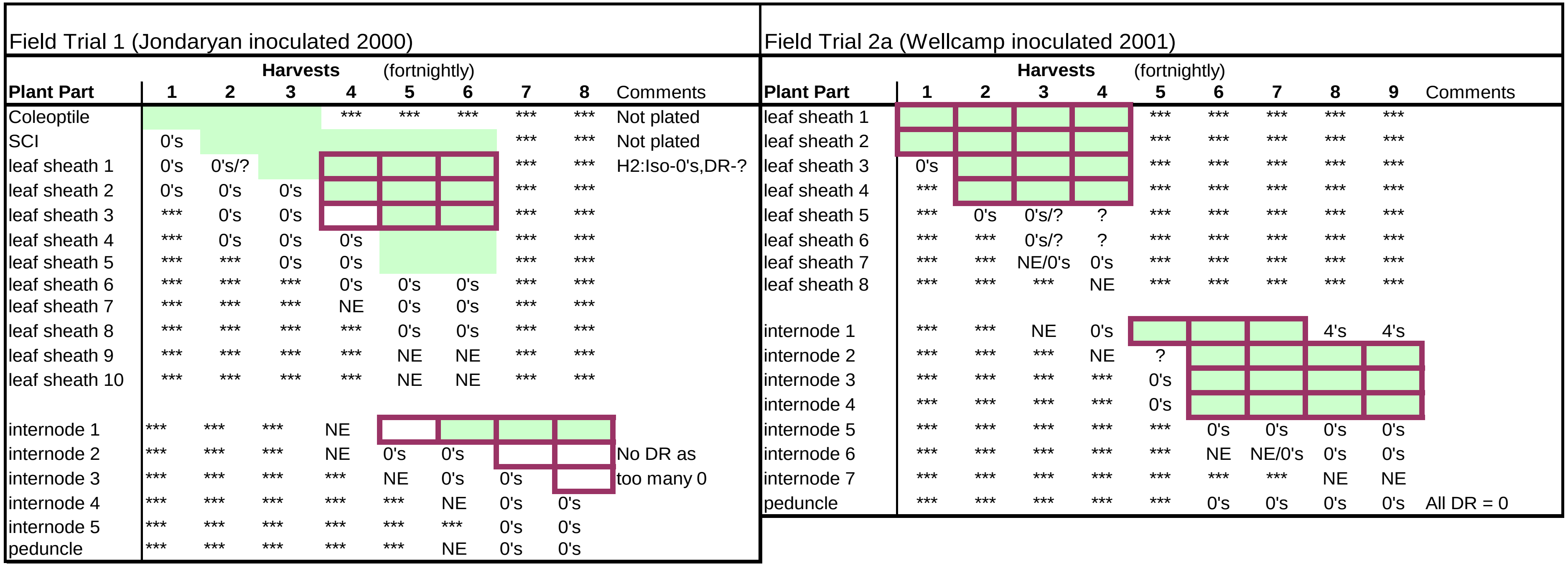
a) Jondaryan inoculated field trial (2000)

Harvest	Date	Age (weeks)	Plant Development	Zadoks Scale
1	20-Jul	4	2 leaf Sheaths	Seedling Growth
2	4-Aug	6	4 leaf sheaths (1° tiller)/ 2 tillers	Tilllering
3	18-Aug	8	5 leaf sheaths (1° tiller)/ 3-4 tillers	Tillering
4	1-Sep	10	6-7 leaf sheath (1° tiller)/ 3-4 tillers/ internodes emerging	Stem Elongation
5	14-Sep	12	2-4 internodes (1° tiller)/ up to 4 tillers	Booting
6	2-Oct	14.5	up to 4 internodes (1° tiller)/ up to 4 tillers/ heads emerged from boot/ pollen dispersed	Ear Emergence/ Anthesis
7	12-Oct	16	mainly 4 internodes + peduncle (1° tiller)/ soft grain	Milk/ Dough Developmnet
8	31-Oct	18.5	mainly 4 internodes + peduncle (1° tiller)/ caryopsis hard/ straw dead	Ripening

b) Wellcamp inoculated field trial (2001)

Harvest	Date	Age (weeks)	Plant Development	Zadoks Scale
1	17-Jul	5	3 leaf sheaths	Seedling Growth
2	2-Aug	7	4-5 leaf sheaths (1° tiller)/ 3-4 tillers	Tillering
3	16-Aug	9	6-7 leaf sheaths (1° tiller)/ up to 9 tillers	Tillering
4	30-Aug	11	8 leaf sheaths (1° tiller)/ up to 9 tillers/ internodes emerging	Stem Elongation
5	13-Sep	13	4 internodes (1° tiller)/ up to 12 tillers	Booting
6	1-Oct	16	5-6 internodes (1° tiller)/ up to 12 tillers (mostly sterile)/ heads emerged from boot (still soft)/ pollen dispersed	Ear Emergence/ Anthesis
7	15-Oct	18	5-6 internodes (1° tiller)/ seed firm/ little milk/ late milk	Milk Development
8	29-Oct	20	5-6 internodes + peduncle (1° tiller)/ soft grain	Dough Development
9	15-Nov	22	5-6 internodes + peduncle (1° tiller)/ caryopsis hard	Ripening

Table 3.3 Plant parts which had expanded at each harvest and those that were included in the analysis for the Jondaryan trial (2000) and the Wellcamp trial (2001). An indication of why expanded plant material was not included in the analysis has also been made.



Field Trial 1 (Jondaryan inoculated 2000)

	Harvests	(fortnightly)							
Plant Part	1	2	3	4	5	6	7	8	Comments
Coleoptile	🟩	🟩	🟩	***	***	***	***	***	Not plated
SCI	0's	🟩	🟩	🟩	🟩	🟩	***	***	Not plated
leaf sheath 1	0's	0's/?	🟩	🟩 □	🟩 □	🟩 □	***	***	H2:Iso-0's,DR-?
leaf sheath 2	0's	0's	0's	🟩 □	🟩 □	🟩 □	***	***	
leaf sheath 3	***	0's	0's	□	🟩 □	🟩 □	***	***	
leaf sheath 4	***	0's	0's	0's	🟩	🟩	***	***	
leaf sheath 5	***	***	0's	0's	🟩	🟩	***	***	
leaf sheath 6	***	***	***	0's	0's	0's	***	***	
leaf sheath 7	***	***	***	NE	0's	0's	***	***	
leaf sheath 8	***	***	***	***	0's	0's	***	***	
leaf sheath 9	***	***	***	***	NE	NE	***	***	
leaf sheath 10	***	***	***	***	NE	NE	***	***	
internode 1	***	***	***	NE	□	🟩 □	🟩 □	🟩 □	
internode 2	***	***	***	NE	0's	0's	□	□	No DR as
internode 3	***	***	***	***	NE	0's	0's	□	too many 0
internode 4	***	***	***	***	***	NE	0's	0's	
internode 5	***	***	***	***	***	***	0's	0's	
peduncle	***	***	***	***	***	NE	0's	0's	

Field Trial 2a (Wellcamp inoculated 2001)

	Harvests	(fortnightly)								
Plant Part	1	2	3	4	5	6	7	8	9	Comments
leaf sheath 1	🟩 □	🟩 □	🟩 □	🟩 □	***	***	***	***	***	
leaf sheath 2	🟩 □	🟩 □	🟩 □	🟩 □	***	***	***	***	***	
leaf sheath 3	0's	🟩 □	🟩 □	🟩 □	***	***	***	***	***	
leaf sheath 4	***	🟩 □	🟩 □	🟩 □	***	***	***	***	***	
leaf sheath 5	***	0's	0's/?	?	***	***	***	***	***	
leaf sheath 6	***	***	0's/?	?	***	***	***	***	***	
leaf sheath 7	***	***	NE/0's	0's	***	***	***	***	***	
leaf sheath 8	***	***	***	NE	***	***	***	***	***	
internode 1	***	***	NE	0's	🟩 □	🟩 □	🟩 □	4's	4's	
internode 2	***	***	***	NE	?	🟩 □	🟩 □	🟩 □	🟩 □	
internode 3	***	***	***	***	0's	🟩 □	🟩 □	🟩 □	🟩 □	
internode 4	***	***	***	***	0's	🟩 □	🟩 □	🟩 □	🟩 □	
internode 5	***	***	***	***	***	0's	0's	0's	0's	
internode 6	***	***	***	***	***	NE	NE/0's	0's	0's	
internode 7	***	***	***	***	***	***	***	NE	NE	
peduncle	***	***	***	***	***	0's	0's	0's	0's	All DR = 0

🟩 Disease Rating	Analysed
□ Isolations	Analysed
DR	Disease Rating
Iso	Isolations
***	Tissue not developed or not collected
0's	Data contains too many zero's
NE	Not Enough: data for that tissue too sparse
?	A lot of 0's but susceptible genotypes diseased
4's	Data contains too many four's
H2	Harvest 2

3.2.2 Environmental effects on plant growth and disease severity within trials

Differences were seen in plant development between the two trials. In the Jondaryan trial up to 4 tillers developed per plant. In the Wellcamp trial up to 12 tillers developed on some plants (Table 3.2). This is almost certainly a result of increased moisture availability in this second trial. In fact, as the plants began to tiller at Wellcamp, the amount of plant material became too great to be processed in a reasonable time and it was decided that only the 1st five tillers would be examined. The extent of fungal infection in the Wellcamp trial was higher than in the Jondaryan trial, where it took a longer time for disease to become established (sections 3.2.4-3.2.5).

Unfortunately the majority of individual plants in the synthetic hexaploid CPI133814 rows were selectively removed by birds in the Wellcamp field trial soon after emergence!! Field staff at the Wellcamp research station have previously noted an apparent preference for synthetic hexaploid seedlings among the local cockatoo flocks. Fortunately sufficient CPI133814 plants remained to allow harvest at two sampling times and we chose to collect these at harvests 5 (booting) and 9 (ripening) (13 and 22 WAP respectively).

3.2.3 Data analysis and presentation

Raw data of both disease rating scores and isolation counts are presented in Excel spreadsheets in Appendix 3A for the Jondaryan trial and Appendix 3B for the Wellcamp trial. The analysis output for each trial is presented in Appendix 3C (Jondaryan trial) and Appendix 3D (Wellcamp trial). As described in Chapter 2 for the seedling trials, several data sets were omitted from this analysis due to a small number of values or limited variance in these field trials. These results included particular harvests or plant parts where ratings or isolations data contained a large proportion of zero's within the replicates for that plant part. Table 3.3 summarises the data collected and the measurements which were included in the analysis. For consistency both analysed and unanalysed data has been presented in the results section of this chapter.

Firstly, the probabilities from the analysis are presented for each trial indicating significance of each factor and interaction for each plant part. A factor or interaction was considered significant where the probability was < 0.01. The unanalysed and analysed results are then presented in bar charts following the disease or fungal progression (isolations) at each harvest for each genotype of each tiller. The analysed results are given as means ± 95% confidence interval of difference. Unanalysed data is presented as means ± standard error (SE).

Charts are presented for disease ratings and for isolation data for all plant parts expanded at each harvest. Along with each chart is a table for that plant part recording the number of parts that had expanded at that harvest (bold) and the number of those plant parts diseased or infected (readings > 0) (incidence).

3.2.4 Field trial disease ratings

Coleoptile

Coleoptiles were assessed in the Jondaryan field trial for the first three harvests (4, 6 and 8 weeks after planting). From this data a significant harvest effect and harvest/genotype interaction (Table 3.4b) were evident in this tissue (charts presented in Appendix 3E (Figure 3E.1)).

At 4 weeks after planting (WAP) most coleoptiles (COL) in each genotype had developed lesions and by 6 WAP all coleoptiles were lesioned (Table 3.4a). The mean disease rating of all genotypes except Sunco increased significantly (Figure 3.4) between 4 and 6 WAP, with differences between 6 and 8 WAP not significant. Overall there was no consistent pattern of differences in degree of lesion development between host genotypes. While at 4 WAP Vasco showed significantly higher disease symptoms than Puseas, at 6 WAP symptoms in Vasco were significantly higher than Sunco. All other differences between genotypes at each harvest were not significant. The coleoptile tissue had started to break down and was absent from many plants at 10 WAP and was therefore not collected from this time.

Figure 3.4 Mean disease rating of the coleoptile (4-8 WAP) and the sub-crown internode (4-14.5 WAP) in the Jondaryan trial. * Indicates data for the harvest was included in the analysis and represents means ± 95% CI of error. Unanalysed data = means ± SE.

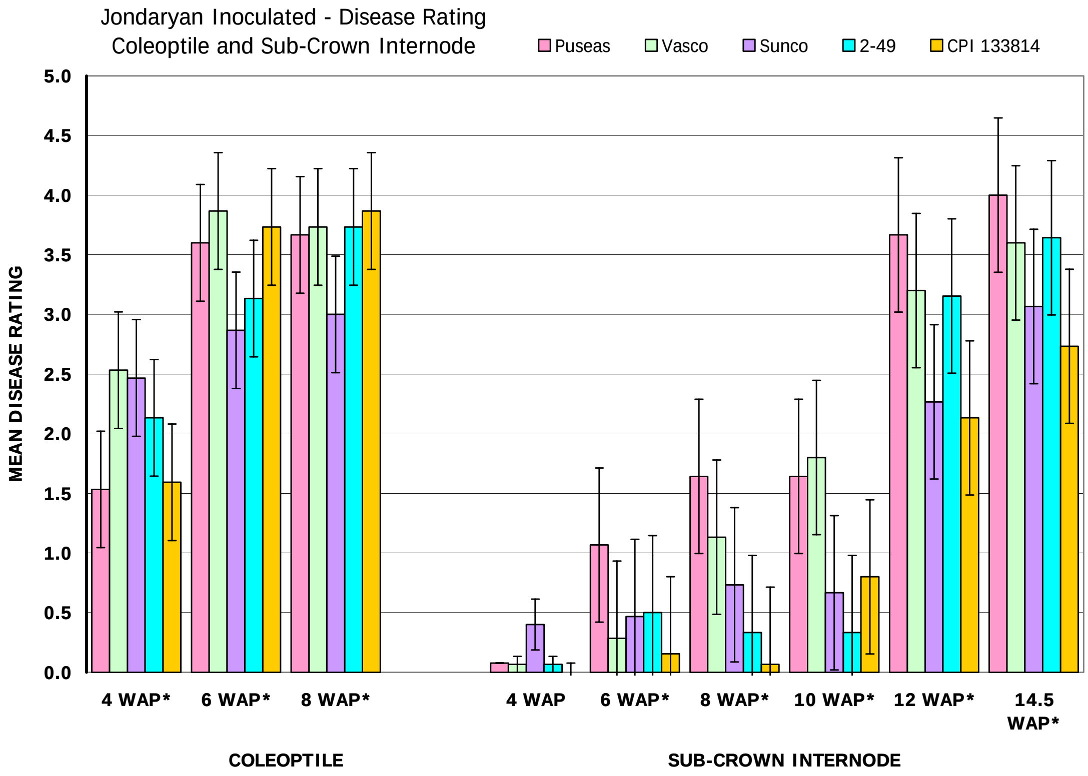


Table 3.4a Number of coleoptiles and sub crown internodes collected at each harvest (bold) with the number of those diseased (below) in the Jondaryan field trial.

PART	Coleoptile			Sub Crown Internode					
HARVEST	4 WAP	6 WAP	8 WAP	4 WAP	6 WAP	8 WAP	10 WAP	12 WAP	14.5 W
Puseas	**15**	**15**	**15**	**13**	**15**	**14**	**14**	**15**	**15**
	14	15	15	1	10	8	10	15	15
Vasco	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**15**
	15	15	15	1	2	8	11	15	15
Sunco	**15**	**15**	**15**	**15**	**15**	**15**	**14**	**15**	**15**
	15	15	15	4	5	3	6	9	14
2-49	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**14**	**14**
	13	15	15	1	4	5	3	12	14
CPI133814	**15**	**15**	**15**	**14**	**13**	**15**	**15**	**15**	**15**
	15	15	15	0	2	1	4	10	13

Table 3.4b Probabilities for each factor and interaction in disease rating data for the coleoptile (4, 6, 8 WAP) and subcrown internode (6, 8, 10, 12, 14.5 WAP) in the Jondaryan trial.

Disease Ratings	**Fixed Term**						
Jondaryan	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Coleoptile	<0.001	0.091		<0.001			
Sub Crown Intern	<0.001	<0.001		0.403			

Sub Crown Internode

Sub crown internode tissues were assessed in the Jondaryan field trial up to the 6th harvest at 14.5 WAP. Limited lesions had developed on the sub crown internodes (SCI) at 4 WAP, and this harvest was not included in the analysis. Only the mean disease rating of Sunco was higher than the other genotypes at this harvest (Figure 3.4). From the analysis the disease rating of the subcrown internode (SCI) had a significant (P<0.001) harvest and genotype effect. The interaction of these factors was not significant (Table 3.4b) (Charts of significant factors presented in Appendix 3E (Figure 3E.1)).

Only slight increases in disease were seen on the SCI at each harvest up to 10 WAP (Figure 3.4) with the number of plants in each genotype with readings >0 still low in the partially resistant genotypes at this time (Table 3.4a). At 12 WAP there was an increase in the mean disease rating of all genotypes (Figure 3.4) which corresponded with an increase in the number of plants infected at this time (Table 3.4a). At this harvest ratings for CPI133814 and Sunco were significantly lower than Puseas. At 14.5 WAP almost all SCI were lesioned and the increase in the mean disease rating seen in all genotypes was not significant. Only CPI 133814 had a mean disease rating significantly lower than Puseas at 14.5 WAP (Table 3.4a, Figure 3.4).

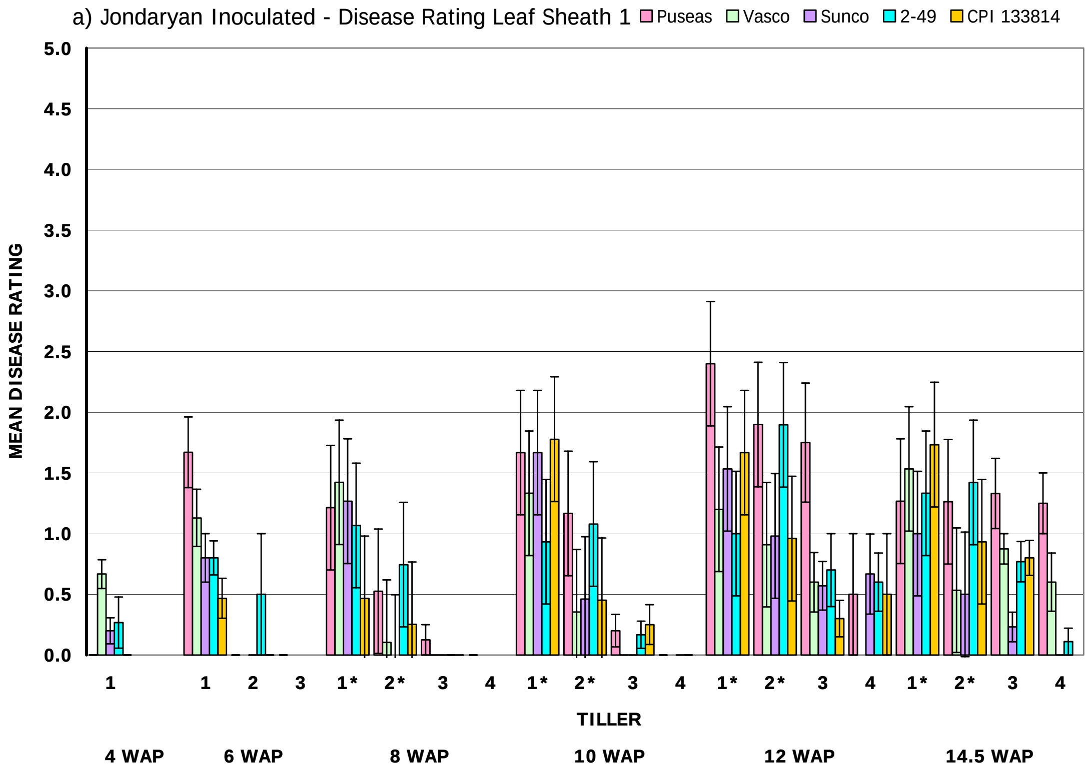
Over all harvests the disease rating for Puseas was significantly higher than for Sunco, CPI133814 and 2-49. Vasco was also significantly higher than CPI133814 (Appendix 3E (Figure 3E.1)).

Leaf Sheath 1

Jondaryan trial

Leaf sheaths were collected in the 1st six harvests up to 14.5 WAP in the Jondaryan trial. Lesions on the 1st leaf sheaths (LS 1) had developed on the primary tiller of 8, 4 and 3 out of 15 Vasco, 2-49 and Sunco plants respectively at 4 WAP (Table 3.5a). Data for the 1st two tillers were analysed over 8, 10, 12 and 14.5 WAP. Harvest, tiller and the tiller/genotype interactions were highly significant (P< 0.001). The genotype effect was also strong (P<0.011) (Table 3.5c). Overall the mean disease rating significantly increased at each harvest up to 12 WAP and dropped between 12 and 14.5 WAP (not significant) (Appendix 3E (Figure 3E.2)). The mean disease

Figure 3.5 Mean disease rating of Leaf Sheath 1 in the a) Jondaryan trial (4-14.5 WAP) and the b) Wellcamp trial (5-11 WAP). *Tillers and/or Harvest included in analysis.


a) Jondaryan Inoculated - Disease Rating Leaf Sheath 1

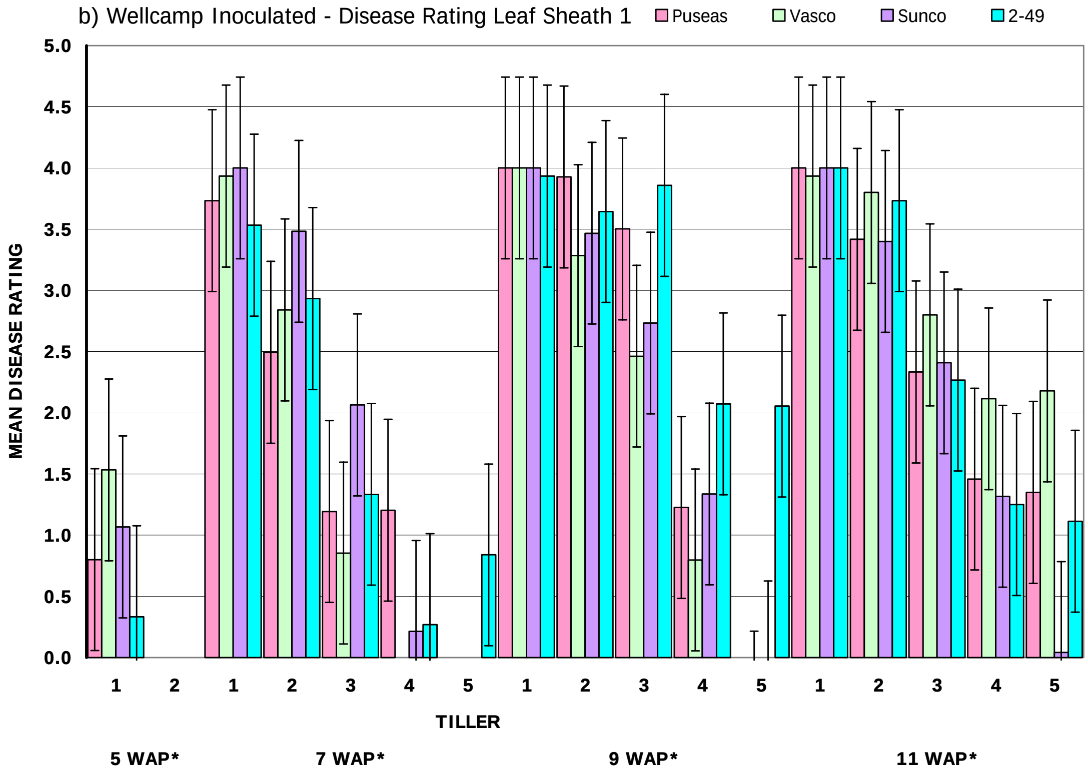

b) Wellcamp Inoculated - Disease Rating Leaf Sheath 1

Table 3.5a Number of expanded Leaf Sheath 1's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	4 WAP	6 WAP			8 WAP				10 WAP				12 WAP				14.5 WAP			
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**15**	**15**	**7**	**3**	**14**	**9**	**8**	**2**	**15**	**12**	**10**	**2**	**15**	**10**	**9**	**2**	**14**	**14**	**9**	**4**
	0	13	0	0	13	4	1	0	13	6	2	0	15	10	8	1	13	14	8	4
Vasco	**15**	**15**			**15**	**5**	**5**		**15**	**11**	**4**		**15**	**9**	**5**		**15**	**10**	**8**	**5**
	8	13			15	0	0		14	4	0		14	8	3		15	6	7	3
Sunco	**15**	**15**	**8**		**15**	**6**	**2**		**15**	**11**	**8**	**3**	**15**	**10**	**7**	**3**	**15**	**14**	**13**	**6**
	3	10	0		12	0	0		14	6	0	0	15	8	4	2	15	7	3	0
2-49	**15**	**15**	**6**		**15**	**11**	**6**	**1**	**15**	**13**	**12**	**7**	**15**	**11**	**9**	**5**	**15**	**14**	**13**	**9**
	4	11	1		11	5	0	0	14	6	2	0	13	11	5	3	15	12	9	1
CPI133814	**15**	**15**	**4**		**15**	**11**	**7**		**14**	**11**	**8**		**15**	**12**	**11**	**2**	**15**	**15**	**15**	
	0	6	0		6	3	0		14	3	1		15	8	4	1	15	14	11	

Table 3.5 b Number of expanded Leaf Sheath 1's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	5 WAP	7 WAP					9 WAP					11 WAP				
TILLER	**1**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**15**	**15**	**10**	**6**	**1**		**15**	**13**	**12**	**6**		**15**	**12**	**12**	**9**	**4**
	8	15	8	4	1		15	13	12	4		15	12	11	8	4
Vasco	**15**	**15**	**14**	**10**			**15**	**14**	**12**	**6**	**1**	**15**	**14**	**15**	**11**	**8**
	11	15	14	6			15	14	11	3	0	15	14	14	9	8
Sunco	**15**	**15**	**12**	**9**	**4**		**15**	**15**	**13**	**11**	**4**	**15**	**15**	**12**	**7**	**5**
	10	15	12	7	2		15	15	12	7	0	15	14	11	5	1
2-49	**15**	**15**	**15**	**15**	**3**	**1**	**15**	**14**	**14**	**14**	**9**	**15**	**14**	**15**	**13**	**9**
	4	15	14	9	1	0	15	14	14	12	7	15	14	14	10	6
CPI133814	**Not collected**															

Table 3.5c Probabilities for each factor and interaction in disease rating data for Leaf Sheath 1 in the Jondaryan (8, 10, 12, 14.5 WAP) and Wellcamp trials (5, 7, 9, 11 WAP).

Disease Ratings	Fixed Term						
Leaf Sheath 1	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	<0.001	0.011	<0.001	0.028	0.04	<0.001	0.167
Wellcamp	<0.001	0.193	<0.001	0.003	<0.001	0.066	0.023

rating of LS1 was significantly higher for the primary tiller than tiller 2 in Vasco, Sunco and CPI133814. Differences were not significant between the two tillers in Puseas and 2-49. In the primary tiller Puseas was significantly higher than only 2-49. However, in the 2nd tiller Puseas was significantly higher than Vasco, Sunco and CPI133814 with no significant differences between Puseas and 2-49 in the 2nd tiller (Appendix 3E (Figure 3E.2)).

Wellcamp trial

In the Wellcamp trial, data for up to five tillers were collected over the 1st four harvests (5-11 WAP). All expanded LS1's were showing symptoms of disease in all genotypes at 7 WAP (Table 3.5a).

Data from all harvests were included in the analysis of LS1 at Wellcamp. There was a significant ($P<0.001$) harvest and tiller effect with a strong harvest/genotype ($P<0.003$) and harvest/tiller ($P<0.001$) interaction (Table 3.5c). Charts of these interactions are presented in Appendix 3E (Figure 3E.2).

Differences between genotypes in each tiller at each harvest were mostly not significant for LS 1 in this trial (Figure 3.5b). Generally the mean disease rating increased in each tiller between 5 and 7, and between 7 and 9 WAP. Also tillers 3, 4 and 5 were usually significantly lower than the primary tiller with the 2nd tiller rated in between. A couple of significant differences were seen between genotypes in the 5th tiller at 9 and 11 WAP, however they involved uneven plant numbers and may be based more on incidence than severity (Table 3.5b).

Leaf Sheath 2

Jondaryan trial

The 2nd LS had emerged at 4 WAP and was collected up till the 6th harvest at 14.5 WAP. Lesions had begun to develop on the 2nd LS of some plants in all genotypes except 2-49 at 6 WAP (Table 3.6b; Figure 3.6a). Differences within each genotype between the primary and 2nd tiller were not significant except in CPI133814 at 14.5 WAP (Figure 3.6a).

The 1st two tillers of LS2 were analysed over the three harvests (10, 12 and 14.5 WAP). The three main factors harvest, genotype and tiller were all significant for LS2 ($P<0.001$) (Table 3.6c). The two way interactions harvest/genotype ($P=0.012$) and genotype/tiller ($P=0.011$) were also quite strong. Charts of factors and interactions for LS2 are presented in Appendix 3E (Figure 3E.3). The mean disease rating of LS2 significantly increased overall from 10 to 12 WAP. With all harvests combined Puseas was significantly higher than all other genotypes (Appendix 3E (Figure 3E.3)).

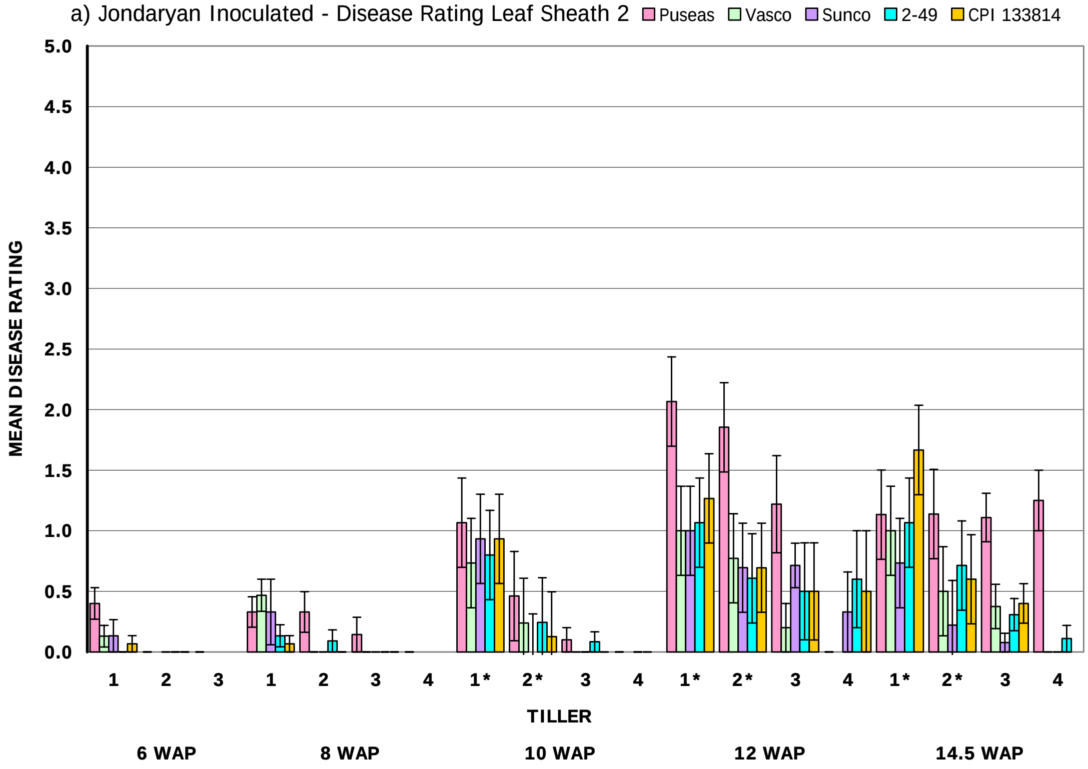
The main differences between genotypes were seen at 12 WAP where the mean disease rating of Puseas was significantly higher than all other genotypes in the primary and 2nd tiller. At 14.5 WAP Puseas was significantly higher than Sunco in the 2nd tiller and significantly higher than all genotypes in the 3rd (Figure 3.6a).

Wellcamp trial

The 2nd LS had expanded at 5 WAP and was collected over four harvests till 11 WAP. Data from all of these harvests were included in the analysis. At 5 WAP only a few plants of Puseas, Vasco and Sunco had developed lesions (Table 3.6b) while most were lesioned by 7 WAP. Differences between genotypes in each tiller at any one harvest were not significant (Figure 3.6b).

From the analysis, harvest ($P< 0.001$), genotype ($P=0.006$) and tiller ($P< 0.001$) were each highly significant (Table 3.6c). Overall the mean disease rating increased sharply between 5 and 7 WAP coinciding with the development of tillers (Table 3.6b) and continued to increase less significantly up to 11 WAP. The significant genotype effect is more difficult to interpret with overall means only ranging from 1.367 for Vasco to 1.252 for 2-49 (Appendix 3E (Figure 3E.3)). Error values are not available at this level as the number of plants (n) is very different for each value. The overall disease rating of LS2 for each tiller was quite different with the primary tiller averaging 2.77, the 2nd tiller 1.73, the 3rd tiller 0.79 and the 4th and 5th tillers 0.11 and 0.15 respectively (Appendix 3E (Figure 3E.3)).

Figure 3.6 Mean disease rating of Leaf Sheath 2 in the a) Jondaryan trial (6-14.5 WAP) and the b) Wellcamp trial (5-11 WAP). *Tillers and/or Harvest included in analysis.



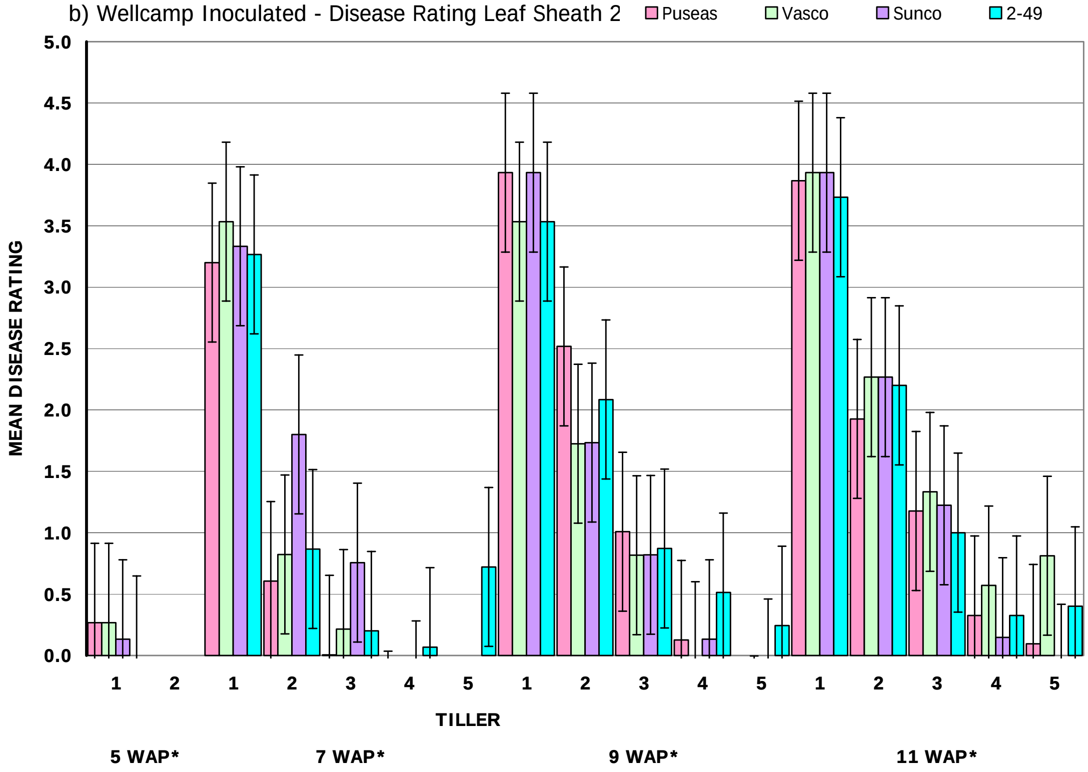


Table 3.6a Number of expanded Leaf Sheath 2's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**4 WAP**	**6 WAP**			**8 WAP**				**10 WAP**				**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**15**	**15**	**7**	**3**	**15**	**9**	**8**	**2**	**15**	**12**	**10**	**2**	**15**	**10**	**9**	**2**	**15**	**14**	**9**	**4**
	0	6	0	0	5	3	1	0	10	4	1	0	15	10	7	0	15	14	8	4
Vasco	**15**	**15**			**15**	**5**	**5**		**15**	**11**	**4**		**15**	**9**	**5**		**15**	**10**	**8**	**5**
	0	2			7	0	0		11	3	0		15	6	1		15	5	3	0
Sunco	**15**	**15**	**8**		**15**	**6**	**2**		**15**	**11**	**8**	**3**	**15**	**10**	**7**	**3**	**15**	**14**	**13**	**6**
	0	1	0		2	0	0		11	0	0	0	13	7	5	1	11	3	1	0
2-49	**15**	**15**	**6**		**15**	**11**	**6**	**1**	**15**	**13**	**12**	**7**	**15**	**12**	**10**	**5**	**15**	**14**	**13**	**9**
	0	0	0		2	1	0	0	12	2	1	0	14	7	2	2	15	9	4	1
CPI133814	**15**	**15**	**4**		**15**	**11**	**7**		**15**	**11**	**8**		**15**	**12**	**11**	**2**	**15**	**15**	**15**	
	0	1	0		1	0	0		10	1	0		14	6	3	1	15	9	5	

Table 3.6 b Number of expanded Leaf Sheath 2's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**5 WAP**	**7 WAP**					**9 WAP**					**11 WAP**				
TILLER	**1**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**15**	**15**	**10**	**5**	**1**		**15**	**13**	**12**	**6**		**15**	**12**	**12**	**9**	**4**
	4	13	4	1	0		15	12	10	1		15	11	7	3	1
Vasco	**15**	**15**	**14**	**10**			**15**	**14**	**12**	**6**	**1**	**15**	**15**	**15**	**11**	**8**
	4	14	10	2			15	11	7	1	0	15	15	12	6	5
Sunco	**15**	**15**	**12**	**9**	**4**		**15**	**15**	**13**	**11**	**4**	**15**	**15**	**13**	**7**	**5**
	2	15	9	4	0		15	13	8	2	0	15	13	9	2	0
2-49	**15**	**15**	**15**	**15**	**3**	**1**	**15**	**14**	**14**	**14**	**9**	**15**	**15**	**15**	**13**	**9**
	0	14	11	3	0	0	15	13	11	5	3	15	14	10	5	4
CPI133814	**Not collected**															

Table 3.6c Probabilities for each factor and interaction in disease rating data for Leaf Sheath 2 in the Jondaryan (10, 12, 14.5 WAP) and Wellcamp (5, 7, 9, 11 WAP) trials.

Disease Ratings Leaf Sheath 2	**Fixed Term**						
	Harvest	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	<0.001	<0.001	<0.001	0.012	0.062	0.011	0.439
Wellcamp	<0.001	0.006	<0.001	0.442	0.079	0.734	0.477

Leaf Sheath 3

Jondaryan trial

Leaf sheath 3 had expanded at 6 WAP and was collected over five harvests until 14.5 WAP. Disease symptom development was quite slow in this tissue with an incidence of > 50% not reached in the primary tiller until 12 WAP (Table 3.7a). A limited number of lesions were recorded on the secondary tillers LS3's.

Puseas was generally higher than the other genotypes in all tillers at each harvest (Figure 3.7a) and analysis of the primary and 2nd tillers over harvests 5 and 6 (12 and 14.5 WAP) showed a significant genotype effect ($P<0.001$) (Table 3.7c). There was also a significant tiller effect ($P<0.001$) with the primary tiller averaging 0.99 over harvests 5 and 6 and the 2nd tiller 0.47 (Appendix 3E (Figure 3E.4)).

Wellcamp trial

The 3rd LS was collected from 5 to 11 WAP in the Wellcamp trial. Most plants of each genotype had developed lesions by 7 WAP on the primary tiller (Table 3.7b) and > 50 % of LS3's of all genotypes had disease symptoms on the 2nd tiller by 11 WAP. No significant differences between genotypes were seen at each harvest in any tiller (Figure 3.7b).

LS 3 was analysed over harvest 2, 3 and 4 (7, 9 and 11 WAP) and only a tiller effect was significant ($P<0.001$)). The primary tiller averaged a mean disease rating of 2.67 with the remaining tillers below 0.7 (Appendix 3E (Figure 3E.4)).

Leaf Sheath 4

Jondaryan trial

The 4th LS was expanded at 6 WAP and data was collected in the Jondaryan trial up to 14.5 WAP. Disease started to establish in this plant part at 12 WAP in the primary tiller. At 14.5 WAP less than half the 2-49, Sunco and CPI133814 plants sampled had developed lesions (Table 3.8a).

Puseas was significantly higher than all other genotypes in the primary tiller at 12 WAP and higher than 2-49 at 14.5 WAP (Figure 3.8a). Only the primary tiller was included in the analysis over 12 and 14.5 WAP and the genotype effect was highly significant ($P < 0.001$) (Table 3.8c). Overall Puseas LS3 averaged a mean disease rating of 1.3 with the other genotypes between 0.4 and 0.6 (Appendix 3E (Figure 3E. 5)).

Wellcamp trial

Leaf sheath 4 was collected from 4 to 11 WAP in the Wellcamp trial. There was no significant difference between genotypes in any tillers at each harvest (Figure 3.8b). The number of diseased LS 4's was also very similar between genotypes at each harvest (Table 3.8b).

Data over all three harvests were included in the analysis and a highly significant harvest and tiller effect ($P<0.001$) was present (Table 3.8c). A jump in the mean disease rating of LS 4 occurred between 9 and 11 WAP. This was most obvious in Puseas, Vasco and Sunco primary tiller with a small increase in the 2nd tiller of all genotypes at 11 WAP (Figure 3.8b). Overall the primary tiller averaged 1.24 and the remaining tillers below 0.21 (Appendix 3E (Figure 3E.5)).

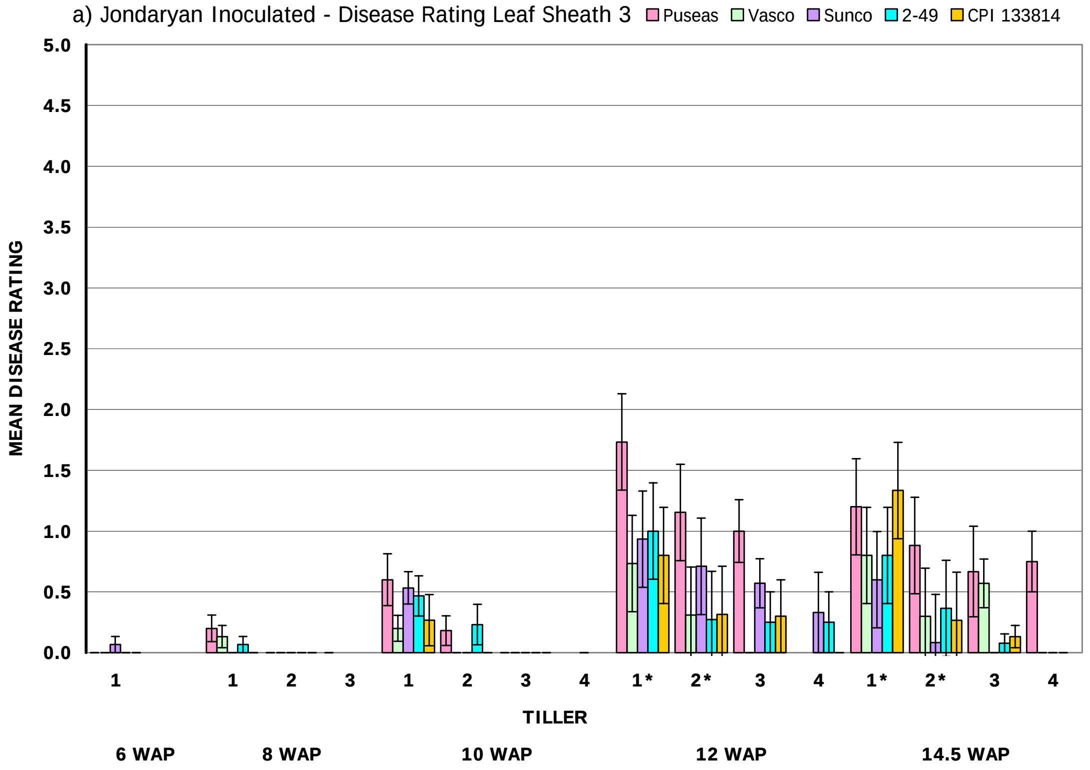
Leaf Sheath 5

Jondaryan trial

The 5th LS had expanded on the primary tiller of some plants at 8 WAP and was collected until 14.5 WAP. No disease was recorded at 8 WAP and by 14.5 WAP 11 Puseas, 9 Vasco, 3 CPI133814 and only 1 2-49 and Sunco LS5 had developed lesions on the primary tiller (Table 3.9a). At 14.5 WAP the disease rating on Puseas was significantly higher than 2-49 and Sunco for the primary tiller (Figure 3.9a) and only Puseas had developed lesions on LS5 of the 2nd and 3rd tillers (Table 3.9a; Figure 3.9a).

LS 5 was analysed over 12 and 14.5 WAP in the primary tiller only. Genotype was highly significant ($P<0.001$) (Table 3.9c) with the mean disease rating of Puseas significantly higher than all the other genotypes (Appendix 3E (Figure 3E.5)).

Figure 3.7 Mean disease rating of Leaf Sheath 3 in the a) Jondaryan trial (6-14.5 WAP) and the b) Wellcamp trial (5-11 WAP). *Tillers and/or Harvest included in analysis.



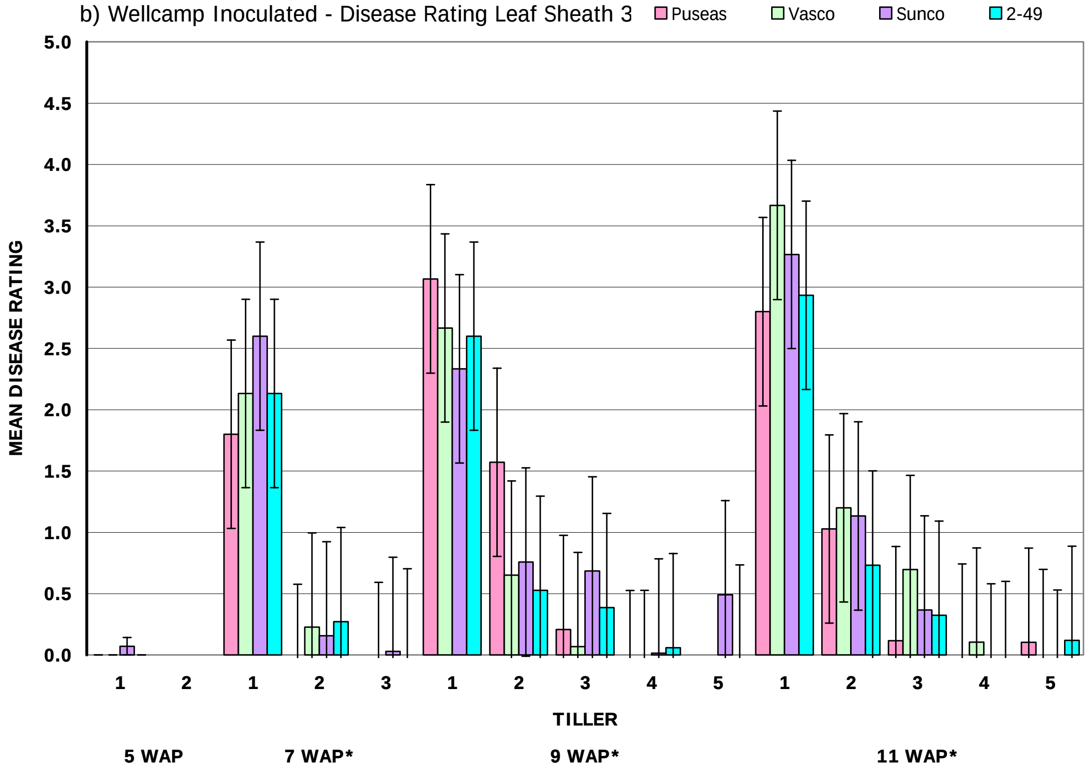


Table 3.7a Number of expanded Leaf Sheath 3's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**6 WAP**	**8 WAP**			**10 WAP**				**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**15**	**15**	**7**	**3**	**15**	**11**	**7**		**15**	**10**	**6**	**2**	**15**	**14**	**9**	**4**
	0	3	0	0	7	2	0		14	6	5	0	15	10	3	3
Vasco	**15**	**15**	**5**		**15**	**11**	**3**		**15**	**9**	**5**		**15**	**10**	**7**	**5**
	0	2	0		3	0	0		11	3	0		11	3	4	0
Sunco	**15**	**15**	**5**		**15**	**10**	**4**	**2**	**15**	**10**	**7**	**3**	**15**	**14**	**13**	**6**
	1	0	0		8	0	0	0	12	7	4	1	9	1	0	0
2-49	**15**	**15**	**7**	**1**	**15**	**13**	**11**	**1**	**15**	**12**	**8**	**4**	**15**	**13**	**13**	**9**
	0	1	0	0	6	2	0	0	12	2	1	1	11	5	1	0
CPI133814	**12**	**15**	**6**		**15**	**10**	**6**		**15**	**11**	**11**	**2**	**15**	**15**	**15**	
	0	0	0		2	0	0		10	1	1	0	12	3	2	

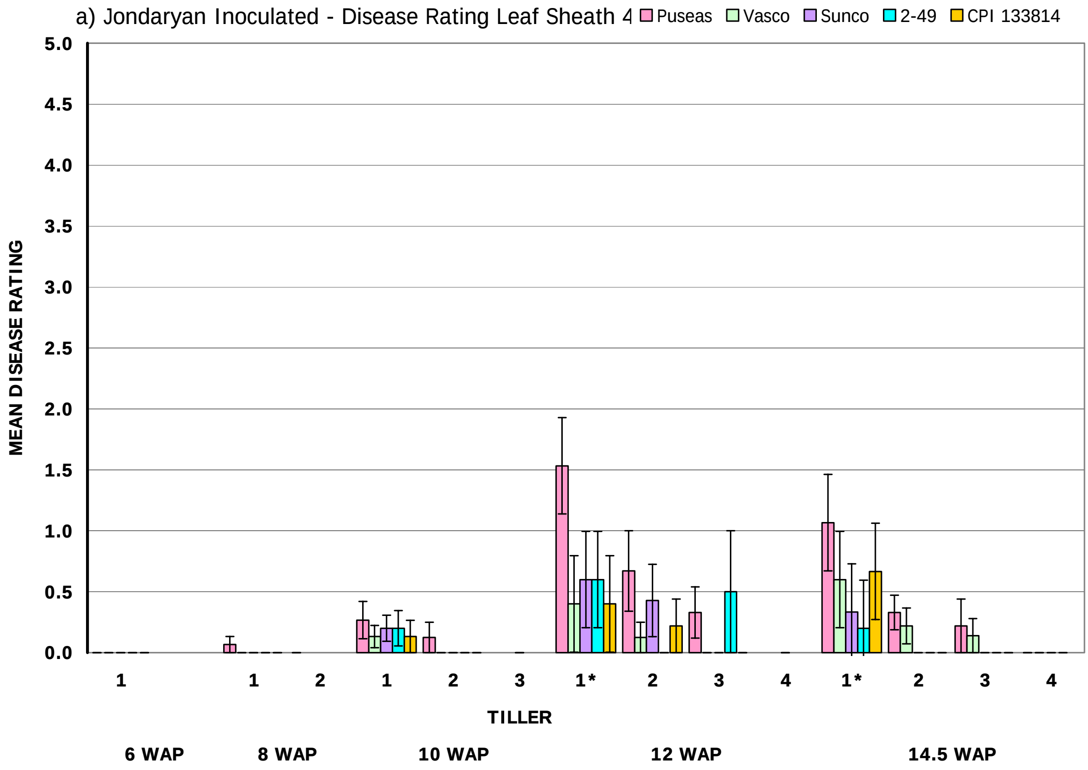
Table 3.7 b Number of expanded Leaf Sheath 3's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**5 WAP**	**7 WAP**			**9 WAP**					**11 WAP**				
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**6**	**15**	**4**	**1**	**15**	**13**	**11**	**2**		**15**	**12**	**8**	**5**	**3**
	0	12	1	0	15	8	2	0		15	6	2	0	0
Vasco	**11**	**15**	**9**	**1**	**15**	**14**	**10**	**4**		**15**	**15**	**15**	**9**	**5**
	0	13	2	0	14	7	2	0		15	10	5	2	1
Sunco	**14**	**15**	**8**	**5**	**15**	**14**	**11**	**10**		**15**	**15**	**12**	**6**	**2**
	1	12	2	1	15	8	4	0		15	12	5	0	0
2-49	**10**	**15**	**13**	**4**	**15**	**14**	**14**	**11**	**7**	**15**	**15**	**13**	**9**	**7**
	0	12	2	0	14	8	6	2	1	15	10	4	0	3
CPI133814	**Not collected**													

Table 3.7c Probabilities for each factor and interaction in disease rating data for Leaf Sheath 3 in the Jondaryan (12, 14.5 WAP) and Wellcamp (7, 9, 11 WAP) trials.

Disease Ratings	**Fixed Term**						
Leaf Sheath 3	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	0.114	<0.001	<0.001	0.163	0.561	0.304	0.212
Wellcamp	0.587	0.048	<0.001	0.241	0.236	0.464	0.77

Figure 3.8 Mean disease rating of Leaf Sheath 4 in the a) Jondaryan trial (6-14.5 WAP) and the b) Wellcamp trial (7-11 WAP). *Tillers and/or Harvest included in analysis.



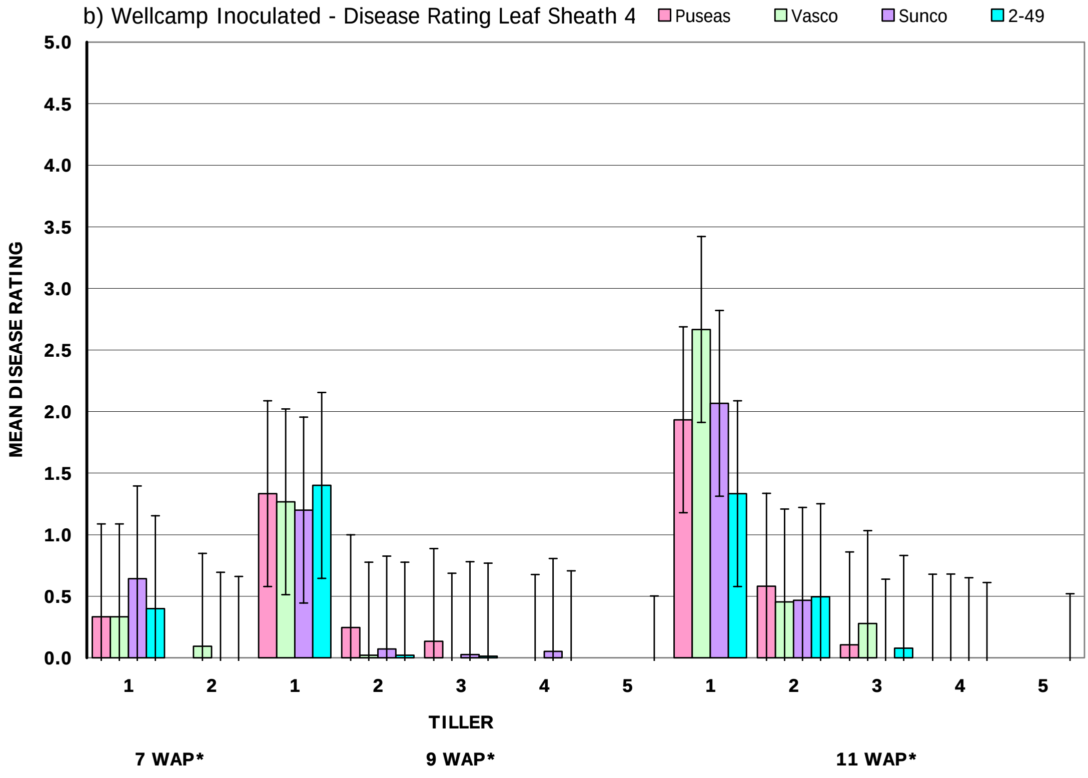


Table 3.8a Number of expanded Leaf Sheath 4’s assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**6 WAP**	**8 WAP**		**10 WAP**			**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**10**	**15**	**2**	**15**	**8**		**15**	**6**	**6**		**15**	**12**	**9**	**2**
	0	1	0	3	1		14	3	2		14	4	1	0
Vasco	**6**	**15**		**15**	**5**		**15**	**8**	**3**		**15**	**9**	**7**	**3**
	0	0		2	0		6	1	0		8	2	1	0
Sunco	**13**	**14**		**15**	**5**	**2**	**15**	**7**	**4**	**2**	**15**	**14**	**11**	**4**
	0	0		3	0	0	9	2	0	0	5	0	0	0
2-49	**9**	**15**	**1**	**15**	**11**		**15**	**8**	**4**	**1**	**15**	**13**	**13**	**7**
	0	0	0	2	0		8	1	1	0	3	0	0	0
CPI133814		**13**		**15**	**6**	**1**	**15**	**9**	**4**		**15**	**14**	**7**	
		0		1	0	0	4	1	0		8	0	0	

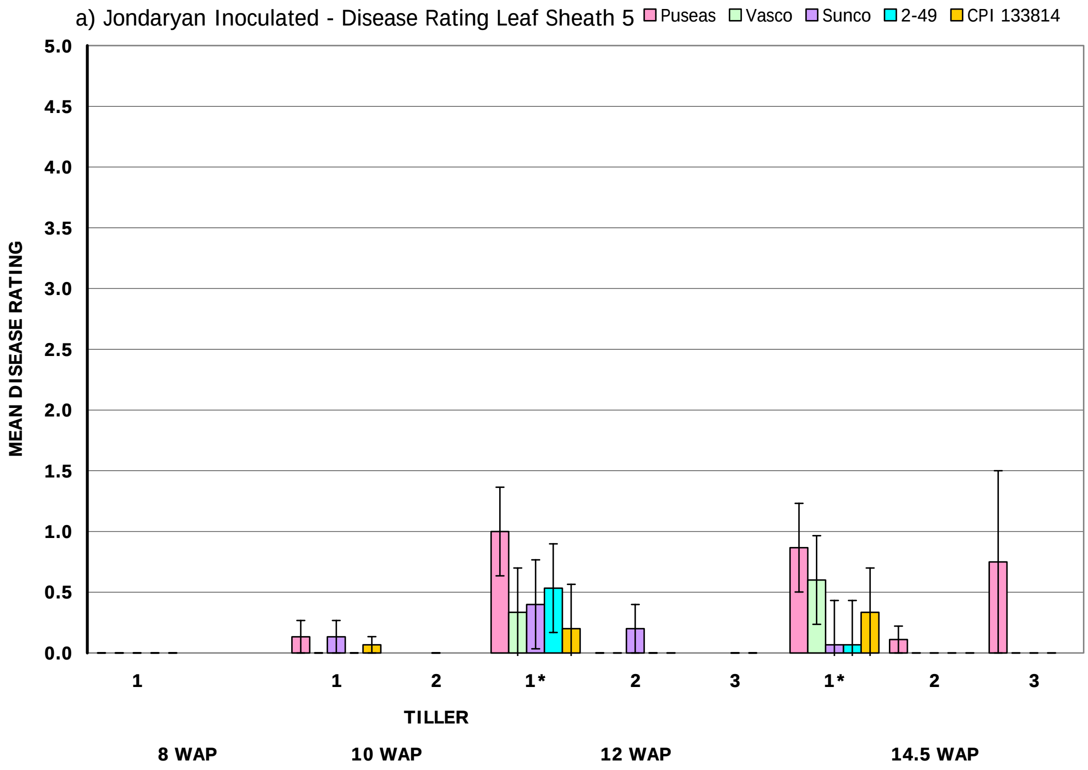
Table 3.8 b Number of expanded Leaf Sheath 4’s assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**7 WAP**		**9 WAP**					**11 WAP**				
TILLER	**1**	**2**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**15**		**15**	**10**	**2**			**15**	**10**	**5**	**1**	
	4		14	2	0			13	2	1	0	
Vasco	**15**	**1**	**15**	**11**	**8**	**1**		**15**	**14**	**11**	**6**	
	5	0	11	1	0	0		15	6	2	0	
Sunco	**14**	**1**	**15**	**13**	**9**	**1**		**15**	**15**	**8**	**3**	
	9	0	13	1	0	0		15	6	0	0	
2-49	**15**	**1**	**15**	**13**	**12**	**5**	**1**	**15**	**14**	**11**	**6**	**5**
	6	0	13	0	0	0	0	12	7	1	0	0
CPI133814	**Not collected**											

Table 3.8c Probabilities for each factor and interaction in disease rating data for Leaf Sheath 4 in the Jondaryan (12, 14.5 WAP) and Wellcamp (7, 9, 11 WAP) trials.

Disease Ratings	**Fixed Term**						
Leaf Sheath 4	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	0.286	<0.001		0.197			
Wellcamp	<0.001	0.057	<0.001	0.413	0.022	0.564	0.364

Figure 3.9 Mean disease rating of Leaf Sheath 5 in the a) Jondaryan trial (8-14.5 WAP) and the b) Wellcamp trial (7-11 WAP). *Tillers and/or Harvest included in analysis.


a) Jondaryan Inoculated - Disease Rating Leaf Sheath 5

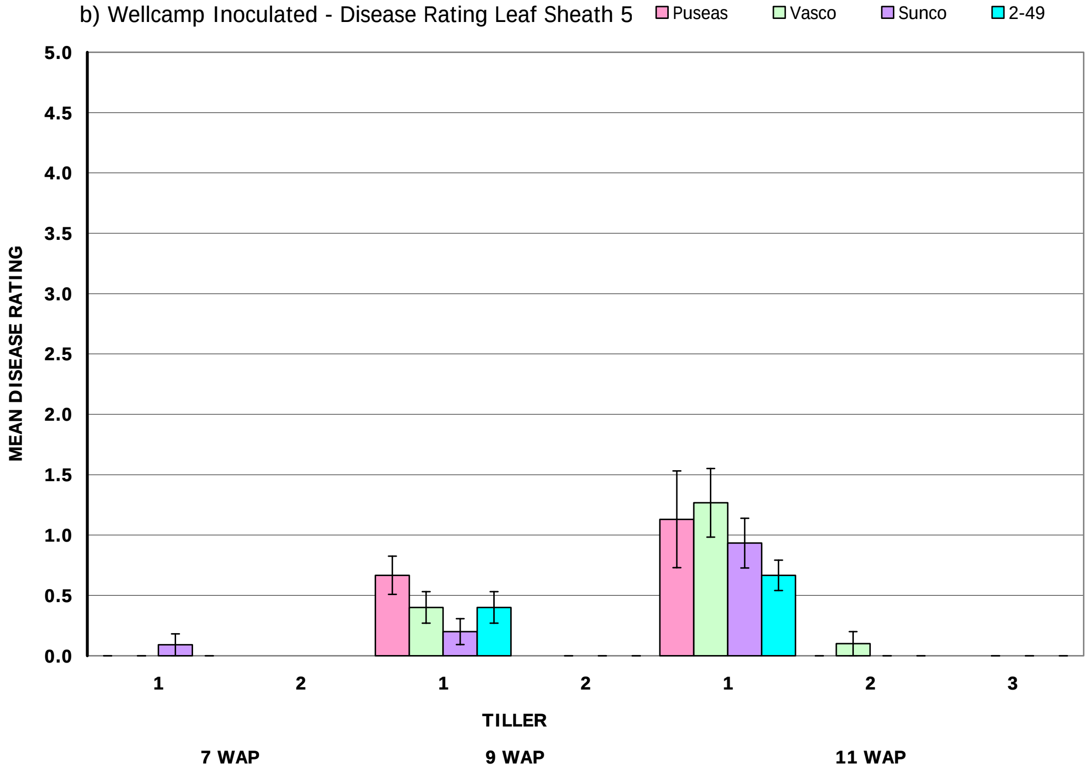

b) Wellcamp Inoculated - Disease Rating Leaf Sheath 5

Table 3.9a Number of expanded Leaf Sheath 5’s assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**8 WAP**	**10 WAP**		**12 WAP**			**14.5 WAP**		
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**1**	**2**	**3**
Puseas	**13**	**15**		**15**	**4**		**15**	**9**	**4**
	0	2		9	0		11	1	1
Vasco	**10**	**15**		**15**	**4**		**15**	**7**	**5**
	0	0		5	0		9	0	0
Sunco	**12**	**15**	**3**	**15**	**5**	**2**	**15**	**14**	**8**
	0	2	0	4	1	0	1	0	0
2-49	**13**	**15**		**15**	**5**	**2**	**15**	**13**	**11**
	0	0		4	0	0	1	0	0
CPI133814	**5**	**15**	**1**	**15**	**3**		**15**	**8**	**1**
	0	1	0	2	0		3	0	0

Table 3.9 b Number of expanded Leaf Sheath 5’s assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**7 WAP**	**9 WAP**			**11 WAP**		
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**
Puseas	**7**	**15**	**1**		**15**	**4**	**1**
	0	9	0		8	0	0
Vasco	**11**	**15**	**4**		**15**	**10**	**4**
	0	6	0		11	1	0
Sunco	**11**	**15**	**5**		**15**	**14**	**4**
	1	3	0		10	0	0
2-49	**12**	**15**	**8**	**2**	**15**	**12**	**6**
	0	6	0	0	10	0	0
CPI133814	**Not collected**						

Table 3.9c Probabilities for each factor and interaction in disease rating data for Leaf Sheath 5 in the Jondaryan (12, 14.5 WAP) trial.

Disease Ratings Leaf Sheath 5	**Fixed Term**						
	Harvest	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	0.356	<0.001		0.224			
Wellcamp	not analysed						

Table 3.9 d Number of expanded Leaf Sheath 6 and 7's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

Plant Part	**Leaf Sheath 6**						**Leaf Sheath 7**		
HARVEST	**10 WAP**	**12 WAP**		**14.5 WAP**			**12 WAP**	**14.5 WAP**	
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**1**	**1**	**2**
Puseas	**12**	**13**		**15**	**5**	**2**	**11**	**14**	**1**
	1	5		6	1	1	1	0	0
Vasco	**15**	**15**		**15**	**5**	**2**	**14**	**15**	**1**
	0	1		4	0	0	0	0	0
Sunco	**13**	**15**	**2**	**15**	**8**	**2**	**14**	**15**	**1**
	1	2	0	0	0	0	0	0	0
2-49	**10**	**15**	**2**	**15**	**8**	**4**	**14**	**15**	**5**
	0	2	0	0	0	0	1	0	0
CPI133814	**5**	**15**		**15**	**2**		**11**	**15**	**1**
	0	1		2	0		0	0	0

Table 3.9 e Number of expanded Leaf Sheath 6, 7 and 8's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

Plant Part	**Leaf Sheath 6**			**Leaf Sheath 7**		**Leaf Sheath 8**
HARVEST	**9 WAP**	**11 WAP**		**9 WAP**	**11 WAP**	**11 WAP**
TILLER	**1**	**1**	**2**	**1**	**1**	**1**
Puseas	**12**	**12**		**3**	**7**	**3**
	2	1		0	0	0
Vasco	**12**	**15**	**4**	**5**	**15**	**13**
	2	9	0	0	0	0
Sunco	**15**	**15**	**6**	**6**	**15**	**9**
	0	5	0	0	0	0
2-49	**14**	**15**	**6**	**8**	**15**	**10**
	0	3	0	0	0	0
CPI133814	**Not collected**			**Not collected**		

Wellcamp trial

Leaf sheath 5 was collected in the Wellcamp field trial over three harvests from 7 to 11 WAP. Only 1 Sunco LS 5 was diseased at 7 WAP and approximately 10 out of 15 primary tiller LS5's were lesioned in all genotypes at 11 WAP (Table 3.9b).

At 9 WAP Puseas was significantly higher than Sunco and at 11 WAP Vasco was significantly higher than 2-49 (Figure 3.9b). Data for LS5 was not analysed in the Wellcamp trial.

Leaf Sheaths 6, 7 and 8

Jondaryan trial

Leaf sheaths 6 and 7 were collected in the Jondaryan trial up to 14.5 WAP. Limited plants had developed lesions on these inner LS's (Table 3.9d) and they were not included in the analysis.

Wellcamp trial

Leaf sheaths 6, 7 and 8 were collected at 9 and 11 WAP in the Wellcamp trial and they also had limited symptoms of disease (Table 3.9e). Data for these LS's were not analysed.

Internode 1

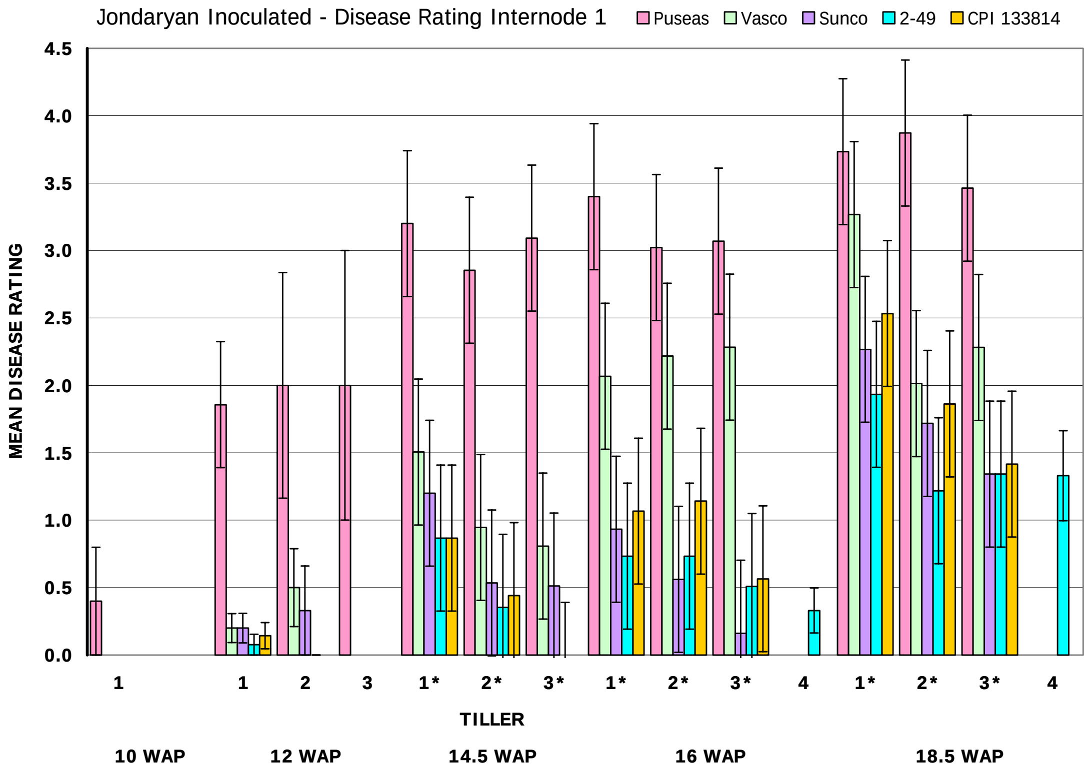
Jondaryan trial

The 1st internode (I1) had begun to expand in Puseas at 10 WAP and was collected over the five harvests to maturity at 18.5 WAP (Table 3.10a). Incidence of disease was highest in Puseas in all tillers and all harvests except at the final harvest (18.5 WAP) where most expanded 1st internodes showed symptoms of disease in all genotypes (Table 3.10a).

Generally the mean disease rating increased at each harvest and differences between tillers within each genotype were not significant (Figure 3.10a). The mean disease rating of Puseas I1 was significantly higher than Sunco, 2-49 and CPI133814 at all harvests in all tillers.

Data for I1 was analysed for the 1st three tillers at 14.5, 16 and 18.5 WAP in the Jondaryan trial. A highly significant genotype ($P<0.001$) effect was not unexpected (Table 3.10c) with the overall mean disease rating of Puseas at 3.3, Vasco approaching a mean of 2.0 and the other genotypes around 1.0 (Appendix 3E (Figure 3E.6)).

Figure 3.10 Mean disease rating of Internode 1 in the a) Jondaryan trial (10-18.5 WAP) and the b) Wellcamp trial (13-22 WAP). *Tillers and/or Harvest included in analysis.



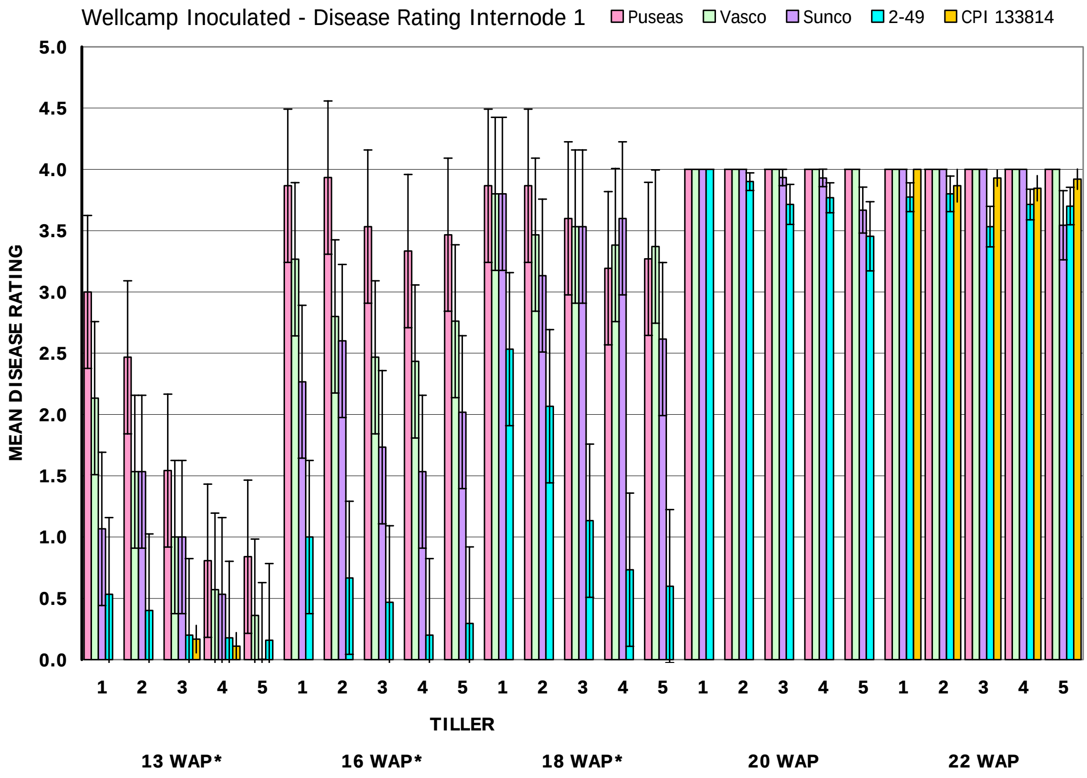


Table 3.10a Number of expanded Internode 1's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**10 WAP**	**12 WAP**			**14.5 WAP**				**16 WAP**				**18.5 WAP**			
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**9**	**14**	**5**	**3**	**15**	**12**	**7**	**3**	**15**	**12**	**10**		**15**	**13**	**9**	**1**
	0	10	4	3	15	12	7	2	15	12	10		15	13	9	0
Vasco		**15**	**4**		**14**	**7**	**6**		**15**	**12**	**6**		**15**	**12**	**8**	
		3	2		13	7	5		15	12	6		15	12	8	
Sunco		**15**	**3**		**15**	**13**	**9**		**15**	**10**	**5**		**15**	**14**	**9**	
		3	1		13	7	4		14	6	1		15	14	8	
2-49		**12**	**3**		**15**	**13**	**8**		**15**	**15**	**12**	**9**	**15**	**14**	**11**	**3**
		1	0		13	5	0		9	10	7	3	15	12	10	3
CPI133814		**14**			**15**	**9**			**15**	**14**	**10**		**15**	**14**	**13**	
		2			11	4			15	12	6		14	12	10	

Table 3.10 b Number of expanded Internode 1's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**11 WAP**			**13 WAP**					**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**10**	**7**	**4**	**15**	**15**	**14**	**10**	**6**	**15**	**15**	**15**	**15**	**15**	**15**	**15**	**15**	**14**	**10**	**15**	**15**	**15**	**14**	**11**	**15**	**15**	**15**	**10**	**8**
	4	1	0	14	14	11	4	3	15	15	15	15	15	15	15	15	14	10	15	15	15	14	11	15	15	15	10	8
Vasco	**14**	**9**	**6**	**15**	**15**	**15**	**12**	**10**	**15**	**15**	**15**	**14**	**10**	**15**	**15**	**15**	**13**	**10**	**15**	**15**	**15**	**10**	**5**	**15**	**15**	**15**	**11**	**8**
	2	2	1	14	11	8	5	4	15	15	13	13	10	15	15	15	12	10	15	15	15	10	5	15	15	15	11	8
Sunco	**7**	**3**	**1**	**15**	**15**	**15**	**15**	**11**	**15**	**15**	**15**	**13**	**13**	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**14**	**12**	**15**	**15**	**15**	**14**	**11**
	3	0	0	11	11	11	6	2	14	14	14	14	10	15	15	15	15	14	15	15	15	14	12	15	15	15	14	11
2-49	**9**	**2**	**1**	**15**	**15**	**15**	**14**	**11**	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**15**	**12**	**14**	**14**	**14**	**13**	**11**	**15**	**15**	**15**	**14**	**10**
	0	0	0	8	6	3	2	1	11	7	7	3	3	15	15	11	10	8	14	14	14	13	11	15	15	15	14	10
CPI133814				**14**	**13**	**12**	**9**	**3**																**15**	**15**	**15**	**13**	**12**
				0	0	2	0	1																15	15	15	13	12

Table 3.10c Probabilities for each factor and interaction in disease rating data for Internode 1 in the Jondaryan (14.5, 16, 18.5 WAP) and Wellcamp (13, 16, 18 WAP) trials.

Disease Ratings Internode 1	**Fixed Term**						
	Harvest	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	<0.001	<0.001	<0.001	0.294	0.003	0.117	0.042
Wellcamp	<0.001	<0.001	<0.001	0.01	0.005	0.317	<0.001

Harvest and tiller were highly significant ($P<0.001$) but there was also a significant harvest/tiller interaction ($P=0.003$) (Table 3.10c). This interaction was mainly explained by very similar disease ratings of the primary tiller at 14.5 and 16 WAP with a sharp increase in disease at 18.5 WAP. The mean disease rating of the 2nd and 3rd tiller increased more gradually over these harvests (Appendix 3E (Figure 3E.6)).

Wellcamp trial

I1 had begun to expand in Puseas at 9 WAP and was collected in the Wellcamp trial up to maturity at 22 WAP. Data for CPI133814 was only collected at 13 and 22 WAP (Table 3.10b). The number of plants with disease symptoms on I1 was lowest in 2-49 at all harvests up to 18 WAP. At 20 and 22 WAP incidence was 100 % in all tillers (Table 3.10b). At these last two harvests the mean disease rating of I1 had reached a maximum of 4 in Puseas and Vasco and was between 3.5 and 4 in 2-49, Sunco and CPI133814 (22 WAP only) (Figure 3.10b).

The mean disease rating increased at each harvest in all genotypes between 13 and 18 WAP (Figure 3.10b). 2-49 was significantly lower than Puseas in all tillers at 13 WAP, significantly lower than Puseas and Vasco in all tillers at 16 WAP and significantly lower than Puseas, Vasco and Sunco at 18 WAP in all tillers except the 2nd (Figure 3.10b). The mean disease rating of Sunco was significantly lower than Puseas in all tillers at 16 WAP, but not significantly different from Puseas in any tillers 2 weeks later (18 WAP).

Disease rating data for I1 was analysed for 5 tillers over the 3 harvests 13, 16 and 18 WAP. All factors were highly significant ($P<0.001$) as was the harvest/ genotype/tiller interaction (Table 3.10c). This interaction is due to the differential development of disease in each genotype and the differences expressed between tillers. Line charts of this interaction are presented in Appendix 3E (Figure 3E.6 and 3E.7). Generally in Puseas, Vasco and 2-49 the primary tiller had the greatest disease followed in order by the 2nd, 3rd and 4th and 5th tillers In Sunco differences between tillers were not significant. In Puseas and Vasco the differences between tillers were significant at 13 WAP but as the tissues approached maximum disease in all tillers the disease ratings were not significantly different at 16 and 18 WAP. In 2-49 on the other hand differences between tillers were not significant at 13 WAP as infection was initiated, became larger at 16 WAP and were highly significant at 18 WAP (Figure 3.10b, Appendix 3E (Figures 3E.6 and 3E.7)).

Internode 2

Jondaryan trial

Internode 2 (I2) had expanded at 12 WAP and was collected in the Jondaryan trial over four harvests till 18.5 WAP. Disease symptoms were recorded on only 3 Puseas plants at 12 WAP (Table 3.11a). At 18 WAP disease incidence of the primary tiller out of 15 plants sampled was 13 in Puseas, 9 in Vasco, 4 in Sunco, 3 in 2-49 and 7 in CPI133814.

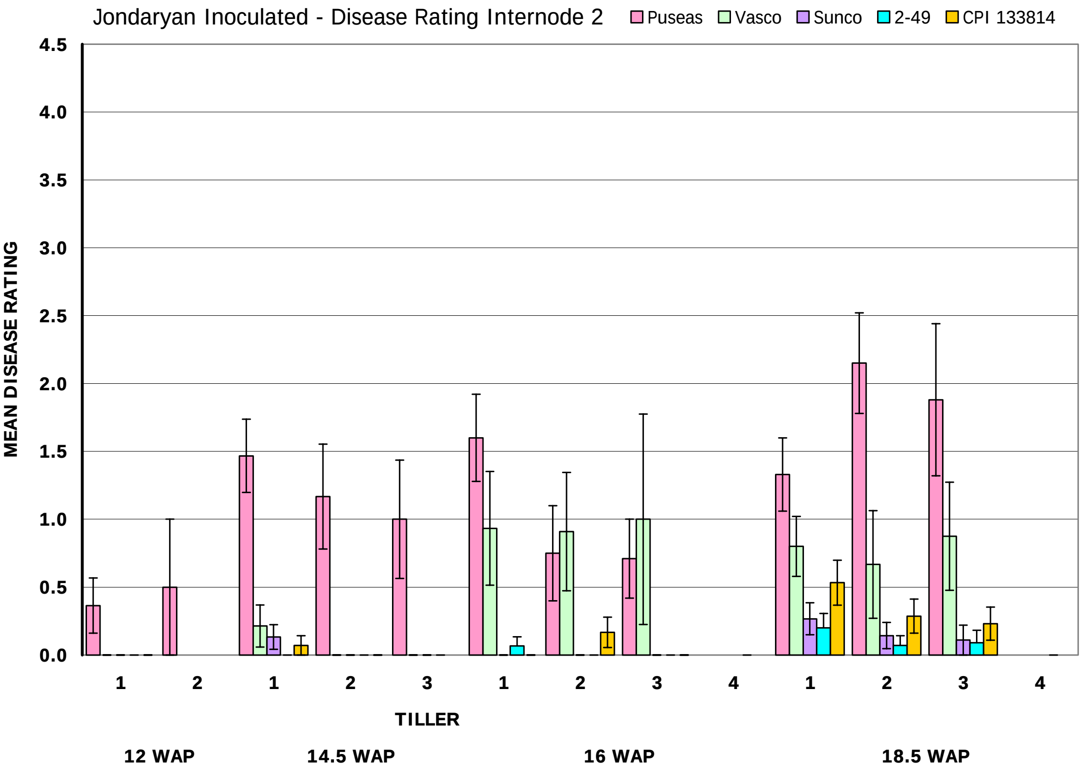
At 12 and 14.5 WAP the mean disease rating of I2 was significantly higher in Puseas than the other genotypes in all tillers (Figure 3.11a). At 16 WAP Vasco was not significantly different from Puseas and these were both higher than 2-49 and Sunco. At 18.5 WAP Puseas was significantly higher than Vasco which was significantly higher than the rating of Sunco, 2-49 and CPI133814 (Figure 3.11a). Data for I2 was not analysed in the Jondaryan trial.

Wellcamp trial

I2 had begun to expand at 11 WAP and was collected up to maturity at 22 WAP. Some plants had developed lesions on this plant part in all genotypes except 2-49 by 13 WAP (Table 3.11b). At 16 WAP disease incidence was high in all tillers of Puseas and Vasco. Approximately one third of Sunco I2's were diseased in each tiller while only one 2-49 I2 was lesioned at this time. Disease symptoms were not recorded on the majority of plants in 2-49 tillers until 20 WAP (Table 3.11b).

The mean disease ratings of the primary and 2nd tillers were significantly higher in Puseas than Vasco and Sunco at 13 WAP (Figure 3.11b). At 16 WAP the differences between Puseas and Vasco were not significant in any tiller. Sunco was significantly lower than Puseas in the 1st 4 tillers and lower than Vasco in the primary and 2nd tiller at 16 WAP. At 18 WAP Sunco was significantly lower than Puseas and Vasco in the primary and 2nd tiller and by 22 WAP significantly lower than Puseas in the mean disease rating of the 5th tiller only. At 18 and 20 WAP 2-49 was significantly lower than Puseas and Vasco in all tillers and significantly lower than Puseas, Vasco

Figure 3.11 Mean disease rating of Internode 2 in the a) Jondaryan trial (12-18.5 WAP) and the b) Wellcamp trial (13-22 WAP). *Tillers and/or Harvest included in analysis.



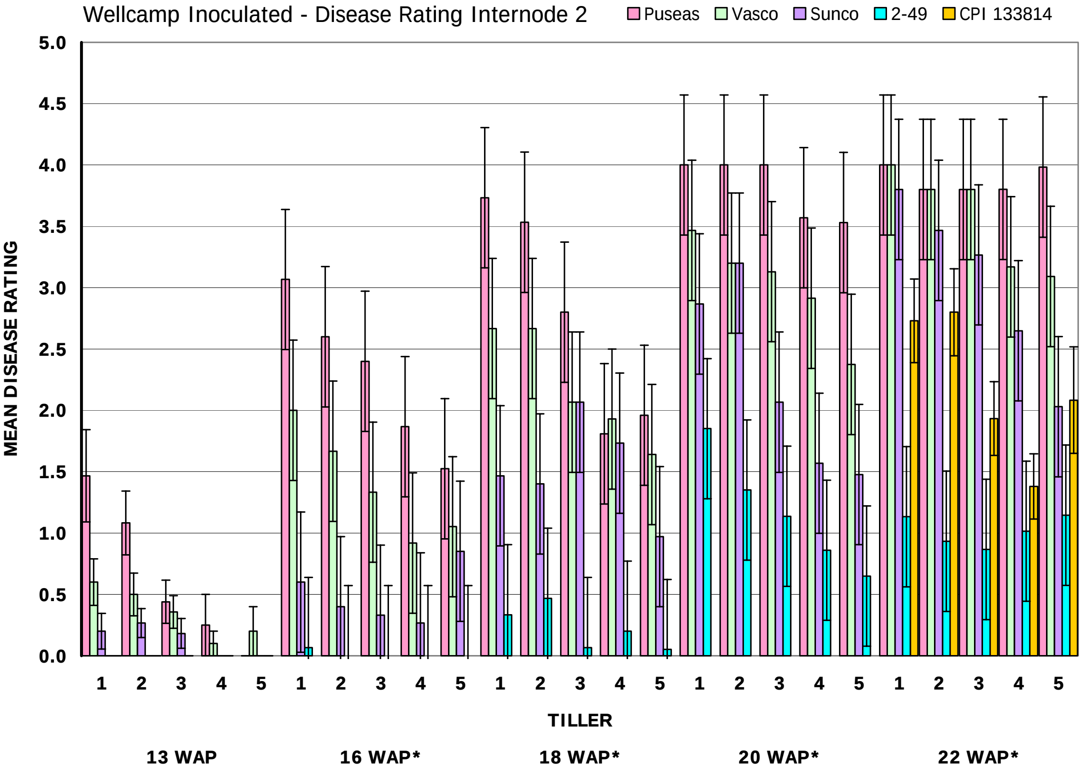


Table 3.11a Number of expanded Internode 2’s assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**10 WAP**	**12 WAP**	**14.5 WAP**			**16 WAP**				**18.5 WAP**			
TILLER	**1**	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**1**	**11**	**15**	**12**	**7**	**15**	**12**	**7**		**15**	**13**	**9**	**1**
	0	3	13	7	4	13	2	4		13	11	7	0
Vasco		**11**	**14**	**7**	**5**	**15**	**11**	**5**		**15**	**12**	**8**	
		0	2	0	0	5	4	2		9	3	4	
Sunco		**11**	**15**	**13**	**8**	**15**	**10**	**5**		**15**	**14**	**9**	
		0	2	0	0	0	0	0		4	2	1	
2-49		**7**	**15**	**11**	**4**	**15**	**15**	**10**	**7**	**15**	**14**	**11**	**3**
		0	0	0	0	1	0	0	0	3	1	1	0
CPI133814		**10**	**15**	**4**		**15**	**12**	**9**		**15**	**14**	**13**	
		0	1	0		0	2	0		7	4	3	

Table 3.11 b Number of expanded Internode 2’s assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**13 WAP**					**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**15**	**12**	**9**	**8**	**3**	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**14**	**10**	**15**	**15**	**15**	**14**	**11**	**15**	**15**	**15**	**10**	**8**
	10	9	4	1	0	15	14	13	10	10	15	15	15	10	8	15	15	15	14	11	15	15	15	10	8
Vasco	**15**	**14**	**14**	**10**	**5**	**15**	**15**	**15**	**14**	**10**	**15**	**15**	**15**	**12**	**9**	**15**	**15**	**15**	**10**	**5**	**15**	**15**	**15**	**11**	**8**
	7	6	5	1	1	11	11	10	9	7	14	13	13	13	9	15	15	15	10	5	15	15	15	11	8
Sunco	**15**	**15**	**11**	**11**	**11**	**15**	**15**	**15**	**12**	**12**	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**14**	**12**	**15**	**15**	**15**	**14**	**11**
	2	4	2	0	0	5	5	3	2	5	15	11	12	12	11	15	15	15	12	10	15	15	15	14	9
2-49	**15**	**13**	**11**	**5**	**3**	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**15**	**12**	**14**	**14**	**14**	**13**	**11**	**15**	**15**	**15**	**14**	**10**
	0	0	0	0	0	1	0	0	0	0	4	4	1	3	1	13	14	11	10	8	15	13	11	13	9
CPI133814	**9**	**5**	**1**	**1**																	**15**	**15**	**15**	**13**	**12**
	0	0	0	0																	15	15	15	12	11

Table 3.11c Probabilities for each factor and interaction in disease rating data for Internode 2 in the Wellcamp (16, 18, 20 and 22 WAP) trial.

Disease Ratings Internode 2	**Fixed Term**						
	Harvest	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	not analysed						
Wellcamp	<0.001	<0.001	<0.001	0.007	0.447	0.044	<0.001

and Sunco in all but one tiller at 22 WAP (Figure 3.11b). CPI133814 was not included in the analysis and therefore has differently calculated error bars however it was rated between 2-49 and Sunco for each tiller at 22 WAP.

Data for I2 was analysed over five tillers 16, 18, 20 and 22 WAP. Each factor-harvest, genotype and tiller were highly significant ($P<0.001$). The harvest/genotype ($P=0.007$) and harvest/genotype/tiller ($P<0.001$) interactions were also significant (Table 3.11c). Charts of the 3-way interaction are presented in Appendix 3E (Figures 3E.8 and 3E.9).

In Puseas the mean disease rating of the 4th and 5th tiller I2's were significantly lower than the primary tiller at 16 WAP, and lower then the primary and 2nd tiller at 18 WAP. There was a significant increase in the mean disease rating of the 3rd, 4th and 5th tillers between 18 and 20 WAP and at this time differences between tillers were no longer significant as they all approached the maximum disease rating of 4. (Figure 3.11b, Appendix 3E (Figures 3E.8 and 3E.9)).

In Vasco the mean disease rating generally increased at the same rate in each tiller at each harvest. The primary and 2nd tillers were usually higher than the 4th and 5th tillers however differences between tillers were not significant at any harvest (Figure 3.11b, Appendix 3E (Figures 3E.8 and 3E.9)).

In Sunco differences between tillers were not significant at 16 and 18 WAP. At 20 WAP the disease increased sharply in the primary and 2nd tiller, and these were significantly higher than the others at 20 WAP. The mean disease rating of Sunco increased in all tillers at 22 WAP and the primary, 2nd and 3rd tiller were significantly higher than the 5th at this harvest (Appendix 3E (Figures 3E.8 and 3E.9), Figure 3.11b).

At 16 and 18 WAP disease was very low in 2-49 and differences between tillers were not significant. At 20 WAP the mean disease rating increased in all tillers. This increase was greatest in the primary tiller and at 20 WAP it was significantly higher than the 5th tiller. Differences between tillers were not significant at 22 WAP (Figure 3.11b, Appendix 3E (Figures 3E.8 and 3E.9)).

Internode 3

Jondaryan trial

The 3rd internode (I3) had started to expand in the Jondaryan trial at 12 WAP and was collected until maturity at 18.5 WAP (Table 3.12a). Disease was recorded in up to 5 plants in Puseas from 12 WAP and up to 3 Vasco plants from 16 WAP. One 2-49, and two CPI133814 plants had lesions on the primary tiller I3 at 18.5 WAP (Table 3.12a, Figure 3.12a). Data for I3 was not analysed in this trial.

Wellcamp trial

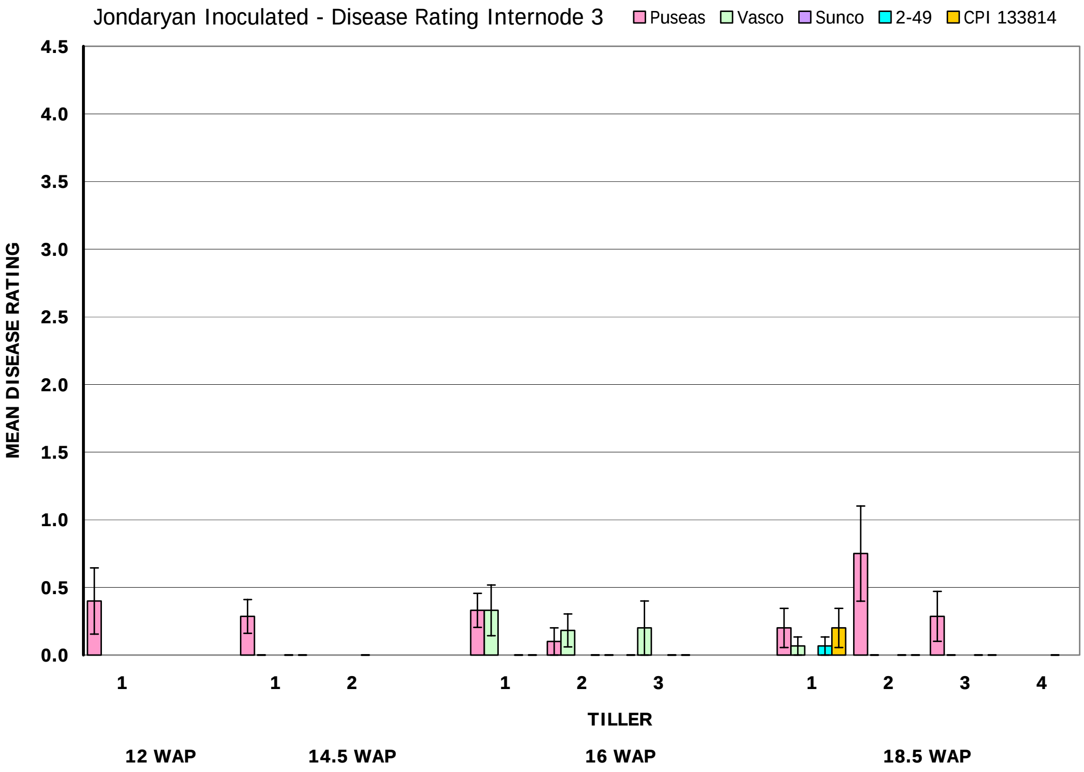
In the Wellcamp trial I3 was collected over five harvests from 13 to 22 WAP. Disease was first recorded in Puseas at 13 WAP and in Vasco and Sunco (only 1 plant) at 16 WAP (Table 3.12b). Lesions on 2-49 I3 were only recorded on a hand full of plants throughout the trial.

At 16 WAP the mean disease rating of Sunco was significantly lower than Puseas and Vasco in the primary and 2nd tillers. At 18 and 20 WAP the rating of Puseas primary tiller was significantly higher than all other genotypes. Sunco was significantly lower than Puseas in all tillers at 20 and 22 WAP and lower than Vasco in the 3rd, 4th and 5th tillers at these harvests (Figure 3.12b). CPI 133814 was significantly lower than Puseas, Vasco and Sunco in all tillers at 22 WAP however the difference between Sunco and CPI133814 were not significant in the 4th and 5th tillers (Figure 3.12b).

I3 data from the Wellcamp trial was analysed over 18, 20 and 22 WAP. All factors and 2 way interactions were highly significant (P =or< 0.002) in this internode (Table 3.12c). The 3-way interaction was also highly significant ($P<0.005$) and charts of this are presented for each genotype in Appendix 3E (Figure 3E.10).

At 18 WAP the mean disease rating in Puseas I3 primary tiller was significantly higher than the 3rd, 4th and 5th tiller. Between 18 and 20 WAP the mean disease rating increased significantly in the 2nd and 4th tillers and at 20 WAP the primary and 2nd tiller were significantly higher than the others. Between 18 and 20 WAP only the

Figure 3.12 Mean disease rating of Internode 3 in the a) Jondaryan trial (12-18.5 WAP) and the b) Wellcamp trial (13-22 WAP). * Harvest included in analysis.



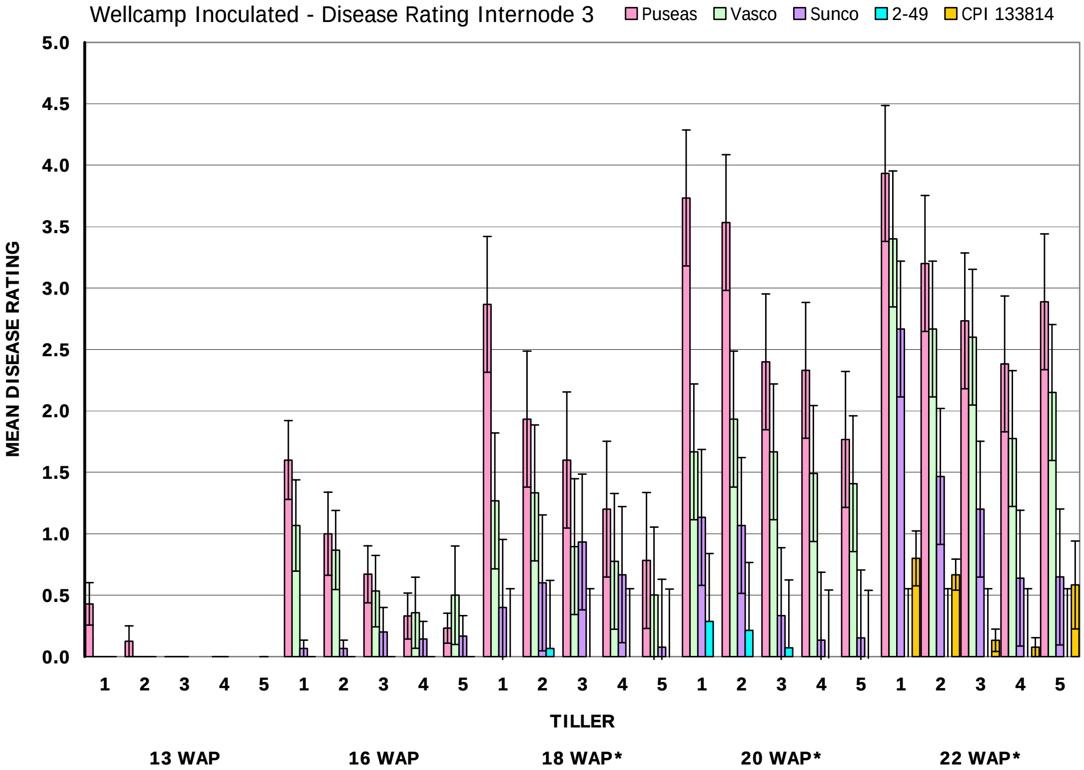


Table 3.12a Number of expanded Internode 3's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

HARVEST	**12 WAP**	**14.5 WAP**		**16 WAP**				**18.5 WAP**			
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**5**	**14**	**1**	**15**	**10**	**4**		**15**	**12**	**7**	**1**
	2	4	0	5	1	0		2	5	2	0
Vasco	**1**	**12**		**15**	**11**	**5**		**15**	**12**	**7**	
	0	0		3	2	1		1	0	0	
Sunco	**2**	**14**		**15**	**10**	**5**		**15**	**14**	**9**	
	0	0		0	0	0		0	0	0	
2-49	**1**	**8**	**3**	**15**	**12**	**9**	**6**	**15**	**14**	**11**	**3**
	0	0	0	0	0	0	0	1	0	0	0
CPI133814		**10**	**1**	**15**	**12**	**6**		**15**	**13**	**9**	
		0	0	0	0	0		2	0	0	

Table 3.12 b Number of expanded Internode 3's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**13 WAP**					**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**14**	**8**	**5**	**1**		**15**	**15**	**15**	**15**	**13**	**15**	**15**	**15**	**13**	**10**	**15**	**15**	**15**	**14**	**11**	**15**	**15**	**15**	**10**	**8**
	5	1	0	0		12	7	4	3	3	14	14	10	6	5	15	15	15	11	9	15	15	15	10	8
Vasco	**15**	**12**	**8**	**7**	**1**	**15**	**15**	**15**	**14**	**10**	**15**	**15**	**14**	**11**	**9**	**15**	**15**	**15**	**10**	**5**	**15**	**15**	**15**	**11**	**8**
	0	0	0	0	0	8	7	4	2	2	10	9	6	5	4	13	13	12	9	3	15	15	14	8	6
Sunco	**15**	**11**	**10**	**10**	**5**	**15**	**15**	**15**	**12**	**12**	**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**14**	**12**	**15**	**15**	**15**	**14**	**11**
	0	0	0	0	0	1	1	1	1	1	4	4	8	4	1	11	11	4	2	2	14	12	12	8	6
2-49	**6**	**4**	**1**			**15**	**15**	**15**	**15**	**14**	**15**	**15**	**15**	**15**	**12**	**14**	**14**	**14**	**13**	**11**	**15**	**15**	**15**	**14**	**10**
	0	0	0			0	0	0	0	0	0	1	0	0	0	4	3	1	0	0	0	0	0	0	0
CPI133814	**not developed**																				**15**	**15**	**15**	**13**	**12**
																					8	10	2	1	3

Table 3.12c Probabilities for each factor and interaction in disease rating data for Internode 3 in the Wellcamp (16, 18, 20, 22 WAP) trials.

Disease Ratings Internode 3	**Fixed Term**						
	Harvest	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	not analysed						
Wellcamp	<0.001	<0.001	<0.001	<0.001	0.002	<0.001	0.005

5th tiller increased significantly and at the final harvest 22 WAP the primary tiller was only higher than the 3rd and 4th tillers in Puseas (Appendix 3E (Figure 3E.10)).

In Vasco differences between tillers were not significant at 18 and 20 WAP. Disease increased in each tiller between 18 and 20 and between 20 and 22 WAP and at this final harvest the mean disease rating of the primary tiller in Vasco was significantly higher than the 4th and 5th (Appendix 3E (Figure 3E.10)).

In Sunco differences in the mean disease rating of each tiller at each harvest were mostly not significant. Only the rating of the primary tiller increased significantly between 20 and 22 WAP and at this final harvest the primary tiller was significantly higher than the 4th and 5th. All other levels of interaction were not significant in the mean disease rating of Sunco I3.

Disease in 2-49 was either absent or very low and no significant differences were seen between harvests or between tillers in this genotype (Appendix 3E (Figures 3E.10, 3E.11)).

Internode 4

Jondaryan trial

The 4th internode (I4) was collected over three harvests from 14.5 to 18.5 WAP in the Jondaryan trial. Only 1 Puseas primary tiller recorded lesions on I4 (Table 3.13a)

Wellcamp trial

In the Wellcamp trial I4 had expanded in some plants at 13 WAP and was collected until maturity at 22 WAP. Disease symptoms were first recorded in Puseas and Vasco at 16 WAP and in two Sunco plants at 18 WAP (Table 3.13b). No lesions were recorded on I4 in 2-49.

At 16 and 18 WAP differences between genotypes were not significant. At 20 WAP Puseas was significantly higher than Vasco and Sunco in the primary and 2nd tiller, with no symptoms of disease recorded in Sunco on the 3rd, 4th and 5th tillers (Figure 3.13). At 22 WAP the mean disease rating in Sunco was significantly lower than Puseas and Vasco in the first three tillers and lower than Puseas in the 5th.

Data for I4 was analysed over 18, 20 and 22 WAP in the Wellcamp trial. All factors were highly significant (P<0.001) as were the two-way interactions, harvest/genotype (P=0.004) harvest/tiller (P=0.005) and tiller/genotype (P<0.001) (Table 3.13c). Charts of these two-way interactions are presented in Appendix 3E (Figure 3E.12).

In the harvest/genotype interaction disease was quite limited in Sunco and differences in the mean disease rating over the three harvests were not significant. While the mean disease rating of Puseas I4 never reached the maximum of 4, after a sharp increase in disease between 18 and 20 WAP, differences between 20 and 22 WAP were not significant. In Vasco the mean disease rating increased gradually at each harvest but differences between 18 and 22 WAP were still not significant.

In the harvest/tiller interaction the mean disease rating of the primary tiller increased at each harvest with the rating at 22 WAP significantly higher than at 18 WAP. Disease mostly increased at each harvest in the remaining tillers however differences between tillers and between harvests were not significant.

Figure 3.13 Mean disease rating of Internode 4 in the Wellcamp trial (16-22 WAP). * Harvest included in analysis.

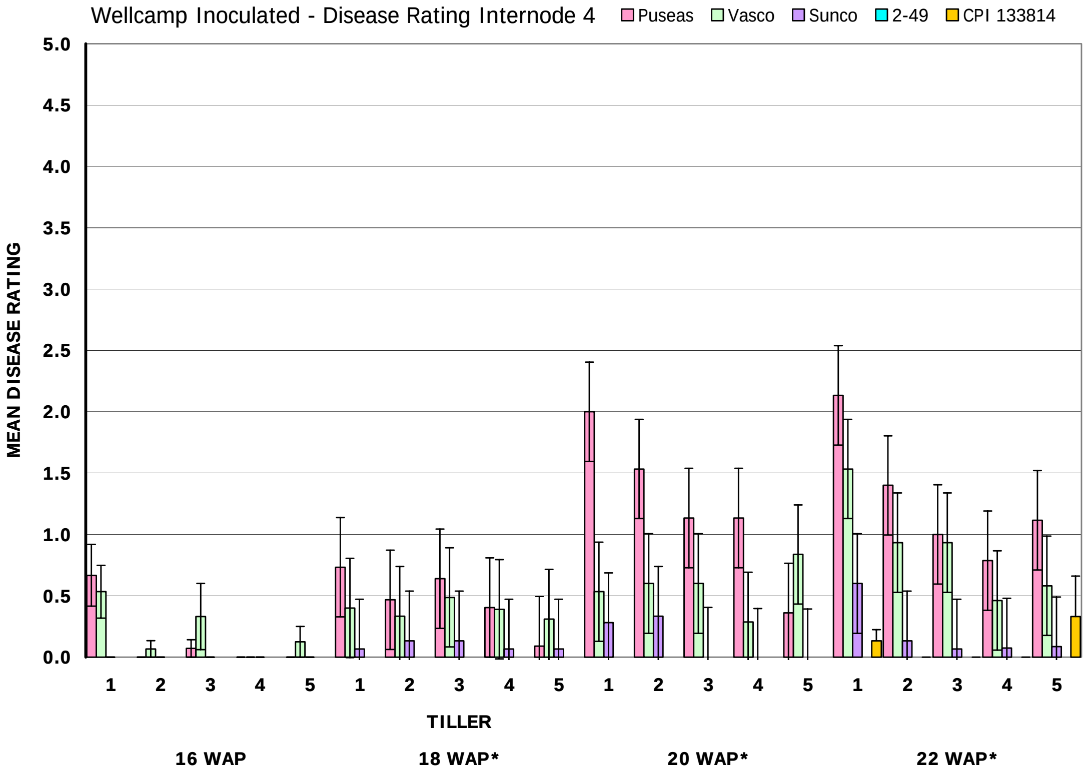


Table 3.13a Number of expanded Internode 4's and peduncles assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Jondaryan trial.

Plant Part	**Internode 4**								**Peduncle**								
HARVEST	**14.5 WAP**	**16 WAP**				**18.5 WAP**			**14.5 WAP**	**16 WAP**				**18.5 WAP**			
TILLER	**1**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**1**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**5**	**14**	**3**			**10**	**5**	**2**	**0**	**11**	**3**	**1**		**12**	**5**	**4**	**1**
	0	1	0			0	0	0	0	0	0	0		0	0	0	0
Vasco	**1**	**12**	**5**	**1**		**12**	**10**	**6**	**1**	**15**	**7**	**3**		**15**	**11**	**6**	
	0	0	0	0		0	0	0	0	0	0	0		0	0	0	
Sunco		**12**	**7**	**3**		**12**	**11**	**7**		**15**	**8**	**1**		**14**	**13**	**8**	
		0	0	0		0	0	0		0	0	0		0	0	0	
2-49	**2**	**12**	**11**	**5**	**2**	**15**	**10**	**7**	**3**	**14**	**10**	**9**	**3**	**15**	**11**	**7**	**1**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CPI133814	**2**	**15**	**10**	**3**		**15**	**12**	**9**		**15**	**7**	**2**		**15**	**11**	**5**	
	0	0	0	0		0	0	0		0	0	0		0	0	0	

Table 3.13 b Number of expanded Internode 4's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**13 WAP**	**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**10**	**15**	**15**	**14**	**8**	**8**	**15**	**15**	**14**	**11**	**10**	**15**	**15**	**15**	**13**	**11**	**15**	**15**	**15**	**10**	**8**
	0	6	0	1	0	0	9	5	6	4	1	14	13	10	6	3	14	11	10	5	3
Vasco	**6**	**15**	**15**	**15**	**11**	**8**	**15**	**15**	**14**	**11**	**8**	**15**	**15**	**15**	**10**	**5**	**15**	**15**	**15**	**11**	**8**
	0	6	1	2	0	1	3	3	2	2	1	6	7	5	3	2	12	10	8	3	3
Sunco	**8**	**15**	**15**	**15**	**12**	**12**	**15**	**15**	**15**	**15**	**14**	**14**	**15**	**15**	**14**	**12**	**15**	**15**	**15**	**14**	**11**
	0	0	0	0	0	0	1	2	2	1	1	4	2	0	0	0	8	2	1	1	1
2-49		**15**	**15**	**15**	**14**	**9**	**15**	**15**	**15**	**14**	**12**	**14**	**14**	**14**	**13**	**11**	**15**	**15**	**15**	**14**	**10**
	not	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CPI133814	**developed**																**15**	**15**	**15**	**12**	**12**
																	2	0	0	0	1

Table 3.13c Probabilities for each factor and interaction in disease rating data for Internode 4 in the Wellcamp (16, 18, 20, 22 WAP) trial.

Disease Ratings	**Fixed Term**						
Internode 4	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	not analysed						
Wellcamp	<0.001	<0.001	<0.001	0.004	0.005	<0.001	0.423

Table 3.13 d Number of expanded Internode 5's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**14**	**10**	**6**	**3**	**2**	**15**	**14**	**14**	**8**	**4**	**15**	**15**	**15**	**11**	**9**	**15**	**15**	**10**	**5**	**4**
	2	0	1	0	0	3	1	2	0	0	7	4	3	3	0	6	4	2	0	0
Vasco	**15**	**11**	**10**	**5**	**1**	**14**	**14**	**10**	**7**	**3**	**15**	**15**	**15**	**8**	**4**	**15**	**15**	**14**	**10**	**4**
	1	0	0	0	0	1	1	1	1	0	1	1	1	0	1	6	3	1	0	0
Sunco	**14**	**14**	**11**	**5**	**5**	**15**	**15**	**15**	**15**	**11**	**14**	**15**	**15**	**12**	**7**	**15**	**15**	**15**	**14**	**9**
	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
2-49	**11**	**7**	**6**	**2**	**3**	**15**	**15**	**10**	**8**	**3**	**14**	**14**	**14**	**12**	**9**	**15**	**15**	**15**	**14**	**9**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CPI133814																**13**	**15**	**14**	**11**	**8**
																0	0	0	0	1

Table 3.13e Number of expanded Internode 6's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**16 WAP**	**18 WAP**				**20 WAP**				**22 WAP**				
TILLER	**1**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**5**
Puseas		**1**		**1**		**9**	**4**	**5**	**2**	**8**	**5**			
		0		1		1	4	0	0	0	0			
Vasco	**1**	**1**				**10**	**9**	**5**		**7**	**4**	**4**	**1**	
	0	0				0	0	0	0	1	1	0	0	
Sunco	**5**	**11**	**6**	**6**	**3**	**8**	**9**	**6**	**2**	**14**	**10**	**9**	**6**	**3**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2-49		**4**	**3**	**2**		**7**	**4**	**3**	**2**	**6**				
	0	0	0	0		0	0	0	0	0				
CPI133814										**9**	**5**	**4**	**2**	
										0	0	0	0	

Table 3.13f Number of expanded Peduncle's assessed at each harvest (bold) and the number of those with disease ratings >0 (below) in the Wellcamp trial.

HARVEST	**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**13**	**12**	**10**	**8**	**4**	**14**	**15**	**14**	**9**	**7**	**14**	**14**	**15**	**12**	**10**	**14**	**14**	**13**	**7**	**7**
	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Vasco	**15**	**14**	**12**	**8**	**4**	**15**	**14**	**11**	**10**	**7**	**15**	**15**	**15**	**8**	**4**	**15**	**15**	**15**	**10**	**8**
	1	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Sunco	**15**	**14**	**13**	**11**	**11**	**15**	**15**	**15**	**14**	**14**	**14**	**15**	**15**	**12**	**7**	**14**	**14**	**15**	**12**	**12**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2-49	**15**	**13**	**10**	**8**	**5**	**15**	**15**	**15**	**14**	**12**	**14**	**14**	**14**	**13**	**11**	**15**	**15**	**15**	**14**	**9**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CPI133814																**9**	**13**	**12**	**11**	**11**
																0	0	0	0	1

The level of disease in each tiller was quite different for each genotype. In Puseas the primary tiller was significantly higher than all other tillers. The 2nd tiller was also significantly higher than the 5th. No differences were significant between tillers in the other genotypes (Appendix 3E (Figure 3E.12)). Puseas I4 disease rating was significantly higher than 2-49 and Sunco in all tillers and higher than Vasco in the primary and 2nd. Vasco was also higher than Sunco in the primary, 3rd and 5th tiller.

Internode 5, 6 and the peduncle

Jondaryan trial

Only four internodes developed consistently in the Jondaryan trial. The peduncle emerged in some plants at 14.5 WAP and was collected over the next two harvests 16 and 18.5 WAP. No disease symptoms were recorded on the peduncle in the Jondaryan trial (Table 3.13a).

Wellcamp trial

A 5th and 6th internode (I5 and I6) and the peduncle were collected in the Wellcamp trial over four harvests 16 to 22 WAP. Disease symptoms were not recorded on these plant parts in 2-49 (Tables 3.13 d, e and f).

One Sunco 2nd tiller and one CPI133814 5th tiller had lesions on I5 at 18 and 22 WAP respectively (Table 3.13d). Lesions were recorded on I5 in several Puseas and Vasco plants at 16 and 18 WAP. At 22 WAP 6 primary tillers were lesioned in each of Vasco and Puseas. Differences in the mean disease rating of Puseas and Vasco I5 were mostly not significant (data not shown).

Lesions on I6 and on the peduncle were rare in the Wellcamp field trial and were generally observed in Vasco and Puseas (Tables 3.13 e and f).

3.2.5 Field trial isolation counts

Leaf Sheath 1

Jondaryan trial

Isolations from LS1 were first recorded in two Vasco plants in the Jondaryan trial at 4 WAP (Table 3.14a). The fungus was recovered from a few plants of each genotype by 8 WAP with the majority of primary tiller LS1's infected at 10 WAP (Table 3.15a). 100% incidence was never recorded for any LS's in this trial (Tables 3.14a-3.18a).

Differences in the mean number of isolations from LS1 were mostly not significant between genotypes or between tillers at each harvest (Figure 3.14a). Some of the 3rd tiller isolations particularly from CPI133814, Sunco and 2-49 were significantly lower than some of the primary tiller isolations however the 3rd tiller isolations were not included in the analysis and do not have the stringent 95% confidence interval of error associated with the values.

I1 isolation counts were analysed for the primary and 2nd tiller over the three harvests 10, 12 and 14.5 WAP. The tiller effect was highly significant ($P< 0.001$) (Table 3.14c) with the square root (sqrt) of infection counts for the primary tiller averaging 1.653 and the 2nd tiller 0.779 (Appendix 3E (Figure 3E.13)).

Wellcamp trial

A higher incidence of infection was seen in LS1 early in the Wellcamp trial with 7 Vasco, 4 Puseas and Sunco and 1 2-49 LS1 infected at the 1st harvest 5 WAP (Table 3.14b). However, as seen in the Jondaryan trial, differences in the number of isolations between genotypes and within genotypes between tillers were again mostly not significant for LS1 at each harvest (Figure 3.14b).

All collected data was analysed for LS1 in the Wellcamp trial. A highly significant tiller ($P<0.001$) and harvest ($P=0.004$) effect were present (Table 3.14c). Error values (SED) were not available at each of these levels as the number of plants (n) is very different for each value. Values for these factors were calculated from the data

Figure 3.14 Mean number of isolations from Leaf Sheath 1 in the a) Jondaryan trial (4-14.5 WAP) and the b) Wellcamp trial (5-11 WAP). *Tillers and/or Harvest included in analysis.

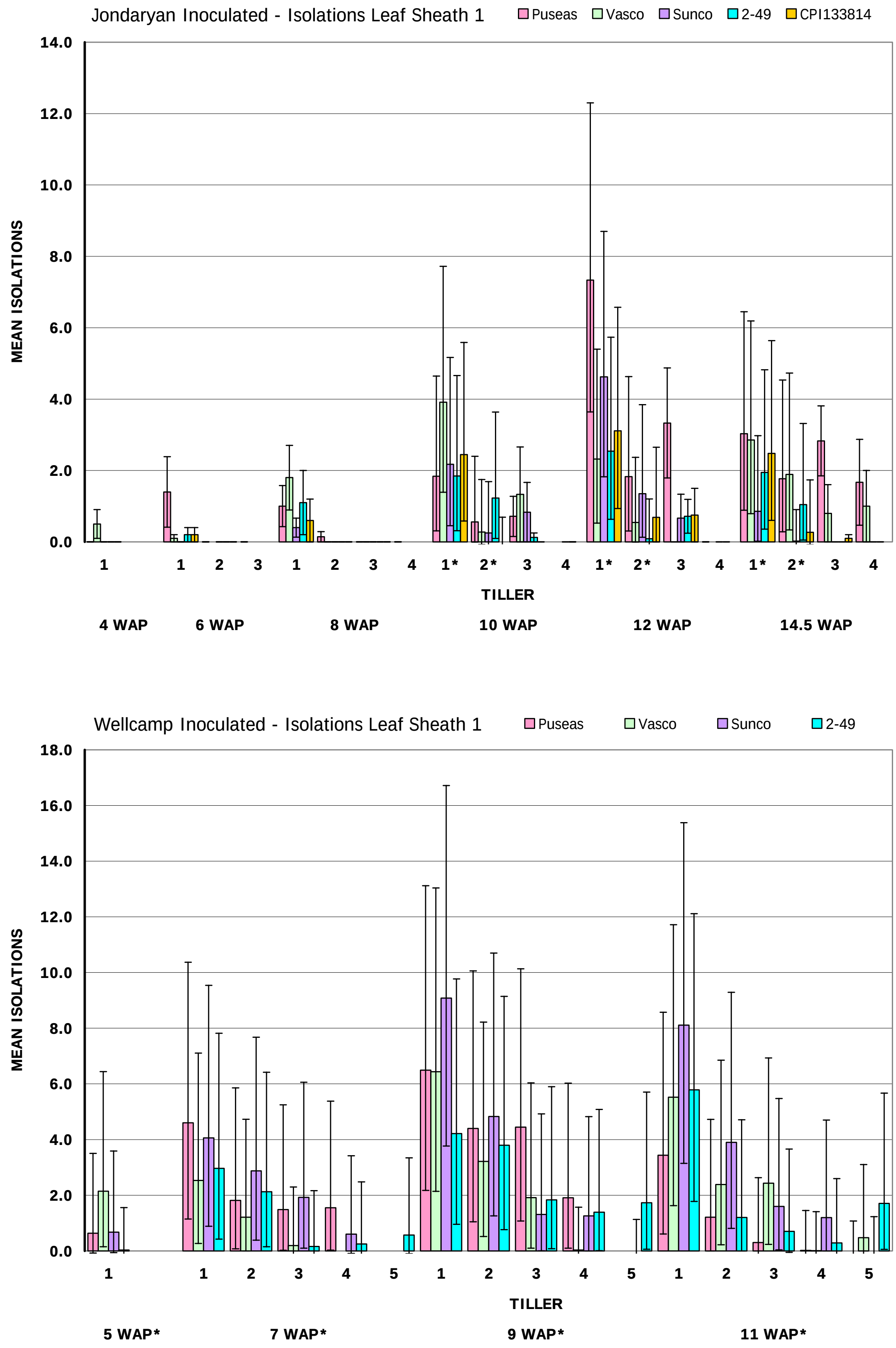


Table 3.14a Number of expanded Leaf Sheath 1's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	**4 WAP**	**6 WAP**		**8 WAP**				**10 WAP**				**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**10**	**10**	**3**	**9**	**7**	**6**	**2**	**10**	**8**	**7**		**10**	**7**	**6**	**2**	**10**	**9**	**6**	**3**
	0	3	0	2	1	0	0	7	4	2		9	5	4	0	8	8	5	2
Vasco	**10**	**10**		**10**	**5**	**5**		**10**	**8**	**3**		**10**	**7**	**3**		**10**	**6**	**5**	**3**
	2	1		5	0	0		9	3	1		7	3	0		7	5	1	1
Sunco	**10**	**10**	**5**	**10**	**5**	**2**		**10**	**6**	**6**	**2**	**10**	**8**	**6**	**2**	**10**	**9**	**9**	**2**
	0	0	0	2	0	0		7	2	1	0	9	4	1	0	6	1	0	0
2-49	**10**	**10**	**4**	**10**	**7**	**3**	**1**	**10**	**8**	**8**	**5**	**10**	**8**	**6**	**3**	**10**	**9**	**8**	**6**
	0	1	0	2	0	0	0	7	4	1	0	6	2	1	0	6	5	0	0
CPI133814	**10**	**10**	**2**	**10**	**8**	**6**		**9**	**7**	**6**		**10**	**9**	**8**	**1**	**10**	**10**	**9**	
	0	1	0	1	0	0		7	1	0		7	4	1	0	7	3	1	

Table 3.14b Number of expanded Leaf Sheath 1's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**5 WAP**			**7 WAP**					**9 WAP**					**11 WAP**				
TILLER	**1**	**2**	3	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**10**			**10**	**6**	**2**			**9**	**9**	**8**	**5**		**10**	**8**	**8**	**6**	**2**
	4			9	3	1			7	7	6	3		6	4	2	1	0
Vasco	**10**			**10**	**10**	**8**			**10**	**10**	**7**	**3**		**10**	**10**	**10**	**7**	**4**
	7			6	5	2			9	7	5	1		8	6	6	2	2
Sunco	**10**			**10**	**10**	**7**			**9**	**10**	**8**	**3**		**10**	**10**	**9**	**4**	**3**
	4			9	10	5			9	9	4	0		9	8	4	1	0
2-49	**10**			**10**	**10**	**10**	**1**		**9**	**10**	**10**	**7**		**10**	**8**	**9**	**9**	**6**
	1			7	7	2	0		6	7	5	4		8	3	3	2	3
CPI133814	**Not collected**																	

Table 3.14c Probabilities for each factor and interaction in the isolation data for Leaf Sheath 1 in the Jondaryan (10, 12, 14.5 WAP) and Wellcamp trials (5, 7, 9, 11 WAP).

Isolations	**Fixed Term**						
Leaf Sheath 1	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	0.235	0.355	<0.001	0.409	0.135	0.544	0.308
Wellcamp	0.004	0.722	<0.001	0.565	0.774	0.047	0.868

provided for the 3-way interaction and charts of the sqrt of infection counts are presented in Appendix 3E (Figure 3E.13).

Overall the infection counts (sqrt) increased from 0.814 at 5 WAP to 1.377 and 1.753 at 7 and 9 WAP respectively. At 11 WAP the sqrt of infection counts decreased to 1.162. The infection counts (sqrt) were highest in the primary tiller (1.896) followed by the 2nd (1.613), 3rd (1.373), 4th (0.751) and 5th tiller (0.579).

Leaf Sheath 2

Jondaryan trial

Fpg was first isolated from LS2 8 WAP in the Jondaryan trail. At 14.5 WAP isolations were made from all four tillers in Puseas, three in Vasco, two tillers in 2-49 and only the primary tiller in CPI133814 and Sunco. A Low number of isolations were made from 3 tillers in CPI133814, Sunco and 2-49 LS2's at earlier harvests (Table 3.15a).

The mean numbers of isolations made from each tiller of each genotype were again mostly not significant (Figure 3.15a). The sqrt of isolation counts from LS2 were analysed over the primary and 2nd tiller 10, 12 and 14.5 WAP. A tiller effect was highly significant ($P<0.001$) (Table 3.15c), with the mean isolations (sqrt) from the primary tiller more than double that of the 2nd tiller (Appendix 3E (Figure 3E.14)).

Wellcamp trial

Isolations were made from the 2nd LS at the 1st harvest (5 WAP) in the Wellcamp trial (Table 3.15b). At 9 and 11 WAP isolations were made from the majority of primary and 2nd tiller LS2's with limited isolations from the 3rd, 4th and 5th tillers in all genotypes.

Differences in the number of isolations from each genotype were not significant in each tiller at each harvest (Figure 3.15b). Analysis of all LS2 isolation counts indicated a highly significant ($P<0.001$) harvest and tiller effect (Table 3.15c). The overall isolations counts (sqrt) ranged from 1.617 for the primary tiller, 1.43 for the 2nd tiller with the remaining tillers below 0.71 (Appendix 3E (Figure 3E.14)). As seen in LS1 the mean number of isolations increased from 5 to 7 to 9 WAP and decreased between 9 and 11 WAP (Appendix 3E (Figure 3E.14)). SED from the analysis of LS2 were also not available at this level due to differences in n.

Leaf Sheath 3

Jondaryan trial

LS3 isolations were recorded from a few plants in all genotypes at 10 WAP in the Jondaryan trial (Table 3.16a). The fungus was recovered from up to 3 tillers in Puseas, Sunco and CPI133814 and up to 2 tillers in Vasco and 2-49.

At 12 WAP the mean isolations from Puseas primary tiller were significantly higher than isolations made from any Vasco and CPI133814 tillers and higher than the 2nd and 3rd tillers in Sunco (Figure 3.16a). All other differences were not significant.

Data for the primary and 2nd tiller of LS3 was analysed over 10, 12 and 14.5 WAP. A highly significant ($P<0.001$) tiller effect was present (Table 3.16c). The mean number of isolations (sqrt) from the primary tiller was 0.719 compared with 0.267 from the 2nd tiller (Appendix 3E (Figure 3E.15)).

Wellcamp trial

Fpg was reisolated from one Sunco LS3 at 5 WAP and from all genotypes at 7 WAP (Table 3.16b). Differences between genotypes in the mean number of isolations from LS3 at each harvest were only significant when uninfected tillers were compared with infected tillers (Figure 3.16b). ie when LS3 was infected differences between genotypes in the amount of infection were not significant.

LS3 data for up to 5 tillers was analysed over 3 harvests 7, 9 and 11 WAP in the Wellcamp trial. The tiller effect was highly significant ($P<0.001$) as was the harvest/genotype interaction ($P=0.011$) (Table3.16c). The primary tiller was significantly higher than all other tillers and the 2nd tiller was higher than the 3rd, 4th and 5th tillers (Appendix 3E (Figure 3E.15)). At 7 WAP the mean isolation counts (sqrt) of Sunco tillers was 1.5 compared to 0.5 for the other genotypes. At 9 WAP the mean isolations from Sunco and Vasco had dropped, while Puseas increased and the values of 2-49 were very similar. At 11 WAP isolations from Vasco increased, Puseas decreased and 2-49 and Sunco remained very similar. However, with a 95%

Figure 3.15 Mean number of isolations from Leaf Sheath 2 in the a) Jondaryan trial (8-14.5 WAP) and the b) Wellcamp trial (5-11 WAP). *Tillers and/or Harvest included in analysis.

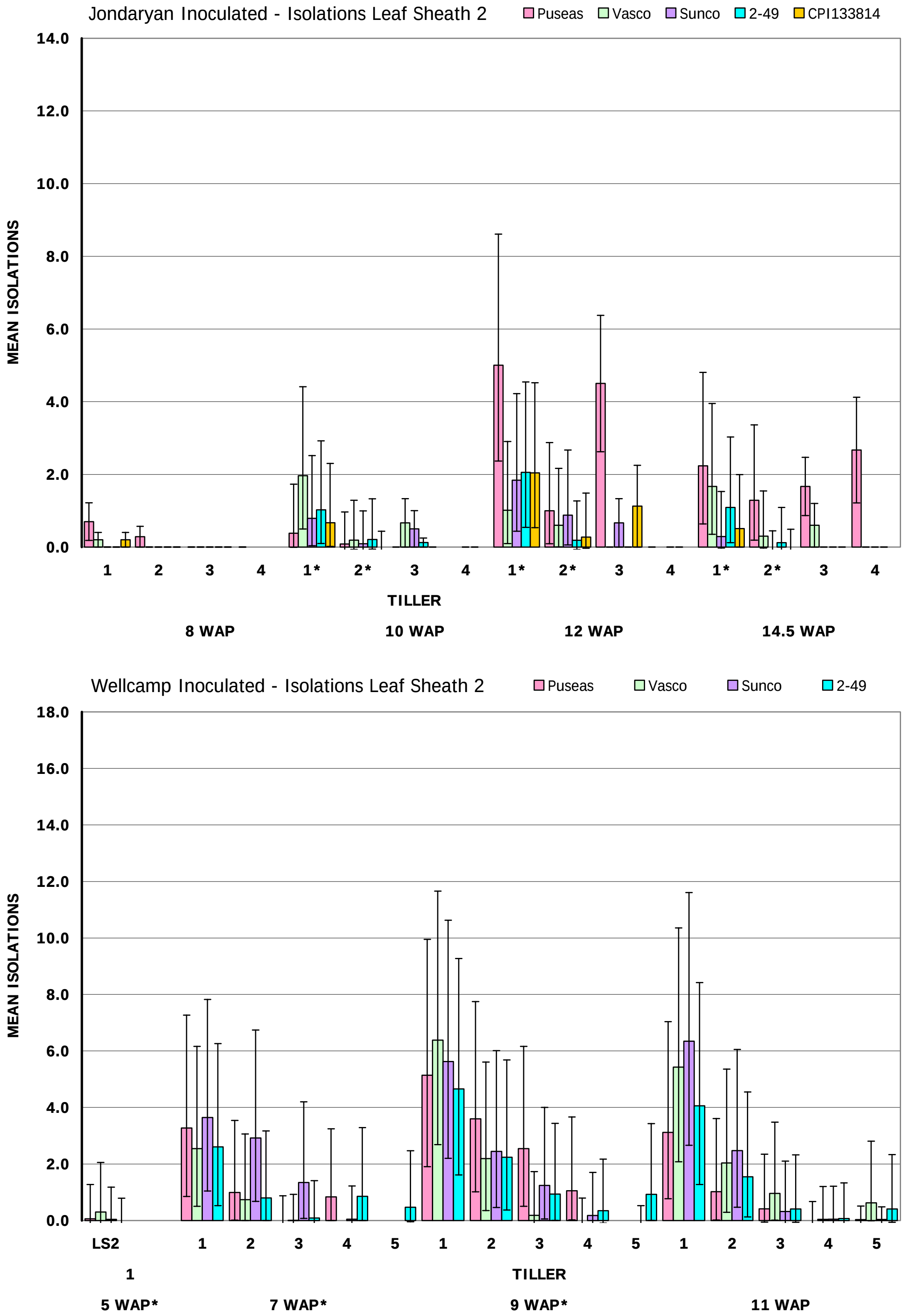


Table 3.15a Number of expanded Leaf Sheath 2's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	**4 WAP**	**6 WAP**		**8 WAP**				**10 WAP**				**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**10**	**10**	**3**	**10**	**7**	**6**	**2**	**10**	**8**	**7**		**10**	**7**	**6**	**2**	**10**	**9**	**6**	**3**
	0	0	0	1	1	0	0	3	2	0		9	4	4	0	8	6	3	2
Vasco	**10**	**10**		**10**	**5**	**5**		**10**	**8**	**3**		**10**	**7**	**3**		**10**	**6**	**5**	**3**
	0	0		1	0	0		9	2	1		5	3	0		7	3	1	0
Sunco	**10**	**10**	**5**	**10**	**5**	**2**		**10**	**6**	**6**	**2**	**10**	**8**	**6**	**2**	**10**	**9**	**9**	**2**
	0	0	0	0	0	0		5	1	1	0	7	4	1	0	4	0	0	0
2-49	**10**	**10**	**4**	**10**	**7**	**3**	**1**	**10**	**8**	**8**	**5**	**10**	**8**	**7**	**3**	**10**	**9**	**8**	**6**
	0	0	0	0	0	0	0	6	2	1	0	6	2	0	0	6	2	0	0
CPI133814	**10**	**10**	**2**	**10**	**8**	**6**		**10**	**7**	**6**		**10**	**9**	**8**	**1**	**10**	**10**	**9**	
	0	0	0	1	0	0		5	0	0		6	2	1	0	4	0	0	

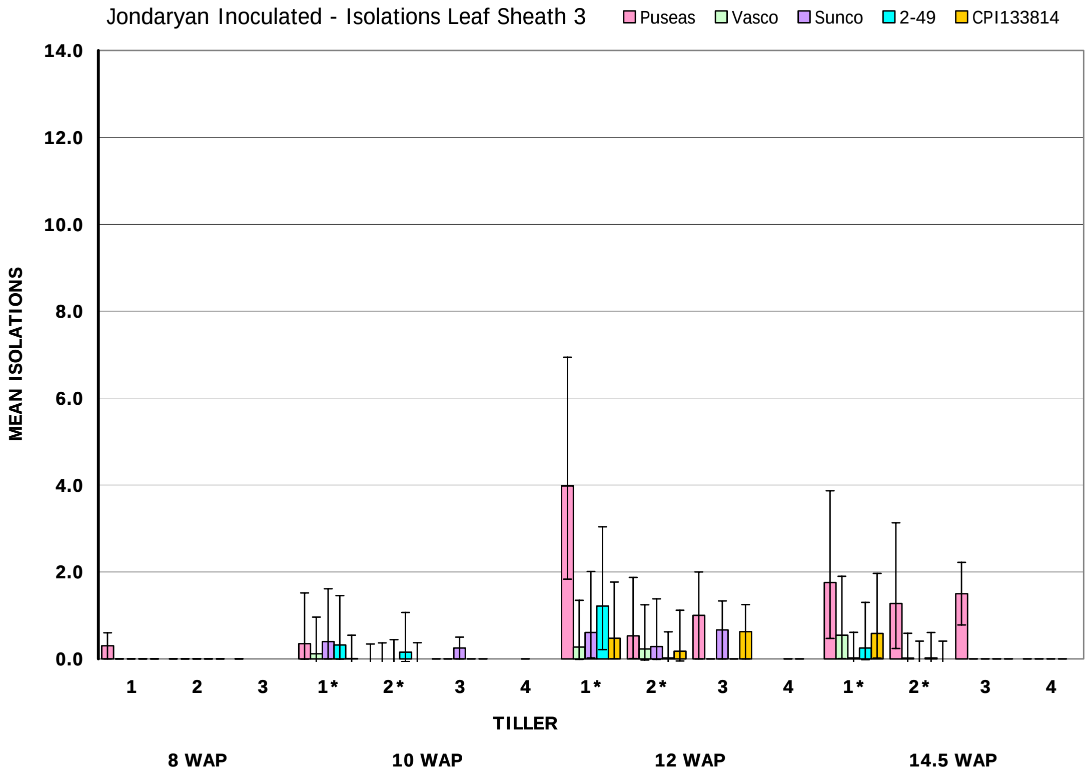
Table 3.15b Number of expanded Leaf Sheath 2's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**5 WAP**			**7 WAP**				**9 WAP**					**11 WAP**				
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**10**			**10**	**6**	**2**		**10**	**9**	**8**	**5**		**10**	**8**	**8**	**6**	**2**
	2			8	5	1		8	6	5	3		6	3	2	0	0
Vasco	**10**			**10**	**10**	**8**		**10**	**10**	**8**	**3**		**10**	**10**	**10**	**7**	**4**
	3			6	5	0		10	6	2	0		8	6	3	2	1
Sunco	**10**			**10**	**10**	**7**		**10**	**10**	**9**	**8**	**3**	**10**	**10**	**9**	**5**	**3**
	1			8	8	4		9	7	4	2	0	9	6	2	1	0
2-49	**10**			**10**	**10**	**10**	**1**	**9**	**10**	**10**	**10**	**7**	**10**	**9**	**9**	**9**	**6**
	0			7	5	1	0	7	6	5	3	3	8	4	3	1	1
CPI133814	**Not collected**																

Table 3.15c Probabilities for each factor and interaction in the isolation data for Leaf Sheath 2 in the Jondaryan (10, 12, 14.5 WAP) and Wellcamp trials (5, 7, 9, 11 WAP).

Isolations	**Fixed Term**						
Leaf Sheath 2	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	0.025	0.169	<0.001	0.403	0.747	0.817	0.442
Wellcamp	<0.001	0.656	<0.001	0.54	0.866	0.283	0.869

Figure 3.16 Mean number of isolations from Leaf Sheath 3 in the a) Jondaryan trial (8-14.5 WAP) and the b) Wellcamp trial (5-11 WAP). *Tillers and/or Harvest included in analysis.



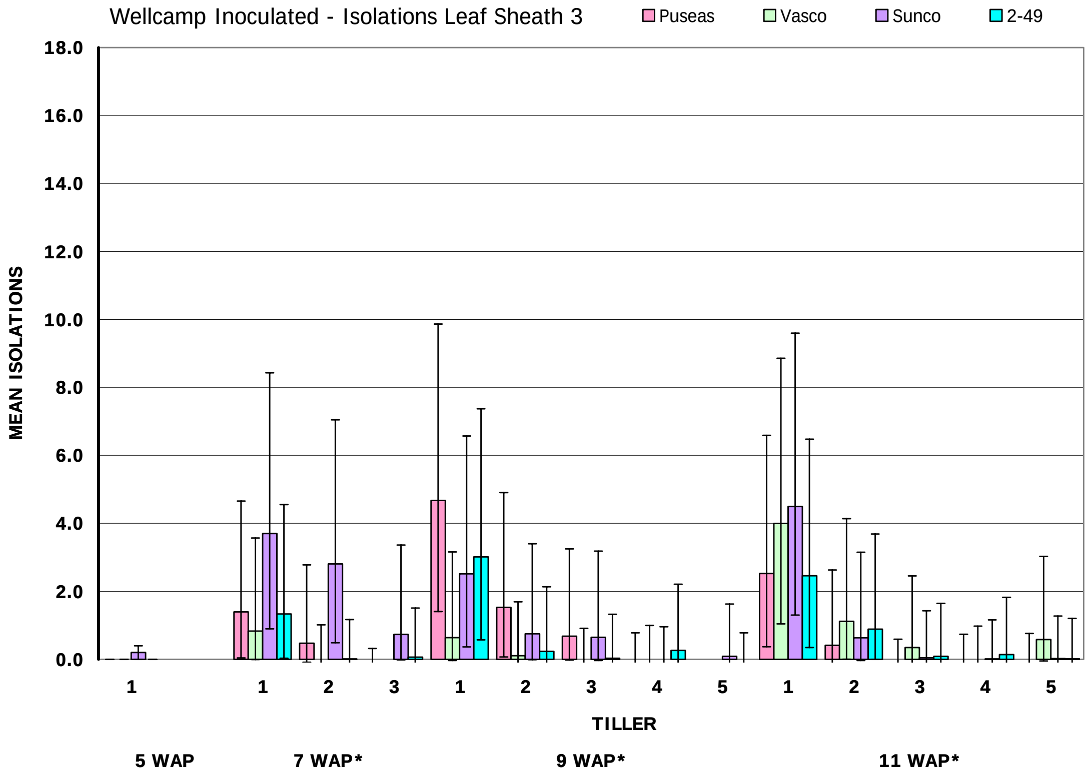


Table 3.16a Number of expanded Leaf Sheath 3's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	**6 WAP**	**8 WAP**			**10 WAP**				**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**10**	**10**	**5**	**3**	**10**	**8**	**4**		**10**	**7**	**4**	**2**	**10**	**9**	**6**	**3**
	0	0	0	0	3	0	0		9	3	1	0	8	6	3	0
Vasco	**10**	**10**	**5**	1	**10**	**7**	**3**		**10**	**7**	**2**		**10**	**6**	**4**	**3**
	0	0	0	0	3	0	0		3	2	0		4	1	0	0
Sunco	**10**	**10**	**5**		**10**	**6**	**3**	**2**	**10**	**8**	**6**	**2**	**10**	**9**	**9**	**2**
	0	0	0		4	0	1	0	4	2	1	0	1	0	0	0
2-49	**10**	**10**	**4**	**1**	**10**	**8**	**8**	**1**	**10**	**8**	**5**	**2**	**10**	**8**	**8**	**6**
	0	0	0	0	3	2	0	0	5	1	0	0	3	1	0	0
CPI133814	**10**	**10**	**6**		**10**	**7**	**4**		**10**	**9**	**8**	**1**	**10**	**10**	**9**	
	0	0	0		1	0	0		3	1	1	0	4	0	0	

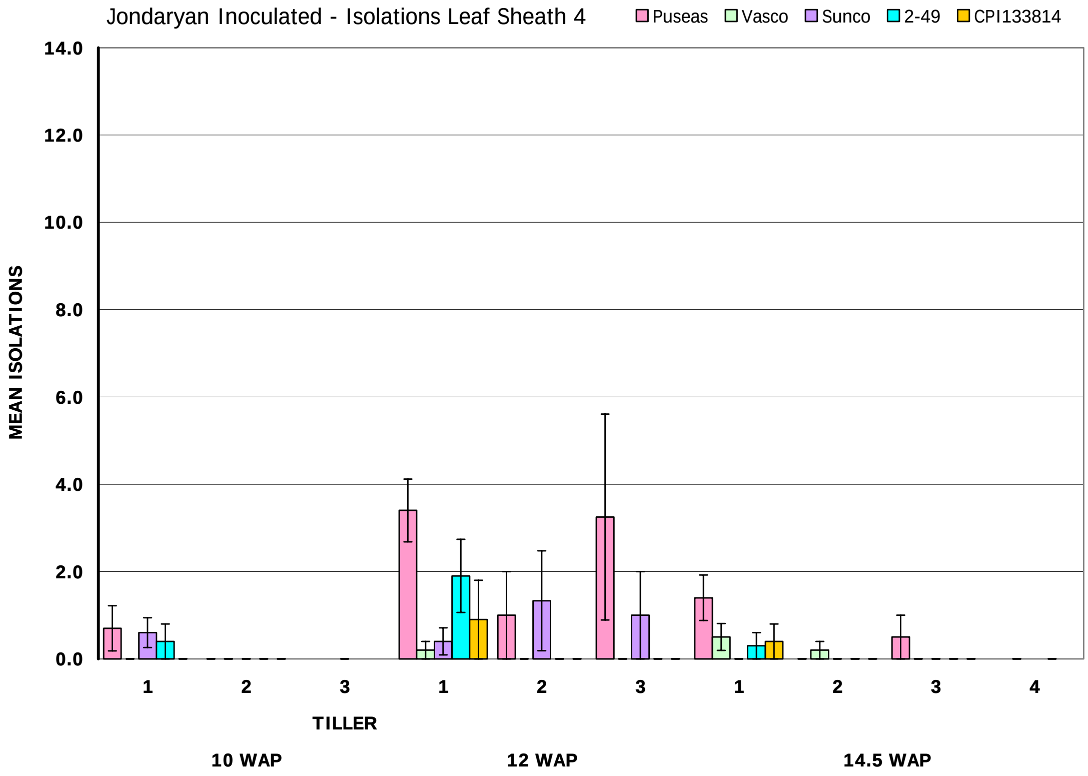
Table 3.16b Number of expanded Leaf Sheath 3's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**5 WAP**			**7 WAP**			**9 WAP**					**11 WAP**				
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**4**			**10**	**3**	**1**	**10**	**9**	**8**	**2**		**10**	**8**	**5**	**4**	**2**
	0			6	1	0	5	4	3	0		6	2	0	0	0
Vasco	**8**			**10**	**6**		**10**	**10**	**7**	**3**		**10**	**10**	**9**	**5**	**3**
	0			4	0		3	2	0	0		8	4	1	0	1
Sunco	**10**			**10**	**6**	**5**	**10**	**10**	**8**	**8**	1	**10**	**10**	**9**	**4**	**1**
	1			9	5	2	7	4	3	0	0	8	4	1	0	0
2-49	**8**			**10**	**8**	**3**	**10**	**10**	**10**	**8**	**6**	**10**	**9**	**8**	**6**	**5**
	0			6	0	0	6	2	1	2	0	6	4	1	1	0
CPI133814	**Not collected**															

Table 3.16c Probabilities for each factor and interaction in the isolation data for Leaf Sheath 3 in the Jondaryan (10, 12, 14.5 WAP) and Wellcamp trials (7, 9, 11 WAP).

Isolations	**Fixed Term**						
Leaf Sheath 3	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	0.013	0.06	<0.001	0.403	0.663	0.593	0.078
Wellcamp	0.595	0.559	<0.001	0.011	0.793	0.958	0.89

Figure 3.17 Mean number of isolations from Leaf Sheath 4 in the a) Jondaryan trial (10-14.5 WAP) and the b) Wellcamp trial (7-11 WAP). *Tillers and/or Harvest included in analysis.



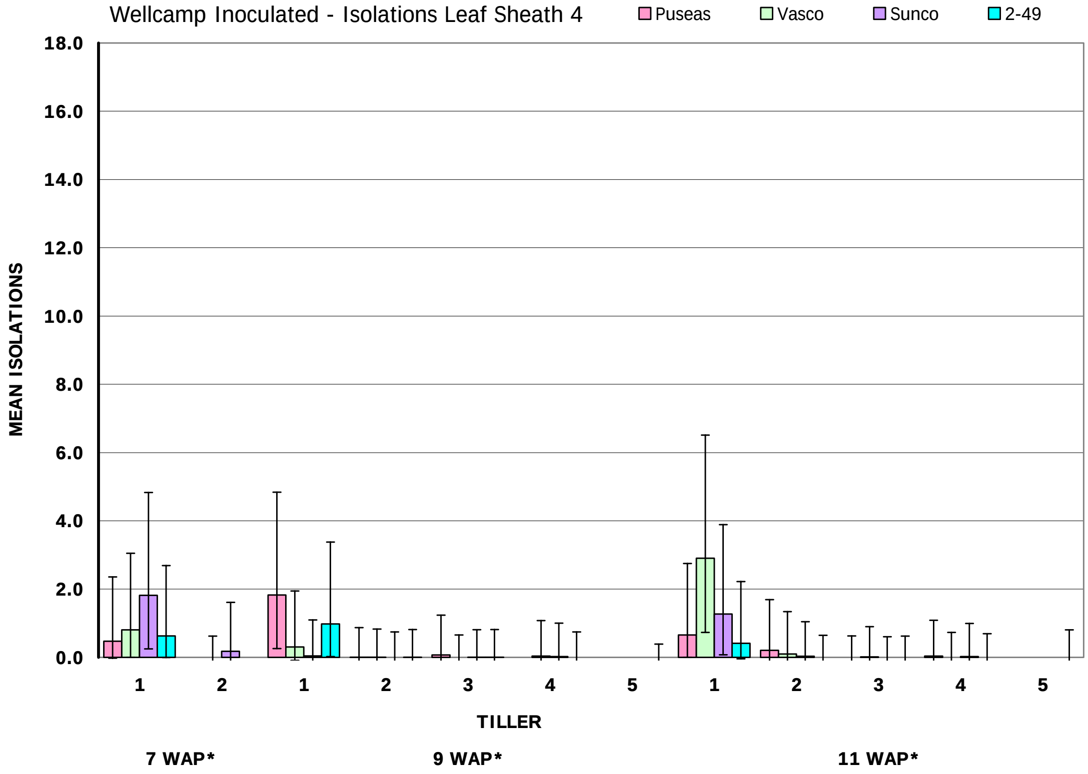


Table 3.17a Number of expanded Leaf Sheath 4's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	**6 WAP**	**8 WAP**		**10 WAP**			**12 WAP**				**14.5 WAP**			
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**6**	**10**	**2**	**10**	**5**		**10**	**4**	**4**		**10**	**8**	**6**	**1**
	0	0	0	2	0		8	1	2		7	0	1	0
Vasco	**5**	**10**		**10**	**3**		**10**	**6**	**2**		**10**	**5**	**4**	**2**
	0	0		0	0		2	0	0		3	1	0	0
Sunco	**8**	**9**		**10**	**4**	**2**	**10**	**6**	**3**	**1**	**10**	**9**	**7**	**2**
	0	0		3	0	0	2	2	1	0	0	0	0	0
2-49	**6**	**10**	**1**	**10**	**8**		**10**	**4**	**3**		**10**	**8**	**8**	**4**
	0	0	0	1	0		4	0	0		1	0	0	0
CPI133814		**9**		**10**	**4**		**10**	**8**	**2**		**10**	**9**	**6**	
		0		0	0		1	0	0		1	0	0	

Table 3.17b Number of expanded Leaf Sheath 4's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**7 WAP**			**9 WAP**					**11 WAP**				
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**10**			**10**	**6**	**2**			**10**	**6**	**4**	**1**	
	1			6	0	0			3	1	0	0	
Vasco	**10**	**1**		**10**	**8**	**7**	**1**		**10**	**9**	**7**	**4**	
	4	0		3	1	0	0		7	1	0	0	
Sunco	**9**	**1**		**10**	**9**	**7**	**1**		**10**	**9**	**6**	**2**	
	6	0		1	0	0	0		5	1	0	0	
2-49	**10**			**10**	**9**	**9**	**5**	**1**	**10**	**9**	**7**	**5**	**4**
	4			4	0	0	0	0	3	0	0	0	0
CPI133814	**Not collected**												

Table 3.17c Probabilities for each factor and interaction in the isolation data for Leaf Sheath 4 in the Wellcamp (7, 9, 11 WAP) trial.

Isolations	**Fixed Term**						
Leaf Sheath 4	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	not analysed						
Wellcamp	0.004	0.619	<0.001	0.084	0.709	0.983	0.89

CI of error of 1.32 differences between these genotypes or differences between harvests were never significant (Appendix 3E (Figure 3E.15)).

Leaf Sheath 4

Jondaryan trial

Isolations from LS4 were quite limited in most genotypes in the Jondaryan trial. 8 and 7 out of 10 Puseas primary tiller LS4's were infected at 12 and 14.5 (Table 3.17a).

At 12 WAP the mean isolations from Puseas primary tiller were significantly higher than isolations from Vasco, Sunco and CPI133814. 2-49 was almost significantly lower as well (Figure 3.17a). At 14.5 WAP isolations from Puseas primary tiller, were significantly higher than all genotypes. Data for LS4 isolations were not analysed.

Wellcamp trial

In the Wellcamp trial isolations were made from some LS4's in all genotypes at 7 WAP. Isolations were mostly restricted to the primary tiller in this plant part (Table 3.17b). Differences between genotypes in each tiller were not significant at any harvest (Figure 3.17b).

LS4 isolations were analysed in up to 5 tillers 7, 9 and 11 WAP. Tiller ($P<0.001$) and harvest ($P=0.004$) were highly significant (Table 3.17c). The primary tiller was significantly higher than all other tillers for LS4 isolations (Appendix 3E (Figure 3E.15)). At 7 WAP the mean number of isolations from LS4 was 0.681 compared with 0.235 and 0.295 for the next two harvests (Appendix 3E (Figure 3E.15)).

Leaf Sheaths 5, 6, 7 and 8

Jondaryan trial

Fpg was reisolated from 7 and 5 out of 10 Puseas primary tiller LS5's at 12 and 14.5 WAP respectively (Table 3.17d). It was randomly recorded in one or two LS6 of each genotype over 10 and 12 WAP (Table 3.17d). Data for LS5 and LS6 from the Jondaryan trial were not analysed.

Table 3.17d Number of expanded Leaf Sheath 5 and 6’s assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

Plant Part	**Leaf Sheath 5**									**Leaf Sheath 6**					
HARVEST	**8 WAP**	**10 WAP**		**12 WAP**			**14.5 WAP**			**10 WAP**	**12 WAP**		**14.5 WAP**		
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**1**	**2**	**1**	**2**	**3**
Puseas	**10**	**10**		**10**	**3**	**1**	**10**	**7**	**3**	**9**	**9**		**10**	**4**	**2**
	0	1		7	0	0	5	0	1	0	2		0	0	0
Vasco	**8**	**10**		**10**	**3**		**9**	**4**	**4**	**10**	**10**		**9**	**4**	**3**
	0	0		2	0		3	0	0	0	0		2	0	0
Sunco	**8**	**10**	**2**	**10**	**4**	**1**	**10**	**9**	**4**	**8**	**10**	**1**	**10**	**6**	**2**
	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
2-49	**9**	**9**		**10**	**3**	**1**	**10**	**8**	**6**	**6**	**10**	**1**	**10**	**5**	**1**
	0	1		2	0	0	0	0	0	0	1	0	0	0	0
CPI133814	**5**	**10**		**10**	**2**		**10**	**7**	**1**	**2**	**10**		**10**	**3**	
	0	0		1	0		1	1	0	0	1		0	1	

Table 3.17e Number of expanded Leaf Sheaths 5, 6 and 7 assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

Plant Part	**Leaf Sheath 5**									**Leaf Sheath 6**			**Leaf Sheath 7**	
HARVEST	**7 WAP**			**9 WAP**			**11 WAP**			**9 WAP**	**11 WAP**		**9 WAP**	**11 WAP**
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**1**	**2**	**1**	**1**
Puseas	**3**			**10**			**10**	**3**	**1**	**8**	**8**		**1**	**5**
	0			3			2	0	0	0	0		0	0
Vasco	**8**			**10**	**4**		**10**	**7**	**5**	**8**	**10**	**4**	**3**	**10**
	0			1	0		6	1	0	0	0	0	0	0
Sunco	**8**			**10**	**5**		**10**	**8**	**3**	**10**	**10**	**7**	**3**	**10**
	3			2	0		1	0	0	0	0	0	0	0
2-49	**10**			**10**	**6**	**2**	**10**	**7**	**5**	**10**	**10**	**4**	**7**	**10**
	2			2	0	0	3	0	0	0	0	0	0	0
CPI133814	**Not collected**									**Not collected**			**Not collected**	

Wellcamp trial

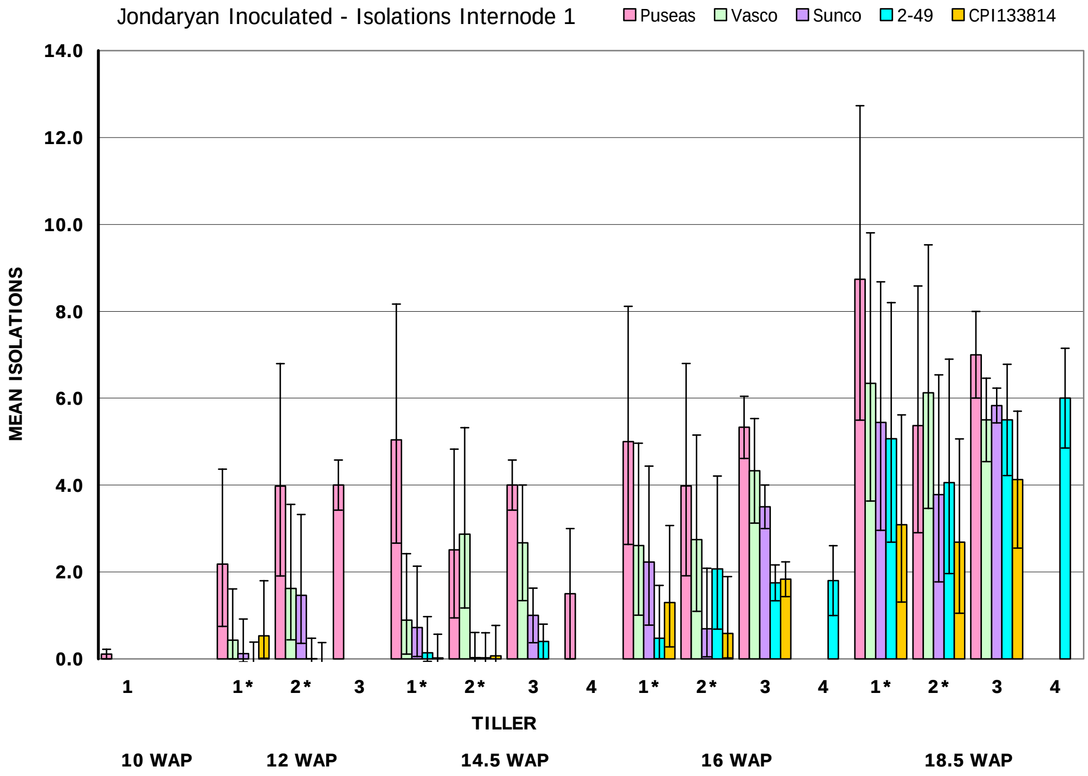
In the Wellcamp trial isolations from LS5 were first recorded in 2-49 and Sunco at 7 WAP and in a few plants of all genotypes at 9 WAP (Table 3.17e). At 11 WAP there were 6 Vasco, 2 Puseas, 3 2-49 and 1 Sunco plant with isolations made from the primary tiller LS5. No isolations were recorded from LS6, 7 and 8 in the Wellcamp field trial (Table 3.17e). Data for these LS’s were not analysed.

Internode 1

Jondaryan trial

In the Jondaryan field trial *Fpg* was first reisolated from 1 Puseas I1 at 10 WAP, from Vasco, Sunco and CPI133814 at 12 WAP and from 2-49 at 14.5 WAP (Table

Figure 3.18 Mean number of isolations from Internode 1 in the a) Jondaryan trial (10-18.5 WAP) and the b) Wellcamp trial (13-22 WAP). *Tillers and/or Harvest included in analysis.



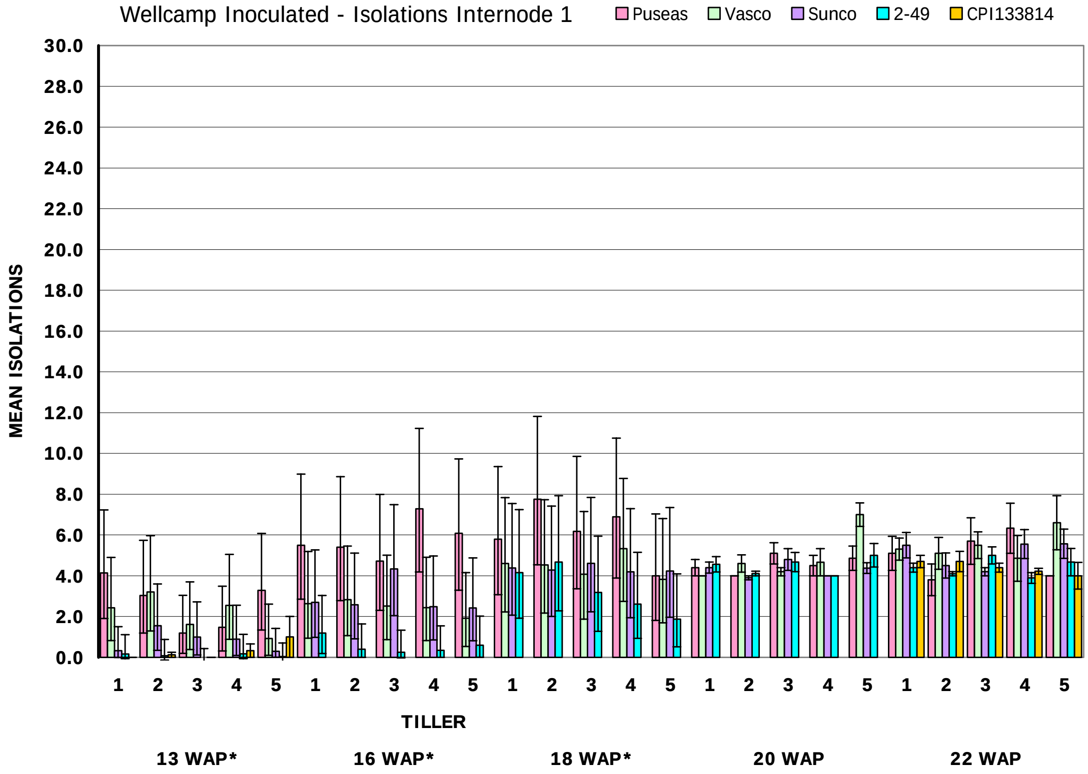


Table 3.18a Number of expanded Internode 1's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	10 WAP	12 WAP			14.5 WAP				16 WAP				18.5 WAP			
TILLER	1	1	2	3	1	2	3	4	1	2	3	4	1	2	3	4
Puseas	**9**	**9**	**4**	**3**	**10**	**7**	**4**	**1**	**10**	**7**	**6**		**10**	**9**	**5**	**1**
	1	7	4	3	10	6	4	1	10	7	6		10	9	5	1
Vasco	**1**	**10**	**3**		**10**	**4**	**3**		**10**	**7**	**3**		**10**	**7**	**4**	
	0	4	3		6	4	1		8	5	3		10	7	4	
Sunco	**1**	**9**	**2**		**10**	**9**	**5**		**10**	**5**	**2**		**10**	**9**	**6**	
	0	1	1		5	1	2		8	3	2		10	9	6	
2-49		**8**	**2**		**10**	**8**	**4**		**10**	**10**	**8**	**5**	**10**	**9**	**6**	**3**
		0	0		2	1	1		4	8	6	3	9	7	5	3
CPI133814		**9**			**10**	**6**			**10**	**8**	**5**		**10**	**9**	**8**	
		4			1	1			7	4	5		8	7	5	

Table 3.18b Number of expanded Internode 1's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	9 WAP			11 WAP			13 WAP					16 WAP					18 WAP					22 WAP				
TILLER	1	2	3	1	2	3	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
Puseas	**6**			**7**	**4**	**2**	**10**	**10**	**9**	**8**	**5**	**10**	**10**	**10**	**10**	**10**	**10**	**10**	**10**	**9**	**7**	**10**	**10**	**10**	**6**	**4**
	4			0	0	0	9	9	5	4	4	10	9	9	10	9	10	10	9	9	6	9	8	9	6	4
Vasco				**9**	**5**	**3**	**10**	**10**	**10**	**8**	**6**	**10**	**10**	**10**	**9**	**5**	**10**	**10**	**10**	**8**	**6**	**10**	**10**	**10**	**7**	**5**
				0	1	1	8	9	6	6	3	8	8	8	7	4	10	10	10	8	5	10	10	10	6	5
Sunco				**4**	**2**	**1**	**10**	**10**	**10**	**10**	**8**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**8**	**7**
				0	0	0	3	6	5	5	2	8	9	10	7	6	10	10	10	10	8	10	9	10	8	7
2-49				**7**	**1**	**1**	**10**	**10**	**10**	**9**	**7**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**10**	**8**	**10**	**10**	**10**	**9**	**6**
				1	0	0	2	0	0	2	1	6	4	3	4	4	10	10	8	9	5	10	10	10	9	6
CPI133814							**9**	**8**	**7**	**6**	**2**											**10**	**10**	**10**	**9**	**8**
							0	1	0	0	1											10	10	10	9	7

Table 3.18c Probabilities for each factor and interaction in the isolation data for Internode 1 in the Jondaryan (12, 14.5, 16, 18.5 WAP) and Wellcamp (13, 16, 18 WAP) trials.

Isolations Internode 1	Fixed Term						
	Harvest	Genotype	Tiller	Harv/Geno	Harv/Till	Till/Geno	Harv/Geno/Till
Jondaryan	<0.001	<0.001	0.118	0.338	0.024	0.035	0.17
Wellcamp	<0.001	<0.001	0.058	0.276	0.648	0.55	0.623

3.18a). At the final harvest (18.5 WAP) all expanded Puseas, Vasco and Sunco and the majority of 2-49 and CPI133814 I1's were infected in all tillers (Table 3.18a).

Differences were seen between genotypes in the severity of infection of I1 in each tiller at each harvest. The number of isolations from I1 was generally higher in Puseas than Vasco; however the differences were usually not significant (Figure 3.18a). At 14.5 WAP Puseas was significantly higher than Sunco, 2-49 and CPI133814 in all tillers. At 16 WAP Puseas was significantly higher than 2-49 and CPI133814 in 2 tillers and at 18.5 WAP most differences between genotypes were not significant (Figure 3.18a).

Isolation data for I1 was analysed for the primary and 2nd tiller over the four harvests 12 to 18.5 WAP. Harvest and genotype were highly significant ($P<0.001$) (Table 3.18c). The mean isolations from the primary and 2nd tillers of all genotypes were not significantly different at 12 and 14.5 WAP. There was a significant increase between 14.5 and 16 and between 16 and 18 WAP (Appendix 3E (Figure 3E.16)). Over the 4 harvests Puseas was significantly higher than Sunco, CPI133814 and 2-49 with Vasco also higher than 2-49 and CPI133814 (Appendix 3E (Figure 3E.16)).

Wellcamp trial

Isolations were first made from Puseas I1 9 WAP in the Wellcamp trial (Table 3.18b). In Puseas and Vasco isolations were recorded in the majority of expanded I1's in all tillers at 13 WAP. Approximately half of Sunco I1's were infected and only a few 2-49 and CPI133814 plants recorded I1 isolations at this time. By 20 WAP 100% incidence of infection was reached in all tillers of all genotypes (Table 3.18c).

The number of isolations from Puseas I1 was significantly higher than 2-49 in most tillers at 13 and 16 WAP. By 18 WAP differences between genotypes were not significant (Figure 3.18b).

I1 data was analysed across all 5 tillers at 13, 16 and 18 WAP in the Wellcamp trial. The harvest and genotype effects were highly significant ($P<0.001$) (Table 3.18c).

The mean number of isolations increased at each harvest with the isolations at 13 WAP significantly lower than the 16 and 18 WAP harvests (Appendix 3E (Figure 3E.16)). With harvests and tillers combined 2-49 was significantly lower than Sunco, Vasco and Puseas, and Sunco was significantly lower than Puseas (Appendix 3E (Figure 3E.16)).

Internode 2

Jondaryan trial

Isolations were first recorded in Puseas and Vasco at 12 WAP in the Jondaryan trial (Table 3.19a). *Fpg* was reisolated from 1 Sunco I2 at 14.5 and 1 Sunco and 1 CPI133814 I2 at 16 WAP. Isolations were only recorded in 2-49 tillers at the final harvest (18.5 WAP).

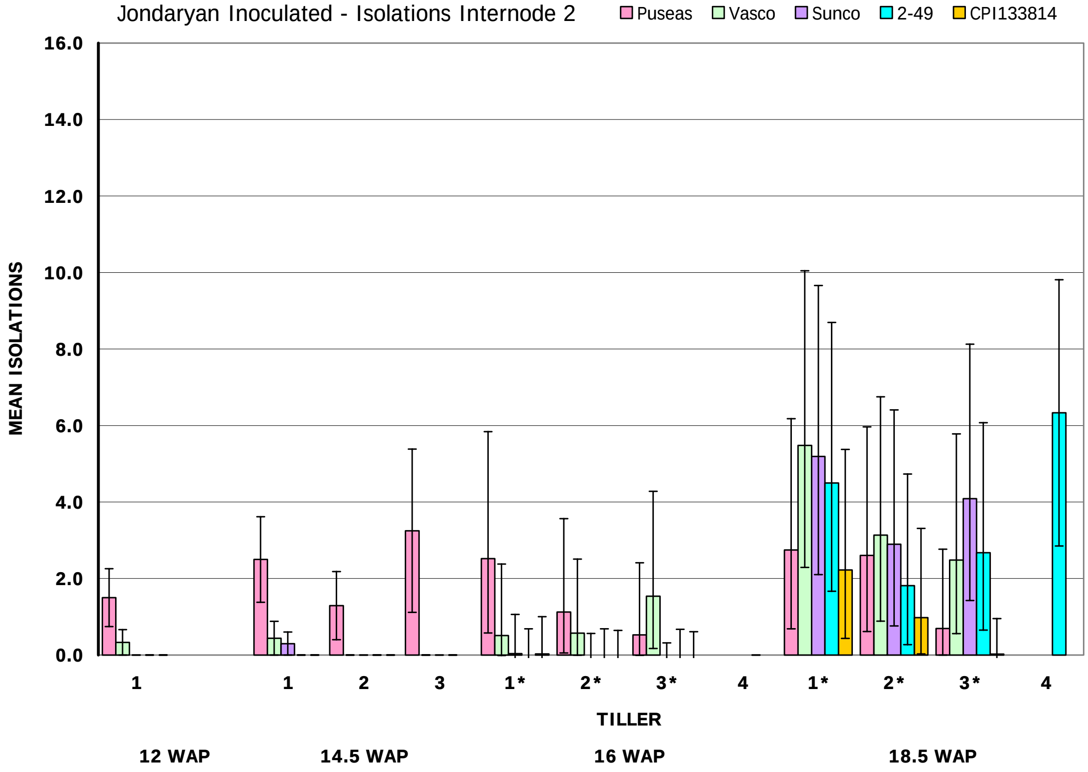
The mean numbers of isolations from Puseas and Vasco tillers were mostly significantly higher than Sunco, CPI133814 and 2-49 at 12, 14.5 and 16 WAP (Figure 3.19a). Consistent isolations from all genotypes were only recorded at 18.5 WAP and differences between genotypes were not significant (Figure 3.19a). This may indicate that differences between genotypes in I2 isolations are more associated with incidence (Table 3.19a) than severity of infection (Figure 3.19a).

I2 isolations were analysed over three tillers at 16 and 18 WAP in the Jondaryan trial. From this data a significant harvest ($P<0.001$) and tiller ($P=0.001$) effect as well as a significant harvest/genotype interaction ($P=0.006$) were present (Table 3.19c). The average of the primary tiller was significantly higher than the 3rd tiller over these two harvests (Appendix 3E (Figure 3E.17)). The mean number of isolations from I2 increased in all genotypes from 16 to 18.5 WAP, however the difference between the two harvests were only significant in 2-49 and CPI133814 (Appendix 3E (Figure 3E.17)).

Wellcamp trial

Isolations were recorded from some I2's of all genotypes except CPI133814 at 13 WAP (Table 3.19b). By 18 WAP the pathogen was reisolated from the majority of I2's, except for the 3rd, 4th and 5th tillers of 2-49 (Table 3.19b).

Figure 3.19 Mean number of isolations from Internode 2 in the a) Jondaryan trial (12-18.5 WAP) and the b) Wellcamp trial (13-22 WAP). *Tillers and/or Harvest included in analysis.



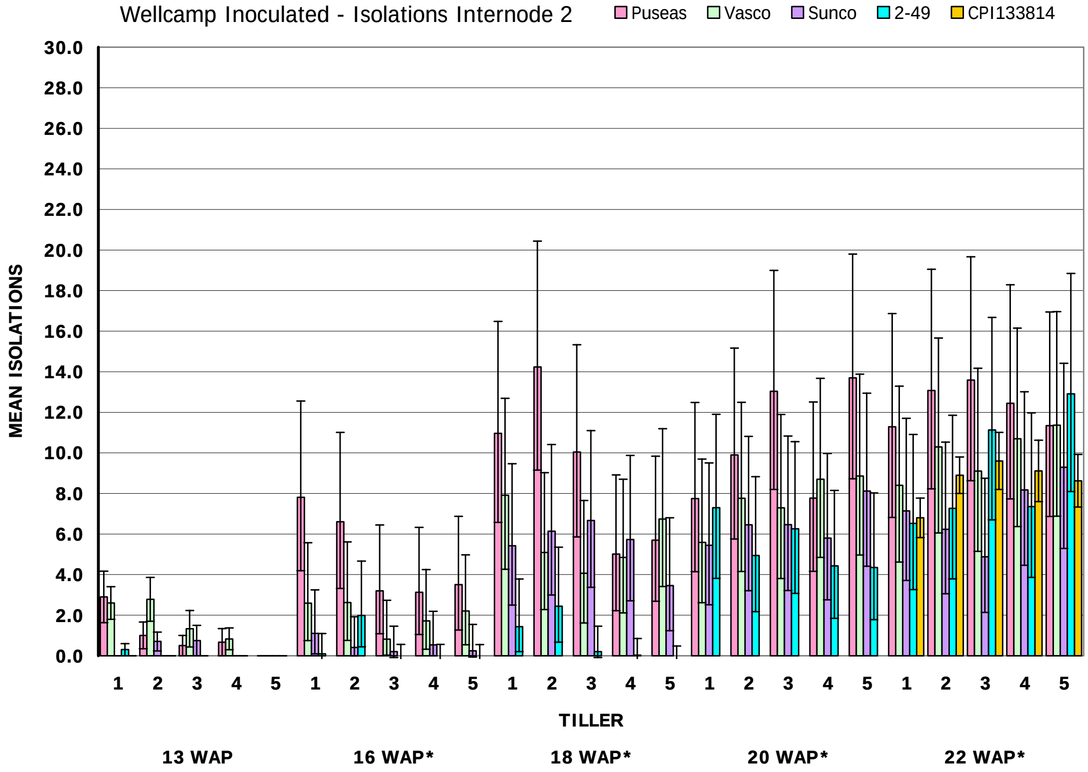


Table 3.19a Number of expanded Internode 2's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	**10 WAP**	**12 WAP**		**14.5 WAP**			**16 WAP**				**18.5 WAP**			
TILLER	**1**	**1**	**2**	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**1**	**8**	**1**	**10**	**6**	**4**	**10**	**7**	**4**		**10**	**9**	**5**	**1**
	0	3	1	4	2	2	8	3	2		6	6	3	1
Vasco		**6**		**10**	**4**	**2**	**10**	**6**	**2**		**10**	**7**	**4**	
		1		1	0	0	3	3	2		9	5	4	
Sunco		**6**		**10**	**8**	**3**	**10**	**5**	**2**		**10**	**9**	**6**	
		0		1	0	0	1	0	0		10	6	6	
2-49		**3**		**10**	**6**	**2**	**10**	**10**	**6**	**3**	**10**	**9**	**6**	**3**
		0		0	0	0	0	0	0	0	7	5	4	2
CPI133814		**7**		**9**	**2**		**10**	**7**	**5**		**10**	**9**	**8**	
		0		0	0		1	0	0		6	4	1	

Table 3.19b Number of expanded Internode 2's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**11 WAP**			**13 WAP**					**16 WAP**					**18 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**4**			**10**	**8**	**6**	**6**	**3**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**9**	**6**	**10**	**10**	**10**	**6**	**4**
	0			5	2	1	1	0	9	9	5	7	6	10	10	9	6	3	10	9	10	6	4
Vasco	**3**			**10**	**9**	**9**	**6**	**2**	**10**	**10**	**10**	**9**	**5**	**10**	**10**	**10**	**8**	**6**	**10**	**10**	**10**	**7**	**5**
	0			6	6	3	2	0	6	6	4	5	3	9	7	7	7	5	10	10	10	7	5
Sunco	**1**			**10**	**10**	**8**	**8**	**8**	**10**	**10**	**10**	**10**	**8**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**9**	**7**
	1			0	2	1	0	0	5	4	2	3	3	10	10	9	10	7	10	9	9	9	7
2-49				**10**	**8**	**7**	**3**	**2**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**10**	**8**	**10**	**10**	**10**	**9**	**6**
				1	0	0	0	0	1	1	0	0	0	7	7	3	1	0	9	9	10	9	6
CPI133814				**6**	**4**	**1**	**1**												**10**	**10**	**10**	**9**	**8**
				0	0	0	0												10	10	10	9	8

Table 3.19c Probabilities for each factor and interaction in the isolation data for Internode 2 in the Jondaryan (16, 18.5 WAP) and Wellcamp trials (16, 18, 20, 22 WAP).

Isolations Internode 2	**Fixed Term**						
	Harvest	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	<0.001	0.036	0.001	0.006	0.213	0.724	0.68
Wellcamp	<0.001	<0.001	0.104	0.002	<0.001	0.405	0.179

Isolations from Puseas and sometimes Vasco I2 were significantly higher than 2-49 in most tillers at 13, 16 and 18 WAP. Differences between Puseas and Sunco were only significant in the primary and 2nd tiller at 16 WAP. At 20 WAP Puseas was significantly higher than 2-49 in the 5th tiller only and at 22 WAP differences between genotypes were not significant in any tillers (Figure 3.19b).

I2 isolation data was analysed over the 5 tillers 16, 18, 20 and 22 WAP in the Wellcamp trial. Both harvest and genotype were highly significant ($P<0.001$). However, significant harvest/tiller ($P<0.001$) and harvest/genotype ($P=0.002$) interactions were also present (Table 3.19c).

At 16 WAP 2-49 was significantly lower than Puseas and Vasco with Sunco also significantly lower than Puseas. There was a significant increase in isolations from Sunco at 18 WAP and 2-49 was significantly lower than all genotypes at this time. There was a significant increase in the mean number of isolations from 2-49 between 18 and 20 WAP and differences between genotypes were not significant at the last two harvests 20 and 22 WAP (Appendix 3E (Figure 3E.17)).

The harvest/tiller interaction was interesting with the mean numbers of isolations not significantly different between tillers at 16 WAP. At 18 WAP the 5th tiller isolations were significantly lower than the primary and 2nd tiller, and the 4th was also significantly lower than the 2nd. At 20 and 22 WAP differences between tillers were again not significant (Appendix 3E (Figure 3E.16)).

Internode 3

Jondaryan trial

Limited isolations were recorded from I3 in the Jondaryan trial (Table 3.20a). At maturity (18.5 WAP) only 1 Puseas, 4 Vasco, 2 Sunco, 3 2-49 and 1 CPI133814 primary tiller I3's were infected with *Fpg*.

Differences between genotypes in each tiller at each harvest were not significant (Figure 3.20a). Data for I3 was only analysed for the primary tiller at 18.5 WAP and the genotype effect was not significant (Table 3.20c).

Wellcamp trial

Isolations were first recorded in Puseas and Vasco I3 at 13 WAP, in 1 Sunco tiller at 16 WAP and in 2-49 at 18 WAP (Table 3.20b). At 22 WAP all I3's of Puseas and Vasco were infected and the majority of 2-49, Sunco and CPI133814 plants sampled had isolations from I3.

At 16 WAP differences in the number of isolations between Puseas and Vasco were not significant in any tillers (Figure 3.20b). At 18 WAP isolations from Puseas were significantly higher than all other genotypes in the primary tiller and higher than 2-49 in the 2nd and 3rd tillers. At 20 WAP Puseas was higher than 2-49 in all tillers and higher than Sunco in the 3rd, 4th and 5th tillers. At 22 WAP differences between genotypes were not significant in the primary tiller, 2-49 was significantly lower than Puseas and Vasco in the 2nd and 4th and 5th tillers (Figure 3.20b).

All 5 tillers were included in the analysis of I3 over the 4 harvests 16 to 22 WAP in the Wellcamp trial. The effects harvest, tiller and genotype were all highly significant ($P<0.001$) for this plant part (Table 3.20c). Charts of these factors are presented in Appendix 3E (Figure 3E.18). There was a significant increase in the number of isolations from I3 at each harvest analysed. Overall 2-49 and Sunco were significantly lower than Puseas and Vasco. The primary tiller was significantly higher than the 3rd, 4th and 5th, and the 2nd tiller was also significantly higher than the 4th and 5th tillers (Appendix 3E (Figure 3E.18)).

Internode 4

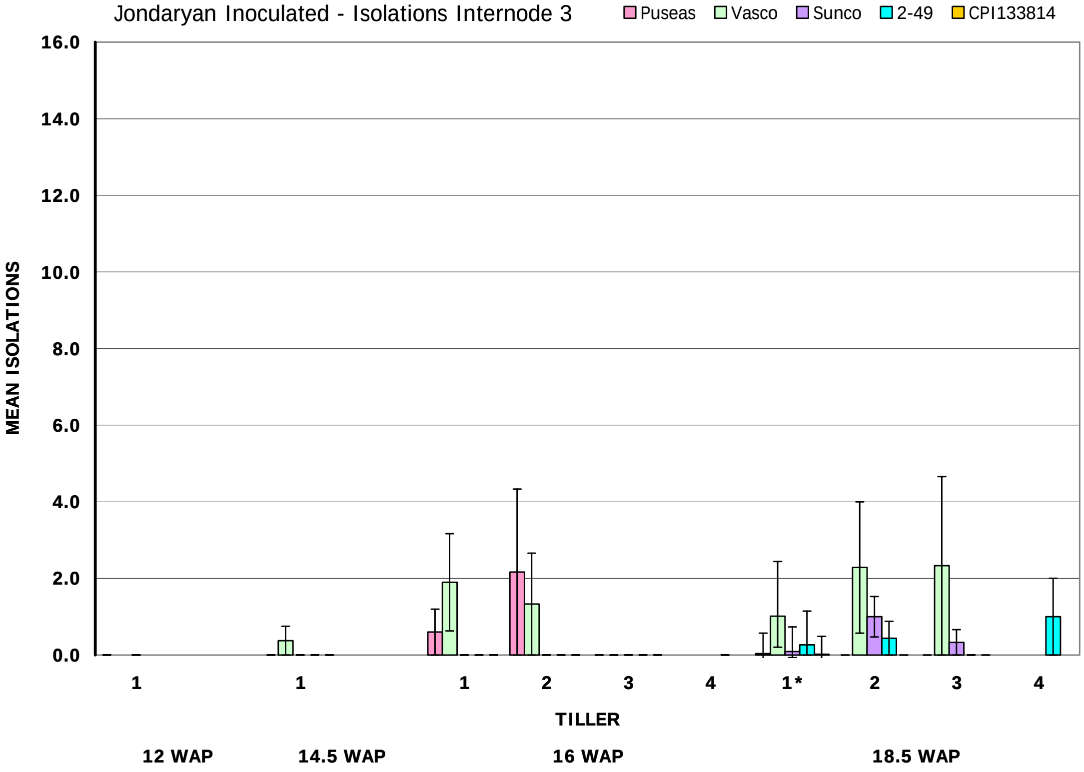
Jondaryan trial

Isolations from I4 were only made in a couple of Vasco plants throughout the Jondaryan trial (Table 3.21a) and this data was not analysed.

Wellcamp trial

In the Wellcamp trial isolations were first made from I4 at 16 WAP in Puseas and Vasco, 18 WAP in Sunco and 20 WAP in 2-49. CPI133814 was only collected at 22 WAP and isolations were recorded from I4 in all tillers at this time (Table 3.21b).

Figure 3.20 Mean number of isolations from Internode 3 in the a) Jondaryan trial (12-18.5 WAP) and the b) Wellcamp trial (13-22 WAP). *Tillers and/or Harvest included in analysis.



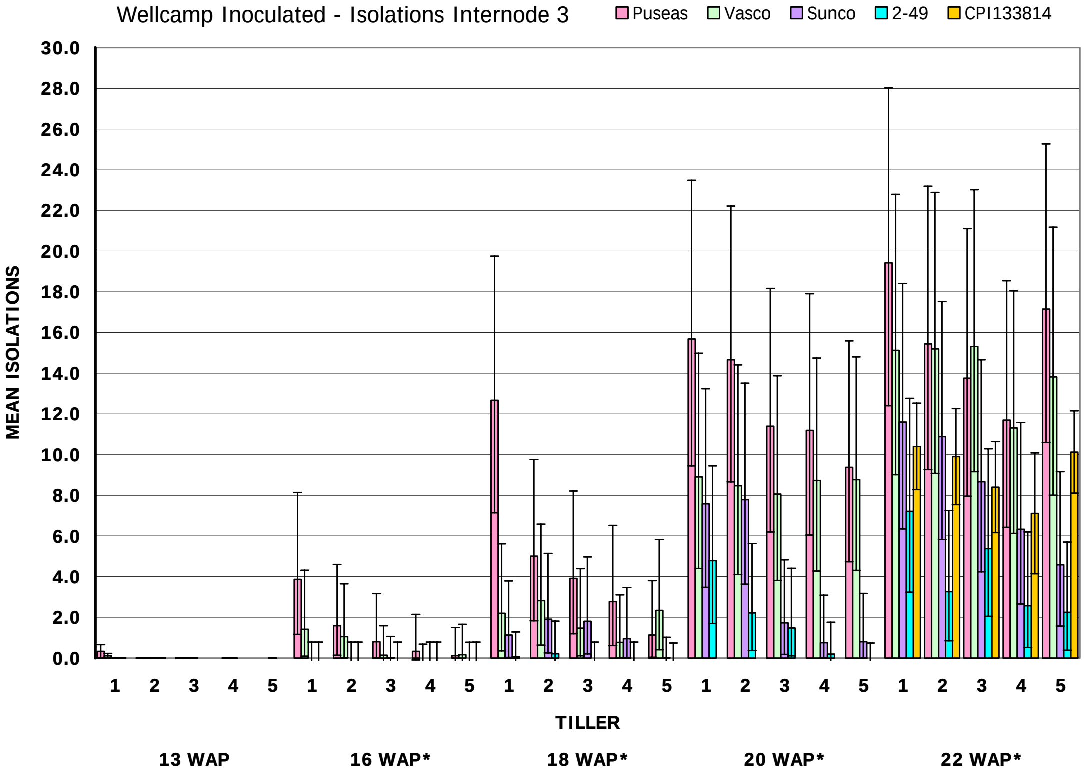


Table 3.20a Number of expanded Internode 3's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	12 WAP	14.5 WAP		16 WAP				18.5 WAP			
TILLER	1	1	2	1	2	3	4	1	2	3	4
Puseas	**4**	**9**	**1**	**10**	**6**	**2**		**9**	**8**	**4**	**1**
	0	0	0	1	1	0		1	0	0	0
Vasco		**8**		**10**	**6**	**2**		**10**	**7**	**3**	
		0		2	1	0		4	2	1	
Sunco		**9**		**10**	**5**	**2**		**10**	**9**	**5**	
		0		0	0	0		2	3	1	
2-49		**4**	**1**	**10**	**8**	**5**	**3**	**10**	**8**	**6**	**3**
		0	0	0	0	0	0	3	1	0	1
CPI133814		**7**	**1**	**10**	**7**	**2**		**10**	**8**	**4**	
		0	0	0	0	0		1	0	0	

Table 3.20b Number of expanded Internode 3's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	13 WAP			16 WAP					18 WAP					20 WAP					22 WAP				
TILLER	1	2	3	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
Puseas	**9**	**3**		**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**8**	**6**	**10**	**10**	**10**	**9**	**7**	**10**	**10**	**10**	**6**	**4**
	1	0		6	4	4	1	2	9	7	5	4	3	10	8	10	8	7	10	10	7	6	4
Vasco	**9**	**5**	**1**	**10**	**10**	**10**	**9**	**5**	**10**	**10**	**9**	**7**	**5**	**10**	**10**	**10**	**5**	**4**	**10**	**10**	**10**	**7**	**5**
	1	0	0	4	3	1	5	1	7	6	3	3	3	10	10	9	5	4	10	10	10	7	5
Sunco	**10**	**7**	**4**	**10**	**10**	**10**	**9**	**8**	**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**9**	**8**	**10**	**9**	**10**	**9**	**7**
	0	0	0	0	0	1	0	0	6	6	5	5	1	9	9	6	4	3	10	8	8	7	5
2-49	**4**			**10**	**10**	**10**	**10**	**9**	**10**	**10**	**10**	**10**	**8**	**9**	**9**	**9**	**8**	**7**	**10**	**10**	**10**	**9**	**6**
	0			0	0	0	0	0	1	2	0	0	0	8	6	5	2	0	8	7	7	6	5
CPI133814	**not developed**																		**10**	**10**	**10**	**9**	**8**
																			9	9	8	7	8

Table 3.20c Probabilities for each factor and interaction in the isolation data for Internode 3 in the Jondaryan (18.5 WAP) and Wellcamp trials (16, 18, 20, 22 WAP).

Isolations Internode 3	Fixed Term						
	Harvest	Genotype	Tiller	Harv/Geno	Harv/Till	Till/Geno	Harv/Geno/Till
Jondaryan		0.172					
Wellcamp	<0.001	<0.001	<0.001	0.363	0.661	0.283	0.121

At 16 and 18 WAP differences in the number of isolations between genotypes were not significant (Figure 3.21). At 20 WAP the isolations from Puseas primary tiller were significantly higher than all tillers of all genotypes. At 22 WAP Puseas and Vasco had similar isolation counts in the primary tiller and these were significantly higher than the other genotypes. Isolations from 2-49 I4 were significantly lower than Puseas and Vasco in all tillers at this final harvest.

All I4 tillers were analysed in the Wellcamp trial over 16, 18, 20 and 22 WAP. The factors harvest, genotype and tiller were all highly significant for this plant part as were all the two–way interactions ($P<0.001$) (Table 3.21c).

While the overall difference in infection between genotypes at each harvest was not great enough to be significant at the 95% CI level, patterns of change in levels of infection at each harvest were seen in each genotype. There was very little or no change in the number of isolations at each harvest in 2-49 and Sunco, while Puseas had a sharp increase between 18 and 20 WAP with little difference between 20 and 22 WAP. Vasco had a more gradual increase at each harvest (Appendix 3E (Figure 3E.18)).

Differences in the number of isolations from each tiller were not significant within genotypes, except Puseas primary tiller was significantly higher than the 5th. However the extent of difference between genotypes varied for each tiller. Puseas was significantly higher than 2-49 and Sunco in the primary tiller, significantly higher than 2-49 in the 2nd tiller and differences in the 3rd, 4th and 5th tiller were not significant (Appendix 3E (Figure 3E.18)).

Internodes 5 and 6 and the Peduncle

Jondaryan trial

Internode 5 did not consistently expand in all genotypes in the Jondaryan trail and therefore is not included in these results. Isolations were attempted from the peduncle 16 and 18.5 WAP and no isolations were recorded in any genotypes from this tissue (Table 3.22a).

Wellcamp trial

Isolations were recorded from I5 in the Wellcamp trial from 18 WAP (Table 3.22b). At 22 WAP isolations were made from all tillers in Vasco, from the 1st 3 tillers in Puseas and Sunco and from only 1 tiller in 2-49 and CPI133814.

Data for I5 isolations was not analysed however differences between genotypes were sometimes significant (Figure 3.22). At 20 WAP isolations from Puseas primary tiller were much higher than the other genotypes. At 22 WAP Vasco was usually significantly highest in each tiller (Figure 3.22).

Isolations were made from I6 in only a couple of Puseas and Vasco plants across the Wellcamp field trial (Table 3.22c). Single isolations were also recorded from the peduncle in Puseas, Vasco and one CPI133814 5th tiller at 22 WAP (Table 3.22d).

Figure 3.21 Mean number of isolations from Internode 4 in the Wellcamp trial (13-22 WAP). *Tillers and/or Harvest included in analysis.

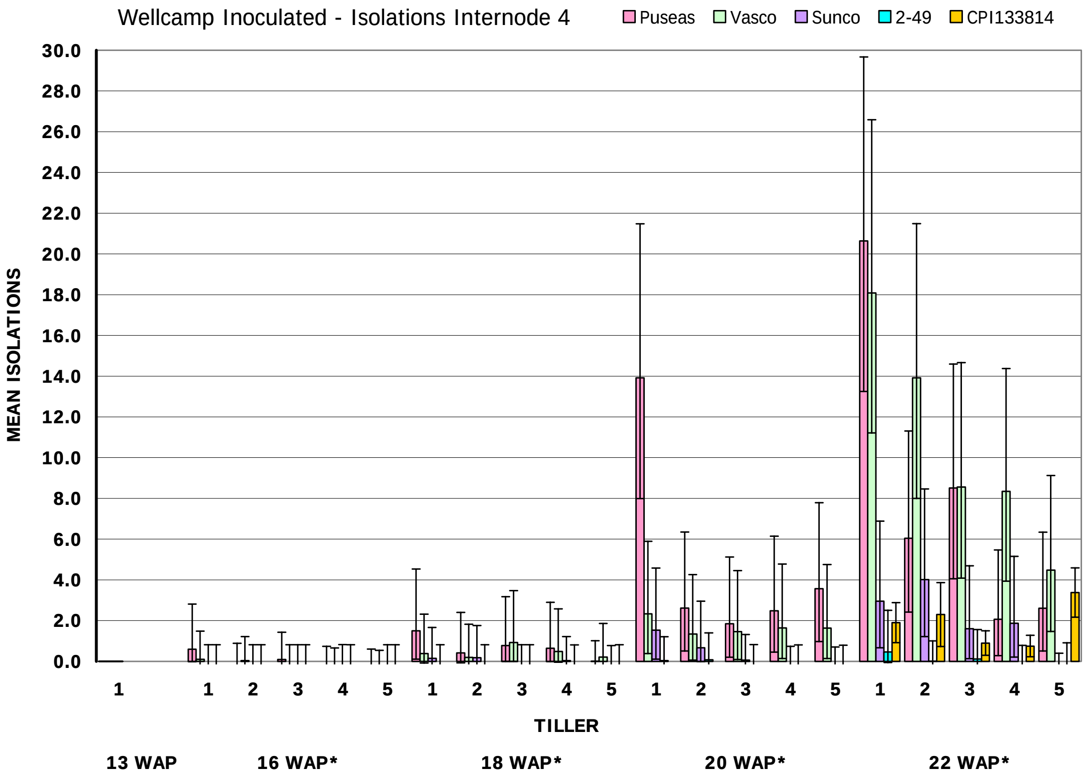


Table 3.21a Number of expanded Internode 4's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	14.5 WAP	16 WAP			18.5 WAP		
TILLER	**1**	**1**	**2**	**3**	**1**	**2**	**3**
Puseas	**3**	**9**	**1**		**7**	**4**	**1**
	0	0	0		0	0	0
Vasco	**1**	**8**	**4**	**1**	**7**	**7**	**3**
	0	1	0	0	1	1	0
Sunco		**7**	**3**	**1**	**9**	**8**	**4**
		0	0	0	0	0	0
2-49	**1**	**8**	**7**	**3**	**9**	**5**	**4**
	0	0	0	0	0	0	0
CPI133814	**2**	**10**	**6**	**1**	**10**	**7**	**4**
	0	0	0	0	0	0	0

Table 3.21b Number of expanded Internode 4's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	13 WAP	16 WAP					18 WAP					20 WAP					22 WAP				
TILLER	**1**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**6**	**10**	**10**	**9**	**7**	**5**	**10**	**10**	**9**	**7**	**6**	**10**	**10**	**10**	**9**	**7**	**10**	**10**	**10**	**6**	**4**
	0	3	0	2	1	0	5	2	3	2	0	10	6	5	5	3	9	8	4	3	2
Vasco	**5**	**10**	**10**	**10**	**6**	**4**	**10**	**10**	**9**	**7**	**5**	**10**	**10**	**10**	**5**	**4**	**10**	**10**	**10**	**7**	**5**
	0	1	1	0	0	0	2	1	2	2	1	6	5	6	3	2	10	9	9	6	4
Sunco	**5**	**10**	**10**	**10**	**9**	**8**	**10**	**10**	**10**	**10**	**9**	**9**	**10**	**10**	**9**	**8**	**10**	**10**	**10**	**9**	**7**
	0	0	0	0	0	0	1	2	0	1	0	4	4	1	0	0	6	6	5	4	1
2-49		**10**	**10**	**10**	**10**	**6**	**10**	**10**	**10**	**9**	**8**	**9**	**9**	**9**	**8**	**7**	**10**	**10**	**10**	**9**	**6**
	not	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	3	1	2	0	1
CPI133814	**developed**																**10**	**10**	**10**	**8**	**8**
																	4	3	2	2	5

Table 3.21c Probabilities for each factor and interaction in the isolation data for Internode 4 in the Wellcamp trial (16, 18, 20, 22 WAP).

Isolations	**Fixed Term**						
Internode 4	**Harvest**	**Genotype**	**Tiller**	**Harv/Geno**	**Harv/Till**	**Till/Geno**	**Harv/Geno/Till**
Jondaryan	not analysed						
Wellcamp	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	0.651

Figure 3.22 Mean number of isolations from Internode 5 in the Wellcamp trial (18-22 WAP). *Tillers and/or Harvest included in analysis.

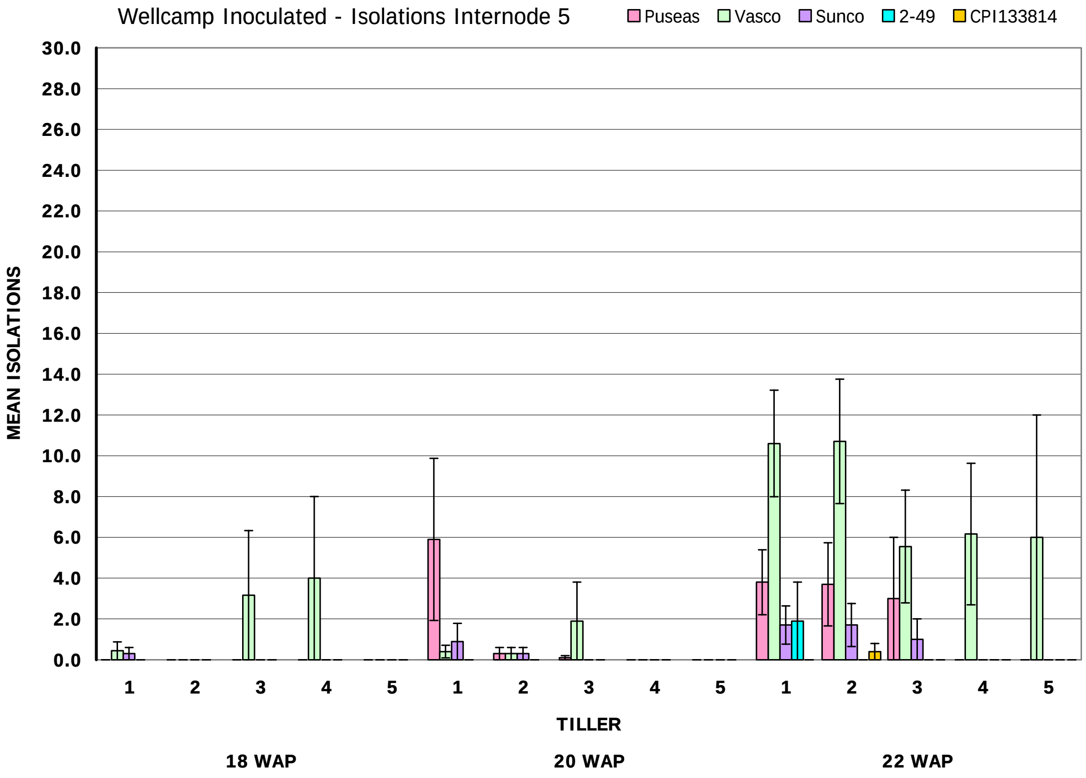


Table 3.22a Number of expanded Peduncle's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Jondaryan trial.

HARVEST	**16 WAP**				**18.5 WAP**			
TILLER	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**
Puseas	**7**	**1**	**1**		**9**	**4**	**3**	**1**
	0	0	0		0	0	0	0
Vasco	**8**	**3**	**1**		**10**	**7**	**3**	
	0	0	0		0	0	0	
Sunco	**10**	**4**	**1**		**10**	**8**	**5**	
	0	0	0		0	0	0	
2-49	**9**	**6**	**5**	**2**	**10**	**7**	**4**	**1**
	0	0	0	0	0	0	0	0
CPI133814	**10**	**3**	**1**		**10**	**7**	**3**	
	0	0	0		0	0	0	

Table 3.22b Number of expanded Internode 5's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**9**	**7**	**4**	**1**	**1**	**10**	**9**	**8**	**4**	**2**	**10**	**10**	**10**	**7**	**5**	**10**	**10**	**6**	**3**	**2**
	0	0	0	0	0	0	0	0	0	0	4	3	1	0	0	5	4	1	0	0
Vasco	**10**	**7**	**6**	**4**	**1**	**9**	**9**	**5**	**5**	**2**	**10**	**10**	**10**	**5**	**4**	**10**	**10**	**9**	**6**	**3**
	0	0	0	0	0	1	0	0	1	0	2	1	1	0	0	8	7	4	3	1
Sunco	**9**	**9**	**9**	**7**	**4**	**1**	**10**	**10**	**10**	**8**	**9**	**10**	**10**	**8**	**4**	**10**	**10**	**10**	**8**	**6**
	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	3	3	1	0	0
2-49	**10**	**7**	**5**	**2**	**3**	**10**	**10**	**5**	**4**	**2**	**9**	**9**	**9**	**8**	**6**	**10**	**10**	**10**	**9**	**5**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
CPI133814																**9**	**10**	**10**	**7**	**6**
																0	1	0	0	0

Table 3.22c Number of expanded Internode 6's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**16 WAP**			**18 WAP**				**20 WAP**				**22 WAP**				
TILLER	**1**	**2**	**3**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**1**	**2**	**3**	**4**	**5**
Puseas				**1**				**7**	**2**	**3**	**1**	**5**	**2**			
				0				2	0	0	0	1	1			
Vasco	**1**			**1**				**7**	**5**	**4**		**5**	**2**	**2**	**1**	
	0			0				0	0	0		1	1	1	1	
Sunco	**5**			**8**	**4**	**4**	**2**	**6**	**6**	**4**	**1**	**9**	**7**	**6**	**2**	**2**
	0			0	0	0	0	0	0	0	0	0	0	0	0	0
2-49				**4**	**3**	**1**		**5**	**3**	**2**	**1**	**4**				
	0			0	0	0		0	0	0	0	0				
CPI133814												**7**	**3**	**2**		
												0	0	0		

Table 3.22d Number of expanded Peduncle's assessed at each harvest (bold) and the number of those with isolations >0 (below) in the Wellcamp trial.

HARVEST	**16 WAP**					**18 WAP**					**20 WAP**					**22 WAP**				
TILLER	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**	**1**	**2**	**3**	**4**	**5**
Puseas	**8**	**8**	**6**	**6**	**3**	**9**	**10**	**9**	**6**	**3**	**10**	**9**	**10**	**8**	**6**	**9**	**9**	**8**	**5**	**3**
	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1
Vasco	**10**	**10**	**8**	**6**	**3**	**10**	**9**	**8**	**5**	**4**	**10**	**10**	**10**	**5**	**3**	**10**	**10**	**10**	**6**	**5**
	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1
Sunco	**10**	**9**	**9**	**7**	**7**	**10**	**10**	**10**	**6**	**9**	**9**	**10**	**10**	**8**	**4**	**9**	**10**	**10**	**7**	**7**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2-49	**10**	**5**	**6**	**5**	**3**	**10**	**10**	**10**	**9**	**8**	**9**	**9**	**9**	**8**	**7**	**10**	**10**	**10**	**9**	**5**
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CPI133814																**6**	**8**	**8**	**7**	**8**
																0	0	0	0	1

3.2.6 Wellcamp head and grain observations at later harvests

Out of a possible 75 tillers examined for each genotype at each harvest, tiller number ranged from 60 to 74 (Table 3.23). While differences between genotypes were not very high Vasco consistently had the lowest tiller number at each harvest. The number of tillers examined with no heads was highest in Puseas at each harvest and lowest in 2-49. The number of heads with pinched grain was high in Puseas in all 3 harvests and ranged from 7 to 9 over the 3 harvests in Vasco. All 2-49 heads contained healthy grain, while Sunco ranged from 0 to 5 heads with pinched grain across the 3 harvests.

From this data a % of healthy heads was obtained ((tiller number - (tillers with no heads + tillers with pinched grain)) / tiller number)*100) which differed greatly across the genotypes. Puseas had the lowest number of healthy heads, falling below 50% with a value of 45.07% at harvest 7 to 35.94% at harvest 9. Once again it was not surprising that 2-49 had the highest number of healthy heads, ranging from 98.61% to 97.10%. The % of healthy heads in Vasco ranged from 59.70% to 76.56%, while Sunco ranged from 85.92% to 97.30%. At harvest 9 all genotypes had the upper internodes and head covered in black sooty mould.

3.2.7 Correlation of disease rating and isolation data

X-Y scatter plots of each correlation are presented in Appendix 3F. A modest correlation (r = 0.5647-0.696) was found when leaf sheath or internode data from each trial was examined (Table 3.24). When both leaf sheath and internode data were combined and separated for each harvest in each trial strong correlations were seen for Harvest 7 (r = 0.7405) in both trials. In the Wellcamp trial Harvest 1 (r = 0.8388) also had a strong correlation while Harvest 1 had a weak correlation in the Jondaryan trial (r = 0.3665). In the Wellcamp trial Harvest 3 and 6 were also strong, while the final harvest was weak (r = 0.3801). The remaining correlations by harvest were modest with r values ranging from 0.4-0.69. When correlations were separated by genotype in each trial all genotypes had a modest correlation (Table 3.24).

Table 3.23: The number of tillers examined, those with no heads developed, the number of heads with pinched grain (whiteheads) and the % of healthy heads for each genotype at harvests 7, 8 and 9.

Harvest 7	tiller number	no heads	pinched grain	%healthy heads
Puseas	71	23	16	45.07
Vasco	67	20	7	59.70
2-49	72	1	0	98.61
Sunco	74	1	1	97.30
Harvest 8	tiller number	no heads	pinched grain	%healthy heads
Puseas	71	14	30	38.03
Vasco	60	9	7	73.33
2-49	66	1	0	98.48
Sunco *	71	5	5	85.92
Harvest 9	tiller number	no heads	pinched grain	%healthy heads
Puseas	64	14	27	35.94
Vasco	64	6	9	76.56
2-49	69	2	0	97.10
Sunco	71	7	0	90.14

* 7 extra heads were missing/partly missing in Sunco but appeared to have been chewed off (mice or birds?) and therefore not included in total.

Table 3.24 Correlations of disease rating and isolation data for the Jondaryan and Wellcamp field trials. Pearson correlation coefficients (r) were used to calculate r^2 values. Correlation strength presented according to (Fowler et al., 1998) pg 132.

Jondaryan Field Trial variables		**coefficient of determination (r^2)**	**correlation coefficient (r)**	**correlation strength**
Plant part	Leaf Sheaths	0.3388	0.5821	modest
	Internodes	0.3521	0.5934	modest
Harvest	1	0.1343	0.3665	weak
	2	0.1855	0.4307	modest
	3	0.2863	0.5351	modest
	4	0.3142	0.5605	modest
	5	0.4113	0.6413	modest
	6	0.3380	0.5814	modest
	7	0.5483	0.7405	strong
	8	0.2670	0.5167	modest
Genotype	Puseas	0.4804	0.6931	modest
	Vasco	0.3180	0.5639	modest
	Sunco	0.2254	0.4748	modest
	2-49	0.2244	0.4737	modest
	CPI133814	0.2785	0.5277	modest

Wellcamp Field Trial variables		**coefficient of determination (r^2)**	**correlation coefficient (r)**	**correlation strength**
Plant part	Leaf Sheaths	0.4844	0.6960	modest
	Internodes	0.3189	0.5647	modest
Harvest	1	0.7036	0.8388	very strong
	2	0.3881	0.6230	modest
	3	0.5322	0.7295	strong
	4	0.4827	0.6948	modest
	5	0.4699	0.6855	modest
	6	0.5654	0.7519	strong
	7	0.5225	0.7228	strong
	8	0.3036	0.5510	modest
	9	0.1445	0.3801	weak
Genotype	Puseas	0.3545	0.5954	modest
	Vasco	0.2985	0.5464	modest
	Sunco	0.3296	0.5741	modest
	2-49	0.2272	0.4767	modest
	CPI133814	0.1193	0.3454	modest

3.3 Discussion

Extensive symptoms of crown rot were induced in both field trials although conducted under very different moisture regimes. Both field trials were planted into Self Mulching Black Vertisol soil typical of the Darling Downs with no major deficiencies or excesses reported from the physical and chemical analysis. Severity of symptoms increased throughout the growing season in all wheat genotypes along with a progression of *Fpg* through each plant part. Differences were seen between susceptible and partially resistant wheat genotypes in the severity of disease symptom development and in the extent of fungal colonisation in both trials. These differences were however only significant at particular harvests or in particular tillers and this varied with the plant part examined. Others have also observed a similar variability in separation of genotypes at different stages of infection and maturity. For example, Klein et al. (1985) assessed the number of healthy seedlings 39, 64 and 102 DAP in *Fpg* inoculated canisters and found that the greatest differences between wheat cultivars was at 64 DAP. At 39 and at 102 DAP only the most susceptible genotypes were statistically separated from the others.

3.3.1 Differences between trials

3.3.1.1 Differences in plant development

There was a marked difference in overall plant size within genotypes between the two trials. While the different genotypes tested varied in tiller number, up to 12 tillers were produced by any one plant in the Wellcamp trial compared to a maximum of 4 tillers in the Jondaryan trial. Under severe drought stress wheat plants may maintain only the primary, or a very few tillers, either not producing or aborting some secondary tillers (Cook and Veseth, 1991). In the Jondaryan trial it is very likely that the moisture stress early in the season resulted in low tiller numbers in all plants.

3.3.1.2 Differences in establishment of infection and disease severity

Mean disease ratings of the coleoptile at the first harvest of the Jondaryan trial was still below 2.5 in all genotypes, indicating lesions covering just over one half of the surface at 4 WAP, with a maximum of 4 still not reached at 8 WAP. This is more than likely due to the dryness of the surface soil that surrounds the coleoptile particularly as it separates from around the leaf sheaths underneath. Only a handful of plants had lesions reported on the 1st LS at the first harvest and disease continued to progress quite slowly through LS tissue in all genotypes in this trial.

In comparison, infection of coleoptiles and LS's in seedling trials occurs more rapidly, reflecting the much higher humidity's and water availability under these controlled conditions. Mean disease rating of the 1st LS was above 3 for Puseas and 2-49 at 21 days after planting (DAP) in seedling trials (Chapter 2 Figure 2.3). In contrast the mean disease rating of the LS's never reached a score of 3 throughout the Jondaryan trial. Liddell and Burgess (1985) and Liddell and Burgess (1988) demonstrated that growth of *F. graminearum* Group 1 is strongly inhibited in dry soil, an effect which would slow initiation of new infections.

Initial infection and subsequent lesion development occurred more rapidly in the field trial conducted at Wellcamp. This 2nd trial had more rainfall events and half as many days with temperatures below 0, contributing to establishment of disease earlier in the season. The mean disease rating of the 1st LS of the primary tiller was above 3.5 in all genotypes by the 2nd harvest (8 WAP) at Wellcamp, whereas in the Jondaryan trial the mean disease rating of the 1st LS was only recorded above 2.0 on one occasion in Puseas primary tillers at 12 WAP (Harvest 5). Backhouse et al. (1997) reported that the availability of soil moisture affects the rate at which plants become infected during the season. Limited moisture may disrupt hyphal activity in soil residues slowing down initiation of infection and hyphal activity throughout the trial, resulting in delayed progress of disease. Humidity at the infection zone is also important. Humidity readings were not collected on site in either trial, however *G. zeae* is presumed to be inactive at relative humidities below 90% (Schneider, 1954 cited in Burgess and Griffin, 1968).

Lower temperatures in the Jondaryan trial may also have affected pathogen vigour. Klein et al. (1985) demonstrated higher disease levels in wheat plants grown at 22^0C than those grown with a diurnal temperature range of 10-20^0C. Disease severity increased significantly with increasing temperatures when 22 day old seedlings were assessed at 13, 19 and 25^0 C (Wildermuth and McNamara, 1994).

3.3.2 Disease symptom development in field trials

3.3.2.1 Coleoptile tissue

This is the first report detailing crown rot disease rating of the coleoptile in field trials. The coleoptile covers the subcrown internode and base of the 1st leaf sheath and it is therefore a significant point of infection when infection takes place in germinating seedlings. Between 4 and 6 WAP the DR increased in all genotypes except Sunco, with differences between 6 and 8 WAP not significant (Figure 3.4). While the DR of Sunco coleoptiles were not significantly different between any harvests, it is noted that Sunco had the lowest mean disease rating at the 2nd and 3rd harvest. Overall, however, differences between genotypes in the extent of coleoptile lesion development at each harvest were mostly not significant and lacked any consistent pattern. Even in seedling trials where high moisture conditions are maintained and coleoptiles exhibit severe lesioning, the still hydrated coleoptile tissue was shown to offer no resistance to crown rot in any wheat genotype examined (Lusted, 1998). These results suggest that early infection of the coleoptile occurs similarly in all genotypes, but that complete colonisation of the coleoptile during its later senescence is impeded under dry field conditions. This is likely under even moderately dry conditions as the coleoptile separates from the tissue underneath following emergence and becomes totally exposed at or near the soil surface.

In discussing disease severity of coleoptile tissue in field trials the natural process of senescence must be considered. It is possible that the rapid browning of coleoptiles infected with *Fpg* may be associated with senescence rather than disease. Furthermore, fungal re-isolation results from these tissues may reflect saprophytic growth. Senescence of wheat coleoptiles (%dead and dying microscopic fields counted) was reported to be as high as 91% by 15 days in glasshouse trials (Lewis and Deacon, 1982). In these experiments while wheat senesced more rapidly than barley, differences between the two wheat cultivars assessed were not significant. The slower rate of browning of Sunco coleoptiles in the Jondaryan field trial may reflect a slower rate of senescence in this genotype.

3.3.2.2 Sub-crown internodes (SCI)

In seedling trials the mean disease rating of the SCI varied between genotypes but the severity of lesion development was not consistent with overall field reactions to crown rot (Lusted, 1998, Wildermuth and McNamara, 1994). At 21 DAP the SCI mean disease rating of Puseas, Vasco and CPI133814 were significantly lower than 2-49 (Lusted, 1998). In the Jondaryan field trial the overall (mean of 5 harvests) disease rating of Puseas SCI was significantly higher than Sunco, 2-49 and CPI133814, with Vasco also higher than CPI133814. However at any one harvest, differences between Puseas and 2-49 were not significant and at 14.5 WAP no differences between genotypes were significant. Wildermuth and McNamara (1994) reported that Puseas was generally rated highest for SCI lesioning with differences between 2-49 and Vasco not significant. They also found that ratings of the SCI had the lowest correlations with overall field performance of a genotype, a conclusion entirely consistent with the findings of this present study.

3.3.2.3 Leaf sheaths

Disease severity in leaf sheaths generally increased as the season progressed in both field trials. Differences between genotypes in the disease rating of leaf sheath tissue of each tiller were mostly not significant at any one harvest or between successive harvests in either trial.

In the Jondaryan trial disease progressed quite slowly through leaf sheaths of all genotypes with a similar rate of both disease incidence (number of plants with disease symptoms) and disease severity (lesion spread over the leaf sheaths of each tiller). The severity of disease was usually highest in Puseas and while usually not significantly so at each harvest in each tiller, an overall genotype effect was significant ($P<0.01$) in the 1st 5 LS's analysed in this trial (Tables 3.5- 3.9c).

Genotypes were usually not separated on the basis of disease incidence or disease severity of any of the LS's at Wellcamp and the overall genotype effect was only significant ($P=0.006$) in LS2 in this trial.

There were smaller differences between genotypes in each leaf sheath at Wellcamp compared to the Jondaryan trial but where genotype was significant Puseas and Vasco had the highest disease ratings. Bai et al. (2001) reported a decreased variation in Fusarium head blight symptoms between susceptible and moderately resistant genotypes in the field than that observed under glasshouse conditions. However a strong correlation between the results of the two trials was still present.

Wildermuth and McNamara (1994) reported that at 13^{0}C no significant differences were expressed between cultivars, at 19^{0}C cultivars could be separated into 3 groups and at 25^{0}C 4 susceptibility groups could be distinguished. The Wellcamp trial was conducted in a warmer environment compared to Jondaryan indicating that temperature differences may not be as important in distinguishing between susceptible and partially resistant genotypes in leaf sheath tissue in the field.

It is interesting that greater differences were seen between genotypes in the disease development of leaf sheaths in the Jondaryan trial, which had lower overall disease levels, than the Wellcamp trial. This suggests that when moisture is not limited earlier in the growing season differences between genotypes with regard to symptom expression, may be less pronounced under field conditions. Other authors have noted an absence or decline of basal browning under wet field conditions (eg Wildermuth et al., 1997b, Felton et al., 1998). However we have reported fairly extensive lesioning of crown tissue early in the growing season at Wellcamp.

When genotypes and tillers were combined for analysis a significant harvest effect was seen in the first 2 LS's in both trials. In the Wellcamp trial the greatest difference in disease severity in LS1 and LS2 was seen between the first 2 harvests conducted at 5 and 7 WAP coinciding with a sharp increase in the disease rating of the primary tiller and initial symptom development of the secondary tillers (Figures 3.5b, 3.6b).

In the Jondaryan trial increases in disease severity of the 1st 2 LS's were quite gradual across all harvests included in the analysis up to 12 WAP (Figures 3.5a and 3.6a). LS3, 4 and 5 were only analysed over harvest 5 and 6 (12 and 14.5 WAP) in the Jondaryan trial and differences between these harvests were also not significant.

The greatest differences in the mean disease rating of LS tissue were seen between tillers. In both trials tiller was highly significant ($P<0.001$) for all leaf sheaths analysed. This was generally as expected with the primary tiller leaf sheaths having the highest disease and the progressively younger tillers having progressively lower disease ratings. The 2 and 3 way interactions were usually not significant in the analysis of LS disease ratings indicating that once diseased, the progression occurred at the same rate at each harvest, in each tiller, for each genotype.

Measurements of disease severity in LS tissues are not usually included in field trial assessments and it has been difficult to associate such measurements with the current literature. These results suggest that such measurements while important in seedling trials (Wildermuth and McNamara, 1994) are not very useful for distinguishing between susceptible and partially resistant genotypes in field screening trials.

In the current study such measurements were required to follow the progression of disease in the field and have shown that disease incidence and severity in LS's was similar in both the susceptible and partially resistant genotypes at the time when symptoms of disease were initiated on internode tissues.

3.3.2.4 Internodes

Internodes showed symptoms of disease soon after their expansion 10-12 WAP in both field trials. Symptoms of disease developed on internodes progressively throughout the growing season with the rate of development different between partially resistant and susceptible genotypes. Each factor: harvest, genotype and tiller, were highly significant in all analysed internodes with strong 2 and 3 way interactions also observed in the mean disease rating of these tissues.

In the Jondaryan trial only I1 was included in the analysis over the 1st 3 tillers. Disease symptoms increased at each harvest in this plant part with a highly significant genotype effect (Figure 3.10a). Puseas had much higher disease levels in this tissue than recorded by all other genotypes in all tillers at all harvests, except Vasco at 16 WAP. At this harvest Vasco was also significantly higher than the more resistant 2-49, CPI133814 and Sunco. Significant symptom development also occurred on the 2nd internode in the majority of Puseas and Vasco expanded tillers at 18.5 WAP (maturity) in the Jondaryan field trial (Figure 3.11a). In comparison only limited lesioning of higher internodes were recorded in 2-49, CPI133814 and Sunco at maturity.

In the Wellcamp trial disease incidence in the stems of all tillers was 100% in all genotypes at maturity (Table 3.10b). However partial resistance was still clearly distinguished in the disease severity of each internode tissue at earlier harvests. A harvest/genotype/tiller interaction was highly significant in the 1st 3 internodes and all 3 two-way interactions were highly significant in I4. Differences between genotypes were most clearly expressed early in the infection of each internode. For example the disease rating of 2-49 and Sunco I1's were still significantly lower than Puseas and Vasco at 18 WAP but at 20 and 22 WAP differences between genotypes were no longer significant in this tissue (Figure 3.10b). At 20 WAP differences in I2 were significant (Figure 3.11b) and at 22 WAP differences in I3 were significant (Figure 3.12b). Levels of disease in Sunco internodes were usually higher than 2-49 and became not significantly different from the susceptible genotypes sooner. Disease was only examined in CPI133814 at 22 WAP and it was higher than 2-49 but lower than Puseas and Vasco.

At maturity disease symptoms in the Wellcamp trial were not seen above the 2nd internode in 2-49. Lesions were seen as high as the 4th internode in Sunco (mostly on the primary tiller), while stem browning was recorded as high as the 5th and 6th internodes in Puseas and Vasco respectively (Tables 3.10-3.13).

Highly significant differences were also seen within genotypes in the development of disease on internodes of each analysed tiller in the Wellcamp trial. In the 1st 2 internodes Puseas generally showed significant differences between older and younger tillers at the earlier harvests and as time went on these differences between tillers became smaller. Vasco and Sunco behaved in a similar fashion with differences between tillers more stable over time. The internodes of 2-49 tillers became diseased more slowly and therefore smaller differences were seen between tillers earlier and these differences became more significant over time as disease progressed more quickly in the primary tiller of 2-49. It is possible that if more tillers were collected greater differences would be seen between genotypes later in the season.

The proportion of diseased tillers at maturity is often used as a measure of resistance in field trials (e.g. Dodman and Wildermuth, 1987, Purss, 1966). When the mean percentage of tillers with stem browning beyond the 2nd internode was assessed at maturity partial resistance in the genotype Gala was clearly expressed (Purss, 1966). In the current study genotypes could not be separated on the basis of disease incidence of I1 at maturity in either trial. However, significant differences were observed in this tissue at earlier harvest times (particularly 16 WAP) and partially resistant and susceptible genotypes could be clearly distinguished on the basis of disease severity in higher internodes at maturity.

3.3.3 *Fpg* localisation

3.3.3.1 Leaf sheaths

Differences between genotypes in the mean number of isolations from LS's were mostly not significant at any one harvest, with the overall genotype effect not significant in isolations from LS's in either trial. While most differences between genotypes were not significant, isolations from this tissue were highest in Puseas in the Jondaryan trial, with little differences between the other genotypes. In the Wellcamp trial no differences in isolations from LS's were clearly distinguished between genotypes.

The tiller effect was highly significant ($P<0.001$) in the 1st 3 LS's analysed over 10, 12 and 14.5 WAP in the Jondaryan trial and in the 1st 4 LS's analysed over 5-11 WAP in the Wellcamp trial. As seen in the disease ratings of this tissue the differences between tillers relate to age and time of infection with the primary tiller having the highest number of isolations and progressively lower numbers of isolations recorded from younger tissues.

As new tillers emerge through the leaf sheaths of older tillers (initially the primary tiller) their leaf bases may become infected through direct contact with these older leaf sheaths at the crown, as reported by Purss (1966). However there is also the possibility that infection occurs directly through the crown of the plant from the base of the primary tiller. In the Jondaryan trial overall infection levels were lower than in the Wellcamp trial and infection of the leaf sheaths of younger tillers were delayed for some time (2-3 weeks after expansion). In the Wellcamp trial *Fpg* was reisolated from the leaf sheaths of secondary tillers soon after their expansion.

3.3.3.2 Internode isolations

Isolations from internode tissue revealed pronounced differences between genotypes at each harvest. The number of isolations increased over time in both trials with a highly significant ($P<0.001$) harvest effect in all internodes analysed. Genotype was also highly significant ($P<0.001$) in I1 in the Jondaryan trial and in all analysed internodes in the Wellcamp trial. In some cases different genotypes had greater increases between different harvests leading to significant harvest/genotype interaction in I2 in both trials and in I4 in the Wellcamp trial. There was no tiller effect in isolations from I1 in either trial or I2 in the Wellcamp trial. However, differences between tillers were highly significant in higher internodes with all two way interactions significant in I4 in the Wellcamp trial.

In the Jondaryan trial *Fpg* moved into the stem sooner in the more susceptible Puseas, and this variety had the highest number of isolations from I1 at almost all harvests. While at 14.5 WAP isolations from Puseas I1 were significantly higher than from the partially resistant Sunco, 2-49 and CPI133814 in all 4 tillers, these significant differences between genotypes had disappeared by 18.5 WAP (maturity). Isolations from I2 and I3 were also lower in the partially resistant varieties at most harvests, but not significantly different from Puseas and Vasco at maturity.

In the Wellcamp trial *Fpg* was isolated from I1 of all genotypes at around the same time (13 WAP) with no tiller effect in this tissue. There was a highly significant (P<0.001) genotype effect, with the number of isolations from each tiller initially highest in Puseas which was significantly greater than 2-49 in most tillers at 13 and 16 WAP (Figure 3.18). Differences between genotypes from 18 WAP onwards were mostly not significant in I1.

Fpg moved up the stem of Puseas and Vasco at a faster rate than the more resistant genotypes, colonising the majority of I2's at 13 WAP in Puseas and Vasco, 16 WAP in Sunco but not until 18 WAP in 2-49. By 20 WAP isolations from Puseas were only significantly higher than 2-49 in the 5th tiller I2 with differences between genotypes in the number of isolations from I2 not significant at maturity.

A similar pattern was seen in each internode higher up the stem. Isolations were consistently made from each internode firstly from Puseas and Vasco usually a harvest later from Sunco and another harvest later from 2-49. At maturity the number of isolations from I3 was significantly lower in 2-49 than Puseas in 3 of the 5 tillers examined with a small number recorded from 2-49 I4's. Isolations from Sunco were consistently lower than Puseas and Vasco however at maturity the differences from I4 were only significant in the primary and the 5th tiller. Isolations from CPI133814 were recorded from at least one I4 of each tiller at maturity, however the mean number was usually significantly lower than Vasco. At maturity isolations from I5 were highest from Vasco.

The absence of a significant tiller/genotype interaction in the 1st to 3rd internodes suggests that once colonised, stem infections progress at the same rate in each tiller of the same genotype. This is in contrast to the significant harvest/genotype/tiller interaction discussed above for the disease rating data of these internodes. Wearing and Burgess (1979) cited in Liddell and Burgess (1988) demonstrated that *Fpg* is capable of saprophytic growth in culture at very low water potentials. The results of the current field trials have shown that at the end of the season the fungus progressed up the stem at a faster rate than disease symptoms developed particularly in the Wellcamp trial. This suggests that as the straw dries out the fungus has switched to saprophytic growth. It was at maturity that the weakest correlation of disease rating and isolation data was found in the Wellcamp trial (as discussed below section 3.3.4).

Compared to the Wellcamp trial, at Jondaryan *Fpg* was mostly restricted to the 2nd internode in all genotypes at maturity. This trial was conducted under extremely dry conditions which may have resulted in a level of straw dryness which inhibited saprophytic spread. Movement of the fungus up the leaf sheath tissue was also inhibited in this trial with isolations from higher segments (data not presented) of leaf sheaths earlier in the season low in all genotypes.

Purss (1966) reported on the progress of crown rot infection and disease development in wheat genotypes. The most resistant genotype in these trials was Gala and while it expressed lower levels of disease reaction at maturity Purss reported in contrast to our results that Gala did not show lower levels of infection at harvests prior to maturity. However, this conclusion was reached from an overall plant incidence measurement where a plant was counted as infected if the fungus was isolated from any tissue. In these early field experiments (Purss, 1966) conflicting results can be observed throughout the season in two field trials. At Irvingdale the percentage of plants infected at maturity was highest in Gala (partially resistant) with Puseas (susceptible) ranked amongst the lowest of the genotypes screened. Whereas at Millmerran the opposite occurred with Puseas recording the highest percentage of infected plants and Gala having the lowest. This indicates that incidence of infected plants at maturity is not a reliable measure of crown rot resistance. The seed of genotypes tested in Purss's field trials were sown (both inoculated and un-inoculated) into fields which reported heavy crown rot disease in the previous season. While he found higher levels of disease in inoculated plants early in the season the differences in severity between non-inoculated and inoculated plants at the end of the season were not as high as expected. Dodman and Wildermuth (1987) found that either inoculation of seed or exposure to natural field inoculum produced overall lower levels of disease in field trials, with the clearest differences between susceptible and partially resistant genotypes achieved when inoculum was applied onto or into the soil (as was done in the current field trials).

When isolations from each internode up the stem were conducted by Purss (1966), differences between Puseas and Gala were also not significant. These measurements were however conducted at maturity. The resistance in 2-49 is considered to be stronger than that expressed by Gala, as it incorporates some resistance loci from Gluyas Early as well as from Gala (Bovill et al., 2006). While *Fpg* infections had progressed as high as the 3rd internode in 2-49 at maturity, differences between susceptible and partially resistant genotypes were expressed in lower internodes at earlier harvests and the fungus was consistently isolated from higher internodes in Puseas than 2-49 even at the final harvest in the Wellcamp trial.

3.3.4 Correlation between disease symptoms and fungal isolations

Usually when an individual plant was diseased *Fpg* was isolated from its tissue and visa versa. On some occasions however this was not the case. In the Jondaryan trial isolations were not always made from lesioned leaf sheaths. For example, at 6 and 8 WAP most primary tillers LS1's showed symptoms of disease however *Fpg* was only reisolated from a handful of plants at these times. This was observed in all genotypes in this trial and could also be seen at 10, 12 and 14.5 WAP in LS2 and at 12 and 14.5 WAP in LS3. This also occurred but to a lesser extent in leaf sheath tissue in the Wellcamp trial. For example, in LS1, while 100% incidence of disease was observed on the primary tiller at 7, 9 and 11 WAP, *Fpg* was subsequently reisolated from only 6 to 9 of the 10 plants examined for each genotype (Tables 3.5b, 3.15b). This may reflect a general variability in the isolation procedure or, as discussed in Chapter 2 (section 2.3.2), may be a result of the difficulty associated with re-isolating the pathogen from older tissues.

In the Wellcamp trial quite the opposite occurred in partially resistant internode tissue examined at later harvests. Visible disease symptoms were not observed on 2-49 stems beyond the 2nd internode. *Fpg* was however reisolated from most 2-49 I3's at the final harvest (22 WAP). This was also seen to a lesser extent in Sunco and CPI133814 where the fungus was isolated from some I5's and I4's that were symptom free. These symptomless infections were not observed in either Puseas or Vasco, where all internodes from which *Fpg* was isolated showed significant disease symptoms.

A modest correlation between disease rating and isolations was found for all genotypes when leaf sheath or internode data from each trial was examined (Table 3.24). Differences were seen in correlation strength when data were separated by harvest. In the Wellcamp trial the strongest correlation of disease rating and isolation data was at the 1st harvest (r = 0.8388) where infection and disease was established in the LS's of the primary tiller. In contrast Harvest 1 had a weak correlation in the Jondaryan trial (r = 0.3665) reflecting the slower initiation of infection and disease in the Jondaryan trial compared to the strong development of infection in the Wellcamp trial. Correlation of data for harvest 7 (r = 0.7405) in the Jondaryan trial and 6 (r = 0.7519) and 7 (r = 0.7228) in the Wellcamp trial were also strong. These harvests were around milk/dough development where strong differences between susceptible and partially resistant genotypes were observed in internode tissue. In the Wellcamp trial the weakest correlation between disease rating and isolation data was seen at the final harvest (r = 0.3801), where a higher number of isolations were recorded from non diseased partially resistant tissues.

3.3.5 Analysis

Separating the data into plant parts for analysis had the advantage of allowing comparisons to be made across harvests examining data over time. The downfall of analysing over several harvests is that as the plants grew data was being added to the pool leading to unequal sample sizes. Significant differences between genotypes appear to be expressed in the early stages of infection, where zero infection scores in some lines frequently led to exclusion from the formal analysis due to low variance. Also on several occasions particularly when dealing with the isolation counts large differences between genotypes were not statistically significant. For example the mean isolations from tiller 2 I4 in Sunco (4.02) were not significantly different from Vasco (13.92) at maturity (Figure 3.21). While there appeared to be a much lower amount of *Fpg* in all Sunco I4's compared to Vasco tillers, the analysis suggested differences were not significant due to the variability in this statistic between individual plants. 95% Confidence intervals of error were used to account for the large sampling error associated with field trials (personal communication with Dr Ashley Plank, USQ statistician). Standard error is commonly used to determine differences between treatments in experimental trials and this value was almost doubled in the current experiments. The analysis used may have been too strict to detect some important differences between genotypes.

3.3.6 Overall Genotypic differences (resistance)

Dodman and Wildermuth (1987) suggested that partial resistance as expressed in the variety Gala may be due to initial penetration following strong differences in disease symptoms between a susceptible and resistant genotype when spores were sprayed directly onto tillers. When spores were injected into tillers no differences in disease severity between the two genotypes were observed. However they concluded in agreement with Purss (1966) that resistance is most clearly expressed in the development of diseased symptoms. Resistance to penetration requires histological examination as has been achieved for other plant pathogen interactions (For example FHB studies conducted by (Pritsch et al., 2000 and Ribichich et al., 2000)).

In agreement with Dodman and Wildermuth (1987) stronger differences between genotypes were maintained throughout the growing season in the current field trials when internodes were assessed for disease symptom development rather than re-isolation of the pathogen. However statistically significant differences were observed between genotypes in the rates of infection of each internode, only at different harvest times. Infection and disease development was consistently lowest in 2-49. While Sunco seemed to be as diseased as Vasco throughout the season (particularly in leaf sheath tissue) differences between these genotypes became clearer as higher internodes and younger tillers were assessed. Symptom expression in Sunco was also usually lower than Puseas. Partial resistance in Sunco while not as strong could not be clearly distinguished from 2-49. There was not a particular time or plant part that stood out which expressed statistically significant differences between these genotypes. The synthetic hexaploid wheat CPI133814 also showed slowing down of disease and infection at a rate in between but usually not significantly different from Sunco and 2-49. It was unfortunate that disease progress could not be followed in this genotype in the Wellcamp trial, due to bird damage.

The genotypes could be rated in order of increasing susceptibility to crown rot as 2-49, CPI133814, Sunco, Vasco and Puseas from the disease and isolation assessments conducted in both field trials. This was clearly confirmed by the condition of the heads and grain (Table 3.23) examined at the final 3 harvests in the Wellcamp trial. While levels of infection in internodes was higher than expected in partially resistant genotypes at maturity it was encouraging to observe > 90% of healthy heads in 2-49 and Sunco cf with 36% for Puseas.

The clearest genotypic differences in disease symptom development in these field trials were seen on stem tissues at around 16 WAP in both trials. At this time the disease rating of I1 was significantly lowest in all tillers of 2-49, with Sunco disease ratings also lower than Vasco (not significant) and Puseas. Lesioning of I2 was also lower in the partially resistant genotypes at 16 WAP. This period prior to maturity characterised by ear emergence – milk development, is also the most useful time for whitehead rating and should be considered as a superior point of symptom analysis whenever 1) small differences between genotypes are being analysed or 2) Populations constructed for research purposes such as marker analysis are being phenotyped.

Chapter 4: Effectiveness of Partially Resistant Sources in Hexaploid Wheats Against a Range of *Fusarium pseudograminearum* Isolates

4.0 Introduction

Host specificity of a pathogen may be limited to one species of plant or to even one or a few varieties within a species (Oku, 1994). However within every host/pathogen relationship varying degrees of host damage can occur. The ability of a host organism to prevent or limit disease is defined as resistance, and this may be expressed as complete or incomplete (partial) resistance, race non-specific (resistant to all races of a pathogen) or race specific (resistant to some but not all races of a pathogen) (Keller et al., 2000). If different isolates of a pathogenic species cause disease in the same subset of varieties of a particular host they are considered to be of the same race or pathotype. If it is thought that different races or pathotypes occur, this needs to be confirmed by testing against a standard set of host varieties that display genetically different resistances (Brown, 1998).

In wheat, race-specificity is most commonly seen in the rust pathogens *Puccinia graminis* (stem rust), *P. recondita* (leaf rust) and *P. striiformis* (stripe rust) (McIntosh et al., 1995) but has also been reported in *Blumeria graminis* f.sp. *tritici* (wheat powdery mildew) (Yahiaoui et al., 2006), *Mycosphaerella graminicola* (septoria tritici blotch) (Cowger et al., 2000), *Ustilago tritici* (loose smut) (Jones and Dhitaphichit, 1991), *Neovossia indica* (karnal bunt) (Datta et al., 1999) with conflicting reports regarding pathogenicity of *Bipolaris sorokiniana* (teleomorph *Cochliobolus sativus*) isolates causing spot blotch and common root rot in wheat and barley (e.g. (Duveiller and Altamirano, 2000, Meldrum et al., 2004).

In contrast, studies on *F. graminearum* and *F. culmorum* indicate that there are no race specific patterns in Fusarium head blight (FHB) infection of wheat (Mesterhazy et al., 1999). While strong environment and year interactions have been observed, variance in FHB due to wheat genotype/strain factors are very small and non specific. Furthermore resistance to FHB against *F. culmorum*, *F. graminearum* and *Microdochium nivale* seem to be of the same type (Van Eeuwijk et al., 1995).

In recent years several research groups have reported a high level of genetic diversity within *Fpg* populations (Akinsanmi et al., 2006a, Bentley et al., 2005b, Bentley et al., 2005a, Bentley et al., 2008) however no studies have been conducted to determine whether differences in pathogenicity for crown rot occur between different *Fpg* isolates.

An understanding of this issue is important for two main reasons. Firstly, the occurrence of pathotypes in the Australian environment against which current sources of resistance are ineffective will reduce their long-term usefulness when deployed. An awareness of interactions between fungal isolates and host genotypes is of great importance to the reliability of resistance screening and understanding the durability of current sources of resistance. A host/isolate interaction may point to vertical (qualitative) resistance controlled by major genes, with a high potential for *Fpg* isolates to adapt and overcome these resistances (Miedaner, 1997).

Secondly, molecular markers currently under development for marker-assisted selection of crown rot resistance (Collard et al., 2005, Bovill et al., 2006) are based upon phenotypic data obtained from host responses to a mixed inoculum increased from a small number of aggressive field isolates, and thus if race-specific isolates are present, the markers may only prove useful for selecting lines that show effective resistance to a subset of isolates in the environment (Mohan et al., 1997).

Recent studies have indicated that *Fpg* varies in it’s aggressiveness for crown rot in wheat (Akinsanmi et al., 2004, Akinsanmi et al., 2006b). However these reports are based on crown rot bioassays using a single wheat variety (Kennedy). Further studies suggested that *Fpg* isolates could be placed into three pathogenicity groups based on degree of FHB symptom development in 9 wheat genotypes (Akinsanmi et al., 2006c). The current study aims to determine whether *Fpg* isolates differ in ability to cause crown rot in several wheat genotypes ranging in susceptibility to this disease. To achieve this we have challenged a selection of partially resistant and susceptible host genotypes with a range of pathogen isolates collected from across Australia.

4.1 Methods

Two seedling experiments were conducted in controlled environment growth rooms at the LRC. Three replicates of nine wheat genotypes ranging in susceptibility to crown rot were exposed to 7 isolates of *F. pseudograminearum* inoculum using a layered pot design as previously described (Section 2.1.2 & 2.1.3). For these experiments seedlings were harvested and rated for crown rot disease severity at 21 days after planting only. Each of three replicates in each experiment were rated by different personnel. In each trial these were the author and two technical staff at the USQ.

4.1.1 Inoculum production

Six *F. pseudograminearum* isolates collected from SA, WA and NSW were provided by Prof Lester Burgess (University of Sydney, NSW). A 7th isolate from Qld was provided by Dr Graham Wildermuth (LRC, Farming Systems Institute, DPI&F, Qld) (Table 4.1).

Table 4.1 Location of collection of F. pseudograminearum isolates

Inoculum	Isolate	Location collected
1	F12464	SA
2	F13691	Walgett, NSW
3	F13718	Spring Ridge, NSW
4	F13911	Quirindi, NSW
5	F14843	WA
6	F14944	WA
7	A03#24	Tara, Qld
8	mixed	3 Qld isolates

Single spores from each isolate were grown on CZA and used to inoculate flasks of sterilised wheat/barley grain. Flasks were incubated at 22^0C for three weeks and shaken daily after one week to allow uniform colonisation of the grain. Colonised grain from each flask was dried on blotting paper at 25^0C for 2 ½ weeks and then ground to pass through a 2mm sieve to obtain inoculum chaff for each isolate.

Detailed instructions are outlined in appendix 4A. A mixed inoculum (produced from 3 aggressive isolates reisolated from infected crop plants in the previous season) used in crown rot seedling screening at LRC was included for comparison.

4.1.2 Plant material

Genotypes were selected for their varied response to crown rot infection as determined in numerous field and seedling trials conducted at LRC, and in other screening programs. These wheat genotypes varied in resistance and genetic backgrounds. Table 4.2 lists the genotypes selected and the expected susceptibility to *Fpg* infection. More complete descriptions of the cultivars Puseas, 2-49 and CPI133814 can be found in Chapter 2 Methods (2.1.1) and Sunco and Vasco have been introduced in Chapter 3 Methods (3.1.2).

Table 4.2 Susceptibility of wheat genotypes to crown rot.

Genotype	Susceptibility
2-49	partial seedling/ adult resistance
CPI133814	partial seedling/ adult resistance
IRN497	partial seedling/ adult resistance
W21MMT70	partial seedling/ adult resistance
Sunco	partial adult resistance
Hartog	susceptible
Janz	susceptible
Vasco	very susceptible
Puseas	very susceptible

Also included in these trials is the wheat variety Hartog which consistently demonstrates a susceptible reaction in the field and is rated as having low levels of resistance to crown rot (QDPI&F, 2007). However, glasshouse trials have found Hartog to vary in susceptiblity sometimes showing higher levels of partial resistance as seedlings (Wildermuth and McNamara, 1994, Wildermuth et al., 2001). Janz is also considered susceptible to crown rot in both seedling and adult plant trials (Liu et al., 2004, Wallwork et al., 2004, Wildermuth and Morgan, 2004).

The breeding line IRN497 has been shown to have both seedling and adult partial resistance to crown rot (Wildermuth and McNamara, 1994), while W21MMT70 has been identified with levels of partial resistance often as good as that seen in 2-49 in both seedling and field trials (Bovill et al., 2006).

4.1.3 Measurement of disease severity

At 21 days after planting, the 1st three leaf sheaths of up to 10 plants from each pot were rated for disease using a scale from 0-4.

0 = no lesions visible

1 = 1-24%

2 = 25-49%

3 = 50-74%

4 = >75% of surface covered by lesions.

The values obtained for each of the three leaf sheaths were added to give a disease rating out of 12. A mean disease rating was obtained from three replicates of up to 10 plants per pot for each inoculum/genotype treatment.

4.1.4 Growth rates of *F. pseudograminearum* isolates

A single germinated macroconidia of each isolate was plated onto the centre of CZA plates. Two plates were inoculated for each isolate. The distance (mm) each colony radiated from the inoculation point was measured daily for three days. This was repeated and a mean growth rate for each isolate obtained.

4.1.5 Data analysis

Treatments within the two experiments were replicated three times and arranged in a randomised block design. Data was analysed with the assistance of Dr Ashley Plank (Department of Maths and Computing, USQ) using SPSS 14.0 for Windows.
Univariate Analysis of Variance was used to determine significance of the factors genotype, inoculum, experiment and all 2, and 3 way interactions. Genotype was treated as a fixed variable while experiment and isolate were classed as random effects. Variance component estimates were also performed using the Minimum Norm Quadratic Unbiased Estimation method. Variance estimates for genotype were not available as this analysis allows estimates of the variation in the dependent variable attributable to each random effect in the model only. The correlation between mean growth rate on CZA plates and mean disease rating for each inoculum was also examined.

4.2 Results

During inoculum production, the extent of mycelial growth (grain colonisation) varied between isolates (Figure 4.1a) Seven days after grain inoculation prior to breaking up of clumps in the grain it was evident that isolates F14994, F13911 and F14843 had greater mycelial growth within each flask (Figure 4.1b). These isolates are highlighted with an asterisk in Table 4.3 for comparison. This increased growth was obviously different from the other isolates in both replicates except in F14843, where 1 flask had less growth then the other. This flask was later discarded due to contamination (Appendix 4A).

Differences occurred in the severity of disease produced in the two experiments, with Experiment 1 consistently yielding higher disease ratings than Experiment 2. It was discovered at the completion of the 2nd experiment that night time temperature in the glasshouse was not being controlled or recorded as intended. Consequently this 2nd experiment, conducted in June 2004, would have been subjected to cooler (particularly overnight) temperatures then the 1st trial conducted in May.

While differences in severity between the trials were evident the patterns of disease across each genotype and across each inoculum were the same (Figures 4.3, 4.4) with susceptible genotypes having higher disease ratings then partially resistant genotypes when challenged with any inoculum. Figure 4.2 shows restricted lesion development in 2-49 compared to Puseas when challenged with the mixed inoculum in Experiment 1.

All raw data is presented in Appendix 4B and the analysis output in Appendix 4C. Analysis of Variance indicated the three main factors genotype (host), inoculum and experiment were highly significant as were the two way interactions genotype*experiment and genotype*inoculum (Table 4.3). Variance component estimates are presented in Table 4.4. Variation due to the differences in disease severity between experiments accounted for just over 13% of the total variance.

Figure 4.1 Flasks containing colonised grain during inoculum production. a) comparison of all isolates. b) isolates F14994, F13911 and F14843 which produced greater mycelial growth than other isolates.

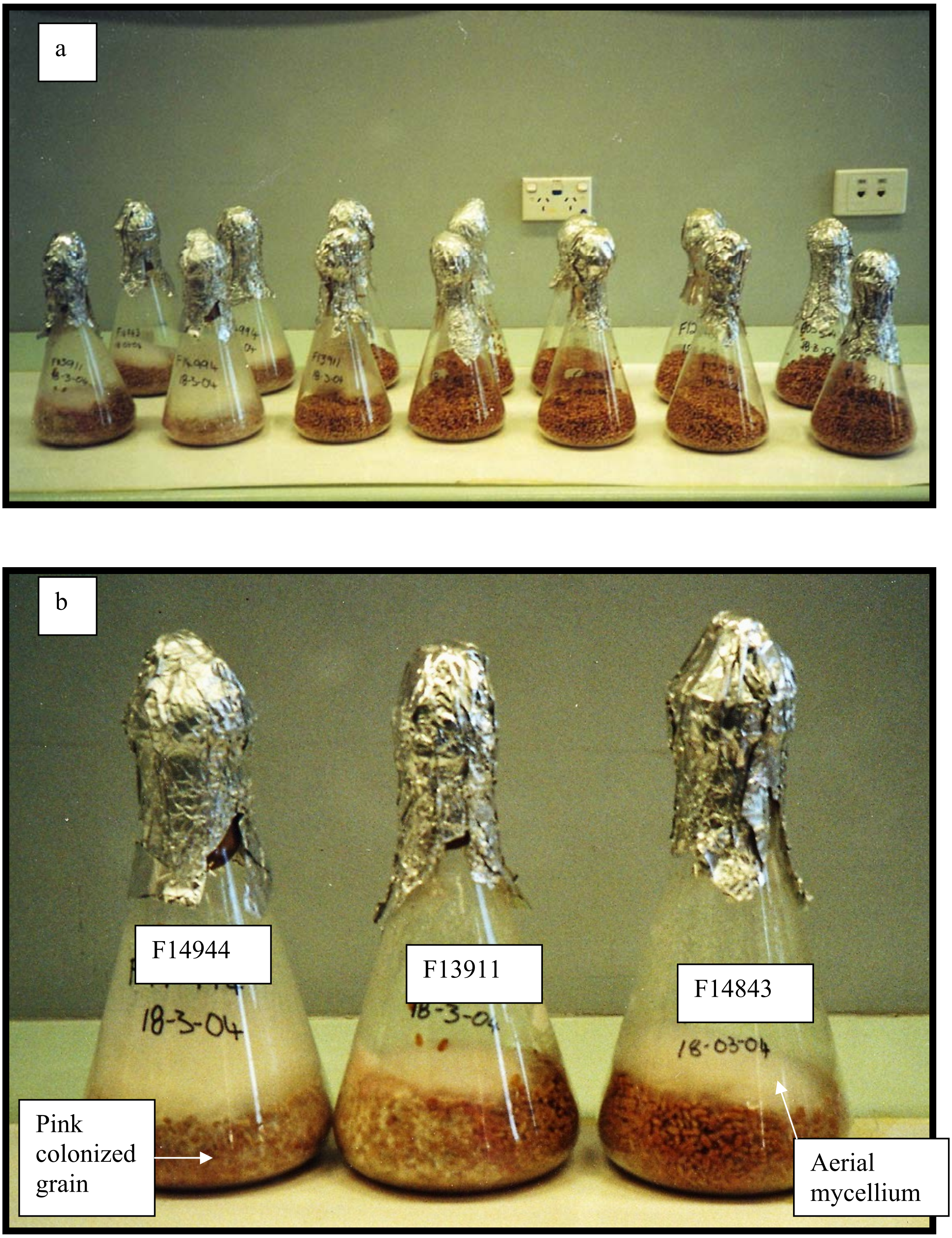


Figure 4.2 Puseas and 2-49 seedlings infected with the mixed inoculum 19 days after planting in Experiment 1.

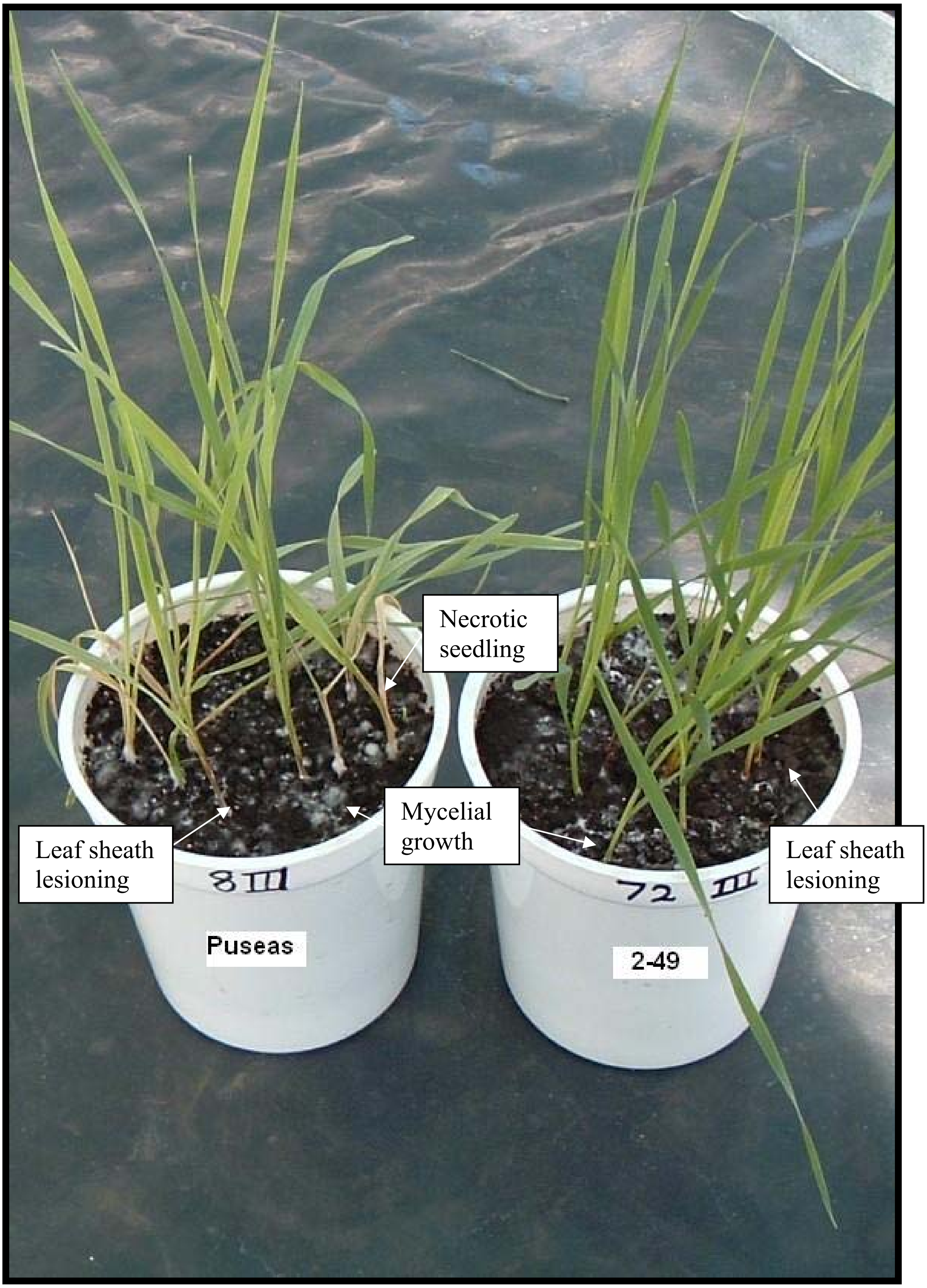


Table 4.3 Tests of between subject effects

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Hypothesis	6837.81	1	6837.81	35.831	0.007
	Error	637.079	3.338	190.833		
Genotype	Hypothesis	628.693	8	78.587	14.944	0.000
	Error	71.36	13.569	5.259		
Inoculum	Hypothesis	657.193	7	93.885	35.995	0.000
	Error	52.2	20.013	2.608		
Experiment	Hypothesis	98.23	1	98.23	22.878	0.001
	Error	36.268	8.447	4.294		
Genotype * Inoculum	Hypothesis	125.821	56	2.247	2.442	0.001
	Error	51.531	56	0.92		
Genotype * Experiment	Hypothesis	31.458	8	3.932	4.273	0.000
	Error	51.531	56	0.92		
Inoculum * Experiment	Hypothesis	8.972	7	1.282	1.393	0.227
	Error	51.531	56	0.92		
Genotype * Inoculum * Experiment	Hypothesis	51.531	56	0.92	1.299	0.089
	Error	204.044	288	0.708		

Table 4.4 Variance estimates using the Minimum Norm Quadratic Unbiased Estimation method (Weight = 1 for Random Effects and Residual).

Component	Estimate	%
Var(Inoculum)	1.69	51.78
Var(Experiment)	0.435	13.33
Var(Inoculum * Genotype)	0.221	6.77
Var(Experiment * Genotype)	0.126	3.86
Var(Inoculum * Experiment)	0.013	0.4
Var(Inoculum * Experiment * Genotype)	0.071	2.18
Var(Error)	0.708	21.69
TOTAL	3.264	100.01

4.2.1 Host genotype effect

The mean disease rating of Exp 1 was higher than Exp 2 in all genotypes, however the difference between experiments was significant in the more susceptible Puseas and Vasco and the partially resistant 2-49, CPI133814 and IRN497 when compared to the remaining genotypes (Figure 4.3), resulting in a genotype*experiment interaction. The mean range between the highest scoring genotype (Puseas) and the lowest (2-49) was 4.6 for Exp1 and 3.4 for Exp 2. The combined mean disease rating of genotypes ranged from 2.09 for 2-49 to 6.09 for Puseas when inoculum data was pooled. The order of susceptibility was as expected (Table 4.2) for all genotypes except for Hartog, which had a mean disease rating lower than Sunco and not significantly different from that of W21MMT70 (Figure 4.3). Differences between experiments were more pronounced at either end of the scale in the more susceptible and more resistant genotypes. Nevertheless the genotype*experiment interaction contributed less than 3 % of the variance (Table 4.4).

4.2.2 Inoculum effect

The inoculum*experiment interaction was not significant and contributed very little to the variance estimates of the experiments (Tables 4.3 & 4.4). Each isolate caused comparable levels of disease across experiments with Exp1 significantly higher than Exp 2 with all inoculum except the lowest (F14843) and highest (A03#24) disease causing isolates which were not significantly different across experiments (Figure 4.4). Fungal isolates differed significantly in the average severity of the symptoms they induced across all host genotypes. Inoculum isolate was the highest variance component, contributing over half the variation observed (Table 4.4). The mean disease rating of the combined genotypes varied for each inoculum from 1.32 for F14843 collected in WA to 5.39 for A03#24 collected in Qld (Figure 4.4). F14843 and F13691 (NSW) were significantly lower than all other isolates and A03#24 was significantly higher (Figure 4.4). The remaining isolates had a mean disease rating between 4 and 5 when experiments were combined.

4.2.2.1 Measurement of isolate growth rates on CZA

Growth rates on CZA^{++} agar were measured individually for each isolate and compared with disease levels. Significant differences were seen in the growth rates of isolates on this medium (Table 4.5). Growth of F12464 was significantly greater than all other isolates while F14843 and F14944 were significantly slower (Table 4.4). A correlation of mean disease rating with growth rate was not significant (Figure and Table 4.5).

Figure 4.3 Mean disease rating of each genotype across all inoculum for each experiment and experiments combined. Error bars represent the upper and lower bounds of the 95% confidence interval.

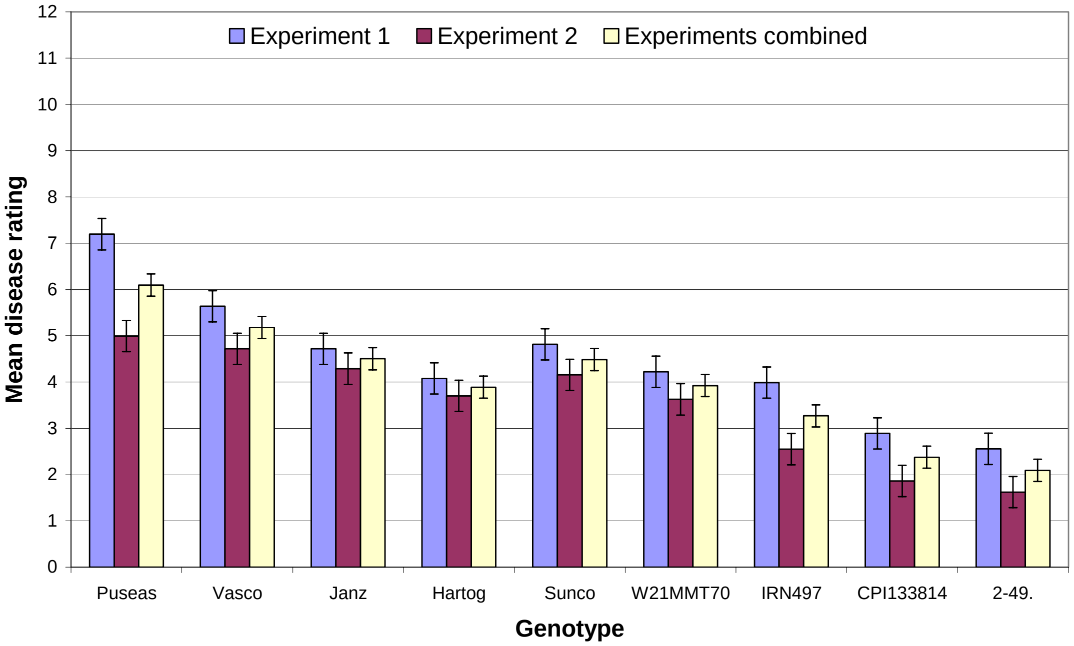


Figure 4.4 Mean disease rating of each inoculum across all genotypes for each experiment and experiments combined. Error bars represent the upper and lower bounds of the 95% confidence interval.

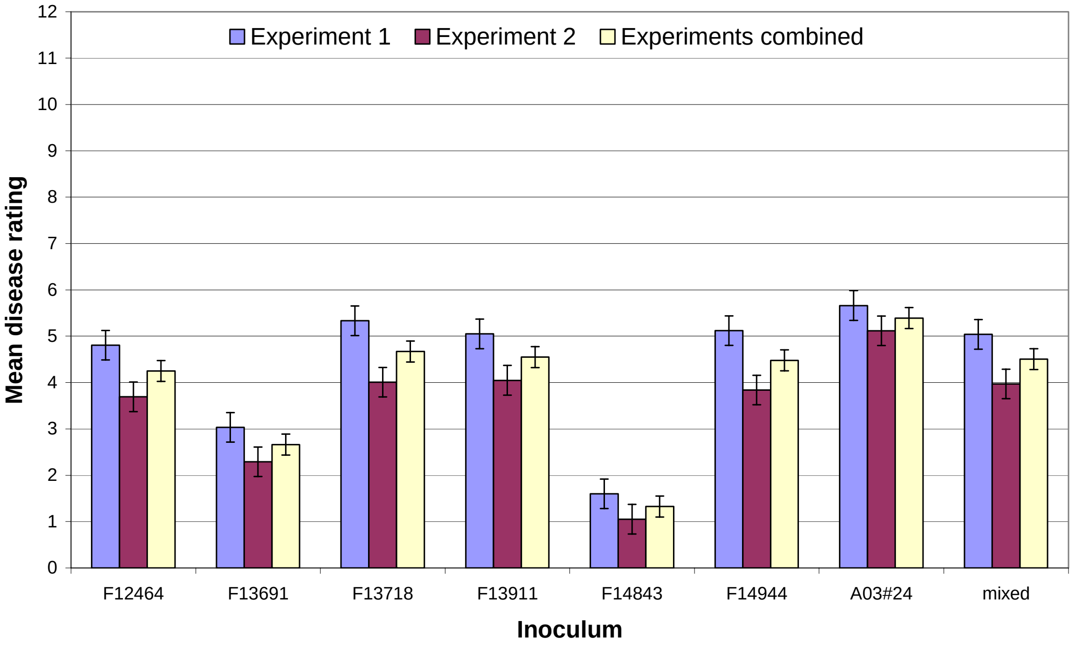
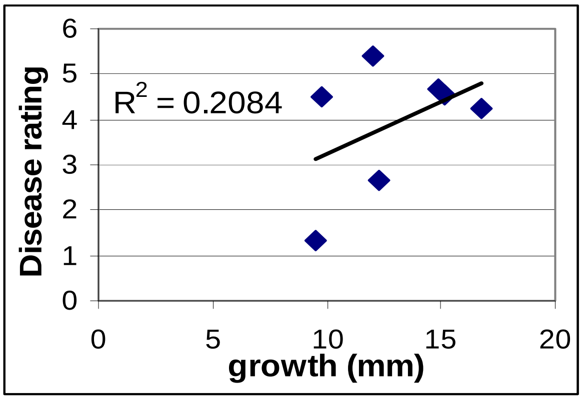


Table 4.5 Comparison of mean disease rating and mean growth rate of each isolate. Identical letters next to growth rate values are assigned to values which are not significantly different.

Inoculum	Disease rating	Growth rate
F14843*	1.33	9.50 a
F13691	2.66	12.25 b
F12464	4.25	16.75 d
F14944*	4.48	9.75 a
mixed	4.50	not measured
F13911*	4.55	15.12 c
F13718	4.67	14.88 c
A03#24	5.39	12.0 b
MEAN	3.98	12.89
Std. Error	0.12	0.82
correlation coefficient (r)		0.456
sig (two-tailed)		0.303

* isolates with a higher degree of grain colonisation during inoculum production

Figure 4.5 Correlation of mean disease rating and growth rate on agar for F. pseudograminearum isolates.



4.2.3 Genotype/inoculum interactions

The genotype*inoculum interaction was highly significant (Table 4.3). However it contributed less than 7 % to the total variance in the data (Table 4.4). The order of susceptibility of each genotype is generally as expected for individual isolates with the more susceptible genotypes always higher than the partially resistant ones (Figure 4.6). Isolates F13691 and F14843 induced significantly lower disease ratings than the other isolates tested and A03#24 caused significantly higher levels of disease in the very susceptible host genotype Puseas (Figure 4.6).

Figure 4.6 Mean disease rating of 9 wheat genotypes challenged with 8 geographically diverse Fpg isolates. Error bars represent the upper and lower bounds of the 95% confidence interval. Lines between data points are for illustration purposes only.

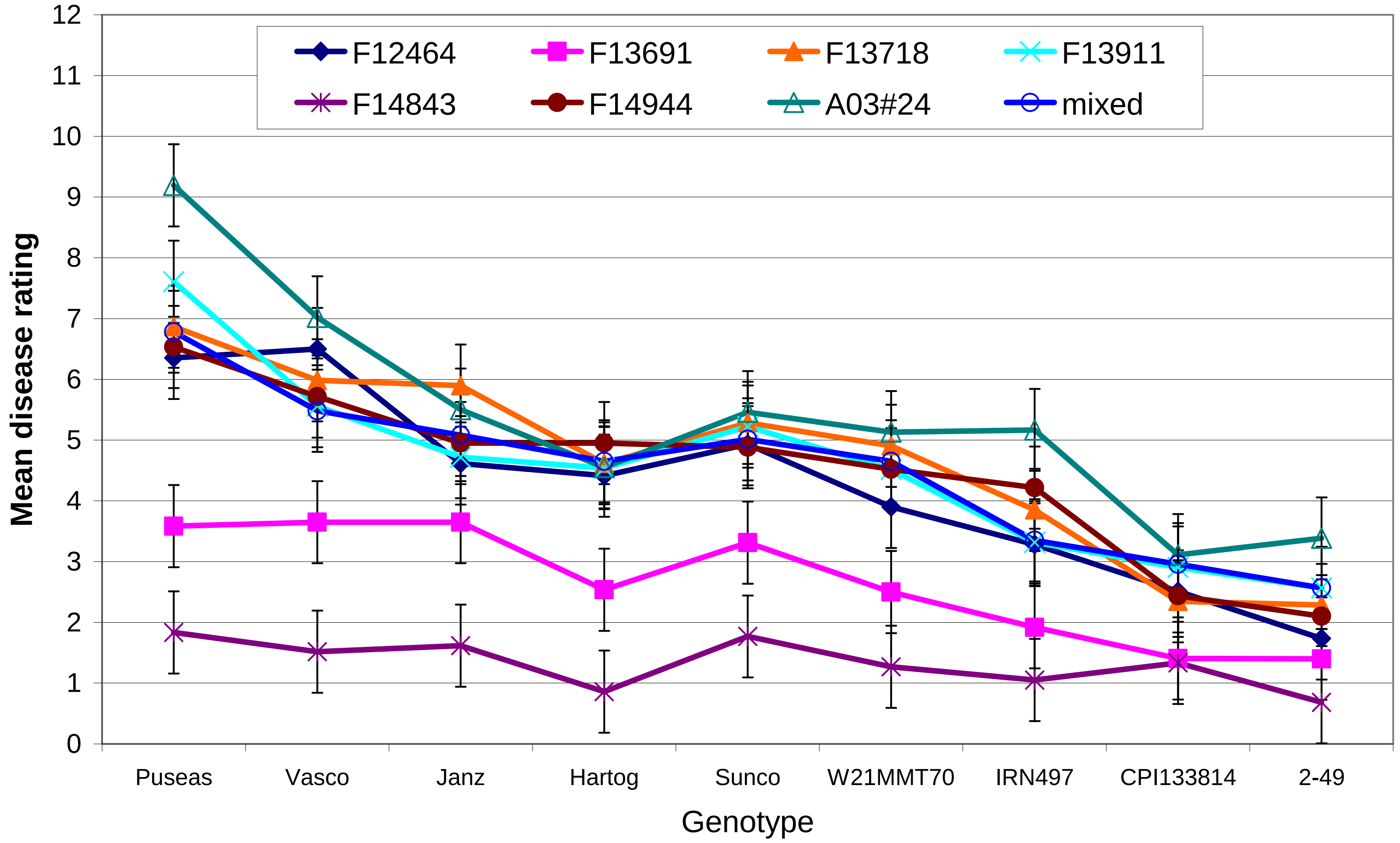


Table 4.6 Tests of between subject effects (Inoculum F14843 and F13691 removed from data).

Source		**Type III Sum of Squares**	**df**	**Mean Square**	**F**	**Sig.**
Intercept	Hypothesis	6976.06	1	6976.061	71.466	0.055
	Error	113.7	1.1648	97.614		
Genotype	Hypothesis	658.394	8	82.299	16.115	0.000
	Error	43.1831	8.4558	5.107		
Inoculum	Hypothesis	41.5249	5	8.305	6.670	0.024
	Error	6.84865	5.5	1.245		
Experiment	Hypothesis	90.3677	1	90.368	18.060	0.003
	Error	38.2566	7.6454	5.004		
Genotype * Inoculum	Hypothesis	46.4871	40	1.162	1.191	0.292
	Error	39.0422	40	0.976		
Genotype * Experiment	Hypothesis	39.3666	8	4.921	5.042	0.000
	Error	39.0422	40	0.976		
Inoculum * Experiment	Hypothesis	5.2954	5	1.059	1.085	0.383
	Error	39.0422	40	0.976		
Genotype * Inoculum * Experiment	Hypothesis	39.0422	40	0.976	1.190	0.217
	Error	177.205	216	0.820		

Table 4.7 Variance estimates using the Minimum Norm Quadratic Unbiased Estimation method (Weight = 1 for Random Effects and Residual). (Inoculum F14843 and F13691 removed from data).

Component	Estimate	%
Var(Inoculum)	0.131	7.35
Var(Experiment)	0.527	29.56
Var(Inoculum * Genotype)	0.031	1.74
Var(Experiment * Genotype)	0.219	12.28
Var(Inoculum * Experiment)	0.003	0.17
Var(Inoculum * Experiment * Genotype)	0.052	2.91
Var(Error)	0.82	45.99
TOTAL	1.783	100

The mean disease ratings of 2-49 and CPI133814 were significantly lower than the susceptible Puseas, Vasco and Janz with all isolates except F14843. The disease ratings of F14843 were so low that it was not possible to discern a genotype effect (Figure 4.6). W21MMT70, Sunco, Hartog and Janz were not significantly different from each other when challenged with any isolate.

4.2.3.1 Analysis of aggressive isolates

To further examine the genotype*inoculum interaction the lowest disease causing (least aggressive) isolates F13691 and F14843 were filtered out of the data and the univariate analysis of variance and variance component estimations re-run. This resulted in the interaction genotype*inoculum no longer being significant (Table 4.6) and contributing less than 2% to the variance in the data set (Table 4.7). It also resulted in a very significant reduction in the variance estimate for inoculum down to 7.35 %.

4.3 Discussion

Three major groupings of susceptibility to crown rot were distinguished in these seedling trials. Moderately resistant (2-49 and CPI133814), highly susceptible (Puseas and Vasco) and moderately susceptible (the remainder of genotypes). IRN497 was often grouped with the partially resistant genotypes, otherwise not significantly different from the susceptible Hartog and Janz. This may be a function of the lack of differentiating power in the seedling assay, for genotypes with modest resistance levels. Mesterhazy (1988) also reported changes in ranking order between genotypes close to each other in resistance to FHB when 21 genotypes were challenged with 4 isolates each of *F. culmorum* and *F. graminearum*. In spite of this, stable genotype rankings were found overall with the most resistant and most susceptible reactions always expressed. In the present study the mean ranking of all genotypes was as expected with the exception of Hartog. Nevertheless while this genotype is considered susceptible in field trials it has previously been rated not significantly different from 2-49 in seedling trials of the same design (Wildermuth and McNamara, 1994, Wildermuth et al., 2001).

Differences seen in the severity of disease between the two experiments has been accounted for by the difference in overnight temperatures between the two trials. Previous research has shown that crown rot infection is best achieved at temperatures around 25^0C and that at lower temperatures differences between genotypes may not be as clear (Wildermuth and McNamara, 1994).

Differences were seen between fungal isolates both in growth rates measured on agar and in colonisation of grain during inoculum production. A correlation of mean disease rating of each isolate with mean growth rate was not significant. Akinsanmi et al. (2006b) reported a weak association between growth rate and aggressiveness of *Fg* and *Fpg* isolates. While statistical analysis was not conducted in the present study, a relationship between colonisation of grain during inoculum production and mean disease severity of each isolate was not observed. Of the three isolates with increased colonisation of grain, isolate F14843 had the lowest mean disease rating while isolates F14944 and F13911 were ranked 4th and 5th respectively in order of increasing severity out of the 8 inoculum tested (Table 4.3). These results suggest that saprophytic growth rates do not predict aggressiveness on living host tissue.

Mesterhazy et al. (1999) also reported problems relating to differential levels of mycelium growth on CZA medium between isolates of *F. graminearum* and *F. culmorum*, indicating that control of fungal biomass was very difficult. They commented that previous research (Mesterhazy, 1977, cited in Mesterhazy et al., 1999) had determined that dilution or concentration of inoculum to achieve the same biomass affected the aggressiveness of isolates.

While isolates differed significantly in the severity of disease produced across wheat genotypes, the geographical source of the isolate was not a factor. F14843 (WA) and F13691 (NSW) were significantly lower than all other isolates however the other NSW and WA isolates produced high levels of disease.

If different races or pathotypes existed within these *Fpg* isolates then we would expect some of the wheat lines previously identified as resistant to show susceptible levels of disease with some isolates, such that the relative rankings of host genotype disease severity varied significantly between isolates. The three way interaction between genotype inoculum and experiment was never significant and the genotype*inoculum interaction was examined with experiments combined (Figure 4.6).

All isolates with the exception of F14843, were pathogenic to all genotypes but varied in aggressiveness. Isolate F13691 produced fairly low levels of disease in each genotype, however partially resistant and susceptible genotypes were still clearly distinguished. This indicates that pathogenic specialisation within these isolates is low. This is in agreement with studies on the pathogenicity of *Fpg* isolates causing FHB in wheat (Akinsanmi et al., 2006c).

Differences in aggressiveness have been reported across individual isolates in a number of different Fusarium species including *F. culmorum* and *F. graminearum* causing head blight in wheat (Mesterhazy et al., 1999), *F. culmorum* infection of barley seedlings (Hestbjerg et al., 2002) and in Fusarium wilt of pigeonpea caused by *F. udum* (Kiprop et al., 2002).

Akinsanmi et al. (2004) showed a high degree of variation in aggressiveness between and within Fusarium species causing crown rot and head blight in the wheat cultivar Kennedy. A strong relationship between previous crop and aggressiveness of isolates causing each disease was found, with isolates from wheat following wheat crops more aggressive for crown rot and isolates from wheat following maize or sorghum more aggressive for FHB. A subsequent AFLP analysis of 67 *Fpg* isolates revealed a significant association between genotypic diversity (AFLP clusters) and aggressiveness for FHB or crown rot (Akinsanmi et al., 2006c).

Mishra et al. (2006) reported a high genetic diversity within *Fpg* populations isolated from wheat seed in Western Canada however this data was not associated with variation in the disease-causing ability of the isolates. A recent study on the genetic structure of Australian *Fpg* populations (Bentley et al., 2008) also reported high levels of gene and genotypic diversity. AFLP analysis revealed low genetic differentiation between south central and southwestern populations but clear regional differentiation of northeastern and southern populations. In this current study both these populations have been (serendipitously) sampled with one isolate from South Australia and two from WA likely to fall into the south/southwestern population while the remaining isolates should group within the northeastern population.

In these experiments differences between partial resistance and susceptibility to crown rot has been shown using each isolate of *Fpg*. However as resistance in this disease is usually measured by a scale comparing the differential rate of disease between genotypes some fungal isolates, due to low aggressiveness, may not distinguish between genotypes which show a low degree of partial resistance. In discussions on FHB resistance Mesterhazy et al. (2005) reported that differentiation of genotype susceptibilities is not possible if disease causing capacity of a particular isolate is too low. This may be the case with isolate F14843 in the current trials. Hence choice of a highly aggressive isolate is likely to give clearer differences of response between host genotypes differing in susceptibility.

Mesterhazy (1988) suggested the use of an inoculum containing several isolates differing in aggressiveness for FHB screening due to the differences in genetic diversity for aggressiveness amongst *F. culmorum* and *F .graminearum* populations. In the experiments presented here both single aggressive isolates and the mixed inoculum separated the most partially resistant and the most susceptible genotypes.

Differences in aggressiveness within *Fpg* isolates shown in the current experiments, and for a single cultivar (Akinsanmi et al., 2004), highlight the importance of using a range of wheat standards differing in susceptibility to crown rot in screening for crown rot resistance with unknown fungal isolates.

A great deal of the variation in aggressiveness in head blight of winter rye caused by *Fusarium culmorum* was shown to be genetically inherited in a quantitative nature (Miedaner, 1997). The results in these trials support the hypothesis that sources of crown rot resistance are stable and quantitative (Collard et al., 2005), which suggests that competent resistance screening for crown rot can be achieved using any isolate aggressive enough to distinguish between genotypes. However only a small number of isolates were included in the current study and as distinct regional populations have been identified (Bentley et al., 2008) a wider assessment of the degree of virulence on known resistant lines of a range of isolates within each regional population should be performed to confirm the lack of pathogenic race structure within Australian *Fpg* populations.

Chapter 5 Conclusion

5.1 Introduction

Infection of the host by *Fpg* can occur at any time (Purss, 1966). In an emerging seedling this may occur soon after germination. Infection is closely followed by development of disease symptoms on infected tissues. The spread of the pathogen within host tissues from this time until yield is compromised at maturity has been poorly understood for some time (Burgess et al., 1981). This study was conducted to address this issue with the aim of identifying critical differences in crown rot infection seen between susceptible and resistant cereal genotypes. Different sources of resistance were included to determine if they act in the same fashion. Seedling and field trials were conducted with individual plants harvested at intervals throughout the trials. Each expanded plant part was separated and rated for disease severity and the number of *Fpg* colonies re-isolated from each tissue recorded. Analysis was conducted on each plant part using the REML procedure in Genstat. The fixed factors: harvest, genotype, tiller and experiment (seedling trials) and the corresponding two and three way interactions were examined to detect where individual means were significantly different. A preliminary examination of the pathogenicity of *Fpg* isolates against a range of wheat genotypes was also conducted.

5.2 Major Findings

1. Lower disease ratings were shown in seedlings of partially resistant wheat genotypes when compared to susceptible wheat genotypes. The oat variety Cleanleaf was consistently rated lower than all wheat genotypes. The barley variety Tallon had disease ratings similar to the more susceptible wheat variety Puseas.

2. Colonisation by *Fpg* was less extensive in seedlings of partially resistant wheat genotypes compared to susceptible material, with a lower number of isolations recorded from partially resistant tissues at each harvest.

3. The oat variety (Cleanleaf) tested in these seedling trials was not immune to fungal spread or disease development, however the resistance offered by this genotype was at a higher level than seen by any of the wheat genotypes tested.

4. Coleoptile material offers no resistance allowing a build up of infective hyphae in all genotypes.

5. Pot trials have confirmed that differences between genotypes in the extent of disease symptom development and fungal spread are clearly expressed in the leaf sheath tissues of pot grown seedlings.

6. Statistically significant differences between genotypes were not expressed in the disease rating or isolation of *Fpg* from leaf sheath tissue in field trials even at the seedling stage.

7. Strong differences were seen between partially resistant and susceptible wheat genotypes in both disease rating and isolations from internodes tissues and this could be detected soon after stem extension commenced.

8. Both colonization and disease symptoms are initially slowed in recently-formed tissues of partially resistant genotypes however at later harvest times these same tissues may be as diseased as the tissues of susceptible genotypes. This was most clearly seen in the leaf sheaths in seedling trials and in the internodes of field grown plants. This resistance appears to be a resistance to spread similar to the Type II resistance detected in FHB.

9. Correlations of disease ratings and isolation count data sets were always positive and highly significant. The strength of correlation in seedling leaf sheaths were usually strong whether data was separated according to genotype, plant part or harvest. However, only a modest correlation of disease rating and isolation data was seen in barley and oat seedlings compared to strong correlations for the three wheat genotypes examined.

10. In field trials strong correlations of disease rating and isolation data were seen from harvests 6 and 7 conducted during anthesis to milk development. Strong differences between susceptible and partially resistant genotypes were observed in internode tissues at these times.

11. There was no evidence of stable pathogenic races in the isolates examined in these experiments. The growth of all isolates was partially inhibited in a consistent manner on resistant genotypes when compared to very susceptible genotypes.

12. These results confirm significant differences in the aggressiveness of *Fpg* isolates on wheat, evidenced by variation in mean disease severity between isolates growing on a range of host genotypes.

5.3 General Discussion

Seedling Trials

In emerged seedlings the coleoptile tissue of all genotypes is highly susceptible to colonisation by *Fpg* which allows a rapid build up of infective hyphae to move into the underlying leaf sheath tissues. While coleoptile material offers no resistance, differences between host genotypes in the rate and extent of infection is clearly distinguished in the leaf sheaths of developing seedlings. In these seedling trials both the disease rating and isolation data for each leaf sheath were initially significantly lower in the partially resistant bread wheat 2-49, the synthetic hexaploid CPI 133814 and the oat variety Cleanleaf when compared to the susceptible bread wheat Puseas and the Barley variety Tallon. At later harvest times differences between the barley and wheat genotypes became non significant in older leaf sheaths. Also, the fungus progressed through to each younger leaf sheath at a slower rate in the partially resistant tissue, than seen in the susceptible tissue.

The disease ratings and isolation counts for the oat variety Cleanleaf also increased over time but at an even slower rate than observed in the partially resistant wheat genotypes CPI133814 and 2-49. At all harvests the isolation counts from all Cleanleaf leaf sheaths were significantly lower than the susceptible Puseas and Tallon except at 14 DAP in Exp 2.2.

Growth of *Fpg* through leaf sheath tissue was inhibited to the same extent in 2-49 and CPI133814 seedlings. Whether the resistances of these genotypes acts in a similar fashion is however unclear. Both genotypes have been shown to offer both seedling and adult plant resistance (Wildermuth and McNamara, 1994, Wildermuth et al., 2003) and it is possible that while the strength of resistance may be similar, the type of resistance may be very different. Molecular analysis of crown rot resistance has shown that the resistance expressed in 2-49 is associated with molecular markers across the whole genome (Collard et al., 2005) while resistance detected from CPI133814 up to this point has been confined to the D genome (William Bovill unpublished). Further studies based around microscopy, gene expression studies and tissue biochemistry are needed to determine how these resistances are operating.

While stem and leaf sheath browning are usually severe in crown rot infected barley genotypes associated yield losses have been reported to be low (Denis and Wallwork, unpublished, cited in Wallwork et al., 2004, Backhouse et al., 1997, Hekimhan et al., 2004). Oats have previously been reported to have high levels of resistance to crown rot (Nelson and Burgess, 1994, Wildermuth and Purss, 1971) and the height of stem colonisation may be lower in oats then either wheat or barley. In the current seedling trials the resistance expressed in the oat variety Cleanleaf was superior to that observed in the wheat or barley genotypes. A modest correlation between disease rating and isolation data was observed for Cleanleaf and Tallon compared to strong correlations in this data for the three wheat genotypes. It is unfortunate that space restrictions at planting and the time required to process samples led to the exclusion of these cereals from the current field trial experiments. The inclusion of barley and oats in such a study would be very informative with regards to the resistance or tolerance these genotypes may offer.

Field Trials

Four bread wheat genotypes Puseas and Vasco (susceptible), 2-49 and Sunco (partially resistant) and the synthetic hexaploid wheat CPI133814 (partially resistant) were assessed from seedlings to maturity for their field reaction to infection with *Fpg*. Symptoms of crown rot disease were observed in all genotypes with severity of symptoms and re-isolation of *Fpg* from infected tissue increasing at each harvest through each plant part. Genotypic differences were observed in both severity of disease and in the extent of fungal colonisation in two field trials conducted under very different moisture regimes.

The marked difference in plant size between the two trials has been accounted for by the lack of rainfall during the Jondaryan trial, where only 4 tillers were produced per plant compared to up 12 tillers per plant at Wellcamp (Cook and Veseth, 1991). Disease severity in the Jondaryan trial was also much lower than that observed at Wellcamp. The dryness of the surrounding soil seemed to not only slow establishment and progression of disease through the plant (Backhouse et al., 1997, Liddell and Burgess, 1985, Liddell and Burgess, 1988), but also restrains the growth of *Fpg* and subsequent symptom development up the length of both internode and leaf sheath tissues. In the moister Wellcamp trial both disease symptom development and colonisation by *Fpg* occurred through each plant at a faster rate with higher segments of each plant part becoming diseased and *Fpg* being readily re-isolated from higher sections of both internode and leaf sheath tissues. Consistent lower temperatures at the Jondaryan trial may have also affected pathogen vigour as greater symptoms of disease have been demonstrated with increasing temperatures (up to 25^0C) in controlled environment cabinets (Klein et al., 1985, Wildermuth and McNamara, 1994).

Although there were clear differences between the two trials in plant growth patterns and disease development, significant genotypic differences were still detected between susceptible and partially resistant wheat cultivars in both experiments. Coleoptile tissue was assessed for symptom development in the Jondaryan field trial and, as clearly established in seedling trials (Lusted, 1998), offers no resistance in any genotype under field conditions. Disease ratings of the sub-crown internode were inconsistent across genotypes and in agreement with (Wildermuth and McNamara, 1994) offered the lowest correlations with overall field performance of a genotype.

Genotypic differences in leaf sheath tissue in both disease rating and isolation data were mostly not statistically significant at each harvest under these field conditions compared to the highly significant differences detected in seedling trials. The overall genotype effect (harvest and tiller combined for each plant part) was highly significant in the disease rating data for the 1st 5 LS's in the Jondaryan trial and only in LS2 at Wellcamp. This was surprising with greater differences expected under higher disease pressure at Wellcamp suggesting that differences between genotypes in symptom expression may be less pronounced under moister field conditions. Alternatively resistance expressed in these genotypes may be associated with a higher tolerance of drier environments or that the pathogen is less able to overcome the resistances under drier field conditions.

It is possible that combining leaf sheaths for rating may produce more statistically significant scores between genotypes. Adding the disease rating score of the 1st three leaf sheaths was shown to have the highest correlation with field performance of each genotype examined by Wildermuth and McNamara (1994). In the current trials tiller was shown to be highly significant in the disease rating of all leaf sheaths with differences between tillers usually according to age (ie primary tiller having the highest level of disease). It may have been better to separate tiller rather than plant part in the analysis of these results allowing plant parts that were closer in age to be pooled. However in these trials genotypic differences were expected to be detected at the harvest/genotype/tiller level of interaction. Increasing sample size may have achieved this.

Consistent with the disease ratings of leaf sheaths, the isolation scores were also not statistically different between genotypes, with the overall genotype effect not significant in any leaf sheath analysed, indicating that resistance was not detected in leaf sheaths in the field. However I feel that the statistics have not detected what I consider to be fairly large differences in levels of infection between genotypes particularly at Jondaryan. The number of isolations from Puseas leaf sheaths was often twice as high as other genotypes particularly in the primary tiller (Tables 3.14, 3.15 and 3.16). In retrospect the particular statistical design employed carried insufficient power to draw out such differences.

Stem elongation was initiated at the 4th harvest (10-11 weeks after planting) and significantly different disease rating and isolations scores were observed between genotypes at all harvests from this time to maturity. The development of disease on internodes was delayed in the partially resistant genotypes. At maturity disease symptoms in the Wellcamp trial were restricted to the 2nd internode in 2-49, the 4th (mainly primary tiller) in Sunco, while lesions were recorded as high as the 5th and 6th internodes in Puseas and Vasco respectively (Tables 3.10-3.13). Limited lesioning beyond the 2nd internode was observed in all genotypes at maturity in the Jondaryan trial, however the severity of symptoms was still lower in the partially resistant genotypes in these 1st two internodes even at maturity.

When crown rot is assessed in field trials disease assessments are usually conducted on mature plants. However a high variability in cultivar reaction is often found between trials (e.g. Purss, 1966, Wallwork et al., 2004), making it difficult to standardize screening of large numbers of germplasm. In our field experiments differences were still observed between genotypes in the severity of disease symptoms in the 1st internode in the Jondaryan trial however in the moister Wellcamp trial differences in this tissue at maturity were no longer significant. This highlights the influence of environmental conditions on disease severity measurements. An index of susceptibility relative to the highly susceptible standard Puseas is used in field screening trials conducted at LRC (Wildermuth and McNamara, 1994) in an attempt to allow for fluctuations in overall disease severity between trials.

While genotypic differences were detected in certain tissues at maturity in the current experiments, more consistent differences were seen around milk/dough development in both field trials. Correlations of disease rating and isolation counts were strong for harvest 7 ($r = 0.7405$) in the Jondaryan trial and 6 ($r = 0.7519$) and 7 ($r = 0.7228$) in the Wellcamp trial. The weakest correlation between disease rating and isolation data was seen at the final harvest ($r = 0.3801$) in the Wellcamp trial. The period between flowering and seed formation would be the most appropriate time to test for genotypic differences in crown rot screening trials. It has been suggested that large scale varietal screening assessments prior to maturity would be impractical (personal communication with Steven Simpfendorfer NSW DPI). Large amounts of material currently harvested at maturity can be left to dry and then processed for disease assessment in the following months. In spite of this any smaller scale studies examining critical research populations should consider this approach and whether active drying or cold room treatment of plants harvested prior to maturity would enable the materials to be analysed over a period of time without changes in visible stem browning.

Pathogenicity

In agreement with studies on the pathogenicity of *Fpg* isolates causing FHB in wheat (Akinsanmi et al., 2006c), pathogenic specialisation for crown rot in wheat was low amongst the isolates examined in the current experiments. All isolates with the exception of F14843, were pathogenic to all genotypes but varied in aggressiveness. Isolate F13691 produced low levels of disease in each genotype, with only the most susceptible statistically distinguished from the most resistant genotype. However, the genotypes were still rated in order of susceptibility. These results suggest that any isolate aggressive enough to distinguish between genotypes can be used in resistance screening for crown rot. Further pathogenicity experiments need to be conducted with a broader isolate range. Considering the recent identification of two distinct regional populations amongst Australian *Fpg* isolates (Bentley et al., 2008) a larger number of isolates from each of these regions could be tested for pathogenicity and aggressiveness in the future.

Detecting resistance

Disease ratings of the partially resistant wheat genotype 2-49 and the synthetic hexaploid wheat CPI133814 were consistently lower than the more susceptible Puseas in all experiments conducted in this project suggesting that resistance to crown rot is relatively stable under challenge by multiple isolates of the pathogen. Similar conclusions have been reached for FHB and foot rot caused by *F. graminearum* and *F. culmorum* in wheat and rye (Bai and Shaner, 1996, Miedaner and Schilling, 1996, Van Eeuwijk et al., 1995), indicating horizontal resistance to these pathogens. However, I consistently encountered difficulty in discriminating between moderately susceptible and moderately resistant genotypes using the current rating techniques (for example differences between Sunco and Vasco were often not statistically significant). While crown rot screening aims to identify superior levels of resistance, it is just as important to be able to identify moderate levels as well. One of the best sources of partial resistance comes from 2-49, created from a cross between two moderately resistant varieties (Gala and Gluyas Early). The genotype

Sumai 3, one of the best sources of FHB resistance, was also created from two moderately resistant varieties (Bai and Shaner, 1994). Being able to discriminate between different levels of resistance in screening trials is very important as the hunt for new sources continues.

Crown rot symptom development is most severe under drought conditions particularly when a wet start to the season is followed with a dry finish. We have demonstrated a higher level of pathogen growth and disease severity in all plants grown under higher moisture conditions and Smiley et al. (2005) demonstrated lower yields in high precipitation trials in the absence of increased whitehead formation. Whether the greater volume of pathogen in the plant stems disrupts the translocation system to developing heads or whether stress at the crown region leads to late tiller abortion is unclear. A complete blocking of the translocation system by hyphal biomass would be expected to be associated with extensive wilting of infected genotypes. This has not been reported. Resistance to crown rot may lie in the ability of the genotype to tolerate moisture stress which would be compounded by infection in extremely dry conditions during grain fill. It is unfortunate that whitehead analysis was not conducted during the Jondaryan trial as such information would have been very informative associated with the current disease severity and isolation scores collected. Based on the results in Tables/Figures 3.19 and 3.20, it appears that at the end of the season as the maturing plant dries off, growth of the fungus is no longer impeded in previously resistant tissues with the fungus possibly switching to saprophytic growth. The extent of spread through the straw is at this point likely to be determined by local moisture conditions.

The resistance examined in these experiments is associated with a slowing of pathogen spread through leaf sheath tissue in seedlings and up the stems of more mature plants in field trials. This may be similar to the Type II resistance (resistance to spread) seen in wheat heads infected with Fusarium Head Blight (Muthomi et al., 2002, Ribichich et al., 2000). Type II resistance has also been shown to be associated with a slowing down of pathogen spread rather than a complete inhibition. This resistance response points to processes that act as barriers such as reinforcing of cell walls with lignin or suberin, or accumulation of antimicrobial secondary metabolites (Osbourn, 2001). There may also be a level of resistance to penetration operating along with resistance to spread. Dodman and Wildermuth (1987) reported that resistance was more clearly expressed when spores were sprayed onto the base of stems rather than when spores were injected into stems, suggesting that resistance to penetration and/or spread will require detailed histological investigations. In the histological experiments conducted in the current project initial penetration was not observed and the mechanism's by which *Fpg* enters the plant remains unclear.

Varietal difference to crown rot infection was observed very soon after disease identification (McKnight and Hart, 1966, Purss, 1966). However our understanding of this resistance is still quite limited. Since the 1960's, producing this resistance consistently in experimental trials has proved difficult. One of the recommendations of Purss (1966) was that resistance screening needs to be standardised to control for the high variability due to environment. Different techniques have been tested throughout the last 40 years, including techniques to increase efficiency such as testing for resistance in seedlings (Wildermuth and McNamara, 1994 and others). However to date, different techniques are still being used to screen winter cereals for crown rot resistance across the country and conflicting results are not uncommon. This issue needs to be addressed in order to pool the information obtained through extensive experimentation nationwide, leading to a better understanding of the very complex wheat crown rot host pathogen relationship.

5.4 Future Directions

There has been a need for a long time to understand the histology of the crown rot pathogen and the resistance subsequently asserted by the host. One of the aims of the current project was to address this issue examining infected tissues with basic and fluorescent microscopy. Time limitations and work-up of timely methodologies restricted these experiments and they have not been included in this dissertation. This approach is currently being followed up by Noel Knight, a current PhD student at USQ. Varying concentrations of conidia always led to extensive growth of mycelium on the surface of inoculated leaf sheaths in both susceptible and partially resistant genotypes which greatly hampered the visualisation of penetration sites. It is possible that some sort of pressure such as that provided within the soil medium is required to encourage penetration and in the absence of such force the fungus produces enough mycelium so as to produce a mat prior to penetration. *Fg* has been reported to produce a mat of mycelium in the subcuticular space prior to cell wall penetration of isolated wheat and barley caryopses (Jansen et al., 2005). The extensive colonisation of the coleoptile of both susceptible and partial resistant genotypes as discussed in Chapter 2 may also be important prior to initial penetration of the underlying leaf sheath tissue. Extensive microscopy still needs to be performed to examine initial infection and aid determination of resistance mechanisms.

Real-Time PCR technologies (Okubara et al., 2005) have also become available since the commencement of my project which can be used to quantify hyphal biomass during infection. This direction is also currently being pursued by Noel Knight at USQ as part of his PhD project. These techniques will allow a much more accurate measurement of real differences in fungal spread between susceptible and partially resistant genotypes. In recent years Real-Time PCR has also been used in gene expression studies of this host-pathogen relationship (Desmond et al., 2006). Several defense genes were induced more rapidly and to a higher level in Sunco compared to the susceptible genotype Kennedy during the first two days after inoculation. The role of these defense genes in the resistance response deserves greater examination.

Two factors critical to farmers with crown rot infected paddocks are the impact of disease on crop yield and the level of inoculum which may carry over in subsequent seasons. The PreDicta B soil test developed by SARDI and CSIRO is now available to monitor pathogen levels in cereal paddocks and farmers may strive to reduce the impact of crown rot through integrated control measures such as fallowing and crop rotation. Reducing the amount of intial inoculum is however crucial and an examination of the differences in inoculum carry over contributed by different genotypes is important. Studies by Verrell et al. (2006) have shown differences in plant biomass partitioning between susceptible and partially resistant genotypes which will certainly impact inoculum carry over. The correlation of disease symptom development and actual yield loss also warrants further attention. Several studies have reported losses in potential yield (eg Dodman and Wildermuth, 1987, Klein et al., 1991) however inoculated and uninoculated plots need to be compared as a measure of both tolerance and resistance of cereal genotypes to crown rot disease.

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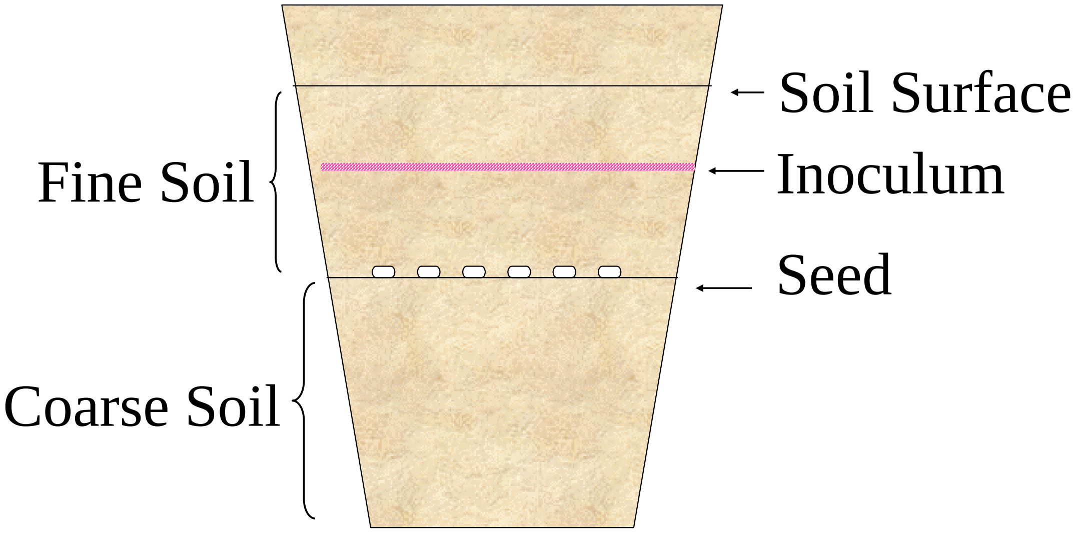
Appendix 2A
Layered-pot design



Appendix 2B

Czapek Dox Agar With Antibiotics

MATERIALS:

Agar	15gms
$NaNO_3$	3gms
K_2HPO_4	1gm
Mg SO_4 $7H_2O$	0.5gms
KCl	0.5gms
$FeSO_4$ $7H_2O$.EDTA	10mls
Sucrose (10%)	30gms
Yeast	1gm
H2O (distilled)	1000mls

STOCK SOLUTIONS

Streptomycin:	1g/50mls sterile distilled water (SDW)
Achromycin:	0.25g/50mls SDW
Allisan (Dichloran):	(50%ai) 0.1g/100mls SDW

$FeSO_4$ $7H_20$.EDTA: 1.2g of EDTA (di-sodium salt) and 1g of $FeSO_4.7H_20$ dissolved in 200mls of SDW.

METHODS

The yeast was first dissolved with water and put aside. Water was placed on a hotplate with a stirrer and dry ingredients were measured out into a beaker and added to the water when it was warm. The solution was left stirring until lumps dissolved. (On some occasions heating was achieved using a microwave for approximately 15 minutes on high, stirring manually a couple of times). Beaker was removed from hotplate or microwave before boiling and FeSO4 7H2O and yeast paste was added and stirred. The agar was poured through a funnel into a 250ml-measuring cylinder and then into Schott bottles. The agar was autoclaved at 121^0 C for 16mins and left to cool.

Prior to use the agar was melted in a microwave and allowed to cool until it could be held for approximately 6secs. 1ml Achromycin, 1.25mls Streptomycin, and 1.5 mls of Allisan were added to each bottle and plates poured immediately. Approximately 20 plates were poured per bottle of agar.

Experiment	Harvest	Genotype	Rep	Plant	Tiller	Part	Disese Rating	Infection (total)	Infection (1/4)	Infection (2/4)
1	1	Puseas	1	1	1	LS1	3	4	2.5	1.5
1	1	Puseas	1	1	1	LS2	1	5	2	2
1	1	Puseas	1	1	1	LS3	0	0	0	0
1	1	Puseas	1	2	1	LS1	2	5	2.5	2.5
1	1	Puseas	1	2	1	LS2	1	1	1	0
1	1	Puseas	1	2	1	LS3	0	0	0	0
1	1	Puseas	1	3	1	LS1	3	7	2.5	3.5
1	1	Puseas	1	3	1	LS2	1	6	0	3
1	1	Puseas	1	3	1	LS3	0	0	0	0
1	1	Puseas	1	4	1	LS1	3	8	2	2
1	1	Puseas	1	4	1	LS2	1	6	0.5	3.5
1	1	Puseas	1	4	1	LS3	0	0	0	0
1	1	Puseas	1	5	1	LS1	3	11	3.5	3.5
1	1	Puseas	1	5	1	LS2	1	5	1	3
1	1	Puseas	1	5	1	LS3	0	0	0	0
1	1	Puseas	2	1	1	LS1	3			
1	1	Puseas	2	1	1	LS2	1			
1	1	Puseas	2	1	1	LS3	0			
1	1	Puseas	2	2	1	LS1	1			
1	1	Puseas	2	2	1	LS2	0			
1	1	Puseas	2	2	1	LS3	0			
1	1	Puseas	2	3	1	LS1	1			
1	1	Puseas	2	3	1	LS2	0			
1	1	Puseas	2	3	1	LS3	0			
1	1	Puseas	2	4	1	LS1	1			
1	1	Puseas	2	4	1	LS2	0			
1	1	Puseas	2	4	1	LS3	0			
1	1	Puseas	2	5	1	LS1	2			
1	1	Puseas	2	5	1	LS2	1			
1	1	Puseas	2	5	1	LS3	0			
1	1	2-49	1	1	1	LS1	1	2	2	0
1	1	2-49	1	1	1	LS2	0	1	1	0
1	1	2-49	1	1	1	LS3	0	0	0	0
1	1	2-49	1	2	1	LS1	1	3	2	1
1	1	2-49	1	2	1	LS2	0	1	1	0
1	1	2-49	1	2	1	LS3	0	0	0	0
1	1	2-49	1	3	1	LS1	2	3	2.5	0.5
1	1	2-49	1	3	1	LS2	0	1	1	0
1	1	2-49	1	3	1	LS3	0	0	0	0
1	1	2-49	1	4	1	LS1	1	3	2	1
1	1	2-49	1	4	1	LS2	0	0	0	0
1	1	2-49	1	4	1	LS3	0	0	0	0
1	1	2-49	1	5	1	LS1	1	3	2.5	0.5
1	1	2-49	1	5	1	LS2	0	0	0	0
1	1	2-49	1	5	1	LS3	0	0	0	0
1	1	2-49	2	1	1	LS1	2			
1	1	2-49	2	1	1	LS2	0			
1	1	2-49	2	1	1	LS3	0			
1	1	2-49	2	2	1	LS1	1			
1	1	2-49	2	2	1	LS2	0			
1	1	2-49	2	2	1	LS3	0			
1	1	2-49	2	3	1	LS1	1			
1	1	2-49	2	3	1	LS2	0			

1	1	2-49	2	3	1	LS3	0			
1	1	2-49	2	4	1	LS1	1			
1	1	2-49	2	4	1	LS2	0			
1	1	2-49	2	4	1	LS3	0			
1	1	2-49	2	5	1	LS1	1			
1	1	2-49	2	5	1	LS2	0			
1	1	2-49	2	5	1	LS3	0			
1	1	CPI133814	1	1	1	LS1	0	3	2	1
1	1	CPI133814	1	1	1	LS2	0	0	0	0
1	1	CPI133814	1	1	1	LS3	0	0	0	0
1	1	CPI133814	1	2	1	LS1	1	3	1.5	1.5
1	1	CPI133814	1	2	1	LS2	0	0	0	0
1	1	CPI133814	1	2	1	LS3	0	0	0	0
1	1	CPI133814	1	3	1	LS1	1	4	2.5	1.5
1	1	CPI133814	1	3	1	LS2	0	0	0	0
1	1	CPI133814	1	3	1	LS3	0	0	0	0
1	1	CPI133814	1	4	1	LS1	1	0	0	0
1	1	CPI133814	1	4	1	LS2	0	0	0	0
1	1	CPI133814	1	4	1	LS3	0	0	0	0
1	1	CPI133814	1	5	1	LS1	0	2	1.5	0.5
1	1	CPI133814	1	5	1	LS2	0	0	0	0
1	1	CPI133814	1	5	1	LS3	0	0	0	0
1	1	CPI133814	2	1	1	LS1	1			
1	1	CPI133814	2	1	1	LS2	0			
1	1	CPI133814	2	1	1	LS3	0			
1	1	CPI133814	2	2	1	LS1	1			
1	1	CPI133814	2	2	1	LS2	0			
1	1	CPI133814	2	2	1	LS3	0			
1	1	CPI133814	2	3	1	LS1	1			
1	1	CPI133814	2	3	1	LS2	0			
1	1	CPI133814	2	3	1	LS3	0			
1	1	CPI133814	2	4	1	LS1	0			
1	1	CPI133814	2	4	1	LS2	0			
1	1	CPI133814	2	4	1	LS3	0			
1	1	CPI133814	2	5	1	LS1	1			
1	1	CPI133814	2	5	1	LS2	0			
1	1	CPI133814	2	5	1	LS3	0			
1	1	Tallon	1	1	1	LS1	3	2	0	2
1	1	Tallon	1	1	1	LS2	1	1	1	0
1	1	Tallon	1	1	1	LS3	0	0	0	0
1	1	Tallon	1	2	1	LS1	3	2	0	2
1	1	Tallon	1	2	1	LS2	1	1	1	0
1	1	Tallon	1	2	1	LS3	0	0	0	0
1	1	Tallon	1	3	1	LS1	3	5	2.5	2.5
1	1	Tallon	1	3	1	LS2	1	2	2	0
1	1	Tallon	1	3	1	LS3	0	0	0	0
1	1	Tallon	1	4	1	LS1	3	2	0	2
1	1	Tallon	1	4	1	LS2	1	2	2	0
1	1	Tallon	1	4	1	LS3	0	1	1	0
1	1	Tallon	1	5	1	LS1	4	6	2	2
1	1	Tallon	1	5	1	LS2	1	0	0	0
1	1	Tallon	1	5	1	LS3	0	0	0	0
1	1	Tallon	2	1	1	LS1	3			
1	1	Tallon	2	1	1	LS2	1			
1	1	Tallon	2	1	1	LS3	0			

1	1	Tallon	2	2	1	LS1	2			
1	1	Tallon	2	2	1	LS2	1			
1	1	Tallon	2	2	1	LS3	0			
1	1	Tallon	2	3	1	LS1	3			
1	1	Tallon	2	3	1	LS2	1			
1	1	Tallon	2	3	1	LS3	0			
1	1	Tallon	2	4	1	LS1	4			
1	1	Tallon	2	4	1	LS2	1			
1	1	Tallon	2	4	1	LS3	0			
1	1	Tallon	2	5	1	LS1	3			
1	1	Tallon	2	5	1	LS2	1			
1	1	Tallon	2	5	1	LS3	0			
1	1	Cleanleaf	1	1	1	LS1	1	1	0	1
1	1	Cleanleaf	1	1	1	LS2	0	0	0	0
1	1	Cleanleaf	1	1	1	LS3	0	0	0	0
1	1	Cleanleaf	1	2	1	LS1	0	0	0	0
1	1	Cleanleaf	1	2	1	LS2	0	0	0	0
1	1	Cleanleaf	1	2	1	LS3	0	0	0	0
1	1	Cleanleaf	1	3	1	LS1	0	0	0	0
1	1	Cleanleaf	1	3	1	LS2	0	0	0	0
1	1	Cleanleaf	1	3	1	LS3	0	0	0	0
1	1	Cleanleaf	1	4	1	LS1	0	0	0	0
1	1	Cleanleaf	1	4	1	LS2	0	0	0	0
1	1	Cleanleaf	1	4	1	LS3	0	0	0	0
1	1	Cleanleaf	1	5	1	LS1	0	3	0	0
1	1	Cleanleaf	1	5	1	LS2	0	0	0	0
1	1	Cleanleaf	1	5	1	LS3	0	0	0	0
1	1	Cleanleaf	2	1	1	LS1	0			
1	1	Cleanleaf	2	1	1	LS2	0			
1	1	Cleanleaf	2	1	1	LS3	0			
1	1	Cleanleaf	2	2	1	LS1	0			
1	1	Cleanleaf	2	2	1	LS2	0			
1	1	Cleanleaf	2	2	1	LS3	0			
1	1	Cleanleaf	2	3	1	LS1	0			
1	1	Cleanleaf	2	3	1	LS2	0			
1	1	Cleanleaf	2	3	1	LS3	0			
1	1	Cleanleaf	2	4	1	LS1	0			
1	1	Cleanleaf	2	4	1	LS2	0			
1	1	Cleanleaf	2	4	1	LS3	0			
1	1	Cleanleaf	2	5	1	LS1	0			
1	1	Cleanleaf	2	5	1	LS2	0			
1	1	Cleanleaf	2	5	1	LS3	0			
1	2	Puseas	1	1	1	LS1	3	4	2	1
1	2	Puseas	1	1	1	LS2	2	2	1	1
1	2	Puseas	1	1	1	LS3	1	3	1	1
1	2	Puseas	1	1	1	LS4	0	0	0	0
1	2	Puseas	1	1	1	LS5	0	0	0	0
1	2	Puseas	1	2	1	LS1	4	6	2	1
1	2	Puseas	1	2	1	LS2	4	8	3	2
1	2	Puseas	1	2	1	LS3	4	8	2	2
1	2	Puseas	1	2	1	LS4	1	0	0	0
1	2	Puseas	1	2	1	LS5	0	0	0	0
1	2	Puseas	1	3	1	LS1	4	3	1	0
1	2	Puseas	1	3	1	LS2	4	6	2	2
1	2	Puseas	1	3	1	LS3	4	5	2	1

1	2	Puseas	1	3	1	LS4	4	4	0	1
1	2	Puseas	1	4	1	LS1	2	3	2	1
1	2	Puseas	1	4	1	LS2	1	1	1	0
1	2	Puseas	1	4	1	LS3	0	0	0	0
1	2	Puseas	1	4	1	LS4	0	0	0	0
1	2	Puseas	1	4	1	LS5	0	0	0	0
1	2	Puseas	1	5	1	LS1	3	4	3	1
1	2	Puseas	1	5	1	LS2	3	4	2	2
1	2	Puseas	1	5	1	LS3	1	2	2	0
1	2	Puseas	1	5	1	LS4	0	0	0	0
1	2	Puseas	2	1	1	LS1	4			
1	2	Puseas	2	1	1	LS2	4			
1	2	Puseas	2	1	1	LS3	4			
1	2	Puseas	2	2	1	LS1	4			
1	2	Puseas	2	2	1	LS2	4			
1	2	Puseas	2	2	1	LS3	4			
1	2	Puseas	2	3	1	LS1	4			
1	2	Puseas	2	3	1	LS2	4			
1	2	Puseas	2	3	1	LS3	4			
1	2	Puseas	2	4	1	LS1	3			
1	2	Puseas	2	4	1	LS2	3			
1	2	Puseas	2	4	1	LS3	1			
1	2	Puseas	2	4	1	LS4	0			
1	2	Puseas	2	4	1	LS5	0			
1	2	Puseas	2	5	1	LS1	4			
1	2	Puseas	2	5	1	LS2	1			
1	2	Puseas	2	5	1	LS3	0			
1	2	Puseas	2	5	1	LS4	0			
1	2	Puseas	2	5	1	LS5	0			
1	2	2-49	1	1	1	LS1	4	4	1	2
1	2	2-49	1	1	1	LS2	2	3	2	1
1	2	2-49	1	1	1	LS3	0	1	0	1
1	2	2-49	1	1	1	LS4	0	0	0	0
1	2	2-49	1	1	1	LS5	0	0	0	0
1	2	2-49	1	1	2	S1	1	2	0	1
1	2	2-49	1	2	1	LS1	4	4	2	1
1	2	2-49	1	2	1	LS2	1	2	1	0
1	2	2-49	1	2	1	LS3	0	0	0	0
1	2	2-49	1	2	1	LS4	0	0	0	0
1	2	2-49	1	2	1	LS5	0	0	0	0
1	2	2-49	1	3	1	LS1	4	4	2	1.5
1	2	2-49	1	3	1	LS2	2	3	2	1
1	2	2-49	1	3	1	LS3	0	3	2	1
1	2	2-49	1	3	1	LS4	0	0	0	0
1	2	2-49	1	3	1	LS5	0	0	0	0
1	2	2-49	1	4	1	LS1	2	3	2	1
1	2	2-49	1	4	1	LS2	1	1	1	0
1	2	2-49	1	4	1	LS3	0	0	0	0
1	2	2-49	1	4	1	LS4	0	0	0	0
1	2	2-49	1	4	1	LS5	0	0	0	0
1	2	2-49	1	4	2	S1	0	0	0	0
1	2	2-49	1	4	2	LS1	0	0	0	0
1	2	2-49	1	4	3	S1	0	0	0	0
1	2	2-49	1	5	1	LS1	3	4	2	1
1	2	2-49	1	5	1	LS2	1	2	2	0

1	2	2-49	1	5	1	LS3	0	0	0	0
1	2	2-49	1	5	1	LS4	0	0	0	0
1	2	2-49	1	5	1	LS5	0	0	0	0
1	2	2-49	2	1	1	LS1	3			
1	2	2-49	2	1	1	LS2	1			
1	2	2-49	2	1	1	LS3	0			
1	2	2-49	2	1	1	LS4	0			
1	2	2-49	2	1	1	LS5	0			
1	2	2-49	2	1	2	S1	0			
1	2	2-49	2	1	2	LS1	0			
1	2	2-49	2	2	1	LS1	3			
1	2	2-49	2	2	1	LS2	2			
1	2	2-49	2	2	1	LS3	0			
1	2	2-49	2	2	1	LS4	0			
1	2	2-49	2	2	1	LS5	0			
1	2	2-49	2	2	2	S1	0			
1	2	2-49	2	2	2	LS1	0			
1	2	2-49	2	2	3	S1	0			
1	2	2-49	2	3	1	LS1	4			
1	2	2-49	2	3	1	LS2	2			
1	2	2-49	2	3	1	LS3	0			
1	2	2-49	2	3	1	LS4	0			
1	2	2-49	2	3	1	LS5	0			
1	2	2-49	2	3	2	S1	0			
1	2	2-49	2	4	1	LS1	4			
1	2	2-49	2	4	1	LS2	1			
1	2	2-49	2	4	1	LS3	0			
1	2	2-49	2	4	1	LS4	0			
1	2	CPI133814	1	1	1	LS1	2	4	2	1.5
1	2	CPI133814	1	1	1	LS2	0	1	0	1
1	2	CPI133814	1	1	1	LS3	0	0	0	0
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1	2	CPI133814	1	2	1	LS1	3	4	2	1
1	2	CPI133814	1	2	1	LS2	2	4	2	2
1	2	CPI133814	1	2	1	LS3	3	4	1	0
1	2	CPI133814	1	2	1	LS4	0	0	0	0
1	2	CPI133814	1	2	2	S1	1	3	0	0.5
1	2	CPI133814	1	3	1	LS1	1	2	1.5	0.5
1	2	CPI133814	1	3	1	LS2	0	0	0	0
1	2	CPI133814	1	3	1	LS3	0	0	0	0
1	2	CPI133814	1	3	1	LS4	0	0	0	0
1	2	CPI133814	1	4	1	LS1	3	3	1.5	1.5
1	2	CPI133814	1	4	1	LS2	1	1	1	0
1	2	CPI133814	1	4	1	LS3	0	0	0	0
1	2	CPI133814	1	4	1	LS4	0	0	0	0
1	2	CPI133814	1	5	1	LS1	2	3	1.5	1.5
1	2	CPI133814	1	5	1	LS2	0	1	0	0
1	2	CPI133814	1	5	1	LS3	0	0	0	0
1	2	CPI133814	1	5	1	LS4	0	0	0	0
1	2	CPI133814	2	1	1	LS1	2			
1	2	CPI133814	2	1	1	LS2	0			
1	2	CPI133814	2	1	1	LS3	0			
1	2	CPI133814	2	1	1	LS4	0			
1	2	CPI133814	2	1	2	S1	0			
1	2	CPI133814	2	2	1	LS1	4			

1	2	CPI133814	2	2	1	LS2	1			
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1	2	CPI133814	2	2	2	S1	1			
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1	2	CPI133814	2	3	1	LS3	0			
1	2	CPI133814	2	3	1	LS4	0			
1	2	CPI133814	2	3	2	S1	1			
1	2	CPI133814	2	3	2	LS1	0			
1	2	CPI133814	2	4	1	LS1	3			
1	2	CPI133814	2	4	1	LS2	0			
1	2	CPI133814	2	4	1	LS3	0			
1	2	CPI133814	2	4	1	LS4	0			
1	2	CPI133814	2	5	1	LS1	1			
1	2	CPI133814	2	5	1	LS2	1			
1	2	CPI133814	2	5	1	LS3	0			
1	2	CPI133814	2	5	1	LS4	0			
1	2	CPI133814	2	5	2	S1	0			
1	2	CPI133814	2	5	2	LS1	0			
1	2	Tallon	1	1	1	LS1	4	7	2	2
1	2	Tallon	1	1	1	LS2	4	5	2	1
1	2	Tallon	1	1	1	LS3	4	5	2	1
1	2	Tallon	1	1	1	LS4	4	4	1	1
1	2	Tallon	1	1	1	LS5	1	0	0	0
1	2	Tallon	1	2	1	LS1	4	5	1	2
1	2	Tallon	1	2	1	LS2	3	2	1.5	0.5
1	2	Tallon	1	2	1	LS3	1	3	1	1
1	2	Tallon	1	2	1	LS4	0	0	0	0
1	2	Tallon	1	2	1	LS5	0	0	0	0
1	2	Tallon	1	3	1	LS1	4	3	1	0
1	2	Tallon	1	3	1	LS2	4	4	1	1
1	2	Tallon	1	3	1	LS3	3	1	1	0
1	2	Tallon	1	3	1	LS4	0	0	0	0
1	2	Tallon	1	3	1	LS5	0	0	0	0
1	2	Tallon	1	4	1	LS1	4	4	1	0
1	2	Tallon	1	4	1	LS2	4	5	1.5	1.5
1	2	Tallon	1	4	1	LS3	4	7	2	2
1	2	Tallon	1	4	1	LS4	4	4	2	0
1	2	Tallon	1	4	1	LS5	2	1	0	1
1	2	Tallon	1	5	1	LS1	4	4	1	1
1	2	Tallon	1	5	1	LS2	1	1	1	0
1	2	Tallon	1	5	1	LS3	0	0	0	0
1	2	Tallon	1	5	1	LS4	0	0	0	0
1	2	Tallon	1	5	1	LS5	0	0	0	0
1	2	Tallon	2	1	1	LS1	4			
1	2	Tallon	2	1	1	LS2	4			
1	2	Tallon	2	1	1	LS3	1			
1	2	Tallon	2	1	1	LS4	1			
1	2	Tallon	2	1	1	LS5	0			
1	2	Tallon	2	1	2	S1	0			
1	2	Tallon	2	1	2	LS1	0			
1	2	Tallon	2	1	3	S1	0			
1	2	Tallon	2	1	3	LS1	0			
1	2	Tallon	2	2	1	LS1	4			

1	2	Tallon	2	2	1	LS2	4			
1	2	Tallon	2	2	1	LS3	1			
1	2	Tallon	2	2	1	LS4	0			
1	2	Tallon	2	2	1	LS5	0			
1	2	Tallon	2	3	1	LS1	4			
1	2	Tallon	2	3	1	LS2	3			
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1	2	Tallon	2	3	1	LS4	0			
1	2	Tallon	2	3	1	LS5	0			
1	2	Tallon	2	4	1	LS1	4			
1	2	Tallon	2	4	1	LS2	4			
1	2	Tallon	2	4	1	LS3	3			
1	2	Tallon	2	4	1	LS4	0			
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1	2	Tallon	2	4	2	S1	0			
1	2	Tallon	2	4	3	S1	0			
1	2	Tallon	2	5	1	LS1	4			
1	2	Tallon	2	5	1	LS2	4			
1	2	Tallon	2	5	1	LS3	4			
1	2	Tallon	2	5	1	LS4	4			
1	2	Tallon	2	5	1	LS5	0			
1	2	Cleanleaf	1	1	1	LS1	2	1	0	1
1	2	Cleanleaf	1	1	1	LS2	0	0	0	0
1	2	Cleanleaf	1	1	1	LS3	0	0	0	0
1	2	Cleanleaf	1	1	1	LS4	0	0	0	0
1	2	Cleanleaf	1	1	1	LS5	0	0	0	0
1	2	Cleanleaf	1	2	1	LS1	2	3	1	1
1	2	Cleanleaf	1	2	1	LS2	1	0	0	0
1	2	Cleanleaf	1	2	1	LS3	0	0	0	0
1	2	Cleanleaf	1	2	1	LS4	0	0	0	0
1	2	Cleanleaf	1	3	1	LS1	2	2	1	1
1	2	Cleanleaf	1	3	1	LS2	1	0	0	0
1	2	Cleanleaf	1	3	1	LS3	0	0	0	0
1	2	Cleanleaf	1	3	1	LS4	0	0	0	0
1	2	Cleanleaf	1	3	1	LS5	0	0	0	0
1	2	Cleanleaf	1	4	1	LS1	1	2	0	1
1	2	Cleanleaf	1	4	1	LS2	1	1	1	0
1	2	Cleanleaf	1	4	1	LS3	0	0	0	0
1	2	Cleanleaf	1	4	1	LS4	0	0	0	0
1	2	Cleanleaf	1	4	1	LS5	0	0	0	0
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1	2	Cleanleaf	1	5	1	LS5	0	0	0	0
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1	2	Cleanleaf	2	1	1	LS3	0			
1	2	Cleanleaf	2	1	1	LS4	0			
1	2	Cleanleaf	2	1	1	LS5	0			
1	2	Cleanleaf	2	2	1	LS1	0			
1	2	Cleanleaf	2	2	1	LS2	0			
1	2	Cleanleaf	2	2	1	LS3	0			
1	2	Cleanleaf	2	2	1	LS4	0			
1	2	Cleanleaf	2	2	1	LS5	0			

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1	2	Cleanleaf	2	3	1	LS3	0			
1	2	Cleanleaf	2	3	1	LS4	0			
1	2	Cleanleaf	2	3	1	LS5	0			
1	2	Cleanleaf	2	4	1	LS1	0			
1	2	Cleanleaf	2	4	1	LS2	0			
1	2	Cleanleaf	2	4	1	LS3	0			
1	2	Cleanleaf	2	4	1	LS4	0			
1	2	Cleanleaf	2	4	1	LS5	0			
1	2	Cleanleaf	2	4	2	S1	0			
1	2	Cleanleaf	2	4	2	LS1	0			
1	2	Cleanleaf	2	5	1	LS1	1			
1	2	Cleanleaf	2	5	1	LS2	0			
1	2	Cleanleaf	2	5	1	LS3	0			
1	2	Cleanleaf	2	5	1	LS4	0			
1	2	Cleanleaf	2	5	1	LS5	0			
1	2	Cleanleaf	2	5	2	S1	0			
1	2	Cleanleaf	2	5	2	LS1	0			
1	3	Puseas	1	1	1	LS1	4	4	3	1
1	3	Puseas	1	1	1	LS2	4	6	3	1
1	3	Puseas	1	1	1	LS3	2	5	3	2
1	3	Puseas	1	1	1	LS4	2	5	3	2
1	3	Puseas	1	1	1	LS5	1	4	4	0
1	3	Puseas	1	1	1	LS6	0	1	1	0
1	3	Puseas	1	2	1	LS1	4	10	3	2
1	3	Puseas	1	2	1	LS2	4	9	3	3
1	3	Puseas	1	2	1	LS3	4	9	2	2
1	3	Puseas	1	2	1	LS4	2	1	1	0
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1	3	Puseas	1	3	1	LS2	4	10	2	2
1	3	Puseas	1	3	1	LS3	4	8	2	2
1	3	Puseas	1	3	1	LS4	3	6	2	2.5
1	3	Puseas	1	3	1	LS5	1	2	1	1
1	3	Puseas	1	3	1	LS6	1	1	1	0
1	3	Puseas	1	4	1	LS1	4	3	2	1
1	3	Puseas	1	4	1	LS2	1	4	4	0
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1	3	Puseas	1	4	1	LS4	0	0	0	0
1	3	Puseas	1	4	1	LS5	0	0	0	0
1	3	Puseas	1	4	1	LS6	0	0	0	0
1	3	Puseas	1	4	1	LS7	0	0	0	0
1	3	Puseas	1	4	1	I1	0	0	0	0
1	3	Puseas	1	5	1	LS1	4	11	3	2.5
1	3	Puseas	1	5	1	LS2	4	6	2	1
1	3	Puseas	1	5	1	LS3	4	9	3	4
1	3	Puseas	1	5	1	LS4	1	0	0	0
1	3	Puseas	1	5	1	LS5	0	0	0	0
1	3	Puseas	1	5	1	LS6	0	0	0	0
1	3	Puseas	2	1	1	LS1	4			
1	3	Puseas	2	1	1	LS2	4			
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1	3	Puseas	2	2	1	LS1	4			
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1	3	Puseas	2	2	1	LS3	1			
1	3	Puseas	2	2	1	LS4	0			
1	3	Puseas	2	2	1	LS5	0			
1	3	Puseas	2	2	1	LS6	0			
1	3	Puseas	2	2	1	LS7	0			
1	3	Puseas	2	2	2	S1	1			
1	3	Puseas	2	2	2	LS1	0			
1	3	Puseas	2	2	2	LS2	0			
1	3	Puseas	2	3	1	LS1	4			
1	3	Puseas	2	3	1	LS2	4			
1	3	Puseas	2	3	1	LS3	4			
1	3	Puseas	2	3	1	LS4	4			
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1	3	Puseas	2	5	1	LS1	3			
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1	3	Puseas	2	5	1	LS3	2			
1	3	Puseas	2	5	1	LS4	1			
1	3	Puseas	2	5	1	LS5	0			
1	3	Puseas	2	5	1	LS6	0			
1	3	Puseas	2	5	1	I1	0			
1	3	2-49	1	1	1	LS1	4	3	2	1
1	3	2-49	1	1	1	LS2	4	7	3	2
1	3	2-49	1	1	1	LS3	1	1	1	0
1	3	2-49	1	1	1	LS4	0	1	1	0
1	3	2-49	1	1	1	LS5	0	0	0	0
1	3	2-49	1	1	1	LS6	0	0	0	0
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1	3	2-49	1	1	2	LS1	1	2	1.5	0.5
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1	3	2-49	1	1	3	LS1	1	0	0	0
1	3	2-49	1	1	3	LS2	0	0	0	0
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1	3	2-49	1	2	1	LS5	0	0	0	0
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1	3	2-49	1	2	2	LS1	0	2	1	1
1	3	2-49	1	2	2	LS2	0	0	0	0
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1	3	2-49	1	3	1	LS3	4	7	3	2
1	3	2-49	1	3	1	LS4	0	1	1	0
1	3	2-49	1	3	1	LS5	0	1	1	0
1	3	2-49	1	3	1	LS6	0	0	0	0
1	3	2-49	1	4	1	LS1	4	4	2	1.5
1	3	2-49	1	4	1	LS2	3	3	2.5	0.5
1	3	2-49	1	4	1	LS3	1	0	0	0

1	3	2-49	1	4	1	LS4	0	0	0	0
1	3	2-49	1	4	1	LS5	0	0	0	0
1	3	2-49	1	4	1	LS6	0	0	0	0
1	3	2-49	1	4	2	S1	3	3	2	1
1	3	2-49	1	4	2	LS1	1	1	1	0
1	3	2-49	1	4	2	LS2	1	0	0	0
1	3	2-49	1	4	2	LS3	0	0	0	0
1	3	2-49	1	4	3	S1	1	1	1	0
1	3	2-49	1	4	3	LS1	0	0	0	0
1	3	2-49	1	4	3	LS2	0	0	0	0
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1	3	2-49	1	5	1	LS3	3	5	3	2
1	3	2-49	1	5	1	LS4	1	1	1	0
1	3	2-49	1	5	1	LS5	0	0	0	0
1	3	2-49	1	5	1	LS6	0	0	0	0
1	3	2-49	1	5	2	S1	4	4	1	1
1	3	2-49	1	5	2	LS1	1	2	1	1
1	3	2-49	1	5	2	LS2	1	1	1	0
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1	3	2-49	2	1	2	S1	3			
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1	3	2-49	2	2	1	LS3	1			
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1	3	2-49	2	5	3	LS2	0			
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1	3	CPI133814	1	1	1	LS2	2	4	3	1
1	3	CPI133814	1	1	1	LS3	1	5	3	2
1	3	CPI133814	1	1	1	LS4	0	0	0	0
1	3	CPI133814	1	1	1	LS5	0	0	0	0
1	3	CPI133814	1	1	2	S1	4	7	2.5	2
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1	3	CPI133814	1	2	1	LS4	0	0	0	0
1	3	CPI133814	1	2	1	LS5	0	0	0	0
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1	3	CPI133814	1	3	1	LS4	1	0	0	0
1	3	CPI133814	1	3	1	LS5	0	0	0	0
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1	3	CPI133814	1	3	2	LS1	1	1	1	0
1	3	CPI133814	1	3	2	LS2	0	0	0	0
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1	3	CPI133814	1	4	1	LS3	1	0	0	0
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1	3	CPI133814	1	5	1	LS1	4	6	1	2
1	3	CPI133814	1	5	1	LS2	1	2	2	0
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1	3	CPI133814	1	5	1	LS4	0	0	0	0
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1	3	CPI133814	2	1	1	LS5	0			
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1	3	CPI133814	2	5	2	LS2	0			
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1	3	Tallon	1	2	1	LS2	4	9	3	2
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1	3	Tallon	2	1	1	LS4	2			
1	3	Tallon	2	1	1	LS5	1			
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1	3	Tallon	2	2	1	LS3	4			
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1	3	Cleanleaf	1	1	1	LS4	0	0	0	0
1	3	Cleanleaf	1	1	1	LS5	0	0	0	0
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1	3	Cleanleaf	1	1	2	S1	1	2	1	1
1	3	Cleanleaf	1	1	2	LS1	0	0	0	0
1	3	Cleanleaf	1	1	2	LS2	0	0	0	0
1	3	Cleanleaf	1	2	1	LS1	2	1	1	0
1	3	Cleanleaf	1	2	1	LS2	1	0	0	0
1	3	Cleanleaf	1	2	1	LS3	0	0	0	0
1	3	Cleanleaf	1	2	1	LS4	0	0	0	0
1	3	Cleanleaf	1	2	1	LS5	0	0	0	0
1	3	Cleanleaf	1	3	1	LS1	1	0	0	0
1	3	Cleanleaf	1	3	1	LS2	0	0	0	0
1	3	Cleanleaf	1	3	1	LS3	0	0	0	0
1	3	Cleanleaf	1	3	1	LS4	0	0	0	0
1	3	Cleanleaf	1	4	1	LS1	1	1	0	1
1	3	Cleanleaf	1	4	1	LS2	1	1	1	0
1	3	Cleanleaf	1	4	1	LS3	0	0	0	0
1	3	Cleanleaf	1	4	1	LS4	0	0	0	0
1	3	Cleanleaf	1	4	1	LS5	0	0	0	0
1	3	Cleanleaf	1	4	1	LS6	0	0	0	0

1	3	Cleanleaf	1	4	2	S1	0	0	0	0
1	3	Cleanleaf	1	4	2	LS1	0	0	0	0
1	3	Cleanleaf	1	5	1	LS1	2	1	0	0.5
1	3	Cleanleaf	1	5	1	LS2	1	0	0	0
1	3	Cleanleaf	1	5	1	LS3	0	0	0	0
1	3	Cleanleaf	1	5	1	LS4	0	0	0	0
1	3	Cleanleaf	1	5	1	LS5	0	0	0	0
1	3	Cleanleaf	1	5	1	LS6	0	0	0	0
1	3	Cleanleaf	2	1	1	LS1	1			
1	3	Cleanleaf	2	1	1	LS2	1			
1	3	Cleanleaf	2	1	1	LS3	0			
1	3	Cleanleaf	2	1	1	LS4	0			
1	3	Cleanleaf	2	1	1	LS5	0			
1	3	Cleanleaf	2	1	2	S1	0			
1	3	Cleanleaf	2	1	2	LS1	0			
1	3	Cleanleaf	2	1	2	LS2	0			
1	3	Cleanleaf	2	2	1	LS1	1			
1	3	Cleanleaf	2	2	1	LS2	1			
1	3	Cleanleaf	2	2	1	LS3	0			
1	3	Cleanleaf	2	2	1	LS4	0			
1	3	Cleanleaf	2	2	1	LS5	0			
1	3	Cleanleaf	2	2	1	LS6	0			
1	3	Cleanleaf	2	3	1	LS1	1			
1	3	Cleanleaf	2	3	1	LS2	0			
1	3	Cleanleaf	2	3	1	LS3	0			
1	3	Cleanleaf	2	3	1	LS4	0			
1	3	Cleanleaf	2	3	1	LS5	0			
1	3	Cleanleaf	2	3	1	LS6	0			
1	3	Cleanleaf	2	3	2	S1	0			
1	3	Cleanleaf	2	3	2	LS1	0			
1	3	Cleanleaf	2	3	2	LS2	0			
1	3	Cleanleaf	2	3	2	LS3	0			
1	3	Cleanleaf	2	4	1	LS1	0			
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1	3	Cleanleaf	2	4	1	LS3	0			
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1	3	Cleanleaf	2	5	1	LS1	1			
1	3	Cleanleaf	2	5	1	LS2	0			
1	3	Cleanleaf	2	5	1	LS3	0			
1	3	Cleanleaf	2	5	1	LS4	0			
1	3	Cleanleaf	2	5	1	LS5	0			
1	3	Cleanleaf	2	5	2	S1	0			
1	3	Cleanleaf	2	5	2	LS1	0			
1	3	Cleanleaf	2	5	2	LS2	0			
1	4	Puseas	1	1	1	LS1	4	8	3	1
1	4	Puseas	1	1	1	LS2	3	9	4	5
1	4	Puseas	1	1	1	LS3	2	1	0	1
1	4	Puseas	1	1	1	LS4	1	0	0	0
1	4	Puseas	1	1	1	LS5	0	0	0	0
1	4	Puseas	1	1	1	LS6	0	0	0	0
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1	4	Puseas	1	1	1	I1	0	0	0	0
1	4	Puseas	1	1	2	S1	4			
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1	4	Puseas	1	1	2	LS2	0	0	0	0

1	4	Puseas	1	2	1	LS1	4	12	3	3
1	4	Puseas	1	2	1	LS2	4	15	4	3
1	4	Puseas	1	2	1	LS3	4	8	1	1
1	4	Puseas	1	2	1	LS4	3	8	1	4
1	4	Puseas	1	2	1	LS5	1	3	0	1
1	4	Puseas	1	2	1	LS6	0	0	0	0
1	4	Puseas	1	2	1	LS7	0	0	0	0
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1	4	Puseas	1	3	1	LS2	4	13	1	4
1	4	Puseas	1	3	1	LS3	4	14	3	4
1	4	Puseas	1	3	1	LS4	4	17	4.5	4.5
1	4	Puseas	1	3	1	LS5	4	12	3	3
1	4	Puseas	1	4	1	LS1	4	10	4	2
1	4	Puseas	1	4	1	LS2	4	13	3	4
1	4	Puseas	1	4	1	LS3	4	12	3.5	4
1	4	Puseas	1	4	1	LS4	4	15	4	4
1	4	Puseas	1	4	1	LS5	4	12	3	2
1	4	Puseas	1	5	1	LS1	4	8	4	3
1	4	Puseas	1	5	1	LS2	4	12	3	3.5
1	4	Puseas	1	5	1	LS3	3	9	4	3.5
1	4	Puseas	1	5	1	LS4	1	1	1	0
1	4	Puseas	1	5	1	LS5	0	0	0	0
1	4	Puseas	1	5	1	LS6	0	0	0	0
1	4	Puseas	1	5	1	LS7	0	0	0	0
1	4	Puseas	2	1	1	LS1	4			
1	4	Puseas	2	1	1	LS2	4			
1	4	Puseas	2	1	1	LS3	4			
1	4	Puseas	2	1	1	LS4	4			
1	4	Puseas	2	2	1	LS1	4			
1	4	Puseas	2	2	1	LS2	4			
1	4	Puseas	2	2	1	LS3	4			
1	4	Puseas	2	2	1	LS4	4			
1	4	Puseas	2	2	1	LS5	4			
1	4	Puseas	2	3	1	LS1	4			
1	4	Puseas	2	3	1	LS2	2			
1	4	Puseas	2	3	1	LS3	2			
1	4	Puseas	2	3	1	LS4	2			
1	4	Puseas	2	3	1	LS5	1			
1	4	Puseas	2	3	1	LS6	0			
1	4	Puseas	2	3	1	LS7	0			
1	4	Puseas	2	3	2	S1	3			
1	4	Puseas	2	3	2	LS1	0			
1	4	Puseas	2	3	2	LS2	0			
1	4	Puseas	2	3	2	LS3	0			
1	4	Puseas	2	3	3	S1	1			
1	4	Puseas	2	3	3	LS1	0			
1	4	Puseas	2	3	3	LS2	0			
1	4	Puseas	2	3	3	LS3	0			
1	4	Puseas	2	3	4	S1	1			
1	4	Puseas	2	3	4	LS1	0			
1	4	Puseas	2	3	4	LS2	0			
1	4	Puseas	2	4	1	LS1	4			
1	4	Puseas	2	4	1	LS2	4			
1	4	Puseas	2	4	1	LS3	4			
1	4	Puseas	2	5	1	LS1	4			

1	4	Puseas	2	5	1	LS2	4			
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1	4	Puseas	2	5	1	LS4	4			
1	4	2-49	1	1	1	LS1	4	7	1	2
1	4	2-49	1	1	1	LS2	1	4	3	1
1	4	2-49	1	1	1	LS3	1	1	1	0
1	4	2-49	1	1	1	LS4	0	0	0	0
1	4	2-49	1	1	1	LS5	0	0	0	0
1	4	2-49	1	1	1	LS6	0	0	0	0
1	4	2-49	1	1	2	S1	1	2	2	0
1	4	2-49	1	1	2	LS1	1	0	0	0
1	4	2-49	1	1	2	LS2	0	0	0	0
1	4	2-49	1	1	2	LS3	0	0	0	0
1	4	2-49	1	1	3	S1	0	0	0	0
1	4	2-49	1	1	3	LS1	0	0	0	0
1	4	2-49	1	1	3	LS2	0	0	0	0
1	4	2-49	1	2	1	LS1	4	9	4	3
1	4	2-49	1	2	1	LS2	4	4	1	2
1	4	2-49	1	2	1	LS3	3	8	4	3
1	4	2-49	1	2	1	LS4	3	5	3	2
1	4	2-49	1	2	1	LS5	1	3	2.5	0.5
1	4	2-49	1	2	1	LS6	0	0	0	0
1	4	2-49	1	2	1	I1	1	3	1	0.5
1	4	2-49	1	3	1	LS1	4	4	3	1
1	4	2-49	1	3	1	LS2	4	10	3	3
1	4	2-49	1	3	1	LS3	1	0	0	0
1	4	2-49	1	3	1	LS4	1	0	0	0
1	4	2-49	1	3	1	LS5	0	0	0	0
1	4	2-49	1	3	1	LS6	0	0	0	0
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1	4	2-49	1	3	2	LS3	0	0	0	0
1	4	2-49	1	3	3	S1	1	0	0	0
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1	4	2-49	1	4	1	LS1	4	7	1	2.5
1	4	2-49	1	4	1	LS2	2	1	1	0
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1	4	2-49	1	4	1	LS4	0	0	0	0
1	4	2-49	1	4	1	LS5	0	0	0	0
1	4	2-49	1	4	1	LS6	0	0	0	0
1	4	2-49	1	4	2	S1	1	3	2	1
1	4	2-49	1	4	2	LS1	1	1	1	0
1	4	2-49	1	4	2	LS2	0	1	1	0
1	4	2-49	1	4	2	LS3	0	1	1	0
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1	4	2-49	1	4	3	LS2	0	0	0	0
1	4	2-49	1	4	3	LS3	0	0	0	0
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1	4	2-49	1	5	1	LS2	2	3	2	1
1	4	2-49	1	5	1	LS3	1	0	0	0
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1	4	2-49	1	5	1	LS5	0	0	0	0
1	4	2-49	1	5	1	LS6	0	0	0	0
1	4	2-49	1	5	2	S1	1	2	1.5	0.5
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1	4	2-49	1	5	3	LS1	0	0	0	0
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1	4	2-49	2	1	1	LS5	0			
1	4	2-49	2	1	1	LS6	0			
1	4	2-49	2	1	2	S1	4			
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1	4	2-49	2	1	2	LS3	0			
1	4	2-49	2	1	3	S1	1			
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1	4	2-49	2	3	3	LS1	1			
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1	4	CPI133814	1	1	1	LS2	0	6	3	2.5
1	4	CPI133814	1	1	1	LS3	0	0	0	0
1	4	CPI133814	1	1	1	LS4	0	0	0	0
1	4	CPI133814	1	1	1	LS5	0	0	0	0
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1	4	CPI133814	1	2	1	LS5	0	0	0	0
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1	4	CPI133814	1	3	1	LS2	2	5	2	3
1	4	CPI133814	1	3	1	LS3	1	0	0	0
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1	4	CPI133814	1	3	1	LS5	0	0	0	0
1	4	CPI133814	1	3	2	S1	1	1	0	1
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1	4	CPI133814	2	1	1	LS4	0			
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1	4	CPI133814	2	1	1	LS6	0			
1	4	CPI133814	2	1	2	S1	1			
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1	4	CPI133814	2	4	1	LS6	0			
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1	4	CPI133814	2	4	2	LS1	0			
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1	4	CPI133814	2	5	2	LS3	0			
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1	4	Tallon	1	1	1	LS2	4	15	4	3
1	4	Tallon	1	1	1	LS3	4	8	2	2
1	4	Tallon	1	1	1	LS4	4	5	1	0
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1	4	Tallon	1	2	1	LS2	4	10	3	2
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1	4	Tallon	1	2	1	LS5	4	15	4	5
1	4	Tallon	1	2	1	LS6	4	12	5	5
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1	4	Tallon	1	2	2	S1	4	5	1	1
1	4	Tallon	1	2	2	LS1	1	2	0	1
1	4	Tallon	1	2	2	LS2	0	0	0	0
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1	4	Tallon	1	3	1	LS2	4	13	3	3

1	4	Tallon	1	3	1	LS3	4	11	3	2
1	4	Tallon	1	3	1	LS4	4	9	2.5	1.5
1	4	Tallon	1	3	1	LS5	4	11	2.5	2.5
1	4	Tallon	1	4	1	LS1	4	16	4	3
1	4	Tallon	1	4	1	LS2	4	15	4	4
1	4	Tallon	1	4	1	LS3	4	15	4	4
1	4	Tallon	1	4	1	LS4	3	12	4	4.5
1	4	Tallon	1	4	1	LS5	3	9	3	5
1	4	Tallon	1	4	1	LS6	1	3	3	0
1	4	Tallon	1	4	1	LS7	0	0	0	0
1	4	Tallon	1	4	2	S1	4	10	2	3
1	4	Tallon	1	4	2	LS1	4	10	2	3
1	4	Tallon	1	4	2	LS2	2	1	1	0
1	4	Tallon	1	5	1	LS1	4	6	3	3
1	4	Tallon	1	5	1	LS2	4	15	3	4
1	4	Tallon	1	5	1	LS3	4	16	3	4
1	4	Tallon	1	5	1	LS4	4	14	3	3
1	4	Tallon	1	5	1	LS5	4	16	4	5
1	4	Tallon	1	5	1	LS6	4	13	2	3
1	4	Tallon	1	5	1	LS7	4	7	0	2
1	4	Tallon	2	1	1	LS1	4			
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1	4	Tallon	2	1	1	LS3	4			
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1	4	Tallon	2	1	1	LS5	4			
1	4	Tallon	2	1	1	LS6	4			
1	4	Tallon	2	1	1	LS7	2			
1	4	Tallon	2	1	2	S1	4			
1	4	Tallon	2	1	2	LS1	4			
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1	4	Tallon	2	2	1	LS1	4			
1	4	Tallon	2	2	1	LS2	4			
1	4	Tallon	2	2	1	LS3	4			
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1	4	Tallon	2	2	1	LS5	4			
1	4	Tallon	2	2	1	LS6	4			
1	4	Tallon	2	3	1	LS1	4			
1	4	Tallon	2	3	1	LS2	4			
1	4	Tallon	2	3	1	LS3	4			
1	4	Tallon	2	3	1	LS4	4			
1	4	Tallon	2	3	1	LS5	3			
1	4	Tallon	2	3	1	LS6	3			
1	4	Tallon	2	3	1	LS7	1			
1	4	Tallon	2	4	1	LS1	4			
1	4	Tallon	2	4	1	LS2	4			
1	4	Tallon	2	4	1	LS3	4			
1	4	Tallon	2	4	1	LS4	4			
1	4	Tallon	2	5	1	LS1	4			
1	4	Tallon	2	5	1	LS2	4			
1	4	Tallon	2	5	1	LS3	4			
1	4	Tallon	2	5	1	LS4	4			
1	4	Tallon	2	5	1	LS5	3			
1	4	Tallon	2	5	1	LS6	1			
1	4	Tallon	2	5	1	LS7	0			
1	4	Tallon	2	5	2	S1	1			

1	4	Tallon	2	5	2	LS1	0			
1	4	Cleanleaf	1	1	1	LS1	1	5	0	2
1	4	Cleanleaf	1	1	1	LS2	0	0	0	0
1	4	Cleanleaf	1	1	1	LS3	0	0	0	0
1	4	Cleanleaf	1	1	1	LS4	0	0	0	0
1	4	Cleanleaf	1	1	1	LS5	0	0	0	0
1	4	Cleanleaf	1	1	1	LS6	0	0	0	0
1	4	Cleanleaf	1	2	1	LS1	1	2	2	0
1	4	Cleanleaf	1	2	1	LS2	0	0	0	0
1	4	Cleanleaf	1	2	1	LS3	0	0	0	0
1	4	Cleanleaf	1	2	1	LS4	0	0	0	0
1	4	Cleanleaf	1	2	1	LS5	0	0	0	0
1	4	Cleanleaf	1	3	1	LS1	0	2	1.5	0.5
1	4	Cleanleaf	1	3	1	LS2	0	0	0	0
1	4	Cleanleaf	1	3	1	LS3	0	0	0	0
1	4	Cleanleaf	1	3	1	LS4	0	0	0	0
1	4	Cleanleaf	1	3	1	LS5	0	0	0	0
1	4	Cleanleaf	1	4	1	LS1	1	0	0	0
1	4	Cleanleaf	1	4	1	LS2	0	0	0	0
1	4	Cleanleaf	1	4	1	LS3	0	0	0	0
1	4	Cleanleaf	1	4	1	LS4	0	0	0	0
1	4	Cleanleaf	1	4	1	LS5	0	0	0	0
1	4	Cleanleaf	1	4	1	LS6	0	0	0	0
1	4	Cleanleaf	1	5	1	LS1	1	4	3	1
1	4	Cleanleaf	1	5	1	LS2	0	0	0	0
1	4	Cleanleaf	1	5	1	LS3	0	0	0	0
1	4	Cleanleaf	1	5	1	LS4	0	0	0	0
1	4	Cleanleaf	1	5	1	LS5	0	0	0	0
1	4	Cleanleaf	2	1	1	LS1	3			
1	4	Cleanleaf	2	1	1	LS2	1			
1	4	Cleanleaf	2	1	1	LS3	1			
1	4	Cleanleaf	2	1	1	LS4	0			
1	4	Cleanleaf	2	1	1	LS5	0			
1	4	Cleanleaf	2	1	1	LS6	0			
1	4	Cleanleaf	2	2	1	LS1	1			
1	4	Cleanleaf	2	2	1	LS2	0			
1	4	Cleanleaf	2	2	1	LS3	0			
1	4	Cleanleaf	2	2	1	LS4	0			
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1	4	Cleanleaf	2	2	1	LS6	0			
1	4	Cleanleaf	2	3	1	LS1	1			
1	4	Cleanleaf	2	3	1	LS2	0			
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1	4	Cleanleaf	2	3	1	LS4	0			
1	4	Cleanleaf	2	3	1	LS5	0			
1	4	Cleanleaf	2	3	1	LS6	0			
1	4	Cleanleaf	2	3	2	S1	0			
1	4	Cleanleaf	2	3	2	LS1	0			
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1	4	Cleanleaf	2	3	2	LS3	0			
1	4	Cleanleaf	2	4	1	LS1	0			
1	4	Cleanleaf	2	4	1	LS2	0			
1	4	Cleanleaf	2	4	1	LS3	0			
1	4	Cleanleaf	2	4	1	LS4	0			
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1	4	Cleanleaf	2	4	1	LS6	0			
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1	4	Cleanleaf	2	5	1	LS2	0			
1	4	Cleanleaf	2	5	1	LS3	0			
1	4	Cleanleaf	2	5	1	LS4	0			
1	4	Cleanleaf	2	5	1	LS5	0			
1	4	Cleanleaf	2	5	1	LS6	0			
1	4	Cleanleaf	2	5	2	S1	0			
1	4	Cleanleaf	2	5	2	LS1	0			
1	4	Cleanleaf	2	5	2	LS2	0			
1	4	Cleanleaf	2	5	2	LS3	0			
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1	5	Puseas	1	1	1	LS2	4	5	2	2
1	5	Puseas	1	1	1	LS3	4	9	0	3
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1	5	Puseas	1	1	1	LS6	4	16	4	4
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1	5	Puseas	1	2	1	LS1	4	9	4	3
1	5	Puseas	1	2	1	LS2	3	11	6	3
1	5	Puseas	1	2	1	LS3	3	12	2.5	3
1	5	Puseas	1	2	1	LS4	3	16	5	5
1	5	Puseas	1	2	1	LS5	3	12	4	4
1	5	Puseas	1	2	1	LS6	1	2	2	0
1	5	Puseas	1	2	1	LS7	0	1	1	0
1	5	Puseas	1	2	1	LS8	0	0	0	0
1	5	Puseas	1	2	1	I1	1	3	0	0
1	5	Puseas	1	2	1	I2	0	0	0	0
1	5	Puseas	1	2	2	S1	0	0	0	0
1	5	Puseas	1	2	2	LS1	0	0	0	0
1	5	Puseas	1	2	2	LS2	0	0	0	0
1	5	Puseas	1	2	3	S1	0	0	0	0
1	5	Puseas	1	2	3	LS1	0	0	0	0
1	5	Puseas	1	2	3	LS2	0	0	0	0
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1	5	Puseas	1	3	1	LS2	4	11	2	3
1	5	Puseas	1	3	1	LS3	4	11	2	2
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1	5	Puseas	1	3	1	LS6	4	10	2	2
1	5	Puseas	1	3	1	LS7	3	5	1	3
1	5	Puseas	1	3	1	LS8	0	1	1	0
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1	5	Puseas	1	4	1	LS2	4	11	4	4
1	5	Puseas	1	4	1	LS3	4	8	3	2
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1	5	Puseas	1	4	1	LS5	4	12	3.5	2.5
1	5	Puseas	1	5	1	LS1	4	8	3	2
1	5	Puseas	1	5	1	LS2	4	14	2	4
1	5	Puseas	1	5	1	LS3	4	13	2	3.5
1	5	Puseas	1	5	1	LS4	4	13	4	3
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1	5	Puseas	1	5	1	LS6	2	4	2	2
1	5	Puseas	1	5	1	LS7	0	3	2	1
1	5	Puseas	1	5	1	LS8	0	2	2	0

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1	5	Puseas	2	2	1	LS1	4			
1	5	Puseas	2	2	1	LS2	4			
1	5	Puseas	2	2	1	LS3	4			
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1	5	Puseas	2	2	1	LS6	3			
1	5	Puseas	2	2	1	LS7	1			
1	5	Puseas	2	2	1	LS8	0			
1	5	Puseas	2	2	1	LS9	0			
1	5	Puseas	2	2	1	I1	1			
1	5	Puseas	2	2	1	I2	1			
1	5	Puseas	2	2	1	I3	0			
1	5	Puseas	2	2	2	S1	2			
1	5	Puseas	2	2	2	LS1	1			
1	5	Puseas	2	2	2	LS2	0			
1	5	Puseas	2	2	2	LS3	0			
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1	5	Puseas	2	3	1	LS2	4			
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1	5	Puseas	2	3	1	LS6	4			
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1	5	Puseas	2	5	1	LS5	3			
1	5	Puseas	2	5	1	LS6	3			
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1	5	Puseas	2	5	1	I1	1			
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1	5	Puseas	2	5	3	S1	4			
1	5	Puseas	2	5	3	LS1	1			
1	5	Puseas	2	5	3	LS2	0			
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1	5	2-49	1	1	1	LS1	4	9	2	1
1	5	2-49	1	1	1	LS2	3	4	2	1.5
1	5	2-49	1	1	1	LS3	2	1	1	0
1	5	2-49	1	1	1	LS4	2	4	1	3
1	5	2-49	1	1	1	LS5	0	0	0	0
1	5	2-49	1	1	1	LS6	0	0	0	0
1	5	2-49	1	1	1	LS7	0	0	0	0
1	5	2-49	1	1	1	LS8	0	0	0	0
1	5	2-49	1	1	2	S1	4	3	1	1
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1	5	2-49	1	1	2	LS4	0	0	0	0
1	5	2-49	1	1	3	S1	3	1	1	0
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1	5	2-49	1	1	3	LS2	0	0	0	0
1	5	2-49	1	1	3	LS3	0	0	0	0
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1	5	2-49	1	2	1	LS2	4	3	1	2
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1	5	2-49	1	3	1	LS7	0	0	0	0
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1	5	2-49	1	3	3	LS2	0	0	0	0

1	5	2-49	1	3	3	LS3	0	0	0	0
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1	5	2-49	1	4	1	LS6	0	0	0	0
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1	5	2-49	1	4	2	LS2	0	0	0	0
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1	5	2-49	1	4	2	LS4	0	0	0	0
1	5	2-49	1	4	3	S1	4	3	3	0
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1	5	2-49	2	1	1	LS7	0			
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1	5	2-49	2	1	2	LS5	0			
1	5	2-49	2	1	3	S1	3			
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1	5	2-49	2	1	3	LS3	0			
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1	5	2-49	2	3	1	LS5	2
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1	5	2-49	2	4	2	LS2	1
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1	5	CPI133814	2	1	1	LS7	0			
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1	5	Tallon	1	2	2	S1	4	1	1	0
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1	5	Tallon	1	3	1	LS1	4	10	2	3
1	5	Tallon	1	3	1	LS2	4	13	3	4
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1	5	Cleanleaf	1	2	1	LS4	0	0	0	0
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1	5	Cleanleaf	1	3	1	LS3	2	1	1	0
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1	5	Cleanleaf	1	3	1	LS5	0	0	0	0
1	5	Cleanleaf	1	3	1	LS6	0	0	0	0
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2	2	Tallon	4	3	1	LS3	1	3	3	0
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2	2	Tallon	4	6	1	LS3	2			
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2	2	Tallon	4	7	1	LS2	4			
2	2	Tallon	4	7	1	LS3	4			
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2	2	Tallon	4	9	1	LS3	4			
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2	2	Cleanleaf	3	4	1	LS2	0	0	0	0
2	2	Cleanleaf	3	4	1	LS3	0	0	0	0
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2	2	Cleanleaf	3	5	1	LS2	0	3	1	2
2	2	Cleanleaf	3	5	1	LS3	0	0	0	0
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2	2	Cleanleaf	3	8	1	LS3	0			
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2	2	Cleanleaf	4	7	1	LS3	0			
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2	3	Tallon	4	10	1	LS1	4			
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2	4	CPI133814	4	3	1	I1	1	0	0	0
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2	4	CPI133814	4	4	1	I1	1	0	0	0
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2	4	CPI133814	4	7	1	LS3	1			
2	4	CPI133814	4	7	1	LS4	0			
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2	4	Tallon	3	6	1	LS3	4			
2	4	Tallon	3	7	1	LS1	4			
2	4	Tallon	3	7	1	LS2	4			
2	4	Tallon	3	7	1	LS3	4			
2	4	Tallon	3	8	1	LS1	4			
2	4	Tallon	3	8	1	LS2	4			
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2	4	Tallon	3	9	1	LS1	4			
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2	4	Tallon	3	9	1	LS3	1			
2	4	Tallon	3	9	1	LS4	0			
2	4	Tallon	3	9	1	LS5	0			
2	4	Tallon	3	9	1	I1	0			
2	4	Tallon	3	9	1	I2	0			
2	4	Tallon	3	9	1	I3	0			
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2	4	Tallon	4	8	1	LS1	4			
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2	4	Tallon	4	10	1	LS1	4			
2	4	Tallon	4	10	1	LS2	4			
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2	4	Cleanleaf	3	1	1	LS2	0	10	3	3.5
2	4	Cleanleaf	3	1	1	LS3	0	2	2	0
2	4	Cleanleaf	3	1	1	LS4	0	0	0	0
2	4	Cleanleaf	3	1	1	I1	0	3	2	1
2	4	Cleanleaf	3	1	1	I2	0	0	0	0
2	4	Cleanleaf	3	1	1	I3	0	0	0	0
2	4	Cleanleaf	3	2	1	LS1	1	3	2	1
2	4	Cleanleaf	3	2	1	LS2	1	1	1	0
2	4	Cleanleaf	3	2	1	LS3	0	0	0	0
2	4	Cleanleaf	3	2	1	LS4	0	0	0	0
2	4	Cleanleaf	3	2	1	I1	1	1	1	0
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2	4	Cleanleaf	3	2	1	I3	0	0	0	0
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2	4	Cleanleaf	3	3	1	LS5	0	0	0	0
2	4	Cleanleaf	3	3	1	I1	0	0	0	0
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2	4	Cleanleaf	3	6	1	LS5	0			
2	4	Cleanleaf	3	6	1	I1	0			
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2	4	Cleanleaf	3	7	1	LS5	0			
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2	4	Cleanleaf	3	7	1	I2	0			
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2	4	Cleanleaf	4	7	1	I2	0			
2	4	Cleanleaf	4	7	1	I3	0			
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3	3

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0	0

1	4
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3	2
3	3
2	4
5	1
6	2
3	4
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3	4
3	4
3	2
2	2
3	2
2	2
1	2

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0	0
0	0
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3	1
3	0
3	2
4	2
2	2
3	2

2.5	1
1	0
0	0
1	1
0	0
3	2
1	0
2	0
0	0
2	2
0	0
0	0
0	0
0	0
3	3
2	2
0	4
2	0
0	0
2.5	2
2	2
0	0

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3	0
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3	2
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5	5
3	2
4	2.5
2	1
2	4
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1	1
0	0
2	3
4	3
4	3.5
1.5	3
1	2
1.5	3
3.5	1
3	2
3	1

3	3
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4	4
4	3
4	3
3	1
2	1
1	0
3	0
3	3
3	1
3	1
4	2
1	2
3	1

2	0
3.5	0
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4	3
3	1
2	0
3	3
6.5	4.5
4	3
3	0
4	1
3	2
1	1
0	0
2	2
4	2
3	2
0	3
0	0
0	0
1	0
0	0
0	0

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3	3
3	3
5	4
5	4
3	1
3	3
5	0

2	2
3	2
4	2
4	2
4	4
5	4
6	6

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0	0
0	0
0	0
2	1
0	0
1	0
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2	3
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3.5	4
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2	0

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2	2
4	4
4	3
4	0
3	2
3	3
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3	1
4	3
3	3
2	1
3	2
3	3
3	1
3	1

2	4
4	4
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1	2
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4	4
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4	4
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4	2

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Appendix 2D
Seedling Trial Analysis Output

```
GenStat Release 6.1  (PC/Windows 2000)         11 February 2004 14:12:17
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              ________________________________________

              GenStat Sixth Edition
              GenStat Procedure Library Release PL14
              ________________________________________

   1  %CD 'C:/KerryBell/QCCA/ClimateChange2003/climarc files'
   2  "Cassandra Percy (UQ) and Graham Wildermuth (supervisor)
file=PotTrialExp1&2.gen
  -3  42 day pot trial experiments 1 & 2
  -4
  -5  2 experiments x 2 reps / 5 Genotypes / 5 Harvest times / 5 or 10 plants / up to 4 tillers /
plant part
  -6
  -7  Experiment 1: Rep 1 & 2, only rep 1 was used for isolations, 6 plants per pot and only
5 measured
  -8  Experiment 2: Rep 3 & 4, up to 13 plants per pot and disease rating on up to 10,
isolation counts for isolations
  -9
 -10  Approximately every fortnight (harvest times), 5 plants were taken from each plot.
 -11
 -12  Each plant was divided into its tillers (tiller 1 being the main tiller),
 -13  and each node was given a disease rating (0-4) and
 -14  then divided into 4 parts, these was placed out on agar
 -15  and the number of 'infections' were counted. The sum of the infections
 -16  across these parts were analysed (=isolation counts).
 -17
 -18  Genotypes:
 -19  2-49
 -20  CPI133814
 -21  Puseas
 -22  Tallon
 -23  Cleanleaf
 -24
 -25  Plant parts:
 -26  levels 1...5:   I1 to I5 (Internode)
 -27  levels 6...14:   LS1 to LS9 (Leaf Sheath)
 -28  level 15: N
 -29  level 16, 17: S1 and S5 (Sheath)
```

```
 -30
 -31  ANALYSES: An ar(1) parameter was attempted to be fitted across harvests,
 -32  but many times the REML analysis did not converge or produce sensible results
 -33  so this parameter was dropped in these instances. If the parameter was non-significant
 -34  (by comparing change in deviance to 2.8) then it was also dropped out.
 -35
 -36  Plant parts analysed for tiller 1 and across relevant harvest times
 -37  - Disease Rating: none for internodes or sheaths; LS1 (H1-5), LS2 (H1-5), LS3 (H2-5), LS4 (H3-5)
 -38  - Isolation Counts: none for internodes or sheaths; LS1 (H1-5), LS2 (H1-5), LS3 (H2-5)
 -39  other parts were not analysed due to lack of values or high proportion of zeros or the same value.
 -40
 -41  The approximate lsd's are calculated by
 -42  lsd = SED x t
 -43  where the degrees of freedom for t depend on the term you are comparing the levels of.
 -44
 -45  Note in table below if not all levels of experiment, genotype and harvest are present,
 -46  then the values of t are underestimated as residual degrees of freedom will be less.
 -47
 -48  5 Harvest times (Disease Rating)
 -49  Term = Experiment, residual/error df=1, t=12.71
 -50  Term = Genotype, residual/error df=8, t=2.306
 -51  Term = Genotype.Experiment, residual/error approx df=8; t~2.306
 -52  Term = Harvest, residual/error df=60, t=2.00
 -53  Term = Harvest.Exp or Harvest.Geno or Harvest.Exp.Geno, residual/error approx df=60; t~2.00
 -54
 -55  4 Harvest times (Disease Rating) [as per 5 harvest times except ...]
 -56  Term = Harvest, residual/error df=30, t=2.04
 -57  Term = Harvest.Exp or Harvest.Geno or Harvest.Exp.Geno, residual/error approx df=30; t~2.04
 -58
 -59  3 Harvest times (Disease Rating) [as per 5 harvest times except ...]
 -60  Term = Harvest, residual/error df=20, t=2.09
 -61  Term = Harvest.Exp or Harvest.Geno or Harvest.Exp.Geno, residual/error approx df=20; t~2.09
 -62
 -63  5 Harvest times (Isolations) - experiment 2 only
 -64  Term = Genotype, residual/error df=8, t=2.306
 -65  Term = Harvest, residual/error df=60, t=2.00
 -66  Term = Harvest.Exp or Harvest.Geno or Harvest.Exp.Geno, residual/error approx df=60; t~2.00
 -67
 -68  4 Harvest times (Isolations) [as per 5 harvest times except ...] - experiment 2 only
```

```
 -69  Term = Harvest, residual/error df=30, t=2.04
 -70  Term = Harvest.Exp or Harvest.Geno or Harvest.Exp.Geno, residual/error approx
df=30; t~2.04
 -71  "
  72
  73  set [outprint=dot]
  74  import file='C:/KerryBell/Biometry/CassandraPercy(UQ)/42day pottrial Exp1&2.xls';
\
  75    sheetname='Sheet1'

 *** Loading Spreadsheet File ***

Catalogue of file C:\DOCUME~1\BELLK\LOCALS~1\TEMP\GENSTAT\G61D27.GSH

Sheet Title:
Data read from C:\KerryBell\Biometry\CassandraPercy(UQ)\42day pottrial
Exp1&2.xls [SHEET1]A1:M3546

Sheet Type: vector
Index       Type    Nval   Name
    1    variate    3545   Experiment
    2    variate    3545   Harvest
    4       text    3545   Genotype
    5    variate    3545   Rep
    6    variate    3545   Plant
    7    variate    3545   Tiller
    9       text    3545   Part
   10    variate    3545   Disease_Rating
   11    variate    3545   Infection_total
   12    variate    3545   Infection_1_4
   13    variate    3545   Infection_2_4
   14    variate    3545   Infection_3_4
   15    variate    3545   Infection_4_4

Missing indices are used by unnamed or system structures. These store ancillary
information, for example factor labels.
  76  group [redefine=yes] Harvest, Genotype, Rep, Plant, Tiller, Part, Experiment
  77  facproduct factors=!P(Rep, Genotype); product=plot
  78  page
```

```
  79
  80
"=================================================================
=========
 -81      PART = I1, I2, I3, I4, I5 - no analyses done due to too many zeros or too sparse
 -82
==================================================================
========"
  83
  84
"=================================================================
=========
 -85                      PART = LS1 (Disease rating: harvest 1 to 5; Infection count: harvest 1 to
5)
 -86
==================================================================
========"
  87
  88  "**** LS1 Disease Rating (Harvests 1 to 5, only tiller 1) ****"
  89
  90  subset [condition=(Part.eq.6).and.(Harvest.ge.1).and.(Harvest.le.5).and.(Tiller.eq.1);
setlevel=yes] \
  91   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
  92   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
  93
  94  vcomp [fixed=nexp*ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
  95  \vstruct [nplot.nharv] factor=nharv; model="ar "uniform
  96  reml [print=means, wald, comp, mod,dev] ndr

96.............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+nexp+ngeno+nharv.nexp+nharv.ngeno+nexp.ngeno+n
harv.nexp.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 720

* Residual term has been added to model
```

```
* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                     0.0047      0.0090
nplot                    0.0000       BOUND
nplot.nharv                  0.0687      0.0212
nplot.nharv.nplant           0.0000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.253    0.0143


*** Deviance: -2*Log-Likelihood ***


               Deviance   d.f.

                 -65.83   665

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                   528.83           4       132.21      <0.001
  nexp                      0.03           1         0.03       0.856
  ngeno                   818.05           4       204.51      <0.001
  nharv.nexp                 33.33           4         8.33      <0.001
  nharv.ngeno                86.01          16         5.38      <0.001
  nexp.ngeno                 28.67           4         7.17      <0.001
  nharv.nexp.ngeno              57.65          16         3.60      <0.001
```

```
* Dropping individual terms from full fixed model

   nharv.nexp.ngeno              57.65          16         3.60     <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            2.975    Standard error:  0.0475



*** Table of predicted means for nharv ***

   nharv    1.000    2.000    3.000    4.000    5.000
            1.505    3.162    3.292    3.249    3.667

Standard error of differences:     Average       0.1038
                                   Maximum       0.1041
                                   Minimum       0.1035


*** Table of predicted means for nexp ***

    nexp    1.000    2.000
            2.966    2.984

Standard error of differences:     0.09504



*** Table of predicted means for ngeno ***

       ngeno         2-49    Cleanleaf    CPI133814       Puseas       Tallon
                    3.364        1.227        2.933        3.596        3.755

Standard error of differences:     Average       0.1038
                                   Maximum       0.1042
                                   Minimum       0.1035


*** Table of predicted means for nharv.nexp ***

         nexp    1.000    2.000
        nharv
```

```
          1.000    1.460    1.549
          2.000    2.929    3.396
          3.000    3.300    3.285
          4.000    3.140    3.358
          5.000    4.000    3.333

Standard error of differences:     Average       0.1551
                                   Maximum       0.1627
                                   Minimum       0.1378

Average variance of differences:               0.02416

Standard error of differences for same level of factor:

                    nharv        nexp
Average          0.1620      0.1465
Maximum           0.1627      0.1548
Minimum           0.1617      0.1378
Average variance of differences:
                0.02626     0.02153



*** Table of predicted means for nharv.ngeno ***

          ngeno         2-49    Cleanleaf    CPI133814       Puseas       Tallon
          nharv
          1.000        1.400        0.175        0.845        2.329        2.775
          2.000        3.648        1.401        3.063        3.700        4.000
          3.000        3.875        1.100        3.538        3.949        4.000
          4.000        3.899        0.959        3.387        4.000        4.000
          5.000        4.000        2.500        3.833        4.000        4.000

Standard error of differences:     Average       0.2320
                                   Maximum       0.2357
                                   Minimum       0.2309

Standard error of differences for same level of factor:

                    nharv       ngeno
Average          0.2320      0.2320
Maximum           0.2355      0.2357
Minimum           0.2309      0.2309



*** Table of predicted means for nexp.ngeno ***
```

```
          ngeno        2-49    Cleanleaf    CPI133814       Puseas       Tallon
           nexp
          1.000       3.249        1.520        2.720        3.520        3.820
          2.000       3.480        0.934        3.147        3.671        3.690

Standard error of differences:     Average       0.1551
                                   Maximum       0.1636
                                   Minimum       0.1375

Average variance of differences:               0.02416

Standard error of differences for same level of factor:

                   nexp       ngeno
Average           0.1465      0.1620
Maximum           0.1548      0.1632
Minimum           0.1375      0.1616
Average variance of differences:
                0.02153     0.02626



*** Table of predicted means for nharv.nexp.ngeno ***

                  ngeno        2-49    Cleanleaf    CPI133814       Puseas
          nharv        nexp
          1.000       1.000       1.200        0.100        0.700        2.200
                      2.000       1.600        0.250        0.990        2.457
          2.000       1.000       3.446        1.300        2.400        3.500
                      2.000       3.850        1.503        3.726        3.900
          3.000       1.000       3.800        1.300        3.500        3.900
                      2.000       3.950        0.900        3.575        3.999
          4.000       1.000       3.800        0.900        3.000        4.000
                      2.000       3.999        1.019        3.775        3.999
          5.000       1.000       4.000        4.000        4.000        4.000
                      2.000       4.000        1.000        3.667        4.000


                  ngeno      Tallon
          nharv        nexp
          1.000       1.000       3.100
                      2.000       2.450
          2.000       1.000       4.000
                      2.000       3.999
          3.000       1.000       4.000
                      2.000       4.000
```

```
         4.000        1.000        4.000
                      2.000        4.001
         5.000        1.000        4.000
                      2.000        4.000

Standard error of differences:     Average       0.3315
                                   Maximum       0.3496
                                   Minimum       0.3065

Average variance of differences:                 0.1101

Standard error of differences for same level of factor:

                   nharv        nexp       ngeno
Average           0.3318      0.3276      0.3318
Maximum           0.3496      0.3496      0.3496
Minimum           0.3065      0.3065      0.3065
Average variance of differences:
                  0.1103      0.1077      0.1103
```

```
  98
  99  "**** LS1 Isolation counts (total) (Harvests 1 to 5, only tiller 1, experiment 2 only)
****"
 100
 101  subset
[condition=(Part.eq.6).and.(Harvest.ge.1).and.(Harvest.le.5).and.(Rep.ge.3).and.(Tiller.eq.1
).and.(Plant.le.5); setlevel=yes] \
 102   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 103   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 104
 105  "WON'T CONVERGE FOR SOME BIZARRE REASON"
 106  \vcomp [fixed=ngeno*nharv] random=nrep+nplot+nplot.nharv+nplot.nharv.nplant;
const=pos
 107  \reml [print=means, wald, comp, mod,dev; maxc=100] sqrt(ntotal)
 108  \vkeep means=gmean; term=ngeno
 109  \print 'Back-transformed means' & gmean**2
 110  \delete [redefine=yes] tmean
 111
 112  "ANOVA CAN BE USED IN THIS CASE AS ALL COMBINATIONS ARE
PRESENT"
 113  treatment ngeno*nharv
 114  block nrep/nplot/nharv
 115  anova [fprob=yes; pse=diff, lsd] sqrt(ntotal)

115..............................................................................

***** Analysis of variance *****

Variate: SQRT(ntotal)

Source of variation     d.f.(m.v.)      s.s.       m.s.    v.r.  F pr.

nrep stratum              1          0.0213     0.0213    0.08

nrep.nplot stratum
ngeno                    4         45.4954    11.3738   42.45  0.002
Residual                  4          1.0717     0.2679    0.41

nrep.nplot.nharv stratum
nharv                    4         74.3036    18.5759   28.77  <.001
nharv.ngeno              16          6.2884     0.3930    0.61  0.841
Residual                 20         12.9155     0.6458    1.89

nrep.nplot.nharv.*Units* stratum
                      199(1)      68.0748     0.3421
```

```
Total                   248(1)     204.9696


* MESSAGE: the following units have large residuals.

nrep 3.00   nplot 3 Cleanleaf  nharv 2.00         0.595   s.e. 0.227
nrep 3.00   nplot 3 Puseas     nharv 4.00         0.460   s.e. 0.227
nrep 4.00   nplot 4 Cleanleaf  nharv 2.00        -0.595   s.e. 0.227
nrep 4.00   nplot 4 Puseas     nharv 4.00        -0.460   s.e. 0.227

nrep 3.00   nplot 3 CPI133814  nharv 5.00   *units* 1
                                           -2.448   s.e. 0.522
nrep 4.00   nplot 4 Cleanleaf  nharv 3.00   *units* 1
                                           -2.045   s.e. 0.522


***** Tables of means *****

Variate: SQRT(ntotal)

Grand mean  2.493

   nharv     1.00     2.00     3.00     4.00     5.00
          1.644    2.155    2.545    3.014    3.106

   ngeno      2-49 Cleanleaf CPI133814    Puseas    Tallon
           2.537     1.783     2.302     2.890     2.951

   nharv    ngeno      2-49 Cleanleaf CPI133814    Puseas    Tallon
    1.00            1.585     1.329     1.352     1.979     1.972
    2.00            2.242     1.350     2.162     2.403     2.616
    3.00            2.725     1.674     2.466     2.951     2.908
    4.00            3.144     1.991     2.889     3.519     3.527
    5.00            2.987     2.571     2.643     3.599     3.733


*** Standard errors of differences of means ***

Table                nharv       ngeno       nharv
                                             ngeno
rep.                   50          50          10
s.e.d.             0.1607      0.1035      0.3377
d.f.                   20           4       23.12
Except when comparing means with the same level(s) of
 ngeno                                     0.3594
 d.f.                                          20
```

```
(Not adjusted for missing values)

*** Least significant differences of means (5% level) ***

Table             nharv      ngeno      nharv
                                        ngeno
rep.                 50         50         10
l.s.d.           0.3353     0.2874     0.6984
d.f.                 20          4      23.12
Except when comparing means with the same level(s) of
 ngeno                                 0.7497
 d.f.                                     20

(Not adjusted for missing values)


***** Missing values *****

Variate: SQRT(ntotal)

 Unit  estimate
   96     0.707

Max. no. iterations 2

 116  akeep means=gmean; term=ngeno
 117  akeep means=hmean; term=nharv
 118  print 'Back-transformed means' & hmean**2 & gmean**2


 Back-transformed means


           hmean** 2
     nharv
     1.000      2.701
     2.000      4.643
     3.000      6.476
     4.000      9.083
     5.000      9.650


           gmean** 2
     ngeno
      2-49      6.434
   Cleanleaf      3.179
```

```
  CPI133814       5.301
     Puseas       8.353
     Tallon       8.710

119  delete [redefine=yes] hmean, gmean
120
121  page
```

```
 122
 123
"==============================================================
=========
-124                      PART = LS2 (Disease rating: harvest 1 to 5; Infection count: harvest 1
to 5)
-125
==============================================================
========"
 126
 127  "**** LS2 Disease Rating (Harvests 1 to 5, only tiller 1) ****"
 128
 129  subset [condition=(Part.eq.7).and.(Harvest.ge.1).and.(Harvest.le.5).and.(Tiller.eq.1);
setlevel=yes] \
 130   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 131   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 132
 133  vcomp [fixed=nexp*ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 134  \vstruct [nplot.nharv] factor=nharv; model="ar "uniform
 135  reml [print=means, wald, comp, mod,dev] ndr

135.............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+nexp+ngeno+nharv.nexp+nharv.ngeno+nexp.ngeno+n
harv.nexp.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 720

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.
```

```
nrep                    0.0007      0.0033
nplot                   0.0000       BOUND
nplot.nharv                0.0000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

nplot.nharv.nplant           Identity      Sigma2           0.532    0.0291


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                378.68   666

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                  1338.94           4       334.74      <0.001
  nexp                     6.26          1        6.26       0.012
  ngeno                  1328.57           4       332.14      <0.001
  nharv.nexp                79.74           4       19.94      <0.001
  nharv.ngeno               257.71          16       16.11      <0.001
  nexp.ngeno                60.09           4       15.02      <0.001
  nharv.nexp.ngeno            100.58          16        6.29      <0.001

* Dropping individual terms from full fixed model

  nharv.nexp.ngeno            100.58          16        6.29      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
          2.247    Standard error:  0.0314



*** Table of predicted means for nharv ***

   nharv    1.000    2.000    3.000    4.000    5.000
            0.438    1.975    2.693    2.702    3.425

Standard error of differences:     Average      0.09051
                                   Maximum      0.09120
                                   Minimum      0.08986


*** Table of predicted means for nexp ***

    nexp    1.000    2.000
            2.170    2.324

Standard error of differences:     0.06271



*** Table of predicted means for ngeno ***

      ngeno        2-49    Cleanleaf    CPI133814       Puseas       Tallon
                  2.371        0.658        1.838        3.088        3.278

Standard error of differences:     Average      0.09051
                                   Maximum      0.09143
                                   Minimum      0.08983


*** Table of predicted means for nharv.nexp ***

         nexp    1.000    2.000
        nharv
        1.000    0.340    0.535
        2.000    1.789    2.161
        3.000    2.500    2.887
        4.000    2.380    3.023
        5.000    3.840    3.011

Standard error of differences:     Average       0.1287
                                   Maximum       0.1467
                                   Minimum       0.1049
```

```
Average variance of differences:            0.01675

Standard error of differences for same level of factor:

                 nharv       nexp
Average          0.1305      0.1265
Maximum          0.1323      0.1467
Minimum          0.1296      0.1049
Average variance of differences:
               0.01704    0.01638



*** Table of predicted means for nharv.ngeno ***

        ngeno        2-49    Cleanleaf    CPI133814      Puseas      Tallon
        nharv
        1.000       0.200        0.000        0.083       0.956       0.950
        2.000       1.447        0.389        1.322       3.125       3.592
        3.000       3.325        0.475        2.207       3.611       3.850
        4.000       3.133        0.301        2.277       3.797       4.000
        5.000       3.750        2.125        3.302       3.950       4.000

Standard error of differences:     Average      0.2024
                                  Maximum      0.2108
                                  Minimum      0.1998

Average variance of differences:            0.04096

Standard error of differences for same level of factor:

                 nharv      ngeno
Average          0.2024      0.2024
Maximum          0.2104      0.2108
Minimum          0.1998      0.1998
Average variance of differences:
               0.04096    0.04096



*** Table of predicted means for nexp.ngeno ***

        ngeno        2-49    Cleanleaf    CPI133814      Puseas      Tallon
         nexp
        1.000       2.169        0.980        1.500       2.960       3.240
        2.000       2.573        0.336        2.176       3.215       3.317
```

```
Standard error of differences:    Average      0.1287
                                 Maximum      0.1467
                                 Minimum      0.1043

Average variance of differences:              0.01675

Standard error of differences for same level of factor:

                  nexp      ngeno
Average         0.1265     0.1305
Maximum         0.1467     0.1333
Minimum         0.1043     0.1294
Average variance of differences:
              0.01638    0.01704



*** Table of predicted means for nharv.nexp.ngeno ***

            ngeno       2-49   Cleanleaf   CPI133814      Puseas
    nharv        nexp
    1.000       1.000      0.000       0.000       0.000       0.700
                2.000      0.400       0.000       0.166       1.211
    2.000       1.000      1.444       0.500       0.500       3.000
                2.000      1.450       0.279       2.144       3.250
    3.000       1.000      3.100       0.600       1.600       3.500
                2.000      3.550       0.350       2.814       3.721
    4.000       1.000      2.600       0.100       1.500       3.700
                2.000      3.666       0.501       3.054       3.894
    5.000       1.000      3.700       3.700       3.900       3.900
                2.000      3.800       0.550       2.704       4.000


            ngeno     Tallon
    nharv        nexp
    1.000       1.000      1.000
                2.000      0.900
    2.000       1.000      3.500
                2.000      3.684
    3.000       1.000      3.700
                2.000      4.000
    4.000       1.000      4.000
                2.000      4.001
    5.000       1.000      4.000
                2.000      4.000
```

```
Standard error of differences:     Average       0.2851
                                   Maximum       0.3352
                                   Minimum       0.2307

Average variance of differences:                0.08226

Standard error of differences for same level of factor:

                 nharv        nexp       ngeno
Average          0.2853      0.2827      0.2853
Maximum          0.3352      0.3352      0.3352
Minimum          0.2307      0.2307      0.2307
Average variance of differences:
                0.08229     0.08192     0.08229
```

```
 137
 138  "**** LS2 Isolation counts (total) (Harvests 1 to 5, only tiller 1, experiment 2 only)
****"
 139
 140  subset
[condition=(Part.eq.7).and.(Harvest.ge.1).and.(Harvest.le.5).and.(Rep.ge.3).and.(Tiller.eq.1
).and.(Plant.le.5); setlevel=yes] \
 141   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 142   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 143
 144  vcomp [fixed=ngeno*nharv] random=nrep+nplot+nplot.nharv+nplot.nharv.nplant;
const=pos
 145  reml [print=means, wald, comp, mod,dev; maxc=50] sqrt(ntotal)

145...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+nharv.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 250

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                     0.0000       BOUND
nplot                    0.0026      0.0201
nplot.nharv                 0.0000       BOUND


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.
```

```
nplot.nharv.nplant          Identity     Sigma2           0.723    0.0689


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                209.91    221

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term             Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                       214.77          4       53.69       <0.001
  ngeno                       165.10          4       41.28       <0.001
  nharv.ngeno                  14.65         16        0.92        0.550

* Dropping individual terms from full fixed model

  nharv.ngeno                  14.65         16        0.92        0.550

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.899    Standard error:  0.0561



*** Table of predicted means for nharv ***

  nharv    1.000    2.000    3.000    4.000    5.000
           0.695    1.439    1.897    2.563    2.900

Standard error of differences:      0.1700
```

```
*** Table of predicted means for ngeno ***

    ngeno      2-49   Cleanleaf   CPI133814     Puseas     Tallon
              1.858       0.746       1.572      2.608      2.710

Standard error of differences:     0.1774



*** Table of predicted means for nharv.ngeno ***

    ngeno      2-49   Cleanleaf   CPI133814     Puseas     Tallon
    nharv
    1.000     0.615       0.000       0.541      1.021      1.297
    2.000     1.185       0.488       0.906      2.350      2.265
    3.000     1.848       0.473       1.710      2.496      2.959
    4.000     2.769       1.106       2.098      3.336      3.509
    5.000     2.873       1.664       2.602      3.835      3.523

Standard error of differences:    Average      0.3830
                                  Maximum      0.3835
                                  Minimum      0.3802

Standard error of differences for same level of factor:

              nharv      ngeno
Average      0.3835     0.3802
Maximum      0.3835     0.3802
Minimum      0.3835     0.3802


 146  vkeep means=hmean; term=nharv
 147  vkeep means=gmean; term=ngeno
 148  print 'Back-transformed means' & hmean**2 & gmean**2


 Back-transformed means


          hmean** 2
    nharv
    1.000     0.483
    2.000     2.070
    3.000     3.599
    4.000     6.571
    5.000     8.407
```

```
           gmean** 2
      ngeno
       2-49       3.452
  Cleanleaf       0.557
  CPI133814       2.470
     Puseas       6.800
     Tallon       7.347

149  delete [redefine=yes] hmean, tmean
150  page
```

```
 151
 152
"=================================================================
=========
-153                      PART = LS3 (Disease rating: harvest 2 to 5; Infection count: harvest 2
to 5)
-154
=================================================================
========"
 155
 156  "**** LS3 Disease Rating (Harvests 2 to 5, only tiller 1) ****"
 157
 158  subset [condition=(Part.eq.8).and.(Harvest.ge.2).and.(Harvest.le.5).and.(Tiller.eq.1);
setlevel=yes] \
 159   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 160   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 161
 162  vcomp [fixed=nexp*ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 163  \vstruct [nplot.nharv] factor=nharv; model="ar "uniform
 164  reml [print=means, wald, comp, mod,dev] ndr

164...................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+nexp+ngeno+nharv.nexp+nharv.ngeno+nexp.ngeno+n
harv.nexp.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 564

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.
```

```
nrep                    0.000      0.007
nplot                   0.000      BOUND
nplot.nharv                0.000      BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

nplot.nharv.nplant           Identity      Sigma2            1.051     0.065


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                653.85   520

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                    193.14           3        64.38      <0.001
  nexp                       3.07           1         3.07       0.080
  ngeno                    812.03           4       203.01      <0.001
  nharv.nexp                  5.78           3         1.93       0.123
  nharv.ngeno                41.52          12         3.46      <0.001
  nexp.ngeno                 10.86           4         2.71       0.028
  nharv.nexp.ngeno             29.97          12         2.50       0.003

* Dropping individual terms from full fixed model

  nharv.nexp.ngeno             29.97          12         2.50       0.003

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
           1.950    Standard error:  0.0456



*** Table of predicted means for nharv ***

   nharv    2.000    3.000    4.000    5.000
           0.969    1.970    2.190    2.671

Standard error of differences:     Average       0.1283
                               Maximum       0.1300
                               Minimum       0.1267


*** Table of predicted means for nexp ***

    nexp    1.000    2.000
           1.880    2.020

Standard error of differences:     0.09117



*** Table of predicted means for ngeno ***

      ngeno         2-49    Cleanleaf    CPI133814       Puseas       Tallon
                 1.660        0.181        1.305        3.167        3.438

Standard error of differences:     Average       0.1435
                               Maximum       0.1460
                               Minimum       0.1415

Average variance of differences:              0.02058


*** Table of predicted means for nharv.nexp ***

        nexp    1.000    2.000
       nharv
       2.000    0.940    0.998
       3.000    1.880    2.060
       4.000    1.960    2.420
       5.000    2.740    2.603

Standard error of differences:     Average       0.1808
                               Maximum       0.2062
```

```
                              Minimum      0.1488

Average variance of differences:             0.03298

Standard error of differences for same level of factor:

                nharv      nexp
Average         0.1817     0.1796
Maximum         0.1876     0.2062
Minimum         0.1788     0.1488
Average variance of differences:
              0.03301    0.03293



*** Table of predicted means for nharv.ngeno ***

       ngeno       2-49    Cleanleaf    CPI133814      Puseas      Tallon
       nharv
       2.000      0.200       0.000       0.350       2.088       2.208
       3.000      1.800       0.025       1.181       3.194       3.650
       4.000      2.117       0.050       1.456       3.434       3.895
       5.000      2.525       0.650       2.232       3.950       4.000

Standard error of differences:     Average      0.2869
                              Maximum      0.3086
                              Minimum      0.2807

Average variance of differences:             0.08233

Standard error of differences for same level of factor:

                nharv      ngeno
Average         0.2868     0.2868
Maximum         0.3086     0.3086
Minimum         0.2807     0.2807
Average variance of differences:
              0.08233    0.08233



*** Table of predicted means for nexp.ngeno ***

       ngeno       2-49    Cleanleaf    CPI133814      Puseas      Tallon
        nexp
       1.000      1.350       0.300       1.150       3.175       3.425
       2.000      1.971       0.063       1.460       3.158       3.451
```

```
Standard error of differences:     Average       0.2020
                                   Maximum       0.2308
                                   Minimum       0.1643

Average variance of differences:              0.04121

Standard error of differences for same level of factor:

                  nexp       ngeno
Average          0.2007      0.2031
Maximum          0.2308      0.2110
Minimum          0.1643      0.1996
Average variance of differences:
               0.04117     0.04125



*** Table of predicted means for nharv.nexp.ngeno ***

              ngeno        2-49     Cleanleaf    CPI133814      Puseas
        nharv        nexp
        2.000       1.000       0.000       0.000       0.300       2.300
                    2.000       0.400       0.000       0.400       1.875
        3.000       1.000       2.000       0.000       0.800       3.000
                    2.000       1.600       0.050       1.563       3.389
        4.000       1.000       1.400       0.100       0.800       3.500
                    2.000       2.833       0.000       2.111       3.368
        5.000       1.000       2.000       1.100       2.700       3.900
                    2.000       3.050       0.200       1.765       4.000


              ngeno       Tallon
        nharv        nexp
        2.000       1.000       2.100
                    2.000       2.316
        3.000       1.000       3.600
                    2.000       3.700
        4.000       1.000       4.000
                    2.000       3.790
        5.000       1.000       4.000
                    2.000       4.000

Standard error of differences:     Average       0.4035
                                   Maximum       0.4711
                                   Minimum       0.3242
```

```
Average variance of differences:                0.1647

Standard error of differences for same level of factor:

                  nharv        nexp       ngeno
Average          0.4037      0.4013      0.4037
Maximum          0.4711      0.4710      0.4710
Minimum          0.3242      0.3242      0.3242
Average variance of differences:
                 0.1647      0.1647      0.1647
```

```
 166
 167  "**** LS3 Isolation counts (total) (Harvests 2 to 5, only tiller 1, experiment 2 only)
****"
 168
 169  subset
[condition=(Part.eq.8).and.(Harvest.ge.2).and.(Harvest.le.5).and.(Rep.ge.3).and.(Tiller.eq.1
).and.(Plant.le.5); setlevel=yes] \
 170   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 171   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 172
 173  vcomp [fixed=ngeno*nharv] random=nrep+nplot+nplot.nharv+nplot.nharv.nplant;
const=pos
 174  reml [print=means, wald, comp, mod,dev; maxc=50] sqrt(ntotal)

174..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+nharv.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 195 (1 units excluded due to zero weights or missing values)

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                     0.0118      0.0362
nplot                    0.0256      0.0463
nplot.nharv                  0.0000       BOUND


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.
```

```
nplot.nharv.nplant           Identity      Sigma2             0.757    0.0821


*** Deviance: -2*Log-Likelihood ***


                 Deviance   d.f.

                   174.88   171

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                      68.85           3        22.95      <0.001
   ngeno                     153.11            4        38.28      <0.001
   nharv.ngeno                    23.75          12         1.98       0.022

* Dropping individual terms from full fixed model

   nharv.ngeno                    23.75          12         1.98       0.022

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           1.510    Standard error:  0.1112



*** Table of predicted means for nharv ***

   nharv    2.000    3.000    4.000    5.000
           0.823    1.197    2.114    1.906

Standard error of differences:     Average       0.1765
                                   Maximum       0.1790
                                   Minimum       0.1740
```

```
Average variance of differences:              0.03116


*** Table of predicted means for ngeno ***

      ngeno        2-49    Cleanleaf    CPI133814      Puseas      Tallon
                 1.204        0.124        0.958        2.494        2.770

Standard error of differences:     Average       0.2541
                                   Maximum       0.2564
                                   Minimum       0.2519


*** Table of predicted means for nharv.ngeno ***

       ngeno        2-49    Cleanleaf    CPI133814      Puseas      Tallon
       nharv
       2.000       0.400       0.009       0.260       1.608       1.837
       3.000       0.415       0.000       0.500       2.123       2.948
       4.000       2.211       0.315       1.724       2.893       3.428
       5.000       1.791       0.173       1.348       3.352       2.864

Standard error of differences:     Average       0.4210
                                   Maximum       0.4528
                                   Minimum       0.3890

Average variance of differences:               0.1774

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.4259      0.3946
Maximum          0.4528      0.4133
Minimum          0.4206      0.3890
Average variance of differences:
                 0.1814      0.1558


 175  vkeep means=hgmean; term=nharv.ngeno
 176  print 'Back-transformed means' & hgmean**2


 Back-transformed means


               hgmean** 2
```

```
      nharv       2.000       3.000       4.000       5.000
      ngeno
       2-49       0.160       0.172       4.887       3.209
  Cleanleaf       0.000       0.000       0.099       0.030
  CPI133814       0.068       0.250       2.973       1.818
     Puseas       2.584       4.506       8.370      11.238
     Tallon       3.375       8.693      11.754       8.204

 177  delete [redefine=yes] hgmean, tmean
 178  page
```

```
 179
 180
"=================================================================
=========
-181                      PART = LS4 (Disease rating: harvest 3 to 5; Infection count: not
analysed)
-182
==================================================================
========"
 183
 184  "**** LS4 Disease Rating (Harvests 3 to 5, only tiller 1) ****"
 185
 186  subset [condition=(Part.eq.9).and.(Harvest.ge.3).and.(Harvest.le.5).and.(Tiller.eq.1);
setlevel=yes] \
 187   Experiment, Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 188   nexp, nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 189
 190  vcomp [fixed=nexp*ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 191  \vstruct [nplot.nharv] factor=nharv; model="ar "uniform
 192  reml [print=means, wald, comp, mod,dev] ndr

192.............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+nexp+ngeno+nharv.nexp+nharv.ngeno+nexp.ngeno+n
harv.nexp.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 285

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.
```

```
nrep                    0.0000     BOUND
nplot                   0.0000     BOUND
nplot.nharv                0.0635    0.0687


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

nplot.nharv.nplant           Identity      Sigma2            0.739    0.0708


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                252.08   251

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      42.27          2       21.14      <0.001
  nexp                       40.55          1       40.55      <0.001
  ngeno                     324.36            4       81.09      <0.001
  nharv.nexp                   1.52           2        0.76       0.468
  nharv.ngeno                  15.12           8        1.89       0.057
  nexp.ngeno                   25.77           4        6.44      <0.001
  nharv.nexp.ngeno                19.04           8        2.38       0.015

* Dropping individual terms from full fixed model

  nharv.nexp.ngeno                19.04           8        2.38       0.015

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
          1.302    Standard error:  0.0686



*** Table of predicted means for nharv ***

   nharv    3.000    4.000    5.000
            0.825    1.284    1.795

Standard error of differences:     Average       0.1678
                                   Maximum       0.1725
                                   Minimum       0.1589

Average variance of differences:               0.02820


*** Table of predicted means for nexp ***

    nexp    1.000    2.000
            1.613    0.990

Standard error of differences:      0.1371



*** Table of predicted means for ngeno ***

       ngeno        2-49    Cleanleaf    CPI133814       Puseas       Tallon
                   0.936        0.033        0.558        2.115        2.865

Standard error of differences:     Average       0.2152
                                   Maximum       0.2572
                                   Minimum       0.1812

Average variance of differences:               0.04699


*** Table of predicted means for nharv.nexp ***

        nexp    1.000    2.000
       nharv
       3.000    1.078    0.573
       4.000    1.523    1.046
       5.000    2.240    1.351

Standard error of differences:     Average       0.2363
```

```
                                  Maximum      0.2765
                                  Minimum      0.2062

Average variance of differences:              0.05639

Standard error of differences for same level of factor:

                 nharv       nexp
Average          0.2369      0.2355
Maximum          0.2611      0.2765
Minimum          0.2241      0.2062
Average variance of differences:
               0.05639     0.05639



*** Table of predicted means for nharv.ngeno ***

        ngeno        2-49    Cleanleaf    CPI133814       Puseas       Tallon
        nharv
        3.000       0.331        0.000        0.100        1.439        2.257
        4.000       0.869        0.000        0.394        2.507        2.651
        5.000       1.608        0.100        1.181        2.400        3.688

Standard error of differences:     Average      0.3689
                                  Maximum      0.5687
                                  Minimum      0.2985

Average variance of differences:               0.1410

Standard error of differences for same level of factor:

                 nharv      ngeno
Average          0.3695      0.3676
Maximum          0.5331      0.5461
Minimum          0.3050      0.2985
Average variance of differences:
                0.1410      0.1410



*** Table of predicted means for nexp.ngeno ***

        ngeno        2-49    Cleanleaf    CPI133814       Puseas       Tallon
         nexp
        1.000       0.746        0.067        0.733        2.971        3.550
        2.000       1.126        0.000        0.383        1.259        2.180
```

```
Standard error of differences:     Average       0.3014
                                   Maximum       0.4374
                                   Minimum       0.2469

Average variance of differences:                0.09399

Standard error of differences for same level of factor:

                  nexp       ngeno
Average          0.3012      0.3014
Maximum          0.4374      0.4030
Minimum          0.2469      0.2473
Average variance of differences:
                0.09399     0.09399



*** Table of predicted means for nharv.nexp.ngeno ***

             ngeno         2-49    Cleanleaf    CPI133814       Puseas
      nharv       nexp
      3.000      1.000        0.338        0.000        0.200        2.100
             2.000        0.324        0.000        0.000        0.777
      4.000      1.000        0.600        0.000        0.100        3.014
             2.000        1.139        0.000        0.687        2.000
      5.000      1.000        1.300        0.200        1.900        3.800
             2.000        1.915        0.000        0.463        1.000


             ngeno       Tallon
      nharv       nexp
      3.000      1.000        2.750
             2.000        1.763
      4.000      1.000        3.900
             2.000        1.402
      5.000      1.000        4.000
             2.000        3.375

Standard error of differences:     Average       0.5150
                                   Maximum        1.041
                                   Minimum       0.3815

Average variance of differences:                 0.2820

Standard error of differences for same level of factor:
```

```
                 nharv        nexp       ngeno
Average          0.5155      0.5147      0.5140
Maximum          0.9621       1.041      0.9910
Minimum          0.4015      0.3815      0.3815
Average variance of differences:
                 0.2820      0.2820      0.2820


 194
 195  "**** LS4 Isolation counts (total) ****"
 196
 197  "not analysed"
```

Appendix 2E

SPSS Output of Disease Rating and Isolation Data

Correlations

Correlations all data

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.76	1.720	1772
Infection (total)	3.81	4.578	1772

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.817**
	Sig. (2-tailed)		.000
	N	1772	1772
Infection (total)	Pearson Correlation	.817**	1
	Sig. (2-tailed)	.000	
	N	1772	1772

**. Correlation is significant at the 0.01 level (2-tailed).

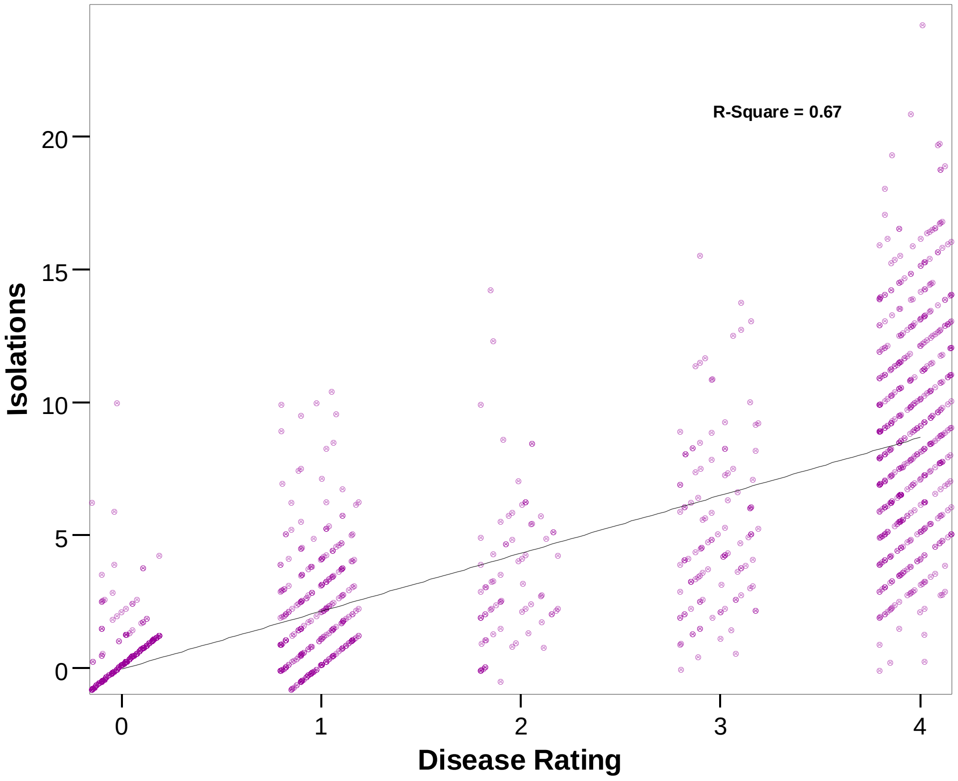
Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.876**
		Sig. (2-tailed)	.	.000
		N	1772	1772
	Infection (total)	Correlation Coefficient	.876**	1.000
		Sig. (2-tailed)	.000	.
		N	1772	1772

**. Correlation is significant at the 0.01 level (2-tailed).

Figure 2E.1 x-y scatter plot with line of best fit for all data combined.



Correlations Exp1

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.59	1.695	808
Infection (total)	3.13	4.102	808

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.826**
	Sig. (2-tailed)		.000
	N	808	808
Infection (total)	Pearson Correlation	.826**	1
	Sig. (2-tailed)	.000	
	N	808	808

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.895**
		Sig. (2-tailed)	.	.000
		N	808	808
	Infection (total)	Correlation Coefficient	.895**	1.000
		Sig. (2-tailed)	.000	.
		N	808	808

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations Exp2

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.90	1.728	964
Infection (total)	4.38	4.871	964

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.812**
	Sig. (2-tailed)		.000
	N	964	964
Infection (total)	Pearson Correlation	.812**	1
	Sig. (2-tailed)	.000	
	N	964	964

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.861**
		Sig. (2-tailed)	.	.000
		N	964	964
	Infection (total)	Correlation Coefficient	.861**	1.000
		Sig. (2-tailed)	.000	.
		N	964	964

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations LS1

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	2.79	1.461	419
Infection (total)	5.94	4.165	419

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.680**
	Sig. (2-tailed)		.000
	N	419	419
Infection (total)	Pearson Correlation	.680**	1
	Sig. (2-tailed)	.000	
	N	419	419

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.737**
		Sig. (2-tailed)	.	.000
		N	419	419
	Infection (total)	Correlation Coefficient	.737**	1.000
		Sig. (2-tailed)	.000	.
		N	419	419

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations LS2

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	2.06	1.695	415
Infection (total)	4.67	4.950	415

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.775**
	Sig. (2-tailed)		.000
	N	415	415
Infection (total)	Pearson Correlation	.775**	1
	Sig. (2-tailed)	.000	
	N	415	415

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.844**
		Sig. (2-tailed)	.	.000
		N	415	415
	Infection (total)	Correlation Coefficient	.844**	1.000
		Sig. (2-tailed)	.000	.
		N	415	415

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations LS3

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.67	1.727	343
Infection (total)	3.72	4.695	343

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.868**
	Sig. (2-tailed)		.000
	N	343	343
Infection (total)	Pearson Correlation	.868**	1
	Sig. (2-tailed)	.000	
	N	343	343

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.886**
		Sig. (2-tailed)	.	.000
		N	343	343
	Infection (total)	Correlation Coefficient	.886**	1.000
		Sig. (2-tailed)	.000	.
		N	343	343

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations LS4

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.03	1.461	186
Infection (total)	2.19	4.125	186

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.851**
	Sig. (2-tailed)		.000
	N	186	186
Infection (total)	Pearson Correlation	.851**	1
	Sig. (2-tailed)	.000	
	N	186	186

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.811**
		Sig. (2-tailed)	.	.000
		N	186	186
	Infection (total)	Correlation Coefficient	.811**	1.000
		Sig. (2-tailed)	.000	.
		N	186	186

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations LS5

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	.79	1.404	122
Infection (total)	1.93	4.165	122

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.919**
	Sig. (2-tailed)		.000
	N	122	122
Infection (total)	Pearson Correlation	.919**	1
	Sig. (2-tailed)	.000	
	N	122	122

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.874**
		Sig. (2-tailed)	.	.000
		N	122	122
	Infection (total)	Correlation Coefficient	.874**	1.000
		Sig. (2-tailed)	.000	.
		N	122	122

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations I1

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	.86	1.255	63
Infection (total)	1.60	2.575	63

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.681**
	Sig. (2-tailed)		.000
	N	63	63
Infection (total)	Pearson Correlation	.681**	1
	Sig. (2-tailed)	.000	
	N	63	63

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.714**
		Sig. (2-tailed)	.	.000
		N	63	63
	Infection (total)	Correlation Coefficient	.714**	1.000
		Sig. (2-tailed)	.000	.
		N	63	63

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations 14 DAP

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	.89	1.055	175
Infection (total)	1.89	2.274	175

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.713**
	Sig. (2-tailed)		.000
	N	175	175
Infection (total)	Pearson Correlation	.713**	1
	Sig. (2-tailed)	.000	
	N	175	175

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.751**
		Sig. (2-tailed)	.	.000
		N	175	175
	Infection (total)	Correlation Coefficient	.751**	1.000
		Sig. (2-tailed)	.000	.
		N	175	175

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations 21 DAP

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.79	1.677	270
Infection (total)	2.63	2.829	270

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.846**
	Sig. (2-tailed)		.000
	N	270	270
Infection (total)	Pearson Correlation	.846**	1
	Sig. (2-tailed)	.000	
	N	270	270

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.888**
		Sig. (2-tailed)	.	.000
		N	270	270
	Infection (total)	Correlation Coefficient	.888**	1.000
		Sig. (2-tailed)	.000	.
		N	270	270

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations 28 DAP

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.78	1.713	386
Infection (total)	3.28	3.925	386

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.849**
	Sig. (2-tailed)		.000
	N	386	386
Infection (total)	Pearson Correlation	.849**	1
	Sig. (2-tailed)	.000	
	N	386	386

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.883**
		Sig. (2-tailed)	.	.000
		N	386	386
	Infection (total)	Correlation Coefficient	.883**	1.000
		Sig. (2-tailed)	.000	.
		N	386	386

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations 35 DAP

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.83	1.792	431
Infection (total)	4.81	5.429	431

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.886**
	Sig. (2-tailed)		.000
	N	431	431
Infection (total)	Pearson Correlation	.886**	1
	Sig. (2-tailed)	.000	
	N	431	431

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.896**
		Sig. (2-tailed)	.	.000
		N	431	431
	Infection (total)	Correlation Coefficient	.896**	1.000
		Sig. (2-tailed)	.000	.
		N	431	431

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations 42 DAP

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.97	1.783	510
Infection (total)	4.65	5.157	510

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.793**
	Sig. (2-tailed)		.000
	N	510	510
Infection (total)	Pearson Correlation	.793**	1
	Sig. (2-tailed)	.000	
	N	510	510

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.858**
		Sig. (2-tailed)	.	.000
		N	510	510
	Infection (total)	Correlation Coefficient	.858**	1.000
		Sig. (2-tailed)	.000	.
		N	510	510

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations Puseas

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	2.65	1.649	311
Infection (total)	6.54	5.327	311

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.800**
	Sig. (2-tailed)		.000
	N	311	311
Infection (total)	Pearson Correlation	.800**	1
	Sig. (2-tailed)	.000	
	N	311	311

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.828**
		Sig. (2-tailed)	.	.000
		N	311	311
	Infection (total)	Correlation Coefficient	.828**	1.000
		Sig. (2-tailed)	.000	.
		N	311	311

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations Tallon

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	3.19	1.373	303
Infection (total)	7.22	4.764	303

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.698**
	Sig. (2-tailed)		.000
	N	303	303
Infection (total)	Pearson Correlation	.698**	1
	Sig. (2-tailed)	.000	
	N	303	303

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.718**
		Sig. (2-tailed)	.	.000
		N	303	303
	Infection (total)	Correlation Coefficient	.718**	1.000
		Sig. (2-tailed)	.000	.
		N	303	303

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations 2-49

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.60	1.619	421
Infection (total)	2.67	3.381	421

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.817**
	Sig. (2-tailed)		.000
	N	421	421
Infection (total)	Pearson Correlation	.817**	1
	Sig. (2-tailed)	.000	
	N	421	421

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.848**
		Sig. (2-tailed)	.	.000
		N	421	421
	Infection (total)	Correlation Coefficient	.848**	1.000
		Sig. (2-tailed)	.000	.
		N	421	421

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations CPI133814

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	1.43	1.542	351
Infection (total)	2.81	3.925	351

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.816**
	Sig. (2-tailed)		.000
	N	351	351
Infection (total)	Pearson Correlation	.816**	1
	Sig. (2-tailed)	.000	
	N	351	351

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.852**
		Sig. (2-tailed)	.	.000
		N	351	351
	Infection (total)	Correlation Coefficient	.852**	1.000
		Sig. (2-tailed)	.000	.
		N	351	351

**. Correlation is significant at the 0.01 level (2-tailed).

Correlations Cleanleaf

Descriptive Statistics

	Mean	Std. Deviation	N
Disease Rating	.39	.806	386
Infection (total)	1.08	2.076	386

Correlations

		Disease Rating	Infection (total)
Disease Rating	Pearson Correlation	1	.554**
	Sig. (2-tailed)		.000
	N	386	386
Infection (total)	Pearson Correlation	.554**	1
	Sig. (2-tailed)	.000	
	N	386	386

**. Correlation is significant at the 0.01 level (2-tailed).

Nonparametric Correlations

Correlations

			Disease Rating	Infection (total)
Spearman's rho	Disease Rating	Correlation Coefficient	1.000	.739**
		Sig. (2-tailed)	.	.000
		N	386	386
	Infection (total)	Correlation Coefficient	.739**	1.000
		Sig. (2-tailed)	.000	.
		N	386	386

**. Correlation is significant at the 0.01 level (2-tailed).

Harvest	Genotype	Rep	Plant	Tiller	Part	Disese Rating	Infection (total)	Infection(1/4)	Infection (2/4)	Infection (3/4)	Infection (4/4)
1	Puseas	1	1	1	C	1					
1	Puseas	1	1	1	SCI	1					
1	Puseas	1	1	1	LS1	0	0	0	0	0	0
1	Puseas	1	1	1	LS2	0	0	0	0	0	0
1	Puseas	1	2	1	C	2					
1	Puseas	1	2	1	SCI	0					
1	Puseas	1	2	1	LS1	0	0	0	0	0	0
1	Puseas	1	2	1	LS2	0	0	0	0	0	0
1	Puseas	1	3	1	C	1					
1	Puseas	1	3	1	SCI	0					
1	Puseas	1	3	1	LS1	0	0	0	0	0	0
1	Puseas	1	3	1	LS2	0	0	0	0	0	0
1	Puseas	1	4	1	C	2					
1	Puseas	1	4	1	SCI	0					
1	Puseas	1	4	1	LS1	0	0	0	0	0	0
1	Puseas	1	4	1	LS2	0	0	0	0	0	0
1	Puseas	1	5	1	C	3					
1	Puseas	1	5	1	SCI	0					
1	Puseas	1	5	1	LS1	0	0	0	0	0	0
1	Puseas	1	5	1	LS2	0	0	0	0	0	0
1	Puseas	2	1	1	C	2					
1	Puseas	2	1	1	SCI	0					
1	Puseas	2	1	1	LS1	0	0	0	0	0	0
1	Puseas	2	1	1	LS2	0	0	0	0	0	0
1	Puseas	2	2	1	C	1					
1	Puseas	2	2	1	LS1	0	0	0	0	0	0
1	Puseas	2	2	1	LS2	0	0	0	0	0	0
1	Puseas	2	3	1	C	1					
1	Puseas	2	3	1	LS1	0	0	0	0	0	0
1	Puseas	2	3	1	LS2	0	0	0	0	0	0
1	Puseas	2	4	1	C	1					
1	Puseas	2	4	1	SCI	0					
1	Puseas	2	4	1	LS1	0	0	0	0	0	0
1	Puseas	2	4	1	LS2	0	0	0	0	0	0
1	Puseas	2	5	1	C	1					

1	Puseas	2	5	1	SCI	0					
1	Puseas	2	5	1	LS1	0	0	0	0	0	0
1	Puseas	2	5	1	LS2	0	0	0	0	0	0
1	Puseas	3	1	1	C	4					
1	Puseas	3	1	1	SCI	0					
1	Puseas	3	1	1	LS1	0					
1	Puseas	3	1	1	LS2	0					
1	Puseas	3	2	1	C	1					
1	Puseas	3	2	1	SCI	0					
1	Puseas	3	2	1	LS1	0					
1	Puseas	3	2	1	LS2	0					
1	Puseas	3	3	1	C	0					
1	Puseas	3	3	1	SCI	0					
1	Puseas	3	3	1	LS1	0					
1	Puseas	3	3	1	LS2	0					
1	Puseas	3	4	1	C	2					
1	Puseas	3	4	1	SCI	0					
1	Puseas	3	4	1	LS1	0					
1	Puseas	3	4	1	LS2	0					
1	Puseas	3	5	1	C	1					
1	Puseas	3	5	1	SCI	0					
1	Puseas	3	5	1	LS1	0					
1	Puseas	3	5	1	LS2	0					
1	Vasco	1	1	1	C	4					
1	Vasco	1	1	1	SCI	0					
1	Vasco	1	1	1	LS1	1	0	0	0	0	0
1	Vasco	1	1	1	LS2	0	0	0	0	0	0
1	Vasco	1	2	1	C	4					
1	Vasco	1	2	1	SCI	0					
1	Vasco	1	2	1	LS1	1	4	3	1	0	0
1	Vasco	1	2	1	LS2	0	0	0	0	0	0
1	Vasco	1	3	1	C	4					
1	Vasco	1	3	1	SCI	0					
1	Vasco	1	3	1	LS1	1	0	0	0	0	0
1	Vasco	1	3	1	LS2	0	0	0	0	0	0
1	Vasco	1	4	1	C	1					

1	Vasco	1	4	1	SCI	0					
1	Vasco	1	4	1	LS1	1	0	0	0	0	0
1	Vasco	1	4	1	LS2	0	0	0	0	0	0
1	Vasco	1	5	1	C	1					
1	Vasco	1	5	1	SCI	0					
1	Vasco	1	5	1	LS1	1	0	0	0	0	0
1	Vasco	1	5	1	LS2	0	0	0	0	0	0
1	Vasco	2	1	1	C	3					
1	Vasco	2	1	1	SCI	0					
1	Vasco	2	1	1	LS1	0	0	0	0	0	0
1	Vasco	2	1	1	LS2	0	0	0	0	0	0
1	Vasco	2	2	1	C	1					
1	Vasco	2	2	1	SCI	0					
1	Vasco	2	2	1	LS1	0	0	0	0	0	0
1	Vasco	2	2	1	LS2	0	0	0	0	0	0
1	Vasco	2	3	1	C	3					
1	Vasco	2	3	1	SCI	0					
1	Vasco	2	3	1	LS1	0	0	0	0	0	0
1	Vasco	2	3	1	LS2	0	0	0	0	0	0
1	Vasco	2	4	1	C	1					
1	Vasco	2	4	1	SCI	0					
1	Vasco	2	4	1	LS1	0	0	0	0	0	0
1	Vasco	2	4	1	LS2	0	0	0	0	0	0
1	Vasco	2	5	1	C	4					
1	Vasco	2	5	1	SCI	1					
1	Vasco	2	5	1	LS1	1	1	1	0	0	0
1	Vasco	2	5	1	LS2	0	0	0	0	0	0
1	Vasco	3	1	1	C	2					
1	Vasco	3	1	1	SCI	0					
1	Vasco	3	1	1	LS1	0					
1	Vasco	3	1	1	LS2	0					
1	Vasco	3	2	1	C	4					
1	Vasco	3	2	1	SCI	0					
1	Vasco	3	2	1	LS1	1					
1	Vasco	3	2	1	LS2	0					
1	Vasco	3	3	1	C	1					

1	Vasco	3	3	1	SCI	0					
1	Vasco	3	3	1	LS1	0					
1	Vasco	3	3	1	LS2	0					
1	Vasco	3	4	1	C	4					
1	Vasco	3	4	1	SCI	0					
1	Vasco	3	4	1	LS1	3					
1	Vasco	3	4	1	LS2	0					
1	Vasco	3	5	1	C	1					
1	Vasco	3	5	1	SCI	0					
1	Vasco	3	5	1	LS1	0					
1	Vasco	3	5	1	LS2	0					
1	2-49	1	1	1	C	4					
1	2-49	1	1	1	SCI	0					
1	2-49	1	1	1	LS1	0	0	0	0	0	0
1	2-49	1	1	1	LS2	0	0	0	0	0	0
1	2-49	1	2	1	C	2					
1	2-49	1	2	1	SCI	0					
1	2-49	1	2	1	LS1	0	0	0	0	0	0
1	2-49	1	2	1	LS2	0	0	0	0	0	0
1	2-49	1	3	1	C	2					
1	2-49	1	3	1	SCI	0					
1	2-49	1	3	1	LS1	1	0	0	0	0	0
1	2-49	1	3	1	LS2	0	0	0	0	0	0
1	2-49	1	4	1	C	0					
1	2-49	1	4	1	SCI	0					
1	2-49	1	4	1	LS1	0	0	0	0	0	0
1	2-49	1	4	1	LS2	0	0	0	0	0	0
1	2-49	1	5	1	C	3					
1	2-49	1	5	1	SCI	0					
1	2-49	1	5	1	LS1	0	0	0	0	0	0
1	2-49	1	5	1	LS2	0	0	0	0	0	0
1	2-49	2	1	1	C	1					
1	2-49	2	1	1	SCI	0					
1	2-49	2	1	1	LS1	0	0	0	0	0	0
1	2-49	2	1	1	LS2	0	0	0	0	0	0
1	2-49	2	2	1	C	1					

1	2-49	2	2	1	SCI	0					
1	2-49	2	2	1	LS1	0	0	0	0	0	0
1	2-49	2	2	1	LS2	0	0	0	0	0	0
1	2-49	2	3	1	C	4					
1	2-49	2	3	1	SCI	0					
1	2-49	2	3	1	LS1	1	0	0	0	0	0
1	2-49	2	3	1	LS2	0	0	0	0	0	0
1	2-49	2	4	1	C	1					
1	2-49	2	4	1	SCI	0					
1	2-49	2	4	1	LS1	0	0	0	0	0	0
1	2-49	2	4	1	LS2	0	0	0	0	0	0
1	2-49	2	5	1	C	0					
1	2-49	2	5	1	SCI	0					
1	2-49	2	5	1	LS1	0	0	0	0	0	0
1	2-49	2	5	1	LS2	0	0	0	0	0	0
1	2-49	3	1	1	C	1					
1	2-49	3	1	1	SCI	0					
1	2-49	3	1	1	LS1	0					
1	2-49	3	1	1	LS2	0					
1	2-49	3	2	1	C	4					
1	2-49	3	2	1	SCI	0					
1	2-49	3	2	1	LS1	1					
1	2-49	3	2	1	LS2	0					
1	2-49	3	3	1	C	4					
1	2-49	3	3	1	SCI	0					
1	2-49	3	3	1	LS1	0					
1	2-49	3	3	1	LS2	0					
1	2-49	3	4	1	C	1					
1	2-49	3	4	1	SCI	0					
1	2-49	3	4	1	LS1	0					
1	2-49	3	4	1	LS2	0					
1	2-49	3	5	1	C	4					
1	2-49	3	5	1	SCI	1					
1	2-49	3	5	1	LS1	1					
1	2-49	3	5	1	LS2	0					
1	Sunco	1	1	1	C	1					

1	Sunco	1	1	1	SCI	0					
1	Sunco	1	1	1	LS1	0	0	0	0	0	0
1	Sunco	1	1	1	LS2	0	0	0	0	0	0
1	Sunco	1	2	1	C	2					
1	Sunco	1	2	1	SCI	0					
1	Sunco	1	2	1	LS1	0	0	0	0	0	0
1	Sunco	1	2	1	LS2	0	0	0	0	0	0
1	Sunco	1	3	1	C	2					
1	Sunco	1	3	1	SCI	0					
1	Sunco	1	3	1	LS1	0	0	0	0	0	0
1	Sunco	1	3	1	LS2	0	0	0	0	0	0
1	Sunco	1	4	1	C	1					
1	Sunco	1	4	1	SCI	0					
1	Sunco	1	4	1	LS1	0	0	0	0	0	0
1	Sunco	1	4	1	LS2	0	0	0	0	0	0
1	Sunco	1	5	1	C	4					
1	Sunco	1	5	1	SCI	0					
1	Sunco	1	5	1	LS1	0	0	0	0	0	0
1	Sunco	1	5	1	LS2	0	0	0	0	0	0
1	Sunco	2	1	1	C	3					
1	Sunco	2	1	1	SCI	1					
1	Sunco	2	1	1	LS1	0	0	0	0	0	0
1	Sunco	2	1	1	LS2	0	0	0	0	0	0
1	Sunco	2	2	1	C	4					
1	Sunco	2	2	1	SCI	0					
1	Sunco	2	2	1	LS1	0	0	0	0	0	0
1	Sunco	2	2	1	LS2	0	0	0	0	0	0
1	Sunco	2	3	1	C	4					
1	Sunco	2	3	1	SCI	3					
1	Sunco	2	3	1	LS1	1	0	0	0	0	0
1	Sunco	2	3	1	LS2	0	0	0	0	0	0
1	Sunco	2	4	1	C	4					
1	Sunco	2	4	1	SCI	0					
1	Sunco	2	4	1	LS1	1	0	0	0	0	0
1	Sunco	2	4	1	LS2	0	0	0	0	0	0
1	Sunco	2	5	1	C	1					

1	Sunco	2	5	1	SCI	0					
1	Sunco	2	5	1	LS1	0	0	0	0	0	0
1	Sunco	2	5	1	LS2	0	0	0	0	0	0
1	Sunco	3	1	1	C	3					
1	Sunco	3	1	1	SCI	1					
1	Sunco	3	1	1	LS1	0					
1	Sunco	3	1	1	LS2	0					
1	Sunco	3	2	1	C	1					
1	Sunco	3	2	1	SCI	0					
1	Sunco	3	2	1	LS1	0					
1	Sunco	3	2	1	LS2	0					
1	Sunco	3	3	1	C	4					
1	Sunco	3	3	1	SCI	1					
1	Sunco	3	3	1	LS1	1					
1	Sunco	3	3	1	LS2	0					
1	Sunco	3	4	1	C	2					
1	Sunco	3	4	1	SCI	0					
1	Sunco	3	4	1	LS1	0					
1	Sunco	3	4	1	LS2	0					
1	Sunco	3	5	1	C	1					
1	Sunco	3	5	1	SCI	0					
1	Sunco	3	5	1	LS1	0					
1	Sunco	3	5	1	LS2	0					
1	CPI133814	1	1	1	C	3					
1	CPI133814	1	1	1	SCI	0					
1	CPI133814	1	1	1	LS1	0	0	0	0	0	0
1	CPI133814	1	1	1	LS2	0	0	0	0	0	0
1	CPI133814	1	2	1	C	1					
1	CPI133814	1	2	1	SCI	0					
1	CPI133814	1	2	1	LS1	0	0	0	0	0	0
1	CPI133814	1	2	1	LS2	0	0	0	0	0	0
1	CPI133814	1	3	1	C	2					
1	CPI133814	1	3	1	SCI	0					
1	CPI133814	1	3	1	LS1	0	0	0	0	0	0
1	CPI133814	1	3	1	LS2	0	0	0	0	0	0
1	CPI133814	1	4	1	C	4					

1	CPI133814	1	4	1	SCI	0					
1	CPI133814	1	4	1	LS1	0	0	0	0	0	0
1	CPI133814	1	4	1	LS2	0	0	0	0	0	0
1	CPI133814	1	5	1	C	2					
1	CPI133814	1	5	1	LS1	0	0	0	0	0	0
1	CPI133814	1	5	1	LS2	0	0	0	0	0	0
1	CPI133814	1	1	1	C	1					
1	CPI133814	1	1	1	SCI	0					
1	CPI133814	2	1	1	LS1	0	0	0	0	0	0
1	CPI133814	2	1	1	LS2	0	0	0	0	0	0
1	CPI133814	2	2	1	C	1					
1	CPI133814	2	2	1	SCI	0					
1	CPI133814	2	2	1	LS1	0	0	0	0	0	0
1	CPI133814	2	2	1	LS2	0	0	0	0	0	0
1	CPI133814	2	3	1	C	1					
1	CPI133814	2	3	1	SCI	0					
1	CPI133814	2	3	1	LS1	0	0	0	0	0	0
1	CPI133814	2	3	1	LS2	0	0	0	0	0	0
1	CPI133814	2	4	1	C	1					
1	CPI133814	2	4	1	SCI	0					
1	CPI133814	2	4	1	LS1	0	0	0	0	0	0
1	CPI133814	2	4	1	LS2	0	0	0	0	0	0
1	CPI133814	2	5	1	C	2					
1	CPI133814	2	5	1	SCI	0					
1	CPI133814	2	5	1	LS1	0	0	0	0	0	0
1	CPI133814	2	5	1	LS2	0	0	0	0	0	0
1	CPI133814	3	1	1	C	1					
1	CPI133814	3	1	1	SCI	0					
1	CPI133814	3	1	1	LS1	0					
1	CPI133814	3	1	1	LS2	0					
1	CPI133814	3	2	1	C	1					
1	CPI133814	3	2	1	SCI	0					
1	CPI133814	3	2	1	LS1	0					
1	CPI133814	3	2	1	LS2	0					
1	CPI133814	3	3	1	C	1					
1	CPI133814	3	3	1	SCI	0					

1	CPI133814	3	3	1	LS1	0					
1	CPI133814	3	3	1	LS2	0					
1	CPI133814	3	4	1	C	1					
1	CPI133814	3	4	1	SCI	0					
1	CPI133814	3	4	1	LS1	0					
1	CPI133814	3	4	1	LS2	0					
1	CPI133814	3	5	1	C	2					
1	CPI133814	3	5	1	SCI	0					
1	CPI133814	3	5	1	LS1	0					
1	CPI133814	3	5	1	LS2	0					
2	Puseas	1	1	1	C	3					
2	Puseas	1	1	1	SCI	2					
2	Puseas	1	1	1	LS1	2	2	2	0	0	0
2	Puseas	1	1	1	LS2	1	0	0	0	0	0
2	Puseas	1	1	1	LS3	0	0	0	0	0	0
2	Puseas	1	2	1	C	3					
2	Puseas	1	2	1	SCI	0					
2	Puseas	1	2	1	LS1	3	0	0	0	0	0
2	Puseas	1	2	1	LS2	0	0	0	0	0	0
2	Puseas	1	2	1	LS3	0	0	0	0	0	0
2	Puseas	1	2	1	LS4	0	0	0	0	0	0
2	Puseas	1	3	1	C	4					
2	Puseas	1	3	1	SCI	1					
2	Puseas	1	3	1	LS1	2	0	0	0	0	0
2	Puseas	1	3	1	LS2	0	0	0	0	0	0
2	Puseas	1	3	1	LS3	0	0	0	0	0	0
2	Puseas	1	4	1	C	4					
2	Puseas	1	4	1	SCI	3					
2	Puseas	1	4	1	LS1	2	2	2	0	0	0
2	Puseas	1	4	1	LS2	1	0	0	0	0	0
2	Puseas	1	4	1	LS3	0	0	0	0	0	0
2	Puseas	1	5	1	C	4					
2	Puseas	1	5	1	SCI	1					
2	Puseas	1	5	1	LS1	4	10	4	3	3	0
2	Puseas	1	5	1	LS2	1	0	0	0	0	0
2	Puseas	1	5	1	LS3	0	0	0	0	0	0

2	Puseas	1	5	1	LS4	0	0	0	0	0	0
2	Puseas	2	1	1	C	4					
2	Puseas	2	1	1	SCI	1					
2	Puseas	2	1	1	LS1	0	0	0	0	0	0
2	Puseas	2	1	1	LS2	0	0	0	0	0	0
2	Puseas	2	1	1	LS3	0	0	0	0	0	0
2	Puseas	2	1	1	LS4	0	0	0	0	0	0
2	Puseas	2	1	2	LS1	0	0	0	0	0	0
2	Puseas	2	1	2	LS2	0	0	0	0	0	0
2	Puseas	2	2	1	C	4					
2	Puseas	2	2	1	SCI	0					
2	Puseas	2	2	1	LS1	1	0	0	0	0	0
2	Puseas	2	2	1	LS2	0	0	0	0	0	0
2	Puseas	2	2	1	LS3	0	0	0	0	0	0
2	Puseas	2	2	1	LS4	0	0	0	0	0	0
2	Puseas	2	2	2	LS1	0	0	0	0	0	0
2	Puseas	2	2	2	LS2	0	0	0	0	0	0
2	Puseas	2	3	1	C	3					
2	Puseas	2	3	1	SCI	0					
2	Puseas	2	3	1	LS1	0	0	0	0	0	0
2	Puseas	2	3	1	LS2	0	0	0	0	0	0
2	Puseas	2	3	1	LS3	0	0	0	0	0	0
2	Puseas	2	4	1	C	3					
2	Puseas	2	4	1	SCI	0					
2	Puseas	2	4	1	LS1	1	0	0	0	0	0
2	Puseas	2	4	1	LS2	0	0	0	0	0	0
2	Puseas	2	4	1	LS3	0	0	0	0	0	0
2	Puseas	2	4	1	LS4	0	0	0	0	0	0
2	Puseas	2	4	2	LS1	0	0	0	0	0	0
2	Puseas	2	4	2	LS2	0	0	0	0	0	0
2	Puseas	2	5	1	C	4					
2	Puseas	2	5	1	SCI	0					
2	Puseas	2	5	1	LS1	1	0	0	0	0	0
2	Puseas	2	5	1	LS2	0	0	0	0	0	0
2	Puseas	2	5	1	LS3	0	0	0	0	0	0
2	Puseas	2	5	1	LS4	0	0	0	0	0	0

2	Puseas	3	1	1	C	4					
2	Puseas	3	1	1	SCI	4					
2	Puseas	3	1	1	LS1	1					
2	Puseas	3	1	1	LS2	0					
2	Puseas	3	1	1	LS3	0					
2	Puseas	3	1	1	LS4	0					
2	Puseas	3	1	2	LS1	0					
2	Puseas	3	1	2	LS2	0					
2	Puseas	3	1	3	LS1	0					
2	Puseas	3	1	3	LS2	0					
2	Puseas	3	2	1	C	4					
2	Puseas	3	2	1	SCI	1					
2	Puseas	3	2	1	LS1	2					
2	Puseas	3	2	1	LS2	1					
2	Puseas	3	2	1	LS3	0					
2	Puseas	3	2	1	LS4	0					
2	Puseas	3	2	2	LS1	0					
2	Puseas	3	2	2	LS2	0					
2	Puseas	3	3	1	C	2					
2	Puseas	3	3	1	SCI	1					
2	Puseas	3	3	1	LS1	1					
2	Puseas	3	3	1	LS2	0					
2	Puseas	3	3	1	LS3	0					
2	Puseas	3	4	1	C	4					
2	Puseas	3	4	1	SCI	1					
2	Puseas	3	4	1	LS1	2					
2	Puseas	3	4	1	LS2	1					
2	Puseas	3	4	1	LS3	0					
2	Puseas	3	4	1	LS4	0					
2	Puseas	3	4	2	LS1	0					
2	Puseas	3	4	2	LS2	0					
2	Puseas	3	4	3	LS1	0					
2	Puseas	3	4	3	LS2	0					
2	Puseas	3	5	1	C	4					
2	Puseas	3	5	1	SCI	1					
2	Puseas	3	5	1	LS1	3					

2	Puseas	3	5	1	LS2	1					
2	Puseas	3	5	1	LS3	0					
2	Puseas	3	5	1	LS4	0					
2	Puseas	3	5	2	LS1	0					
2	Puseas	3	5	2	LS2	0					
2	Puseas	3	5	3	LS1	0					
2	Puseas	3	5	3	LS2	0					
2	Vasco	1	1	1	C	4					
2	Vasco	1	1	1	SCI	0					
2	Vasco	1	1	1	LS1	1	0	0	0	0	0
2	Vasco	1	1	1	LS2	0	0	0	0	0	0
2	Vasco	1	1	1	LS3	0	0	0	0	0	0
2	Vasco	1	1	1	LS4	0	0	0	0	0	0
2	Vasco	1	2	1	C	4					
2	Vasco	1	2	1	SCI	1					
2	Vasco	1	2	1	LS1	4	0	0	0	0	0
2	Vasco	1	2	1	LS2	1	0	0	0	0	0
2	Vasco	1	2	1	LS3	0	0	0	0	0	0
2	Vasco	1	2	1	LS4	0	0	0	0	0	0
2	Vasco	1	3	1	C	4					
2	Vasco	1	3	1	SCI	3					
2	Vasco	1	3	1	LS1	2	1	1	0	0	0
2	Vasco	1	3	1	LS2	1	0	0	0	0	0
2	Vasco	1	3	1	LS3	0	0	0	0	0	0
2	Vasco	1	3	1	LS4	0	0	0	0	0	0
2	Vasco	1	4	1	C	4					
2	Vasco	1	4	1	SCI	0					
2	Vasco	1	4	1	LS1	1	0	0	0	0	0
2	Vasco	1	4	1	LS2	0	0	0	0	0	0
2	Vasco	1	4	1	LS3	0	0	0	0	0	0
2	Vasco	1	5	1	C	4					
2	Vasco	1	5	1	SCI	0					
2	Vasco	1	5	1	LS1	0	0	0	0	0	0
2	Vasco	1	5	1	LS2	0	0	0	0	0	0
2	Vasco	1	5	1	LS3	0	0	0	0	0	0
2	Vasco	2	1	1	C	4					

2	Vasco	2	1	1	SCI	0					
2	Vasco	2	1	1	LS1	1	0	0	0	0	0
2	Vasco	2	1	1	LS2	0	0	0	0	0	0
2	Vasco	2	1	1	LS3	0	0	0	0	0	0
2	Vasco	2	2	1	C	4					
2	Vasco	2	2	1	SCI	0					
2	Vasco	2	2	1	LS1	1	0	0	0	0	0
2	Vasco	2	2	1	LS2	0	0	0	0	0	0
2	Vasco	2	2	1	LS3	0	0	0	0	0	0
2	Vasco	2	3	1	C	4					
2	Vasco	2	3	1	SCI	0					
2	Vasco	2	3	1	LS1	1	0	0	0	0	0
2	Vasco	2	3	1	LS2	0	0	0	0	0	0
2	Vasco	2	3	1	LS3	0	0	0	0	0	0
2	Vasco	2	3	1	LS4	0	0	0	0	0	0
2	Vasco	2	4	1	C	4					
2	Vasco	2	4	1	SCI	0					
2	Vasco	2	4	1	LS1	1	0	0	0	0	0
2	Vasco	2	4	1	LS2	0	0	0	0	0	0
2	Vasco	2	4	1	LS3	0	0	0	0	0	0
2	Vasco	2	4	1	LS4	0	0	0	0	0	0
2	Vasco	2	5	1	C	4					
2	Vasco	2	5	1	LS1	1	0	0	0	0	0
2	Vasco	2	5	1	LS2	0	0	0	0	0	0
2	Vasco	2	5	1	LS3	0	0	0	0	0	0
2	Vasco	3	1	1	C	4					
2	Vasco	3	1	1	SCI	0					
2	Vasco	3	1	1	LS1	1					
2	Vasco	3	1	1	LS2	0					
2	Vasco	3	1	1	LS3	0					
2	Vasco	3	2	1	C	4					
2	Vasco	3	2	1	SCI	0					
2	Vasco	3	2	1	LS1	1					
2	Vasco	3	2	1	LS2	0					
2	Vasco	3	2	1	LS3	0					
2	Vasco	3	3	1	C	3					

2	Vasco	3	3	1	SCI	0					
2	Vasco	3	3	1	LS1	0					
2	Vasco	3	3	1	LS2	0					
2	Vasco	3	3	1	LS3	0					
2	Vasco	3	4	1	C	3					
2	Vasco	3	4	1	SCI	0					
2	Vasco	3	4	1	LS1	1					
2	Vasco	3	4	1	LS2	0					
2	Vasco	3	4	1	LS3	0					
2	Vasco	3	5	1	C	4					
2	Vasco	3	5	1	SCI	0					
2	Vasco	3	5	1	LS1	1					
2	Vasco	3	5	1	LS2	0					
2	Vasco	3	5	1	LS3	0					
2	Vasco	3	5	1	LS4	0					
2	2-49	1	1	1	C	4					
2	2-49	1	1	1	SCI	2					
2	2-49	1	1	1	LS1	2	0	0	0	0	0
2	2-49	1	1	1	LS2	0	0	0	0	0	0
2	2-49	1	1	1	LS3	0	0	0	0	0	0
2	2-49	1	1	1	LS4	0	0	0	0	0	0
2	2-49	1	2	1	C	3					
2	2-49	1	2	1	LS1	0	0	0	0	0	0
2	2-49	1	2	1	LS2	0	0	0	0	0	0
2	2-49	1	2	1	LS3	0	0	0	0	0	0
2	2-49	1	2	2	LS1	0	0	0	0	0	0
2	2-49	1	2	2	LS2	0	0	0	0	0	0
2	2-49	1	3	1	C	3					
2	2-49	1	3	1	SCI	0					
2	2-49	1	3	1	LS1	1	0	0	0	0	0
2	2-49	1	3	1	LS2	0	0	0	0	0	0
2	2-49	1	3	1	LS3	0	0	0	0	0	0
2	2-49	1	4	1	C	3					
2	2-49	1	4	1	SCI	0					
2	2-49	1	4	1	LS1	1	2	0	0	2	0
2	2-49	1	4	1	LS2	0	0	0	0	0	0

2	2-49	1	4	1	LS3	0	0	0	0	0	0
2	2-49	1	4	1	LS4	0	0	0	0	0	0
2	2-49	1	5	1	C	4					
2	2-49	1	5	1	SCI	0					
2	2-49	1	5	1	LS1	1	0	0	0	0	0
2	2-49	1	5	1	LS2	0	0	0	0	0	0
2	2-49	1	5	1	LS3	0	0	0	0	0	0
2	2-49	1	5	1	LS4	0	0	0	0	0	0
2	2-49	1	5	2	LS1	0	0	0	0	0	0
2	2-49	1	5	2	LS2	0	0	0	0	0	0
2	2-49	2	1	1	C	3					
2	2-49	2	1	1	SCI	0					
2	2-49	2	1	1	LS1	1	0	0	0	0	0
2	2-49	2	1	1	LS2	0	0	0	0	0	0
2	2-49	2	1	1	LS3	0	0	0	0	0	0
2	2-49	2	2	1	C	4					
2	2-49	2	2	1	SCI	1					
2	2-49	2	2	1	LS1	1	0	0	0	0	0
2	2-49	2	2	1	LS2	0	0	0	0	0	0
2	2-49	2	2	1	LS3	0	0	0	0	0	0
2	2-49	2	2	1	LS4	0	0	0	0	0	0
2	2-49	2	3	1	C	2					
2	2-49	2	3	1	SCI	0					
2	2-49	2	3	1	LS1	0	0	0	0	0	0
2	2-49	2	3	1	LS2	0	0	0	0	0	0
2	2-49	2	3	1	LS3	0	0	0	0	0	0
2	2-49	2	4	1	C	2					
2	2-49	2	4	1	SCI	0					
2	2-49	2	4	1	LS1	1	0	0	0	0	0
2	2-49	2	4	1	LS2	0	0	0	0	0	0
2	2-49	2	4	1	LS3	0	0	0	0	0	0
2	2-49	2	4	1	LS4	0	0	0	0	0	0
2	2-49	2	4	2	LS1	3	0	0	0	0	0
2	2-49	2	4	2	LS2	0	0	0	0	0	0
2	2-49	2	5	1	C	3					
2	2-49	2	5	1	SCI	0					

2	2-49	2	5	1	LS1	0	0	0	0	0	0
2	2-49	2	5	1	LS2	0	0	0	0	0	0
2	2-49	2	5	1	LS3	0	0	0	0	0	0
2	2-49	2	5	1	LS4	0	0	0	0	0	0
2	2-49	2	5	2	LS1	0	0	0	0	0	0
2	2-49	2	5	2	LS2	0	0	0	0	0	0
2	2-49	3	1	1	C	3					
2	2-49	3	1	1	SCI	0					
2	2-49	3	1	1	LS1	0					
2	2-49	3	1	1	LS2	0					
2	2-49	3	1	1	LS3	0					
2	2-49	3	2	1	C	4					
2	2-49	3	2	1	SCI	1					
2	2-49	3	2	1	LS1	1					
2	2-49	3	2	1	LS2	0					
2	2-49	3	2	1	LS3	0					
2	2-49	3	2	1	LS4	0					
2	2-49	3	2	2	LS1	0					
2	2-49	3	2	2	LS2	0					
2	2-49	3	3	1	C	4					
2	2-49	3	3	1	SCI	3					
2	2-49	3	3	1	LS1	1					
2	2-49	3	3	1	LS2	0					
2	2-49	3	3	1	LS3	0					
2	2-49	3	3	1	LS4	0					
2	2-49	3	3	2	LS1	0					
2	2-49	3	3	2	LS2	0					
2	2-49	3	4	1	C	3					
2	2-49	3	4	1	SCI	0					
2	2-49	3	4	1	LS1	1					
2	2-49	3	4	1	LS2	0					
2	2-49	3	4	1	LS3	0					
2	2-49	3	4	1	LS4	0					
2	2-49	3	5	1	C	2					
2	2-49	3	5	1	SCI	0					
2	2-49	3	5	1	LS1	1					

2	2-49	3	5	1	LS2	0					
2	2-49	3	5	1	LS3	0					
2	Sunco	1	1	1	C	4					
2	Sunco	1	1	1	SCI	1					
2	Sunco	1	1	1	LS1	1	0	0	0	0	0
2	Sunco	1	1	1	LS2	0	0	0	0	0	0
2	Sunco	1	1	1	LS3	0	0	0	0	0	0
2	Sunco	1	1	1	LS4	0	0	0	0	0	0
2	Sunco	1	1	2	LS1	0	0	0	0	0	0
2	Sunco	1	1	2	LS2	0	0	0	0	0	0
2	Sunco	1	2	1	C	2					
2	Sunco	1	2	1	SCI	1					
2	Sunco	1	2	1	LS1	1	0	0	0	0	0
2	Sunco	1	2	1	LS2	0	0	0	0	0	0
2	Sunco	1	2	1	LS3	0	0	0	0	0	0
2	Sunco	1	3	1	C	2					
2	Sunco	1	3	1	SCI	0					
2	Sunco	1	3	1	LS1	0	0	0	0	0	0
2	Sunco	1	3	1	LS2	0	0	0	0	0	0
2	Sunco	1	3	1	LS3	0	0	0	0	0	0
2	Sunco	1	4	1	C	3					
2	Sunco	1	4	1	SCI	0					
2	Sunco	1	4	1	LS1	0	0	0	0	0	0
2	Sunco	1	4	1	LS2	0	0	0	0	0	0
2	Sunco	1	4	1	LS3	0	0	0	0	0	0
2	Sunco	1	4	1	LS4	0	0	0	0	0	0
2	Sunco	1	4	2	LS1	0	0	0	0	0	0
2	Sunco	1	4	2	LS2	0	0	0	0	0	0
2	Sunco	1	5	1	C	3					
2	Sunco	1	5	1	SCI	0					
2	Sunco	1	5	1	LS1	1	0	0	0	0	0
2	Sunco	1	5	1	LS2	0	0	0	0	0	0
2	Sunco	1	5	1	LS3	0	0	0	0	0	0
2	Sunco	1	5	1	LS4	0	0	0	0	0	0
2	Sunco	1	5	2	LS1	0	0	0	0	0	0
2	Sunco	1	5	2	LS2	0	0	0	0	0	0

2	Sunco	2	1	1	C	4					
2	Sunco	2	1	1	SCI	3					
2	Sunco	2	1	1	LS1	3	0	0	0	0	0
2	Sunco	2	1	1	LS2	2	0	0	0	0	0
2	Sunco	2	1	1	LS3	1	0	0	0	0	0
2	Sunco	2	1	1	LS4	0	0	0	0	0	0
2	Sunco	2	2	1	C	2					
2	Sunco	2	2	1	SCI	0					
2	Sunco	2	2	1	LS1	1	0	0	0	0	0
2	Sunco	2	2	1	LS2	0	0	0	0	0	0
2	Sunco	2	2	1	LS3	0	0	0	0	0	0
2	Sunco	2	2	1	LS4	0	0	0	0	0	0
2	Sunco	2	3	1	C	4					
2	Sunco	2	3	1	SCI	0					
2	Sunco	2	3	1	LS1	0	0	0	0	0	0
2	Sunco	2	3	1	LS2	0	0	0	0	0	0
2	Sunco	2	3	1	LS3	0	0	0	0	0	0
2	Sunco	2	3	1	LS4	0	0	0	0	0	0
2	Sunco	2	3	2	LS1	0	0	0	0	0	0
2	Sunco	2	3	2	LS2	0	0	0	0	0	0
2	Sunco	2	4	1	C	2					
2	Sunco	2	4	1	SCI	0					
2	Sunco	2	4	1	LS1	1	0	0	0	0	0
2	Sunco	2	4	1	LS2	0	0	0	0	0	0
2	Sunco	2	4	1	LS3	0	0	0	0	0	0
2	Sunco	2	4	1	LS4	0	0	0	0	0	0
2	Sunco	2	4	2	LS1	0	0	0	0	0	0
2	Sunco	2	4	2	LS2	0	0	0	0	0	0
2	Sunco	2	5	1	C	4					
2	Sunco	2	5	1	SCI	1					
2	Sunco	2	5	1	LS1	1	0	0	0	0	0
2	Sunco	2	5	1	LS2	0	0	0	0	0	0
2	Sunco	2	5	1	LS3	0	0	0	0	0	0
2	Sunco	2	5	1	LS4	0	0	0	0	0	0
2	Sunco	3	1	1	C	3					
2	Sunco	3	1	1	SCI	0					

2	Sunco	3	1	1	LS1	1					
2	Sunco	3	1	1	LS2	0					
2	Sunco	3	1	1	LS3	0					
2	Sunco	3	1	1	LS4	0					
2	Sunco	3	1	2	LS1	0					
2	Sunco	3	1	2	LS2	0					
2	Sunco	3	2	1	C	1					
2	Sunco	3	2	1	SCI	0					
2	Sunco	3	2	1	LS1	0					
2	Sunco	3	2	1	LS2	0					
2	Sunco	3	2	1	LS3	0					
2	Sunco	3	2	1	LS4	0					
2	Sunco	3	2	2	LS1	0					
2	Sunco	3	2	2	LS2	0					
2	Sunco	3	3	1	C	3					
2	Sunco	3	3	1	SCI	0					
2	Sunco	3	3	1	LS1	0					
2	Sunco	3	3	1	LS2	0					
2	Sunco	3	3	1	LS3	0					
2	Sunco	3	3	1	LS4	0					
2	Sunco	3	3	2	LS1	0					
2	Sunco	3	3	2	LS2	0					
2	Sunco	3	4	1	C	4					
2	Sunco	3	4	1	SCI	1					
2	Sunco	3	4	1	LS1	1					
2	Sunco	3	4	1	LS2	0					
2	Sunco	3	4	1	LS3	0					
2	Sunco	3	4	1	LS4	0					
2	Sunco	3	5	1	C	2					
2	Sunco	3	5	1	SCI	0					
2	Sunco	3	5	1	LS1	1					
2	Sunco	3	5	1	LS2	0					
2	Sunco	3	5	1	LS3	0					
2	Sunco	3	5	1	LS4	0					
2	CPI133814	1	1	1	C	4					
2	CPI133814	1	1	1	SCI	0					

2	CPI133814	1	1	1	LS1	0	0	0	0	0	0
2	CPI133814	1	1	1	LS2	0	0	0	0	0	0
2	CPI133814	1	1	1	LS3	0	0	0	0	0	0
2	CPI133814	1	2	1	C	4					
2	CPI133814	1	2	1	SCI	0					
2	CPI133814	1	2	1	LS1	0	0	0	0	0	0
2	CPI133814	1	2	1	LS2	0	0	0	0	0	0
2	CPI133814	1	2	1	LS3	0	0	0	0	0	0
2	CPI133814	1	3	1	C	3					
2	CPI133814	1	3	1	SCI	0					
2	CPI133814	1	3	1	LS1	2	0	0	0	0	0
2	CPI133814	1	3	1	LS2	1	0	0	0	0	0
2	CPI133814	1	3	1	LS3	0	0	0	0	0	0
2	CPI133814	1	4	1	C	4					
2	CPI133814	1	4	1	SCI	0					
2	CPI133814	1	4	1	LS1	0	0	0	0	0	0
2	CPI133814	1	4	1	LS2	0	0	0	0	0	0
2	CPI133814	1	4	1	LS3	0	0	0	0	0	0
2	CPI133814	1	5	1	C	4					
2	CPI133814	1	5	1	SCI	0					
2	CPI133814	1	5	1	LS1	0	2	0	1	1	0
2	CPI133814	1	5	1	LS2	0	0	0	0	0	0
2	CPI133814	1	5	1	LS3	0	0	0	0	0	0
2	CPI133814	2	1	1	C	4					
2	CPI133814	2	1	1	SCI	0					
2	CPI133814	2	1	1	LS1	1	0	0	0	0	0
2	CPI133814	2	1	1	LS2	0	0	0	0	0	0
2	CPI133814	2	1	1	LS3	0	0	0	0	0	0
2	CPI133814	2	2	1	C	4					
2	CPI133814	2	2	1	SCI	0					
2	CPI133814	2	2	1	LS1	1	0	0	0	0	0
2	CPI133814	2	2	1	LS2	0	0	0	0	0	0
2	CPI133814	2	2	1	LS3	0	0	0	0	0	0
2	CPI133814	2	3	1	C	4					
2	CPI133814	2	3	1	SCI	1					
2	CPI133814	2	3	1	LS1	0	0	0	0	0	0

2	CPI133814	2	3	1	LS2	0	0	0	0	0	0
2	CPI133814	2	3	1	LS3	0	0	0	0	0	0
2	CPI133814	2	4	1	C	3					
2	CPI133814	2	4	1	SCI	0					
2	CPI133814	2	4	1	LS1	1	0	0	0	0	0
2	CPI133814	2	4	1	LS2	0	0	0	0	0	0
2	CPI133814	2	4	1	LS3	0	0	0	0	0	0
2	CPI133814	2	4	2	LS1	0	0	0	0	0	0
2	CPI133814	2	4	2	LS2	0	0	0	0	0	0
2	CPI133814	2	5	1	C	4					
2	CPI133814	2	5	1	SCI	0					
2	CPI133814	2	5	1	LS1	0	0	0	0	0	0
2	CPI133814	2	5	1	LS2	0	0	0	0	0	0
2	CPI133814	2	5	1	LS3	0	0	0	0	0	0
2	CPI133814	2	5	2	LS1	0	0	0	0	0	0
2	CPI133814	2	5	2	LS2	0	0	0	0	0	0
2	CPI133814	3	1	1	C	4					
2	CPI133814	3	1	1	SCI	0					
2	CPI133814	3	1	1	LS1	0					
2	CPI133814	3	1	1	LS2	0					
2	CPI133814	3	1	1	LS3	0					
2	CPI133814	3	1	2	LS1	0					
2	CPI133814	3	1	2	LS2	0					
2	CPI133814	3	2	1	C	3					
2	CPI133814	3	2	1	SCI	0					
2	CPI133814	3	2	1	LS1	0					
2	CPI133814	3	2	1	LS2	0					
2	CPI133814	3	3	1	C	4					
2	CPI133814	3	3	1	LS1	1					
2	CPI133814	3	3	1	LS2	0					
2	CPI133814	3	4	1	C	3					
2	CPI133814	3	4	1	LS1	0					
2	CPI133814	3	4	1	LS2	0					
2	CPI133814	3	5	1	C	4					
2	CPI133814	3	5	1	SCI	1					
2	CPI133814	3	5	1	LS1	1					

2	CPI133814	3	5	1	LS2	0					
2	CPI133814	3	5	1	LS3	0					
2	CPI133814	3	5	2	LS1	0					
2	CPI133814	3	5	2	LS2	0					
3	Puseas	1	1	1	C	3					
3	Puseas	1	1	1	SCI	0					
3	Puseas	1	1	1	LS1	1	0	0	0	0	0
3	Puseas	1	1	1	LS2	0	0	0	0	0	0
3	Puseas	1	1	1	LS3	0	0	0	0	0	0
3	Puseas	1	1	1	LS4	0	0	0	0	0	0
3	Puseas	1	1	1	LS5	0	0	0	0	0	0
3	Puseas	1	1	2	LS1	0	0	0	0	0	0
3	Puseas	1	1	2	LS2	0	0	0	0	0	0
3	Puseas	1	1	2	LS3	0	0	0	0	0	0
3	Puseas	1	1	3	LS1	0	0	0	0	0	0
3	Puseas	1	1	3	LS2	0	0	0	0	0	0
3	Puseas	1	2	1	C	4					
3	Puseas	1	2	1	SCI	0					
3	Puseas	1	2	1	LS1	1	0	0	0	0	0
3	Puseas	1	2	1	LS2	0	0	0	0	0	0
3	Puseas	1	2	1	LS3	0	0	0	0	0	0
3	Puseas	1	2	1	LS4	0	0	0	0	0	0
3	Puseas	1	2	1	LS5	0	0	0	0	0	0
3	Puseas	1	2	2	LS1	0	0	0	0	0	0
3	Puseas	1	2	2	LS2	0	0	0	0	0	0
3	Puseas	1	2	3	LS1	0	0	0	0	0	0
3	Puseas	1	2	3	LS2	0	0	0	0	0	0
3	Puseas	1	3	1	C	4					
3	Puseas	1	3	1	SCI	0					
3	Puseas	1	3	1	LS1	1	2	2	0	0	0
3	Puseas	1	3	1	LS2	0	0	0	0	0	0
3	Puseas	1	3	1	LS3	0	0	0	0	0	0
3	Puseas	1	3	1	LS4	0	0	0	0	0	0
3	Puseas	1	3	1	LS5	0	0	0	0	0	0
3	Puseas	1	4	1	C	4					
3	Puseas	1	4	1	SCI	3					

3	Puseas	1	4	1	LS2	0	0	0	0	0	0
3	Puseas	1	4	1	LS3	0	0	0	0	0	0
3	Puseas	1	4	1	LS4	0	0	0	0	0	0
3	Puseas	1	4	1	LS5	0	0	0	0	0	0
3	Puseas	1	5	1	C	4					
3	Puseas	1	5	1	SCI	4					
3	Puseas	1	5	1	LS1	1	2	2	0	0	0
3	Puseas	1	5	1	LS2	1	5	3	2	0	0
3	Puseas	1	5	1	LS3	1	0	0	0	0	0
3	Puseas	1	5	1	LS4	0	0	0	0	0	0
3	Puseas	1	5	1	LS5	0	0	0	0	0	0
3	Puseas	1	5	2	LS1	1	1	1	0	0	0
3	Puseas	1	5	2	LS2	1	0	0	0	0	0
3	Puseas	2	1	1	C	4					
3	Puseas	2	1	1	SCI	0					
3	Puseas	2	1	1	LS1	2	0	0	0	0	0
3	Puseas	2	1	1	LS2	0	0	0	0	0	0
3	Puseas	2	1	1	LS3	0	0	0	0	0	0
3	Puseas	2	1	1	LS4	0	0	0	0	0	0
3	Puseas	2	1	1	LS5	0	0	0	0	0	0
3	Puseas	2	1	1	LS6	0	0	0	0	0	0
3	Puseas	2	1	2	LS1	0	0	0	0	0	0
3	Puseas	2	1	2	LS2	0	0	0	0	0	0
3	Puseas	2	1	2	LS3	0	0	0	0	0	0
3	Puseas	2	1	2	LS4	0	0	0	0	0	0
3	Puseas	2	1	3	LS1	0	0	0	0	0	0
3	Puseas	2	1	3	LS2	0	0	0	0	0	0
3	Puseas	2	1	3	LS3	0	0	0	0	0	0
3	Puseas	2	1	4	LS1	0	0	0	0	0	0
3	Puseas	2	1	4	LS2	0	0	0	0	0	0
3	Puseas	2	2	1	C	3					
3	Puseas	2	2	1	SCI	4					
3	Puseas	2	2	1	LS1	2	0	0	0	0	0
3	Puseas	2	2	1	LS2	1	0	0	0	0	0
3	Puseas	2	2	1	LS3	1	0	0	0	0	0
3	Puseas	2	2	1	LS4	0	0	0	0	0	0

3	Puseas	2	2	1	LS5	0	0	0	0	0	0
3	Puseas	2	2	2	LS1	2	0	0	0	0	0
3	Puseas	2	2	2	LS2	1	2	1	1	0	0
3	Puseas	2	2	2	LS3	0	0	0	0	0	0
3	Puseas	2	2	3	LS1	1	0	0	0	0	0
3	Puseas	2	2	3	LS2	1	0	0	0	0	0
3	Puseas	2	2	3	LS3	0	0	0	0	0	0
3	Puseas	2	3	1	C	4					
3	Puseas	2	3	1	SCI	4					
3	Puseas	2	3	1	LS1	1	0	0	0	0	0
3	Puseas	2	3	1	LS2	1	0	0	0	0	0
3	Puseas	2	3	1	LS3	0	0	0	0	0	0
3	Puseas	2	3	1	LS4	0	0	0	0	0	0
3	Puseas	2	3	1	LS5	0	0	0	0	0	0
3	Puseas	2	3	2	LS1	1	0	0	0	0	0
3	Puseas	2	3	2	LS2	1	0	0	0	0	0
3	Puseas	2	3	2	LS3	0	0	0	0	0	0
3	Puseas	2	3	3	LS1	0	0	0	0	0	0
3	Puseas	2	3	3	LS2	0	0	0	0	0	0
3	Puseas	2	4	1	C	4					
3	Puseas	2	4	1	SCI	0					
3	Puseas	2	4	1	LS1	1	0	0	0	0	0
3	Puseas	2	4	1	LS2	1	0	0	0	0	0
3	Puseas	2	4	1	LS3	0	0	0	0	0	0
3	Puseas	2	4	1	LS4	0	0	0	0	0	0
3	Puseas	2	4	1	LS5	0	0	0	0	0	0
3	Puseas	2	4	2	LS1	0	0	0	0	0	0
3	Puseas	2	4	2	LS2	0	0	0	0	0	0
3	Puseas	2	4	2	LS3	0	0	0	0	0	0
3	Puseas	2	4	2	LS4	0	0	0	0	0	0
3	Puseas	2	4	3	LS1	0	0	0	0	0	0
3	Puseas	2	4	3	LS2	0	0	0	0	0	0
3	Puseas	2	4	3	LS3	0	0	0	0	0	0
3	Puseas	2	4	4	LS1	0	0	0	0	0	0
3	Puseas	2	4	4	LS2	0	0	0	0	0	0
3	Puseas	2	5	1	C	4					

3	Puseas	2	5	1	SCI	4					
3	Puseas	2	5	1	LS1	2	5	3	2	0	0
3	Puseas	2	5	1	LS2	1	2	2	0	0	0
3	Puseas	2	5	1	LS3	1	3	2	1	0	0
3	Puseas	2	5	1	LS4	1	0	0	0	0	0
3	Puseas	2	5	1	LS5	0	0	0	0	0	0
3	Puseas	3	1	1	C	4					
3	Puseas	3	1	1	SCI	2					
3	Puseas	3	1	1	LS1	2					
3	Puseas	3	1	1	LS2	0					
3	Puseas	3	1	1	LS3	0					
3	Puseas	3	1	1	LS4	0					
3	Puseas	3	1	1	LS5	0					
3	Puseas	3	1	2	LS1	1					
3	Puseas	3	1	2	LS2	0					
3	Puseas	3	1	2	LS3	0					
3	Puseas	3	1	3	LS1	0					
3	Puseas	3	1	3	LS2	0					
3	Puseas	3	2	1	C	3					
3	Puseas	3	2	1	SCI	1					
3	Puseas	3	2	1	LS1	1					
3	Puseas	3	2	1	LS2	0					
3	Puseas	3	2	1	LS3	0					
3	Puseas	3	2	1	LS4	0					
3	Puseas	3	2	1	LS5	0					
3	Puseas	3	3	1	C	2					
3	Puseas	3	3	1	SCI	1					
3	Puseas	3	3	1	LS1	0					
3	Puseas	3	3	1	LS2	0					
3	Puseas	3	3	1	LS3	0					
3	Puseas	3	3	1	LS4	0					
3	Puseas	3	3	1	LS5	0					
3	Puseas	3	4	1	C	4					
3	Puseas	3	4	1	SCI	0					
3	Puseas	3	4	1	LS1	1					
3	Puseas	3	4	1	LS2	0					

3	Puseas	3	4	1	LS3	0					
3	Puseas	3	4	1	LS4	0					
3	Puseas	3	5	1	C	4					
3	Puseas	3	5	1	LS1	1					
3	Puseas	3	5	1	LS2	0					
3	Puseas	3	5	1	LS3	0					
3	Puseas	3	5	1	LS4	0					
3	Puseas	3	5	2	LS1	0					
3	Puseas	3	5	2	LS2	0					
3	Puseas	3	5	2	LS3	0					
3	Puseas	3	5	3	LS1	0					
3	Puseas	3	5	3	LS2	0					
3	Vasco	1	1	1	C	4					
3	Vasco	1	1	1	SCI	3					
3	Vasco	1	1	1	LS1	1	0	0	0	0	0
3	Vasco	1	1	1	LS2	0	0	0	0	0	0
3	Vasco	1	1	1	LS3	0	0	0	0	0	0
3	Vasco	1	1	1	LS4	0	0	0	0	0	0
3	Vasco	1	2	1	C	4					
3	Vasco	1	2	1	SCI	0					
3	Vasco	1	2	1	LS1	1	2	2	0	0	0
3	Vasco	1	2	1	LS2	0	0	0	0	0	0
3	Vasco	1	2	1	LS3	0	0	0	0	0	0
3	Vasco	1	2	1	LS4	0	0	0	0	0	0
3	Vasco	1	2	2	LS1	0	0	0	0	0	0
3	Vasco	1	2	2	LS2	0	0	0	0	0	0
3	Vasco	1	2	2	LS3	0	0	0	0	0	0
3	Vasco	1	2	3	LS1	0	0	0	0	0	0
3	Vasco	1	2	3	LS2	0	0	0	0	0	0
3	Vasco	1	3	1	C	4					
3	Vasco	1	3	1	SCI	1					
3	Vasco	1	3	1	LS1	1	0	0	0	0	0
3	Vasco	1	3	1	LS2	0	0	0	0	0	0
3	Vasco	1	3	1	LS3	0	0	0	0	0	0
3	Vasco	1	3	1	LS4	0	0	0	0	0	0
3	Vasco	1	3	1	LS5	0	0	0	0	0	0

3	Vasco	1	4	1	C	3					
3	Vasco	1	4	1	SCI	2					
3	Vasco	1	4	1	LS1	1	0	0	0	0	0
3	Vasco	1	4	1	LS2	0	0	0	0	0	0
3	Vasco	1	4	1	LS3	0	0	0	0	0	0
3	Vasco	1	4	1	LS4	0	0	0	0	0	0
3	Vasco	1	4	1	LS5	0	0	0	0	0	0
3	Vasco	1	4	2	LS1	0	0	0	0	0	0
3	Vasco	1	4	2	LS2	0	0	0	0	0	0
3	Vasco	1	4	2	LS3	0	0	0	0	0	0
3	Vasco	1	4	3	LS1	0	0	0	0	0	0
3	Vasco	1	4	3	LS2	0	0	0	0	0	0
3	Vasco	1	5	1	C	4					
3	Vasco	1	5	1	SCI	0					
3	Vasco	1	5	1	LS1	1	0	0	0	0	0
3	Vasco	1	5	1	LS2	1	0	0	0	0	0
3	Vasco	1	5	1	LS3	0	0	0	0	0	0
3	Vasco	1	5	1	LS4	0	0	0	0	0	0
3	Vasco	1	5	1	LS5	0	0	0	0	0	0
3	Vasco	1	5	2	LS1	0	0	0	0	0	0
3	Vasco	1	5	2	LS2	0	0	0	0	0	0
3	Vasco	1	5	2	LS3	0	0	0	0	0	0
3	Vasco	1	5	3	LS1	0	0	0	0	0	0
3	Vasco	1	5	3	LS2	0	0	0	0	0	0
3	Vasco	2	1	1	C	4					
3	Vasco	2	1	1	SCI	0					
3	Vasco	2	1	1	LS1	1	1	1	0	0	0
3	Vasco	2	1	1	LS2	0	0	0	0	0	0
3	Vasco	2	1	1	LS3	0	0	0	0	0	0
3	Vasco	2	1	1	LS4	0	0	0	0	0	0
3	Vasco	2	1	1	LS5	0	0	0	0	0	0
3	Vasco	2	1	2	LS1	0	0	0	0	0	0
3	Vasco	2	1	2	LS2	0	0	0	0	0	0
3	Vasco	2	1	2	LS3	0	0	0	0	0	0
3	Vasco	2	1	3	LS1	0	0	0	0	0	0
3	Vasco	2	1	3	LS2	0	0	0	0	0	0

3	Vasco	2	2	1	C	4					
3	Vasco	2	2	1	SCI	1					
3	Vasco	2	2	1	LS1	4	9	4	4	1	0
3	Vasco	2	2	1	LS2	1	2	2	0	0	0
3	Vasco	2	2	1	LS3	0	0	0	0	0	0
3	Vasco	2	2	1	LS4	0	0	0	0	0	0
3	Vasco	2	2	1	LS5	0	0	0	0	0	0
3	Vasco	2	3	1	C	4					
3	Vasco	2	3	1	SCI	2					
3	Vasco	2	3	1	LS1	1	2	2	0	0	0
3	Vasco	2	3	1	LS2	0	0	0	0	0	0
3	Vasco	2	3	1	LS3	0	0	0	0	0	0
3	Vasco	2	3	1	LS4	0	0	0	0	0	0
3	Vasco	2	3	1	LS5	0	0	0	0	0	0
3	Vasco	2	4	1	C	2					
3	Vasco	2	4	1	SCI	0					
3	Vasco	2	4	1	LS1	1	0	0	0	0	0
3	Vasco	2	4	1	LS2	1	0	0	0	0	0
3	Vasco	2	4	1	LS3	0	0	0	0	0	0
3	Vasco	2	4	1	LS4	0	0	0	0	0	0
3	Vasco	2	4	1	LS5	0	0	0	0	0	0
3	Vasco	2	5	1	C	4					
3	Vasco	2	5	1	SCI	3					
3	Vasco	2	5	1	LS1	1	4	3	1	0	0
3	Vasco	2	5	1	LS2	1	0	0	0	0	0
3	Vasco	2	5	1	LS3	0	0	0	0	0	0
3	Vasco	2	5	1	LS4	0	0	0	0	0	0
3	Vasco	2	5	1	LS5	0	0	0	0	0	0
3	Vasco	2	5	2	LS1	0	0	0	0	0	0
3	Vasco	2	5	2	LS2	0	0	0	0	0	0
3	Vasco	2	5	2	LS3	0	0	0	0	0	0
3	Vasco	2	5	3	LS1	0	0	0	0	0	0
3	Vasco	2	5	3	LS2	0	0	0	0	0	0
3	Vasco	3	1	1	C	4					
3	Vasco	3	1	1	SCI	0					
3	Vasco	3	1	1	LS1	1					

3	Vasco	3	1	1	LS2	0					
3	Vasco	3	1	1	LS3	0					
3	Vasco	3	1	1	LS4	0					
3	Vasco	3	2	1	C	3					
3	Vasco	3	2	1	SCI	0					
3	Vasco	3	2	1	LS1	2					
3	Vasco	3	2	1	LS2	1					
3	Vasco	3	2	1	LS3	1					
3	Vasco	3	2	1	LS4	0					
3	Vasco	3	3	1	C	4					
3	Vasco	3	3	1	SCI	0					
3	Vasco	3	3	1	LS1	1					
3	Vasco	3	3	1	LS2	0					
3	Vasco	3	3	1	LS3	0					
3	Vasco	3	3	1	LS4	0					
3	Vasco	3	3	1	LS5	0					
3	Vasco	3	4	1	C	4					
3	Vasco	3	4	1	SCI	1					
3	Vasco	3	4	1	LS1	2					
3	Vasco	3	4	1	LS2	1					
3	Vasco	3	4	1	LS3	0					
3	Vasco	3	4	1	LS4	0					
3	Vasco	3	5	1	C	4					
3	Vasco	3	5	1	SCI	4					
3	Vasco	3	5	1	LS1	4					
3	Vasco	3	5	1	LS2	1					
3	Vasco	3	5	1	LS3	1					
3	Vasco	3	5	1	LS4	0					
3	Vasco	3	5	1	LS1	0					
3	2-49	1	1	1	C	4					
3	2-49	1	1	1	SCI	1					
3	2-49	1	1	1	LS1	0	0	0	0	0	0
3	2-49	1	1	1	LS2	0	0	0	0	0	0
3	2-49	1	1	1	LS3	0	0	0	0	0	0
3	2-49	1	1	1	LS4	0	0	0	0	0	0
3	2-49	1	1	1	LS5	0	0	0	0	0	0

3	2-49	1	1	2	LS1	0	0	0	0	0	0
3	2-49	1	1	2	LS2	0	0	0	0	0	0
3	2-49	1	2	1	C	3					
3	2-49	1	2	1	SCI	0					
3	2-49	1	2	1	LS1	0	0	0	0	0	0
3	2-49	1	2	1	LS2	0	0	0	0	0	0
3	2-49	1	2	1	LS3	0	0	0	0	0	0
3	2-49	1	2	1	LS4	0	0	0	0	0	0
3	2-49	1	2	1	LS5	0	0	0	0	0	0
3	2-49	1	2	2	LS1	0	0	0	0	0	0
3	2-49	1	2	2	LS2	0	0	0	0	0	0
3	2-49	1	3	1	C	4					
3	2-49	1	3	1	SCI	0					
3	2-49	1	3	1	LS1	1	2	2	0	0	0
3	2-49	1	3	1	LS2	0	0	0	0	0	0
3	2-49	1	3	1	LS3	0	0	0	0	0	0
3	2-49	1	3	1	LS4	0	0	0	0	0	0
3	2-49	1	3	1	LS5	0	0	0	0	0	0
3	2-49	1	4	1	C	4					
3	2-49	1	4	1	SCI	0					
3	2-49	1	4	1	LS1	0	0	0	0	0	0
3	2-49	1	4	1	LS2	0	0	0	0	0	0
3	2-49	1	4	1	LS3	0	0	0	0	0	0
3	2-49	1	4	1	LS4	0	0	0	0	0	0
3	2-49	1	4	1	LS5	0	0	0	0	0	0
3	2-49	1	4	2	LS1	0	0	0	0	0	0
3	2-49	1	4	2	LS2	0	0	0	0	0	0
3	2-49	1	5	1	C	4					
3	2-49	1	5	1	SCI	1					
3	2-49	1	5	1	LS1	2	9	3	2	2	2
3	2-49	1	5	1	LS2	1	0	0	0	0	0
3	2-49	1	5	1	LS3	1	0	0	0	0	0
3	2-49	1	5	1	LS4	0	0	0	0	0	0
3	2-49	1	5	1	LS5	0	0	0	0	0	0
3	2-49	1	5	2	LS1	3	0	0	0	0	0
3	2-49	1	5	2	LS2	1	0	0	0	0	0

3	2-49	1	5	2	LS3	0	0	0	0	0	0
3	2-49	1	5	2	LS4	0	0	0	0	0	0
3	2-49	1	5	3	LS1	0	0	0	0	0	0
3	2-49	1	5	3	LS2	0	0	0	0	0	0
3	2-49	1	5	3	LS3	0	0	0	0	0	0
3	2-49	1	5	4	LS1	0	0	0	0	0	0
3	2-49	1	5	4	LS2	0	0	0	0	0	0
3	2-49	2	1	1	C	4					
3	2-49	2	1	1	SCI	0					
3	2-49	2	1	1	LS1	1	0	0	0	0	0
3	2-49	2	1	1	LS2	0	0	0	0	0	0
3	2-49	2	1	1	LS3	0	0	0	0	0	0
3	2-49	2	1	1	LS4	0	0	0	0	0	0
3	2-49	2	1	1	LS5	0	0	0	0	0	0
3	2-49	2	1	2	LS1	1	0	0	0	0	0
3	2-49	2	1	2	LS2	0	0	0	0	0	0
3	2-49	2	1	2	LS3	0	0	0	0	0	0
3	2-49	2	1	3	LS1	0	0	0	0	0	0
3	2-49	2	1	3	LS2	0	0	0	0	0	0
3	2-49	2	2	1	C	4					
3	2-49	2	2	1	SCI	0					
3	2-49	2	2	1	LS1	1	0	0	0	0	0
3	2-49	2	2	1	LS2	0	0	0	0	0	0
3	2-49	2	2	1	LS3	0	0	0	0	0	0
3	2-49	2	2	1	LS4	0	0	0	0	0	0
3	2-49	2	3	1	C	4					
3	2-49	2	3	1	SCI	1					
3	2-49	2	3	1	LS1	2	0	0	0	0	0
3	2-49	2	3	1	LS2	0	0	0	0	0	0
3	2-49	2	3	1	LS3	0	0	0	0	0	0
3	2-49	2	3	1	LS4	0	0	0	0	0	0
3	2-49	2	3	1	LS5	0	0	0	0	0	0
3	2-49	2	4	1	C	3					
3	2-49	2	4	1	SCI	0					
3	2-49	2	4	1	LS1	1	0	0	0	0	0
3	2-49	2	4	1	LS2	0	0	0	0	0	0

3	2-49	2	4	1	LS3	0	0	0	0	0	0
3	2-49	2	4	1	LS4	0	0	0	0	0	0
3	2-49	2	4	1	LS5	0	0	0	0	0	0
3	2-49	2	4	2	LS1	2	0	0	0	0	0
3	2-49	2	4	2	LS2	0	0	0	0	0	0
3	2-49	2	4	2	LS3	0	0	0	0	0	0
3	2-49	2	4	3	LS1	0	0	0	0	0	0
3	2-49	2	4	3	LS2	0	0	0	0	0	0
3	2-49	2	5	1	C	3					
3	2-49	2	5	1	SCI	0					
3	2-49	2	5	1	LS1	1	0	0	0	0	0
3	2-49	2	5	1	LS2	0	0	0	0	0	0
3	2-49	2	5	1	LS3	0	0	0	0	0	0
3	2-49	2	5	1	LS4	0	0	0	0	0	0
3	2-49	2	5	1	LS5	0	0	0	0	0	0
3	2-49	2	5	2	LS1	1	0	0	0	0	0
3	2-49	2	5	2	LS2	0	0	0	0	0	0
3	2-49	2	5	2	LS3	0	0	0	0	0	0
3	2-49	2	5	3	LS1	0	0	0	0	0	0
3	2-49	2	5	3	LS2	0	0	0	0	0	0
3	2-49	3	1	1	C	4					
3	2-49	3	1	1	SCI	0					
3	2-49	3	1	1	LS1	4					
3	2-49	3	1	1	LS2	1					
3	2-49	3	1	1	LS3	0					
3	2-49	3	1	1	LS4	0					
3	2-49	3	1	1	LS5	0					
3	2-49	3	1	2	LS1	1					
3	2-49	3	1	2	LS2	0					
3	2-49	3	1	2	LS3	0					
3	2-49	3	2	1	C	4					
3	2-49	3	2	1	SCI	1					
3	2-49	3	2	1	LS1	1					
3	2-49	3	2	1	LS2	0					
3	2-49	3	2	1	LS3	0					
3	2-49	3	2	1	LS4	0					

3	2-49	3	2	1	LS5	0					
3	2-49	3	3	1	C	4					
3	2-49	3	3	1	SCI	0					
3	2-49	3	3	1	LS1	0					
3	2-49	3	3	1	LS2	0					
3	2-49	3	3	1	LS3	0					
3	2-49	3	3	1	LS4	0					
3	2-49	3	3	1	LS5	0					
3	2-49	3	3	2	LS1	0					
3	2-49	3	3	2	LS2	0					
3	2-49	3	3	2	LS3	0					
3	2-49	3	3	3	LS1	0					
3	2-49	3	3	3	LS2	0					
3	2-49	3	4	1	C	3					
3	2-49	3	4	1	SCI	1					
3	2-49	3	4	1	LS1	1					
3	2-49	3	4	1	LS2	0					
3	2-49	3	4	1	LS3	0					
3	2-49	3	4	1	LS4	0					
3	2-49	3	4	1	LS5	0					
3	2-49	3	4	2	LS1	0					
3	2-49	3	4	2	LS2	0					
3	2-49	3	5	1	C	4					
3	2-49	3	5	1	SCI	0					
3	2-49	3	5	1	LS1	1					
3	2-49	3	5	1	LS2	0					
3	2-49	3	5	1	LS3	0					
3	2-49	3	5	1	LS4	0					
3	2-49	3	5	2	LS1	0					
3	2-49	3	5	2	LS2	0					
3	2-49	3	5	2	LS3	0					
3	2-49	3	5	3	LS1	0					
3	2-49	3	5	3	LS2	0					
3	Sunco	1	1	1	C	1					
3	Sunco	1	1	1	SCI	0					
3	Sunco	1	1	1	LS1	0	0	0	0	0	0

3	Sunco	1	1	1	LS2	0	0	0	0	0	0
3	Sunco	1	1	1	LS3	0	0	0	0	0	0
3	Sunco	1	1	1	LS4	0	0	0	0	0	0
3	Sunco	1	2	1	C	3					
3	Sunco	1	2	1	SCI	0					
3	Sunco	1	2	1	LS1	2	2	0	1	1	0
3	Sunco	1	2	1	LS2	0	0	0	0	0	0
3	Sunco	1	2	1	LS3	0	0	0	0	0	0
3	Sunco	1	2	1	LS4	0	0	0	0	0	0
3	Sunco	1	2	1	LS5	0	0	0	0	0	0
3	Sunco	1	2	2	LS1	0	0	0	0	0	0
3	Sunco	1	2	2	LS2	0	0	0	0	0	0
3	Sunco	1	2	2	LS3	0	0	0	0	0	0
3	Sunco	1	3	1	C	3					
3	Sunco	1	3	1	SCI	0					
3	Sunco	1	3	1	LS1	1	0	0	0	0	0
3	Sunco	1	3	1	LS2	0	0	0	0	0	0
3	Sunco	1	3	1	LS3	0	0	0	0	0	0
3	Sunco	1	3	1	LS4	0					
3	Sunco	1	4	1	C	4					
3	Sunco	1	4	1	SCI	4					
3	Sunco	1	4	1	LS1	1	0	0	0	0	0
3	Sunco	1	4	1	LS2	0	0	0	0	0	0
3	Sunco	1	4	1	LS3	0	0	0	0	0	0
3	Sunco	1	4	1	LS4	0	0	0	0	0	0
3	Sunco	1	4	1	LS5	0	0	0	0	0	0
3	Sunco	1	4	2	LS1	0	0	0	0	0	0
3	Sunco	1	4	2	LS2	0	0	0	0	0	0
3	Sunco	1	4	2	LS3	0	0	0	0	0	0
3	Sunco	1	5	1	C	2					
3	Sunco	1	5	1	SCI	0					
3	Sunco	1	5	1	LS1	1	0	0	0	0	0
3	Sunco	1	5	1	LS2	0	0	0	0	0	0
3	Sunco	1	5	1	LS3	0	0	0	0	0	0
3	Sunco	1	5	1	LS4	0	0	0	0	0	0
3	Sunco	1	5	1	LS5	0	0	0	0	0	0

3	Sunco	2	1	1	C	3					
3	Sunco	2	1	1	SCI	0					
3	Sunco	2	1	1	LS1	1	0	0	0	0	0
3	Sunco	2	1	1	LS2	0	0	0	0	0	0
3	Sunco	2	1	1	LS3	0	0	0	0	0	0
3	Sunco	2	1	1	LS4	0	0	0	0	0	0
3	Sunco	2	1	1	LS5	0	0	0	0	0	0
3	Sunco	2	1	2	LS1	0	0	0	0	0	0
3	Sunco	2	1	2	LS2	0	0	0	0	0	0
3	Sunco	2	1	2	LS3	0	0	0	0	0	0
3	Sunco	2	1	3	LS1	0	0	0	0	0	0
3	Sunco	2	1	3	LS2	0	0	0	0	0	0
3	Sunco	2	2	1	C	4					
3	Sunco	2	2	1	SCI	0					
3	Sunco	2	2	1	LS1	2	0	0	0	0	0
3	Sunco	2	2	1	LS2	0	0	0	0	0	0
3	Sunco	2	2	1	LS3	0	0	0	0	0	0
3	Sunco	2	2	1	LS4	0	0	0	0	0	0
3	Sunco	2	2	1	LS5	0	0	0	0	0	0
3	Sunco	2	2	2	LS1	0	0	0	0	0	0
3	Sunco	2	2	2	LS2	0	0	0	0	0	0
3	Sunco	2	2	2	LS3	0	0	0	0	0	0
3	Sunco	2	3	1	C	3					
3	Sunco	2	3	1	SCI	0					
3	Sunco	2	3	1	LS1	1	2	2	0	0	0
3	Sunco	2	3	1	LS2	0	0	0	0	0	0
3	Sunco	2	3	1	LS3	0	0	0	0	0	0
3	Sunco	2	3	1	LS4	0	0	0	0	0	0
3	Sunco	2	3	1	LS5	0	0	0	0	0	0
3	Sunco	2	3	2	LS1	0	0	0	0	0	0
3	Sunco	2	3	2	LS2	0	0	0	0	0	0
3	Sunco	2	3	2	LS3	0	0	0	0	0	0
3	Sunco	2	3	3	LS1	0	0	0	0	0	0
3	Sunco	2	3	3	LS2	0	0	0	0	0	0
3	Sunco	2	4	1	C	4					
3	Sunco	2	4	1	SCI	0					

3	Sunco	2	4	1	LS1	1	0	0	0	0	0
3	Sunco	2	4	1	LS2	0	0	0	0	0	0
3	Sunco	2	4	1	LS3	0	0	0	0	0	0
3	Sunco	2	4	1	LS4	0	0	0	0	0	0
3	Sunco	2	4	1	LS5	0	0	0	0	0	0
3	Sunco	2	5	1	C	2					
3	Sunco	2	5	1	SCI	0					
3	Sunco	2	5	1	LS1	0	0	0	0	0	0
3	Sunco	2	5	1	LS2	0	0	0	0	0	0
3	Sunco	2	5	1	LS3	0	0	0	0	0	0
3	Sunco	2	5	1	LS4	0	0	0	0	0	0
3	Sunco	2	5	1	LS5	0	0	0	0	0	0
3	Sunco	3	1	1	C	2					
3	Sunco	3	1	1	SCI	0					
3	Sunco	3	1	1	LS1	1					
3	Sunco	3	1	1	LS2	0					
3	Sunco	3	1	1	LS3	0					
3	Sunco	3	1	1	LS4	0					
3	Sunco	3	1	1	LS5	0					
3	Sunco	3	1	2	LS1	0					
3	Sunco	3	1	2	LS2	0					
3	Sunco	3	2	1	C	4					
3	Sunco	3	2	1	SCI	3					
3	Sunco	3	2	1	LS1	3					
3	Sunco	3	2	1	LS2	1					
3	Sunco	3	2	1	LS3	0					
3	Sunco	3	2	1	LS4	0					
3	Sunco	3	2	1	LS5	0					
3	Sunco	3	3	1	C	4					
3	Sunco	3	3	1	SCI	4					
3	Sunco	3	3	1	LS1	4					
3	Sunco	3	3	1	LS2	4					
3	Sunco	3	3	1	LS3	0					
3	Sunco	3	3	1	LS4	0					
3	Sunco	3	3	1	LS5	0					
3	Sunco	3	4	1	C	3					

3	Sunco	3	4	1	SCI	0					
3	Sunco	3	4	1	LS1	0					
3	Sunco	3	4	1	LS2	0					
3	Sunco	3	4	1	LS3	0					
3	Sunco	3	4	1	LS4	0					
3	Sunco	3	5	1	C	3					
3	Sunco	3	5	1	SCI	0					
3	Sunco	3	5	1	LS1	1					
3	Sunco	3	5	1	LS2	0					
3	Sunco	3	5	1	LS3	0					
3	Sunco	3	5	1	LS4	0					
3	Sunco	3	5	1	LS5	0					
3	CPI133814	1	1	1	C	4					
3	CPI133814	1	1	1	SCI	0					
3	CPI133814	1	1	1	LS1	0	0	0	0	0	0
3	CPI133814	1	1	1	LS2	0	0	0	0	0	0
3	CPI133814	1	1	1	LS3	0	0	0	0	0	0
3	CPI133814	1	1	1	LS4	0	0	0	0	0	0
3	CPI133814	1	1	1	LS5	0	0	0	0	0	0
3	CPI133814	1	1	2	LS1	0	0	0	0	0	0
3	CPI133814	1	1	2	LS2	0	0	0	0	0	0
3	CPI133814	1	1	2	LS3	0	0	0	0	0	0
3	CPI133814	1	1	3	LS1	0	0	0	0	0	0
3	CPI133814	1	1	3	LS2	0	0	0	0	0	0
3	CPI133814	1	2	1	C	4					
3	CPI133814	1	2	1	SCI	0					
3	CPI133814	1	2	1	LS1	0	0	0	0	0	0
3	CPI133814	1	2	1	LS2	0	0	0	0	0	0
3	CPI133814	1	2	1	LS3	0	0	0	0	0	0
3	CPI133814	1	3	1	C	4					
3	CPI133814	1	3	1	SCI	0					
3	CPI133814	1	3	1	LS1	0	0	0	0	0	0
3	CPI133814	1	3	1	LS2	0	0	0	0	0	0
3	CPI133814	1	3	1	LS3	0	0	0	0	0	0
3	CPI133814	1	3	1	LS4	0	0	0	0	0	0
3	CPI133814	1	3	2	LS1	0	0	0	0	0	0

3	CPI133814	1	3	2	LS2	0	0	0	0	0	0
3	CPI133814	1	4	1	C	4					
3	CPI133814	1	4	1	SCI	0					
3	CPI133814	1	4	1	LS1	0	0	0	0	0	0
3	CPI133814	1	4	1	LS2	0	0	0	0	0	0
3	CPI133814	1	4	1	LS3	0	0	0	0	0	0
3	CPI133814	1	4	1	LS4	0	0	0	0	0	0
3	CPI133814	1	4	2	LS1	0	0	0	0	0	0
3	CPI133814	1	4	2	LS2	0	0	0	0	0	0
3	CPI133814	1	5	1	C	4					
3	CPI133814	1	5	1	SCI	1					
3	CPI133814	1	5	1	LS1	1	0	0	0	0	0
3	CPI133814	1	5	1	LS2	0	0	0	0	0	0
3	CPI133814	1	5	1	LS3	0	0	0	0	0	0
3	CPI133814	1	5	1	LS4	0	0	0	0	0	0
3	CPI133814	1	5	1	LS5	0	0	0	0	0	0
3	CPI133814	1	5	2	LS1	1	0	0	0	0	0
3	CPI133814	1	5	2	LS2	0	0	0	0	0	0
3	CPI133814	1	5	2	LS3	0	0	0	0	0	0
3	CPI133814	1	5	3	LS1	0	0	0	0	0	0
3	CPI133814	1	5	3	LS2	0	0	0	0	0	0
3	CPI133814	2	1	1	C	4					
3	CPI133814	2	1	1	SCI	0					
3	CPI133814	2	1	1	LS1	0	0	0	0	0	0
3	CPI133814	2	1	1	LS2	0	0	0	0	0	0
3	CPI133814	2	1	1	LS3	0	0	0	0	0	0
3	CPI133814	2	1	1	LS4	0	0	0	0	0	0
3	CPI133814	2	1	2	LS1	0	0	0	0	0	0
3	CPI133814	2	1	2	LS2	0	0	0	0	0	0
3	CPI133814	2	1	2	LS3	0	0	0	0	0	0
3	CPI133814	2	1	3	LS1	0	0	0	0	0	0
3	CPI133814	2	1	3	LS2	0	0	0	0	0	0
3	CPI133814	2	2	1	C	4					
3	CPI133814	2	2	1	SCI	0					
3	CPI133814	2	2	1	LS1	0	0	0	0	0	0
3	CPI133814	2	2	1	LS2	0	0	0	0	0	0

3	CPI133814	2	2	1	LS3	0	0	0	0	0	0
3	CPI133814	2	2	1	LS4	0	0	0	0	0	0
3	CPI133814	2	3	1	C	3					
3	CPI133814	2	3	1	SCI	0					
3	CPI133814	2	3	1	LS1	1	0	0	0	0	0
3	CPI133814	2	3	1	LS2	0	0	0	0	0	0
3	CPI133814	2	3	1	LS3	0	0	0	0	0	0
3	CPI133814	2	3	1	LS4	0	0	0	0	0	0
3	CPI133814	2	3	1	LS5	0	0	0	0	0	0
3	CPI133814	2	3	2	LS1	0	0	0	0	0	0
3	CPI133814	2	3	2	LS2	0	0	0	0	0	0
3	CPI133814	2	3	2	LS3	0	0	0	0	0	0
3	CPI133814	2	3	3	LS1	0	0	0	0	0	0
3	CPI133814	2	3	3	LS2	0	0	0	0	0	0
3	CPI133814	2	4	1	C	4					
3	CPI133814	2	4	1	SCI	0					
3	CPI133814	2	4	1	LS1	1	6	2	2	1	1
3	CPI133814	2	4	1	LS2	1	2	1	1	0	0
3	CPI133814	2	4	1	LS3	0	0	0	0	0	0
3	CPI133814	2	4	1	LS4	0	0	0	0	0	0
3	CPI133814	2	4	1	LS5	0	0	0	0	0	0
3	CPI133814	2	4	2	LS1	1	0	0	0	0	0
3	CPI133814	2	4	2	LS2	0	0	0	0	0	0
3	CPI133814	2	4	2	LS3	0	0	0	0	0	0
3	CPI133814	2	4	3	LS1	0	0	0	0	0	0
3	CPI133814	2	4	3	LS2	0	0	0	0	0	0
3	CPI133814	2	5	1	C	4					
3	CPI133814	2	5	1	SCI	0					
3	CPI133814	2	5	1	LS1	0	0	0	0	0	0
3	CPI133814	2	5	1	LS2	0	0	0	0	0	0
3	CPI133814	2	5	1	LS3	0	0	0	0	0	0
3	CPI133814	2	5	1	LS4	0	0	0	0	0	0
3	CPI133814	2	5	1	LS5	0	0	0	0	0	0
3	CPI133814	2	5	2	LS1	0	0	0	0	0	0
3	CPI133814	2	5	2	LS2	0	0	0	0	0	0
3	CPI133814	2	5	2	LS3	0	0	0	0	0	0

3	CPI133814	2	5	3	LS1	0	0	0	0	0	0
3	CPI133814	2	5	3	LS2	0	0	0	0	0	0
3	CPI133814	3	1	1	C	4					
3	CPI133814	3	1	1	SCI	0					
3	CPI133814	3	1	1	LS1	2					
3	CPI133814	3	1	1	LS2	0					
3	CPI133814	3	1	1	LS3	0					
3	CPI133814	3	1	1	LS4	0					
3	CPI133814	3	1	2	LS1	1					
3	CPI133814	3	1	2	LS2	0					
3	CPI133814	3	1	3	LS1	0					
3	CPI133814	3	1	3	LS2	0					
3	CPI133814	3	2	1	C	4					
3	CPI133814	3	2	1	SCI	0					
3	CPI133814	3	2	1	LS1	1					
3	CPI133814	3	2	1	LS2	0					
3	CPI133814	3	2	1	LS3	0					
3	CPI133814	3	2	1	LS4	0					
3	CPI133814	3	2	2	LS1	0					
3	CPI133814	3	2	2	LS2	0					
3	CPI133814	3	3	1	C	4					
3	CPI133814	3	3	1	SCI	0					
3	CPI133814	3	3	1	LS1	0					
3	CPI133814	3	3	1	LS2	0					
3	CPI133814	3	3	1	LS3	0					
3	CPI133814	3	3	1	LS4	0					
3	CPI133814	3	4	1	C	3					
3	CPI133814	3	4	1	SCI	0					
3	CPI133814	3	4	1	LS1	0					
3	CPI133814	3	4	1	LS2	0					
3	CPI133814	3	4	1	LS3	0					
3	CPI133814	3	4	2	LS1	0					
3	CPI133814	3	4	2	LS2	0					
3	CPI133814	3	5	1	C	4					
3	CPI133814	3	5	1	SCI	0					
3	CPI133814	3	5	1	LS1	1					

3	CPI133814	3	5	1	LS2	0					
3	CPI133814	3	5	1	LS3	0					
3	CPI133814	3	5	1	LS4	0					
4	Puseas	1	1	1	SCI	2					
4	Puseas	1	1	1	LS1	0	0	0	0	0	0
4	Puseas	1	1	1	LS2	0	0	0	0	0	0
4	Puseas	1	1	1	LS3	0	0	0	0	0	0
4	Puseas	1	1	1	LS4	0	0	0	0	0	0
4	Puseas	1	1	1	LS5	0	0	0	0	0	0
4	Puseas	1	1	1	I1	0	0	0	0	0	0
4	Puseas	1	1	1	I2	0	0	0	0	0	0
4	Puseas	1	2	1	SCI	1					
4	Puseas	1	2	1	LS1	1	4	2	1	1	0
4	Puseas	1	2	1	LS2	0	0	0	0	0	0
4	Puseas	1	2	1	LS3	0	0	0	0	0	0
4	Puseas	1	2	1	LS4	0	0	0	0	0	0
4	Puseas	1	2	1	LS5	0	0	0	0	0	0
4	Puseas	1	2	1	LS6	0	0	0	0	0	0
4	Puseas	1	2	1	I1	0	0	0	0	0	0
4	Puseas	1	3	1	SCI	0					
4	Puseas	1	3	1	LS1	1	3	0	1	1	1
4	Puseas	1	3	1	LS2	0	0	0	0	0	0
4	Puseas	1	3	1	LS3	0	0	0	0	0	0
4	Puseas	1	3	1	LS4	0	0	0	0	0	0
4	Puseas	1	3	1	LS5	0	0	0	0	0	0
4	Puseas	1	3	1	LS6	0	0	0	0	0	0
4	Puseas	1	3	1	I1	0	0	0	0	0	0
4	Puseas	1	3	2	LS1	0	0	0	0	0	0
4	Puseas	1	3	2	LS2	0	0	0	0	0	0
4	Puseas	1	3	2	LS3	0	0	0	0	0	0
4	Puseas	1	3	3	LS1	0	0	0	0	0	0
4	Puseas	1	3	3	LS2	0	0	0	0	0	0
4	Puseas	1	4	1	SCI	4					
4	Puseas	1	4	1	LS1	3	6	2	2	2	0
4	Puseas	1	4	1	LS2	2	6	3	1	2	0
4	Puseas	1	4	1	LS3	1	6	3	2	1	0

4	Puseas	1	4	1	LS4	1	5	3	2	0	0
4	Puseas	1	4	1	LS5	1	5	4	1	0	0
4	Puseas	1	4	1	LS6	1	0	0	0	0	0
4	Puseas	1	4	2	LS1	4	4	1	1	1	1
4	Puseas	1	4	2	LS2	1	2	0	1	1	0
4	Puseas	1	4	2	LS3	1	0	0	0	0	0
4	Puseas	1	4	2	LS4	1	0	0	0	0	0
4	Puseas	1	5	1	SCI	2					
4	Puseas	1	5	1	LS1	1	2	2	0	0	0
4	Puseas	1	5	1	LS2	1	0	0	0	0	0
4	Puseas	1	5	1	LS3	0	0	0	0	0	0
4	Puseas	1	5	1	LS4	0	0	0	0	0	0
4	Puseas	1	5	1	LS5	0	0	0	0	0	0
4	Puseas	1	5	1	LS6	0	0	0	0	0	0
4	Puseas	1	5	1	I1	0	0	0	0	0	0
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4	Puseas	1	5	2	LS2	0	0	0	0	0	0
4	Puseas	1	5	2	LS3	0	0	0	0	0	0
4	Puseas	1	5	3	LS1	0	4	3	1	0	0
4	Puseas	1	5	3	LS2	0	0	0	0	0	0
4	Puseas	2	1	1	LS1	2	3	2	1	0	0
4	Puseas	2	1	1	LS2	1	0	0	0	0	0
4	Puseas	2	1	1	LS3	0	0	0	0	0	0
4	Puseas	2	1	1	LS4	0	0	0	0	0	0
4	Puseas	2	1	1	LS5	0	0	0	0	0	0
4	Puseas	2	1	1	LS6	0	0	0	0	0	0
4	Puseas	2	1	1	I1	0	0	0	0	0	0
4	Puseas	2	1	2	LS1	0	0	0	0	0	0
4	Puseas	2	1	2	LS2	0	0	0	0	0	0
4	Puseas	2	1	2	LS3	0	0	0	0	0	0
4	Puseas	2	1	2	LS4	0	0	0	0	0	0
4	Puseas	2	1	3	LS1	0	0	0	0	0	0
4	Puseas	2	1	3	LS2	0	0	0	0	0	0
4	Puseas	2	1	3	LS3	0	0	0	0	0	0
4	Puseas	2	2	1	SCI	0					
4	Puseas	2	2	1	LS1	2	5	2	2	1	0

4	Puseas	2	2	1	LS2	1	3	2	1	0	0
4	Puseas	2	2	1	LS3	1	3	3	0	0	0
4	Puseas	2	2	1	LS4	0	0	0	0	0	0
4	Puseas	2	2	1	LS5	0	0	0	0	0	0
4	Puseas	2	2	1	LS6	0	0	0	0	0	0
4	Puseas	2	2	1	I1	0	1	1	0	0	0
4	Puseas	2	2	2	LS1	2	1	1	0	0	0
4	Puseas	2	2	2	LS2	1	0	0	0	0	0
4	Puseas	2	2	2	LS3	0	0	0	0	0	0
4	Puseas	2	2	2	LS4	0	0	0	0	0	0
4	Puseas	2	2	3	LS1	1	0	0	0	0	0
4	Puseas	2	2	3	LS2	0	0	0	0	0	0
4	Puseas	2	2	3	LS3	0	0	0	0	0	0
4	Puseas	2	3	1	SCI	0					
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4	Puseas	2	3	1	LS2	1	0	0	0	0	0
4	Puseas	2	3	1	LS3	1	0	0	0	0	0
4	Puseas	2	3	1	LS4	0	0	0	0	0	0
4	Puseas	2	3	1	LS5	0	0	0	0	0	0
4	Puseas	2	3	1	LS6	0	0	0	0	0	0
4	Puseas	2	3	1	I1	0	0	0	0	0	0
4	Puseas	2	3	2	LS1	0	0	0	0	0	0
4	Puseas	2	3	2	LS2	0	0	0	0	0	0
4	Puseas	2	3	2	LS3	0	0	0	0	0	0
4	Puseas	2	3	2	LS4	0	0	0	0	0	0
4	Puseas	2	3	3	LS1	0	0	0	0	0	0
4	Puseas	2	3	3	LS2	0	0	0	0	0	0
4	Puseas	2	3	3	LS3	0	0	0	0	0	0
4	Puseas	2	3	4	LS1	0					
4	Puseas	2	3	4	LS2	0					
4	Puseas	2	4	1	SCI	0					
4	Puseas	2	4	1	LS1	2	0	0	0	0	0
4	Puseas	2	4	1	LS2	2	0	0	0	0	0
4	Puseas	2	4	1	LS3	1	0	0	0	0	0
4	Puseas	2	4	1	LS4	0	0	0	0	0	0
4	Puseas	2	4	1	LS5	0	0	0	0	0	0

4	Puseas	2	4	1	LS6	0	0	0	0	0	0
4	Puseas	2	4	1	I1	0	0	0	0	0	0
4	Puseas	2	4	2	LS1	1	0	0	0	0	0
4	Puseas	2	4	2	LS2	0	0	0	0	0	0
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4	Puseas	2	4	2	LS4	0	0	0	0	0	0
4	Puseas	2	4	3	LS1	0	0	0	0	0	0
4	Puseas	2	4	3	LS2	0	0	0	0	0	0
4	Puseas	2	4	3	LS3	0	0	0	0	0	0
4	Puseas	2	5	1	SCI	2					
4	Puseas	2	5	1	LS1	2	4	2	1	1	0
4	Puseas	2	5	1	LS2	2	4	2	2	0	0
4	Puseas	2	5	1	LS3	1	3	3	0	0	0
4	Puseas	2	5	1	LS4	1	2	2	0	0	0
4	Puseas	2	5	1	LS5	0	0	0	0	0	0
4	Puseas	2	5	1	LS6	0	0	0	0	0	0
4	Puseas	2	5	1	I1	0	0	0	0	0	0
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4	Puseas	2	5	2	LS2	1	2	2	0	0	0
4	Puseas	2	5	2	LS3	1	0	0	0	0	0
4	Puseas	2	5	2	LS4	0	0	0	0	0	0
4	Puseas	2	5	3	LS1	1	1	1	0	0	0
4	Puseas	2	5	3	LS2	1	0	0	0	0	0
4	Puseas	2	5	3	LS3	0					
4	Puseas	3	1	1	SCI	4					
4	Puseas	3	1	1	LS1	4					
4	Puseas	3	1	1	LS2	3					
4	Puseas	3	1	1	LS3	3					
4	Puseas	3	1	1	LS4	2					
4	Puseas	3	1	1	LS5	1					
4	Puseas	3	1	1	I1	4					
4	Puseas	3	1	2	LS1	4					
4	Puseas	3	1	2	LS2	3					
4	Puseas	3	2	1	SCI	1					
4	Puseas	3	2	1	LS1	0					
4	Puseas	3	2	1	LS2	0					

4	Puseas	3	2	1	LS3	0					
4	Puseas	3	2	1	LS4	0					
4	Puseas	3	2	1	LS5	0					
4	Puseas	3	2	1	LS6	0					
4	Puseas	3	2	2	LS1	0					
4	Puseas	3	2	2	LS2	0					
4	Puseas	3	2	2	LS3	0					
4	Puseas	3	2	2	LS4	0					
4	Puseas	3	2	3	LS1	0					
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4	Puseas	3	2	4	LS1	0					
4	Puseas	3	2	4	LS2	0					
4	Puseas	3	3	1	SCI	2					
4	Puseas	3	3	1	LS1	1					
4	Puseas	3	3	1	LS2	1					
4	Puseas	3	3	1	LS3	0					
4	Puseas	3	3	1	LS4	0					
4	Puseas	3	3	1	LS5	0					
4	Puseas	3	3	1	LS6	0					
4	Puseas	3	3	2	LS1	0					
4	Puseas	3	3	2	LS2	0					
4	Puseas	3	3	2	LS3	0					
4	Puseas	3	3	2	LS4	0					
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4	Puseas	3	3	3	LS2	0					
4	Puseas	3	3	3	LS3	0					
4	Puseas	3	4	1	SCI	4					
4	Puseas	3	4	1	LS1	4					
4	Puseas	3	4	1	LS2	2					
4	Puseas	3	4	1	LS3	1					
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4	Puseas	3	4	1	LS5	0					
4	Puseas	3	5	1	SCI	1					
4	Puseas	3	5	1	LS1	1					
4	Puseas	3	5	1	LS2	0					

4	Puseas	3	5	1	LS3	0					
4	Puseas	3	5	1	LS4	0					
4	Puseas	3	5	1	LS5	0					
4	Puseas	3	5	1	LS6	0					
4	Puseas	3	5	2	LS1	0					
4	Puseas	3	5	2	LS2	0					
4	Puseas	3	5	2	LS3	0					
4	Puseas	3	5	3	LS1	0					
4	Puseas	3	5	3	LS2	0					
4	Vasco	1	1	1	SCI	4					
4	Vasco	1	1	1	LS1	1	6	3	1	1	1
4	Vasco	1	1	1	LS2	1	3	2	1	0	0
4	Vasco	1	1	1	LS3	1	0	0	0	0	0
4	Vasco	1	1	1	LS4	1	0	0	0	0	0
4	Vasco	1	1	1	LS5	0	0	0	0	0	0
4	Vasco	1	1	1	LS6	0	0	0	0	0	0
4	Vasco	1	1	2	LS1	1	0	0	0	0	0
4	Vasco	1	1	2	LS2	1	0	0	0	0	0
4	Vasco	1	1	2	LS3	0	0	0	0	0	0
4	Vasco	1	2	1	SCI	4					
4	Vasco	1	2	1	LS1	1	3	2	1	0	0
4	Vasco	1	2	1	LS2	0	3	1	1	1	0
4	Vasco	1	2	1	LS3	0	0	0	0	0	0
4	Vasco	1	2	1	LS4	0	0	0	0	0	0
4	Vasco	1	2	1	LS5	0	0	0	0	0	0
4	Vasco	1	2	1	LS6	0	0	0	0	0	0
4	Vasco	1	3	1	SCI	0					
4	Vasco	1	3	1	LS1	1	5	2	2	1	0
4	Vasco	1	3	1	LS2	1	4	3	1	0	0
4	Vasco	1	3	1	LS3	0	0	0	0	0	0
4	Vasco	1	3	1	LS4	0	0	0	0	0	0
4	Vasco	1	3	1	LS5	0	0	0	0	0	0
4	Vasco	1	3	1	LS6	0	0	0	0	0	0
4	Vasco	1	3	2	LS1	1	2	1	1	0	0
4	Vasco	1	3	2	LS2	1	6	1	2	2	1
4	Vasco	1	3	2	LS3	0	0	0	0	0	0

4	Vasco	1	3	2	LS4	0	0	0	0	0	0
4	Vasco	1	4	1	SCI	2					
4	Vasco	1	4	1	LS1	1	4	1	1	1	1
4	Vasco	1	4	1	LS2	0	1	0	1	0	0
4	Vasco	1	4	1	LS3	0	0	0	0	0	0
4	Vasco	1	4	1	LS4	0	0	0	0	0	0
4	Vasco	1	4	1	LS5	0	0	0	0	0	0
4	Vasco	1	4	1	LS6	0	0	0	0	0	0
4	Vasco	1	5	1	SCI	3					
4	Vasco	1	5	1	LS1	1	5	2	2	1	0
4	Vasco	1	5	1	LS2	1	1	1	0	0	0
4	Vasco	1	5	1	LS3	0	1	1	0	0	0
4	Vasco	1	5	1	LS4	0	0	0	0	0	0
4	Vasco	1	5	1	LS5	0	0	0	0	0	0
4	Vasco	1	5	1	LS6	0	0	0	0	0	0
4	Vasco	1	5	2	LS1	0	0	0	0	0	0
4	Vasco	1	5	2	LS2	0	0	0	0	0	0
4	Vasco	1	5	2	LS3	0	0	0	0	0	0
4	Vasco	1	5	2	LS4	0	0	0	0	0	0
4	Vasco	1	5	3	LS1	0	0	0	0	0	0
4	Vasco	1	5	3	LS2	0	0	0	0	0	0
4	Vasco	1	5	3	LS3	0	0	0	0	0	0
4	Vasco	2	1	1	SCI	1					
4	Vasco	2	1	1	LS1	2	0	0	0	0	0
4	Vasco	2	1	1	LS2	1	0	0	0	0	0
4	Vasco	2	1	1	LS3	1	0	0	0	0	0
4	Vasco	2	1	1	LS4	0	0	0	0	0	0
4	Vasco	2	1	1	LS5	0	0	0	0	0	0
4	Vasco	2	1	1	LS6	0	0	0	0	0	0
4	Vasco	2	1	2	LS1	1	0	0	0	0	0
4	Vasco	2	1	2	LS2	0	0	0	0	0	0
4	Vasco	2	1	2	LS3	0	0	0	0	0	0
4	Vasco	2	2	1	SCI	0					
4	Vasco	2	2	1	LS1	1	5	1	2	1	1
4	Vasco	2	2	1	LS2	1	2	0	2	0	0
4	Vasco	2	2	1	LS3	0	0	0	0	0	0

4	Vasco	2	2	1	LS4	0	0	0	0	0	0
4	Vasco	2	2	1	LS5	0	0	0	0	0	0
4	Vasco	2	2	1	LS6	0	0	0	0	0	0
4	Vasco	2	2	2	LS1	0	0	0	0	0	0
4	Vasco	2	2	2	LS2	0	0	0	0	0	0
4	Vasco	2	2	2	LS3	0	0	0	0	0	0
4	Vasco	2	3	1	SCI	4					
4	Vasco	2	3	1	LS1	2	4	2	1	1	0
4	Vasco	2	3	1	LS2	1	2	2	0	0	0
4	Vasco	2	3	1	LS3	1	1	1	0	0	0
4	Vasco	2	3	1	LS4	1	0	0	0	0	0
4	Vasco	2	3	1	LS5	0	0	0	0	0	0
4	Vasco	2	3	1	LS6	0	0	0	0	0	0
4	Vasco	2	3	2	LS1	1	2	1	1	0	0
4	Vasco	2	3	2	LS2	1	1	1	0	0	0
4	Vasco	2	3	2	LS3	0	0	0	0	0	0
4	Vasco	2	4	1	SCI	4					
4	Vasco	2	4	1	LS1	3	6	2	2	1	1
4	Vasco	2	4	1	LS2	1	4	2	1	1	0
4	Vasco	2	4	1	LS3	0	2	2	0	0	0
4	Vasco	2	4	1	LS4	0	0	0	0	0	0
4	Vasco	2	4	1	LS5	0	0	0	0	0	0
4	Vasco	2	4	1	LS6	0	0	0	0	0	0
4	Vasco	2	4	2	LS1	0	2	2	0	0	0
4	Vasco	2	4	2	LS2	0	0	0	0	0	0
4	Vasco	2	4	2	LS3	0	0	0	0	0	0
4	Vasco	2	4	2	LS4	0	0	0	0	0	0
4	Vasco	2	4	3	LS1	0	0	0	0	0	0
4	Vasco	2	4	3	LS2	0	0	0	0	0	0
4	Vasco	2	4	3	LS3	0	0	0	0	0	0
4	Vasco	2	5	1	SCI	1					
4	Vasco	2	5	1	LS1	1	6	2	2	1	1
4	Vasco	2	5	1	LS2	1	3	2	1	0	0
4	Vasco	2	5	1	LS3	0	0	0	0	0	0
4	Vasco	2	5	1	LS4	0	0	0	0	0	0
4	Vasco	2	5	1	LS5	0	0	0	0	0	0

4	Vasco	2	5	1	LS6	0	0	0	0	0	0
4	Vasco	2	5	2	LS1	0	0	0	0	0	0
4	Vasco	2	5	2	LS2	0	0	0	0	0	0
4	Vasco	2	5	2	LS3	0	0	0	0	0	0
4	Vasco	2	5	2	LS4	0	0	0	0	0	0
4	Vasco	2	5	3	LS1	0	4	1	2	1	0
4	Vasco	2	5	3	LS2	0	2	1	1	0	0
4	Vasco	2	5	3	LS3	0	0	0	0	0	0
4	Vasco	3	1	1	SCI	1					
4	Vasco	3	1	1	LS1	2					
4	Vasco	3	1	1	LS2	1					
4	Vasco	3	1	1	LS3	0					
4	Vasco	3	1	1	LS4	0					
4	Vasco	3	1	1	LS5	0					
4	Vasco	3	1	1	LS6	0					
4	Vasco	3	2	1	SCI	1					
4	Vasco	3	2	1	LS1	1					
4	Vasco	3	2	1	LS2	1					
4	Vasco	3	2	1	LS3	0					
4	Vasco	3	2	1	LS4	0					
4	Vasco	3	2	1	LS5	0					
4	Vasco	3	2	1	LS6	0					
4	Vasco	3	3	1	SCI	0					
4	Vasco	3	3	1	LS1	0					
4	Vasco	3	3	1	LS2	0					
4	Vasco	3	3	1	LS3	0					
4	Vasco	3	3	1	LS4	0					
4	Vasco	3	3	1	LS5	0					
4	Vasco	3	3	1	LS6	0					
4	Vasco	3	3	2	LS1	0					
4	Vasco	3	3	2	LS2	0					
4	Vasco	3	3	2	LS3	0					
4	Vasco	3	3	2	LS4	0					
4	Vasco	3	4	1	SCI	2					
4	Vasco	3	4	1	LS1	1					
4	Vasco	3	4	1	LS2	0					

4	Vasco	3	4	1	LS3	0					
4	Vasco	3	4	1	LS4	0					
4	Vasco	3	4	1	LS5	0					
4	Vasco	3	4	1	LS6	0					
4	Vasco	3	4	2	LS1	0					
4	Vasco	3	4	2	LS2	0					
4	Vasco	3	4	2	LS3	0					
4	Vasco	3	4	3	LS1	0					
4	Vasco	3	4	3	LS2	0					
4	Vasco	3	5	1	SCI	0					
4	Vasco	3	5	1	LS1	2					
4	Vasco	3	5	1	LS2	1					
4	Vasco	3	5	1	LS3	0					
4	Vasco	3	5	1	LS4	0					
4	Vasco	3	5	1	LS5	0					
4	Vasco	3	5	1	LS6	0					
4	Vasco	3	5	2	LS1	0					
4	Vasco	3	5	2	LS2	0					
4	Vasco	3	5	2	LS3	0					
4	2-49	1	1	1	SCI	0					
4	2-49	1	1	1	LS1	1	5	2	2	1	0
4	2-49	1	1	1	LS2	1	3	3	0	0	0
4	2-49	1	1	1	LS3	1	2	2	0	0	0
4	2-49	1	1	1	LS4	0	0	0	0	0	0
4	2-49	1	1	1	LS5	0	0	0	0	0	0
4	2-49	1	1	1	LS6	0	0	0	0	0	0
4	2-49	1	1	1	LS7	0	0	0	0	0	0
4	2-49	1	1	2	LS1	2	6	2	2	1	1
4	2-49	1	1	2	LS2	0	0	0	0	0	0
4	2-49	1	1	2	LS3	0	0	0	0	0	0
4	2-49	1	1	2	LS4	0	0	0	0	0	0
4	2-49	1	1	3	LS1	0	0	0	0	0	0
4	2-49	1	1	3	LS2	0	0	0	0	0	0
4	2-49	1	1	3	LS3	0	0	0	0	0	0
4	2-49	1	1	4	LS1	0	0	0	0	0	0
4	2-49	1	1	4	LS2	0	0	0	0	0	0

4	2-49	1	1	4	LS3	0	0	0	0	0	0
4	2-49	1	2	1	SCI	0					
4	2-49	1	2	1	LS1	1	5	2	2	0	1
4	2-49	1	2	1	LS2	1	4	2	1	0	1
4	2-49	1	2	1	LS3	1	4	2	2	0	0
4	2-49	1	2	1	LS4	1	0	0	0	0	0
4	2-49	1	2	1	LS5	0	0	0	0	0	0
4	2-49	1	2	1	LS6	0	0	0	0	0	0
4	2-49	1	2	2	LS1	4	4	1	1	1	1
4	2-49	1	2	2	LS2	2	3	1	1	1	0
4	2-49	1	2	2	LS3	2	2	1	1	0	0
4	2-49	1	2	2	LS4	0	0	0	0	0	0
4	2-49	1	2	3	LS1	1	0	0	0	0	0
4	2-49	1	2	3	LS2	0	0	0	0	0	0
4	2-49	1	2	3	LS3	0	0	0	0	0	0
4	2-49	1	2	4	LS1	0	0	0	0	0	0
4	2-49	1	2	4	LS2	0	0	0	0	0	0
4	2-49	1	3	1	SCI	0					
4	2-49	1	3	1	LS1	1	5	1	2	1	1
4	2-49	1	3	1	LS2	1	5	2	2	1	0
4	2-49	1	3	1	LS3	2	5	1	2	2	0
4	2-49	1	3	1	LS4	2	4	2	1	1	0
4	2-49	1	3	1	LS5	0	1	0	1	0	0
4	2-49	1	4	1	SCI	3					
4	2-49	1	4	1	LS1	1	4	2	1	1	0
4	2-49	1	4	1	LS2	1	2	2	0	0	0
4	2-49	1	4	1	LS3	1	0	0	0	0	0
4	2-49	1	4	1	LS4	0	0	0	0	0	0
4	2-49	1	4	1	LS5	0	0	0	0	0	0
4	2-49	1	5	1	SCI	1					
4	2-49	1	5	1	LS1	1	3	1	1	1	0
4	2-49	1	5	1	LS2	1	0	0	0	0	0
4	2-49	1	5	1	LS3	1	0	0	0	0	0
4	2-49	1	5	1	LS4	0	0	0	0	0	0
4	2-49	1	5	1	LS5	0	0	0	0	0	0
4	2-49	1	5	1	LS6	0	0	0	0	0	0

4	2-49	1	5	2	LS1	3	4	1	1	1	1
4	2-49	1	5	2	LS2	1	1	1	0	0	0
4	2-49	1	5	2	LS3	1	1	1	0	0	0
4	2-49	1	5	2	LS4	0	0	0	0	0	0
4	2-49	1	5	3	LS1	1	1	1	0	0	0
4	2-49	1	5	3	LS2	1	1	1	0	0	0
4	2-49	1	5	3	LS3	0	0	0	0	0	0
4	2-49	1	5	4	LS1	0	0	0	0	0	0
4	2-49	1	5	4	LS2	0	0	0	0	0	0
4	2-49	2	1	1	SCI	0					
4	2-49	2	1	1	LS1	0	2	1	1	0	0
4	2-49	2	1	1	LS2	0	1	1	0	0	0
4	2-49	2	1	1	LS3	0	0	0	0	0	0
4	2-49	2	1	1	LS4	0	0	0	0	0	0
4	2-49	2	1	1	LS5	0	0	0	0	0	0
4	2-49	2	1	1	LS6	0	0	0	0	0	0
4	2-49	2	1	2	LS1	0	2	0	1	1	0
4	2-49	2	1	2	LS2	0	0	0	0	0	0
4	2-49	2	1	2	LS3	0	0	0	0	0	0
4	2-49	2	1	2	LS4	0	0	0	0	0	0
4	2-49	2	1	3	LS1	0	0	0	0	0	0
4	2-49	2	1	3	LS2	0	0	0	0	0	0
4	2-49	2	1	3	LS3	0	0	0	0	0	0
4	2-49	2	2	1	SCI	0					
4	2-49	2	2	1	LS1	1	0	0	0	0	0
4	2-49	2	2	1	LS2	0	0	0	0	0	0
4	2-49	2	2	1	LS3	0	0	0	0	0	0
4	2-49	2	2	1	LS4	0	0	0	0	0	0
4	2-49	2	2	1	LS5	0	0	0	0	0	0
4	2-49	2	2	2	LS1	3	0	0	0	0	0
4	2-49	2	2	2	LS2	0	0	0	0	0	0
4	2-49	2	2	2	LS3	0	0	0	0	0	0
4	2-49	2	2	2	LS4	0	0	0	0	0	0
4	2-49	2	2	3	LS1	0	0	0	0	0	0
4	2-49	2	2	3	LS2	0	0	0	0	0	0
4	2-49	2	2	3	LS3	0	0	0	0	0	0

4	2-49	2	3	1	SCI	1					
4	2-49	2	3	1	LS1	1	0	0	0	0	0
4	2-49	2	3	1	LS2	1	0	0	0	0	0
4	2-49	2	3	1	LS3	0	0	0	0	0	0
4	2-49	2	3	1	LS4	0	0	0	0	0	0
4	2-49	2	3	1	LS5	0	0	0	0	0	0
4	2-49	2	3	1	LS6	0	0	0	0	0	0
4	2-49	2	3	2	LS1	1	0	0	0	0	0
4	2-49	2	3	2	LS2	0	0	0	0	0	0
4	2-49	2	3	2	LS3	0	0	0	0	0	0
4	2-49	2	3	2	LS4	0	0	0	0	0	0
4	2-49	2	3	3	LS1	0	0	0	0	0	0
4	2-49	2	3	3	LS2	0	0	0	0	0	0
4	2-49	2	3	3	LS3	0	0	0	0	0	0
4	2-49	2	4	1	SCI	0					
4	2-49	2	4	1	LS1	1	3	2	1	0	0
4	2-49	2	4	1	LS2	1	3	2	1	0	0
4	2-49	2	4	1	LS3	0	0	0	0	0	0
4	2-49	2	4	1	LS4	0	0	0	0	0	0
4	2-49	2	4	1	LS5	0	0	0	0	0	0
4	2-49	2	4	1	LS6	0	0	0	0	0	0
4	2-49	2	4	2	LS1	0	0	0	0	0	0
4	2-49	2	4	2	LS2	0	0	0	0	0	0
4	2-49	2	4	2	LS3	0	0	0	0	0	0
4	2-49	2	4	2	LS4	0	0	0	0	0	0
4	2-49	2	4	3	LS1	0	0	0	0	0	0
4	2-49	2	4	3	LS2	0	0	0	0	0	0
4	2-49	2	4	3	LS3	0	0	0	0	0	0
4	2-49	2	4	4	LS1	0	0	0	0	0	0
4	2-49	2	4	4	LS2	0	0	0	0	0	0
4	2-49	2	5	1	SCI	0					
4	2-49	2	5	1	LS1	1	0	0	0	0	0
4	2-49	2	5	1	LS2	1	0	0	0	0	0
4	2-49	2	5	1	LS3	0	0	0	0	0	0
4	2-49	2	5	1	LS4	0	0	0	0	0	0
4	2-49	2	5	1	LS5	0	0	0	0	0	0

4	2-49	2	5	1	LS6	0	0	0	0	0	0
4	2-49	2	5	2	LS1	1	0	0	0	0	0
4	2-49	2	5	2	LS2	0	0	0	0	0	0
4	2-49	2	5	2	LS3	0	0	0	0	0	0
4	2-49	2	5	2	LS4	0	0	0	0	0	0
4	2-49	2	5	3	LS1	0	0	0	0	0	0
4	2-49	2	5	3	LS2	0	0	0	0	0	0
4	2-49	2	5	3	LS3	0	0	0	0	0	0
4	2-49	2	5	4	LS1	0	0	0	0	0	0
4	2-49	2	5	4	LS2	0	0	0	0	0	0
4	2-49	3	1	1	SCI	0					
4	2-49	3	1	1	LS1	1					
4	2-49	3	1	1	LS2	0					
4	2-49	3	1	1	LS3	0					
4	2-49	3	1	1	LS4	0					
4	2-49	3	1	1	LS5	0					
4	2-49	3	1	2	LS1	0					
4	2-49	3	1	2	LS2	0					
4	2-49	3	1	2	LS3	0					
4	2-49	3	2	1	SCI	0					
4	2-49	3	2	1	LS1	1					
4	2-49	3	2	1	LS2	1					
4	2-49	3	2	1	LS3	0					
4	2-49	3	2	1	LS4	0					
4	2-49	3	2	1	LS5	0					
4	2-49	3	2	2	LS1	0					
4	2-49	3	2	2	LS2	0					
4	2-49	3	2	2	LS3	0					
4	2-49	3	2	2	LS4	0					
4	2-49	3	2	3	LS1	0					
4	2-49	3	2	3	LS2	0					
4	2-49	3	2	3	LS3	0					
4	2-49	3	3	1	SCI	0					
4	2-49	3	3	1	LS1	1					
4	2-49	3	3	1	LS2	1					
4	2-49	3	3	1	LS3	1					

4	2-49	3	3	1	LS4	0					
4	2-49	3	3	1	LS5	0					
4	2-49	3	3	1	LS6	0					
4	2-49	3	3	2	LS1	0					
4	2-49	3	3	2	LS2	0					
4	2-49	3	3	2	LS3	0					
4	2-49	3	3	3	LS1	0					
4	2-49	3	3	3	LS2	0					
4	2-49	3	4	1	SCI	0					
4	2-49	3	4	1	LS1	1					
4	2-49	3	4	1	LS2	1					
4	2-49	3	4	1	LS3	0					
4	2-49	3	4	1	LS4	0					
4	2-49	3	4	1	LS5	0					
4	2-49	3	4	1	LS6	0					
4	2-49	3	4	2	LS1	0					
4	2-49	3	4	2	LS2	0					
4	2-49	3	4	2	LS3	0					
4	2-49	3	4	2	LS4	0					
4	2-49	3	4	3	LS1	0					
4	2-49	3	4	3	LS2	0					
4	2-49	3	4	3	LS3	0					
4	2-49	3	4	4	LS1	0					
4	2-49	3	4	4	LS2	0					
4	2-49	3	5	1	SCI	0					
4	2-49	3	5	1	LS1	1					
4	2-49	3	5	1	LS2	1					
4	2-49	3	5	1	LS3	0					
4	2-49	3	5	1	LS4	0					
4	2-49	3	5	1	LS5	0					
4	2-49	3	5	1	LS6	0					
4	2-49	3	5	2	LS1	0					
4	2-49	3	5	2	LS2	0					
4	2-49	3	5	2	LS3	0					
4	2-49	3	5	2	LS4	0					
4	2-49	3	5	3	LS1	0					

4	2-49	3	5	3	LS2	0					
4	2-49	3	5	3	LS3	0					
4	2-49	3	5	4	LS1	0					
4	2-49	3	5	4	LS2	0					
4	Sunco	1	1	1	SCI	0					
4	Sunco	1	1	1	LS1	3	4	1	1	1	1
4	Sunco	1	1	1	LS2	2	3	1	1	1	0
4	Sunco	1	1	1	LS3	1	2	2	0	0	0
4	Sunco	1	1	1	LS4	0	3	3	0	0	0
4	Sunco	1	1	1	LS5	0	0	0	0	0	0
4	Sunco	1	1	1	LS6	0	0	0	0	0	0
4	Sunco	1	1	1	I1	0	0	0	0	0	0
4	Sunco	1	1	2	LS1	1	3	2	1	0	0
4	Sunco	1	1	2	LS2	0	3	2	1	0	0
4	Sunco	1	1	2	LS3	0	0	0	0	0	0
4	Sunco	1	1	2	LS4	0	0	0	0	0	0
4	Sunco	1	1	2	LS5	0	0	0	0	0	0
4	Sunco	1	1	3	LS1	0	5	2	2	1	0
4	Sunco	1	1	3	LS2	0	3	2	1	0	0
4	Sunco	1	1	3	LS3	0	1	1	0	0	0
4	Sunco	1	1	3	LS4	0	0	0	0	0	0
4	Sunco	1	1	4	LS1	0	0	0	0	0	0
4	Sunco	1	1	4	LS2	0	0	0	0	0	0
4	Sunco	1	1	4	LS3	0	0	0	0	0	0
4	Sunco	1	2	1	SCI	2					
4	Sunco	1	2	1	LS1	2	0	0	0	0	0
4	Sunco	1	2	1	LS2	1	0	0	0	0	0
4	Sunco	1	2	1	LS3	1	0	0	0	0	0
4	Sunco	1	2	1	LS4	1	0	0	0	0	0
4	Sunco	1	2	1	LS5	0	0	0	0	0	0
4	Sunco	1	2	1	LS6	0	0	0	0	0	0
4	Sunco	1	3	1	SCI	1					
4	Sunco	1	3	1	LS1	1	0	0	0	0	0
4	Sunco	1	3	1	LS2	1	0	0	0	0	0
4	Sunco	1	3	1	LS3	0	0	0	0	0	0
4	Sunco	1	3	1	LS4	0	0	0	0	0	0

4	Sunco	1	3	1	LS5	0	0	0	0	0	0
4	Sunco	1	3	1	LS6	0	0	0	0	0	0
4	Sunco	1	3	2	LS1	0	0	0	0	0	0
4	Sunco	1	3	2	LS2	0	0	0	0	0	0
4	Sunco	1	3	2	LS3	0	0	0	0	0	0
4	Sunco	1	3	3	LS1	0	0	0	0	0	0
4	Sunco	1	3	3	LS2	0	0	0	0	0	0
4	Sunco	1	4	1	SCI	0					
4	Sunco	1	4	1	LS1	1	0	0	0	0	0
4	Sunco	1	4	1	LS2	0	0	0	0	0	0
4	Sunco	1	4	1	LS3	0	0	0	0	0	0
4	Sunco	1	4	1	LS4	0	0	0	0	0	0
4	Sunco	1	4	1	LS5	0	0	0	0	0	0
4	Sunco	1	5	1	SCI	0					
4	Sunco	1	5	1	LS1	3	7	2	2	2	1
4	Sunco	1	5	1	LS2	1	3	0	2	1	0
4	Sunco	1	5	1	LS3	0	2	0	1	1	0
4	Sunco	1	5	1	LS4	0	1	0	1	0	0
4	Sunco	1	5	1	LS5	0	0	0	0	0	0
4	Sunco	1	5	1	LS6	0	0	0	0	0	0
4	Sunco	2	1	1	SCI	0					
4	Sunco	2	1	1	LS1	1	6	3	1	2	0
4	Sunco	2	1	1	LS2	1	4	2	1	1	0
4	Sunco	2	1	1	LS3	0	3	2	1	0	0
4	Sunco	2	1	1	LS4	0	0	0	0	0	0
4	Sunco	2	1	1	LS5	0	0	0	0	0	0
4	Sunco	2	1	1	LS6	0	0	0	0	0	0
4	Sunco	2	1	2	LS1	0	0	0	0	0	0
4	Sunco	2	1	2	LS2	0	0	0	0	0	0
4	Sunco	2	1	2	LS3	0	0	0	0	0	0
4	Sunco	2	1	2	LS4	0	0	0	0	0	0
4	Sunco	2	1	3	LS1	0	0	0	0	0	0
4	Sunco	2	1	3	LS2	0	0	0	0	0	0
4	Sunco	2	1	3	LS3	0	0	0	0	0	0
4	Sunco	2	2	1	SCI	1					
4	Sunco	2	2	1	LS1	1	3	2	1	0	0

4	Sunco	2	2	1	LS2	1	2	1	1	0	0
4	Sunco	2	2	1	LS3	1	0	0	0	0	0
4	Sunco	2	2	1	LS4	0	0	0	0	0	0
4	Sunco	2	2	1	LS5	0	0	0	0	0	0
4	Sunco	2	2	1	LS6	0	0	0	0	0	0
4	Sunco	2	2	2	LS1	0	3	1	1	1	0
4	Sunco	2	2	2	LS2	0	0	0	0	0	0
4	Sunco	2	2	2	LS3	0	0	0	0	0	0
4	Sunco	2	2	2	LS4	0	0	0	0	0	0
4	Sunco	2	2	3	LS1	0	0	0	0	0	0
4	Sunco	2	2	3	LS2	0	0	0	0	0	0
4	Sunco	2	2	3	LS3	0	0	0	0	0	0
4	Sunco	2	3	1	SCI	2					
4	Sunco	2	3	1	LS1	1	3	1	1	1	0
4	Sunco	2	3	1	LS2	1	0	0	0	0	0
4	Sunco	2	3	1	LS3	1	0	0	0	0	0
4	Sunco	2	3	1	LS4	0	0	0	0	0	0
4	Sunco	2	3	1	LS5	0	0	0	0	0	0
4	Sunco	2	3	1	LS6	0	0	0	0	0	0
4	Sunco	2	3	2	LS1	1	0	0	0	0	0
4	Sunco	2	3	2	LS2	0	0	0	0	0	0
4	Sunco	2	3	2	LS3	0	0	0	0	0	0
4	Sunco	2	3	2	LS4	0	0	0	0	0	0
4	Sunco	2	3	2	LS5	0	0	0	0	0	0
4	Sunco	2	3	3	LS1	0	0	0	0	0	0
4	Sunco	2	3	3	LS2	0	0	0	0	0	0
4	Sunco	2	3	3	LS3	0	0	0	0	0	0
4	Sunco	2	3	3	LS4	0	0	0	0	0	0
4	Sunco	2	3	4	LS1	0	0	0	0	0	0
4	Sunco	2	3	4	LS2	0	0	0	0	0	0
4	Sunco	2	3	4	LS3	0	0	0	0	0	0
4	Sunco	2	4	1	SCI	1					
4	Sunco	2	4	1	LS1	1	6	2	2	2	0
4	Sunco	2	4	1	LS2	0	4	2	1	1	0
4	Sunco	2	4	1	LS3	0	3	2	1	0	0
4	Sunco	2	4	1	LS4	0	2	2	0	0	0

4	Sunco	2	4	1	LS5	0	0	0	0	0	0
4	Sunco	2	5	1	SCI	1					
4	Sunco	2	5	1	LS1	4	3	2	1	0	0
4	Sunco	2	5	1	LS2	2	0	0	0	0	0
4	Sunco	2	5	1	LS3	1	0	0	0	0	0
4	Sunco	2	5	1	LS4	1	0	0	0	0	0
4	Sunco	2	5	1	LS5	1	0	0	0	0	0
4	Sunco	2	5	1	LS6	1	2	2	0	0	0
4	Sunco	2	5	2	LS1	1	0	0	0	0	0
4	Sunco	2	5	2	LS2	0	0	0	0	0	0
4	Sunco	2	5	2	LS3	0	0	0	0	0	0
4	Sunco	2	5	3	LS1	0	0	0	0	0	0
4	Sunco	2	5	3	LS2	0	0	0	0	0	0
4	Sunco	3	1	1	SCI	0					
4	Sunco	3	1	1	LS1	4					
4	Sunco	3	1	1	LS2	2					
4	Sunco	3	1	1	LS3	1					
4	Sunco	3	1	1	LS4	1					
4	Sunco	3	1	1	LS5	1					
4	Sunco	3	1	1	LS6	0					
4	Sunco	3	1	1	LS7	0					
4	Sunco	3	1	2	LS1	1					
4	Sunco	3	1	2	LS2	0					
4	Sunco	3	1	2	LS3	0					
4	Sunco	3	2	1	SCI	0					
4	Sunco	3	2	1	LS1	1					
4	Sunco	3	2	1	LS2	0					
4	Sunco	3	2	1	LS3	0					
4	Sunco	3	2	1	LS4	0					
4	Sunco	3	2	1	LS5	0					
4	Sunco	3	2	1	LS6	0					
4	Sunco	3	2	2	LS1	0					
4	Sunco	3	2	2	LS2	0					
4	Sunco	3	2	2	LS3	0					
4	Sunco	3	3	1	SCI	0					
4	Sunco	3	3	1	LS1	0					

4	Sunco	3	3	1	LS2	0					
4	Sunco	3	3	1	LS3	0					
4	Sunco	3	3	1	LS4	0					
4	Sunco	3	3	1	LS5	0					
4	Sunco	3	3	1	LS6	0					
4	Sunco	3	3	2	LS1	0					
4	Sunco	3	3	2	LS2	0					
4	Sunco	3	3	2	LS3	0					
4	Sunco	3	3	3	LS1	0					
4	Sunco	3	3	3	LS2	0					
4	Sunco	3	4	1	SCI	0					
4	Sunco	3	4	1	LS1	1					
4	Sunco	3	4	1	LS2	1					
4	Sunco	3	4	1	LS3	1					
4	Sunco	3	4	1	LS4	0					
4	Sunco	3	4	1	LS5	0					
4	Sunco	3	4	1	LS6	0					
4	Sunco	3	4	1	LS7	0					
4	Sunco	3	4	2	LS1	0					
4	Sunco	3	4	2	LS2	0					
4	Sunco	3	4	2	LS3	0					
4	Sunco	3	4	2	LS4	0					
4	Sunco	3	4	2	LS5	0					
4	Sunco	3	5	1	SCI	2					
4	Sunco	3	5	1	LS1	1					
4	Sunco	3	5	1	LS2	1					
4	Sunco	3	5	1	LS3	1					
4	Sunco	3	5	1	LS4	0					
4	Sunco	3	5	1	LS5	0					
4	Sunco	3	5	1	LS6	0					
4	Sunco	3	5	2	LS1	1					
4	Sunco	3	5	2	LS2	0					
4	Sunco	3	5	3	LS1	0					
4	Sunco	3	5	3	LS2	0					
4	Sunco	3	5	4	LS1	0					
4	Sunco	3	5	4	LS2	0					

4	CPI133814	1	1	1	SCI	0					
4	CPI133814	1	1	1	LS1	1	1	1	0	0	0
4	CPI133814	1	1	1	LS2	0	0	0	0	0	0
4	CPI133814	1	1	1	LS3	0	0	0	0	0	0
4	CPI133814	1	1	1	LS4	0	0	0	0	0	0
4	CPI133814	1	1	1	LS5	0	0	0	0	0	0
4	CPI133814	1	2	1	SCI	2					
4	CPI133814	1	2	1	LS1	1	3	2	1	0	0
4	CPI133814	1	2	1	LS2	1	3	2	1	0	0
4	CPI133814	1	2	1	LS3	0	0	0	0	0	0
4	CPI133814	1	2	1	LS4	0	0	0	0	0	0
4	CPI133814	1	2	1	LS5	0	0	0	0	0	0
4	CPI133814	1	3	1	SCI	4					
4	CPI133814	1	3	1	LS1	1	0	0	0	0	0
4	CPI133814	1	3	1	LS2	1	0	0	0	0	0
4	CPI133814	1	3	1	LS3	0	0	0	0	0	0
4	CPI133814	1	3	1	LS4	0	0	0	0	0	0
4	CPI133814	1	3	1	LS5	0	0	0	0	0	0
4	CPI133814	1	4	1	SCI	2					
4	CPI133814	1	4	1	LS1	1	7	3	2	2	0
4	CPI133814	1	4	1	LS2	0	4	2	1	1	0
4	CPI133814	1	4	1	LS3	0	0	0	0	0	0
4	CPI133814	1	4	1	LS4	0	0	0	0	0	0
4	CPI133814	1	4	1	LS5	0	0	0	0	0	0
4	CPI133814	1	4	2	LS1	0	1	1	0	0	0
4	CPI133814	1	4	2	LS2	0	0	0	0	0	0
4	CPI133814	1	4	2	LS3	0	0	0	0	0	0
4	CPI133814	1	4	3	LS1	0	0	0	0	0	0
4	CPI133814	1	4	3	LS2	0	0	0	0	0	0
4	CPI133814	1	5	1	SCI	0					
4	CPI133814	1	5	1	LS1	1	4	3	1	0	0
4	CPI133814	1	5	1	LS2	1	1	0	1	0	0
4	CPI133814	1	5	1	LS3	0	0	0	0	0	0
4	CPI133814	1	5	1	LS4	0	0	0	0	0	0
4	CPI133814	1	5	1	LS5	0	0	0	0	0	0
4	CPI133814	1	5	2	LS1	1	0	0	0	0	0

4	CPI133814	1	5	2	LS2	1	0	0	0	0	0
4	CPI133814	1	5	2	LS3	0	0	0	0	0	0
4	CPI133814	2	1	1	SCI	0					
4	CPI133814	2	1	1	LS1	2	2	1	1	0	0
4	CPI133814	2	1	1	LS2	1	0	0	0	0	0
4	CPI133814	2	1	1	LS3	1	0	0	0	0	0
4	CPI133814	2	1	1	LS4	0	0	0	0	0	0
4	CPI133814	2	1	1	LS5	0	0	0	0	0	0
4	CPI133814	2	1	1	LS6	0	0	0	0	0	0
4	CPI133814	2	1	2	LS1	1	0	0	0	0	0
4	CPI133814	2	1	2	LS2	0	0	0	0	0	0
4	CPI133814	2	1	2	LS3	0	0	0	0	0	0
4	CPI133814	2	1	2	LS4	0	0	0	0	0	0
4	CPI133814	2	1	3	LS1	1	0	0	0	0	0
4	CPI133814	2	1	3	LS2	0	0	0	0	0	0
4	CPI133814	2	1	3	LS3	0	0	0	0	0	0
4	CPI133814	2	2	1	SCI	0					
4	CPI133814	2	2	1	LS1	1	7	3	2	2	0
4	CPI133814	2	2	1	LS2	0	3	2	1	0	0
4	CPI133814	2	2	1	LS3	0	0	0	0	0	0
4	CPI133814	2	2	1	LS4	0	0	0	0	0	0
4	CPI133814	2	2	1	LS5	0	0	0	0	0	0
4	CPI133814	2	2	1	LS6	0	0	0	0	0	0
4	CPI133814	2	2	2	LS1	1	0	0	0	0	0
4	CPI133814	2	2	2	LS2	0	0	0	0	0	0
4	CPI133814	2	2	2	LS3	0	0	0	0	0	0
4	CPI133814	2	2	2	LS4	0	0	0	0	0	0
4	CPI133814	2	2	3	LS1	1	0	0	0	0	0
4	CPI133814	2	2	3	LS2	0	0	0	0	0	0
4	CPI133814	2	2	3	LS3	0	0	0	0	0	0
4	CPI133814	2	3	1	SCI	0					
4	CPI133814	2	3	1	LS1						
4	CPI133814	2	3	1	LS2	2	0	0	0	0	0
4	CPI133814	2	3	1	LS3	0	0	0	0	0	0
4	CPI133814	2	3	1	LS4	0	0	0	0	0	0
4	CPI133814	2	3	1	LS5	0	0	0	0	0	0

4	CPI133814	2	3	2	LS1	0	0	0	0	0	0
4	CPI133814	2	3	2	LS2	0	0	0	0	0	0
4	CPI133814	2	3	2	LS3	0	0	0	0	0	0
4	CPI133814	2	3	3	LS1	0	0	0	0	0	0
4	CPI133814	2	3	3	LS2	0	0	0	0	0	0
4	CPI133814	2	4	1	SCI	0					
4	CPI133814	2	4	1	LS1	2	7	3	2	2	0
4	CPI133814	2	4	1	LS2	1	3	2	1	0	0
4	CPI133814	2	4	1	LS3	0	1	1	0	0	0
4	CPI133814	2	4	1	LS4	0	0	0	0	0	0
4	CPI133814	2	4	1	LS5	0	0	0	0	0	0
4	CPI133814	2	4	2	LS1	0	0	0	0	0	0
4	CPI133814	2	4	2	LS2	0	0	0	0	0	0
4	CPI133814	2	4	2	LS3	0	0	0	0	0	0
4	CPI133814	2	4	2	LS4	0	0	0	0	0	0
4	CPI133814	2	4	3	LS1	0	0	0	0	0	0
4	CPI133814	2	4	3	LS2	0	0	0	0	0	0
4	CPI133814	2	4	3	LS3	0	0	0	0	0	0
4	CPI133814	2	5	1	SCI	0					
4	CPI133814	2	5	1	LS1	3	0	0	0	0	0
4	CPI133814	2	5	1	LS2	2	0	0	0	0	0
4	CPI133814	2	5	1	LS3	0	0	0	0	0	0
4	CPI133814	2	5	1	LS4	0	0	0	0	0	0
4	CPI133814	2	5	1	LS5	0	0	0	0	0	0
4	CPI133814	2	5	2	LS1	2	0	0	0	0	0
4	CPI133814	2	5	2	LS2	0	0	0	0	0	0
4	CPI133814	2	5	2	LS3	0	0	0	0	0	0
4	CPI133814	2	5	2	LS4	0	0	0	0	0	0
4	CPI133814	2	5	3	LS1	0	0	0	0	0	0
4	CPI133814	2	5	3	LS2	0	0	0	0	0	0
4	CPI133814	2	5	3	LS3	0	0	0	0	0	0
4	CPI133814	3	1	1	SCI	4					
4	CPI133814	3	1	1	LS1	4					
4	CPI133814	3	1	1	LS2	3					
4	CPI133814	3	1	1	LS3	3					
4	CPI133814	3	1	1	LS4	2					

4	CPI133814	3	1	1	LS5	1					
4	CPI133814	3	2	1	SCI	0					
4	CPI133814	3	2	1	LS1	2					
4	CPI133814	3	2	1	LS2	0					
4	CPI133814	3	2	1	LS3	0					
4	CPI133814	3	2	1	LS4	0					
4	CPI133814	3	2	1	LS5	0					
4	CPI133814	3	2	2	LS1	0					
4	CPI133814	3	2	2	LS2	0					
4	CPI133814	3	3	1	SCI	0					
4	CPI133814	3	3	1	LS1	1					
4	CPI133814	3	3	1	LS2	0					
4	CPI133814	3	3	1	LS3	0					
4	CPI133814	3	3	1	LS4	0					
4	CPI133814	3	3	1	LS5	0					
4	CPI133814	3	3	1	LS6	0					
4	CPI133814	3	3	2	LS1	0					
4	CPI133814	3	3	2	LS2	0					
4	CPI133814	3	3	2	LS3	0					
4	CPI133814	3	3	2	LS4	0					
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4	CPI133814	3	3	3	LS2	0					
4	CPI133814	3	3	3	LS3	0					
4	CPI133814	3	3	3	LS4	0					
4	CPI133814	3	4	1	SCI	0					
4	CPI133814	3	4	1	LS1	2					
4	CPI133814	3	4	1	LS2	1					
4	CPI133814	3	4	1	LS3	0					
4	CPI133814	3	4	1	LS4	0					
4	CPI133814	3	4	1	LS5	0					
4	CPI133814	3	4	1	LS6	0					
4	CPI133814	3	4	2	LS1	0					
4	CPI133814	3	4	2	LS2	0					
4	CPI133814	3	4	2	LS3	0					
4	CPI133814	3	5	1	SCI	0					

4	CPI133814	3	5	1	LS1	3					
4	CPI133814	3	5	1	LS2	1					
4	CPI133814	3	5	1	LS3	0					
4	CPI133814	3	5	1	LS4	0					
4	CPI133814	3	5	1	LS5	0					
4	CPI133814	3	5	1	LS6	0					
4	CPI133814	3	5	2	LS1	0					
4	CPI133814	3	5	2	LS2	0					
4	CPI133814	3	5	2	LS3	0					
4	CPI133814	3	5	2	LS4	0					
4	CPI133814	3	5	3	LS1	0					
4	CPI133814	3	5	3	LS2	0					
4	CPI133814	3	5	3	LS3	0					
5	Puseas	1	1	1	SCI	4					
5	Puseas	1	1	1	LS1	2	9	4	2	3	0
5	Puseas	1	1	1	LS2	1	4	3	1	0	0
5	Puseas	1	1	1	LS3	1	4	3	1	0	0
5	Puseas	1	1	1	LS4	1	2	2	0	0	0
5	Puseas	1	1	1	LS5	1	0	0	0	0	0
5	Puseas	1	1	1	LS6	1	0	0	0	0	0
5	Puseas	1	1	1	LS7	0	0	0	0	0	0
5	Puseas	1	1	1	LS8	0	0	0	0	0	0
5	Puseas	1	1	1	I1	4	4	1	1	1	1
5	Puseas	1	1	1	I2	1	3	3	0	0	0
5	Puseas	1	1	1	I3	1	0	0	0	0	0
5	Puseas	1	1	2	LS1	1	5	2	1	1	1
5	Puseas	1	1	2	LS2	1	4	3	1	0	0
5	Puseas	1	1	2	LS3	1	2	2	0	0	0
5	Puseas	1	2	1	SCI	4					
5	Puseas	1	2	1	LS1	4	9	2	3	2	2
5	Puseas	1	2	1	LS2	4	8	3	3	2	0
5	Puseas	1	2	1	LS3	3	7	3	2	2	0
5	Puseas	1	2	1	LS4	3	6	3	2	1	0
5	Puseas	1	2	1	LS5	2	6	3	3	0	0
5	Puseas	1	2	1	LS6	4	8	3	2	1	2
5	Puseas	1	3	1	SCI	1					

5	Puseas	1	3	1	LS1	2	7	2	3	2	0
5	Puseas	1	3	1	LS2	2	4	2	2	0	0
5	Puseas	1	3	1	LS3	2	5	3	1	1	0
5	Puseas	1	3	1	LS4	1	4	3	1	0	0
5	Puseas	1	3	1	LS5	0	0	0	0	0	0
5	Puseas	1	3	1	LS6	0	0	0	0	0	0
5	Puseas	1	3	1	I1	1	1	1	0	0	0
5	Puseas	1	3	1	I2	0	0	0	0	0	0
5	Puseas	1	4	1	SCI	4					
5	Puseas	1	4	1	LS1	2	13	4	3	3	3
5	Puseas	1	4	1	LS2	2	7	2	2	2	1
5	Puseas	1	4	1	LS3	1	6	3	2	1	0
5	Puseas	1	4	1	LS4	1	5	2	2	1	0
5	Puseas	1	4	1	LS5	1	0	0	0	0	0
5	Puseas	1	4	1	LS6	0	0	0	0	0	0
5	Puseas	1	4	1	LS7	0	0	0	0	0	0
5	Puseas	1	4	1	I1	1	3	2	1	0	0
5	Puseas	1	4	1	I2	0	0	0	0	0	0
5	Puseas	1	4	2	LS1	1	0	0	0	0	0
5	Puseas	1	4	2	LS2	1	0	0	0	0	0
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5	Puseas	1	4	3	LS1	0	0	0	0	0	0
5	Puseas	1	4	3	LS2	0	0	0	0	0	0
5	Puseas	1	5	1	SCI	3					
5	Puseas	1	5	1	LS1	1	0	0	0	0	0
5	Puseas	1	5	1	LS2	1	0	0	0	0	0
5	Puseas	1	5	1	LS3	0	0	0	0	0	0
5	Puseas	1	5	1	LS4	0	0	0	0	0	0
5	Puseas	1	5	1	LS5	0	0	0	0	0	0
5	Puseas	1	5	1	LS6	0	0	0	0	0	0
5	Puseas	1	5	1	LS7	0	0	0	0	0	0
5	Puseas	1	5	1	I1	0	0	0	0	0	0
5	Puseas	1	5	1	I2	0	0	0	0	0	0
5	Puseas	2	1	1	SCI	4					
5	Puseas	2	1	1	LS1	1	6	3	2	1	0
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5	Puseas	2	1	1	LS3	1	3	3	0	0	0
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5	Puseas	2	1	1	LS5	0	0	0	0	0	0
5	Puseas	2	1	1	LS6	0	0	0	0	0	0
5	Puseas	2	1	1	LS7	0	0	0	0	0	0
5	Puseas	2	1	1	I1	0	0	0	0	0	0
5	Puseas	2	1	1	I2	0	0	0	0	0	0
5	Puseas	2	1	2	LS1	1	0	0	0	0	0
5	Puseas	2	1	2	LS2	1	0	0	0	0	0
5	Puseas	2	1	2	LS3	0	0	0	0	0	0
5	Puseas	2	1	2	LS4	0	0	0	0	0	0
5	Puseas	2	1	2	LS5	0	0	0	0	0	0
5	Puseas	2	1	2	I1	1	2	2	0	0	0
5	Puseas	2	1	3	LS1	1	0	0	0	0	0
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5	Puseas	2	1	4	LS3	0	0	0	0	0	0
5	Puseas	2	2	1	SCI	4					
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5	Puseas	2	2	1	LS2	3	10	4	4	2	0
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5	Puseas	2	2	1	LS4	2	4	4	0	0	0
5	Puseas	2	2	1	LS5	2	1	1	0	0	0
5	Puseas	2	2	1	LS6	0	0	0	0	0	0
5	Puseas	2	2	1	LS7	0	0	0	0	0	0
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5	Puseas	2	2	2	LS2	2	3	3	0	0	0
5	Puseas	2	2	2	LS3	1	3	3	0	0	0
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5	Puseas	2	3	1	LS1	4	10	4	3	3	0
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5	Puseas	2	3	3	LS1	4	5	2	2	1	0
5	Puseas	2	3	3	LS2	4	9	3	3	2	1
5	Puseas	2	4	1	SCI	4					
5	Puseas	2	4	1	LS1	4	8	2	2	2	2
5	Puseas	2	4	1	LS2	1	6	2	1	2	1
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5	Puseas	2	4	1	LS5	1	0	0	0	0	0
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5	Puseas	2	4	1	LS8	0	0	0	0	0	0
5	Puseas	2	4	1	LS9	0	0	0	0	0	0
5	Puseas	2	4	1	LS10	0	0	0	0	0	0
5	Puseas	2	4	1	I1	1	2	2	0	0	0
5	Puseas	2	4	1	I2	0	0	0	0	0	0
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5	Puseas	2	4	2	LS1	1	3	3	0	0	0
5	Puseas	2	4	2	LS2	1	0	0	0	0	0
5	Puseas	2	4	2	LS3	1	0	0	0	0	0
5	Puseas	2	4	2	LS4	0	0	0	0	0	0
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5	Puseas	2	4	3	LS3	1	3	3	0	0	0
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5	Puseas	2	4	4	LS1	0	0	0	0	0	0
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5	Puseas	2	4	4	LS3	0	0	0	0	0	0
5	Puseas	2	5	1	SCI	3					
5	Puseas	2	5	1	LS1	1	7	2	2	2	1
5	Puseas	2	5	1	LS2	1	8	3	3	2	0
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5	Puseas	2	5	1	LS4	1	6	0	0	3	3
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5	Puseas	2	5	1	LS7	0	0	0	0	0	0
5	Puseas	2	5	1	LS8	0	0	0	0	0	0
5	Puseas	2	5	1	I1	4	7	2	2	2	1
5	Puseas	2	5	1	I2	1	4	4	0	0	0
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5	Puseas	2	5	2	LS1	1	4	3	1	0	0
5	Puseas	2	5	2	LS2	2	4	3	1	0	0
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5	Puseas	2	5	2	I1	4	4	2	1	1	0
5	Puseas	2	5	2	I2	1	2	2	0	0	0
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5	Puseas	2	5	3	LS2	2	9	5	4	0	0
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5	Puseas	3	1	1	SCI	4					
5	Puseas	3	1	1	LS1	1					
5	Puseas	3	1	1	LS2	1					

5	Puseas	3	1	1	LS3	1					
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5	Puseas	3	1	1	LS5	0					
5	Puseas	3	1	1	LS6	0					
5	Puseas	3	1	1	LS7	0					
5	Puseas	3	1	1	I1	0					
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5	Puseas	3	2	1	SCI	4					
5	Puseas	3	2	1	LS1	4					
5	Puseas	3	2	1	LS2	2					
5	Puseas	3	2	1	LS3	1					
5	Puseas	3	2	1	LS4	1					
5	Puseas	3	2	1	LS5	1					
5	Puseas	3	2	1	LS6	2					
5	Puseas	3	2	1	LS7	0					
5	Puseas	3	2	1	LS8	0					
5	Puseas	3	2	1	I1	4					
5	Puseas	3	2	2	LS1	3					
5	Puseas	3	2	2	LS2	1					
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5	Puseas	3	2	3	LS2	1					
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5	Puseas	3	3	1	LS1	4					
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5	Puseas	3	3	1	LS4	1					
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5	Puseas	3	4	1	SCI	4					
5	Puseas	3	4	1	LS1	1					
5	Puseas	3	4	1	LS2	1					
5	Puseas	3	4	1	LS3	1					
5	Puseas	3	4	1	LS4	3					
5	Puseas	3	4	1	LS5	0					
5	Puseas	3	4	1	LS6	0					

5	Puseas	3	4	1	LS7	0					
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5	Puseas	3	4	1	I2	0					
5	Puseas	3	4	1	I3	0					
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5	Puseas	3	4	2	I2	0					
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5	Puseas	3	5	1	LS5	2					
5	Puseas	3	5	1	LS6	0					
5	Puseas	3	5	1	LS7	0					
5	Puseas	3	5	1	I1	2					
5	Puseas	3	5	1	I2	0					
5	Puseas	3	5	2	LS1	4					
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5	Puseas	3	5	2	LS4	2					
5	Puseas	3	5	3	LS1	4					
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5	Puseas	3	5	3	LS3	2					
5	Puseas	3	5	3	LS4	1					
5	Vasco	1	1	1	SCI	1					
5	Vasco	1	1	1	LS1	1	3	2	0	1	0
5	Vasco	1	1	1	LS2	1	1	0	1	0	0

5	Vasco	1	1	1	LS3	0	3	0	2	1	0
5	Vasco	1	1	1	LS4	0	0	0	0	0	0
5	Vasco	1	1	1	LS5	0	0	0	0	0	0
5	Vasco	1	1	1	LS6	0	0	0	0	0	0
5	Vasco	1	1	1	LS7	0	0	0	0	0	0
5	Vasco	1	1	1	I1	0	0	0	0	0	0
5	Vasco	1	1	1	I2	0	0	0	0	0	0
5	Vasco	1	2	1	SCI	3					
5	Vasco	1	2	1	LS1	1	0	0	0	0	0
5	Vasco	1	2	1	LS2	1	0	0	0	0	0
5	Vasco	1	2	1	LS3	0	0	0	0	0	0
5	Vasco	1	2	1	LS4	0	0	0	0	0	0
5	Vasco	1	2	1	LS5	0	0	0	0	0	0
5	Vasco	1	2	1	LS6	0	0	0	0	0	0
5	Vasco	1	2	1	LS7	0	0	0	0	0	0
5	Vasco	1	2	1	I1	0	0	0	0	0	0
5	Vasco	1	3	1	SCI	2					
5	Vasco	1	3	1	LS1	3	6	3	0	1	2
5	Vasco	1	3	1	LS2	1	6	2	2	2	0
5	Vasco	1	3	1	LS3	1	0	0	0	0	0
5	Vasco	1	3	1	LS4	1	0	0	0	0	0
5	Vasco	1	3	1	LS5	1	0	0	0	0	0
5	Vasco	1	3	1	LS6	1	0	0	0	0	0
5	Vasco	1	3	1	LS7	0	0	0	0	0	0
5	Vasco	1	3	1	LS8	0	0	0	0	0	0
5	Vasco	1	3	1	I1	1	3	2	1	0	0
5	Vasco	1	3	1	I2	0	0	0	0	0	0
5	Vasco	1	4	1	SCI	2					
5	Vasco	1	4	1	LS1	2	7	2	1	2	2
5	Vasco	1	4	1	LS2	1	3	2	1	0	0
5	Vasco	1	4	1	LS3	1	3	2	1	0	0
5	Vasco	1	4	1	LS4	1	0	0	0	0	0
5	Vasco	1	4	1	LS5	1	0	0	0	0	0
5	Vasco	1	4	1	LS6	0	0	0	0	0	0
5	Vasco	1	4	1	LS7	0	0	0	0	0	0
5	Vasco	1	4	1	LS8	0	0	0	0	0	0

5	Vasco	1	4	1	LS9	0	0	0	0	0	0
5	Vasco	1	4	1	I1	0	0	0	0	0	0
5	Vasco	1	4	1	I2	0	0	0	0	0	0
5	Vasco	1	4	2	LS1	1	3	2	1	0	0
5	Vasco	1	4	2	LS2	1	3	2	1	0	0
5	Vasco	1	4	2	LS3	1	2	2	0	0	0
5	Vasco	1	4	2	LS4	0	0	0	0	0	0
5	Vasco	1	4	3	LS1	1	0	0	0	0	0
5	Vasco	1	4	3	LS2	1	0	0	0	0	0
5	Vasco	1	4	3	LS3	0	0	0	0	0	0
5	Vasco	1	5	1	SCI	4					
5	Vasco	1	5	1	LS1	1	0	0	0	0	0
5	Vasco	1	5	1	LS2	1	0	0	0	0	0
5	Vasco	1	5	1	LS3	0	0	0	0	0	0
5	Vasco	1	5	1	LS4	0	0	0	0	0	0
5	Vasco	1	5	1	LS5	0	0	0	0	0	0
5	Vasco	1	5	1	LS6	0	0	0	0	0	0
5	Vasco	1	5	1	LS7	0	0	0	0	0	0
5	Vasco	1	5	1	I1	0	0	0	0	0	0
5	Vasco	1	5	2	LS1	1	0	0	0	0	0
5	Vasco	1	5	2	LS2	1	0	0	0	0	0
5	Vasco	1	5	2	LS3	0	0	0	0	0	0
5	Vasco	1	5	2	LS4	0	0	0	0	0	0
5	Vasco	2	1	1	SCI	1					
5	Vasco	2	1	1	LS1	1	5	2	2	1	0
5	Vasco	2	1	1	LS2	1	0	0	0	0	0
5	Vasco	2	1	1	LS3	1	0	0	0	0	0
5	Vasco	2	1	1	LS4	0	0	0	0	0	0
5	Vasco	2	1	1	LS5	0	0	0	0	0	0
5	Vasco	2	1	1	LS6	0	0	0	0	0	0
5	Vasco	2	1	1	LS7	0	0	0	0	0	0
5	Vasco	2	1	1	LS8	0	0	0	0	0	0
5	Vasco	2	1	1	I1	0	2	2	0	0	0
5	Vasco	2	1	2	LS1	1	0	0	0	0	0
5	Vasco	2	1	2	LS2	1	0	0	0	0	0
5	Vasco	2	1	2	LS3	0	0	0	0	0	0

5	Vasco	2	1	2	LS4	0	0	0	0	0	0
5	Vasco	2	1	3	LS1	1	0	0	0	0	0
5	Vasco	2	1	3	LS2	0					
5	Vasco	2	1	3	LS3	0	0	0	0	0	0
5	Vasco	2	2	1	SCI	4					
5	Vasco	2	2	1	LS1	2	6	2	1	2	1
5	Vasco	2	2	1	LS2	1	7	3	1	2	1
5	Vasco	2	2	1	LS3	1	3	2	1	0	0
5	Vasco	2	2	1	LS4	1	2	2	0	0	0
5	Vasco	2	2	1	LS5	1	1	1	0	0	0
5	Vasco	2	2	1	LS6	0	0	0	0	0	0
5	Vasco	2	2	1	LS7	0	0	0	0	0	0
5	Vasco	2	2	1	LS8	0	0	0	0	0	0
5	Vasco	2	2	1	LS9	0	0	0	0	0	0
5	Vasco	2	2	1	I1	1	2	2	0	0	0
5	Vasco	2	2	1	I2	0	0	0	0	0	0
5	Vasco	2	2	2	LS1	1	5	1	2	2	0
5	Vasco	2	2	2	LS2	2	3	3	0	0	0
5	Vasco	2	2	2	LS3	1	0	0	0	0	0
5	Vasco	2	2	2	LS4	0	0	0	0	0	0
5	Vasco	2	2	2	LS5	0	0	0	0	0	0
5	Vasco	2	2	2	I1	1	2	1	1	0	0
5	Vasco	2	3	1	SCI	4					
5	Vasco	2	3	1	LS1	1	3	2	1	0	0
5	Vasco	2	3	1	LS2	1	0	0	0	0	0
5	Vasco	2	3	1	LS3	0	0	0	0	0	0
5	Vasco	2	3	1	LS4	0	0	0	0	0	0
5	Vasco	2	3	1	LS5	0	0	0	0	0	0
5	Vasco	2	3	1	LS6	0	0	0	0	0	0
5	Vasco	2	3	1	LS7	0	0	0	0	0	0
5	Vasco	2	3	1	LS8	0	0	0	0	0	0
5	Vasco	2	3	1	I1	0	0	0	0	0	0
5	Vasco	2	3	1	I2	0	0	0	0	0	0
5	Vasco	2	3	2	LS1	1	0	0	0	0	0
5	Vasco	2	3	2	LS2	1	0	0	0	0	0
5	Vasco	2	3	2	LS3	0	0	0	0	0	0

5	Vasco	2	4	1	SCI	4					
5	Vasco	2	4	1	LS1	1	4	2	1	1	0
5	Vasco	2	4	1	LS2	1	5	3	2	0	0
5	Vasco	2	4	1	LS3	1	0	0	0	0	0
5	Vasco	2	4	1	LS4	0	0	0	0	0	0
5	Vasco	2	4	1	LS5	0	0	0	0	0	0
5	Vasco	2	4	1	LS6	0	0	0	0	0	0
5	Vasco	2	4	1	LS7	0	0	0	0	0	0
5	Vasco	2	4	1	I1	0	0	0	0	0	0
5	Vasco	2	4	2	LS1	1	2	2	0	0	0
5	Vasco	2	4	2	LS2	1	3	2	1	0	0
5	Vasco	2	4	2	LS3	1	3	2	1	0	0
5	Vasco	2	4	2	LS4	1	0	0	0	0	0
5	Vasco	2	4	2	LS5	0	0	0	0	0	0
5	Vasco	2	4	2	I1	1	2	2	0	0	0
5	Vasco	2	4	3	LS1	0	0	0	0	0	0
5	Vasco	2	4	3	LS2	0	0	0	0	0	0
5	Vasco	2	4	3	LS3	0	0	0	0	0	0
5	Vasco	2	4	3	LS4	0	0	0	0	0	0
5	Vasco	2	5	1	SCI	4					
5	Vasco	2	5	1	LS1	1	0	0	0	0	0
5	Vasco	2	5	1	LS2	1	0	0	0	0	0
5	Vasco	2	5	1	LS3	1	0	0	0	0	0
5	Vasco	2	5	1	LS4	1	0	0	0	0	0
5	Vasco	2	5	1	LS5	1	0	0	0	0	0
5	Vasco	2	5	1	LS6	0	0	0	0	0	0
5	Vasco	2	5	1	LS7	0	0	0	0	0	0
5	Vasco	2	5	1	I1	1	4	1	1	1	1
5	Vasco	2	5	1	I2	0	2	2	0	0	0
5	Vasco	2	5	2	LS1	0	0	0	0	0	0
5	Vasco	2	5	2	LS2	0	0	0	0	0	0
5	Vasco	2	5	2	LS3	0	0	0	0	0	0
5	Vasco	2	5	2	LS4	0	0	0	0	0	0
5	Vasco	2	5	2	LS5	0	0	0	0	0	0
5	Vasco	2	5	2	I1	0	3	2	1	0	0
5	Vasco	2	5	3	LS1	0	0	0	0	0	0

5	Vasco	2	5	3	LS2	0	0	0	0	0	0
5	Vasco	2	5	3	LS3	0	0	0	0	0	0
5	Vasco	2	5	3	LS4	0	0	0	0	0	0
5	Vasco	3	1	1	SCI	4					
5	Vasco	3	1	1	LS1	1					
5	Vasco	3	1	1	LS2	1					
5	Vasco	3	1	1	LS3	1					
5	Vasco	3	1	1	LS4	0					
5	Vasco	3	1	1	LS5	0					
5	Vasco	3	1	1	LS6	0					
5	Vasco	3	1	1	LS7	0					
5	Vasco	3	1	1	LS8	0					
5	Vasco	3	1	1	I1	0					
5	Vasco	3	1	1	I2	0					
5	Vasco	3	1	2	LS1	1					
5	Vasco	3	1	2	LS2	0					
5	Vasco	3	1	2	LS3	0					
5	Vasco	3	1	2	LS4	0					
5	Vasco	3	1	2	LS5	0					
5	Vasco	3	1	3	LS1	1					
5	Vasco	3	1	3	LS2	0					
5	Vasco	3	1	3	LS3	0					
5	Vasco	3	1	3	LS4	0					
5	Vasco	3	2	1	SCI	4					
5	Vasco	3	2	1	LS1	1					
5	Vasco	3	2	1	LS2	1					
5	Vasco	3	2	1	LS3	1					
5	Vasco	3	2	1	LS4	0					
5	Vasco	3	2	1	LS5	0					
5	Vasco	3	2	1	LS6	0					
5	Vasco	3	2	1	LS7	0					
5	Vasco	3	2	1	I1	0					
5	Vasco	3	2	1	I2	0					
5	Vasco	3	3	1	SCI	4					
5	Vasco	3	3	1	LS1	1					
5	Vasco	3	3	1	LS2	1					

5	Vasco	3	3	1	LS3	1					
5	Vasco	3	3	1	LS4	1					
5	Vasco	3	3	1	LS5	1					
5	Vasco	3	3	1	LS6	0					
5	Vasco	3	3	1	LS7	0					
5	Vasco	3	3	1	LS8	0					
5	Vasco	3	3	1	I1	0					
5	Vasco	3	3	1	I2	0					
5	Vasco	3	3	1	I3	0					
5	Vasco	3	4	1	SCI	3					
5	Vasco	3	4	1	LS1	0					
5	Vasco	3	4	1	LS2	1					
5	Vasco	3	4	1	LS3	1					
5	Vasco	3	4	1	LS4	1					
5	Vasco	3	4	1	LS5	0					
5	Vasco	3	4	1	LS6	0					
5	Vasco	3	4	1	LS7	0					
5	Vasco	3	4	1	I1	0					
5	Vasco	3	4	1	I2	0					
5	Vasco	3	4	2	LS1	1					
5	Vasco	3	4	2	LS2	0					
5	Vasco	3	4	2	LS3	0					
5	Vasco	3	4	2	LS4	0					
5	Vasco	3	4	2	I1	0					
5	Vasco	3	5	1	SCI	4					
5	Vasco	3	5	1	LS1	1					
5	Vasco	3	5	1	LS2	1					
5	Vasco	3	5	1	LS3	1					
5	Vasco	3	5	1	LS4	0					
5	Vasco	3	5	1	LS5	0					
5	Vasco	3	5	1	LS6	0					
5	Vasco	3	5	1	I1	0					
5	Vasco	3	5	1	I2	0					
5	2-49	1	1	1	SCI	4					
5	2-49	1	1	1	LS1	1	7	1	2	2	2
5	2-49	1	1	1	LS2	1	6	2	1.5	1.5	1

5	2-49	1	1	1	LS3	0	5	2	2	1	0
5	2-49	1	1	1	LS4	0	4	2	1	1	0
5	2-49	1	1	1	LS5	0	0	0	0	0	0
5	2-49	1	1	1	LS6	0	0	0	0	0	0
5	2-49	1	1	1	LS7	0	0	0	0	0	0
5	2-49	1	1	1	LS8	0	0	0	0	0	0
5	2-49	1	1	1	I1	0	0	0	0	0	0
5	2-49	1	1	1	I2	0	0	0	0	0	0
5	2-49	1	1	2	LS1	1	0	0	0	0	0
5	2-49	1	1	2	LS2	1	1	1	0	0	0
5	2-49	1	1	2	LS3	0	0	0	0	0	0
5	2-49	1	1	2	LS4	0	0	0	0	0	0
5	2-49	1	1	2	LS5	0	0	0	0	0	0
5	2-49	1	1	2	I1	0	0	0	0	0	0
5	2-49	1	1	3	LS1	0	3	2	1	0	0
5	2-49	1	1	3	LS2	0	0	0	0	0	0
5	2-49	1	1	3	LS3	0	0	0	0	0	0
5	2-49	1	1	3	LS4	0	0	0	0	0	0
5	2-49	1	1	3	LS5	0	0	0	0	0	0
5	2-49	1	1	4	LS1	0	0	0	0	0	0
5	2-49	1	1	4	LS2	0	0	0	0	0	0
5	2-49	1	1	4	LS3	0	0	0	0	0	0
5	2-49	1	2	1	LS1	1	9	2	3	2	2
5	2-49	1	2	1	LS2	1	8	2	2	2	2
5	2-49	1	2	1	LS3	4	8	2	2	2	2
5	2-49	1	2	1	LS4	2	7	2	2	2	1
5	2-49	1	2	1	LS5	2	6	2	3	1	0
5	2-49	1	2	1	LS6	0	2	2	0	0	0
5	2-49	1	2	1	LS7	0	0	0	0	0	0
5	2-49	1	2	1	I1	1	0	0	0	0	0
5	2-49	1	3	1	SCI	4					
5	2-49	1	3	1	LS1	1	9	3	3	2	1
5	2-49	1	3	1	LS2	1	7	2	2	2	1
5	2-49	1	3	1	LS3	1	5	2	2	1	0
5	2-49	1	3	1	LS4	1	5	3	2	0	0
5	2-49	1	3	1	LS5	1	1	1	0	0	0

5	2-49	1	3	1	LS6	0	0	0	0	0	0
5	2-49	1	3	1	LS7	0	0	0	0	0	0
5	2-49	1	3	1	LS8	0	0	0	0	0	0
5	2-49	1	3	1	I1	0	0	0	0	0	0
5	2-49	1	3	1	I2	0	0	0	0	0	0
5	2-49	1	3	2	LS1	3	6	2	1	2	1
5	2-49	1	3	2	LS2	1	6	2	2	1	1
5	2-49	1	3	2	LS3	0	1	1	0	0	0
5	2-49	1	3	2	LS4	0	0	0	0	0	0
5	2-49	1	3	2	LS5	0	0	0	0	0	0
5	2-49	1	3	2	LS6	0	0	0	0	0	0
5	2-49	1	3	2	I1	0	0	0	0	0	0
5	2-49	1	3	3	LS1	1	2	1	1	0	0
5	2-49	1	3	3	LS2	0	0	0	0	0	0
5	2-49	1	3	3	LS3	0	0	0	0	0	0
5	2-49	1	3	3	LS4	0	0	0	0	0	0
5	2-49	1	3	4	LS1	1	0	0	0	0	0
5	2-49	1	3	4	LS2	0	0	0	0	0	0
5	2-49	1	3	4	LS3	0	0	0	0	0	0
5	2-49	1	4	1	SCI	4					
5	2-49	1	4	1	LS1	1	8	3	2	2	1
5	2-49	1	4	1	LS2	0	5	2	2	1	0
5	2-49	1	4	1	LS3	0	4	2	1	1	0
5	2-49	1	4	1	LS4	0	3	2	1	0	0
5	2-49	1	4	1	LS5	0	0	0	0	0	0
5	2-49	1	4	1	LS6	0	0	0	0	0	0
5	2-49	1	4	1	LS7	0	0	0	0	0	0
5	2-49	1	4	1	LS8	0	0	0	0	0	0
5	2-49	1	4	1	I1	0	0	0	0	0	0
5	2-49	1	4	1	I2	0	0	0	0	0	0
5	2-49	1	4	2	LS1	1	0	0	0	0	0
5	2-49	1	4	2	LS2	0	0	0	0	0	0
5	2-49	1	4	2	LS3	0	0	0	0	0	0
5	2-49	1	4	3	LS1	0	0	0	0	0	0
5	2-49	1	4	3	LS2	0	0	0	0	0	0
5	2-49	1	5	1	SCI	3					

5	2-49	1	5	1	LS1	2	5	2	2	1	0
5	2-49	1	5	1	LS2	2	6	2	2	1	1
5	2-49	1	5	1	LS3	1	3	2	1	0	0
5	2-49	1	5	1	LS4	1	0	0	0	0	0
5	2-49	1	5	1	LS5	0	0	0	0	0	0
5	2-49	1	5	1	LS6	0	0	0	0	0	0
5	2-49	1	5	1	LS7	0	0	0	0	0	0
5	2-49	1	5	1	I1	0	0	0	0	0	0
5	2-49	1	5	2	LS1	1	0	0	0	0	0
5	2-49	1	5	2	LS2	0	0	0	0	0	0
5	2-49	1	5	2	LS3	0	0	0	0	0	0
5	2-49	1	5	3	LS1	0	0	0	0	0	0
5	2-49	1	5	3	LS2	0	0	0	0	0	0
5	2-49	2	1	1	SCI	0					
5	2-49	2	1	1	LS1	1	0	0	0	0	0
5	2-49	2	1	1	LS2	1	0	0	0	0	0
5	2-49	2	1	1	LS3	1	0	0	0	0	0
5	2-49	2	1	1	LS4	1	0	0	0	0	0
5	2-49	2	1	1	LS5	0	0	0	0	0	0
5	2-49	2	1	1	LS6	0	0	0	0	0	0
5	2-49	2	1	1	LS7	0	0	0	0	0	0
5	2-49	2	1	1	I1	0	0	0	0	0	0
5	2-49	2	1	2	LS1	1	0	0	0	0	0
5	2-49	2	1	2	LS2	0	0	0	0	0	0
5	2-49	2	1	2	LS3	0	0	0	0	0	0
5	2-49	2	2	1	SCI	4					
5	2-49	2	2	1	LS1	1	5	3	1	1	0
5	2-49	2	2	1	LS2	1	3	1	1	1	0
5	2-49	2	2	1	LS3	1	0	0	0	0	0
5	2-49	2	2	1	LS4	1	0	0	0	0	0
5	2-49	2	2	1	LS5	0	0	0	0	0	0
5	2-49	2	2	1	LS6	0	0	0	0	0	0
5	2-49	2	2	1	LS7	0	0	0	0	0	0
5	2-49	2	2	1	LS8	0	0	0	0	0	0
5	2-49	2	2	1	I1	0	0	0	0	0	0
5	2-49	2	2	1	I2	0	0	0	0	0	0

5	2-49	2	2	2	LS1	4	0	0	0	0	0
5	2-49	2	2	2	LS2	1	0	0	0	0	0
5	2-49	2	2	2	LS3	1	0	0	0	0	0
5	2-49	2	2	2	LS4	0	0	0	0	0	0
5	2-49	2	2	3	LS1	1	0	0	0	0	0
5	2-49	2	2	3	LS2	1	0	0	0	0	0
5	2-49	2	2	3	LS3	0	0	0	0	0	0
5	2-49	2	2	4	LS1	1	0	0	0	0	0
5	2-49	2	2	4	LS2	1	0	0	0	0	0
5	2-49	2	3	1	SCI	2					
5	2-49	2	3	1	LS1	1	0	0	0	0	0
5	2-49	2	3	1	LS2	1	0	0	0	0	0
5	2-49	2	3	1	LS3	0	0	0	0	0	0
5	2-49	2	3	1	LS4	0	0	0	0	0	0
5	2-49	2	3	1	LS5	0	0	0	0	0	0
5	2-49	2	3	1	LS6	0	0	0	0	0	0
5	2-49	2	3	1	LS7	0	0	0	0	0	0
5	2-49	2	3	1	I1	0	0	0	0	0	0
5	2-49	2	3	2	LS1	1	0	0	0	0	0
5	2-49	2	3	2	LS2	0	0	0	0	0	0
5	2-49	2	3	2	LS3	0	0	0	0	0	0
5	2-49	2	3	3	LS1	1	0	0	0	0	0
5	2-49	2	3	3	LS2	0	0	0	0	0	0
5	2-49	2	3	3	LS3	0	0	0	0	0	0
5	2-49	2	4	1	SCI	4					
5	2-49	2	4	1	LS1	1	0	0	0	0	0
5	2-49	2	4	1	LS2	1	0	0	0	0	0
5	2-49	2	4	1	LS3	1	0	0	0	0	0
5	2-49	2	4	1	LS4	0	0	0	0	0	0
5	2-49	2	4	1	LS5	0	0	0	0	0	0
5	2-49	2	4	1	LS6	0	0	0	0	0	0
5	2-49	2	4	1	LS7	0	0	0	0	0	0
5	2-49	2	4	2	LS1	1	0	0	0	0	0
5	2-49	2	4	2	LS2	1	0	0	0	0	0
5	2-49	2	4	2	LS3	0	0	0	0	0	0
5	2-49	2	4	2	LS4	0	0	0	0	0	0

5	2-49	2	4	2	LS5	0	0	0	0	0	0
5	2-49	2	4	3	LS1	0	0	0	0	0	0
5	2-49	2	4	3	LS2	0	0	0	0	0	0
5	2-49	2	4	3	LS3	0	0	0	0	0	0
5	2-49	2	5	1	LS1	1	0	0	0	0	0
5	2-49	2	5	1	LS2	1	0	0	0	0	0
5	2-49	2	5	1	LS3	1	0	0	0	0	0
5	2-49	2	5	1	LS4	0	0	0	0	0	0
5	2-49	2	5	1	LS5	0	0	0	0	0	0
5	2-49	2	5	1	LS6	0	0	0	0	0	0
5	2-49	2	5	1	I1	0	0	0	0	0	0
5	2-49	3	1	1	SCI	4					
5	2-49	3	1	1	LS1	0					
5	2-49	3	1	1	LS2	2					
5	2-49	3	1	1	LS3	1					
5	2-49	3	1	1	LS4	0					
5	2-49	3	1	1	LS5	0					
5	2-49	3	1	1	LS6	0					
5	2-49	3	1	1	LS7	0					
5	2-49	3	1	1	LS8	0					
5	2-49	3	1	1	I1	0					
5	2-49	3	1	1	I2	0					
5	2-49	3	2	1	SCI	4					
5	2-49	3	2	1	LS1	2					
5	2-49	3	2	1	LS2	1					
5	2-49	3	2	1	LS3	1					
5	2-49	3	2	1	LS4	1					
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5	2-49	3	2	1	LS6	0					
5	2-49	3	2	1	LS7	0					
5	2-49	3	2	2	LS1	3					
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5	2-49	3	2	2	LS3	0					
5	2-49	3	2	2	LS4	0					
5	2-49	3	3	1	SCI	0					
5	2-49	3	3	1	LS1	1					

5	2-49	3	3	1	LS2	1					
5	2-49	3	3	1	LS3	1					
5	2-49	3	3	1	LS4	0					
5	2-49	3	3	1	LS5	0					
5	2-49	3	3	1	LS6	0					
5	2-49	3	3	1	LS7	0					
5	2-49	3	3	1	LS8	0					
5	2-49	3	3	1	I1	0					
5	2-49	3	3	2	LS1	4					
5	2-49	3	3	2	LS2	0					
5	2-49	3	3	2	LS3	0					
5	2-49	3	3	2	LS4	0					
5	2-49	3	3	3	LS1	0					
5	2-49	3	3	3	LS2	0					
5	2-49	3	3	3	LS3	0					
5	2-49	3	4	1	SCI	4					
5	2-49	3	4	1	LS1	0					
5	2-49	3	4	1	LS2	1					
5	2-49	3	4	1	LS3	1					
5	2-49	3	4	1	LS4	1					
5	2-49	3	4	1	LS5	2					
5	2-49	3	4	1	LS6	1					
5	2-49	3	4	1	LS7	0					
5	2-49	3	4	1	LS8	0					
5	2-49	3	4	1	LS9	0					
5	2-49	3	4	1	I1	0					
5	2-49	3	4	1	I2	0					
5	2-49	3	4	2	LS1	1					
5	2-49	3	4	2	LS2	0					
5	2-49	3	4	2	LS3	0					
5	2-49	3	4	2	LS4	0					
5	2-49	3	4	2	LS5	0					
5	2-49	3	4	3	LS1	1					
5	2-49	3	4	3	LS2	0					
5	2-49	3	4	3	LS3	0					
5	2-49	3	4	3	LS4	0					

5	2-49	3	4	4	LS1	0					
5	2-49	3	4	4	LS2	0					
5	2-49	3	4	4	LS3	0					
5	2-49	3	5	1	SCI	4					
5	2-49	3	5	1	LS1	1					
5	2-49	3	5	1	LS2	1					
5	2-49	3	5	1	LS3	1					
5	2-49	3	5	1	LS4	1					
5	2-49	3	5	1	LS5	3					
5	2-49	3	5	1	LS6	2					
5	2-49	3	5	1	LS7	1					
5	2-49	3	5	1	LS8	0					
5	2-49	3	5	1	LS9	0					
5	2-49	3	5	1	I1	0					
5	2-49	3	5	1	I2	0					
5	2-49	3	5	1	I3	0					
5	2-49	3	5	2	LS1	2					
5	2-49	3	5	2	LS2	2					
5	2-49	3	5	2	LS3	1					
5	2-49	3	5	2	LS4	0					
5	2-49	3	5	2	LS5	0					
5	2-49	3	5	2	I1	0					
5	2-49	3	5	3	LS1	3					
5	2-49	3	5	3	LS2	4					
5	2-49	3	5	3	LS3	2					
5	2-49	3	5	3	LS4	2					
5	2-49	3	5	3	LS5	0					
5	2-49	3	5	4	LS1	1					
5	2-49	3	5	4	LS2	2					
5	2-49	3	5	4	LS3	1					
5	2-49	3	5	4	LS4	0					
5	Sunco	1	1	1	SCI	4					
5	Sunco	1	1	1	LS1	2	6	2	3	1	0
5	Sunco	1	1	1	LS2	1	3	2	1	0	0
5	Sunco	1	1	1	LS3	1	0	0	0	0	0
5	Sunco	1	1	1	LS4	0	0	0	0	0	0

5	Sunco	1	1	1	LS5	0	0	0	0	0	0
5	Sunco	1	1	1	LS6	0	0	0	0	0	0
5	Sunco	1	1	1	LS7	0	0	0	0	0	0
5	Sunco	1	1	1	LS8	0	0	0	0	0	0
5	Sunco	1	1	1	I1	0	0	0	0	0	0
5	Sunco	1	1	1	I2	0	0	0	0	0	0
5	Sunco	1	1	2	LS1	0	0	0	0	0	0
5	Sunco	1	1	2	LS2	0	0	0	0	0	0
5	Sunco	1	1	2	LS3	0	0	0	0	0	0
5	Sunco	1	2	1	SCI	4					
5	Sunco	1	2	1	LS1	2	7	3	2	1	1
5	Sunco	1	2	1	LS2	1	3	2	1	0	0
5	Sunco	1	2	1	LS3	1	0	0	0	0	0
5	Sunco	1	2	1	LS4	0	0	0	0	0	0
5	Sunco	1	2	1	LS5	0	0	0	0	0	0
5	Sunco	1	2	1	LS6	0	0	0	0	0	0
5	Sunco	1	2	1	LS7	0	0	0	0	0	0
5	Sunco	1	2	1	I1	0	0	0	0	0	0
5	Sunco	1	3	1	SCI	0					
5	Sunco	1	3	1	LS1	1	10	3	3	2	2
5	Sunco	1	3	1	LS2	0	5	3	2	0	0
5	Sunco	1	3	1	LS3	0	0	0	0	0	0
5	Sunco	1	3	1	LS4	0	0	0	0	0	0
5	Sunco	1	3	1	LS5	0	0	0	0	0	0
5	Sunco	1	3	1	LS6	0	0	0	0	0	0
5	Sunco	1	3	1	LS7	0	0	0	0	0	0
5	Sunco	1	3	1	LS8	0	0	0	0	0	0
5	Sunco	1	3	1	I1	0	0	0	0	0	0
5	Sunco	1	3	1	I2	0	0	0	0	0	0
5	Sunco	1	3	2	LS1	1	6	2	2	1	1
5	Sunco	1	3	2	LS2	1	5	2	2	1	0
5	Sunco	1	3	2	LS3	1	5	2	2	1	0
5	Sunco	1	3	2	LS4	2	7	3	2	2	0
5	Sunco	1	3	2	LS5	1	4	1	3	0	0
5	Sunco	1	3	2	LS6	0	2	2	0	0	0
5	Sunco	1	3	2	I1	1	4	1	1	1	1

5	Sunco	1	3	3	LS1	0	4	2	2	0	0
5	Sunco	1	3	3	LS2	1	4	2	2	0	0
5	Sunco	1	3	3	LS3	1	4	2	2	0	0
5	Sunco	1	3	3	LS4	0	3	2	1	0	0
5	Sunco	1	3	3	LS5	0	0	0	0	0	0
5	Sunco	1	3	4	LS1	0	0	0	0	0	0
5	Sunco	1	3	4	LS2	0	0	0	0	0	0
5	Sunco	1	3	4	LS3	0	0	0	0	0	0
5	Sunco	1	3	4	LS4	0	0	0	0	0	0
5	Sunco	1	4	1	SCI	3					
5	Sunco	1	4	1	LS1	3	6	3	3	0	0
5	Sunco	1	4	1	LS2	2	6	2	2	1	1
5	Sunco	1	4	1	LS3	2	7	3	2	2	0
5	Sunco	1	4	1	LS4	1	3	2	1	0	0
5	Sunco	1	4	1	LS5	1	0	0	0	0	0
5	Sunco	1	4	1	LS6	0	0	0	0	0	0
5	Sunco	1	4	1	LS7	0	0	0	0	0	0
5	Sunco	1	4	1	LS8	0	0	0	0	0	0
5	Sunco	1	4	1	I1	1	0	0	0	0	0
5	Sunco	1	4	1	I2	0	0	0	0	0	0
5	Sunco	1	5	1	SCI	4					
5	Sunco	1	5	1	LS1	1	0	0	0	0	0
5	Sunco	1	5	1	LS2	1	0	0	0	0	0
5	Sunco	1	5	1	LS3	0	0	0	0	0	0
5	Sunco	1	5	1	LS4	0	0	0	0	0	0
5	Sunco	1	5	1	LS5	0	0	0	0	0	0
5	Sunco	1	5	1	LS6	0	0	0	0	0	0
5	Sunco	1	5	1	LS7	0	0	0	0	0	0
5	Sunco	1	5	1	I1	0	0	0	0	0	0
5	Sunco	1	5	2	LS1	0	0	0	0	0	0
5	Sunco	1	5	2	LS2	0	0	0	0	0	0
5	Sunco	1	5	2	LS3	0	0	0	0	0	0
5	Sunco	1	5	2	LS4	0	0	0	0	0	0
5	Sunco	1	5	2	LS5	0	0	0	0	0	0
5	Sunco	1	5	2	I1	0	0	0	0	0	0
5	Sunco	1	5	3	LS1	0	0	0	0	0	0

5	Sunco	1	5	3	LS2	0	0	0	0	0	0
5	Sunco	1	5	3	LS3	0	0	0	0	0	0
5	Sunco	2	1	1	SCI	4					
5	Sunco	2	1	1	LS1	1	3	2	1	0	0
5	Sunco	2	1	1	LS2	1	0	0	0	0	0
5	Sunco	2	1	1	LS3	1	2	2	0	0	0
5	Sunco	2	1	1	LS4	1	0	0	0	0	0
5	Sunco	2	1	1	LS5	1	0	0	0	0	0
5	Sunco	2	1	1	LS6	0	0	0	0	0	0
5	Sunco	2	1	1	LS7	0	0	0	0	0	0
5	Sunco	2	1	1	I1	0	0	0	0	0	0
5	Sunco	2	1	2	LS1	1	0	0	0	0	0
5	Sunco	2	1	2	LS2	1	0	0	0	0	0
5	Sunco	2	1	2	LS3	1	0	0	0	0	0
5	Sunco	2	2	1	SCI	0					
5	Sunco	2	2	1	LS1	1	7	2	1	2	2
5	Sunco	2	2	1	LS2	1	4	0	2	2	0
5	Sunco	2	2	1	LS3	1	4	3	1	0	0
5	Sunco	2	2	1	LS4	1	0	0	0	0	0
5	Sunco	2	2	1	LS5	0	0	0	0	0	0
5	Sunco	2	2	1	LS6	0	0	0	0	0	0
5	Sunco	2	2	1	LS7	0	0	0	0	0	0
5	Sunco	2	2	1	LS8	0	0	0	0	0	0
5	Sunco	2	2	1	I1	0	1	1	0	0	0
5	Sunco	2	2	1	I2	0	0	0	0	0	0
5	Sunco	2	2	2	LS1	1	2	2	0	0	0
5	Sunco	2	2	2	LS2	1	2	2	0	0	0
5	Sunco	2	2	2	LS3	1	3	2	1	0	0
5	Sunco	2	2	2	LS4	1	1	1	0	0	0
5	Sunco	2	2	2	LS5	0	0	0	0	0	0
5	Sunco	2	2	3	LS1	1	0	0	0	0	0
5	Sunco	2	2	3	LS2	1	0	0	0	0	0
5	Sunco	2	2	3	LS3	0	0	0	0	0	0
5	Sunco	2	2	3	LS4	0	0	0	0	0	0
5	Sunco	2	3	1	SCI	0					
5	Sunco	2	3	1	LS1	1	5	3	1	1	0

5	Sunco	2	3	1	LS2	1	4	2	2	0	0
5	Sunco	2	3	1	LS3	1	3	2	1	0	0
5	Sunco	2	3	1	LS4	1	1	1	0	0	0
5	Sunco	2	3	1	LS5	0	0	0	0	0	0
5	Sunco	2	3	1	LS6	0	0	0	0	0	0
5	Sunco	2	3	1	LS7	0	0	0	0	0	0
5	Sunco	2	3	1	I1	1	0	0	0	0	0
5	Sunco	2	3	1	I2	0	0	0	0	0	0
5	Sunco	2	3	2	LS1	1	0	0	0	0	0
5	Sunco	2	3	2	LS2	1	0	0	0	0	0
5	Sunco	2	3	2	LS3	1	0	0	0	0	0
5	Sunco	2	3	2	LS4	0	0	0	0	0	0
5	Sunco	2	3	3	LS1	1	0	0	0	0	0
5	Sunco	2	3	3	LS2	1	0	0	0	0	0
5	Sunco	2	3	3	LS3	1	0	0	0	0	0
5	Sunco	2	4	1	SCI	3					
5	Sunco	2	4	1	LS1	1	6	3	2	1	0
5	Sunco	2	4	1	LS2	2	0	0	0	0	0
5	Sunco	2	4	1	LS3	1	0	0	0	0	0
5	Sunco	2	4	1	LS4	1	0	0	0	0	0
5	Sunco	2	4	1	LS5	1	0	0	0	0	0
5	Sunco	2	4	1	LS6	0	0	0	0	0	0
5	Sunco	2	4	1	LS7	0	0	0	0	0	0
5	Sunco	2	4	1	I1	0	0	0	0	0	0
5	Sunco	2	4	2	LS1	1	10	3	3	3	1
5	Sunco	2	4	2	LS2	1	3	2	1	0	0
5	Sunco	2	4	2	LS3	1	0	0	0	0	0
5	Sunco	2	4	2	LS4	0	0	0	0	0	0
5	Sunco	2	4	2	LS5	0	0	0	0	0	0
5	Sunco	2	4	3	LS1	1	0	0	0	0	0
5	Sunco	2	4	3	LS2	1	0	0	0	0	0
5	Sunco	2	4	3	LS3	1	0	0	0	0	0
5	Sunco	2	4	3	LS4	0	0	0	0	0	0
5	Sunco	2	4	4	LS1	1	0	0	0	0	0
5	Sunco	2	4	4	LS2	1	0	0	0	0	0
5	Sunco	2	4	4	LS3	1	0	0	0	0	0

5	Sunco	2	5	1	SCI	0					
5	Sunco	2	5	1	LS1	1	3	2	1	0	0
5	Sunco	2	5	1	LS2	1	2	1	1	0	0
5	Sunco	2	5	1	LS3	1	0	0	0	0	0
5	Sunco	2	5	1	LS4	0	0	0	0	0	0
5	Sunco	2	5	1	LS5	1	0	0	0	0	0
5	Sunco	2	5	1	LS6	1	0	0	0	0	0
5	Sunco	2	5	1	LS7	0	0	0	0	0	0
5	Sunco	2	5	1	LS8	0	0	0	0	0	0
5	Sunco	2	5	1	I1	1	6	2	2	1	1
5	Sunco	2	5	1	I2	0	0	0	0	0	0
5	Sunco	2	5	2	LS1	1	4	3	1	0	0
5	Sunco	2	5	2	LS2	1	2	2	0	0	0
5	Sunco	2	5	2	LS3	1	0	0	0	0	0
5	Sunco	2	5	2	LS4	0	0	0	0	0	0
5	Sunco	2	5	3	LS1	1	0	0	0	0	0
5	Sunco	2	5	3	LS2	1	0	0	0	0	0
5	Sunco	2	5	3	LS3	1	0	0	0	0	0
5	Sunco	3	1	1	SCI	4					
5	Sunco	3	1	1	LS1	1					
5	Sunco	3	1	1	LS2	1					
5	Sunco	3	1	1	LS3	2					
5	Sunco	3	1	1	LS4	2					
5	Sunco	3	1	1	LS5	0					
5	Sunco	3	1	1	LS6	0					
5	Sunco	3	1	1	LS7	0					
5	Sunco	3	1	1	LS8	0					
5	Sunco	3	1	1	I1	0					
5	Sunco	3	1	1	I2	0					
5	Sunco	3	1	2	LS1	2					
5	Sunco	3	1	2	LS2	1					
5	Sunco	3	1	2	LS3	1					
5	Sunco	3	1	2	LS4	0					
5	Sunco	3	1	2	LS5	0					
5	Sunco	3	1	2	LS6	0					
5	Sunco	3	1	2	I1	0					

5	Sunco	3	1	3	LS1	0					
5	Sunco	3	1	3	LS2	0					
5	Sunco	3	1	3	LS3	0					
5	Sunco	3	1	3	LS4	0					
5	Sunco	3	1	3	LS5	0					
5	Sunco	3	1	4	LS1	1					
5	Sunco	3	1	4	LS2	0					
5	Sunco	3	1	4	LS3	0					
5	Sunco	3	1	4	LS4	0					
5	Sunco	3	2	1	SCI	0					
5	Sunco	3	2	1	LS1	1					
5	Sunco	3	2	1	LS2	0					
5	Sunco	3	2	1	LS3	0					
5	Sunco	3	2	1	LS4	0					
5	Sunco	3	2	1	LS5	0					
5	Sunco	3	2	1	LS6	0					
5	Sunco	3	2	1	LS7	0					
5	Sunco	3	2	1	I1	0					
5	Sunco	3	2	1	I2	0					
5	Sunco	3	3	1	SCI	4					
5	Sunco	3	3	1	LS1	2					
5	Sunco	3	3	1	LS2	1					
5	Sunco	3	3	1	LS3	1					
5	Sunco	3	3	1	LS4	1					
5	Sunco	3	3	1	LS5	2					
5	Sunco	3	3	1	LS6	1					
5	Sunco	3	3	1	LS7	0					
5	Sunco	3	3	1	LS8	0					
5	Sunco	3	3	1	I1	0					
5	Sunco	3	3	1	I2	0					
5	Sunco	3	3	2	LS1	1					
5	Sunco	3	3	2	LS2	0					
5	Sunco	3	3	2	LS3	0					
5	Sunco	3	4	1	SCI	0					
5	Sunco	3	4	1	LS1	1					
5	Sunco	3	4	1	LS2	1					

5	Sunco	3	4	1	LS3	1					
5	Sunco	3	4	1	LS4	0					
5	Sunco	3	4	1	LS5	0					
5	Sunco	3	4	1	LS6	0					
5	Sunco	3	4	1	LS7	0					
5	Sunco	3	4	1	I1	0					
5	Sunco	3	4	1	I2	0					
5	Sunco	3	4	1	I3	0					
5	Sunco	3	5	1	SCI	4					
5	Sunco	3	5	1	LS1	4					
5	Sunco	3	5	1	LS2	1					
5	Sunco	3	5	1	LS3	1					
5	Sunco	3	5	1	LS4	1					
5	Sunco	3	5	1	LS5	0					
5	Sunco	3	5	1	LS6	0					
5	Sunco	3	5	1	LS7	0					
5	Sunco	3	5	1	LS8	0					
5	Sunco	3	5	1	I1	0					
5	Sunco	3	5	1	I2	0					
5	Sunco	3	5	1	I3	0					
5	CPI133814	1	1	1	SCI	4					
5	CPI133814	1	1	1	LS1	1	0	0	0	0	0
5	CPI133814	1	1	1	LS2	1	0	0	0	0	0
5	CPI133814	1	1	1	LS3	1	0	0	0	0	0
5	CPI133814	1	1	1	LS4	0	0	0	0	0	0
5	CPI133814	1	1	1	LS5	0	0	0	0	0	0
5	CPI133814	1	1	1	LS6	0	0	0	0	0	0
5	CPI133814	1	1	1	LS7	0	0	0	0	0	0
5	CPI133814	1	1	1	I1	0	0	0	0	0	0
5	CPI133814	1	1	2	LS1	1	0	0	0	0	0
5	CPI133814	1	1	2	LS2	0	0	0	0	0	0
5	CPI133814	1	1	2	LS3	0	0	0	0	0	0
5	CPI133814	1	1	2	LS4	0	0	0	0	0	0
5	CPI133814	1	1	2	LS5	0	0	0	0	0	0
5	CPI133814	1	1	3	LS1	0	0	0	0	0	0
5	CPI133814	1	1	3	LS2	0	0	0	0	0	0

5	CPI133814	1	1	3	LS3	0	0	0	0	0	0
5	CPI133814	1	1	3	LS4	0	0	0	0	0	0
5	CPI133814	1	2	1	SCI	0					
5	CPI133814	1	2	1	LS1	1	0	0	0	0	0
5	CPI133814	1	2	1	LS2	1	0	0	0	0	0
5	CPI133814	1	2	1	LS3	0	0	0	0	0	0
5	CPI133814	1	2	1	LS4	0	0	0	0	0	0
5	CPI133814	1	2	1	LS5	0	0	0	0	0	0
5	CPI133814	1	2	1	LS6	0	0	0	0	0	0
5	CPI133814	1	2	1	I1	0	0	0	0	0	0
5	CPI133814	1	2	1	I2	0	0	0	0	0	0
5	CPI133814	1	2	2	LS1	0	0	0	0	0	0
5	CPI133814	1	2	2	LS2	0	0	0	0	0	0
5	CPI133814	1	2	2	LS3	0	0	0	0	0	0
5	CPI133814	1	3	1	SCI	0					
5	CPI133814	1	3	1	LS1	2	11	3	3	2	3
5	CPI133814	1	3	1	LS2	1	4	2	2	0	0
5	CPI133814	1	3	1	LS3	0	0	0	0	0	0
5	CPI133814	1	3	1	LS4	0	0	0	0	0	0
5	CPI133814	1	3	1	LS5	0	0	0	0	0	0
5	CPI133814	1	3	1	LS6	0	0	0	0	0	0
5	CPI133814	1	3	1	LS7	0	0	0	0	0	0
5	CPI133814	1	3	1	I1	0	3	1	1	1	0
5	CPI133814	1	3	1	I2	0	0	0	0	0	0
5	CPI133814	1	3	2	LS1	0	0	0	0	0	0
5	CPI133814	1	3	2	LS2	0	0	0	0	0	0
5	CPI133814	1	3	2	LS3	0	0	0	0	0	0
5	CPI133814	1	3	2	LS4	0	0	0	0	0	0
5	CPI133814	1	3	3	LS1	0	0	0	0	0	0
5	CPI133814	1	3	3	LS2	0	0	0	0	0	0
5	CPI133814	1	3	3	LS3	0	0	0	0	0	0
5	CPI133814	1	4	1	SCI	1					
5	CPI133814	1	4	1	LS1	1	4	2	2	0	0
5	CPI133814	1	4	1	LS2	1	5	2	2	1	0
5	CPI133814	1	4	1	LS3	1	0	0	0	0	0
5	CPI133814	1	4	1	LS4	0	0	0	0	0	0

5	CPI133814	1	4	1	LS5	0	0	0	0	0	0
5	CPI133814	1	4	1	LS6	0	0	0	0	0	0
5	CPI133814	1	4	1	LS7	0	0	0	0	0	0
5	CPI133814	1	4	1	I1	0	0	0	0	0	0
5	CPI133814	1	4	1	I2	0	0	0	0	0	0
5	CPI133814	1	4	2	LS1	1	7	3	2	1	1
5	CPI133814	1	4	2	LS2	0	0	0	0	0	0
5	CPI133814	1	4	2	LS3	0	0	0	0	0	0
5	CPI133814	1	4	2	LS4	0	0	0	0	0	0
5	CPI133814	1	4	3	LS1	0	0	0	0	0	0
5	CPI133814	1	4	3	LS2	0	0	0	0	0	0
5	CPI133814	1	4	3	LS3	0	0	0	0	0	0
5	CPI133814	1	5	1	SCI	0					
5	CPI133814	1	5	1	LS1	1	6	3	2	1	0
5	CPI133814	1	5	1	LS2	1	2	2	0	0	0
5	CPI133814	1	5	1	LS3	1	0	0	0	0	0
5	CPI133814	1	5	1	LS4	0	0	0	0	0	0
5	CPI133814	1	5	1	LS5	0	0	0	0	0	0
5	CPI133814	1	5	1	LS6	0	0	0	0	0	0
5	CPI133814	1	5	1	LS7	0	0	0	0	0	0
5	CPI133814	1	5	1	I1	0	0	0	0	0	0
5	CPI133814	1	5	1	I2	0	0	0	0	0	0
5	CPI133814	1	5	2	LS1	0	0	0	0	0	0
5	CPI133814	1	5	2	LS2	0	0	0	0	0	0
5	CPI133814	1	5	2	LS3	0	0	0	0	0	0
5	CPI133814	1	5	2	LS4	0	0	0	0	0	0
5	CPI133814	1	5	3	LS1	0	0	0	0	0	0
5	CPI133814	1	5	3	LS2	0	0	0	0	0	0
5	CPI133814	1	5	3	LS3	0	0	0	0	0	0
5	CPI133814	2	1	1	SCI	3					
5	CPI133814	2	1	1	LS1	1	8	2	3	3	0
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5	CPI133814	2	1	1	LS3	2	4	2	1	1	0
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5	CPI133814	2	1	1	LS5	1	0	0	0	0	0
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5	CPI133814	2	1	1	LS7	0	0	0	0	0	0
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5	CPI133814	2	1	1	I2	0	0	0	0	0	0
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5	CPI133814	2	1	2	LS3	4	8	3	3	2	0
5	CPI133814	2	1	2	LS4	2	0	0	0	0	0
5	CPI133814	2	1	3	LS1	1	6	3	2	1	0
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5	CPI133814	2	1	3	LS3	3	5	3	2	0	0
5	CPI133814	2	2	1	SCI	3					
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5	CPI133814	2	2	1	LS2	1	8	2	3	2	1
5	CPI133814	2	2	1	LS3	1	10	3	1	3	3
5	CPI133814	2	2	1	LS4	2	9	3	2	2	2
5	CPI133814	2	2	1	LS5	2	6	3	2	1	0
5	CPI133814	2	2	1	LS6	1	5	2	3	0	0
5	CPI133814	2	2	1	LS7	0	0	0	0	0	0
5	CPI133814	2	2	1	LS8	0	0	0	0	0	0
5	CPI133814	2	3	1	SCI	1					
5	CPI133814	2	3	1	LS1	4	3	2	1	0	0
5	CPI133814	2	3	1	LS2	3	0	0	0	0	0
5	CPI133814	2	3	1	LS3	2	0	0	0	0	0
5	CPI133814	2	3	1	LS4	1	0	0	0	0	0
5	CPI133814	2	3	1	LS5	0	0	0	0	0	0
5	CPI133814	2	3	1	LS6	0	0	0	0	0	0
5	CPI133814	2	3	1	LS7	0	0	0	0	0	0
5	CPI133814	2	3	1	I1	1	1	1	0	0	0
5	CPI133814	2	3	1	I2	0	0	0	0	0	0
5	CPI133814	2	3	2	LS1	1	0	0	0	0	0
5	CPI133814	2	3	2	LS2	1	0	0	0	0	0
5	CPI133814	2	3	2	LS3	0	0	0	0	0	0
5	CPI133814	2	3	2	LS4	0	0	0	0	0	0
5	CPI133814	2	3	3	LS1	0	0	0	0	0	0
5	CPI133814	2	3	3	LS2	0	0	0	0	0	0
5	CPI133814	2	3	3	LS3	0	0	0	0	0	0

5	CPI133814	2	4	1	SCI	4					
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5	CPI133814	2	4	1	LS3	1	3	1	1	0	1
5	CPI133814	2	4	1	LS4	0	0	0	0	0	0
5	CPI133814	2	4	1	LS5	0	0	0	0	0	0
5	CPI133814	2	4	1	LS6	0	0	0	0	0	0
5	CPI133814	2	4	1	LS7	0	0	0	0	0	0
5	CPI133814	2	4	1	I1	0	2	1	1	0	0
5	CPI133814	2	4	1	I2	0	0	0	0	0	0
5	CPI133814	2	4	2	LS1	1	2	1	1	0	0
5	CPI133814	2	4	2	LS2	1	0	0	0	0	0
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5	CPI133814	2	4	3	LS1	1	0	0	0	0	0
5	CPI133814	2	4	3	LS2	0	0	0	0	0	0
5	CPI133814	2	4	3	LS3	0	0	0	0	0	0
5	CPI133814	2	5	1	SCI	4					
5	CPI133814	2	5	1	LS1	3	0	0	0	0	0
5	CPI133814	2	5	1	LS2	3	0	0	0	0	0
5	CPI133814	2	5	1	LS3	1	0	0	0	0	0
5	CPI133814	2	5	1	LS4	1	0	0	0	0	0
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5	CPI133814	2	5	1	I1	0	0	0	0	0	0
5	CPI133814	2	5	1	I2	0	0	0	0	0	0
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5	CPI133814	2	5	2	LS2	1	1	1	0	0	0
5	CPI133814	2	5	2	LS3	0	0	0	0	0	0
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5	CPI133814	2	5	3	LS2	1	0	0	0	0	0
5	CPI133814	2	5	3	LS3	0	0	0	0	0	0
5	CPI133814	2	5	3	LS4	0	0	0	0	0	0

5	CPI133814	2	5	4	LS1	1	0	0	0	0	0
5	CPI133814	2	5	4	LS2	1	0	0	0	0	0
5	CPI133814	2	5	4	LS3	0	0	0	0	0	0
5	CPI133814	3	1	1	SCI	0					
5	CPI133814	3	1	1	LS1	1					
5	CPI133814	3	1	1	LS2	0					
5	CPI133814	3	1	1	LS3	0					
5	CPI133814	3	1	1	LS4	0					
5	CPI133814	3	1	1	LS5	0					
5	CPI133814	3	1	1	LS6	0					
5	CPI133814	3	1	1	I1	0					
5	CPI133814	3	1	1	I2	0					
5	CPI133814	3	2	1	SCI	4					
5	CPI133814	3	2	1	LS1	1					
5	CPI133814	3	2	1	LS2	1					
5	CPI133814	3	2	1	LS3	1					
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5	CPI133814	3	2	1	LS5	0					
5	CPI133814	3	2	1	LS6	0					
5	CPI133814	3	2	1	I1	0					
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5	CPI133814	3	2	2	LS2	1					
5	CPI133814	3	3	1	SCI	4					
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5	CPI133814	3	3	1	LS2	1					
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5	CPI133814	3	3	1	LS4	0					
5	CPI133814	3	3	1	LS5	0					
5	CPI133814	3	3	1	LS6	0					
5	CPI133814	3	3	1	I1	0					
5	CPI133814	3	4	1	SCI	4					
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5	CPI133814	3	4	1	LS2	2					
5	CPI133814	3	4	1	LS3	1					
5	CPI133814	3	4	1	LS4	0					
5	CPI133814	3	4	1	LS5	0					

5	CPI133814	3	4	1	LS6	0					
5	CPI133814	3	4	1	LS7	0					
5	CPI133814	3	4	1	I1	0					
5	CPI133814	3	4	2	LS1	1					
5	CPI133814	3	4	2	LS2	1					
5	CPI133814	3	4	2	LS3	0					
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5	CPI133814	3	4	2	LS5	0					
5	CPI133814	3	4	3	LS1	0					
5	CPI133814	3	4	3	LS2	0					
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5	CPI133814	3	4	4	LS3	0					
5	CPI133814	3	5	1	SCI	0					
5	CPI133814	3	5	1	LS1	1					
5	CPI133814	3	5	1	LS2	1					
5	CPI133814	3	5	1	LS3	0					
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5	CPI133814	3	5	1	LS5	0					
5	CPI133814	3	5	1	LS6	0					
5	CPI133814	3	5	1	LS7	0					
5	CPI133814	3	5	1	I1	0					
5	CPI133814	3	5	1	I2	0					
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5	CPI133814	3	5	2	LS2	0					
5	CPI133814	3	5	2	LS3	0					
5	CPI133814	3	5	3	LS1	0					
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6	Puseas	1	1	1	SCI	4					
6	Puseas	1	1	1	LS1	2	7	1	2	2	2
6	Puseas	1	1	1	LS2	1	2	1	1	0	0
6	Puseas	1	1	1	LS3	1	3	1	2	0	0
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6	Puseas	1	1	1	LS5	1	1	1	0	0	0
6	Puseas	1	1	1	LS6	1	0	0	0	0	0
6	Puseas	1	1	1	LS7	0	0	0	0	0	0
6	Puseas	1	1	1	LS8	0	0	0	0	0	0
6	Puseas	1	1	1	LS9	0	0	0	0	0	0
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6	Puseas	1	1	1	I2	1	0	0	0	0	0
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6	Puseas	1	1	1	I4	0	0	0	0	0	0
6	Puseas	1	1	2	LS1	1	1	1	0	0	0
6	Puseas	1	1	2	LS2	1	3	2	1	0	0
6	Puseas	1	1	2	LS3	1	3	2	1	0	0
6	Puseas	1	2	1	SCI	4					
6	Puseas	1	2	1	LS1	0	2	2	0	0	0
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6	Puseas	1	2	1	LS3	2	1	1	0	0	0
6	Puseas	1	2	1	LS4	1	1	1	0	0	0
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6	Puseas	1	2	1	LS6	0	0	0	0	0	0
6	Puseas	1	2	1	LS7	0	0	0	0	0	0
6	Puseas	1	2	1	LS8	0	0	0	0	0	0
6	Puseas	1	2	1	I1	3	2	1	1	0	0
6	Puseas	1	2	1	I2	1	0	0	0	0	0
6	Puseas	1	2	1	I3	0	0	0	0	0	0
6	Puseas	1	3	1	SCI	4					
6	Puseas	1	3	1	LS1	1	0	0	0	0	0
6	Puseas	1	3	1	LS2	1	0	0	0	0	0
6	Puseas	1	3	1	LS3	1	0	0	0	0	0
6	Puseas	1	3	1	LS4	1	0	0	0	0	0
6	Puseas	1	3	1	LS5	1	0	0	0	0	0
6	Puseas	1	3	1	LS6	0	0	0	0	0	0
6	Puseas	1	3	1	LS7	0	0	0	0	0	0
6	Puseas	1	3	1	LS8	0	0	0	0	0	0
6	Puseas	1	3	1	LS9	0	0	0	0	0	0
6	Puseas	1	3	1	I1	1	1	1	0	0	0
6	Puseas	1	3	1	I2	1	0	0	0	0	0

6	Puseas	1	3	1	I3	0	0	0	0	0	0
6	Puseas	1	3	1	I4	0	0	0	0	0	0
6	Puseas	1	3	2	LS1	1	0	0	0	0	0
6	Puseas	1	3	2	LS2	1	0	0	0	0	0
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6	Puseas	1	3	2	LS5	0	0	0	0	0	0
6	Puseas	1	3	2	LS6	0	0	0	0	0	0
6	Puseas	1	3	2	LS7	0	0	0	0	0	0
6	Puseas	1	3	2	I1	1	1	1	0	0	0
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6	Puseas	1	3	3	LS2	1	0	0	0	0	0
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6	Puseas	1	3	3	LS4	0	0	0	0	0	0
6	Puseas	1	3	3	LS5	0	0	0	0	0	0
6	Puseas	1	3	3	LS6	0	0	0	0	0	0
6	Puseas	1	3	3	LS7	0	0	0	0	0	0
6	Puseas	1	3	3	I1	1	3	3	0	0	0
6	Puseas	1	3	3	I2	0	0	0	0	0	0
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6	Puseas	1	3	4	LS2	1	0	0	0	0	0
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6	Puseas	1	3	4	LS4	0	0	0	0	0	0
6	Puseas	1	3	4	LS5	0	0	0	0	0	0
6	Puseas	1	3	4	I1	0	0	0	0	0	0
6	Puseas	1	4	1	SCI	4					
6	Puseas	1	4	1	LS1	1	2	2	0	0	0
6	Puseas	1	4	1	LS2	1	3	1	2	0	0
6	Puseas	1	4	1	LS3	1	3	2	1	0	0
6	Puseas	1	4	1	LS4	1	2	2	0	0	0
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6	Puseas	1	4	1	LS7	0	0	0	0	0	0
6	Puseas	1	4	1	LS8	0	0	0	0	0	0
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6	Puseas	1	4	1	I2	3	0	0	0	0	0
6	Puseas	1	4	1	I3	1	0	0	0	0	0
6	Puseas	1	4	2	LS1	1	1	1	0	0	0
6	Puseas	1	4	2	LS2	1	1	1	0	0	0
6	Puseas	1	4	2	LS3	1	0	0	0	0	0
6	Puseas	1	4	2	LS4	1	0	0	0	0	0
6	Puseas	1	5	1	SCI	4					
6	Puseas	1	5	1	LS1	2	8	3	3	2	0
6	Puseas	1	5	1	LS2	1	5	3	1	1	0
6	Puseas	1	5	1	LS3	1	3	3	0	0	0
6	Puseas	1	5	1	LS4	1	3	3	0	0	0
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6	Puseas	1	5	1	LS6	0	0	0	0	0	0
6	Puseas	1	5	1	LS7	0	0	0	0	0	0
6	Puseas	1	5	1	I1	4	9	3	3	2	1
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6	Puseas	1	5	2	LS1	2	4	1	1	1	1
6	Puseas	1	5	2	LS2	2	3	1	1	1	0
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6	Puseas	1	5	2	LS5	1	0	0	0	0	0
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6	Puseas	1	5	3	LS4	2	3	2	1	0	0
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6	Puseas	2	1	1	SCI	4					
6	Puseas	2	1	1	LS1	1	4	3	1	0	0
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6	Puseas	2	1	1	LS3	2	4	4	0	0	0
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6	Puseas	2	1	1	LS5	0	0	0	0	0	0
6	Puseas	2	1	1	LS6	0	0	0	0	0	0
6	Puseas	2	1	1	I1	3	14	4	3	3	4
6	Puseas	2	1	1	I2	1	6	3	3	0	0
6	Puseas	2	1	1	I3	0	0	0	0	0	0
6	Puseas	2	1	2	LS1	2	3	1	1	1	0
6	Puseas	2	1	2	LS2	1	0	0	0	0	0
6	Puseas	2	1	2	LS3	1	3	3	0	0	0
6	Puseas	2	1	2	LS4	0	0	0	0	0	0
6	Puseas	2	1	2	LS5	0	0	0	0	0	0
6	Puseas	2	1	2	I1	4	6	2	2	0	2
6	Puseas	2	1	2	I2	1	0	0	0	0	0
6	Puseas	2	2	1	SCI	4					
6	Puseas	2	2	1	LS1	1	6	3	2	1	0
6	Puseas	2	2	1	LS2	1	6	3	3	0	0
6	Puseas	2	2	1	LS3	1	2	2	0	0	0
6	Puseas	2	2	1	LS4	1	1	1	0	0	0
6	Puseas	2	2	1	LS5	1	0	0	0	0	0
6	Puseas	2	2	1	LS6	0	0	0	0	0	0
6	Puseas	2	2	1	LS7	0	0	0	0	0	0
6	Puseas	2	2	1	LS8	0	0	0	0	0	0
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6	Puseas	2	2	1	I1	4	6	2	1	2	1
6	Puseas	2	2	1	I2	1	0	0	0	0	0
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6	Puseas	2	2	2	LS3	0	3	3	0	0	0
6	Puseas	2	2	2	LS4	0	0	0	0	0	0
6	Puseas	2	2	2	I1	2	0	0	0	0	0
6	Puseas	2	2	2	I2	0	0	0	0	0	0
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6	Puseas	2	2	3	LS2	0	0	0	0	0	0
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6	Puseas	2	2	3	LS4	0	0	0	0	0	0
6	Puseas	2	3	1	SCI	4					
6	Puseas	2	3	1	LS1	1	0	0	0	0	0
6	Puseas	2	3	1	LS2	1	0	0	0	0	0
6	Puseas	2	3	1	LS3	1	0	0	0	0	0
6	Puseas	2	3	1	LS4	1	0	0	0	0	0
6	Puseas	2	3	1	LS5	0	0	0	0	0	0
6	Puseas	2	3	1	LS6	0	0	0	0	0	0
6	Puseas	2	3	1	LS7	0	0	0	0	0	0
6	Puseas	2	3	1	LS8	0	0	0	0	0	0
6	Puseas	2	3	1	I1	1	3	2	1	0	0
6	Puseas	2	3	1	I2	0	0	0	0	0	0
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6	Puseas	2	3	2	LS1	1	4	3	1	0	0
6	Puseas	2	3	2	LS2	1	0	0	0	0	0
6	Puseas	2	3	2	LS3	1	0	0	0	0	0
6	Puseas	2	3	2	LS4	0	0	0	0	0	0
6	Puseas	2	3	2	LS5	0	0	0	0	0	0
6	Puseas	2	3	2	LS6	0	0	0	0	0	0
6	Puseas	2	3	2	I1	1	3	2	1	0	0
6	Puseas	2	3	2	I2	0	0	0	0	0	0
6	Puseas	2	3	3	LS1	1	2	2	0	0	0
6	Puseas	2	3	3	LS2	1	0	0	0	0	0
6	Puseas	2	3	3	LS3	1	0	0	0	0	0
6	Puseas	2	3	3	LS4	0	0	0	0	0	0
6	Puseas	2	3	3	LS5	0	0	0	0	0	0
6	Puseas	2	3	3	I1	1	3	1	1	1	0
6	Puseas	2	3	3	I2	0	0	0	0	0	0
6	Puseas	2	4	1	SCI	4					
6	Puseas	2	4	1	LS1	2	7	2	2	2	1
6	Puseas	2	4	1	LS2	1	5	3	2	0	0
6	Puseas	2	4	1	LS3	1	5	3	2	0	0
6	Puseas	2	4	1	LS4	2	5	3	2	0	0
6	Puseas	2	4	1	LS5	2	4	3	1	0	0

6	Puseas	2	4	1	LS6	1	0	0	0	0	0
6	Puseas	2	4	1	LS7	0	0	0	0	0	0
6	Puseas	2	4	1	LS8	0	0	0	0	0	0
6	Puseas	2	4	1	I1	4	7	2	2	2	1
6	Puseas	2	4	1	I2	1	3	3	0	0	0
6	Puseas	2	4	1	I3	0	0	0	0	0	0
6	Puseas	2	4	2	LS1	1	4	3	1	0	0
6	Puseas	2	4	2	LS2	2	8	3	1	2	2
6	Puseas	2	4	2	LS3	2	4	4	0	0	0
6	Puseas	2	4	2	LS4	1	0	0	0	0	0
6	Puseas	2	4	2	LS5	0	0	0	0	0	0
6	Puseas	2	4	2	LS6	0	0	0	0	0	0
6	Puseas	2	4	2	I1	4	7	2	2	2	1
6	Puseas	2	4	2	I2	2	0	0	0	0	0
6	Puseas	2	4	2	I3	0	0	0	0	0	0
6	Puseas	2	4	3	LS1	2	7	3	3	1	0
6	Puseas	2	4	3	LS2	2	4	4	0	0	0
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6	Puseas	2	4	3	LS4	0	0	0	0	0	0
6	Puseas	2	4	3	I1	4	5	1	1	2	1
6	Puseas	2	4	3	I2	3	4	2	2	0	0
6	Puseas	2	4	4	LS1	2	4	1	1	1	1
6	Puseas	2	4	4	LS2	2	3	3	0	0	0
6	Puseas	2	4	4	LS3	1	0	0	0	0	0
6	Puseas	2	4	4	I1	4	3	1	1	1	0
6	Puseas	2	5	1	SCI	4					
6	Puseas	2	5	1	LS1	1	4	4	0	0	0
6	Puseas	2	5	1	LS2	2	2	2	0	0	0
6	Puseas	2	5	1	LS3	1	2	2	0	0	0
6	Puseas	2	5	1	LS4	2	2	2	0	0	0
6	Puseas	2	5	1	LS5	1	0	0	0	0	0
6	Puseas	2	5	1	LS6	1	0	0	0	0	0
6	Puseas	2	5	1	LS7	0	0	0	0	0	0
6	Puseas	2	5	1	I1	4	11	4	3	2	2
6	Puseas	2	5	1	I2	3	9	2	2	3	2
6	Puseas	2	5	1	I3	1	0	0	0	0	0

6	Puseas	2	5	2	LS1	1	2	2	0	0	0
6	Puseas	2	5	2	LS2	1	2	2	0	0	0
6	Puseas	2	5	2	LS3	1	3	3	0	0	0
6	Puseas	2	5	2	LS4	0	0	0	0	0	0
6	Puseas	2	5	2	LS5	0	0	0	0	0	0
6	Puseas	2	5	2	I1	4	5	1	2	1	1
6	Puseas	2	5	2	I2	1	6	2	2	2	0
6	Puseas	2	5	3	LS1	1	2	2	0	0	0
6	Puseas	2	5	3	LS2	1	2	2	0	0	0
6	Puseas	2	5	3	LS3	0	2	2	0	0	0
6	Puseas	2	5	3	LS4	0	0	0	0	0	0
6	Puseas	2	5	3	I1	4	5	2	1	1	1
6	Puseas	2	5	3	I2	1	9	3	2	2	2
6	Puseas	3	1	1	SCI	4					
6	Puseas	3	1	1	LS1	2					
6	Puseas	3	1	1	LS2	1					
6	Puseas	3	1	1	LS3	1					
6	Puseas	3	1	1	LS4	1					
6	Puseas	3	1	1	LS5	0					
6	Puseas	3	1	1	LS6	0					
6	Puseas	3	1	1	LS7	0					
6	Puseas	3	1	1	I1	4					
6	Puseas	3	1	1	I2	3					
6	Puseas	3	1	1	I3	1					
6	Puseas	3	1	1	I4	0					
6	Puseas	3	1	2	LS1	1					
6	Puseas	3	1	2	LS2	1					
6	Puseas	3	1	2	LS3	0					
6	Puseas	3	1	2	LS4	0					
6	Puseas	3	1	2	LS5	0					
6	Puseas	3	1	2	I1	4					
6	Puseas	3	1	2	I2	3					
6	Puseas	3	1	3	LS1	1					
6	Puseas	3	1	3	LS2	1					
6	Puseas	3	1	3	LS3	0					
6	Puseas	3	1	3	LS4	0					

6	Puseas	3	1	3	I1	4					
6	Puseas	3	1	3	I2	2					
6	Puseas	3	2	1	SCI	4					
6	Puseas	3	2	1	LS1	1					
6	Puseas	3	2	1	LS2	1					
6	Puseas	3	2	1	LS3	1					
6	Puseas	3	2	1	LS4	1					
6	Puseas	3	2	1	LS5	0					
6	Puseas	3	2	1	LS6	0					
6	Puseas	3	2	1	LS7	0					
6	Puseas	3	2	1	I1	2					
6	Puseas	3	2	1	I2	0					
6	Puseas	3	2	1	I3	0					
6	Puseas	3	2	2	LS1	2					
6	Puseas	3	2	2	LS2	1					
6	Puseas	3	2	2	LS3	1					
6	Puseas	3	2	2	LS4	0					
6	Puseas	3	2	2	LS5	0					
6	Puseas	3	2	2	I1	1					
6	Puseas	3	2	2	I2	0					
6	Puseas	3	2	3	LS1	2					
6	Puseas	3	2	3	LS2	1					
6	Puseas	3	2	3	LS3	0					
6	Puseas	3	2	3	LS4	0					
6	Puseas	3	2	3	I1	2					
6	Puseas	3	2	3	I2	0					
6	Puseas	3	3	1	SCI	4					
6	Puseas	3	3	1	LS1	2					
6	Puseas	3	3	1	LS2	2					
6	Puseas	3	3	1	LS3	1					
6	Puseas	3	3	1	LS4	1					
6	Puseas	3	3	1	LS5	1					
6	Puseas	3	3	1	LS6	1					
6	Puseas	3	3	1	LS7	0					
6	Puseas	3	3	1	LS8	0					
6	Puseas	3	3	1	I1	4					

6	Puseas	3	3	1	I2	2					
6	Puseas	3	3	1	I3	1					
6	Puseas	3	3	2	LS1	1					
6	Puseas	3	3	2	LS2	1					
6	Puseas	3	3	2	LS3	0					
6	Puseas	3	3	2	I1	1					
6	Puseas	3	3	2	I2	0					
6	Puseas	3	4	1	SCI	4					
6	Puseas	3	4	1	LS1	1					
6	Puseas	3	4	1	LS2	1					
6	Puseas	3	4	1	LS3	2					
6	Puseas	3	4	1	LS4	1					
6	Puseas	3	4	1	LS5	1					
6	Puseas	3	4	1	LS6	1					
6	Puseas	3	4	1	LS7	0					
6	Puseas	3	4	1	I1	4					
6	Puseas	3	4	1	I2	1					
6	Puseas	3	4	1	I3	0					
6	Puseas	3	4	2	LS1	2					
6	Puseas	3	4	2	LS2	1					
6	Puseas	3	4	2	LS3	1					
6	Puseas	3	4	2	LS4	1					
6	Puseas	3	4	2	I1	4					
6	Puseas	3	4	2	I2	2					
6	Puseas	3	5	1	SCI	4					
6	Puseas	3	5	1	LS1	1					
6	Puseas	3	5	1	LS2	1					
6	Puseas	3	5	1	LS3	1					
6	Puseas	3	5	1	LS4	1					
6	Puseas	3	5	1	LS5	1					
6	Puseas	3	5	1	LS6	0					
6	Puseas	3	5	1	LS7	0					
6	Puseas	3	5	1	LS8	0					
6	Puseas	3	5	1	I1	3					
6	Puseas	3	5	1	I2	1					
6	Puseas	3	5	1	I3	0					

6	Puseas	3	5	1	I4	0					
6	Puseas	3	5	2	LS1	1					
6	Puseas	3	5	2	LS2	1					
6	Puseas	3	5	2	LS3	1					
6	Puseas	3	5	2	LS4	0					
6	Puseas	3	5	2	LS5	0					
6	Puseas	3	5	2	LS6	0					
6	Puseas	3	5	2	I1	4					
6	Puseas	3	5	2	I2	1					
6	Puseas	3	5	3	LS1	1					
6	Puseas	3	5	3	LS2	1					
6	Puseas	3	5	3	LS3	0					
6	Puseas	3	5	3	LS4	0					
6	Puseas	3	5	3	LS5	0					
6	Puseas	3	5	3	I1	4					
6	Puseas	3	5	3	I2	1					
6	Puseas	3	5	4	LS1	1					
6	Puseas	3	5	4	LS2	1					
6	Puseas	3	5	4	LS3	0					
6	Puseas	3	5	4	LS4	0					
6	Puseas	3	5	4	I1	4					
6	Vasco	1	1	1	SCI	4					
6	Vasco	1	1	1	LS1	1	3	2	1	0	0
6	Vasco	1	1	1	LS2	1	2	1	1	0	0
6	Vasco	1	1	1	LS3	1	0	0	0	0	0
6	Vasco	1	1	1	LS4	0	0	0	0	0	0
6	Vasco	1	1	1	LS5	0	0	0	0	0	0
6	Vasco	1	1	1	LS6	0	0	0	0	0	0
6	Vasco	1	1	1	LS7	0	0	0	0	0	0
6	Vasco	1	1	1	LS8	0	0	0	0	0	0
6	Vasco	1	1	1	I1	1	0	0	0	0	0
6	Vasco	1	1	1	I2	0	0	0	0	0	0
6	Vasco	1	1	1	I3	0	0	0	0	0	0
6	Vasco	1	2	1	SCI	3					
6	Vasco	1	2	1	LS1	1	0	0	0	0	0
6	Vasco	1	2	1	LS2	1	0	0	0	0	0

6	Vasco	1	2	1	LS3	1	0	0	0	0	0
6	Vasco	1	2	1	LS4	0	0	0	0	0	0
6	Vasco	1	2	1	LS5	0	0	0	0	0	0
6	Vasco	1	2	1	LS6	0	0	0	0	0	0
6	Vasco	1	2	1	LS7	0	0	0	0	0	0
6	Vasco	1	2	1	LS8	0	0	0	0	0	0
6	Vasco	1	2	1	I1	0	0	0	0	0	0
6	Vasco	1	2	1	I2	0	0	0	0	0	0
6	Vasco	1	2	1	I3	0	0	0	0	0	0
6	Vasco	1	3	1	SCI	4					
6	Vasco	1	3	1	LS1	1	4	2	2	0	0
6	Vasco	1	3	1	LS2	1	3	2	1	0	0
6	Vasco	1	3	1	LS3	1	0	0	0	0	0
6	Vasco	1	3	1	LS4	1	0	0	0	0	0
6	Vasco	1	3	1	LS5	1	1	1	0	0	0
6	Vasco	1	3	1	LS6	0	0	0	0	0	0
6	Vasco	1	3	1	LS7	0	0	0	0	0	0
6	Vasco	1	3	1	LS8	0	0	0	0	0	0
6	Vasco	1	3	1	LS9	0	0	0	0	0	0
6	Vasco	1	3	1	I1	1	1	1	0	0	0
6	Vasco	1	3	1	I2	0	0	0	0	0	0
6	Vasco	1	3	1	I3	0	0	0	0	0	0
6	Vasco	1	3	2	LS1	1	3	2	1	0	0
6	Vasco	1	3	2	LS2	1	1	1	0	0	0
6	Vasco	1	3	2	LS3	1	0	0	0	0	0
6	Vasco	1	3	2	LS4	0	0	0	0	0	0
6	Vasco	1	3	2	LS5	0	0	0	0	0	0
6	Vasco	1	3	2	LS6	0	0	0	0	0	0
6	Vasco	1	3	2	I1	1	3	2	1	0	0
6	Vasco	1	3	2	I2	0	0	0	0	0	0
6	Vasco	1	3	3	LS1	1	3	2	1	0	0
6	Vasco	1	3	3	LS2	1	0	0	0	0	0
6	Vasco	1	3	3	LS3	0	0	0	0	0	0
6	Vasco	1	3	3	LS4	0	0	0	0	0	0
6	Vasco	1	3	3	LS5	0	0	0	0	0	0
6	Vasco	1	3	3	I1	0	0	0	0	0	0

6	Vasco	1	3	4	LS1	1	0	0	0	0	0
6	Vasco	1	3	4	LS2	0	0	0	0	0	0
6	Vasco	1	3	4	LS3	0	0	0	0	0	0
6	Vasco	1	4	1	SCI	1					
6	Vasco	1	4	1	LS1	1	3	2	1	0	0
6	Vasco	1	4	1	LS2	1	2	1	1	0	0
6	Vasco	1	4	1	LS3	1	0	0	0	0	0
6	Vasco	1	4	1	LS4	1	0	0	0	0	0
6	Vasco	1	4	1	LS5	1	0	0	0	0	0
6	Vasco	1	4	1	LS6	0	0	0	0	0	0
6	Vasco	1	4	1	LS7	0	0	0	0	0	0
6	Vasco	1	4	1	LS8	0	0	0	0	0	0
6	Vasco	1	4	1	I1	1	1	1	0	0	0
6	Vasco	1	4	1	I2	0	0	0	0	0	0
6	Vasco	1	5	1	SCI	4					
6	Vasco	1	5	1	LS1	3	8	3	1	2	2
6	Vasco	1	5	1	LS2	1	3	1	1	1	0
6	Vasco	1	5	1	LS3	0	3	2	1	0	0
6	Vasco	1	5	1	LS4	0	1	1	0	0	0
6	Vasco	1	5	1	LS5	1	3	2	1	0	0
6	Vasco	1	5	1	LS6	1	4	2	2	0	0
6	Vasco	1	5	1	LS7	0	0	0	0	0	0
6	Vasco	1	5	1	LS8	0	0	0	0	0	0
6	Vasco	1	5	1	LS9	0	0	0	0	0	0
6	Vasco	1	5	1	I1	4	0	0	0	0	0
6	Vasco	1	5	1	I2	2	4	1	1	1	1
6	Vasco	1	5	1	I3	0	3	3	0	0	0
6	Vasco	1	5	1	I4	0	0	0	0	0	0
6	Vasco	1	5	1	P	0	0	0	0	0	0
6	Vasco	1	5	2	LS1	1	3	1	1	1	0
6	Vasco	1	5	2	LS2	1	1	1	0	0	0
6	Vasco	1	5	2	LS3	0	3	2	1	0	0
6	Vasco	1	5	2	LS4	0	0	0	0	0	0
6	Vasco	1	5	3	LS1	0	0	0	0	0	0
6	Vasco	1	5	3	LS2	0	0	0	0	0	0
6	Vasco	2	1	1	SCI	4					

6	Vasco	2	1	1	LS1	1	0	0	0	0	0
6	Vasco	2	1	1	LS2	1	0	0	0	0	0
6	Vasco	2	1	1	LS3	0	0	0	0	0	0
6	Vasco	2	1	1	LS4	0	0	0	0	0	0
6	Vasco	2	1	1	LS5	0	0	0	0	0	0
6	Vasco	2	1	1	LS6	0	0	0	0	0	0
6	Vasco	2	1	1	LS7	0	0	0	0	0	0
6	Vasco	2	1	1	LS8	0	0	0	0	0	0
6	Vasco	2	1	1	I1	2	0	0	0	0	0
6	Vasco	2	1	1	I2	0	0	0	0	0	0
6	Vasco	2	1	1	I3	0	0	0	0	0	0
6	Vasco	2	1	2	LS1	0	0	0	0	0	0
6	Vasco	2	1	2	LS2	0	0	0	0	0	0
6	Vasco	2	1	2	LS3	0	0	0	0	0	0
6	Vasco	2	2	1	SCI	4					
6	Vasco	2	2	1	LS1	1	6	2	2	2	0
6	Vasco	2	2	1	LS2	1	7	3	2	1	1
6	Vasco	2	2	1	LS3	1	5	2	2	1	0
6	Vasco	2	2	1	LS4	1	3	2	1	0	0
6	Vasco	2	2	1	LS5	1	3	3	0	0	0
6	Vasco	2	2	1	LS6	2	6	3	3	0	0
6	Vasco	2	2	1	LS7	0	0	0	0	0	0
6	Vasco	2	2	1	LS8	0	0	0	0	0	0
6	Vasco	2	2	1	LS9	0	0	0	0	0	0
6	Vasco	2	2	1	I1	1	8	2	2	2	2
6	Vasco	2	2	1	I2	0	0	0	0	0	0
6	Vasco	2	2	1	I3	0	0	0	0	0	0
6	Vasco	2	2	2	LS1	0	2	2	0	0	0
6	Vasco	2	2	2	LS2	0	0	0	0	0	0
6	Vasco	2	2	2	LS3	0	0	0	0	0	0
6	Vasco	2	2	2	LS4	1	1	1	0	0	0
6	Vasco	2	2	2	LS5	0	0	0	0	0	0
6	Vasco	2	2	2	LS6	0	0	0	0	0	0
6	Vasco	2	2	2	I1	1	5	2	1	1	1
6	Vasco	2	2	2	I2	0	0	0	0	0	0
6	Vasco	2	2	3	LS1	1	4	2	2	0	0

6	Vasco	2	2	3	LS2	0	0	0	0	0	0
6	Vasco	2	2	3	LS3	1	0	0	0	0	0
6	Vasco	2	2	3	LS4	1	0	0	0	0	0
6	Vasco	2	2	3	LS5	0	0	0	0	0	0
6	Vasco	2	2	3	LS6	0	0	0	0	0	0
6	Vasco	2	2	3	I1	1	4	1	1	1	1
6	Vasco	2	2	3	I2	0	0	0	0	0	0
6	Vasco	2	2	4	LS1	0	3	3	0	0	0
6	Vasco	2	2	4	LS2	0	0	0	0	0	0
6	Vasco	2	2	4	LS3	0	0	0	0	0	0
6	Vasco	2	2	4	LS4	0	0	0	0	0	0
6	Vasco	2	3	1	SCI	4					
6	Vasco	2	3	1	LS1	1	0	0	0	0	0
6	Vasco	2	3	1	LS2	1	0	0	0	0	0
6	Vasco	2	3	1	LS3	0	0	0	0	0	0
6	Vasco	2	3	1	LS4	0	0	0	0	0	0
6	Vasco	2	3	1	LS5	0	0	0	0	0	0
6	Vasco	2	3	1	LS6	0	0	0	0	0	0
6	Vasco	2	3	1	LS7	0	0	0	0	0	0
6	Vasco	2	3	1	LS8	0	0	0	0	0	0
6	Vasco	2	3	1	LS9	0	0	0	0	0	0
6	Vasco	2	4	1	SCI	4					
6	Vasco	2	4	1	LS1	1	11	3	3	3	2
6	Vasco	2	4	1	LS2	1	3	2	1	0	0
6	Vasco	2	4	1	LS3	1	4	2	2	0	0
6	Vasco	2	4	1	LS4	1	1	1	0	0	0
6	Vasco	2	4	1	LS5	1	0	0	0	0	0
6	Vasco	2	4	1	LS6	0	0	0	0	0	0
6	Vasco	2	4	1	LS7	0	0	0	0	0	0
6	Vasco	2	4	1	LS8	0	0	0	0	0	0
6	Vasco	2	4	1	LS9	0	0	0	0	0	0
6	Vasco	2	4	1	I1	1	3	2	1	0	0
6	Vasco	2	4	1	I2	0	0	0	0	0	0
6	Vasco	2	4	1	I3	0	0	0	0	0	0
6	Vasco	2	4	2	LS1	1	4	3	1	0	0
6	Vasco	2	4	2	LS2	1	0	0	0	0	0

6	Vasco	2	4	2	LS3	0	0	0	0	0	0
6	Vasco	2	4	2	LS4	0	0	0	0	0	0
6	Vasco	2	4	2	LS5	0	0	0	0	0	0
6	Vasco	2	4	2	LS6	0	0	0	0	0	0
6	Vasco	2	4	2	I1	1	4	3	1	0	0
6	Vasco	2	4	2	I2	0	0	0	0	0	0
6	Vasco	2	4	3	LS1	1	0	0	0	0	0
6	Vasco	2	4	3	LS2	1	0	0	0	0	0
6	Vasco	2	4	3	LS3	1	0	0	0	0	0
6	Vasco	2	4	3	LS4	0	0	0	0	0	0
6	Vasco	2	4	3	LS5	0	0	0	0	0	0
6	Vasco	2	4	3	LS6	0	0	0	0	0	0
6	Vasco	2	4	3	I1	1	4	1	1	1	1
6	Vasco	2	4	3	I2	0	0	0	0	0	0
6	Vasco	2	5	1	SCI	4					
6	Vasco	2	5	1	LS1	4	8	3	2	2	1
6	Vasco	2	5	1	LS2	1	5	2	2	1	0
6	Vasco	2	5	1	LS3	2	2	2	0	0	0
6	Vasco	2	5	1	LS4	1	0	0	0	0	0
6	Vasco	2	5	1	LS5	1	0	0	0	0	0
6	Vasco	2	5	1	LS6	1	0	0	0	0	0
6	Vasco	2	5	1	LS7	0	0	0	0	0	0
6	Vasco	2	5	1	LS8	0	0	0	0	0	0
6	Vasco	2	5	1	LS9	0	0	0	0	0	0
6	Vasco	2	5	1	I1	2	3	2	1	0	0
6	Vasco	2	5	1	I2	0	0	0	0	0	0
6	Vasco	2	5	1	I3	0	0	0	0	0	0
6	Vasco	2	5	2	LS1	1	7	2	1	2	2
6	Vasco	2	5	2	LS2	1	5	2	1	1	1
6	Vasco	2	5	2	LS3	1	0	0	0	0	0
6	Vasco	2	5	2	LS4	1	0	0	0	0	0
6	Vasco	2	5	2	LS5	0	0	0	0	0	0
6	Vasco	2	5	2	LS6	0	0	0	0	0	0
6	Vasco	2	5	2	LS7	0	0	0	0	0	0
6	Vasco	2	5	2	I1	1	4	1	1	1	1
6	Vasco	2	5	2	I2	0	0	0	0	0	0

6	Vasco	2	5	3	LS1	1	0	0	0	0	0
6	Vasco	2	5	3	LS2	0	0	0	0	0	0
6	Vasco	2	5	3	LS3	0	0	0	0	0	0
6	Vasco	2	5	3	LS4	0	0	0	0	0	0
6	Vasco	2	5	3	LS5	0	0	0	0	0	0
6	Vasco	2	5	4	LS1	1	0	0	0	0	0
6	Vasco	2	5	4	LS2	0	0	0	0	0	0
6	Vasco	2	5	4	LS3	0	0	0	0	0	0
6	Vasco	2	5	4	LS4	0	0	0	0	0	0
6	Vasco	3	1	1	SCI	4					
6	Vasco	3	1	1	LS1	3					
6	Vasco	3	1	1	LS2	1					
6	Vasco	3	1	1	LS3	1					
6	Vasco	3	1	1	LS4	2					
6	Vasco	3	1	1	LS5	1					
6	Vasco	3	1	1	LS6	0					
6	Vasco	3	1	1	LS7	0					
6	Vasco	3	1	1	LS8	0					
6	Vasco	3	1	1	LS9	0					
6	Vasco	3	1	1	I1	1					
6	Vasco	3	1	1	I2	0					
6	Vasco	3	1	1	I3	0					
6	Vasco	3	1	2	LS1	0					
6	Vasco	3	1	2	LS2	0					
6	Vasco	3	1	2	LS3	0					
6	Vasco	3	1	2	LS4	0					
6	Vasco	3	2	1	SCI	4					
6	Vasco	3	2	1	LS1	1					
6	Vasco	3	2	1	LS2	1					
6	Vasco	3	2	1	LS3	0					
6	Vasco	3	2	1	LS4	0					
6	Vasco	3	2	1	LS5	0					
6	Vasco	3	2	1	LS6	0					
6	Vasco	3	2	1	LS7	0					
6	Vasco	3	2	1	LS8	0					
6	Vasco	3	2	1	LS9	0					

6	Vasco	3	2	1	I1	1					
6	Vasco	3	2	1	I2	0					
6	Vasco	3	2	1	I3	0					
6	Vasco	3	2	2	LS1	0					
6	Vasco	3	2	2	LS2	0					
6	Vasco	3	2	2	LS3	0					
6	Vasco	3	2	2	LS4	0					
6	Vasco	3	2	2	LS5	0					
6	Vasco	3	2	2	I1	1					
6	Vasco	3	2	2	I2	0					
6	Vasco	3	2	3	LS1	1					
6	Vasco	3	2	3	LS2	0					
6	Vasco	3	2	3	LS3	0					
6	Vasco	3	2	3	LS4	0					
6	Vasco	3	2	3	I1	1					
6	Vasco	3	2	3	I2	0					
6	Vasco	3	2	4	LS1	0					
6	Vasco	3	2	4	LS2	0					
6	Vasco	3	2	4	LS3	0					
6	Vasco	3	3	1	SCI	4					
6	Vasco	3	3	1	LS1	2					
6	Vasco	3	3	1	LS2	1					
6	Vasco	3	3	1	LS3	1					
6	Vasco	3	3	1	LS4	1					
6	Vasco	3	3	1	LS5	1					
6	Vasco	3	3	1	LS6	1					
6	Vasco	3	3	1	LS7	0					
6	Vasco	3	3	1	LS8	0					
6	Vasco	3	3	1	I1	2					
6	Vasco	3	3	1	I2	0					
6	Vasco	3	3	1	I3	0					
6	Vasco	3	3	2	LS1	1					
6	Vasco	3	3	2	LS2	0					
6	Vasco	3	3	2	LS3	0					
6	Vasco	3	3	2	LS4	0					
6	Vasco	3	3	2	LS5	0					

6	Vasco	3	3	2	I1	1					
6	Vasco	3	3	2	I2	0					
6	Vasco	3	3	3	LS1	1					
6	Vasco	3	3	3	LS2	0					
6	Vasco	3	3	3	LS3	1					
6	Vasco	3	3	3	LS4	0					
6	Vasco	3	3	3	I1	1					
6	Vasco	3	3	3	I2	0					
6	Vasco	3	4	1	SCI	2					
6	Vasco	3	4	1	LS1	1					
6	Vasco	3	4	1	LS2	1					
6	Vasco	3	4	1	LS3	1					
6	Vasco	3	4	1	LS4	1					
6	Vasco	3	4	1	LS5	1					
6	Vasco	3	4	1	LS6	0					
6	Vasco	3	4	1	LS7	0					
6	Vasco	3	4	1	LS8	0					
6	Vasco	3	4	1	I1	1					
6	Vasco	3	4	1	I2	0					
6	Vasco	3	5	1	SCI	4					
6	Vasco	3	5	1	LS1	1					
6	Vasco	3	5	1	LS2	1					
6	Vasco	3	5	1	LS3	1					
6	Vasco	3	5	1	LS4	0					
6	Vasco	3	5	1	LS5	0					
6	Vasco	3	5	1	LS6	0					
6	Vasco	3	5	1	LS7	0					
6	Vasco	3	5	1	LS8	0					
6	Vasco	3	5	1	I1	3					
6	Vasco	3	5	1	I2	1					
6	Vasco	3	5	1	I3	0					
6	Vasco	3	5	2	LS1	1					
6	Vasco	3	5	2	LS2	1					
6	Vasco	3	5	2	LS3	1					
6	Vasco	3	5	2	LS4	0					
6	Vasco	3	5	2	LS5	0					

6	Vasco	3	5	2	LS6	0					
6	Vasco	3	5	2	I1	1					
6	Vasco	3	5	2	I2	0					
6	Vasco	3	5	3	LS1	1					
6	Vasco	3	5	3	LS2	1					
6	Vasco	3	5	3	LS3	1					
6	Vasco	3	5	3	LS4	0					
6	Vasco	3	5	3	LS5	0					
6	Vasco	3	5	3	I1	1					
6	Vasco	3	5	3	I2	0					
6	Vasco	3	5	4	LS1	1					
6	Vasco	3	5	4	LS2	0					
6	Vasco	3	5	4	LS3	0					
6	Vasco	3	5	4	LS4	0					
6	2-49	1	1	1	SCI	4					
6	2-49	1	1	1	LS1	1	0	0	0	0	0
6	2-49	1	1	1	LS2	1	0	0	0	0	0
6	2-49	1	1	1	LS3	0	0	0	0	0	0
6	2-49	1	1	1	LS4	0	0	0	0	0	0
6	2-49	1	1	1	LS5	0	0	0	0	0	0
6	2-49	1	1	1	LS6	0	0	0	0	0	0
6	2-49	1	1	1	LS7	0	0	0	0	0	0
6	2-49	1	1	1	LS8	0	0	0	0	0	0
6	2-49	1	1	1	I1	1	0	0	0	0	0
6	2-49	1	1	1	I2	0	0	0	0	0	0
6	2-49	1	1	2	LS1	1	0	0	0	0	0
6	2-49	1	1	2	LS2	1	0	0	0	0	0
6	2-49	1	1	2	LS3	1	0	0	0	0	0
6	2-49	1	1	2	LS4	0	0	0	0	0	0
6	2-49	1	1	2	LS5	0	0	0	0	0	0
6	2-49	1	1	2	LS6	0	0	0	0	0	0
6	2-49	1	1	2	LS7	0	0	0	0	0	0
6	2-49	1	1	2	I1	0	0	0	0	0	0
6	2-49	1	1	2	I2	0	0	0	0	0	0
6	2-49	1	1	3	LS1	0	0	0	0	0	0
6	2-49	1	1	3	LS2	0	0	0	0	0	0

6	2-49	1	1	3	LS3	0	0	0	0	0	0
6	2-49	1	1	3	LS4	0	0	0	0	0	0
6	2-49	1	1	3	LS5	0	0	0	0	0	0
6	2-49	1	1	3	I1	0	0	0	0	0	0
6	2-49	1	1	4	LS1	0	0	0	0	0	0
6	2-49	1	1	4	LS2	0	0	0	0	0	0
6	2-49	1	1	4	LS3	0	0	0	0	0	0
6	2-49	1	1	4	LS4	0	0	0	0	0	0
6	2-49	1	2	1	SCI	4					
6	2-49	1	2	1	LS1	1	0	0	0	0	0
6	2-49	1	2	1	LS2	1	0	0	0	0	0
6	2-49	1	2	1	LS3	1	0	0	0	0	0
6	2-49	1	2	1	LS4	0	0	0	0	0	0
6	2-49	1	2	1	LS5	0	0	0	0	0	0
6	2-49	1	2	1	LS6	0	0	0	0	0	0
6	2-49	1	2	1	LS7	0	0	0	0	0	0
6	2-49	1	2	1	LS8	0	0	0	0	0	0
6	2-49	1	2	1	I1	1	0	0	0	0	0
6	2-49	1	2	1	I2	0	0	0	0	0	0
6	2-49	1	3	1	SCI	4					
6	2-49	1	3	1	LS1	1	0	0	0	0	0
6	2-49	1	3	1	LS2	1	0	0	0	0	0
6	2-49	1	3	1	LS3	0	0	0	0	0	0
6	2-49	1	3	1	LS4	0	0	0	0	0	0
6	2-49	1	3	1	LS5	0	0	0	0	0	0
6	2-49	1	3	1	LS6	0	0	0	0	0	0
6	2-49	1	3	1	LS7	0	0	0	0	0	0
6	2-49	1	3	1	LS8	0	0	0	0	0	0
6	2-49	1	3	1	I1	0	0	0	0	0	0
6	2-49	1	3	1	I2	0	0	0	0	0	0
6	2-49	1	3	2	LS1	0	0	0	0	0	0
6	2-49	1	3	2	LS2	0	0	0	0	0	0
6	2-49	1	4	1	SCI	4					
6	2-49	1	4	1	LS1	1	5	2	2	1	0
6	2-49	1	4	1	LS2	1	4	2	2	0	0
6	2-49	1	4	1	LS3	0	0	0	0	0	0

6	2-49	1	4	1	LS4	0	0	0	0	0	0
6	2-49	1	4	1	LS5	0	0	0	0	0	0
6	2-49	1	4	1	LS6	0	0	0	0	0	0
6	2-49	1	4	1	LS7	0	0	0	0	0	0
6	2-49	1	4	1	LS8	0	0	0	0	0	0
6	2-49	1	4	1	LS9	0	0	0	0	0	0
6	2-49	1	4	1	I1	0	0	0	0	0	0
6	2-49	1	4	1	I2	0	0	0	0	0	0
6	2-49	1	4	2	LS1	1	2	1	1	0	0
6	2-49	1	4	2	LS2	1	0	0	0	0	0
6	2-49	1	4	2	LS3	0	0	0	0	0	0
6	2-49	1	4	2	LS4	0	0	0	0	0	0
6	2-49	1	4	2	LS5	0	0	0	0	0	0
6	2-49	1	4	2	I1	0	0	0	0	0	0
6	2-49	1	4	3	LS1	2	0	0	0	0	0
6	2-49	1	4	3	LS2	1	0	0	0	0	0
6	2-49	1	4	3	LS3	0	0	0	0	0	0
6	2-49	1	4	3	LS4	0	0	0	0	0	0
6	2-49	1	4	3	LS5	0	0	0	0	0	0
6	2-49	1	4	4	LS1	1	0	0	0	0	0
6	2-49	1	4	4	LS2	1	0	0	0	0	0
6	2-49	1	4	4	LS3	0	0	0	0	0	0
6	2-49	1	5	1	LS1	1	4	2	2	0	0
6	2-49	1	5	1	LS2	1	1	1	0	0	0
6	2-49	1	5	1	LS3	2	4	2	1	1	0
6	2-49	1	5	1	LS4	1	3	2	1	0	0
6	2-49	1	5	1	LS5	1	0	0	0	0	0
6	2-49	1	5	1	LS6	0	0	0	0	0	0
6	2-49	1	5	1	LS7	0	0	0	0	0	0
6	2-49	1	5	1	LS8	0	0	0	0	0	0
6	2-49	1	5	1	I1	1	0	0	0	0	0
6	2-49	1	5	1	I2	0	0	0	0	0	0
6	2-49	1	5	2	LS1	4	4	3	1	0	0
6	2-49	1	5	2	LS2	2	0	0	0	0	0
6	2-49	1	5	2	LS3	0	0	0	0	0	0
6	2-49	1	5	2	LS4	0	0	0	0	0	0

6	2-49	1	5	2	LS5	0	0	0	0	0	0
6	2-49	1	5	2	I1	0	0	0	0	0	0
6	2-49	1	5	3	LS1	1	0	0	0	0	0
6	2-49	1	5	3	LS2	0	0	0	0	0	0
6	2-49	1	5	3	LS3	0	0	0	0	0	0
6	2-49	1	5	3	LS4	0	0	0	0	0	0
6	2-49	2	1	1	SCI	1					
6	2-49	2	1	1	LS1	2	4	3	1	0	0
6	2-49	2	1	1	LS2	1	3	2	1	0	0
6	2-49	2	1	1	LS3	1	1	1	0	0	0
6	2-49	2	1	1	LS4	1	0	0	0	0	0
6	2-49	2	1	1	LS5	0	0	0	0	0	0
6	2-49	2	1	1	LS6	0	0	0	0	0	0
6	2-49	2	1	1	LS7	0	0	0	0	0	0
6	2-49	2	1	1	LS8	0	0	0	0	0	0
6	2-49	2	1	1	LS9	0	0	0	0	0	0
6	2-49	2	1	1	LS10	0	0	0	0	0	0
6	2-49	2	1	1	I1	1	0	0	0	0	0
6	2-49	2	1	1	I2	0	0	0	0	0	0
6	2-49	2	1	1	I3	0	0	0	0	0	0
6	2-49	2	1	1	P	0	0	0	0	0	0
6	2-49	2	1	2	LS1	1	6	2	2	2	0
6	2-49	2	1	2	LS2	1	2	1	1	0	0
6	2-49	2	1	2	LS3	1	0	0	0	0	0
6	2-49	2	1	2	LS4	0	0	0	0	0	0
6	2-49	2	1	2	LS5	0	0	0	0	0	0
6	2-49	2	1	2	LS6	0	0	0	0	0	0
6	2-49	2	1	2	LS7	0	0	0	0	0	0
6	2-49	2	1	2	I1	1	0	0	0	0	0
6	2-49	2	1	2	I2	0	0	0	0	0	0
6	2-49	2	1	2	I3	0	0	0	0	0	0
6	2-49	2	1	3	LS1	1	0	0	0	0	0
6	2-49	2	1	3	LS2	1	0	0	0	0	0
6	2-49	2	1	3	LS3	1	0	0	0	0	0
6	2-49	2	1	3	LS4	0	0	0	0	0	0
6	2-49	2	1	3	LS5	0	0	0	0	0	0

6	2-49	2	1	3	LS6	0	0	0	0	0	0
6	2-49	2	1	3	LS7	0	0	0	0	0	0
6	2-49	2	1	3	I1	0	2	1	1	0	0
6	2-49	2	1	3	I2	0	0	0	0	0	0
6	2-49	2	1	4	LS1	0	0	0	0	0	0
6	2-49	2	1	4	LS2	0	0	0	0	0	0
6	2-49	2	1	4	LS3	0	0	0	0	0	0
6	2-49	2	1	4	LS4	0	0	0	0	0	0
6	2-49	2	2	1	SCI	4					
6	2-49	2	2	1	LS1	1	6	2	2	1	1
6	2-49	2	2	1	LS2	1	3	2	1	0	0
6	2-49	2	2	1	LS3	1	0	0	0	0	0
6	2-49	2	2	1	LS4	0	0	0	0	0	0
6	2-49	2	2	1	LS5	0	0	0	0	0	0
6	2-49	2	2	1	LS6	0	0	0	0	0	0
6	2-49	2	2	1	LS7	0	0	0	0	0	0
6	2-49	2	2	1	LS8	0	0	0	0	0	0
6	2-49	2	2	1	I1	1	4	1	1	1	1
6	2-49	2	2	1	I2	0	0	0	0	0	0
6	2-49	2	2	1	I3	0	0	0	0	0	0
6	2-49	2	2	2	LS1	0	3	1	1	1	0
6	2-49	2	2	2	LS2	0	0	0	0	0	0
6	2-49	2	2	2	LS3	0	0	0	0	0	0
6	2-49	2	2	2	LS4	0	0	0	0	0	0
6	2-49	2	2	2	LS5	0	0	0	0	0	0
6	2-49	2	2	2	LS6	0	0	0	0	0	0
6	2-49	2	2	2	I1	0	0	0	0	0	0
6	2-49	2	2	2	I2	0	0	0	0	0	0
6	2-49	2	2	3	LS1	0	0	0	0	0	0
6	2-49	2	2	3	LS2	0	0	0	0	0	0
6	2-49	2	2	3	LS3	0	0	0	0	0	0
6	2-49	2	2	3	LS4	0	0	0	0	0	0
6	2-49	2	2	3	LS5	0	0	0	0	0	0
6	2-49	2	2	3	I1	0	0	0	0	0	0
6	2-49	2	2	4	LS1	0	0	0	0	0	0
6	2-49	2	2	4	LS2	0	0	0	0	0	0

6	2-49	2	2	4	LS3	0	0	0	0	0	0
6	2-49	2	3	1	SCI	4					
6	2-49	2	3	1	LS1	1	0	0	0	0	0
6	2-49	2	3	1	LS2	1	0	0	0	0	0
6	2-49	2	3	1	LS3	1	0	0	0	0	0
6	2-49	2	3	1	LS4	0	0	0	0	0	0
6	2-49	2	3	1	LS5	0	0	0	0	0	0
6	2-49	2	3	1	LS6	0	0	0	0	0	0
6	2-49	2	3	1	LS7	0	0	0	0	0	0
6	2-49	2	3	1	LS8	0	0	0	0	0	0
6	2-49	2	3	1	I1	1	3	0	0	1	2
6	2-49	2	3	1	I2	0	0	0	0	0	0
6	2-49	2	3	2	LS1	4	0	0	0	0	0
6	2-49	2	3	2	LS2	1	0	0	0	0	0
6	2-49	2	3	2	LS3	0	0	0	0	0	0
6	2-49	2	3	2	LS4	0	0	0	0	0	0
6	2-49	2	3	2	LS5	0	0	0	0	0	0
6	2-49	2	3	2	LS6	0	0	0	0	0	0
6	2-49	2	3	2	LS7	0	0	0	0	0	0
6	2-49	2	3	2	I1	1	3	2	1	0	0
6	2-49	2	3	2	I2	0	0	0	0	0	0
6	2-49	2	3	3	LS1	0	0	0	0	0	0
6	2-49	2	3	3	LS2	0	0	0	0	0	0
6	2-49	2	3	3	LS3	0	0	0	0	0	0
6	2-49	2	3	3	LS4	0	0	0	0	0	0
6	2-49	2	3	3	LS5	0	0	0	0	0	0
6	2-49	2	3	3	I1	0	0	0	0	0	0
6	2-49	2	3	4	LS1	0	0	0	0	0	0
6	2-49	2	3	4	LS2	0	0	0	0	0	0
6	2-49	2	3	4	LS3	0	0	0	0	0	0
6	2-49	2	3	4	LS4	0	0	0	0	0	0
6	2-49	2	4	1	SCI	4					
6	2-49	2	4	1	LS1	1	8	3	2	2	1
6	2-49	2	4	1	LS2	1	3	2	1	0	0
6	2-49	2	4	1	LS3	1	0	0	0	0	0
6	2-49	2	4	1	LS4	0	0	0	0	0	0

6	2-49	2	4	1	LS5	0	0	0	0	0	0
6	2-49	2	4	1	LS6	0	0	0	0	0	0
6	2-49	2	4	1	LS7	0	0	0	0	0	0
6	2-49	2	4	1	LS8	0	0	0	0	0	0
6	2-49	2	4	1	LS9	0	0	0	0	0	0
6	2-49	2	4	1	I1	1	0	0	0	0	0
6	2-49	2	4	1	I2	0	0	0	0	0	0
6	2-49	2	4	1	I3	0	0	0	0	0	0
6	2-49	2	4	2	LS1	1	0	0	0	0	0
6	2-49	2	4	2	LS2	0	0	0	0	0	0
6	2-49	2	4	2	LS3	0	0	0	0	0	0
6	2-49	2	4	2	LS4	0	0	0	0	0	0
6	2-49	2	4	2	LS5	0	0	0	0	0	0
6	2-49	2	4	2	LS6	0	0	0	0	0	0
6	2-49	2	4	2	I1	0	0	0	0	0	0
6	2-49	2	4	2	I2	0	0	0	0	0	0
6	2-49	2	4	3	LS1	1	0	0	0	0	0
6	2-49	2	4	3	LS2	0	0	0	0	0	0
6	2-49	2	4	3	LS3	0	0	0	0	0	0
6	2-49	2	4	3	LS4	0	0	0	0	0	0
6	2-49	2	5	1	SCI	4					
6	2-49	2	5	1	LS1	4	6	2	1	1	2
6	2-49	2	5	1	LS2	2	5	2	1.5	1.5	0
6	2-49	2	5	1	LS3	1	4	2	2	0	0
6	2-49	2	5	1	LS4	0	0	0	0	0	0
6	2-49	2	5	1	LS5	0	0	0	0	0	0
6	2-49	2	5	1	LS6	0	0	0	0	0	0
6	2-49	2	5	1	LS7	0	0	0	0	0	0
6	2-49	2	5	1	LS8	0	0	0	0	0	0
6	2-49	2	5	1	LS9	0	0	0	0	0	0
6	2-49	2	5	1	LS10	0	0	0	0	0	0
6	2-49	2	5	1	I1	1	0	0	0	0	0
6	2-49	2	5	1	I2	0	0	0	0	0	0
6	2-49	2	5	1	I3	0	0	0	0	0	0
6	2-49	2	5	1	I4	0	0	0	0	0	0
6	2-49	2	5	1	P	0	0	0	0	0	0

6	2-49	2	5	2	LS1	2	5	1.5	1.5	1	1
6	2-49	2	5	2	LS2	1	5	2	1	1	1
6	2-49	2	5	2	LS3	1	2	2	0	0	0
6	2-49	2	5	2	LS4	0	0	0	0	0	0
6	2-49	2	5	2	LS5	0	0	0	0	0	0
6	2-49	2	5	2	LS6	0	0	0	0	0	0
6	2-49	2	5	2	LS7	0	0	0	0	0	0
6	2-49	2	5	2	I1	0	0	0	0	0	0
6	2-49	2	5	2	I2	0	0	0	0	0	0
6	2-49	2	5	3	LS1	1	0	0	0	0	0
6	2-49	2	5	3	LS2	0	0	0	0	0	0
6	2-49	2	5	3	LS3	0	0	0	0	0	0
6	2-49	2	5	3	LS4	0	0	0	0	0	0
6	2-49	2	5	3	LS5	0	0	0	0	0	0
6	2-49	2	5	3	LS6	0	0	0	0	0	0
6	2-49	2	5	3	I1	0	0	0	0	0	0
6	2-49	2	5	3	I2	0	0	0	0	0	0
6	2-49	2	5	4	LS1	0	0	0	0	0	0
6	2-49	2	5	4	LS2	0	0	0	0	0	0
6	2-49	2	5	4	LS3	0	0	0	0	0	0
6	2-49	2	5	4	LS4	0	0	0	0	0	0
6	2-49	3	1	1	SCI	4					
6	2-49	3	1	1	LS1	1					
6	2-49	3	1	1	LS2	1					
6	2-49	3	1	1	LS3	1					
6	2-49	3	1	1	LS4	0					
6	2-49	3	1	1	LS5	0					
6	2-49	3	1	1	LS6	0					
6	2-49	3	1	1	LS7	0					
6	2-49	3	1	1	LS8	0					
6	2-49	3	1	1	I1	1					
6	2-49	3	1	1	I2	0					
6	2-49	3	1	1	I3	0					
6	2-49	3	1	2	LS1	1					
6	2-49	3	1	2	LS2	0					
6	2-49	3	1	2	LS3	0					

6	2-49	3	1	2	LS4	0					
6	2-49	3	1	2	LS5	0					
6	2-49	3	1	2	I1	1					
6	2-49	3	1	2	I2	0					
6	2-49	3	1	3	LS1	1					
6	2-49	3	1	3	LS2	1					
6	2-49	3	1	3	LS3	0					
6	2-49	3	1	3	LS4	0					
6	2-49	3	1	3	LS5	0					
6	2-49	3	1	3	I1	0					
6	2-49	3	1	4	LS1	0					
6	2-49	3	1	4	LS2	0					
6	2-49	3	1	4	LS3	0					
6	2-49	3	1	4	LS4	0					
6	2-49	3	2	1	SCI	4					
6	2-49	3	2	1	LS1	2					
6	2-49	3	2	1	LS2	1					
6	2-49	3	2	1	LS3	1					
6	2-49	3	2	1	LS4	1					
6	2-49	3	2	1	LS5	0					
6	2-49	3	2	1	LS6	0					
6	2-49	3	2	1	LS7	0					
6	2-49	3	2	1	LS8	0					
6	2-49	3	2	1	I1	1					
6	2-49	3	2	1	I2	0					
6	2-49	3	2	1	I3	0					
6	2-49	3	2	2	LS1	1					
6	2-49	3	2	2	LS2	1					
6	2-49	3	2	2	LS3	1					
6	2-49	3	2	2	LS4	0					
6	2-49	3	2	2	LS5	0					
6	2-49	3	2	2	I1	0					
6	2-49	3	2	2	I2	0					
6	2-49	3	2	3	LS1	1					
6	2-49	3	2	3	LS2	1					
6	2-49	3	2	3	LS3	0					

6	2-49	3	2	3	LS4	0					
6	2-49	3	2	3	LS5	0					
6	2-49	3	3	1	SCI	4					
6	2-49	3	3	1	LS1	1					
6	2-49	3	3	1	LS2	1					
6	2-49	3	3	1	LS3	1					
6	2-49	3	3	1	LS4	0					
6	2-49	3	3	1	LS5	0					
6	2-49	3	3	1	LS6	0					
6	2-49	3	3	1	LS7	0					
6	2-49	3	3	1	LS8	0					
6	2-49	3	3	1	LS9	0					
6	2-49	3	3	1	I1	1					
6	2-49	3	3	1	I2	0					
6	2-49	3	3	1	I3	0					
6	2-49	3	3	2	LS1	1					
6	2-49	3	3	2	LS2	1					
6	2-49	3	3	2	LS3	0					
6	2-49	3	3	2	LS4	0					
6	2-49	3	3	2	LS5	0					
6	2-49	3	3	2	LS6	0					
6	2-49	3	3	2	I1	1					
6	2-49	3	3	2	I2	0					
6	2-49	3	3	2	I3	0					
6	2-49	3	3	3	LS1	1					
6	2-49	3	3	3	LS2	0					
6	2-49	3	3	3	LS3	0					
6	2-49	3	3	3	LS4	0					
6	2-49	3	3	3	LS5	0					
6	2-49	3	3	3	LS6	0					
6	2-49	3	3	3	I1	0					
6	2-49	3	3	3	I2	0					
6	2-49	3	3	4	LS1	0					
6	2-49	3	3	4	LS2	0					
6	2-49	3	3	4	LS3	0					
6	2-49	3	3	4	LS4	0					

6	2-49	3	4	1	SCI	2					
6	2-49	3	4	1	LS1	1					
6	2-49	3	4	1	LS2	1					
6	2-49	3	4	1	LS3	0					
6	2-49	3	4	1	LS4	0					
6	2-49	3	4	1	LS5	0					
6	2-49	3	4	1	LS6	0					
6	2-49	3	4	1	LS7	0					
6	2-49	3	4	1	LS8	0					
6	2-49	3	4	1	I1	1					
6	2-49	3	4	1	I2	0					
6	2-49	3	4	2	LS1	1					
6	2-49	3	4	2	LS2	0					
6	2-49	3	4	2	LS3	0					
6	2-49	3	4	2	LS4	0					
6	2-49	3	4	2	LS5	0					
6	2-49	3	4	2	I1	0					
6	2-49	3	4	2	I2	0					
6	2-49	3	4	3	LS1	0					
6	2-49	3	4	3	LS2	0					
6	2-49	3	4	3	LS3	0					
6	2-49	3	4	3	LS4	0					
6	2-49	3	5	1	SCI	4					
6	2-49	3	5	1	LS1	1					
6	2-49	3	5	1	LS2	1					
6	2-49	3	5	1	LS3	1					
6	2-49	3	5	1	LS4	0					
6	2-49	3	5	1	LS5	0					
6	2-49	3	5	1	LS6	0					
6	2-49	3	5	1	LS7	0					
6	2-49	3	5	1	LS8	0					
6	2-49	3	5	1	LS9	0					
6	2-49	3	5	1	I1	1					
6	2-49	3	5	1	I2	0					
6	2-49	3	5	1	I3	0					
6	2-49	3	5	1	I4	0					

6	2-49	3	5	1	P	0					
6	2-49	3	5	2	LS1	2					
6	2-49	3	5	2	LS2	1					
6	2-49	3	5	2	LS3	1					
6	2-49	3	5	2	LS4	0					
6	2-49	3	5	2	LS5	0					
6	2-49	3	5	2	LS6	0					
6	2-49	3	5	2	LS7	0					
6	2-49	3	5	2	I1	1					
6	2-49	3	5	2	I2	0					
6	2-49	3	5	2	I3	0					
6	2-49	3	5	3	LS1	1					
6	2-49	3	5	3	LS2	0					
6	2-49	3	5	3	LS3	0					
6	2-49	3	5	3	LS4	0					
6	2-49	3	5	3	LS5	0					
6	2-49	3	5	3	LS6	0					
6	2-49	3	5	3	I1	0					
6	2-49	3	5	3	I2	0					
6	2-49	3	5	4	LS1	0					
6	2-49	3	5	4	LS2	0					
6	2-49	3	5	4	LS3	0					
6	2-49	3	5	4	LS4	0					
6	Sunco	1	1	1	SCI	4	3	1	1	1	0
6	Sunco	1	1	1	LS1	1	0	0	0	0	0
6	Sunco	1	1	1	LS2	1	0	0	0	0	0
6	Sunco	1	1	1	LS3	1	0	0	0	0	0
6	Sunco	1	1	1	LS4	1	0	0	0	0	0
6	Sunco	1	1	1	LS5	0	0	0	0	0	0
6	Sunco	1	1	1	LS6	0	0	0	0	0	0
6	Sunco	1	1	1	LS7	0	0	0	0	0	0
6	Sunco	1	1	1	LS8	0	0	0	0	0	0
6	Sunco	1	1	1	I1	2	2	1	0	0	1
6	Sunco	1	1	1	I2	1	0	0	0	0	0
6	Sunco	1	1	1	I3	0	0	0	0	0	0
6	Sunco	1	2	1	SCI	4					

6	Sunco	1	2	1	LS1	1	3	2	1	0	0
6	Sunco	1	2	1	LS2	1	0	0	0	0	0
6	Sunco	1	2	1	LS3	1	0	0	0	0	0
6	Sunco	1	2	1	LS4	1	0	0	0	0	0
6	Sunco	1	2	1	LS5	0	0	0	0	0	0
6	Sunco	1	2	1	LS6	0	0	0	0	0	0
6	Sunco	1	2	1	LS7	0	0	0	0	0	0
6	Sunco	1	2	1	LS8	0	0	0	0	0	0
6	Sunco	1	2	1	I1	1	0	0	0	0	0
6	Sunco	1	2	1	I2	0	0	0	0	0	0
6	Sunco	1	2	1	I3	0	0	0	0	0	0
6	Sunco	1	2	2	LS1	1	0	0	0	0	0
6	Sunco	1	2	2	LS2	1	0	0	0	0	0
6	Sunco	1	2	2	LS3	0	0	0	0	0	0
6	Sunco	1	2	2	LS4	0	0	0	0	0	0
6	Sunco	1	2	2	LS5	0	0	0	0	0	0
6	Sunco	1	2	2	I1	0	0	0	0	0	0
6	Sunco	1	2	3	LS1	0	0	0	0	0	0
6	Sunco	1	2	3	LS2	0	0	0	0	0	0
6	Sunco	1	2	3	LS3	0	0	0	0	0	0
6	Sunco	1	2	3	LS4	0	0	0	0	0	0
6	Sunco	1	3	1	SCI	4					
6	Sunco	1	3	1	LS1	1	2	2	0	0	0
6	Sunco	1	3	1	LS2	1	3	1	2	0	0
6	Sunco	1	3	1	LS3	1	2	1	1	0	0
6	Sunco	1	3	1	LS4	1	0	0	0	0	0
6	Sunco	1	3	1	LS5	0	0	0	0	0	0
6	Sunco	1	3	1	LS6	0	0	0	0	0	0
6	Sunco	1	3	1	LS7	0	0	0	0	0	0
6	Sunco	1	3	1	LS8	0	0	0	0	0	0
6	Sunco	1	3	1	I1	1	2	2	0	0	0
6	Sunco	1	3	1	I2	0	0	0	0	0	0
6	Sunco	1	3	2	LS1	1	0	0	0	0	0
6	Sunco	1	3	2	LS2	1	0	0	0	0	0
6	Sunco	1	3	2	LS3	0	0	0	0	0	0
6	Sunco	1	3	2	LS4	0	0	0	0	0	0

6	Sunco	1	3	2	LS5	0	0	0	0	0	0
6	Sunco	1	3	2	I1	1	2	1	1	0	0
6	Sunco	1	3	2	I2	0	0	0	0	0	0
6	Sunco	1	3	3	LS1	1	0	0	0	0	0
6	Sunco	1	3	3	LS2	0	0	0	0	0	0
6	Sunco	1	3	3	LS3	0	0	0	0	0	0
6	Sunco	1	3	3	LS4	0	0	0	0	0	0
6	Sunco	1	3	3	LS5	0	0	0	0	0	0
6	Sunco	1	3	3	I1	1	2	1	1	0	0
6	Sunco	1	3	3	I2	0	0	0	0	0	0
6	Sunco	1	4	1	SCI	0					
6	Sunco	1	4	1	LS1	1	0	0	0	0	0
6	Sunco	1	4	1	LS2	1	0	0	0	0	0
6	Sunco	1	4	1	LS3	1	0	0	0	0	0
6	Sunco	1	4	1	LS4	1	0	0	0	0	0
6	Sunco	1	4	1	LS5	1	0	0	0	0	0
6	Sunco	1	4	1	LS6	0	0	0	0	0	0
6	Sunco	1	4	1	LS7	0	0	0	0	0	0
6	Sunco	1	4	1	LS8	0	0	0	0	0	0
6	Sunco	1	4	1	I1	1	2	1	1	0	0
6	Sunco	1	4	1	I2	0	0	0	0	0	0
6	Sunco	1	4	1	I3	0	0	0	0	0	0
6	Sunco	1	4	2	LS1	0	0	0	0	0	0
6	Sunco	1	4	2	LS2	0	0	0	0	0	0
6	Sunco	1	4	2	LS3	0	0	0	0	0	0
6	Sunco	1	4	2	LS4	0	0	0	0	0	0
6	Sunco	1	4	2	LS5	0	0	0	0	0	0
6	Sunco	1	4	2	LS6	0	0	0	0	0	0
6	Sunco	1	4	2	I1	1	0	0	0	0	0
6	Sunco	1	4	2	I2	0	0	0	0	0	0
6	Sunco	1	4	3	LS1	0	0	0	0	0	0
6	Sunco	1	4	3	LS2	0	0	0	0	0	0
6	Sunco	1	4	3	LS3	0	0	0	0	0	0
6	Sunco	1	4	3	LS4	0	0	0	0	0	0
6	Sunco	1	4	3	LS5	0	0	0	0	0	0
6	Sunco	1	4	3	I1	0	0	0	0	0	0

6	Sunco	1	5	1	SCI	4	4	1	1	1	1
6	Sunco	1	5	1	LS1	1	2	2	0	0	0
6	Sunco	1	5	1	LS2	0	0	0	0	0	0
6	Sunco	1	5	1	LS3	0	0	0	0	0	0
6	Sunco	1	5	1	LS4	0	0	0	0	0	0
6	Sunco	1	5	1	LS5	0	0	0	0	0	0
6	Sunco	1	5	1	LS6	0	0	0	0	0	0
6	Sunco	1	5	1	LS7	0	0	0	0	0	0
6	Sunco	1	5	1	LS8	0	0	0	0	0	0
6	Sunco	1	5	1	I1	1	0	0	0	0	0
6	Sunco	1	5	1	I2	0	0	0	0	0	0
6	Sunco	1	5	1	I3	0	0	0	0	0	0
6	Sunco	1	5	2	LS1	0	0	0	0	0	0
6	Sunco	1	5	2	LS2	0	0	0	0	0	0
6	Sunco	1	5	2	LS3	0	0	0	0	0	0
6	Sunco	1	5	2	LS4	0	0	0	0	0	0
6	Sunco	1	5	2	LS5	0	0	0	0	0	0
6	Sunco	1	5	2	LS6	0	0	0	0	0	0
6	Sunco	1	5	2	I1	0	0	0	0	0	0
6	Sunco	1	5	2	I2	0	0	0	0	0	0
6	Sunco	1	5	3	LS1	0	0	0	0	0	0
6	Sunco	1	5	3	LS2	0	0	0	0	0	0
6	Sunco	1	5	3	LS3	0	0	0	0	0	0
6	Sunco	2	1	1	SCI	4					
6	Sunco	2	1	1	LS1	1	6	2	1	1.5	1.5
6	Sunco	2	1	1	LS2	0	5	2	1	1	1
6	Sunco	2	1	1	LS3	0	0	0	0	0	0
6	Sunco	2	1	1	LS4	0	0	0	0	0	0
6	Sunco	2	1	1	LS5	0	0	0	0	0	0
6	Sunco	2	1	1	LS6	0	0	0	0	0	0
6	Sunco	2	1	1	LS7	0	0	0	0	0	0
6	Sunco	2	1	1	LS8	0	0	0	0	0	0
6	Sunco	2	1	1	I1	1	0	0	0	0	0
6	Sunco	2	1	1	I2	0	0	0	0	0	0
6	Sunco	2	1	1	I3	0	0	0	0	0	0
6	Sunco	2	1	2	LS1	1	0	0	0	0	0

6	Sunco	2	1	2	LS2	0	0	0	0	0	0
6	Sunco	2	1	2	LS3	0	0	0	0	0	0
6	Sunco	2	1	2	LS4	0	0	0	0	0	0
6	Sunco	2	1	2	LS5	0	0	0	0	0	0
6	Sunco	2	1	2	LS6	0	0	0	0	0	0
6	Sunco	2	1	2	I1	1	0	0	0	0	0
6	Sunco	2	1	2	I2	0	0	0	0	0	0
6	Sunco	2	1	3	LS1	0	0	0	0	0	0
6	Sunco	2	1	3	LS2	0	0	0	0	0	0
6	Sunco	2	1	3	LS3	0	0	0	0	0	0
6	Sunco	2	1	3	LS4	0	0	0	0	0	0
6	Sunco	2	1	3	LS5	0	0	0	0	0	0
6	Sunco	2	1	3	I1	1	0	0	0	0	0
6	Sunco	2	1	3	I2	0	0	0	0	0	0
6	Sunco	2	2	1	SCI	4					
6	Sunco	2	2	1	LS1	1	0	0	0	0	0
6	Sunco	2	2	1	LS2	1	0	0	0	0	0
6	Sunco	2	2	1	LS3	0	0	0	0	0	0
6	Sunco	2	2	1	LS4	0	0	0	0	0	0
6	Sunco	2	2	1	LS5	0	0	0	0	0	0
6	Sunco	2	2	1	LS6	0	0	0	0	0	0
6	Sunco	2	2	1	LS7	0	0	0	0	0	0
6	Sunco	2	2	1	LS8	0	0	0	0	0	0
6	Sunco	2	2	1	LS9	0	0	0	0	0	0
6	Sunco	2	2	1	I1	0	5	1	1	2	1
6	Sunco	2	2	1	I2	0	0	0	0	0	0
6	Sunco	2	2	1	I3	0	0	0	0	0	0
6	Sunco	2	2	2	LS1	0	0	0	0	0	0
6	Sunco	2	2	2	LS2	0	0	0	0	0	0
6	Sunco	2	2	2	LS3	0	0	0	0	0	0
6	Sunco	2	2	2	LS4	0	0	0	0	0	0
6	Sunco	2	2	2	LS5	0	0	0	0	0	0
6	Sunco	2	2	2	LS6	0	0	0	0	0	0
6	Sunco	2	2	2	LS7	0	0	0	0	0	0
6	Sunco	2	2	2	I1	0	0	0	0	0	0
6	Sunco	2	2	2	I2	0	0	0	0	0	0

6	Sunco	2	2	3	LS1	0	0	0	0	0	0
6	Sunco	2	2	3	LS2	0	0	0	0	0	0
6	Sunco	2	2	3	LS3	0	0	0	0	0	0
6	Sunco	2	2	3	LS4	0	0	0	0	0	0
6	Sunco	2	2	3	LS5	0	0	0	0	0	0
6	Sunco	2	2	3	LS6	0	0	0	0	0	0
6	Sunco	2	2	3	I1	0	3	1	1	1	0
6	Sunco	2	2	3	I2	0	0	0	0	0	0
6	Sunco	2	2	4	LS1	0	0	0	0	0	0
6	Sunco	2	2	4	LS2	0	0	0	0	0	0
6	Sunco	2	2	4	LS3	0	0	0	0	0	0
6	Sunco	2	2	4	LS4	0	0	0	0	0	0
6	Sunco	2	3	1	SCI	1					
6	Sunco	2	3	1	LS1	1	5	2	2	1	0
6	Sunco	2	3	1	LS2	0	2	2	0	0	0
6	Sunco	2	3	1	LS3	0	0	0	0	0	0
6	Sunco	2	3	1	LS4	0	0	0	0	0	0
6	Sunco	2	3	1	LS5	0	0	0	0	0	0
6	Sunco	2	3	1	LS6	0	0	0	0	0	0
6	Sunco	2	3	1	LS7	0	0	0	0	0	0
6	Sunco	2	3	1	LS8	0	0	0	0	0	0
6	Sunco	2	3	1	LS9	0	0	0	0	0	0
6	Sunco	2	3	1	I1	4	4	1	1	1	1
6	Sunco	2	3	1	I2	1	3	3	0	0	0
6	Sunco	2	3	1	I3	0	0	0	0	0	0
6	Sunco	2	3	2	LS1	0	0	0	0	0	0
6	Sunco	2	3	2	LS2	0	0	0	0	0	0
6	Sunco	2	3	2	LS3	0	0	0	0	0	0
6	Sunco	2	3	2	LS4	0	0	0	0	0	0
6	Sunco	2	3	2	LS5	0	0	0	0	0	0
6	Sunco	2	3	2	I1	0	0	0	0	0	0
6	Sunco	2	3	2	I2	0	0	0	0	0	0
6	Sunco	2	3	3	LS1	0	0	0	0	0	0
6	Sunco	2	3	3	LS2	0	0	0	0	0	0
6	Sunco	2	3	3	LS3	0	0	0	0	0	0
6	Sunco	2	4	1	SCI	1					

6	Sunco	2	4	1	LS1	1	0	0	0	0	0
6	Sunco	2	4	1	LS2	1	0	0	0	0	0
6	Sunco	2	4	1	LS3	1	0	0	0	0	0
6	Sunco	2	4	1	LS4	0	0	0	0	0	0
6	Sunco	2	4	1	LS5	0	0	0	0	0	0
6	Sunco	2	4	1	LS6	0	0	0	0	0	0
6	Sunco	2	4	1	LS7	0	0	0	0	0	0
6	Sunco	2	4	1	LS8	0	0	0	0	0	0
6	Sunco	2	4	1	I1	0	0	0	0	0	0
6	Sunco	2	4	1	I2	0	0	0	0	0	0
6	Sunco	2	4	1	I3	0	0	0	0	0	0
6	Sunco	2	4	2	LS1	0	0	0	0	0	0
6	Sunco	2	4	2	LS2	0	0	0	0	0	0
6	Sunco	2	4	2	LS3	0	0	0	0	0	0
6	Sunco	2	4	2	LS4	0	0	0	0	0	0
6	Sunco	2	4	2	LS5	0	0	0	0	0	0
6	Sunco	2	4	2	LS6	0	0	0	0	0	0
6	Sunco	2	4	2	I1	0	0	0	0	0	0
6	Sunco	2	4	2	I2	0	0	0	0	0	0
6	Sunco	2	4	3	LS1	0	0	0	0	0	0
6	Sunco	2	4	3	LS2	0	0	0	0	0	0
6	Sunco	2	4	3	LS3	0	0	0	0	0	0
6	Sunco	2	4	3	LS4	0	0	0	0	0	0
6	Sunco	2	5	1	SCI	4					
6	Sunco	2	5	1	LS1	1	0	0	0	0	0
6	Sunco	2	5	1	LS2	1	0	0	0	0	0
6	Sunco	2	5	1	LS3	1	0	0	0	0	0
6	Sunco	2	5	1	LS4	0	0	0	0	0	0
6	Sunco	2	5	1	LS5	0	0	0	0	0	0
6	Sunco	2	5	1	LS6	0	0	0	0	0	0
6	Sunco	2	5	1	LS7	0	0	0	0	0	0
6	Sunco	2	5	1	LS8	0	0	0	0	0	0
6	Sunco	2	5	1	I1	1	0	0	0	0	0
6	Sunco	2	5	1	I2	0	0	0	0	0	0
6	Sunco	2	5	1	I3	0	0	0	0	0	0
6	Sunco	2	5	2	LS1	1	3	3	0	0	0

6	Sunco	2	5	2	LS2	1	0	0	0	0	0
6	Sunco	2	5	2	LS3	1	0	0	0	0	0
6	Sunco	2	5	2	LS4	0	0	0	0	0	0
6	Sunco	2	5	2	LS5	0	0	0	0	0	0
6	Sunco	2	5	2	LS6	0	0	0	0	0	0
6	Sunco	2	5	2	I1	1	0	0	0	0	0
6	Sunco	2	5	2	I2	0	0	0	0	0	0
6	Sunco	2	5	3	LS1	1	0	0	0	0	0
6	Sunco	2	5	3	LS2	1	0	0	0	0	0
6	Sunco	2	5	3	LS3	0	0	0	0	0	0
6	Sunco	2	5	3	LS4	0	0	0	0	0	0
6	Sunco	2	5	3	LS5	0	0	0	0	0	0
6	Sunco	2	5	3	LS6	0	0	0	0	0	0
6	Sunco	2	5	3	I1	1	0	0	0	0	0
6	Sunco	2	5	3	I2	0	0	0	0	0	0
6	Sunco	2	5	4	LS1	0	0	0	0	0	0
6	Sunco	2	5	4	LS2	0	0	0	0	0	0
6	Sunco	2	5	4	LS3	0	0	0	0	0	0
6	Sunco	3	1	1	SCI	4					
6	Sunco	3	1	1	LS1	1					
6	Sunco	3	1	1	LS2	1					
6	Sunco	3	1	1	LS3	1					
6	Sunco	3	1	1	LS4	0					
6	Sunco	3	1	1	LS5	0					
6	Sunco	3	1	1	LS6	0					
6	Sunco	3	1	1	LS7	0					
6	Sunco	3	1	1	LS8	0					
6	Sunco	3	1	1	I1	2					
6	Sunco	3	1	1	I2	0					
6	Sunco	3	1	1	I3	0					
6	Sunco	3	1	2	LS1	1					
6	Sunco	3	1	2	LS2	0					
6	Sunco	3	1	2	LS3	0					
6	Sunco	3	1	2	LS4	0					
6	Sunco	3	1	2	LS5	0					
6	Sunco	3	1	2	I1	1					

6	Sunco	3	1	2	I2	0					
6	Sunco	3	2	1	SCI	4					
6	Sunco	3	2	1	LS1	1					
6	Sunco	3	2	1	LS2	1					
6	Sunco	3	2	1	LS3	1					
6	Sunco	3	2	1	LS4	1					
6	Sunco	3	2	1	LS5	0					
6	Sunco	3	2	1	LS6	0					
6	Sunco	3	2	1	LS7	0					
6	Sunco	3	2	1	LS8	0					
6	Sunco	3	2	1	I1	1					
6	Sunco	3	2	1	I2	0					
6	Sunco	3	2	1	I3	0					
6	Sunco	3	2	2	LS1	1					
6	Sunco	3	2	2	LS2	0					
6	Sunco	3	2	2	LS3	0					
6	Sunco	3	2	2	LS4	0					
6	Sunco	3	2	2	LS5	0					
6	Sunco	3	2	2	LS6	0					
6	Sunco	3	2	2	I1	1					
6	Sunco	3	2	2	I2	0					
6	Sunco	3	2	3	LS1	0					
6	Sunco	3	2	3	LS2	0					
6	Sunco	3	2	3	LS3	0					
6	Sunco	3	2	3	LS4	0					
6	Sunco	3	2	3	LS5	0					
6	Sunco	3	2	3	I1	0					
6	Sunco	3	2	3	I2	0					
6	Sunco	3	2	4	LS1	0					
6	Sunco	3	2	4	LS2	0					
6	Sunco	3	2	4	LS3	0					
6	Sunco	3	2	4	LS4	0					
6	Sunco	3	3	1	SCI	1					
6	Sunco	3	3	1	LS1	1					
6	Sunco	3	3	1	LS2	0					
6	Sunco	3	3	1	LS3	0					

6	Sunco	3	3	1	LS4	0					
6	Sunco	3	3	1	LS5	0					
6	Sunco	3	3	1	LS6	0					
6	Sunco	3	3	1	LS7	0					
6	Sunco	3	3	1	LS8	0					
6	Sunco	3	3	1	I1	1					
6	Sunco	3	3	1	I2	0					
6	Sunco	3	3	1	I3	0					
6	Sunco	3	3	2	LS1	0					
6	Sunco	3	3	2	LS2	0					
6	Sunco	3	3	2	LS3	0					
6	Sunco	3	3	2	LS4	0					
6	Sunco	3	3	2	LS5	0					
6	Sunco	3	3	2	I1	0					
6	Sunco	3	3	2	I2	0					
6	Sunco	3	3	3	LS1	0					
6	Sunco	3	3	3	LS2	0					
6	Sunco	3	3	3	LS3	0					
6	Sunco	3	3	3	LS4	0					
6	Sunco	3	3	3	I1	0					
6	Sunco	3	3	3	I2	0					
6	Sunco	3	3	4	LS1	0					
6	Sunco	3	3	4	LS2	0					
6	Sunco	3	3	4	LS3	0					
6	Sunco	3	4	1	SCI	4					
6	Sunco	3	4	1	LS1	1					
6	Sunco	3	4	1	LS2	1					
6	Sunco	3	4	1	LS3	0					
6	Sunco	3	4	1	LS4	0					
6	Sunco	3	4	1	LS5	0					
6	Sunco	3	4	1	LS6	0					
6	Sunco	3	4	1	LS7	0					
6	Sunco	3	4	1	LS8	0					
6	Sunco	3	4	1	I1	1					
6	Sunco	3	4	1	I2	0					
6	Sunco	3	4	1	I3	0					

6	Sunco	3	4	2	LS1	1					
6	Sunco	3	4	2	LS2	0					
6	Sunco	3	4	2	LS3	0					
6	Sunco	3	4	2	LS4	0					
6	Sunco	3	4	2	LS5	0					
6	Sunco	3	4	2	LS6	0					
6	Sunco	3	4	2	I1	1					
6	Sunco	3	4	2	I2	0					
6	Sunco	3	4	3	LS1	1					
6	Sunco	3	4	3	LS2	0					
6	Sunco	3	4	3	LS3	0					
6	Sunco	3	4	3	LS4	0					
6	Sunco	3	4	3	LS5	0					
6	Sunco	3	4	3	I1	1					
6	Sunco	3	4	3	I2	0					
6	Sunco	3	4	4	LS1	0					
6	Sunco	3	4	4	LS2	0					
6	Sunco	3	4	4	LS3	0					
6	Sunco	3	4	4	LS4	0					
6	Sunco	3	5	1	SCI	3					
6	Sunco	3	5	1	LS1	1					
6	Sunco	3	5	1	LS2	1					
6	Sunco	3	5	1	LS3	1					
6	Sunco	3	5	1	LS4	0					
6	Sunco	3	5	1	LS5	0					
6	Sunco	3	5	1	LS6	0					
6	Sunco	3	5	1	LS7	0					
6	Sunco	3	5	1	LS8	0					
6	Sunco	3	5	1	LS9	0					
6	Sunco	3	5	1	I1	1					
6	Sunco	3	5	1	I2	0					
6	Sunco	3	5	1	I3	0					
6	Sunco	3	5	2	LS1	0					
6	Sunco	3	5	2	LS2	0					
6	Sunco	3	5	2	LS3	0					
6	Sunco	3	5	2	LS4	0					

6	Sunco	3	5	2	LS5	0					
6	Sunco	3	5	2	I1	0					
6	Sunco	3	5	2	I2	0					
6	Sunco	3	5	3	LS1	0					
6	Sunco	3	5	3	LS2	0					
6	Sunco	3	5	3	LS3	0					
6	Sunco	3	5	3	LS4	0					
6	Sunco	3	5	3	LS5	0					
6	Sunco	3	5	3	I1	0					
6	Sunco	3	5	3	I2	0					
6	Sunco	3	5	4	LS1	0					
6	Sunco	3	5	4	LS2	0					
6	Sunco	3	5	4	LS3	0					
6	Sunco	3	5	4	LS4	0					
6	CPI133814	1	1	1	SCI	4					
6	CPI133814	1	1	1	LS1	4	7	3	2	2	0
6	CPI133814	1	1	1	LS2	4	3	3	0	0	0
6	CPI133814	1	1	1	LS3	3	10	4	1	2	3
6	CPI133814	1	1	1	LS4	3	4	3	1	0	0
6	CPI133814	1	1	1	LS5	3	7	4	3	0	0
6	CPI133814	1	1	1	LS6	1	0	0	0	0	0
6	CPI133814	1	1	1	LS7	0	0	0	0	0	0
6	CPI133814	1	1	1	LS8	0	0	0	0	0	0
6	CPI133814	1	1	1	I1	2	2	1	1	0	0
6	CPI133814	1	1	1	I2	1	0	0	0	0	0
6	CPI133814	1	1	1	I3	0	0	0	0	0	0
6	CPI133814	1	1	2	LS1	1	0	0	0	0	0
6	CPI133814	1	1	2	LS2	1	0	0	0	0	0
6	CPI133814	1	1	2	LS3	0	0	0	0	0	0
6	CPI133814	1	1	2	LS4	0	0	0	0	0	0
6	CPI133814	1	1	2	LS5	0	0	0	0	0	0
6	CPI133814	1	1	2	I1	0	3	1	1	1	0
6	CPI133814	1	1	3	LS1	1	0	0	0	0	0
6	CPI133814	1	1	3	LS2	0	0	0	0	0	0
6	CPI133814	1	1	3	LS3	0	0	0	0	0	0
6	CPI133814	1	1	3	LS4	0	0	0	0	0	0

6	CPI133814	1	2	1	SCI	4					
6	CPI133814	1	2	1	LS1	1	3	2	1	0	0
6	CPI133814	1	2	1	LS2	1	0	0	0	0	0
6	CPI133814	1	2	1	LS3	1	0	0	0	0	0
6	CPI133814	1	2	1	LS4	0	0	0	0	0	0
6	CPI133814	1	2	1	LS5	0	0	0	0	0	0
6	CPI133814	1	2	1	LS6	0	0	0	0	0	0
6	CPI133814	1	2	1	LS7	0	0	0	0	0	0
6	CPI133814	1	2	1	I1	1	0	0	0	0	0
6	CPI133814	1	2	1	I2	0	0	0	0	0	0
6	CPI133814	1	2	2	LS1	1	0	0	0	0	0
6	CPI133814	1	2	2	LS2	1	0	0	0	0	0
6	CPI133814	1	2	2	LS3	0	0	0	0	0	0
6	CPI133814	1	2	2	LS4	0	0	0	0	0	0
6	CPI133814	1	2	2	LS5	0	0	0	0	0	0
6	CPI133814	1	2	2	I1	0	0	0	0	0	0
6	CPI133814	1	2	3	LS1	0	0	0	0	0	0
6	CPI133814	1	2	3	LS2	0	0	0	0	0	0
6	CPI133814	1	2	3	LS3	0	0	0	0	0	0
6	CPI133814	1	2	3	LS4	0	0	0	0	0	0
6	CPI133814	1	3	1	SCI	4					
6	CPI133814	1	3	1	LS1	1	6	2	2	2	0
6	CPI133814	1	3	1	LS2	1	4	3	1	0	0
6	CPI133814	1	3	1	LS3	1	3	3	0	0	0
6	CPI133814	1	3	1	LS4	1	0	0	0	0	0
6	CPI133814	1	3	1	LS5	0	0	0	0	0	0
6	CPI133814	1	3	1	LS6	0	0	0	0	0	0
6	CPI133814	1	3	1	LS7	0	0	0	0	0	0
6	CPI133814	1	3	1	I1	1	0	0	0	0	0
6	CPI133814	1	3	1	I2	0	0	0	0	0	0
6	CPI133814	1	3	1	I3	0	0	0	0	0	0
6	CPI133814	1	3	2	LS1	1	6	2	2	2	0
6	CPI133814	1	3	2	LS2	0	0	0	0	0	0
6	CPI133814	1	3	2	LS3	0	0	0	0	0	0
6	CPI133814	1	3	2	LS4	0	0	0	0	0	0
6	CPI133814	1	3	3	LS1	0	2	2	0	0	0

6	CPI133814	1	3	3	LS2	0	3	0	3	0	0
6	CPI133814	1	3	3	LS3	0	0	0	0	0	0
6	CPI133814	1	3	3	LS4	0	0	0	0	0	0
6	CPI133814	1	4	1	SCI	0					
6	CPI133814	1	4	1	LS1	2	0	0	0	0	0
6	CPI133814	1	4	1	LS2	2	0	0	0	0	0
6	CPI133814	1	4	1	LS3	2	0	0	0	0	0
6	CPI133814	1	4	1	LS4	1	0	0	0	0	0
6	CPI133814	1	4	1	LS5	1	0	0	0	0	0
6	CPI133814	1	4	1	LS6	0	0	0	0	0	0
6	CPI133814	1	4	1	LS7	0	0	0	0	0	0
6	CPI133814	1	4	1	I1	0	0	0	0	0	0
6	CPI133814	1	4	2	LS1	1	0	0	0	0	0
6	CPI133814	1	4	2	LS2	1	0	0	0	0	0
6	CPI133814	1	4	2	LS3	1	0	0	0	0	0
6	CPI133814	1	4	2	LS4	0	0	0	0	0	0
6	CPI133814	1	4	2	LS5	0	0	0	0	0	0
6	CPI133814	1	4	2	I1	1	0	0	0	0	0
6	CPI133814	1	4	3	LS1	1	0	0	0	0	0
6	CPI133814	1	4	3	LS2	1	0	0	0	0	0
6	CPI133814	1	4	3	LS3	1	0	0	0	0	0
6	CPI133814	1	5	1	SCI	2					
6	CPI133814	1	5	1	LS1	4	1	1	0	0	0
6	CPI133814	1	5	1	LS2	3	0	0	0	0	0
6	CPI133814	1	5	1	LS3	3	0	0	0	0	0
6	CPI133814	1	5	1	LS4	1	0	0	0	0	0
6	CPI133814	1	5	1	LS5	0	0	0	0	0	0
6	CPI133814	1	5	1	LS6	0	0	0	0	0	0
6	CPI133814	1	5	1	LS7	0	0	0	0	0	0
6	CPI133814	1	5	1	I1	1	0	0	0	0	0
6	CPI133814	1	5	1	I2	0	0	0	0	0	0
6	CPI133814	1	5	2	LS1	1	0	0	0	0	0
6	CPI133814	1	5	2	LS2	1	0	0	0	0	0
6	CPI133814	1	5	2	LS3	1	0	0	0	0	0
6	CPI133814	1	5	2	LS4	0	0	0	0	0	0
6	CPI133814	1	5	3	LS1	1	0	0	0	0	0

6	CPI133814	1	5	3	LS2	1	0	0	0	0	0
6	CPI133814	1	5	3	LS3	0	0	0	0	0	0
6	CPI133814	2	1	1	SCI	4					
6	CPI133814	2	1	1	LS1	1	7	3	2	2	0
6	CPI133814	2	1	1	LS2	1	4	3	1	0	0
6	CPI133814	2	1	1	LS3	0	3	2	1	0	0
6	CPI133814	2	1	1	LS4	0	0	0	0	0	0
6	CPI133814	2	1	1	LS5	0	0	0	0	0	0
6	CPI133814	2	1	1	LS6	0	0	0	0	0	0
6	CPI133814	2	1	1	LS7	0	0	0	0	0	0
6	CPI133814	2	1	1	LS8	0	0	0	0	0	0
6	CPI133814	2	1	1	LS9	0	0	0	0	0	0
6	CPI133814	2	1	1	I1	1	0	0	0	0	0
6	CPI133814	2	1	1	I2	0	0	0	0	0	0
6	CPI133814	2	1	1	I3	0	0	0	0	0	0
6	CPI133814	2	1	1	I4	0	0	0	0	0	0
6	CPI133814	2	1	2	LS1	1	3	3	0	0	0
6	CPI133814	2	1	2	LS2	0	0	0	0	0	0
6	CPI133814	2	1	2	LS3	0	0	0	0	0	0
6	CPI133814	2	1	2	LS4	0	0	0	0	0	0
6	CPI133814	2	1	2	LS5	0	0	0	0	0	0
6	CPI133814	2	1	2	LS6	0	0	0	0	0	0
6	CPI133814	2	1	2	LS7	0	0	0	0	0	0
6	CPI133814	2	1	2	I1	1	0	0	0	0	0
6	CPI133814	2	1	2	I2	0	0	0	0	0	0
6	CPI133814	2	1	2	I3	0	0	0	0	0	0
6	CPI133814	2	1	3	LS1	1	1	1	0	0	0
6	CPI133814	2	1	3	LS2	0	0	0	0	0	0
6	CPI133814	2	1	3	LS3	0	0	0	0	0	0
6	CPI133814	2	1	3	LS4	0	0	0	0	0	0
6	CPI133814	2	2	1	SCI	1					
6	CPI133814	2	2	1	LS1	1	6	3	2	1	0
6	CPI133814	2	2	1	LS2	1	0				
6	CPI133814	2	2	1	LS3	1	0	0	0	0	0
6	CPI133814	2	2	1	LS4	0	0	0	0	0	0
6	CPI133814	2	2	1	LS5	0	0	0	0	0	0

6	CPI133814	2	2	1	LS6	0	0	0	0	0	0
6	CPI133814	2	2	1	LS7	0	0	0	0	0	0
6	CPI133814	2	2	1	LS8	0	0	0	0	0	0
6	CPI133814	2	2	1	LS9	0	0	0	0	0	0
6	CPI133814	2	2	1	I1	1	0	0	0	0	0
6	CPI133814	2	2	1	I2	0	0	0	0	0	0
6	CPI133814	2	2	1	I3	0	0	0	0	0	0
6	CPI133814	2	2	1	I4	0	0	0	0	0	0
6	CPI133814	2	2	2	LS1	1	0	0	0	0	0
6	CPI133814	2	2	2	LS2	0	0	0	0	0	0
6	CPI133814	2	2	2	LS3	0	0	0	0	0	0
6	CPI133814	2	2	2	LS4	0	0	0	0	0	0
6	CPI133814	2	2	3	LS1	1	0	0	0	0	0
6	CPI133814	2	2	3	LS2	0	0	0	0	0	0
6	CPI133814	2	2	3	LS3	0	0	0	0	0	0
6	CPI133814	2	3	1	SCI	4					
6	CPI133814	2	3	1	LS1	1	0	0	0	0	0
6	CPI133814	2	3	1	LS2	1	0	0	0	0	0
6	CPI133814	2	3	1	LS3	1	0	0	0	0	0
6	CPI133814	2	3	1	LS4	0	0	0	0	0	0
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6	CPI133814	2	3	1	LS7	0	0	0	0	0	0
6	CPI133814	2	3	1	LS8	0	0	0	0	0	0
6	CPI133814	2	3	1	I1	1	0	0	0	0	0
6	CPI133814	2	3	1	I2	0	0	0	0	0	0
6	CPI133814	2	3	1	I3	0	0	0	0	0	0
6	CPI133814	2	3	2	LS1	1	1	1	0	0	0
6	CPI133814	2	3	2	LS2	1	0	0	0	0	0
6	CPI133814	2	3	2	LS3	1	0	0	0	0	0
6	CPI133814	2	3	3	LS1	1	0	0	0	0	0
6	CPI133814	2	3	3	LS2	1	0	0	0	0	0
6	CPI133814	2	3	3	LS3	0	0	0	0	0	0
6	CPI133814	2	4	1	SCI	3					
6	CPI133814	2	4	1	LS1	4	0	0	0	0	0
6	CPI133814	2	4	1	LS2	4	0	0	0	0	0

6	CPI133814	2	4	1	LS3	4	0	0	0	0	0
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6	CPI133814	2	4	1	LS5	1	0	0	0	0	0
6	CPI133814	2	4	1	LS6	1	0	0	0	0	0
6	CPI133814	2	4	1	LS7	0	0	0	0	0	0
6	CPI133814	2	4	1	LS8	0	0	0	0	0	0
6	CPI133814	2	4	1	LS9	0	0	0	0	0	0
6	CPI133814	2	4	1	I1	0	0	0	0	0	0
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6	CPI133814	2	4	1	I3	0	0	0	0	0	0
6	CPI133814	2	4	2	LS1	1	0	0	0	0	0
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6	CPI133814	2	4	2	LS5	0	0	0	0	0	0
6	CPI133814	2	4	2	I1	0	0	0	0	0	0
6	CPI133814	2	4	3	LS1	2	0	0	0	0	0
6	CPI133814	2	4	3	LS2	2	0	0	0	0	0
6	CPI133814	2	4	3	LS3	1	0	0	0	0	0
6	CPI133814	2	4	3	LS4	0	0	0	0	0	0
6	CPI133814	2	4	3	LS5	0	0	0	0	0	0
6	CPI133814	2	5	1	SCI	0					
6	CPI133814	2	5	1	LS1	2	8	3	3	2	0
6	CPI133814	2	5	1	LS2	2	2	2	0	0	0
6	CPI133814	2	5	1	LS3	1	1	1	0	0	0
6	CPI133814	2	5	1	LS4	0	0	0	0	0	0
6	CPI133814	2	5	1	LS5	0	0	0	0	0	0
6	CPI133814	2	5	1	LS6	0	0	0	0	0	0
6	CPI133814	2	5	1	LS7	0	0	0	0	0	0
6	CPI133814	2	5	1	LS8	0	0	0	0	0	0
6	CPI133814	2	5	1	I1	0	0	0	0	0	0
6	CPI133814	2	5	1	I2	0	0	0	0	0	0
6	CPI133814	2	5	1	I3	0	0	0	0	0	0
6	CPI133814	2	5	2	LS1	1	0	0	0	0	0
6	CPI133814	2	5	2	LS2	1	0	0	0	0	0
6	CPI133814	2	5	2	LS3	0	0	0	0	0	0

6	CPI133814	2	5	2	LS4	0	0	0	0	0	0
6	CPI133814	2	5	2	LS5	0	0	0	0	0	0
6	CPI133814	2	5	2	LS6	0	0	0	0	0	0
6	CPI133814	2	5	2	I1	0	0	0	0	0	0
6	CPI133814	2	5	2	I2	0	0	0	0	0	0
6	CPI133814	2	5	3	LS1	1	0	0	0	0	0
6	CPI133814	2	5	3	LS2	0	0	0	0	0	0
6	CPI133814	2	5	3	LS3	0	0	0	0	0	0
6	CPI133814	3	1	1	SCI	4					
6	CPI133814	3	1	1	LS1	1					
6	CPI133814	3	1	1	LS2	1					
6	CPI133814	3	1	1	LS3	1					
6	CPI133814	3	1	1	LS4	0					
6	CPI133814	3	1	1	LS5	0					
6	CPI133814	3	1	1	LS6	0					
6	CPI133814	3	1	1	LS7	0					
6	CPI133814	3	1	1	LS8	0					
6	CPI133814	3	1	1	I1	1					
6	CPI133814	3	1	1	I2	0					
6	CPI133814	3	1	1	I3	0					
6	CPI133814	3	1	2	LS1	1					
6	CPI133814	3	1	2	LS2	0					
6	CPI133814	3	1	2	LS3	0					
6	CPI133814	3	1	2	LS4	0					
6	CPI133814	3	1	3	LS1	1					
6	CPI133814	3	1	3	LS2	0					
6	CPI133814	3	1	3	LS3	0					
6	CPI133814	3	2	1	SCI	4					
6	CPI133814	3	2	1	LS1	1					
6	CPI133814	3	2	1	LS2	1					
6	CPI133814	3	2	1	LS3	1					
6	CPI133814	3	2	1	LS4	1					
6	CPI133814	3	2	1	LS5	0					
6	CPI133814	3	2	1	LS6	0					
6	CPI133814	3	2	1	LS7	0					
6	CPI133814	3	2	1	I1	1					

6	CPI133814	3	2	1	I2	0					
6	CPI133814	3	2	1	I3	0					
6	CPI133814	3	2	2	LS1	1					
6	CPI133814	3	2	2	LS2	1					
6	CPI133814	3	2	2	LS3	0					
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6	CPI133814	3	2	2	I2	0					
6	CPI133814	3	2	3	LS1	1					
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6	CPI133814	3	3	1	SCI	2					
6	CPI133814	3	3	1	LS1	1					
6	CPI133814	3	3	1	LS2	1					
6	CPI133814	3	3	1	LS3	0					
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6	CPI133814	3	3	1	LS5	0					
6	CPI133814	3	3	1	LS6	0					
6	CPI133814	3	3	1	LS7	0					
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6	CPI133814	3	3	2	LS4	0					
6	CPI133814	3	3	2	I1	0					
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6	CPI133814	3	4	1	LS7	0					
6	CPI133814	3	4	1	I1	1					
6	CPI133814	3	4	1	I2	0					
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6	CPI133814	3	4	3	LS2	0					
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6	CPI133814	3	5	1	LS2	1					
6	CPI133814	3	5	1	LS3	1					
6	CPI133814	3	5	1	LS4	1					
6	CPI133814	3	5	1	LS5	0					
6	CPI133814	3	5	1	LS6	0					
6	CPI133814	3	5	1	LS7	0					
6	CPI133814	3	5	1	I1	2					
6	CPI133814	3	5	1	I2	0					
6	CPI133814	3	5	1	I3	0					
6	CPI133814	3	5	2	LS1	1					
6	CPI133814	3	5	2	LS2	1					
6	CPI133814	3	5	2	LS3	1					
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6	CPI133814	3	5	2	I1	1					
6	CPI133814	3	5	2	I2	0					
6	CPI133814	3	5	3	LS1	1					
6	CPI133814	3	5	3	LS2	1					
6	CPI133814	3	5	3	LS3	0					
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7	Puseas	1	1	1	I1	4	4	1	1	1	1

7	Puseas	1	1	1	I2	2	1	1	0	0	0
7	Puseas	1	1	1	I3	1	0	0	0	0	0
7	Puseas	1	1	1	I4	0	0	0	0	0	0
7	Puseas	1	1	1	P	0	0	0	0	0	0
7	Puseas	1	2	1	I1	4	8	3	2	2	1
7	Puseas	1	2	1	I2	1	4	2	1	1	0
7	Puseas	1	2	1	I3	0	0	0	0	0	0
7	Puseas	1	2	1	I4	0	0	0	0	0	0
7	Puseas	1	2	1	P	0	0	0	0	0	0
7	Puseas	1	2	2	I1	4	7	2	2	2	1
7	Puseas	1	2	2	I2	0	0	0	0	0	0
7	Puseas	1	2	2	I3	0	0	0	0	0	0
7	Puseas	1	2	3	I1	4	5	1	2	1	1
7	Puseas	1	3	1	I1	1	2	2	0	0	0
7	Puseas	1	3	1	I2	0	0	0	0	0	0
7	Puseas	1	3	1	I3	0	0	0	0	0	0
7	Puseas	1	3	1	I4	0	0	0	0	0	0
7	Puseas	1	4	1	I1	4	5	1	1	1	2
7	Puseas	1	4	1	I2	1	3	3	0	0	0
7	Puseas	1	4	1	I3	0	0	0	0	0	0
7	Puseas	1	4	1	I4	0	0	0	0	0	0
7	Puseas	1	5	1	I1	4	7	1	2	2	2
7	Puseas	1	5	1	I2	1	2	2	0	0	0
7	Puseas	1	5	1	I3	0	0	0	0	0	0
7	Puseas	1	5	1	I4	0	0	0	0	0	0
7	Puseas	1	5	1	P	0	0	0	0	0	0
7	Puseas	1	5	2	I1	4	6	2	1	1	2
7	Puseas	1	5	2	I2	0	4	2	2	0	0
7	Puseas	1	5	2	I3	0	0	0	0	0	0
7	Puseas	1	5	3	I1	4	4	1	1	1	1
7	Puseas	1	5	3	I2	1	5	3	2	0	0
7	Puseas	2	1	1	I1	4	5	1	2	1	1
7	Puseas	2	1	1	I2	3	4	2	1	1	0
7	Puseas	2	1	1	I3	0	0	0	0	0	0
7	Puseas	2	1	1	I4	0	0	0	0	0	0
7	Puseas	2	1	1	P	0	0	0	0	0	0

7	Puseas	2	1	2	I1	3	2	2	0	0	0
7	Puseas	2	1	2	I2	0	0	0	0	0	0
7	Puseas	2	1	2	I3	0	0	0	0	0	0
7	Puseas	2	1	3	I1	4	4	1	1	1	1
7	Puseas	2	1	3	I2	2	3	2	1	0	0
7	Puseas	2	1	3	I3	0	0	0	0	0	0
7	Puseas	2	2	1	I1	1	1	1	0	0	0
7	Puseas	2	2	1	I2	0	0	0	0	0	0
7	Puseas	2	2	1	I3	0	0	0	0	0	0
7	Puseas	2	2	1	I4	0	0	0	0	0	0
7	Puseas	2	2	1	P	0	0	0	0	0	0
7	Puseas	2	2	2	I1	1	2	2	0	0	0
7	Puseas	2	2	2	I2	0	0	0	0	0	0
7	Puseas	2	3	1	I1	4	4	2	1	0	1
7	Puseas	2	3	1	I2	1	3	2	0	1	0
7	Puseas	2	3	1	I3	0	0	0	0	0	0
7	Puseas	2	3	1	I4	0	0	0	0	0	0
7	Puseas	2	3	2	I1	4	4	1	1	1	1
7	Puseas	2	3	2	I2	1	13	3	4	3	3
7	Puseas	2	3	2	I3	0	0	0	0	0	0
7	Puseas	2	3	3	I1	2	4	1	1	1	1
7	Puseas	2	4	1	I1	4	9	3	3	2	1
7	Puseas	2	4	1	I2	2	4	2	1	1	0
7	Puseas	2	4	1	I3	1	0	0	0	0	0
7	Puseas	2	4	1	I4	0	0	0	0	0	0
7	Puseas	2	4	1	P	0	0	0	0	0	0
7	Puseas	2	4	2	I1	4	5	2	1	1	1
7	Puseas	2	4	2	I2	4	8	2	0	3	3
7	Puseas	2	4	2	I3	1	13	4	3	3	3
7	Puseas	2	4	2	I4	0	0	0	0	0	0
7	Puseas	2	4	3	I1	4	8	4	2	0	2
7	Puseas	2	4	3	I2	0	0	0	0	0	0
7	Puseas	2	5	1	I1	4	9	5	1	0	3
7	Puseas	2	5	1	I2	4	16	5	2	4	5
7	Puseas	2	5	1	I3	1	6	4	2	0	0
7	Puseas	2	5	1	P	0	0	0	0	0	0

7	Puseas	2	5	2	I1	1	5	5	0	0	0
7	Puseas	2	5	2	I2	0	0	0	0	0	0
7	Puseas	2	5	2	I3	0	0	0	0	0	0
7	Puseas	2	5	2	P	0	0	0	0	0	0
7	Puseas	2	5	3	I1	1	7	4	3	0	0
7	Puseas	2	5	3	I2	0	0	0	0	0	0
7	Puseas	2	5	3	I3	0	0	0	0	0	0
7	Puseas	2	5	3	P	0	0	0	0	0	0
7	Puseas	3	1	1	I1	4					
7	Puseas	3	1	1	I2	1					
7	Puseas	3	1	1	I3	0					
7	Puseas	3	1	1	I4	0					
7	Puseas	3	1	1	P	0					
7	Puseas	3	1	2	I1	4					
7	Puseas	3	1	2	I2	1					
7	Puseas	3	1	2	I3	0					
7	Puseas	3	1	2	I4	0					
7	Puseas	3	1	2	P	0					
7	Puseas	3	1	3	I1	4					
7	Puseas	3	1	3	I2	1					
7	Puseas	3	1	3	I3	0					
7	Puseas	3	2	1	I1	4					
7	Puseas	3	2	1	I2	4					
7	Puseas	3	2	1	I3	1					
7	Puseas	3	2	1	I4	1					
7	Puseas	3	2	1	P	0					
7	Puseas	3	2	2	I1	4					
7	Puseas	3	2	2	I2	2					
7	Puseas	3	2	2	I3	0					
7	Puseas	3	2	3	I1	4					
7	Puseas	3	3	1	I1	3					
7	Puseas	3	3	1	I2	1					
7	Puseas	3	3	1	I3	0					
7	Puseas	3	3	1	I4	0					
7	Puseas	3	3	1	P	0					
7	Puseas	3	3	2	I1	1					

7	Puseas	3	3	2	I2	0					
7	Puseas	3	4	1	I1	4					
7	Puseas	3	4	1	I2	2					
7	Puseas	3	4	1	I3	1					
7	Puseas	3	4	1	I4	0					
7	Puseas	3	4	2	I1	4					
7	Puseas	3	4	2	I2	1					
7	Puseas	3	4	2	I3	0					
7	Puseas	3	4	2	I4	0					
7	Puseas	3	4	2	P	0					
7	Puseas	3	4	3	I1	4					
7	Puseas	3	4	3	I2	1					
7	Puseas	3	4	3	I3	0					
7	Puseas	3	5	1	I1	2					
7	Puseas	3	5	1	I2	1					
7	Puseas	3	5	1	I3	0					
7	Puseas	3	5	1	I4	0					
7	Puseas	3	5	1	P	0					
7	Puseas	3	5	2	I1	3					
7	Puseas	3	5	2	I2	0					
7	Puseas	3	5	2	I3	0					
7	Puseas	3	5	3	I1	3					
7	Puseas	3	5	3	I2	0					
7	Vasco	1	1	1	I1	1	3	1	1	1	0
7	Vasco	1	1	1	I2	0	0	0	0	0	0
7	Vasco	1	1	1	I3	0	0	0	0	0	0
7	Vasco	1	1	1	I4	0	0	0	0	0	0
7	Vasco	1	1	1	P	0	0	0	0	0	0
7	Vasco	1	2	1	I1	1	2	2	0	0	0
7	Vasco	1	2	1	I2	0	0	0	0	0	0
7	Vasco	1	2	1	I3	0	0	0	0	0	0
7	Vasco	1	2	1	P	0	0	0	0	0	0
7	Vasco	1	3	1	I1	1	0	0	0	0	0
7	Vasco	1	3	1	I2	0	0	0	0	0	0
7	Vasco	1	3	1	I3	0	0	0	0	0	0
7	Vasco	1	3	1	I4	0	0	0	0	0	0

7	Vasco	1	3	1	P	0	0	0	0	0	0
7	Vasco	1	3	2	I1	1	0	0	0	0	0
7	Vasco	1	4	1	I1	1	2	1	0	1	0
7	Vasco	1	4	1	I2	0	0	0	0	0	0
7	Vasco	1	4	1	I3	0	0	0	0	0	0
7	Vasco	1	4	1	P	0	0	0	0	0	0
7	Vasco	1	4	2	I1	1	4	1	1	1	1
7	Vasco	1	4	2	I2	0	0	0	0	0	0
7	Vasco	1	4	2	I3	0	0	0	0	0	0
7	Vasco	1	5	1	I1	1	0	0	0	0	0
7	Vasco	1	5	1	I2	0	0	0	0	0	0
7	Vasco	1	5	1	I3	0	0	0	0	0	0
7	Vasco	1	5	1	I4	0	0	0	0	0	0
7	Vasco	1	5	1	P	0	0	0	0	0	0
7	Vasco	1	5	2	I1	1	2	2	0	0	0
7	Vasco	1	5	2	I2	0	0	0	0	0	0
7	Vasco	1	5	2	I3	0	0	0	0	0	0
7	Vasco	1	5	3	I1	1	2	2	0	0	0
7	Vasco	2	1	1	I1	2	5	2	1	1	1
7	Vasco	2	1	1	I2	0	0	0	0	0	0
7	Vasco	2	1	1	I3	0	0	0	0	0	0
7	Vasco	2	1	1	I4	0	0	0	0	0	0
7	Vasco	2	1	1	P	0	0	0	0	0	0
7	Vasco	2	2	1	I1	1	6	2	1	1	2
7	Vasco	2	2	1	I2	0	0	0	0	0	0
7	Vasco	2	2	1	I3	0	0	0	0	0	0
7	Vasco	2	2	1	I4	0	0	0	0	0	0
7	Vasco	2	2	1	P	0	0	0	0	0	0
7	Vasco	2	2	2	I1	2	5	2	1	0	2
7	Vasco	2	2	2	I2	0	0	0	0	0	0
7	Vasco	2	2	2	I3	0	0	0	0	0	0
7	Vasco	2	2	2	I4	0	0	0	0	0	0
7	Vasco	2	2	2	P	0	0	0	0	0	0
7	Vasco	2	3	1	I1	4	6	2	1	1	2
7	Vasco	2	3	1	I2	4	5	2	0	1	2
7	Vasco	2	3	1	I3	2	10	3	2	2	3

7	Vasco	2	3	1	I4	0	0	0	0	0	0
7	Vasco	2	3	1	P	0	0	0	0	0	0
7	Vasco	2	3	2	I1	4	4	1	1	1	1
7	Vasco	2	3	2	I2	2	3	2	1	0	0
7	Vasco	2	3	2	I3	0	0	0	0	0	0
7	Vasco	2	3	2	I4	0	0	0	0	0	0
7	Vasco	2	3	2	P	0	0	0	0	0	0
7	Vasco	2	3	3	I1	4	6	2	1	1	2
7	Vasco	2	3	3	I2	0	5	3	1	1	0
7	Vasco	2	3	3	I3	0	0	0	0	0	0
7	Vasco	2	3	3	P	0	0	0	0	0	0
7	Vasco	2	4	1	I1	3	6	2	1	1	2
7	Vasco	2	4	1	I2	1	6	3	1	1	1
7	Vasco	2	4	1	I3	0	0	0	0	0	0
7	Vasco	2	4	1	I4	0	0	0	0	0	0
7	Vasco	2	4	1	P	0	0	0	0	0	0
7	Vasco	2	4	2	I1	3	4	1	1	1	1
7	Vasco	2	4	2	I2	0	2	2	0	0	0
7	Vasco	2	4	2	I3	0	0	0	0	0	0
7	Vasco	2	4	2	I4	0	0	0	0	0	0
7	Vasco	2	4	2	P	0	0	0	0	0	0
7	Vasco	2	5	1	I1	4	4	1	1	1	1
7	Vasco	2	5	1	I2	4	6	2	1	1	2
7	Vasco	2	5	1	I3	2	9	2	2	2	3
7	Vasco	2	5	1	I4	0	7	4	3	0	0
7	Vasco	2	5	1	P	0	0	0	0	0	0
7	Vasco	2	5	2	I1	4	4	1	1	1	1
7	Vasco	2	5	2	I2	4	7	1	2	2	2
7	Vasco	2	5	2	I3	1	8	3	2	3	0
7	Vasco	2	5	2	I4	0	0	0	0	0	0
7	Vasco	2	5	2	P	0	0	0	0	0	0
7	Vasco	2	5	3	I1	4	5	2	1	1	1
7	Vasco	2	5	3	I2	4	4	2	1	1	0
7	Vasco	2	5	3	I3	1	0	0	0	0	0
7	Vasco	2	5	3	I4	0	0	0	0	0	0
7	Vasco	3	1	1	I1	4					

7	Vasco	3	1	1	I2	1					
7	Vasco	3	1	1	I3	0					
7	Vasco	3	1	1	I4	0					
7	Vasco	3	1	1	P	0					
7	Vasco	3	1	2	I1	4					
7	Vasco	3	1	2	I2	1					
7	Vasco	3	1	2	I3	0					
7	Vasco	3	1	2	P	0					
7	Vasco	3	1	3	I1	4					
7	Vasco	3	1	3	I2	0					
7	Vasco	3	1	3	I3	0					
7	Vasco	3	1	3	P	0					
7	Vasco	3	2	1	I1	1					
7	Vasco	3	2	1	I2	0					
7	Vasco	3	2	1	I3	0					
7	Vasco	3	2	1	P	0					
7	Vasco	3	2	2	I1	1					
7	Vasco	3	2	2	I2	0					
7	Vasco	3	2	2	I3	0					
7	Vasco	3	3	1	I1	2					
7	Vasco	3	3	1	I2	0					
7	Vasco	3	3	1	I3	0					
7	Vasco	3	3	1	I4	0					
7	Vasco	3	3	1	P	0					
7	Vasco	3	3	2	I1	1					
7	Vasco	3	3	2	I2	0					
7	Vasco	3	3	2	I3	0					
7	Vasco	3	4	1	I1	1					
7	Vasco	3	4	1	I2	0					
7	Vasco	3	4	1	I3	0					
7	Vasco	3	4	1	I4	0					
7	Vasco	3	4	1	P	0					
7	Vasco	3	4	2	I1	2					
7	Vasco	3	4	2	I2	0					
7	Vasco	3	4	2	I3	0					
7	Vasco	3	4	2	P	0					

7	Vasco	3	4	3	I1	1					
7	Vasco	3	4	3	I2	0					
7	Vasco	3	4	3	I3	0					
7	Vasco	3	5	1	I1	4					
7	Vasco	3	5	1	I2	4					
7	Vasco	3	5	1	I3	1					
7	Vasco	3	5	1	I4	0					
7	Vasco	3	5	1	P	0					
7	Vasco	3	5	2	I1	4					
7	Vasco	3	5	2	I2	3					
7	Vasco	3	5	2	I3	1					
7	Vasco	3	5	2	I4	0					
7	Vasco	3	5	2	P	0					
7	Vasco	3	5	3	I1	4					
7	Vasco	3	5	3	I2	1					
7	Vasco	3	5	3	I3	0					
7	Vasco	3	5	3	P	0					
7	2-49	1	1	1	I1	1	3	1	1	0	1
7	2-49	1	1	1	I2	0	0	0	0	0	0
7	2-49	1	1	1	I3	0	0	0	0	0	0
7	2-49	1	1	1	I4	0	0	0	0	0	0
7	2-49	1	1	1	P	0	0	0	0	0	0
7	2-49	1	1	2	I1	2	4	2	1	0	1
7	2-49	1	1	2	I2	0	0	0	0	0	0
7	2-49	1	1	2	I3	0	0	0	0	0	0
7	2-49	1	1	2	I4	0	0	0	0	0	0
7	2-49	1	1	2	P	0	0	0	0	0	0
7	2-49	1	1	3	I1	1	3	3	0	0	0
7	2-49	1	1	3	I2	0	0	0	0	0	0
7	2-49	1	1	3	I3	0	0	0	0	0	0
7	2-49	1	1	3	P	0	0	0	0	0	0
7	2-49	1	1	4	I1	1	0	0	0	0	0
7	2-49	1	1	4	I2	0	0	0	0	0	0
7	2-49	1	1	4	I3	0	0	0	0	0	0
7	2-49	1	2	1	I1	1	0	0	0	0	0
7	2-49	1	2	1	I2	0	0	0	0	0	0

7	2-49	1	2	1	I3	0	0	0	0	0	0
7	2-49	1	2	2	I1	1	0	0	0	0	0
7	2-49	1	2	2	I2	0	0	0	0	0	0
7	2-49	1	3	1	I1	1	0	0	0	0	0
7	2-49	1	3	1	I2	0	0	0	0	0	0
7	2-49	1	3	1	I3	0	0	0	0	0	0
7	2-49	1	3	1	I4	0	0	0	0	0	0
7	2-49	1	3	1	P	0	0	0	0	0	0
7	2-49	1	3	2	I1	1	3	2	1	0	0
7	2-49	1	3	2	I2	0	0	0	0	0	0
7	2-49	1	3	2	I3	0	0	0	0	0	0
7	2-49	1	3	3	I1	0	2	1	1	0	0
7	2-49	1	4	1	I1	2	4	1	1	1	1
7	2-49	1	4	1	I2	0	0	0	0	0	0
7	2-49	1	4	1	I3	0	0	0	0	0	0
7	2-49	1	4	1	I4	0	0	0	0	0	0
7	2-49	1	4	1	P	0	0	0	0	0	0
7	2-49	1	4	2	I1	0	0	0	0	0	0
7	2-49	1	4	2	I2	0	0	0	0	0	0
7	2-49	1	4	2	I3	0	0	0	0	0	0
7	2-49	1	4	2	I4	0	0	0	0	0	0
7	2-49	1	4	3	I1	0	0	0	0	0	0
7	2-49	1	4	3	I2	0	0	0	0	0	0
7	2-49	1	4	4	I1	0	0	0	0	0	0
7	2-49	1	5	1	I1	2	0	0	0	0	0
7	2-49	1	5	1	I2	1	0	0	0	0	0
7	2-49	1	5	1	I3	0	0	0	0	0	0
7	2-49	1	5	1	P	0	0	0	0	0	0
7	2-49	1	5	2	I1	1	3	2	1	0	0
7	2-49	1	5	2	I2	0	0	0	0	0	0
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7	2-49	2	1	1	I1	1	3	1	2	0	0
7	2-49	2	1	1	I2	0	0	0	0	0	0
7	2-49	2	1	1	I3	0	0	0	0	0	0
7	2-49	2	1	1	I4	0	0	0	0	0	0
7	2-49	2	1	1	P	0	0	0	0	0	0

7	2-49	2	1	2	I1	1	3	2	1	0	0
7	2-49	2	1	2	I2	0	0	0	0	0	0
7	2-49	2	1	2	I3	0	0	0	0	0	0
7	2-49	2	1	2	I4	0	0	0	0	0	0
7	2-49	2	1	2	P	0	0	0	0	0	0
7	2-49	2	1	3	I1	1	3	3	0	0	0
7	2-49	2	1	3	I2	0	0	0	0	0	0
7	2-49	2	1	3	I3	0	0	0	0	0	0
7	2-49	2	1	3	I4	0	0	0	0	0	0
7	2-49	2	1	3	P	0	0	0	0	0	0
7	2-49	2	1	4	I1	1	2	2	0	0	0
7	2-49	2	2	1	I1	0	0	0	0	0	0
7	2-49	2	2	1	I2	0	0	0	0	0	0
7	2-49	2	2	1	I3	0	0	0	0	0	0
7	2-49	2	2	1	I4	0	0	0	0	0	0
7	2-49	2	2	1	P	0	0	0	0	0	0
7	2-49	2	2	2	I1	1	3	2	1	0	0
7	2-49	2	2	2	I2	0	0	0	0	0	0
7	2-49	2	2	2	I3	0	0	0	0	0	0
7	2-49	2	2	2	I4	0	0	0	0	0	0
7	2-49	2	2	2	P	0	0	0	0	0	0
7	2-49	2	2	3	I1	0	2	2	0	0	0
7	2-49	2	2	3	I2	0	0	0	0	0	0
7	2-49	2	2	3	I3	0	0	0	0	0	0
7	2-49	2	2	3	I4	0	0	0	0	0	0
7	2-49	2	2	3	P	0	0	0	0	0	0
7	2-49	2	3	1	I1	0	0	0	0	0	0
7	2-49	2	3	1	I2	0	0	0	0	0	0
7	2-49	2	3	1	I3	0	0	0	0	0	0
7	2-49	2	3	1	I4	0	0	0	0	0	0
7	2-49	2	3	1	P	0	0	0	0	0	0
7	2-49	2	3	2	I1	1	3	2	1	0	0
7	2-49	2	3	2	I2	0	0	0	0	0	0
7	2-49	2	3	2	I3	0	0	0	0	0	0
7	2-49	2	3	2	I4	0	0	0	0	0	0
7	2-49	2	3	2	P	0	0	0	0	0	0

7	2-49	2	3	3	I1	1	0	0	0	0	0
7	2-49	2	3	3	I2	0	0	0	0	0	0
7	2-49	2	3	3	I3	0	0	0	0	0	0
7	2-49	2	3	3	I4	0	0	0	0	0	0
7	2-49	2	3	3	P	0	0	0	0	0	0
7	2-49	2	3	4	I1	0	0	0	0	0	0
7	2-49	2	3	4	I2	0	0	0	0	0	0
7	2-49	2	3	4	I3	0	0	0	0	0	0
7	2-49	2	3	4	I4	0	0	0	0	0	0
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7	2-49	2	4	1	I3	0	0	0	0	0	0
7	2-49	2	4	1	I4	0	0	0	0	0	0
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7	2-49	2	4	2	I1	0	4	4	0	0	0
7	2-49	2	4	2	I2	0	0	0	0	0	0
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7	2-49	2	4	2	I4	0	0	0	0	0	0
7	2-49	2	4	2	P	0	0	0	0	0	0
7	2-49	2	5	1	I1	1	2	2	0	0	0
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7	2-49	2	5	1	I4	0	0	0	0	0	0
7	2-49	2	5	1	P	0	0	0	0	0	0
7	2-49	2	5	2	I1	1	3	2	1	0	0
7	2-49	2	5	2	I2	0	0	0	0	0	0
7	2-49	2	5	2	I3	0	0	0	0	0	0
7	2-49	2	5	2	I4	0	0	0	0	0	0
7	2-49	2	5	2	P	0	0	0	0	0	0
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7	2-49	2	5	3	I2	0	0	0	0	0	0
7	2-49	2	5	3	I3	0	0	0	0	0	0
7	2-49	2	5	3	P	0	0	0	0	0	0
7	2-49	2	5	4	I1	0	4	4	0	0	0
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7	2-49	2	5	4	I3	0	0	0	0	0	0
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7	2-49	3	1	1	I2	0					
7	2-49	3	1	1	I3	0					
7	2-49	3	1	1	I4	0					
7	2-49	3	1	1	P	0					
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7	2-49	3	2	4	I2	0					
7	2-49	3	2	4	I3	0					
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7	2-49	3	3	3	P	0					
7	2-49	3	3	4	I1	1					
7	2-49	3	3	4	I2	0					
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7	2-49	3	4	1	I1	1					
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7	2-49	3	4	3	P	0					
7	2-49	3	4	4	I1	0					
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7	2-49	3	4	4	I3	0					
7	2-49	3	4	4	I4	0					
7	2-49	3	4	4	P	0					
7	2-49	3	5	1	I1	0					
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7	2-49	3	5	2	I3	0					
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7	2-49	3	5	3	I2	0					
7	2-49	3	5	3	I3	0					
7	2-49	3	5	3	P	0					
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7	Sunco	1	1	1	I3	0	0	0	0	0	0
7	Sunco	1	1	1	P	0	0	0	0	0	0
7	Sunco	1	1	2	I1	1	1	1	0	0	0
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7	Sunco	1	1	2	I3	0	0	0	0	0	0
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7	Sunco	1	2	1	I3	0	0	0	0	0	0
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7	Sunco	1	3	1	I2	0	0	0	0	0	0
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7	Sunco	1	3	1	I4	0	0	0	0	0	0
7	Sunco	1	3	1	P	0	0	0	0	0	0
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7	Sunco	1	4	1	I2	0	0	0	0	0	0
7	Sunco	1	4	1	I3	0	0	0	0	0	0
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7	Sunco	1	4	2	I1	0	0	0	0	0	0
7	Sunco	1	4	2	I2	0	0	0	0	0	0
7	Sunco	1	4	2	I3	0	0	0	0	0	0
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7	Sunco	1	5	1	I1	1	0	0	0	0	0
7	Sunco	1	5	1	I2	0	0	0	0	0	0
7	Sunco	1	5	1	I3	0	0	0	0	0	0

7	Sunco	1	5	1	I4	0	0	0	0	0	0
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7	Sunco	2	1	1	I1	1	4	1	1	1	1
7	Sunco	2	1	1	I2	0	0	0	0	0	0
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7	Sunco	2	2	2	I2	0	0	0	0	0	0
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7	Sunco	2	2	2	I4	0	0	0	0	0	0
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7	CPI133814	2	3	3	I1	0	2	1	1	0	0
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7	CPI133814	2	5	1	P	0	0	0	0	0	0
7	CPI133814	2	5	2	I1	4	4	1	1	1	1
7	CPI133814	2	5	2	I2	1	0	0	0	0	0
7	CPI133814	2	5	2	I3	0	0	0	0	0	0
7	CPI133814	2	5	2	I4	0	0	0	0	0	0
7	CPI133814	2	5	2	P	0	0	0	0	0	0
7	CPI133814	2	5	3	I1	1	3	2	1	0	0
7	CPI133814	2	5	3	I2	0	0	0	0	0	0
7	CPI133814	2	5	3	I3	0	0	0	0	0	0
7	CPI133814	2	5	3	I4	0	0	0	0	0	0
7	CPI133814	2	5	3	P	0	0	0	0	0	0
7	CPI133814	3	1	1	I1	1					
7	CPI133814	3	1	1	I2	0					
7	CPI133814	3	1	1	I3	0					
7	CPI133814	3	1	1	I4	0					
7	CPI133814	3	1	1	P	0					
7	CPI133814	3	1	2	I1	1					
7	CPI133814	3	1	2	I2	0					
7	CPI133814	3	1	2	I3	0					
7	CPI133814	3	1	2	I4	0					
7	CPI133814	3	1	2	P	0					

7	CPI133814	3	1	3	I1	1					
7	CPI133814	3	1	3	I2	0					
7	CPI133814	3	1	3	I3	0					
7	CPI133814	3	1	3	I4	0					
7	CPI133814	3	1	3	P	0					
7	CPI133814	3	2	1	I1	1					
7	CPI133814	3	2	1	I2	0					
7	CPI133814	3	2	1	I3	0					
7	CPI133814	3	2	1	I4	0					
7	CPI133814	3	2	1	P	0					
7	CPI133814	3	2	2	I1	1					
7	CPI133814	3	2	2	I2	0					
7	CPI133814	3	2	2	I3	0					
7	CPI133814	3	3	1	I1	1					
7	CPI133814	3	3	1	I2	0					
7	CPI133814	3	3	1	I3	0					
7	CPI133814	3	3	1	I4	0					
7	CPI133814	3	3	1	P	0					
7	CPI133814	3	3	2	I1	1					
7	CPI133814	3	3	2	I2	0					
7	CPI133814	3	3	2	I3	0					
7	CPI133814	3	3	2	I4	0					
7	CPI133814	3	3	2	P	0					
7	CPI133814	3	3	3	I1	0					
7	CPI133814	3	3	3	I2	0					
7	CPI133814	3	3	3	I3	0					
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7	CPI133814	3	4	1	I2	0					
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7	CPI133814	3	4	1	I4	0					
7	CPI133814	3	4	1	P	0					
7	CPI133814	3	4	2	I1	0					
7	CPI133814	3	4	2	I2	0					
7	CPI133814	3	4	2	I3	0					
7	CPI133814	3	4	2	I4	0					
7	CPI133814	3	4	2	P	0					

7	CPI133814	3	4	3	I1	0				
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7	CPI133814	3	4	3	I3	0				
7	CPI133814	3	4	3	I4	0				
7	CPI133814	3	4	3	P	0				
7	CPI133814	3	5	1	I1	1				
7	CPI133814	3	5	1	I2	0				
7	CPI133814	3	5	1	I3	0				
7	CPI133814	3	5	1	I4	0				
7	CPI133814	3	5	1	P	0				
7	CPI133814	3	5	2	I1	2				
7	CPI133814	3	5	2	I2	1				
7	CPI133814	3	5	2	I3	0				
7	CPI133814	3	5	2	I4	0				
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7	CPI133814	3	5	3	I2	0				
7	CPI133814	3	5	3	I3	0				
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8	Puseas	1	1	1	I2	1	0	0	0	0	0
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8	Puseas	1	1	1	I4	0	0	0	0	0	0
8	Puseas	1	1	1	P	0	0	0	0	0	0
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8	Puseas	1	1	2	I2	2	6	4	2	0	0
8	Puseas	1	1	2	I3	1	0	0	0	0	0
8	Puseas	1	1	2	I4	0	0	0	0	0	0
8	Puseas	1	1	2	P	0	0	0	0	0	0
8	Puseas	1	1	3	I1	4	8	3	1	2	2
8	Puseas	1	1	3	I2	1	3	3	0	0	0
8	Puseas	1	1	3	I3	0	0	0	0	0	0
8	Puseas	1	2	1	I1	4	10	4	3	2	1
8	Puseas	1	2	1	I2	1	0	0	0	0	0
8	Puseas	1	2	1	I3	0	0	0	0	0	0
8	Puseas	1	2	1	I4	0	0	0	0	0	0
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8	Puseas	1	2	2	I2	1	0	0	0	0	0
8	Puseas	1	2	2	I3	0	0	0	0	0	0
8	Puseas	1	3	1	I1	4	10	3	3	2	2
8	Puseas	1	3	1	I2	1	4	3	1	0	0
8	Puseas	1	3	1	I3	0	0	0	0	0	0
8	Puseas	1	3	1	I4	0	0	0	0	0	0
8	Puseas	1	3	1	P	0	0	0	0	0	0
8	Puseas	1	4	1	I1	4	6	2	2	1	1
8	Puseas	1	4	1	I2	1	0	0	0	0	0
8	Puseas	1	4	1	I3	0	0	0	0	0	0
8	Puseas	1	4	1	I4	0	0	0	0	0	0
8	Puseas	1	4	1	P	0	0	0	0	0	0
8	Puseas	1	4	2	I1	4	5	2	2	1	0
8	Puseas	1	4	2	I2	4	0	0	0	0	0
8	Puseas	1	4	2	I3	4	0	0	0	0	0
8	Puseas	1	5	1	I1	4	11	3	3	2	3
8	Puseas	1	5	1	I2	1	8	2	3	3	0
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8	Puseas	1	5	1	I4	0	0	0	0	0	0
8	Puseas	1	5	2	I1	4	5	2	1	1	1
8	Puseas	1	5	2	I2	3	5	3	2	0	0
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8	Puseas	2	1	1	I2	0	9	4	3	2	0
8	Puseas	2	1	1	I3	0	0	0	0	0	0
8	Puseas	2	1	1	I4	0	0	0	0	0	0
8	Puseas	2	1	1	P	0	0	0	0	0	0
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8	Puseas	2	1	2	I2	0	9	3	3	3	0
8	Puseas	2	1	2	I3	0	0	0	0	0	0
8	Puseas	2	1	2	I4	0	0	0	0	0	0
8	Puseas	2	1	2	P	0	0	0	0	0	0
8	Puseas	2	1	3	I1	1	7	2	2	1	2
8	Puseas	2	1	3	I2	0	2	2	0	0	0
8	Puseas	2	1	3	I3	0	0	0	0	0	0
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8	Puseas	2	1	3	P	0	0	0	0	0	0
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8	Puseas	2	1	4	I2	0	4	3	1	0	0
8	Puseas	2	1	4	I3	0	0	0	0	0	0
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8	Puseas	2	2	1	I2	1	8	3	2	3	0
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8	Puseas	2	2	1	I4	0	0	0	0	0	0
8	Puseas	2	2	1	P	0	0	0	0	0	0
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8	Puseas	2	2	2	I2	2	1	1	0	0	0
8	Puseas	2	2	2	I3	0	0	0	0	0	0
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8	Puseas	2	3	1	I2	1	6	4	2	0	0
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8	Puseas	2	3	1	I4	0	0	0	0	0	0
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8	Puseas	2	3	2	I2	3	13	4	3	3	3
8	Puseas	2	3	2	I3	0	0	0	0	0	0
8	Puseas	2	3	2	I4	0	0	0	0	0	0
8	Puseas	2	3	2	P	0	0	0	0	0	0
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8	Puseas	2	3	3	I2	0	0	0	0	0	0
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8	Puseas	2	4	2	I2	3	5	4	1	0	0
8	Puseas	2	4	2	I3	0	0	0	0	0	0
8	Puseas	2	4	2	I4	0	0	0	0	0	0
8	Puseas	2	4	2	P	0	0	0	0	0	0

8	Puseas	2	4	3	I1	4	6	4	2	0	0
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8	Puseas	2	4	3	I3	0	0	0	0	0	0
8	Puseas	2	4	3	P	0	0	0	0	0	0
8	Puseas	2	5	1	I1	4	9	4	2	0	3
8	Puseas	2	5	1	I2	2	12	2	4	4	2
8	Puseas	2	5	1	I3	0	0	0	0	0	0
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8	Puseas	2	5	2	I1	4	5	3	2	0	0
8	Puseas	2	5	2	I2	2	0	0	0	0	0
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8	Puseas	3	1	1	I2	1					
8	Puseas	3	1	1	I3	0					
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8	Puseas	3	2	1	I2	1					
8	Puseas	3	2	1	I3	0					
8	Puseas	3	2	1	P	0					
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8	Puseas	3	2	2	I2	0					
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8	Puseas	3	2	3	I2	1					
8	Puseas	3	2	3	I3	0					
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8	Puseas	3	3	1	I2	0					
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8	Puseas	3	3	2	I1	4					
8	Puseas	3	3	2	I2	1					
8	Puseas	3	3	2	I3	0					
8	Puseas	3	3	3	I1	4					
8	Puseas	3	3	3	I2	4					
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8	Puseas	3	4	1	I2	3					

8	Puseas	3	4	1	I3	1					
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8	Puseas	3	4	1	P	0					
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8	Puseas	3	4	2	I2	3					
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8	Puseas	3	4	3	I2	2					
8	Puseas	3	4	3	I3	1					
8	Puseas	3	4	3	I4	0					
8	Puseas	3	4	3	P	0					
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8	Puseas	3	5	1	I2	4					
8	Puseas	3	5	1	I3	2					
8	Puseas	3	5	1	I4	0					
8	Puseas	3	5	1	P	0					
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8	Puseas	3	5	2	I2	4					
8	Puseas	3	5	2	I3	1					
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8	Puseas	3	5	3	I2	4					
8	Puseas	3	5	3	I3	1					
8	Vasco	1	1	1	I1	4	4	1	1	1	1
8	Vasco	1	1	1	I2	1	7	3	1	2	1
8	Vasco	1	1	1	I3	0	3	2	1	0	0
8	Vasco	1	1	1	I4	0	0	0	0	0	0
8	Vasco	1	1	1	P	0	0	0	0	0	0
8	Vasco	1	1	2	I1	1	9	3	2	2	2
8	Vasco	1	1	2	I2	0	0	0	0	0	0
8	Vasco	1	1	2	I3	0	0	0	0	0	0
8	Vasco	1	1	2	P	0	0	0	0	0	0
8	Vasco	1	2	1	I1	2	6	2	2	2	0
8	Vasco	1	2	1	I2	0	0	0	0	0	0
8	Vasco	1	2	1	I3	0	0	0	0	0	0

8	Vasco	1	2	1	P	0	0	0	0	0	0
8	Vasco	1	3	1	I1	2	7	2	2	2	1
8	Vasco	1	3	1	I2	1	5	2	1	1	1
8	Vasco	1	3	1	I3	0	2	1	1	0	0
8	Vasco	1	3	1	I4	0	0	0	0	0	0
8	Vasco	1	3	1	P	0	0	0	0	0	0
8	Vasco	1	4	1	I1	3	8	2	2	2	2
8	Vasco	1	4	1	I2	0	4	2	1	1	0
8	Vasco	1	4	1	I3	0	0	0	0	0	0
8	Vasco	1	4	1	P	0	0	0	0	0	0
8	Vasco	1	5	1	I1	4	4	1	1	1	1
8	Vasco	1	5	1	I2	1	8	3	2	1	2
8	Vasco	1	5	1	I3	0	0	0	0	0	0
8	Vasco	1	5	1	I4	0	0	0	0	0	0
8	Vasco	1	5	1	P	0	0	0	0	0	0
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8	Vasco	1	5	2	I2	0	7	2	2	2	1
8	Vasco	1	5	2	I3	0	0	0	0	0	0
8	Vasco	1	5	2	I4	0	0	0	0	0	0
8	Vasco	1	5	2	P	0	0	0	0	0	0
8	Vasco	1	5	3	I1	2	4	1	1	1	1
8	Vasco	1	5	3	I2	0	7	2	2	2	1
8	Vasco	1	5	3	I3	0	7	3	2	2	0
8	Vasco	1	5	3	I4	0	0	0	0	0	0
8	Vasco	1	5	3	P	0	0	0	0	0	0
8	Vasco	2	1	1	I1	3	8	3	3	2	0
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8	Vasco	2	1	1	I3	0	0	0	0	0	0
8	Vasco	2	1	1	P	0	0	0	0	0	0
8	Vasco	2	1	2	I1	1	6	2	1	2	1
8	Vasco	2	1	2	I2	0	4	3	1	0	0
8	Vasco	2	1	2	I3	0	0	0	0	0	0
8	Vasco	2	1	2	I4	0	0	0	0	0	0
8	Vasco	2	1	2	P	0	0	0	0	0	0
8	Vasco	2	2	1	I1	4	4	1	1	1	1
8	Vasco	2	2	1	I2	0	6	3	3	0	0

8	Vasco	2	2	1	I3	0	0	0	0	0	0
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8	Vasco	2	2	1	P	0	0	0	0	0	0
8	Vasco	2	2	2	I1	2	5	1	2	1	1
8	Vasco	2	2	2	I2	0	8	4	3	1	0
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8	Vasco	2	2	2	I4	0	0	0	0	0	0
8	Vasco	2	2	2	P	0	0	0	0	0	0
8	Vasco	2	2	3	I1	1	8	2	2	2	2
8	Vasco	2	2	3	I2	0	3	3	0	0	0
8	Vasco	2	2	3	I3	0	0	0	0	0	0
8	Vasco	2	2	3	I4	0	0	0	0	0	0
8	Vasco	2	2	3	P	0	0	0	0	0	0
8	Vasco	2	3	1	I1	4	10	3	3	2	2
8	Vasco	2	3	1	I2	1	12	3	3	3	3
8	Vasco	2	3	1	I3	0	11	4	3	3	1
8	Vasco	2	3	1	I4	0	0	0	0	0	0
8	Vasco	2	3	1	P	0	0	0	0	0	0
8	Vasco	2	3	2	I1	4	4	1	1	1	1
8	Vasco	2	3	2	I2	4	10	3	2	2	3
8	Vasco	2	3	2	I3	0	12	4	3	3	2
8	Vasco	2	3	2	I4	0	3	3	0	0	0
8	Vasco	2	3	2	P	0	0	0	0	0	0
8	Vasco	2	3	3	I1	4	6	2	1	1	2
8	Vasco	2	3	3	I2	1	4	3	1	0	0
8	Vasco	2	3	3	I3	0	0	0	0	0	0
8	Vasco	2	3	3	I4	0	0	0	0	0	0
8	Vasco	2	3	3	P	0	0	0	0	0	0
8	Vasco	2	4	1	I1	4	8	2	2	2	2
8	Vasco	2	4	1	I2	1	11	3	2	2	4
8	Vasco	2	4	1	I3	0	13	4	3	3	3
8	Vasco	2	4	1	I4	0	4	4	0	0	0
8	Vasco	2	4	1	P	0	0	0	0	0	0
8	Vasco	2	4	2	I1	3	10	3	2	2	3
8	Vasco	2	4	2	I2	0	10	3	2	3	2
8	Vasco	2	4	2	I3	0	4	3	1	0	0

8	Vasco	2	4	2	I4	0	0	0	0	0	0
8	Vasco	2	4	2	P	0	0	0	0	0	0
8	Vasco	2	4	3	I1	4	4	1	1	1	1
8	Vasco	2	4	3	I2	1	4	2	2	0	0
8	Vasco	2	5	1	I1	1	6	1	2	2	1
8	Vasco	2	5	1	I2	0	5	3	1	1	0
8	Vasco	2	5	1	I3	0	0	0	0	0	0
8	Vasco	2	5	1	I4	0	0	0	0	0	0
8	Vasco	2	5	1	P	0	0	0	0	0	0
8	Vasco	2	5	2	I1	1	7	2	2	2	1
8	Vasco	2	5	2	I2	0	0	0	0	0	0
8	Vasco	2	5	2	I3	0	0	0	0	0	0
8	Vasco	2	5	2	I4	0	0	0	0	0	0
8	Vasco	2	5	2	P	0	0	0	0	0	0
8	Vasco	3	1	1	I1	4					
8	Vasco	3	1	1	I2	1					
8	Vasco	3	1	1	I3	0					
8	Vasco	3	1	1	I4	0					
8	Vasco	3	1	1	P	0					
8	Vasco	3	1	2	I1	2					
8	Vasco	3	1	2	I2	1					
8	Vasco	3	1	2	I3	0					
8	Vasco	3	1	2	I4	0					
8	Vasco	3	1	3	I1	1					
8	Vasco	3	1	3	I2	0					
8	Vasco	3	1	3	I3	0					
8	Vasco	3	1	3	I4	0					
8	Vasco	3	1	3	P	0					
8	Vasco	3	2	1	I1	2					
8	Vasco	3	2	1	I2	0					
8	Vasco	3	2	1	I3	0					
8	Vasco	3	2	1	I4	0					
8	Vasco	3	2	1	P	0					
8	Vasco	3	2	2	I1	2					
8	Vasco	3	2	2	I2	0					
8	Vasco	3	2	2	I3	0					

8	Vasco	3	2	2	I4	0					
8	Vasco	3	2	2	P	0					
8	Vasco	3	2	3	I1	2					
8	Vasco	3	2	3	I2	0					
8	Vasco	3	2	3	I3	0					
8	Vasco	3	2	3	I4	0					
8	Vasco	3	2	3	P	0					
8	Vasco	3	3	1	I1	4					
8	Vasco	3	3	1	I2	3					
8	Vasco	3	3	1	I3	1					
8	Vasco	3	3	1	I4	0					
8	Vasco	3	3	1	P	0					
8	Vasco	3	3	2	I1	4					
8	Vasco	3	3	2	I2	3					
8	Vasco	3	3	2	I3	0					
8	Vasco	3	3	3	I1	4					
8	Vasco	3	3	3	I2	3					
8	Vasco	3	3	3	I3	0					
8	Vasco	3	4	1	I1	4					
8	Vasco	3	4	1	I2	1					
8	Vasco	3	4	1	I3	0					
8	Vasco	3	4	1	I4	0					
8	Vasco	3	4	1	P	0					
8	Vasco	3	4	2	I1	3					
8	Vasco	3	4	2	I2	0					
8	Vasco	3	4	2	I3	0					
8	Vasco	3	4	2	I4	0					
8	Vasco	3	4	2	P	0					
8	Vasco	3	4	3	I1	4					
8	Vasco	3	4	3	I2	2					
8	Vasco	3	4	3	I3	0					
8	Vasco	3	4	3	I4	0					
8	Vasco	3	4	3	P	0					
8	Vasco	3	5	1	I1	4					
8	Vasco	3	5	1	I2	2					
8	Vasco	3	5	1	I3	0					

8	Vasco	3	5	1	I4	0					
8	Vasco	3	5	1	P	0					
8	Vasco	3	5	2	I1	1					
8	Vasco	3	5	2	I2	0					
8	Vasco	3	5	2	I3	0					
8	Vasco	3	5	2	I4	0					
8	Vasco	3	5	2	P	0					
8	2-49	1	1	1	I1	2	6	2	1	2	1
8	2-49	1	1	1	I2	0	12	4	3	3	2
8	2-49	1	1	1	I3	0	0	0	0	0	0
8	2-49	1	1	1	I4	0	0	0	0	0	0
8	2-49	1	1	1	P	0	0	0	0	0	0
8	2-49	1	1	2	I1	1	3	3	0	0	0
8	2-49	1	1	2	I2	0	0	0	0	0	0
8	2-49	1	1	2	I3	0	0	0	0	0	0
8	2-49	1	1	2	I4	0	0	0	0	0	0
8	2-49	1	1	3	I1	1	4	1	1	1	1
8	2-49	1	1	3	I2	0	5	2	2	1	0
8	2-49	1	1	3	I3	0	0	0	0	0	0
8	2-49	1	2	1	I1	1	12	3	3	3	3
8	2-49	1	2	1	I2	1	8	2	2	2	2
8	2-49	1	2	1	I3	1	2	2	0	0	0
8	2-49	1	2	1	I4	0	0	0	0	0	0
8	2-49	1	2	1	P	0	0	0	0	0	0
8	2-49	1	2	2	I1	1	9	2	2	2	3
8	2-49	1	2	2	I2	0	3	3	0	0	0
8	2-49	1	2	2	I3	0	0	0	0	0	0
8	2-49	1	2	2	P	0	0	0	0	0	0
8	2-49	1	3	1	I1	3	5	1	2	1	1
8	2-49	1	3	1	I2	1	0	0	0	0	0
8	2-49	1	3	1	I3	0	0	0	0	0	0
8	2-49	1	3	1	I4	0	0	0	0	0	0
8	2-49	1	3	1	P	0	0	0	0	0	0
8	2-49	1	3	2	I1	3	5	3	1	1	0
8	2-49	1	3	2	I2	0	0	0	0	0	0
8	2-49	1	3	2	I3	0	0	0	0	0	0

8	2-49	1	3	2	I4	0	0	0	0	0	0
8	2-49	1	3	2	P	0	0	0	0	0	0
8	2-49	1	3	3	I1	4	6	3	2	1	0
8	2-49	1	3	3	I2	1	0	0	0	0	0
8	2-49	1	3	3	I3	0	0	0	0	0	0
8	2-49	1	3	3	I4	0	0	0	0	0	0
8	2-49	1	3	3	P	0	0	0	0	0	0
8	2-49	1	3	4	I1	1	4	2	1	1	0
8	2-49	1	3	4	I2	0	0	0	0	0	0
8	2-49	1	3	4	I3	0	0	0	0	0	0
8	2-49	1	3	4	I4	0	0	0	0	0	0
8	2-49	1	3	4	P	0	0	0	0	0	0
8	2-49	1	4	1	I1	2	4	1	1	1	1
8	2-49	1	4	1	I2	0	8	2	2	2	2
8	2-49	1	4	1	I3	0	3	2	1	0	0
8	2-49	1	4	1	I4	0	0	0	0	0	0
8	2-49	1	4	1	P	0	0	0	0	0	0
8	2-49	1	4	2	I1	2	4	1	1	1	1
8	2-49	1	4	2	I2	0	9	3	2	2	2
8	2-49	1	4	2	I3	0	0	0	0	0	0
8	2-49	1	4	2	I4	0	0	0	0	0	0
8	2-49	1	4	2	P	0	0	0	0	0	0
8	2-49	1	4	3	I1	2	7	2	1	2	2
8	2-49	1	4	3	I2	0	5	2	2	1	0
8	2-49	1	4	3	I3	0	0	0	0	0	0
8	2-49	1	4	3	P	0	0	0	0	0	0
8	2-49	1	5	1	I1	2	4	1	1	1	1
8	2-49	1	5	1	I2	0	6	1	2	2	1
8	2-49	1	5	1	I3	0	0	0	0	0	0
8	2-49	1	5	1	I4	0	0	0	0	0	0
8	2-49	1	5	1	P	0	0	0	0	0	0
8	2-49	2	1	1	I1	4	8	2	2	2	2
8	2-49	2	1	1	I2	0	12	3	3	3	3
8	2-49	2	1	1	I3	0	4	3	1	0	0
8	2-49	2	1	1	I4	0	0	0	0	0	0
8	2-49	2	1	1	P	0	0	0	0	0	0

8	2-49	2	1	2	I1	2	9	3	3	1	2
8	2-49	2	1	2	I2	1	11	4	2	2	3
8	2-49	2	1	2	I3	0	4	3	1	0	0
8	2-49	2	1	2	I4	0	0	0	0	0	0
8	2-49	2	1	2	P	0	0	0	0	0	0
8	2-49	2	1	3	I1	2	7	2	2	1	2
8	2-49	2	1	3	I2	0	6	3	2	1	0
8	2-49	2	1	3	I3	0	0	0	0	0	0
8	2-49	2	1	3	I4	0	0	0	0	0	0
8	2-49	2	1	4	I1	2	8	2	2	2	2
8	2-49	2	1	4	I2	0	12	3	3	3	3
8	2-49	2	1	4	I3	0	3	3	0	0	0
8	2-49	2	2	1	I1	1	0	0	0	0	0
8	2-49	2	2	1	I2	0	0	0	0	0	0
8	2-49	2	2	1	I3	0	0	0	0	0	0
8	2-49	2	2	1	I4	0	0	0	0	0	0
8	2-49	2	2	1	P	0	0	0	0	0	0
8	2-49	2	2	2	I1	1	0	0	0	0	0
8	2-49	2	2	2	I2	0	0	0	0	0	0
8	2-49	2	2	2	I3	0	0	0	0	0	0
8	2-49	2	2	2	P	0	0	0	0	0	0
8	2-49	2	2	3	I1	1	0	0	0	0	0
8	2-49	2	2	3	I2	0	0	0	0	0	0
8	2-49	2	2	3	I3	0	0	0	0	0	0
8	2-49	2	2	3	I4	0	0	0	0	0	0
8	2-49	2	2	3	P	0	0	0	0	0	0
8	2-49	2	3	1	I1	2	5	2	1	1	1
8	2-49	2	3	1	I2	0	9	3	3	3	0
8	2-49	2	3	1	I3	0	0	0	0	0	0
8	2-49	2	3	1	I4	0	0	0	0	0	0
8	2-49	2	3	1	P	0	0	0	0	0	0
8	2-49	2	3	2	I1	1	7	1	2	2	2
8	2-49	2	3	2	I2	0	4	3	1	0	0
8	2-49	2	3	2	I3	0	0	0	0	0	0
8	2-49	2	3	2	I4	0	0	0	0	0	0
8	2-49	2	3	2	P	0	0	0	0	0	0

8	2-49	2	4	1	I1	2	7	2	2	2	1
8	2-49	2	4	1	I2	0	10	3	2	3	2
8	2-49	2	4	1	I3	0	0	0	0	0	0
8	2-49	2	4	1	I4	0	0	0	0	0	0
8	2-49	2	4	1	P	0	0	0	0	0	0
8	2-49	2	4	2	I1	1	13	3	4	3	3
8	2-49	2	4	2	I2	0	4	3	0	1	0
8	2-49	2	4	2	I3	0	0	0	0	0	0
8	2-49	2	4	2	P	0	0	0	0	0	0
8	2-49	2	4	3	I1	2	9	2	3	2	2
8	2-49	2	4	3	I2	0	9	4	3	2	0
8	2-49	2	4	3	I3	0	0	0	0	0	0
8	2-49	2	4	3	I4	0	0	0	0	0	0
8	2-49	2	4	3	P	0	0	0	0	0	0
8	2-49	2	4	4	I1	1	6	1.5	1.5	1.5	1.5
8	2-49	2	4	4	I2	0	7	3	3	1	0
8	2-49	2	4	4	I3	0	0	0	0	0	0
8	2-49	2	5	1	I1	1	7	3	2	2	0
8	2-49	2	5	1	I2	0	0	0	0	0	0
8	2-49	2	5	1	I3	0	0	0	0	0	0
8	2-49	2	5	1	I4	0	0	0	0	0	0
8	2-49	2	5	1	P	0	0	0	0	0	0
8	2-49	2	5	2	I1	0	0	0	0	0	0
8	2-49	2	5	2	I2	0	0	0	0	0	0
8	2-49	2	5	2	I3	0	0	0	0	0	0
8	2-49	2	5	2	I4	0	0	0	0	0	0
8	2-49	3	1	1	I1	2					
8	2-49	3	1	1	I2	1					
8	2-49	3	1	1	I3	0					
8	2-49	3	1	1	I4	0					
8	2-49	3	1	1	P	0					
8	2-49	3	1	2	I1	1					
8	2-49	3	1	2	I2	0					
8	2-49	3	1	2	I3	0					
8	2-49	3	1	2	I4	0					
8	2-49	3	1	2	P	0					

8	2-49	3	1	3	I1	1					
8	2-49	3	1	3	I2	0					
8	2-49	3	1	3	I3	0					
8	2-49	3	1	3	I4	0					
8	2-49	3	1	3	P	0					
8	2-49	3	2	1	I1	1					
8	2-49	3	2	1	I2	0					
8	2-49	3	2	1	I3	0					
8	2-49	3	2	1	I4	0					
8	2-49	3	2	1	P	0					
8	2-49	3	2	2	I1	1					
8	2-49	3	2	2	I2	0					
8	2-49	3	2	2	I3	0					
8	2-49	3	2	2	I4	0					
8	2-49	3	2	2	P	0					
8	2-49	3	2	3	I1	1					
8	2-49	3	2	3	I2	0					
8	2-49	3	2	3	I3	0					
8	2-49	3	2	3	I4	0					
8	2-49	3	2	3	P	0					
8	2-49	3	3	1	I1	3					
8	2-49	3	3	1	I2	0					
8	2-49	3	3	1	I3	0					
8	2-49	3	3	1	I4	0					
8	2-49	3	3	1	P	0					
8	2-49	3	3	2	I1	1					
8	2-49	3	3	2	I2	0					
8	2-49	3	3	2	I3	0					
8	2-49	3	3	2	I4	0					
8	2-49	3	3	2	P	0					
8	2-49	3	3	3	I1	1					
8	2-49	3	3	3	I2	0					
8	2-49	3	3	3	I3	0					
8	2-49	3	4	1	I1	1					
8	2-49	3	4	1	I2	0					
8	2-49	3	4	1	I3	0					

8	2-49	3	4	1	I4	0					
8	2-49	3	4	1	P	0					
8	2-49	3	4	2	I1	0					
8	2-49	3	4	2	I2	0					
8	2-49	3	4	2	I3	0					
8	2-49	3	4	2	I4	0					
8	2-49	3	4	2	P	0					
8	2-49	3	4	3	I1	0					
8	2-49	3	4	3	I2	0					
8	2-49	3	4	3	I3	0					
8	2-49	3	4	3	I4	0					
8	2-49	3	4	3	P	0					
8	2-49	3	5	1	I1	2					
8	2-49	3	5	1	I2	0					
8	2-49	3	5	1	I3	0					
8	2-49	3	5	1	I4	0					
8	2-49	3	5	1	P	0					
8	2-49	3	5	2	I1	2					
8	2-49	3	5	2	I2	0					
8	2-49	3	5	2	I3	0					
8	2-49	3	5	3	I1	1					
8	2-49	3	5	3	I2	0					
8	2-49	3	5	3	I3	0					
8	Sunco	1	1	1	I1	4	7	1	2	2	2
8	Sunco	1	1	1	I2	1	8	3	2	2	1
8	Sunco	1	1	1	I3	0	0	0	0	0	0
8	Sunco	1	1	1	I4	0	0	0	0	0	0
8	Sunco	1	1	1	P	0	0	0	0	0	0
8	Sunco	1	1	2	I1	4	4	1	1	1	1
8	Sunco	1	1	2	I2	1	5	1	2	1	1
8	Sunco	1	1	2	I3	0	4	2	2	0	0
8	Sunco	1	1	2	I4	0	0	0	0	0	0
8	Sunco	1	1	2	P	0	0	0	0	0	0
8	Sunco	1	1	3	I1	2	6	2	1	1	2
8	Sunco	1	1	3	I2	1	4	1	1	0	2
8	Sunco	1	1	3	I3	0	0	0	0	0	0

8	Sunco	1	1	3	I4	0	0	0	0	0	0
8	Sunco	1	1	3	P	0	0	0	0	0	0
8	Sunco	1	2	1	I1	2	5	1	2	1	1
8	Sunco	1	2	1	I2	0	10	3	2	2	3
8	Sunco	1	2	1	I3	0	0	0	0	0	0
8	Sunco	1	2	1	I4	0	0	0	0	0	0
8	Sunco	1	2	1	P	0	0	0	0	0	0
8	Sunco	1	2	2	I1	2	4	1	1	1	1
8	Sunco	1	2	2	I2	0	8	3	2	2	1
8	Sunco	1	2	2	I3	0	3	2	1	0	0
8	Sunco	1	2	2	I4	0	0	0	0	0	0
8	Sunco	1	2	2	P	0	0	0	0	0	0
8	Sunco	1	2	3	I1	1	6	2	1	1	2
8	Sunco	1	2	3	I2	0	7	2	2	1	2
8	Sunco	1	2	3	I3	0	0	0	0	0	0
8	Sunco	1	2	3	P	0	0	0	0	0	0
8	Sunco	1	3	1	I1	3	5	1	2	1	1
8	Sunco	1	3	1	I2	0	3	2	1	0	0
8	Sunco	1	3	1	I3	0	0	0	0	0	0
8	Sunco	1	3	1	I4	0	0	0	0	0	0
8	Sunco	1	3	1	P	0	0	0	0	0	0
8	Sunco	1	3	2	I1	1	9	3	2	2	2
8	Sunco	1	3	2	I2	0	0	0	0	0	0
8	Sunco	1	3	2	I3	0	0	0	0	0	0
8	Sunco	1	3	2	P	0	0	0	0	0	0
8	Sunco	1	4	1	I1	1	7	3	1	1	2
8	Sunco	1	4	1	I2	0	8	3	3	2	0
8	Sunco	1	4	1	I3	0	0	0	0	0	0
8	Sunco	1	4	1	P	0	0	0	0	0	0
8	Sunco	1	4	2	I1	1	1	1	0	0	0
8	Sunco	1	4	2	I2	0	0	0	0	0	0
8	Sunco	1	4	2	I3	0	0	0	0	0	0
8	Sunco	1	4	2	I4	0	0	0	0	0	0
8	Sunco	1	4	2	P	0	0	0	0	0	0
8	Sunco	1	5	1	I1	2	5	2	1	1	1
8	Sunco	1	5	1	I2	0	3	3	0	0	0

8	Sunco	1	5	1	I3	0	0	0	0	0	0
8	Sunco	1	5	1	I4	0	0	0	0	0	0
8	Sunco	1	5	1	P	0	0	0	0	0	0
8	Sunco	1	5	2	I1	2	4	1	1	1	1
8	Sunco	1	5	2	I2	0	5	3	1	0	1
8	Sunco	1	5	2	I3	0	2	2	0	0	0
8	Sunco	1	5	2	I4	0	0	0	0	0	0
8	Sunco	1	5	2	P	0	0	0	0	0	0
8	Sunco	1	5	3	I1	3	6	1	2	2	1
8	Sunco	1	5	3	I2	0	2	2	0	0	0
8	Sunco	1	5	3	I3	0	0	0	0	0	0
8	Sunco	1	5	3	I4	0	0	0	0	0	0
8	Sunco	1	5	3	P	0	0	0	0	0	0
8	Sunco	2	1	1	I1	1	4	2	1	1	0
8	Sunco	2	1	1	I2	0	2	1	1	0	0
8	Sunco	2	1	1	I3	0	1	1	0	0	0
8	Sunco	2	1	1	I4	0	0	0	0	0	0
8	Sunco	2	1	1	P	0	0	0	0	0	0
8	Sunco	2	1	2	I1	1	2	1	1	0	0
8	Sunco	2	1	2	I2	0	0	0	0	0	0
8	Sunco	2	1	2	I3	0	0	0	0	0	0
8	Sunco	2	1	2	I4	0	0	0	0	0	0
8	Sunco	2	1	2	P	0	0	0	0	0	0
8	Sunco	2	1	3	I1	1	6	1	2	2	1
8	Sunco	2	1	3	I2	0	5	3	2	0	0
8	Sunco	2	1	3	I3	0	0	0	0	0	0
8	Sunco	2	1	3	I4	0	0	0	0	0	0
8	Sunco	2	1	3	P	0	0	0	0	0	0
8	Sunco	2	2	1	I1	2	7	2	2	2	1
8	Sunco	2	2	1	I2	0	6	3	2	1	0
8	Sunco	2	2	1	I3	0	0	0	0	0	0
8	Sunco	2	2	1	I4	0	0	0	0	0	0
8	Sunco	2	2	1	P	0	0	0	0	0	0
8	Sunco	2	2	2	I1	1	4	1	1	1	1
8	Sunco	2	2	2	I2	0	10	3	3	3	1
8	Sunco	2	2	2	I3	0	0	0	0	0	0

8	Sunco	2	2	2	I4	0	0	0	0	0	0
8	Sunco	2	2	2	P	0	0	0	0	0	0
8	Sunco	2	2	3	I1	1	4	1	1	1	1
8	Sunco	2	2	3	I2	0	6	1	2	2	1
8	Sunco	2	2	3	I3	0	2	2	0	0	0
8	Sunco	2	3	1	I1	2	4	1	1	1	1
8	Sunco	2	3	1	I2	0	7	3	2	2	0
8	Sunco	2	3	1	I3	0	4	2	2	0	0
8	Sunco	2	3	1	I4	0	0	0	0	0	0
8	Sunco	2	3	1	P	0	0	0	0	0	0
8	Sunco	2	3	2	I1	2	4	1	1	1	1
8	Sunco	2	3	2	I2	0	7	3	2	2	0
8	Sunco	2	3	2	I3	0	0	0	0	0	0
8	Sunco	2	3	2	I4	0	0	0	0	0	0
8	Sunco	2	3	2	P	0	0	0	0	0	0
8	Sunco	2	3	3	I1	1	7	2	2	1	2
8	Sunco	2	3	3	I2	0	5	3	2	0	0
8	Sunco	2	3	3	I3	0	0	0	0	0	0
8	Sunco	2	3	3	I4	0	0	0	0	0	0
8	Sunco	2	3	3	P	0	0	0	0	0	0
8	Sunco	2	4	1	I1	4	6	2	1	2	1
8	Sunco	2	4	1	I2	1	4	2	2	0	0
8	Sunco	2	4	1	I3	0	0	0	0	0	0
8	Sunco	2	4	1	I4	0	0	0	0	0	0
8	Sunco	2	4	1	P	0	0	0	0	0	0
8	Sunco	2	5	1	I1	2	5	1	1	2	1
8	Sunco	2	5	1	I2	0	4	3	1	0	0
8	Sunco	2	5	1	I3	0	0	0	0	0	0
8	Sunco	2	5	1	I4	0	0	0	0	0	0
8	Sunco	2	5	1	P	0	0	0	0	0	0
8	Sunco	2	5	2	I1	1	4	1	1	1	1
8	Sunco	2	5	2	I2	0	5	2	2	1	0
8	Sunco	2	5	2	I3	0	0	0	0	0	0
8	Sunco	2	5	2	I4	0	0	0	0	0	0
8	Sunco	2	5	2	P	0	0	0	0	0	0
8	Sunco	3	1	1	I1	2					

8	Sunco	3	1	1	I2	0					
8	Sunco	3	1	1	I3	0					
8	Sunco	3	1	1	I4	0					
8	Sunco	3	1	1	P	0					
8	Sunco	3	1	2	I1	1					
8	Sunco	3	1	2	I2	0					
8	Sunco	3	1	2	I3	0					
8	Sunco	3	1	2	I4	0					
8	Sunco	3	1	2	P	0					
8	Sunco	3	1	3	I1	1					
8	Sunco	3	1	3	I2	0					
8	Sunco	3	1	3	I3	0					
8	Sunco	3	1	3	I4	0					
8	Sunco	3	1	3	P	0					
8	Sunco	3	2	1	I1	4					
8	Sunco	3	2	1	I2	1					
8	Sunco	3	2	1	I3	0					
8	Sunco	3	2	1	I4	0					
8	Sunco	3	2	1	P	0					
8	Sunco	3	2	2	I1	4					
8	Sunco	3	2	2	I2	1					
8	Sunco	3	2	2	I3	0					
8	Sunco	3	3	1	I1	1					
8	Sunco	3	3	1	I2	0					
8	Sunco	3	3	1	I3	0					
8	Sunco	3	3	1	I4	0					
8	Sunco	3	3	1	P	0					
8	Sunco	3	3	2	I1	1					
8	Sunco	3	3	2	I2	0					
8	Sunco	3	3	2	I3	0					
8	Sunco	3	3	2	I4	0					
8	Sunco	3	3	2	P	0					
8	Sunco	3	3	3	I1	0					
8	Sunco	3	3	3	I2	0					
8	Sunco	3	3	3	I3	0					
8	Sunco	3	3	3	I4	0					

8	Sunco	3	3	3	P	0				
8	Sunco	3	4	1	I1	2				
8	Sunco	3	4	1	I2	0				
8	Sunco	3	4	1	I3	0				
8	Sunco	3	4	1	I4	0				
8	Sunco	3	4	1	P	0				
8	Sunco	3	4	2	I1	1				
8	Sunco	3	4	2	I2	0				
8	Sunco	3	4	2	I3	0				
8	Sunco	3	4	2	I4	0				
8	Sunco	3	4	2	P	0				
8	Sunco	3	4	3	I1	1				
8	Sunco	3	4	3	I2	0				
8	Sunco	3	4	3	I3	0				
8	Sunco	3	4	3	I4	0				
8	Sunco	3	4	3	P	0				
8	Sunco	3	5	1	I1	2				
8	Sunco	3	5	1	I2	1				
8	Sunco	3	5	1	I3	0				
8	Sunco	3	5	1	P	0				
8	Sunco	3	5	2	I1	1				
8	Sunco	3	5	2	I2	0				
8	Sunco	3	5	2	I3	0				
8	Sunco	3	5	2	P	0				
8	CPI133814	1	1	1	I1	4	4	1	1	1	1
8	CPI133814	1	1	1	I2	1	3	2	1	0	0
8	CPI133814	1	1	1	I3	0	0	0	0	0	0
8	CPI133814	1	1	1	I4	0	0	0	0	0	0
8	CPI133814	1	1	1	I5	0	0	0	0	0	0
8	CPI133814	1	1	1	P	0	0	0	0	0	0
8	CPI133814	1	1	2	I1	1	3	1	1	1	0
8	CPI133814	1	1	2	I2	0	3	3	0	0	0
8	CPI133814	1	1	2	I3	0	0	0	0	0	0
8	CPI133814	1	1	3	I1	0	0	0	0	0	0
8	CPI133814	1	1	3	I2	0	0	0	0	0	0
8	CPI133814	1	2	1	I1	2	7	2	1	2	2

8	CPI133814	1	2	1	I2	0	0	0	0	0	0
8	CPI133814	1	2	1	I3	0	0	0	0	0	0
8	CPI133814	1	2	1	I4	0	0	0	0	0	0
8	CPI133814	1	2	1	P	0	0	0	0	0	0
8	CPI133814	1	2	2	I1	1	4	3	1	0	0
8	CPI133814	1	2	2	I2	0	0	0	0	0	0
8	CPI133814	1	2	2	I3	0	0	0	0	0	0
8	CPI133814	1	2	2	I4	0	0	0	0	0	0
8	CPI133814	1	2	2	P	0	0	0	0	0	0
8	CPI133814	1	2	3	I1	1	2	1	1	0	0
8	CPI133814	1	2	3	I2	0	0	0	0	0	0
8	CPI133814	1	3	1	I1	2	6	2	1	1	2
8	CPI133814	1	3	1	I2	0	3	3	0	0	0
8	CPI133814	1	3	1	I3	0	0	0	0	0	0
8	CPI133814	1	3	1	I4	0	0	0	0	0	0
8	CPI133814	1	3	1	P	0	0	0	0	0	0
8	CPI133814	1	3	2	I1	1	0	0	0	0	0
8	CPI133814	1	3	2	I2	0	0	0	0	0	0
8	CPI133814	1	3	3	I1	1	0	0	0	0	0
8	CPI133814	1	3	3	I2	0	0	0	0	0	0
8	CPI133814	1	4	1	I1	4	5	2	1	1	1
8	CPI133814	1	4	1	I2	1	8	3	3	2	0
8	CPI133814	1	4	1	I3	0	0	0	0	0	0
8	CPI133814	1	4	1	I4	0	0	0	0	0	0
8	CPI133814	1	4	1	I5	0	0	0	0	0	0
8	CPI133814	1	4	1	P	0	0	0	0	0	0
8	CPI133814	1	4	2	I1	4	4	1	1	1	1
8	CPI133814	1	4	2	I2	1	9	3	3	3	0
8	CPI133814	1	4	2	I3	0	0	0	0	0	0
8	CPI133814	1	4	2	I4	0	0	0	0	0	0
8	CPI133814	1	4	2	I5	0	0	0	0	0	0
8	CPI133814	1	4	2	P	0	0	0	0	0	0
8	CPI133814	1	4	3	I1	4	9	3	2	2	2
8	CPI133814	1	4	3	I2	1	5	4	1	0	0
8	CPI133814	1	5	1	I1	4	0	0	0	0	0
8	CPI133814	1	5	1	I2	2	0	0	0	0	0

8	CPI133814	1	5	1	I3	2	0	0	0	0	0
8	CPI133814	1	5	1	I4	0	0	0	0	0	0
8	CPI133814	1	5	1	I5	0	0	0	0	0	0
8	CPI133814	1	5	1	P	0	0	0	0	0	0
8	CPI133814	1	5	2	I1	4	5	1	2	1	1
8	CPI133814	1	5	2	I2	1	7	3	2	2	0
8	CPI133814	1	5	2	I3	0	0	0	0	0	0
8	CPI133814	1	5	2	I4	0	0	0	0	0	0
8	CPI133814	1	5	2	I5	0	0	0	0	0	0
8	CPI133814	1	5	2	P	0	0	0	0	0	0
8	CPI133814	1	5	3	I1	2	3	2	1	0	0
8	CPI133814	1	5	3	I2	0	0	0	0	0	0
8	CPI133814	1	5	3	I3	0	0	0	0	0	0
8	CPI133814	1	5	3	I4	0	0	0	0	0	0
8	CPI133814	2	1	1	I1	2	4	1	1	1	1
8	CPI133814	2	1	1	I2	0	7	2	1	2	2
8	CPI133814	2	1	1	I3	0	2	2	0	0	0
8	CPI133814	2	1	1	I4	0	0	0	0	0	0
8	CPI133814	2	1	1	I5	0	0	0	0	0	0
8	CPI133814	2	1	1	P	0	0	0	0	0	0
8	CPI133814	2	1	2	I1	2	0	0	0	0	0
8	CPI133814	2	1	2	I2	0	0	0	0	0	0
8	CPI133814	2	1	2	I3	0	0	0	0	0	0
8	CPI133814	2	1	2	I4	0	0	0	0	0	0
8	CPI133814	2	1	2	I5	0	0	0	0	0	0
8	CPI133814	2	1	2	P	0	0	0	0	0	0
8	CPI133814	2	1	3	I1	1	0	0	0	0	0
8	CPI133814	2	1	3	I2	0	0	0	0	0	0
8	CPI133814	2	1	3	I3	0	0	0	0	0	0
8	CPI133814	2	1	3	I4	0	0	0	0	0	0
8	CPI133814	2	1	3	P	0	0	0	0	0	0
8	CPI133814	2	2	1	I1	0	5	2	2	1	0
8	CPI133814	2	2	1	I2	0	0	0	0	0	0
8	CPI133814	2	2	1	I3	0	0	0	0	0	0
8	CPI133814	2	2	1	I4	0	0	0	0	0	0
8	CPI133814	2	2	1	P	0	0	0	0	0	0

8	CPI133814	2	2	2	I1	0	4	2	1	1	0
8	CPI133814	2	2	2	I2	0	0	0	0	0	0
8	CPI133814	2	2	2	I3	0	0	0	0	0	0
8	CPI133814	2	2	2	I4	0	0	0	0	0	0
8	CPI133814	2	2	2	P	0	0	0	0	0	0
8	CPI133814	2	3	1	I1	3	4	1	1	1	1
8	CPI133814	2	3	1	I2	1	11	4	4	3	0
8	CPI133814	2	3	1	I3	1	0	0	0	0	0
8	CPI133814	2	3	1	I4	0	0	0	0	0	0
8	CPI133814	2	3	1	I5	0	0	0	0	0	0
8	CPI133814	2	3	1	P	0	0	0	0	0	0
8	CPI133814	2	3	2	I1	3	10	4	3	3	0
8	CPI133814	2	3	2	I2	1	0	0	0	0	0
8	CPI133814	2	3	2	I3	0	0	0	0	0	0
8	CPI133814	2	3	2	I4	0	0	0	0	0	0
8	CPI133814	2	3	2	P	0	0	0	0	0	0
8	CPI133814	2	3	3	I1	3	9	3	3	0	3
8	CPI133814	2	3	3	I2	1	0	0	0	0	0
8	CPI133814	2	3	3	I3	0	0	0	0	0	0
8	CPI133814	2	3	3	I4	0	0	0	0	0	0
8	CPI133814	2	3	3	P	0	0	0	0	0	0
8	CPI133814	2	4	1	I1	4	4	1	1	1	1
8	CPI133814	2	4	1	I2	1	7	3	2	2	0
8	CPI133814	2	4	1	I3	0	0	0	0	0	0
8	CPI133814	2	4	1	I4	0	0	0	0	0	0
8	CPI133814	2	4	1	I5	0	0	0	0	0	0
8	CPI133814	2	4	1	P	0	0	0	0	0	0
8	CPI133814	2	4	2	I1	4	4	1	1	1	1
8	CPI133814	2	4	2	I2	0	4	3	1	0	0
8	CPI133814	2	4	2	I3	0	0	0	0	0	0
8	CPI133814	2	4	2	I4	0	0	0	0	0	0
8	CPI133814	2	4	2	I5	0	0	0	0	0	0
8	CPI133814	2	4	2	P	0	0	0	0	0	0
8	CPI133814	2	4	3	I1	4	10	3	3	2	2
8	CPI133814	2	4	3	I2	0	0	0	0	0	0
8	CPI133814	2	4	3	I3	0	0	0	0	0	0

8	CPI133814	2	4	3	I4	0	0	0	0	0	0
8	CPI133814	2	4	3	P	0	0	0	0	0	0
8	CPI133814	2	5	1	I1	1	0	0	0	0	0
8	CPI133814	2	5	1	I2	0	0	0	0	0	0
8	CPI133814	2	5	1	I3	0	0	0	0	0	0
8	CPI133814	2	5	1	I4	0	0	0	0	0	0
8	CPI133814	2	5	1	P	0	0	0	0	0	0
8	CPI133814	3	1	1	I1	4					
8	CPI133814	3	1	1	I2	1					
8	CPI133814	3	1	1	I3	0					
8	CPI133814	3	1	1	I4	0					
8	CPI133814	3	1	1	I5	0					
8	CPI133814	3	1	1	P	0					
8	CPI133814	3	1	2	I1	2					
8	CPI133814	3	1	2	I2	0					
8	CPI133814	3	1	2	I3	0					
8	CPI133814	3	1	2	I4	0					
8	CPI133814	3	1	2	P	0					
8	CPI133814	3	1	3	I1	0					
8	CPI133814	3	1	3	I2	0					
8	CPI133814	3	1	3	I3	0					
8	CPI133814	3	2	1	I1	2					
8	CPI133814	3	2	1	I2	0					
8	CPI133814	3	2	1	I3	0					
8	CPI133814	3	2	1	I4	0					
8	CPI133814	3	2	1	I5	0					
8	CPI133814	3	2	1	P	0					
8	CPI133814	3	2	2	I1	1					
8	CPI133814	3	2	2	I2	0					
8	CPI133814	3	2	2	I3	0					
8	CPI133814	3	2	2	I4	0					
8	CPI133814	3	2	2	I5	0					
8	CPI133814	3	2	2	P	0					
8	CPI133814	3	2	3	I1	1					
8	CPI133814	3	2	3	I2	0					
8	CPI133814	3	2	3	I3	0					

8	CPI133814	3	2	3	I4	0					
8	CPI133814	3	2	3	P	0					
8	CPI133814	3	3	1	I1	1					
8	CPI133814	3	3	1	I2	0					
8	CPI133814	3	3	1	I3	0					
8	CPI133814	3	3	1	I4	0					
8	CPI133814	3	3	1	P	0					
8	CPI133814	3	3	2	I1	0					
8	CPI133814	3	3	2	I2	0					
8	CPI133814	3	3	2	I3	0					
8	CPI133814	3	3	2	I4	0					
8	CPI133814	3	3	2	P	0					
8	CPI133814	3	3	3	I1	0					
8	CPI133814	3	3	3	I2	0					
8	CPI133814	3	3	3	I3	0					
8	CPI133814	3	4	1	I1	3					
8	CPI133814	3	4	1	I2	1					
8	CPI133814	3	4	1	I3	0					
8	CPI133814	3	4	1	I4	0					
8	CPI133814	3	4	1	I5	0					
8	CPI133814	3	4	1	P	0					
8	CPI133814	3	4	2	I1	3					
8	CPI133814	3	4	2	I2	1					
8	CPI133814	3	4	2	I3	0					
8	CPI133814	3	4	2	I4	0					
8	CPI133814	3	4	2	I5	0					
8	CPI133814	3	4	2	P	0					
8	CPI133814	3	4	3	I1	3					
8	CPI133814	3	4	3	I2	1					
8	CPI133814	3	4	3	I3	0					
8	CPI133814	3	4	3	I4	0					
8	CPI133814	3	4	3	P	0					
8	CPI133814	3	5	1	I1	2					
8	CPI133814	3	5	1	I2	0					
8	CPI133814	3	5	1	I3	0					
8	CPI133814	3	5	1	I4	0					

8	CPI133814	3	5	1	P	0					
8	CPI133814	3	5	2	I1	1					
8	CPI133814	3	5	2	I2	0					
8	CPI133814	3	5	2	I3	0					
8	CPI133814	3	5	2	I4	0					
8	CPI133814	3	5	3	I1	1					
8	CPI133814	3	5	3	I2	0					
8	CPI133814	3	5	3	I3	0					
8	CPI133814	3	5	3	I4	0					

Harvest	Genotype	Rep	Plant	Tiller	Part	Disese Rating	Infection (total)	Infection(1/4)	Infection (2/4)	Infection (3/4)	Infection (4/4)	
1	Puseas	1	1	1	LS1	0	0	0	0	0	0	
1	Puseas	1	1	1	LS2	0	0	0	0	0	0	
1	Puseas	1	2	1	LS1	1	0	0	0	0	0	
1	Puseas	1	2	1	LS2	0	0	0	0	0	0	
1	Puseas	1	2	1	LS3	0	0	0	0	0	0	
1	Puseas	1	3	1	LS1	1	4	2	2	0	0	
1	Puseas	1	3	1	LS2	0	0	0	0	0	0	
1	Puseas	1	3	1	LS3	0	0	0	0	0	0	
1	Puseas	1	4	1	LS1	4	8	0	3	3	2	
1	Puseas	1	4	1	LS2	1	1	0	1	0	0	
1	Puseas	1	5	1	LS1	1	0	0	0	0	0	
1	Puseas	1	5	1	LS2	0	0	0	0	0	0	
1	Puseas	2	1	1	LS1	1	3	2	1	0	0	
1	Puseas	2	1	1	LS2	1	2	2	0	0	0	
1	Puseas	2	2	1	LS1	0	0	0	0	0	0	
1	Puseas	2	2	1	LS2	0	0	0	0	0	0	
1	Puseas	2	2	1	LS3	0	0	0	0	0	0	
1	Puseas	2	3	1	LS1	2	2	2	0	0	0	
1	Puseas	2	3	1	LS2	1	0	0	0	0	0	
1	Puseas	2	3	1	LS3	0	0	0	0	0	0	
1	Puseas	2	4	1	LS1	0	0	0	0	0	0	
1	Puseas	2	4	1	LS2	0	0	0	0	0	0	
1	Puseas	2	5	1	LS1	0	0	0	0	0	0	
1	Puseas	2	5	1	LS2	0	0	0	0	0	0	
1	Puseas	3	1	1	LS1	0						
1	Puseas	3	1	1	LS2	0						
1	Puseas	3	2	1	LS1	0						
1	Puseas	3	2	1	LS2	0						
1	Puseas	3	3	1	LS1	1						
1	Puseas	3	3	1	LS2	0						
1	Puseas	3	3	1	LS3	0						
1	Puseas	3	4	1	LS1	0						
1	Puseas	3	4	1	LS2	0						
1	Puseas	3	5	1	LS1	1						
1	Puseas	3	5	1	LS2	1						

1	Puseas	3	5	1	LS3	0						
1	Vasco	1	1	1	LS1	1	1	1	0	0	0	
1	Vasco	1	1	1	LS2	0	0	0	0	0	0	
1	Vasco	1	1	1	LS3	0	0	0	0	0	0	
1	Vasco	1	2	1	LS1	2	6	2	3	1	0	
1	Vasco	1	2	1	LS2	1	3	2	1	0	0	
1	Vasco	1	2	1	LS3	0	0	0	0	0	0	
1	Vasco	1	3	1	LS1	1	0	0	0	0	0	
1	Vasco	1	3	1	LS2	0	0	0	0	0	0	
1	Vasco	1	3	1	LS3	0	0	0	0	0	0	
1	Vasco	1	4	1	LS1	0	0	0	0	0	0	
1	Vasco	1	4	1	LS2	0	0	0	0	0	0	
1	Vasco	1	5	1	LS1	1	0	0	0	0	0	
1	Vasco	1	5	1	LS2	0	0	0	0	0	0	
1	Vasco	1	5	1	LS3	0	0	0	0	0	0	
1	Vasco	2	1	1	LS1	4	6	2	1	2	1	
1	Vasco	2	1	1	LS2	0	0	0	0	0	0	
1	Vasco	2	2	1	LS1	4	7	3	1	2	1	
1	Vasco	2	2	1	LS2	1	3	3	0	0	0	
1	Vasco	2	2	1	LS3	0	0	0	0	0	0	
1	Vasco	2	3	1	LS1	2	5	3	2	0	0	
1	Vasco	2	3	1	LS2	1	4	3	1	0	0	
1	Vasco	2	3	1	LS3	0	0	0	0	0	0	
1	Vasco	2	4	1	LS1	3	6	2	1	2	1	
1	Vasco	2	4	1	LS2	0	0	0	0	0	0	
1	Vasco	2	4	1	LS3	0	0	0	0	0	0	
1	Vasco	2	5	1	LS1	1	2	2	0	0	0	
1	Vasco	2	5	1	LS2	0	0	0	0	0	0	
1	Vasco	2	5	1	LS3	0	0	0	0	0	0	
1	Vasco	3	1	1	LS1	0						
1	Vasco	3	1	1	LS2	0						
1	Vasco	3	2	1	LS1	1						
1	Vasco	3	2	1	LS2	0						
1	Vasco	3	2	1	LS3	0						
1	Vasco	3	3	1	LS1	0						
1	Vasco	3	3	1	LS2	0						

1	Vasco	3	3	1	LS3	0						
1	Vasco	3	4	1	LS1	3						
1	Vasco	3	4	1	LS2	1						
1	Vasco	3	4	1	LS3	0						
1	Vasco	3	5	1	LS1	0						
1	Vasco	3	5	1	LS2	0						
1	2-49	1	1	1	LS1	0	0	0	0	0	0	
1	2-49	1	1	1	LS2	0	0	0	0	0	0	
1	2-49	1	1	1	LS3	0	0	0	0	0	0	
1	2-49	1	2	1	LS1	0	0	0	0	0	0	
1	2-49	1	2	1	LS2	0	0	0	0	0	0	
1	2-49	1	3	1	LS1	0	0	0	0	0	0	
1	2-49	1	3	1	LS2	0	0	0	0	0	0	
1	2-49	1	3	1	LS3	0	0	0	0	0	0	
1	2-49	1	4	1	LS1	0	0	0	0	0	0	
1	2-49	1	4	1	LS2	0	0	0	0	0	0	
1	2-49	1	4	1	LS3	0	0	0	0	0	0	
1	2-49	1	5	1	LS1	0	0	0	0	0	0	
1	2-49	1	5	1	LS2	0	0	0	0	0	0	
1	2-49	1	5	1	LS3	0	0	0	0	0	0	
1	2-49	2	1	1	LS1	1	3	2	1	0	0	
1	2-49	2	1	1	LS2	0	0	0	0	0	0	
1	2-49	2	1	1	LS3	0	0	0	0	0	0	
1	2-49	2	2	1	LS1	0	0	0	0	0	0	
1	2-49	2	2	1	LS2	0	0	0	0	0	0	
1	2-49	2	2	1	LS3	0	0	0	0	0	0	
1	2-49	2	3	1	LS1	1	0	0	0	0	0	
1	2-49	2	3	1	LS2	0	0	0	0	0	0	
1	2-49	2	3	1	LS3	0	0	0	0	0	0	
1	2-49	2	4	1	LS1	0	0	0	0	0	0	
1	2-49	2	4	1	LS2	0	0	0	0	0	0	
1	2-49	2	5	1	LS1	0	0	0	0	0	0	
1	2-49	2	5	1	LS2	0	0	0	0	0	0	
1	2-49	2	5	1	LS3	0	0	0	0	0	0	
1	2-49	3	1	1	LS1	0						
1	2-49	3	1	1	LS2	0						

1	2-49	3	2	1	LS1	2						
1	2-49	3	2	1	LS2	0						
1	2-49	3	2	1	LS3	0						
1	2-49	3	3	1	LS1	1						
1	2-49	3	3	1	LS2	0						
1	2-49	3	4	1	LS1	0						
1	2-49	3	4	1	LS2	0						
1	2-49	3	5	1	LS1	0						
1	2-49	3	5	1	LS2	0						
1	2-49	3	5	1	LS3	0						
1	Sunco	1	1	1	LS1	1	0	0	0	0	0	
1	Sunco	1	1	1	LS2	0	0	0	0	0	0	
1	Sunco	1	1	1	LS3	0	0	0	0	0	0	
1	Sunco	1	2	1	LS1	0	0	0	0	0	0	
1	Sunco	1	2	1	LS2	0	0	0	0	0	0	
1	Sunco	1	2	1	LS3	0	0	0	0	0	0	
1	Sunco	1	3	1	LS1	2	0	0	0	0	0	
1	Sunco	1	3	1	LS2	0	0	0	0	0	0	
1	Sunco	1	3	1	LS3	0	0	0	0	0	0	
1	Sunco	1	4	1	LS1	1	3	3	0	0	0	
1	Sunco	1	4	1	LS2	1	0	0	0	0	0	
1	Sunco	1	4	1	LS3	0	0	0	0	0	0	
1	Sunco	1	5	1	LS1	1	0	0	0	0	0	
1	Sunco	1	5	1	LS2	0	0	0	0	0	0	
1	Sunco	1	5	1	LS3	0	0	0	0	0	0	
1	Sunco	2	1	1	LS1	4	3	0	0	1	2	
1	Sunco	2	1	1	LS2	1	4	3	1	0	0	
1	Sunco	2	1	1	LS3	1	2	2	0	0	0	
1	Sunco	2	2	1	LS1	1	1	0	0	1	0	
1	Sunco	2	2	1	LS2	0	0	0	0	0	0	
1	Sunco	2	2	1	LS3	0	0	0	0	0	0	
1	Sunco	2	3	1	LS1	2	3	1	2	0	0	
1	Sunco	2	3	1	LS2	0	0	0	0	0	0	
1	Sunco	2	3	1	LS3	0	0	0	0	0	0	
1	Sunco	2	4	1	LS1	0	0	0	0	0	0	
1	Sunco	2	4	1	LS2	0	0	0	0	0	0	

1	Sunco	2	4	1	LS3	0	0	0	0	0	0	
1	Sunco	2	5	1	LS1	1	4	0	0	2	2	
1	Sunco	2	5	1	LS2	0	0	0	0	0	0	
1	Sunco	2	5	1	LS3	0	0	0	0	0	0	
1	Sunco	3	1	1	LS1	0						
1	Sunco	3	1	1	LS2	0						
1	Sunco	3	2	1	LS1	2						
1	Sunco	3	2	1	LS2	0						
1	Sunco	3	2	1	LS3	0						
1	Sunco	3	3	1	LS1	0						
1	Sunco	3	3	1	LS2	0						
1	Sunco	3	3	1	LS3	0						
1	Sunco	3	4	1	LS1	0						
1	Sunco	3	4	1	LS2	0						
1	Sunco	3	4	1	LS3	0						
1	Sunco	3	5	1	LS1	1						
1	Sunco	3	5	1	LS2	0						
1	Sunco	3	5	1	LS3	0						
2	Puseas	1	1	1	LS1	4	7	0	1	3	3	
2	Puseas	1	1	1	LS2	3	6	2	3	1	0	
2	Puseas	1	1	1	LS3	1	4	4	0	0	0	
2	Puseas	1	1	1	LS4	0	0	0	0	0	0	
2	Puseas	1	2	1	LS1	4	7	1	1	2	3	
2	Puseas	1	2	1	LS2	4	10	3	2	3	2	
2	Puseas	1	2	1	LS3	4	0	0	0	0	0	
2	Puseas	1	2	1	LS4	0	4	4	0	0	0	
2	Puseas	1	2	1	LS5	0	0	0	0	0	0	
2	Puseas	1	2	2	LS1	4	0	0	0	0	0	
2	Puseas	1	2	2	LS2	1	5	2	3	0	0	
2	Puseas	1	2	2	LS3	0	0	0	0	0	0	
2	Puseas	1	2	3	LS1	0	0	0	0	0	0	
2	Puseas	1	2	3	LS2	0	0	0	0	0	0	
2	Puseas	1	3	1	LS1	4	11	2	3	3	3	
2	Puseas	1	3	1	LS2	4	9	3	1	2	3	
2	Puseas	1	3	1	LS3	3	5	2	2	1	0	
2	Puseas	1	3	1	LS4	1	0	0	0	0	0	

2	Puseas	1	3	2	LS1	4	8	3	2	1	2	
2	Puseas	1	3	2	LS2	1	8	3	2	3	0	
2	Puseas	1	3	2	LS3	0	0	0	0	0	0	
2	Puseas	1	4	1	LS1	4	1	1	0	0	0	
2	Puseas	1	4	1	LS2	2	2	2	0	0	0	
2	Puseas	1	4	1	LS3	0	1	1	0	0	0	
2	Puseas	1	4	1	LS4	0	0	0	0	0	0	
2	Puseas	1	5	1	LS1	4	7	4	3	0	0	
2	Puseas	1	5	1	LS2	4	5	2	1	2	0	
2	Puseas	1	5	1	LS3	1	3	1	1	1	0	
2	Puseas	1	5	1	LS4	0	0	0	0	0	0	
2	Puseas	2	1	1	LS1	4	9	2	3	2	2	
2	Puseas	2	1	1	LS2	4	9	3	3	1	2	
2	Puseas	2	1	1	LS3	4	8	4	0	3	1	
2	Puseas	2	1	1	LS4	2	7	2	3	2	0	
2	Puseas	2	1	1	LS5	0	0	0	0	0	0	
2	Puseas	2	1	2	LS1	4	8	1	3	1	3	
2	Puseas	2	1	2	LS2	2	7	0	2	2	3	
2	Puseas	2	1	2	LS3	1	6	3	2	1	0	
2	Puseas	2	1	3	LS1	4	8	3	3	2	0	
2	Puseas	2	1	3	LS2	1	1	1	0	0	0	
2	Puseas	2	1	3	LS3	0	0	0	0	0	0	
2	Puseas	2	1	4	LS1	2	4	1	3	0	0	
2	Puseas	2	1	4	LS2	0	2	0	2	0	0	
2	Puseas	2	2	1	LS1	2	0	0	0	0	0	
2	Puseas	2	2	1	LS2	0	0	0	0	0	0	
2	Puseas	2	2	1	LS3	0	0	0	0	0	0	
2	Puseas	2	2	1	LS4	0	0	0	0	0	0	
2	Puseas	2	3	1	LS1	4	5	0	0	3	2	
2	Puseas	2	3	1	LS2	4	2	0	2	0	0	
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2	Puseas	2	3	1	LS4	1	5	0	1	0	4	
2	Puseas	2	3	1	LS5	0	0	0	0	0	0	
2	Puseas	2	3	2	LS1	0	0	0	0	0	0	
2	Puseas	2	3	2	LS2	0	0	0	0	0	0	
2	Puseas	2	4	1	LS1	4	5	2	2	1	0	

2	Puseas	2	4	1	LS2	4	2	0	0	2	0	
2	Puseas	2	4	1	LS3	1	4	1	0	3	0	
2	Puseas	2	4	1	LS4	0	0	0	0	0	0	
2	Puseas	2	4	2	LS1	4	9	5	2	2	0	
2	Puseas	2	4	2	LS2	2	7	0	2	3	2	
2	Puseas	2	5	1	LS1	2	3	0	3	0	0	
2	Puseas	2	5	1	LS2	0	0	0	0	0	0	
2	Puseas	2	5	1	LS3	0	0	0	0	0	0	
2	Puseas	2	5	1	LS4	0	0	0	0	0	0	
2	Puseas	2	5	2	LS1	0	0	0	0	0	0	
2	Puseas	2	5	2	LS2	0	3	0	2	1	0	
2	Puseas	3	1	1	LS1	4						
2	Puseas	3	1	1	LS2	4						
2	Puseas	3	1	1	LS3	2						
2	Puseas	3	1	1	LS4	0						
2	Puseas	3	1	2	LS1	3						
2	Puseas	3	1	2	LS2	1						
2	Puseas	3	1	3	LS1	1						
2	Puseas	3	1	3	LS2	0						
2	Puseas	3	2	1	LS1	4						
2	Puseas	3	2	1	LS2	4						
2	Puseas	3	2	1	LS3	3						
2	Puseas	3	2	1	LS4	1						
2	Puseas	3	2	1	LS5	0						
2	Puseas	3	3	1	LS1	4						
2	Puseas	3	3	1	LS2	4						
2	Puseas	3	3	1	LS3	1						
2	Puseas	3	3	1	LS4	0						
2	Puseas	3	3	1	LS5	0						
2	Puseas	3	3	2	LS1	1						
2	Puseas	3	3	2	LS2	0						
2	Puseas	3	3	3	LS1	0						
2	Puseas	3	3	3	LS2	0						
2	Puseas	3	4	1	LS1	4						
2	Puseas	3	4	1	LS2	3						
2	Puseas	3	4	1	LS3	1						

2	Puseas	3	4	1	LS4	0						
2	Puseas	3	4	1	LS5	0						
2	Puseas	3	4	2	LS1	3						
2	Puseas	3	4	2	LS2	0						
2	Puseas	3	4	2	LS3	0						
2	Puseas	3	4	3	LS1	2						
2	Puseas	3	4	3	LS2	0						
2	Puseas	3	5	1	LS1	4						
2	Puseas	3	5	1	LS2	4						
2	Puseas	3	5	1	LS3	2						
2	Puseas	3	5	1	LS4	0						
2	Puseas	3	5	1	LS5	0						
2	Puseas	3	5	2	LS1	2						
2	Puseas	3	5	2	LS2	0						
2	Puseas	3	5	3	LS1	1						
2	Vasco	1	1	1	LS1	4	4	1	1	1	1	
2	Vasco	1	1	1	LS2	4	8	2	2	2	2	
2	Vasco	1	1	1	LS3	4	5	1	1	2	1	
2	Vasco	1	1	1	LS4	1	5	2	2	1	0	
2	Vasco	1	1	1	LS5	0	0	0	0	0	0	
2	Vasco	1	1	2	LS1	1	0	0	0	0	0	
2	Vasco	1	1	2	LS2	0	0	0	0	0	0	
2	Vasco	1	2	1	LS1	4	0	0	0	0	0	
2	Vasco	1	2	1	LS2	0	0	0	0	0	0	
2	Vasco	1	2	1	LS3	0	0	0	0	0	0	
2	Vasco	1	2	1	LS4	0	0	0	0	0	0	
2	Vasco	1	2	1	LS5	0	0	0	0	0	0	
2	Vasco	1	2	2	LS1	1	0	0	0	0	0	
2	Vasco	1	2	2	LS2	0	0	0	0	0	0	
2	Vasco	1	2	2	LS3	0	0	0	0	0	0	
2	Vasco	1	2	3	LS1	0	0	0	0	0	0	
2	Vasco	1	2	3	LS2	0	0	0	0	0	0	
2	Vasco	1	3	1	LS1	4	8	2	2	2	2	
2	Vasco	1	3	1	LS2	4	9	3	3	3	0	
2	Vasco	1	3	1	LS3	4	7	2	1	2	2	
2	Vasco	1	3	1	LS4	0	4	2	1	0	1	

2	Vasco	1	3	1	LS5	0	0	0	0	0	0	
2	Vasco	1	3	2	LS1	4	6	2	1	1	2	
2	Vasco	1	3	2	LS2	1	3	0	1	2	0	
2	Vasco	1	3	2	LS3	0	0	0	0	0	0	
2	Vasco	1	3	2	LS4	0	0	0	0	0	0	
2	Vasco	1	3	3	LS1	1	2	0	0	1	1	
2	Vasco	1	3	3	LS2	1	0	0	0	0	0	
2	Vasco	1	4	1	LS1	4	7	3	3	1	0	
2	Vasco	1	4	1	LS2	4	5	2	2	1	0	
2	Vasco	1	4	1	LS3	1	0	0	0	0	0	
2	Vasco	1	4	1	LS4	0	0	0	0	0	0	
2	Vasco	1	4	1	LS5	0	0	0	0	0	0	
2	Vasco	1	4	2	LS1	4	3	0	0	1	2	
2	Vasco	1	4	2	LS2	1	4	0	0	2	2	
2	Vasco	1	4	2	LS3	0	0	0	0	0	0	
2	Vasco	1	4	3	LS1	0	0	0	0	0	0	
2	Vasco	1	4	3	LS2	0	0	0	0	0	0	
2	Vasco	1	5	1	LS1	4	8	3	1	2	2	
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2	Vasco	1	5	1	LS3	3	5	3	2	0	0	
2	Vasco	1	5	1	LS4	0	0	0	0	0	0	
2	Vasco	1	5	1	LS5	0	0	0	0	0	0	
2	Vasco	1	5	2	LS1	4	7	3	3	1	0	
2	Vasco	1	5	2	LS2	0	2	2	0	0	0	
2	Vasco	1	5	2	LS3	0	0	0	0	0	0	
2	Vasco	1	5	3	LS1	0	3	0	2	1	0	
2	Vasco	1	5	3	LS2	0	0	0	0	0	0	
2	Vasco	2	1	1	LS1	4	0	0	0	0	0	
2	Vasco	2	1	1	LS2	4	0	0	0	0	0	
2	Vasco	2	1	1	LS3	1	0	0	0	0	0	
2	Vasco	2	1	1	LS4	0	0	0	0	0	0	
2	Vasco	2	1	2	LS1	1	0	0	0	0	0	
2	Vasco	2	1	2	LS2	0	0	0	0	0	0	
2	Vasco	2	1	2	LS3	0	0	0	0	0	0	
2	Vasco	2	1	3	LS1	1	0	0	0	0	0	
2	Vasco	2	1	3	LS2	0	0	0	0	0	0	

2	Vasco	2	2	1	LS1	4	0	0	0	0	0	
2	Vasco	2	2	1	LS2	4	0	0	0	0	0	
2	Vasco	2	2	1	LS3	1	0	0	0	0	0	
2	Vasco	2	2	1	LS4	0	0	0	0	0	0	
2	Vasco	2	2	1	LS5	0	0	0	0	0	0	
2	Vasco	2	2	2	LS1	4	0	0	0	0	0	
2	Vasco	2	2	2	LS2	1	0	0	0	0	0	
2	Vasco	2	2	3	LS1	1	0	0	0	0	0	
2	Vasco	2	2	3	LS2	0	0	0	0	0	0	
2	Vasco	2	3	1	LS1	4	0	0	0	0	0	
2	Vasco	2	3	1	LS2	4	0	0	0	0	0	
2	Vasco	2	3	1	LS3	1	0	0	0	0	0	
2	Vasco	2	3	1	LS4	0	0	0	0	0	0	
2	Vasco	2	3	1	LS5	0	0	0	0	0	0	
2	Vasco	2	3	2	LS1	4	6	2	2	2	0	
2	Vasco	2	3	2	LS2	1	3	3	0	0	0	
2	Vasco	2	3	2	LS3	0	0	0	0	0	0	
2	Vasco	2	3	3	LS1	1	0	0	0	0	0	
2	Vasco	2	3	3	LS2	0	0	0	0	0	0	
2	Vasco	2	4	1	LS1	4	6	3	2	1	0	
2	Vasco	2	4	1	LS2	4	5	3	2	0	0	
2	Vasco	2	4	1	LS3	2	0	0	0	0	0	
2	Vasco	2	4	1	LS4	1	3	1	2	0	0	
2	Vasco	2	4	2	LS1	1	0	0	0	0	0	
2	Vasco	2	4	2	LS2	1	0	0	0	0	0	
2	Vasco	2	4	3	LS1	1	0	0	0	0	0	
2	Vasco	2	4	3	LS2	0	0	0	0	0	0	
2	Vasco	2	5	1	LS1	4	10	2	2	3	3	
2	Vasco	2	5	1	LS2	4	7	1	2	1	3	
2	Vasco	2	5	1	LS3	4	4	1	0	1	2	
2	Vasco	2	5	1	LS4	1	9	2	3	1	3	
2	Vasco	2	5	1	LS5	0	0	0	0	0	0	
2	Vasco	2	5	2	LS1	1	3	0	1	2	0	
2	Vasco	2	5	2	LS2	1	3	0	3	0	0	
2	Vasco	3	1	1	LS1	4						
2	Vasco	3	1	1	LS2	4						

2	Vasco	3	1	1	LS3	4						
2	Vasco	3	1	1	LS4	1						
2	Vasco	3	1	1	LS5	0						
2	Vasco	3	1	2	LS1	4						
2	Vasco	3	1	2	LS2	2						
2	Vasco	3	1	2	LS3	1						
2	Vasco	3	1	3	LS1	4						
2	Vasco	3	1	3	LS2	1						
2	Vasco	3	2	1	LS1	4						
2	Vasco	3	2	1	LS2	4						
2	Vasco	3	2	1	LS3	3						
2	Vasco	3	2	1	LS4	0						
2	Vasco	3	2	1	LS5	0						
2	Vasco	3	2	2	LS1	4						
2	Vasco	3	2	2	LS2	1						
2	Vasco	3	2	2	LS3	0						
2	Vasco	3	3	1	LS1	4						
2	Vasco	3	3	1	LS2	3						
2	Vasco	3	3	1	LS3	2						
2	Vasco	3	3	1	LS4	0						
2	Vasco	3	3	1	LS5	0						
2	Vasco	3	3	2	LS1	3						
2	Vasco	3	3	2	LS2	1						
2	Vasco	3	3	2	LS3	1						
2	Vasco	3	3	3	LS1	0						
2	Vasco	3	3	3	LS2	0						
2	Vasco	3	3	3	LS3	0						
2	Vasco	3	4	1	LS1	4						
2	Vasco	3	4	1	LS2	4						
2	Vasco	3	4	1	LS3	2						
2	Vasco	3	4	1	LS4	1						
2	Vasco	3	4	2	LS1	4						
2	Vasco	3	4	2	LS2	2						
2	Vasco	3	5	1	LS1	3						
2	Vasco	3	5	1	LS2	2						
2	Vasco	3	5	1	LS3	0						

2	Vasco	3	5	1	LS4	0						
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2	2-49	1	1	1	LS5	0	0	0	0	0	0	
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2	2-49	1	2	1	LS5	0	0	0	0	0	0	
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2	2-49	1	2	2	LS2	1	3	0	0	1	2	
2	2-49	1	2	2	LS3	0	0	0	0	0	0	
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2	2-49	1	4	1	LS2	0	0	0	0	0	0	
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2	2-49	1	4	1	LS5	0	0	0	0	0	0	
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2	2-49	2	1	1	LS5	0	2	0	0	1	1	
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2	2-49	2	2	2	LS2	1	0	0	0	0	0	
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2	2-49	2	3	1	LS3	4	3	0	0	1	2	
2	2-49	2	3	1	LS4	1	0	0	0	0	0	
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2	2-49	3	1	1	LS1	4						
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2	2-49	3	1	1	LS4	0						
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2	2-49	3	3	3	LS1	4						
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2	2-49	3	4	2	LS2	0						
2	2-49	3	4	2	LS3	0						
2	2-49	3	4	3	LS1	0						
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2	2-49	3	5	1	LS2	1						
2	2-49	3	5	1	LS3	0						
2	2-49	3	5	1	LS4	0						
2	2-49	3	5	2	LS1	1						
2	2-49	3	5	2	LS2	1						
2	2-49	3	5	2	LS3	0						
2	2-49	3	5	3	LS1	0						
2	2-49	3	5	3	LS2	0						
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2	Sunco	1	1	1	LS2	4	0	0	0	0	0	
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2	Sunco	1	1	1	LS4	1	0	0	0	0	0	
2	Sunco	1	1	1	LS5	0	2	0	0	0	2	
2	Sunco	1	1	2	LS1	4	2	1	0	1	0	
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2	Sunco	1	1	2	LS3	0	8	3	3	2	0	
2	Sunco	1	1	2	LS4	0	0	0	0	0	0	
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2	Sunco	1	1	3	LS2	1	3	1	2	0	0	
2	Sunco	1	1	3	LS3	0	0	0	0	0	0	
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2	Sunco	1	2	1	LS1	4	3	0	0	0	3	
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2	Sunco	1	2	1	LS3	3	5	2	1	2	0	
2	Sunco	1	2	1	LS4	1	0	0	0	0	0	
2	Sunco	1	2	1	LS5	0	0	0	0	0	0	
2	Sunco	1	2	2	LS1	4	4	2	0	2	0	
2	Sunco	1	2	2	LS2	4	9	3	2	2	2	

2	Sunco	1	2	2	LS3	0	4	2	1	1	0	
2	Sunco	1	2	3	LS1	1	2	2	0	0	0	
2	Sunco	1	2	3	LS2	0	0	0	0	0	0	
2	Sunco	1	2	3	LS3	0	0	0	0	0	0	
2	Sunco	1	2	4	LS1	0	0	0	0	0	0	
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2	Sunco	1	3	2	LS2	0	3	0	0	2	1	
2	Sunco	1	3	3	LS1	1	0	0	0	0	0	
2	Sunco	1	3	3	LS2	0	0	0	0	0	0	
2	Sunco	1	4	1	LS1	4	0	0	0	0	0	
2	Sunco	1	4	1	LS2	1	0	0	0	0	0	
2	Sunco	1	4	1	LS3	1	0	0	0	0	0	
2	Sunco	1	4	1	LS4	0	0	0	0	0	0	
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2	Sunco	1	4	2	LS2	1	0	0	0	0	0	
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2	Sunco	1	5	1	LS3	4	7	3	1	2	1	
2	Sunco	1	5	1	LS4	1	8	2	1	3	2	
2	Sunco	1	5	1	LS5	0	4	0	4	0	0	
2	Sunco	1	5	2	LS1	4	1	0	1	0	0	
2	Sunco	1	5	2	LS2	1	5	0	2	2	1	
2	Sunco	1	5	2	LS3	0	1	0	0	1	0	
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2	Sunco	1	5	3	LS2	1	3	1	2	0	0	
2	Sunco	1	5	3	LS3	0	3	0	0	3	0	
2	Sunco	1	5	4	LS1	1	3	0	1	2	0	

2	Sunco	1	5	4	LS2	0	3	0	2	1	0	
2	Sunco	2	1	1	LS1	4	6	0	2	2	2	
2	Sunco	2	1	1	LS2	4	8	3	1	3	1	
2	Sunco	2	1	1	LS3	4	4	3	1	0	0	
2	Sunco	2	1	1	LS4	1	1	0	1	0	0	
2	Sunco	2	1	1	LS5	0	0	0	0	0	0	
2	Sunco	2	1	2	LS1	4	6	2	3	1	0	
2	Sunco	2	1	2	LS2	3	5	1	1	3	0	
2	Sunco	2	1	2	LS3	1	4	1	3	0	0	
2	Sunco	2	1	3	LS1	3	4	3	1	0	0	
2	Sunco	2	1	3	LS2	1	4	3	1	0	0	
2	Sunco	2	1	3	LS3	1	0	0	0	0	0	
2	Sunco	2	1	4	LS1	0	0	0	0	0	0	
2	Sunco	2	1	4	LS2	0	0	0	0	0	0	
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2	Sunco	2	2	1	LS2	4	6	0	2	2	2	
2	Sunco	2	2	1	LS3	4	3	1	2	0	0	
2	Sunco	2	2	1	LS4	1	3	2	1	0	0	
2	Sunco	2	2	1	LS5	1	0	0	0	0	0	
2	Sunco	2	2	2	LS1	2	1	0	1	0	0	
2	Sunco	2	2	2	LS2	0	0	0	0	0	0	
2	Sunco	2	3	1	LS1	4	8	3	0	2	3	
2	Sunco	2	3	1	LS2	4	3	0	0	1	2	
2	Sunco	2	3	1	LS3	3	7	1	1	3	2	
2	Sunco	2	3	1	LS4	0	3	0	2	1	0	
2	Sunco	2	3	2	LS1	3	1	0	0	1	0	
2	Sunco	2	3	2	LS2	3	5	1	1	1	2	
2	Sunco	2	4	1	LS1	4	4	1	1	1	1	
2	Sunco	2	4	1	LS2	4	3	1	1	1	0	
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2	Sunco	2	4	1	LS4	1	11	3	3	3	2	
2	Sunco	2	4	1	LS5	0	7	0	4	3	0	
2	Sunco	2	4	2	LS1	4	6	2	2	2	0	
2	Sunco	2	4	2	LS2	4	4	3	0	0	1	
2	Sunco	2	4	2	LS3	1	4	0	2	2	0	
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2	Sunco	2	4	3	LS2	4	6	2	1	2	1	
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2	Sunco	2	5	1	LS3	4	2	2	0	0	0	
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2	Sunco	2	5	1	LS5	0	0	0	0	0	0	
2	Sunco	2	5	2	LS1	4	5	1	2	1	1	
2	Sunco	2	5	2	LS2	1	2	1	0	1	0	
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2	Sunco	3	1	1	LS3	0						
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2	Sunco	3	1	1	LS5	0						
2	Sunco	3	1	2	LS1	1						
2	Sunco	3	1	2	LS2	0						
2	Sunco	3	1	2	LS3	0						
2	Sunco	3	1	3	LS1	0						
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2	Sunco	3	2	1	LS3	3						
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2	Sunco	3	2	2	LS1	4						
2	Sunco	3	2	2	LS2	1						
2	Sunco	3	2	2	LS3	0						
2	Sunco	3	2	3	LS1	2						
2	Sunco	3	2	3	LS2	0						
2	Sunco	3	3	1	LS1	4						
2	Sunco	3	3	1	LS2	4						
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2	Sunco	3	3	1	LS4	0						
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2	Sunco	3	4	1	LS2	4						
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2	Sunco	3	4	1	LS4	1						

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2	Sunco	3	5	1	LS3	0						
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3	Puseas	1	1	1	LS5	1	5	0	0	4	1	
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3	Puseas	1	2	2	LS2	1	7	6	1	0	0	
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3	Puseas	1	5	1	LS5	0	0	0	0	0	0	
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3	Puseas	2	2	1	LS2	4	6	3	2	1	0	
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3	Puseas	2	2	1	LS4	2	6	2	4	0	0	
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3	Vasco	1	1	1	LS3	1	0	0	0	0	0	
3	Vasco	1	1	1	LS4	0	0	0	0	0	0	
3	Vasco	1	1	1	LS5	0	0	0	0	0	0	
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3	Vasco	1	1	2	LS2	1	0	0	0	0	0	
3	Vasco	1	1	2	LS3	0	0	0	0	0	0	
3	Vasco	1	2	1	LS1	4	7	3	2	2	0	
3	Vasco	1	2	1	LS2	4	9	3	3	3	0	
3	Vasco	1	2	1	LS3	4	0	0	0	0	0	

3	Vasco	1	2	1	LS4	1	0	0	0	0	0	
3	Vasco	1	2	1	LS5	1	0	0	0	0	0	
3	Vasco	1	2	1	LS6	0	0	0	0	0	0	
3	Vasco	1	2	1	LS7	0	0	0	0	0	0	
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3	Vasco	1	2	2	LS4	0	0	0	0	0	0	
3	Vasco	1	2	3	LS1	3	9	5	4	0	0	
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3	Vasco	1	2	3	LS3	1	0	0	0	0	0	
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3	Vasco	1	3	1	LS1	4	9	4	4	1	0	
3	Vasco	1	3	1	LS2	3	2	0	2	0	0	
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3	Vasco	1	3	1	LS4	0	0	0	0	0	0	
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3	Vasco	1	3	2	LS3	0	0	0	0	0	0	
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3	Vasco	1	4	3	LS1	0						
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3	Vasco	1	4	3	LS3	0	0	0	0	0	0	
3	Vasco	1	4	3	LS4	0	0	0	0	0	0	

3	Vasco	1	5	1	LS1	4	5	0	3	2	0	
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3	Vasco	1	5	1	LS4	1	0	0	0	0	0	
3	Vasco	1	5	1	LS5	0	0	0	0	0	0	
3	Vasco	1	5	1	LS6	0	0	0	0	0	0	
3	Vasco	1	5	1	LS7	0	0	0	0	0	0	
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3	Vasco	1	5	2	LS4	1	0	0	0	0	0	
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3	Vasco	1	5	4	LS2	1	0	0	0	0	0	
3	Vasco	1	5	4	LS3	0	0	0	0	0	0	
3	Vasco	1	5	4	LS4	0	0	0	0	0	0	
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3	Vasco	2	1	1	LS2	4	8	2	2	2	2	
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3	Vasco	2	1	1	LS5	1	4	4	0	0	0	
3	Vasco	2	1	1	LS6	0	0	0	0	0	0	
3	Vasco	2	1	2	LS1	4	5	1	2	1	1	
3	Vasco	2	1	2	LS2	3	6	3	2	1	0	
3	Vasco	2	1	2	LS3	1	0	0	0	0	0	
3	Vasco	2	1	2	LS4	0	0	0	0	0	0	
3	Vasco	2	1	3	LS1	1	0	0	0	0	0	
3	Vasco	2	1	3	LS2	0	0	0	0	0	0	
3	Vasco	2	2	1	LS1	4	8	2	2	2	2	
3	Vasco	2	2	1	LS2	2	7	2	2	1	2	
3	Vasco	2	2	1	LS3	1	0	0	0	0	0	
3	Vasco	2	2	1	LS4	0	0	0	0	0	0	

3	Vasco	2	2	1	LS5	0	0	0	0	0	0	
3	Vasco	2	2	1	LS6	0	0	0	0	0	0	
3	Vasco	2	2	2	LS1	4	7	2	2	2	1	
3	Vasco	2	2	2	LS2	1	4	1	2	1	0	
3	Vasco	2	2	2	LS3	0	0	0	0	0	0	
3	Vasco	2	2	2	LS4	0	0	0	0	0	0	
3	Vasco	2	2	3	LS1	4	3	2	1	0	0	
3	Vasco	2	2	3	LS2	1	0	0	0	0	0	
3	Vasco	2	2	3	LS3	0	0	0	0	0	0	
3	Vasco	2	2	3	LS4	0	0	0	0	0	0	
3	Vasco	2	2	4	LS1	0	0	0	0	0	0	
3	Vasco	2	2	4	LS2	0	0	0	0	0	0	
3	Vasco	2	2	4	LS3	0	0	0	0	0	0	
3	Vasco	2	3	1	LS1	4	8	2	2	2	2	
3	Vasco	2	3	1	LS2	4	10	2	3	2	3	
3	Vasco	2	3	1	LS3	4	10	3	3	3	1	
3	Vasco	2	3	1	LS4	4	7	3	3	1	0	
3	Vasco	2	3	1	LS5	1	0	0	0	0	0	
3	Vasco	2	3	1	LS6	0	0	0	0	0	0	
3	Vasco	2	3	2	LS1	4	10	3	3	3	1	
3	Vasco	2	3	2	LS2	4	8	3	1	2	2	
3	Vasco	2	3	2	LS3	1	1	1	0	0	0	
3	Vasco	2	3	2	LS4	0	1	1	0	0	0	
3	Vasco	2	3	2	LS5	0	0	0	0	0	0	
3	Vasco	2	3	3	LS1	4	7	2	2	1	2	
3	Vasco	2	3	3	LS2	1	2	0	2	0	0	
3	Vasco	2	3	3	LS3	0	0	0	0	0	0	
3	Vasco	2	3	3	LS4	0	0	0	0	0	0	
3	Vasco	2	4	1	LS1	4	9	3	3	2	1	
3	Vasco	2	4	1	LS2	3	9	3	3	3	0	
3	Vasco	2	4	1	LS3	2	4	3	1	0	0	
3	Vasco	2	4	1	LS4	1	2	2	0	0	0	
3	Vasco	2	4	1	LS5	0	0	0	0	0	0	
3	Vasco	2	4	1	LS6	0	0	0	0	0	0	
3	Vasco	2	4	2	LS1	4	5	2	2	1	0	
3	Vasco	2	4	2	LS2	1	5	3	2	0	0	

3	Vasco	2	4	2	LS3	1	0	0	0	0	0	
3	Vasco	2	4	2	LS4	0	0	0	0	0	0	
3	Vasco	2	4	3	LS1	3	0	0	0	0	0	
3	Vasco	2	4	3	LS2	0	0	0	0	0	0	
3	Vasco	2	4	3	LS3	0	0	0	0	0	0	
3	Vasco	2	4	3	LS4	0	0	0	0	0	0	
3	Vasco	2	5	1	LS1	4	8	3	2	2	1	
3	Vasco	2	5	1	LS2	4	10	3	2	2	3	
3	Vasco	2	5	1	LS3	3	0	0	0	0	0	
3	Vasco	2	5	1	LS4	1	0	0	0	0	0	
3	Vasco	2	5	1	LS5	0	0	0	0	0	0	
3	Vasco	2	5	1	LS6	0	0	0	0	0	0	
3	Vasco	2	5	2	LS1	4	6	1	2	1	2	
3	Vasco	2	5	2	LS2	1	0	0	0	0	0	
3	Vasco	2	5	2	LS3	1	0	0	0	0	0	
3	Vasco	2	5	2	LS4	0	0	0	0	0	0	
3	Vasco	2	5	2	LS5	0	0	0	0	0	0	
3	Vasco	2	5	3	LS1	3	5	4	1	0	0	
3	Vasco	2	5	3	LS2	1	0	0	0	0	0	
3	Vasco	2	5	3	LS3	0	0	0	0	0	0	
3	Vasco	2	5	3	LS4	0	0	0	0	0	0	
3	Vasco	2	5	4	LS1	1	0	0	0	0	0	
3	Vasco	2	5	4	LS2	0	0	0	0	0	0	
3	Vasco	2	5	4	LS3	0	0	0	0	0	0	
3	Vasco	3	1	1	LS1	4						
3	Vasco	3	1	1	LS2	4						
3	Vasco	3	1	1	LS3	2						
3	Vasco	3	1	1	LS4	1						
3	Vasco	3	1	1	LS5	1						
3	Vasco	3	1	1	LS6	0						
3	Vasco	3	1	2	LS1	1						
3	Vasco	3	1	2	LS2	0						
3	Vasco	3	1	2	LS3	0						
3	Vasco	3	1	3	LS1	1						
3	Vasco	3	1	3	LS2	0						
3	Vasco	3	2	1	LS1	4						

3	Vasco	3	2	1	LS2	4						
3	Vasco	3	2	1	LS3	4						
3	Vasco	3	2	1	LS4	4						
3	Vasco	3	2	1	LS5	1						
3	Vasco	3	2	1	LS6	1						
3	Vasco	3	2	1	LS7	0						
3	Vasco	3	2	1	I1	2						
3	Vasco	3	2	2	LS1	4						
3	Vasco	3	2	2	LS2	3						
3	Vasco	3	2	2	LS3	1						
3	Vasco	3	2	2	LS4	0						
3	Vasco	3	2	3	LS1	4						
3	Vasco	3	2	3	LS2	3						
3	Vasco	3	2	3	LS3	0						
3	Vasco	3	2	3	LS4	0						
3	Vasco	3	2	4	LS1	2						
3	Vasco	3	2	4	LS2	0						
3	Vasco	3	2	4	LS3	0						
3	Vasco	3	2	5	LS1	0						
3	Vasco	3	2	5	LS2	0						
3	Vasco	3	3	1	LS1	4						
3	Vasco	3	3	1	LS2	4						
3	Vasco	3	3	1	LS3	3						
3	Vasco	3	3	1	LS4	1						
3	Vasco	3	3	1	LS5	0						
3	Vasco	3	3	1	LS6	0						
3	Vasco	3	3	2	LS1	3						
3	Vasco	3	3	2	LS2	1						
3	Vasco	3	3	2	LS3	0						
3	Vasco	3	3	2	LS4	0						
3	Vasco	3	3	3	LS1	2						
3	Vasco	3	3	3	LS2	1						
3	Vasco	3	3	3	LS3	0						
3	Vasco	3	3	4	LS1	0						
3	Vasco	3	3	4	LS2	0						
3	Vasco	3	4	1	LS1	4						

3	Vasco	3	4	1	LS2	4						
3	Vasco	3	4	1	LS3	4						
3	Vasco	3	4	1	LS4	1						
3	Vasco	3	4	1	LS5	1						
3	Vasco	3	4	1	LS6	1						
3	Vasco	3	4	1	LS7	0						
3	Vasco	3	4	1	LS8	0						
3	Vasco	3	4	2	LS1	4						
3	Vasco	3	4	2	LS2	2						
3	Vasco	3	4	2	LS3	0						
3	Vasco	3	4	2	LS4	0						
3	Vasco	3	4	3	LS1	1						
3	Vasco	3	4	3	LS2	0						
3	Vasco	3	4	3	LS3	0						
3	Vasco	3	4	4	LS1	0						
3	Vasco	3	4	4	LS2	0						
3	Vasco	3	5	1	LS1	4						
3	Vasco	3	5	1	LS2	4						
3	Vasco	3	5	1	LS3	3						
3	Vasco	3	5	1	LS4	1						
3	Vasco	3	5	1	LS5	0						
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3	2-49	1	1	1	LS2	4	5	1	1	2	1	
3	2-49	1	1	1	LS3	1	0	0	0	0	0	
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3	2-49	1	1	1	LS5	1	0	0	0	0	0	
3	2-49	1	1	1	LS6	0	0	0	0	0	0	
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3	2-49	1	1	2	LS1	3	7	2	2	2	1	
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3	2-49	1	1	2	LS3	0	0	0	0	0	0	
3	2-49	1	1	2	LS4	0	0	0	0	0	0	
3	2-49	1	1	2	LS5	0	0	0	0	0	0	
3	2-49	1	1	3	LS1	3	0	0	0	0	0	
3	2-49	1	1	3	LS2	0	0	0	0	0	0	
3	2-49	1	1	3	LS3	0	0	0	0	0	0	

3	2-49	1	1	3	LS4	0	0	0	0	0	0	
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3	2-49	1	1	4	LS2	0	0	0	0	0	0	
3	2-49	1	1	4	LS3	0	0	0	0	0	0	
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3	2-49	1	2	1	LS3	4	7	2	2	2	1	
3	2-49	1	2	1	LS4	2	6	4	2	0	0	
3	2-49	1	2	1	LS5	0	6	5	1	0	0	
3	2-49	1	2	1	LS6	0	0	0	0	0	0	
3	2-49	1	2	1	LS7	0	0	0	0	0	0	
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3	2-49	1	2	2	LS2	3	8	3	2	3	0	
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3	2-49	1	2	2	LS4	0	0	0	0	0	0	
3	2-49	1	2	2	LS5	0	0	0	0	0	0	
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3	2-49	1	2	3	LS4	0	0	0	0	0	0	
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3	2-49	1	3	1	LS4	0	0	0	0	0	0	
3	2-49	1	3	1	LS5	0	0	0	0	0	0	
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3	2-49	1	3	2	LS4	0	0	0	0	0	0	
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3	2-49	1	4	1	LS6	0	0	0	0	0	0	
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3	2-49	1	5	1	LS4	0	0	0	0	0	0	
3	2-49	1	5	1	LS5	0	0	0	0	0	0	
3	2-49	1	5	1	LS6	0	0	0	0	0	0	
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3	2-49	1	5	2	LS3	0	0	0	0	0	0	
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3	2-49	2	1	1	LS6	0	0	0	0	0	0	
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3	2-49	2	2	1	LS6	0	0	0	0	0	0	
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3	2-49	2	2	2	LS5	0	0	0	0	0	0	
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3	2-49	2	2	3	LS3	1	0	0	0	0	0	
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3	2-49	2	2	4	LS2	4	6	2	1	2	1	
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3	2-49	2	2	5	LS1	4	9	3	2	3	1	
3	2-49	2	2	5	LS2	1	8	3	3	2	0	
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3	2-49	2	3	1	LS1	4						
3	2-49	2	3	1	LS2	4						
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3	2-49	2	3	1	LS4	3	9	2	3	2	2	
3	2-49	2	3	1	LS5	1	2	0	2	0	0	
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3	2-49	2	3	1	LS7	0	0	0	0	0	0	
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3	2-49	2	3	3	LS3	0	0	0	0	0	0	
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3	2-49	2	3	4	LS2	0	0	0	0	0	0	

3	2-49	2	4	1	LS1	4	11	3	2	3	3	
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3	2-49	2	4	1	LS4	3	6	1	2	1	2	
3	2-49	2	4	1	LS5	1	0	0	0	0	0	
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3	Sunco	1	1	1	LS3	3	2	2	0	0	0	
3	Sunco	1	1	1	LS4	1	0	0	0	0	0	
3	Sunco	1	1	1	LS5	0	0	0	0	0	0	
3	Sunco	1	1	1	LS6	0	0	0	0	0	0	
3	Sunco	1	1	1	LS7	0	0	0	0	0	0	
3	Sunco	1	1	2	LS1	4	8	2	2	2	2	
3	Sunco	1	1	2	LS2	2	10	2	2	3	3	
3	Sunco	1	1	2	LS3	0	0	0	0	0	0	
3	Sunco	1	1	2	LS4	0	0	0	0	0	0	
3	Sunco	1	1	2	LS5	0	0	0	0	0	0	
3	Sunco	1	1	3	LS1	4	5	2	2	1	0	
3	Sunco	1	1	3	LS2	1	3	2	1	0	0	
3	Sunco	1	1	3	LS3	1	4	4	0	0	0	
3	Sunco	1	1	3	LS4	0	0	0	0	0	0	
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3	Sunco	1	1	4	LS4	0	0	0	0	0	0	
3	Sunco	1	1	5	LS1	0	0	0	0	0	0	
3	Sunco	1	1	5	LS2	0	0	0	0	0	0	
3	Sunco	1	2	1	LS1	4						
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3	Sunco	1	2	1	LS4	3	0	0	0	0	0	
3	Sunco	1	2	1	LS5	0	0	0	0	0	0	
3	Sunco	1	2	1	LS6	0	0	0	0	0	0	
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3	Sunco	1	2	2	LS4	0	0	0	0	0	0	
3	Sunco	1	2	2	LS5	0	0	0	0	0	0	
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3	Sunco	1	2	4	LS2	0	0	0	0	0	0	
3	Sunco	1	2	4	LS3	0	0	0	0	0	0	
3	Sunco	1	3	1	LS1	4	11	3	3	2	3	
3	Sunco	1	3	1	LS2	4	7	4	3	0	0	
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3	Sunco	1	3	1	LS4	1	0	0	0	0	0	
3	Sunco	1	3	1	LS5	0	0	0	0	0	0	
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3	Sunco	1	3	2	LS1	4	10	3	3	1	3	
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3	Sunco	1	3	2	LS4	0	0	0	0	0	0	
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3	Sunco	1	4	1	LS2	3	0	0	0	0	0	
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3	Sunco	1	4	1	LS4	1	0	0	0	0	0	
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3	Sunco	1	4	1	LS6	0	0	0	0	0	0	
3	Sunco	1	4	1	LS7	0	0	0	0	0	0	
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3	Sunco	1	4	2	LS3	0	0	0	0	0	0	
3	Sunco	1	4	2	LS4	0	0	0	0	0	0	
3	Sunco	1	4	3	LS1	2	0	0	0	0	0	
3	Sunco	1	4	3	LS2	0	0	0	0	0	0	
3	Sunco	1	4	3	LS3	0	0	0	0	0	0	
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3	Sunco	1	4	4	LS3	0	0	0	0	0	0	
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3	Sunco	1	5	1	LS6	0	0	0	0	0	0	
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3	Sunco	2	1	1	LS2	4	11	4	3	3	1	
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3	Sunco	2	1	1	LS6	0	0	0	0	0	0	
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3	Sunco	2	1	2	LS4	0	0	0	0	0	0	
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3	Sunco	2	3	1	LS5	0	0	0	0	0	0	
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3	Sunco	2	3	2	LS1	3	0	0	0	0	0	
3	Sunco	2	3	2	LS2	1	0	0	0	0	0	
3	Sunco	2	3	2	LS3	0	0	0	0	0	0	

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3	Sunco	2	3	3	LS1	3	0	0	0	0	0	
3	Sunco	2	3	3	LS2	1	0	0	0	0	0	
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3	Sunco	2	4	3	LS4	0	0	0	0	0	0	
3	Sunco	2	4	4	LS1	0	0	0	0	0	0	
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3	Sunco	2	5	1	LS5	0	0	0	0	0	0	
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3	Sunco	2	5	2	LS3	1	6	3	3	0	0	
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3	Sunco	2	5	3	LS3	1	4	3	1	0	0	
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3	Sunco	2	5	4	LS3	0	0	0	0	0	0	
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3	Sunco	3	1	1	LS3	4						
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3	Sunco	3	1	1	LS5	1						
3	Sunco	3	1	1	LS6	0						
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3	Sunco	3	1	2	LS1	4						
3	Sunco	3	1	2	LS2	3						
3	Sunco	3	1	2	LS3	1						
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3	Sunco	3	1	3	LS1	1						
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3	Sunco	3	2	1	LS5	1						
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3	Sunco	3	3	1	LS3	1						

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3	Sunco	3	3	1	LS8	0						
3	Sunco	3	3	2	LS1	3						
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3	Sunco	3	3	3	LS2	0						
3	Sunco	3	3	3	LS3	0						
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4	Vasco	1	1	1	LS6	1	0	0	0	0	0	
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4	Vasco	1	1	1	LS8	0	0	0	0	0	0	
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4	Vasco	1	1	5	LS1	4	0	0	0	0	0	
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4	Vasco	1	1	5	LS3	0	0	0	0	0	0	
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4	Vasco	1	2	1	LS3	3	0	0	0	0	0	
4	Vasco	1	2	1	LS4	1	0	0	0	0	0	
4	Vasco	1	2	1	LS5	0	0	0	0	0	0	
4	Vasco	1	2	1	LS6	0	0	0	0	0	0	
4	Vasco	1	2	1	LS7	0	0	0	0	0	0	
4	Vasco	1	2	1	I1	0	0	0	0	0	0	
4	Vasco	1	2	2	LS1	4	0	0	0	0	0	
4	Vasco	1	2	2	LS2	1	0	0	0	0	0	
4	Vasco	1	2	2	LS3	1	0	0	0	0	0	
4	Vasco	1	2	2	LS4	0	0	0	0	0	0	
4	Vasco	1	2	2	LS5	0	0	0	0	0	0	
4	Vasco	1	2	3	LS1	1	0	0	0	0	0	
4	Vasco	1	2	3	LS2	1	0	0	0	0	0	
4	Vasco	1	2	3	LS3	0	0	0	0	0	0	
4	Vasco	1	2	3	LS4	0	0	0	0	0	0	
4	Vasco	1	3	1	LS1	4	3	2	1	0	0	
4	Vasco	1	3	1	LS2	4	5	2	1	0	2	
4	Vasco	1	3	1	LS3	4	6	3	1	1	1	
4	Vasco	1	3	1	LS4	1	0	0	0	0	0	
4	Vasco	1	3	1	LS5	1	0	0	0	0	0	
4	Vasco	1	3	1	LS6	0	0	0	0	0	0	
4	Vasco	1	3	1	LS7	0	0	0	0	0	0	
4	Vasco	1	3	1	LS8	0	0	0	0	0	0	
4	Vasco	1	3	1	I1	0	0	0	0	0	0	
4	Vasco	1	3	1	I2	0	0	0	0	0	0	
4	Vasco	1	3	2	LS1	3	0	0	0	0	0	
4	Vasco	1	3	2	LS2	1	2	1	1	0	0	
4	Vasco	1	3	2	LS3	1	0	0	0	0	0	
4	Vasco	1	3	2	LS4	1	0	0	0	0	0	

4	Vasco	1	3	2	LS5	0	0	0	0	0	0	
4	Vasco	1	3	2	LS6	0	0	0	0	0	0	
4	Vasco	1	3	2	I1	0	0	0	0	0	0	
4	Vasco	1	3	3	LS1	2	1	1	0	0	0	
4	Vasco	1	3	3	LS2	1	0	0	0	0	0	
4	Vasco	1	3	3	LS3	0	0	0	0	0	0	
4	Vasco	1	3	3	LS4	0	0	0	0	0	0	
4	Vasco	1	3	3	LS5	0	0	0	0	0	0	
4	Vasco	1	3	3	I1	0	0	0	0	0	0	
4	Vasco	1	3	4	LS1	1	0	0	0	0	0	
4	Vasco	1	3	4	LS2	1	0	0	0	0	0	
4	Vasco	1	3	4	LS3	0	0	0	0	0	0	
4	Vasco	1	3	5	LS1	1	0	0	0	0	0	
4	Vasco	1	3	5	LS2	0	0	0	0	0	0	
4	Vasco	1	4	1	LS1	3	0	0	0	0	0	
4	Vasco	1	4	1	LS2	3	0	0	0	0	0	
4	Vasco	1	4	1	LS3	3	0	0	0	0	0	
4	Vasco	1	4	1	LS4	1	0	0	0	0	0	
4	Vasco	1	4	1	LS5	0	0	0	0	0	0	
4	Vasco	1	4	1	LS6	0	0	0	0	0	0	
4	Vasco	1	4	1	LS7	0	0	0	0	0	0	
4	Vasco	1	4	1	LS8	0	0	0	0	0	0	
4	Vasco	1	4	1	I1	0	0	0	0	0	0	
4	Vasco	1	4	1	I2	0	0	0	0	0	0	
4	Vasco	1	4	2	LS1	2	0	0	0	0	0	
4	Vasco	1	4	2	LS2	1	0	0	0	0	0	
4	Vasco	1	4	2	LS3	0	0	0	0	0	0	
4	Vasco	1	4	2	LS4	0	0	0	0	0	0	
4	Vasco	1	4	2	LS5	0	0	0	0	0	0	
4	Vasco	1	4	2	I1	0	0	0	0	0	0	
4	Vasco	1	4	3	LS1	2	0	0	0	0	0	
4	Vasco	1	4	3	LS2	1	0	0	0	0	0	
4	Vasco	1	4	3	LS3	1	0	0	0	0	0	
4	Vasco	1	4	3	LS4	0	0	0	0	0	0	
4	Vasco	1	4	3	LS5	0	0	0	0	0	0	
4	Vasco	1	4	3	I1	0	0	0	0	0	0	

4	Vasco	1	4	4	LS1	1	0	0	0	0	0	
4	Vasco	1	4	4	LS2	0	0	0	0	0	0	
4	Vasco	1	4	4	LS3	0	0	0	0	0	0	
4	Vasco	1	4	4	LS4	0	0	0	0	0	0	
4	Vasco	1	4	5	LS1	1	0	0	0	0	0	
4	Vasco	1	4	5	LS2	1	0	0	0	0	0	
4	Vasco	1	4	5	LS3	0	0	0	0	0	0	
4	Vasco	1	5	1	LS1	4	7	2	2	2	1	
4	Vasco	1	5	1	LS2	4	7	1	2	2	2	
4	Vasco	1	5	1	LS3	4	4	2	2	0	0	
4	Vasco	1	5	1	LS4	3	5	3	2	0	0	
4	Vasco	1	5	1	LS5	1	0	0	0	0	0	
4	Vasco	1	5	1	LS6	1	0	0	0	0	0	
4	Vasco	1	5	1	LS7	0	0	0	0	0	0	
4	Vasco	1	5	1	LS8	0	0	0	0	0	0	
4	Vasco	1	5	1	I1	0	0	0	0	0	0	
4	Vasco	1	5	2	LS1	4	6	1	2	2	1	
4	Vasco	1	5	2	LS2	4	7	1	2	2	2	
4	Vasco	1	5	2	LS3	3	7	3	2	2	0	
4	Vasco	1	5	2	LS4	1	0	0	0	0	0	
4	Vasco	1	5	2	LS5	0	0	0	0	0	0	
4	Vasco	1	5	2	LS6	0	0	0	0	0	0	
4	Vasco	1	5	2	I1	0	0	0	0	0	0	
4	Vasco	1	5	3	LS1	4	7	2	2	2	1	
4	Vasco	1	5	3	LS2	2	5	3	2	0	0	
4	Vasco	1	5	3	LS3	1	0	0	0	0	0	
4	Vasco	1	5	3	LS4	1	0	0	0	0	0	
4	Vasco	1	5	3	LS5	0	0	0	0	0	0	
4	Vasco	1	5	4	LS1	3	0	0	0	0	0	
4	Vasco	1	5	4	LS2	1	0	0	0	0	0	
4	Vasco	1	5	4	LS3	0	0	0	0	0	0	
4	Vasco	1	5	4	LS4	0	0	0	0	0	0	
4	Vasco	2	1	1	LS1	4	10	3	2	2	3	
4	Vasco	2	1	1	LS2	4	9	2	3	2	2	
4	Vasco	2	1	1	LS3	4	9	3	3	2	1	
4	Vasco	2	1	1	LS4	4	8	3	2	3	0	

4	Vasco	2	1	1	LS5	3	4	3	1	0	0	
4	Vasco	2	1	1	LS6	1	6	0	3	3	0	
4	Vasco	2	1	1	LS7	0	0	0	0	0	0	
4	Vasco	2	1	1	LS8	0	0	0	0	0	0	
4	Vasco	2	1	1	I1	0	0	0	0	0	0	
4	Vasco	2	1	2	LS1	4	5	2	1	1	1	
4	Vasco	2	1	2	LS2	3	9	3	3	1	2	
4	Vasco	2	1	2	LS3	1	6	1	3	2	0	
4	Vasco	2	1	2	LS4	0	0	0	0	0	0	
4	Vasco	2	1	3	LS1	4	4	0	1	2	1	
4	Vasco	2	1	3	LS2	1	0	0	0	0	0	
4	Vasco	2	1	3	LS3	0	0	0	0	0	0	
4	Vasco	2	1	4	LS1	0	0	0	0	0	0	
4	Vasco	2	1	4	LS2	0	0	0	0	0	0	
4	Vasco	2	2	1	LS1	4	9	2	2	2	3	
4	Vasco	2	2	1	LS2	4	11	2	3	3	3	
4	Vasco	2	2	1	LS3	4	5	2	2	1	0	
4	Vasco	2	2	1	LS4	4	7	3	3	1	0	
4	Vasco	2	2	1	LS5	3	1	1	0	0	0	
4	Vasco	2	2	1	LS6	1	0	0	0	0	0	
4	Vasco	2	2	1	LS7	0	0	0	0	0	0	
4	Vasco	2	2	1	LS8	0	0	0	0	0	0	
4	Vasco	2	2	1	I1	1	0	0	0	0	0	
4	Vasco	2	2	2	LS1	4	7	2	1	1	3	
4	Vasco	2	2	2	LS2	1	0	0	0	0	0	
4	Vasco	2	2	2	LS3	0	0	0	0	0	0	
4	Vasco	2	2	3	LS1	4	6	1	2	3	0	
4	Vasco	2	2	3	LS2	1	0	0	0	0	0	
4	Vasco	2	2	3	LS3	0	0	0	0	0	0	
4	Vasco	2	2	4	LS1	0	0	0	0	0	0	
4	Vasco	2	2	4	LS2	0	0	0	0	0	0	
4	Vasco	2	3	1	LS1	4	11	3	3	2	3	
4	Vasco	2	3	1	LS2	4	11	3	3	4	1	
4	Vasco	2	3	1	LS3	3	5	1	2	2	0	
4	Vasco	2	3	1	LS4	2	5	3	2	0	0	
4	Vasco	2	3	1	LS5	1	4	3	1	0	0	

4	Vasco	2	3	1	LS6	1	0	0	0	0	0	
4	Vasco	2	3	1	LS7	0	0	0	0	0	0	
4	Vasco	2	3	1	LS8	0	0	0	0	0	0	
4	Vasco	2	3	1	I1	0	0	0	0	0	0	
4	Vasco	2	3	2	LS1	4	8	2	2	3	1	
4	Vasco	2	3	2	LS2	2	7	3	3	1	0	
4	Vasco	2	3	2	LS3	1	7	2	3	2	0	
4	Vasco	2	3	2	LS4	0	0	0	0	0	0	
4	Vasco	2	3	2	LS5	0	0	0	0	0	0	
4	Vasco	2	3	3	LS1	1	0	0	0	0	0	
4	Vasco	2	3	3	LS2	1	0	0	0	0	0	
4	Vasco	2	3	3	LS3	0	0	0	0	0	0	
4	Vasco	2	3	3	LS4	0	0	0	0	0	0	
4	Vasco	2	4	1	LS1	4	11	3	3	3	2	
4	Vasco	2	4	1	LS2	4	8	3	3	0	2	
4	Vasco	2	4	1	LS3	4	8	2	2	2	2	
4	Vasco	2	4	1	LS4	4	4	2	0	0	2	
4	Vasco	2	4	1	LS5	2	5	2	2	1	0	
4	Vasco	2	4	1	LS6	1	0	0	0	0	0	
4	Vasco	2	4	1	LS7	0	0	0	0	0	0	
4	Vasco	2	4	1	LS8	0	0	0	0	0	0	
4	Vasco	2	4	2	LS1	4	0	0	0	0	0	
4	Vasco	2	4	2	LS2	1	0	0	0	0	0	
4	Vasco	2	4	2	LS3	0	0	0	0	0	0	
4	Vasco	2	4	2	LS4	0	0	0	0	0	0	
4	Vasco	2	4	3	LS1	0	3	2	1	0	0	
4	Vasco	2	4	3	LS2	0	7	2	2	2	1	
4	Vasco	2	5	1	LS1	4	11	3	2	3	3	
4	Vasco	2	5	1	LS2	4	8	3	2	2	1	
4	Vasco	2	5	1	LS3	4	9	2	3	2	2	
4	Vasco	2	5	1	LS4	4	7	3	3	1	0	
4	Vasco	2	5	1	LS5	1	4	4	0	0	0	
4	Vasco	2	5	1	LS6	1	0	0	0	0	0	
4	Vasco	2	5	1	LS7	0	0	0	0	0	0	
4	Vasco	2	5	1	LS8	0	0	0	0	0	0	
4	Vasco	2	5	1	I1	0	0	0	0	0	0	

4	Vasco	2	5	2	LS1	4	8	2	2	2	2	
4	Vasco	2	5	2	LS2	4	8	3	3	2	0	
4	Vasco	2	5	2	LS3	2	8	4	3	1	0	
4	Vasco	2	5	2	LS4	1	6	4	2	0	0	
4	Vasco	2	5	2	LS5	1	6	4	2	0	0	
4	Vasco	2	5	2	LS6	0	0	0	0	0	0	
4	Vasco	2	5	2	I1	1	4	1	1	1	1	
4	Vasco	2	5	3	LS1	4	11	2	4	3	2	
4	Vasco	2	5	3	LS2	3	6	3	2	1	0	
4	Vasco	2	5	3	LS3	2	3	3	0	0	0	
4	Vasco	2	5	3	LS4	1	0	0	0	0	0	
4	Vasco	2	5	3	LS5	0	0	0	0	0	0	
4	Vasco	2	5	4	LS1	4	3	3	0	0	0	
4	Vasco	2	5	4	LS2	1	4	3	1	0	0	
4	Vasco	2	5	4	LS3	1	0	0	0	0	0	
4	Vasco	2	5	4	LS4	0	0	0	0	0	0	
4	Vasco	2	5	5	LS1	4	6	0	2	4	0	
4	Vasco	2	5	5	LS2	3	11	4	3	2	2	
4	Vasco	2	5	5	LS3	1	6	2	4	0	0	
4	Vasco	3	1	1	LS1	4						
4	Vasco	3	1	1	LS2	4						
4	Vasco	3	1	1	LS3	4						
4	Vasco	3	1	1	LS4	4						
4	Vasco	3	1	1	LS5	2						
4	Vasco	3	1	1	LS6	1						
4	Vasco	3	1	1	LS7	0						
4	Vasco	3	1	1	LS8	0						
4	Vasco	3	1	1	I1	0						
4	Vasco	3	1	1	I2	0						
4	Vasco	3	1	2	LS1	4						
4	Vasco	3	1	2	LS2	4						
4	Vasco	3	1	2	LS3	2						
4	Vasco	3	1	2	LS4	1						
4	Vasco	3	1	2	LS5	0						
4	Vasco	3	1	2	I1	0						
4	Vasco	3	1	3	LS1	4						

4	Vasco	3	1	3	LS2	4						
4	Vasco	3	1	3	LS3	3						
4	Vasco	3	1	3	LS4	0						
4	Vasco	3	1	3	I1	0						
4	Vasco	3	1	4	LS1	4						
4	Vasco	3	1	4	LS2	1						
4	Vasco	3	1	4	LS3	0						
4	Vasco	3	1	4	LS4	0						
4	Vasco	3	1	5	LS1	4						
4	Vasco	3	1	5	LS2	1						
4	Vasco	3	1	5	LS3	0						
4	Vasco	3	2	1	LS1	4						
4	Vasco	3	2	1	LS2	4						
4	Vasco	3	2	1	LS3	4						
4	Vasco	3	2	1	LS4	1						
4	Vasco	3	2	1	LS5	0						
4	Vasco	3	2	1	LS6	0						
4	Vasco	3	2	1	LS7	0						
4	Vasco	3	2	1	LS8	0						
4	Vasco	3	2	1	I1	0						
4	Vasco	3	2	1	I2	0						
4	Vasco	3	2	2	LS1	4						
4	Vasco	3	2	2	LS2	1						
4	Vasco	3	2	2	LS3	0						
4	Vasco	3	2	2	LS4	0						
4	Vasco	3	2	3	LS1	4						
4	Vasco	3	2	3	LS2	1						
4	Vasco	3	2	3	LS3	0						
4	Vasco	3	2	3	LS4	0						
4	Vasco	3	2	4	LS1	2						
4	Vasco	3	2	4	LS2	0						
4	Vasco	3	2	4	LS3	0						
4	Vasco	3	2	5	LS1	1						
4	Vasco	3	2	5	LS2	0						
4	Vasco	3	3	1	LS1	4						
4	Vasco	3	3	1	LS2	4						

4	Vasco	3	3	1	LS3	3						
4	Vasco	3	3	1	LS4	1						
4	Vasco	3	3	1	LS5	0						
4	Vasco	3	3	1	LS6	0						
4	Vasco	3	3	1	LS7	0						
4	Vasco	3	3	1	LS8	0						
4	Vasco	3	3	1	I1	0						
4	Vasco	3	3	2	LS1	4						
4	Vasco	3	3	2	LS2	2						
4	Vasco	3	3	2	LS3	1						
4	Vasco	3	3	2	LS4	0						
4	Vasco	3	3	2	LS5	0						
4	Vasco	3	3	2	I1	0						
4	Vasco	3	3	3	LS1	3						
4	Vasco	3	3	3	LS2	0						
4	Vasco	3	3	3	LS3	0						
4	Vasco	3	3	3	LS4	0						
4	Vasco	3	3	3	I1	0						
4	Vasco	3	3	4	LS1	4						
4	Vasco	3	3	4	LS2	2						
4	Vasco	3	3	4	LS3	0						
4	Vasco	3	3	5	LS1	2						
4	Vasco	3	3	5	LS2	1						
4	Vasco	3	4	1	LS1	4						
4	Vasco	3	4	1	LS2	4						
4	Vasco	3	4	1	LS3	4						
4	Vasco	3	4	1	LS4	4						
4	Vasco	3	4	1	LS5	3						
4	Vasco	3	4	1	LS6	1						
4	Vasco	3	4	1	LS7	0						
4	Vasco	3	4	1	I1	1						
4	Vasco	3	4	2	LS1	4						
4	Vasco	3	4	2	LS2	4						
4	Vasco	3	4	2	LS3	3						
4	Vasco	3	4	2	LS4	1						
4	Vasco	3	4	2	I1	1						

4	Vasco	3	4	3	LS1	4						
4	Vasco	3	4	3	LS2	1						
4	Vasco	3	4	3	LS3	0						
4	Vasco	3	5	1	LS1	4						
4	Vasco	3	5	1	LS2	4						
4	Vasco	3	5	1	LS3	3						
4	Vasco	3	5	1	LS4	2						
4	Vasco	3	5	1	LS5	1						
4	Vasco	3	5	1	LS6	0						
4	Vasco	3	5	1	LS7	0						
4	Vasco	3	5	1	LS8	0						
4	Vasco	3	5	1	I1	0						
4	Vasco	3	5	2	LS1	4						
4	Vasco	3	5	2	LS2	1						
4	Vasco	3	5	2	LS3	0						
4	Vasco	3	5	2	LS4	0						
4	Vasco	3	5	2	LS5	0						
4	Vasco	3	5	2	I1	0						
4	Vasco	3	5	3	LS1	1						
4	Vasco	3	5	3	LS2	0						
4	Vasco	3	5	3	LS3	0						
4	Vasco	3	5	3	LS4	0						
4	Vasco	3	5	3	I1	0						
4	Vasco	3	5	4	LS1	1						
4	Vasco	3	5	4	LS2	0						
4	Vasco	3	5	4	LS3	0						
4	Vasco	3	5	4	LS4	0						
4	Vasco	3	5	5	LS1	1						
4	Vasco	3	5	5	LS2	0						
4	Vasco	3	5	5	LS3	0						
4	2-49	1	1	1	LS1	4	0	0	0	0	0	
4	2-49	1	1	1	LS2	4	0	0	0	0	0	
4	2-49	1	1	1	LS3	4	0	0	0	0	0	
4	2-49	1	1	1	LS4	3	0	0	0	0	0	
4	2-49	1	1	1	LS5	1	0	0	0	0	0	
4	2-49	1	1	1	LS6	1	0	0	0	0	0	

4	2-49	1	1	1	LS7	0	0	0	0	0	0	
4	2-49	1	1	1	LS8	0	0	0	0	0	0	
4	2-49	1	1	1	I1	0	0	0	0	0	0	
4	2-49	1	1	2	LS1	4	0	0	0	0	0	
4	2-49	1	1	2	LS2	4	0	0	0	0	0	
4	2-49	1	1	2	LS3	1	0	0	0	0	0	
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4	2-49	3	5	3	LS1	4						

4	2-49	3	5	3	LS2	1						
4	2-49	3	5	3	LS3	0						
4	2-49	3	5	3	LS4	0						
4	2-49	3	5	4	LS1	0						
4	2-49	3	5	4	LS2	0						
4	2-49	3	5	4	LS3	0						
4	2-49	3	5	5	LS1	0						
4	2-49	3	5	5	LS2	0						
4	Sunco	1	1	1	LS1	4	9	3	2	2	2	
4	Sunco	1	1	1	LS2	4	8	2	2	2	2	
4	Sunco	1	1	1	LS3	3	3	2	1	0	0	
4	Sunco	1	1	1	LS4	1	0	0	0	0	0	
4	Sunco	1	1	1	LS5	0	0	0	0	0	0	
4	Sunco	1	1	1	LS6	0	0	0	0	0	0	
4	Sunco	1	1	1	LS7	0	0	0	0	0	0	
4	Sunco	1	1	1	LS8	0	0	0	0	0	0	
4	Sunco	1	1	2	LS1	2	6	3	2	1	0	
4	Sunco	1	1	2	LS2	1	0	0	0	0	0	
4	Sunco	1	1	2	LS3	1	0	0	0	0	0	
4	Sunco	1	1	2	LS4	0	0	0	0	0	0	
4	Sunco	1	1	2	LS5	0	0	0	0	0	0	
4	Sunco	1	1	3	LS1	0	0	0	0	0	0	
4	Sunco	1	1	3	LS2	0	0	0	0	0	0	
4	Sunco	1	2	1	LS1	4	9	3	2	2	2	
4	Sunco	1	2	1	LS2	4	9	2	2	2	3	
4	Sunco	1	2	1	LS3	4	7	3	2	2	0	
4	Sunco	1	2	1	LS4	3	4	3	1	0	0	
4	Sunco	1	2	1	LS5	2	0	0	0	0	0	
4	Sunco	1	2	1	LS6	1	0	0	0	0	0	
4	Sunco	1	2	1	LS7	0	0	0	0	0	0	
4	Sunco	1	2	1	LS8	0	0	0	0	0	0	
4	Sunco	1	2	2	LS1	4	7	3	2	2	0	
4	Sunco	1	2	2	LS2	3	6	3	3	0	0	
4	Sunco	1	2	2	LS3	1	0	0	0	0	0	
4	Sunco	1	2	2	LS4	0	0	0	0	0	0	
4	Sunco	1	2	2	LS5	0	0	0	0	0	0	

4	Sunco	1	2	2	LS6	0	0	0	0	0	0	
4	Sunco	1	2	3	LS1	4	9	3	3	2	1	
4	Sunco	1	2	3	LS2	3	7	4	3	0	0	
4	Sunco	1	2	3	LS3	1	0	0	0	0	0	
4	Sunco	1	2	3	LS4	0	0	0	0	0	0	
4	Sunco	1	2	4	LS1	3	0	0	0	0	0	
4	Sunco	1	2	4	LS2	1	0	0	0	0	0	
4	Sunco	1	2	4	LS3	0	0	0	0	0	0	
4	Sunco	1	2	4	LS4	0	0	0	0	0	0	
4	Sunco	1	2	5	LS1	1	0	0	0	0	0	
4	Sunco	1	2	5	LS2	0	0	0	0	0	0	
4	Sunco	1	2	5	LS3	0	0	0	0	0	0	
4	Sunco	1	3	1	LS1	4	10	3	2	3	2	
4	Sunco	1	3	1	LS2	4	7	3	3	1	0	
4	Sunco	1	3	1	LS3	2	6	2	3	1	0	
4	Sunco	1	3	1	LS4	1	0	0	0	0	0	
4	Sunco	1	3	1	LS5	0	0	0	0	0	0	
4	Sunco	1	3	1	LS6	0	0	0	0	0	0	
4	Sunco	1	3	1	LS7	0	0	0	0	0	0	
4	Sunco	1	3	2	LS1	0	0	0	0	0	0	
4	Sunco	1	3	2	LS2	0	0	0	0	0	0	
4	Sunco	1	3	2	LS3	0	0	0	0	0	0	
4	Sunco	1	3	2	LS4	0	0	0	0	0	0	
4	Sunco	1	3	3	LS1	0	0	0	0	0	0	
4	Sunco	1	3	3	LS2	0	0	0	0	0	0	
4	Sunco	1	3	3	LS3	0	0	0	0	0	0	
4	Sunco	1	3	4	LS1	0	0	0	0	0	0	
4	Sunco	1	3	4	LS2	0	0	0	0	0	0	
4	Sunco	1	4	1	LS1	4	12	4	3	3	2	
4	Sunco	1	4	1	LS2	4	8	2	2	2	2	
4	Sunco	1	4	1	LS3	4	9	3	3	3	0	
4	Sunco	1	4	1	LS4	2	0	0	0	0	0	
4	Sunco	1	4	1	LS5	1	0	0	0	0	0	
4	Sunco	1	4	1	LS6	0	0	0	0	0	0	
4	Sunco	1	4	1	LS7	0	0	0	0	0	0	
4	Sunco	1	4	1	LS8	0	0	0	0	0	0	

4	Sunco	1	4	2	LS1	4	5	2	1	2	0	
4	Sunco	1	4	2	LS2	4	6	2	2	2	0	
4	Sunco	1	4	2	LS3	1	4	3	1	0	0	
4	Sunco	1	4	2	LS4	1	0	0	0	0	0	
4	Sunco	1	4	2	LS5	0	0	0	0	0	0	
4	Sunco	1	4	2	LS6	0	0	0	0	0	0	
4	Sunco	1	4	3	LS1	1	0	0	0	0	0	
4	Sunco	1	4	3	LS2	1	0	0	0	0	0	
4	Sunco	1	4	3	LS3	0	0	0	0	0	0	
4	Sunco	1	4	4	LS1	0					0	
4	Sunco	1	4	4	LS2	0	0	0	0	0	0	
4	Sunco	1	4	4	LS3	0	0	0	0	0	0	
4	Sunco	1	4	5	LS1	0	0	0	0	0	0	
4	Sunco	1	4	5	LS2	0	0	0	0	0	0	
4	Sunco	1	5	1	LS1	4	9	3	1	3	2	
4	Sunco	1	5	1	LS2	3	7	2	2	2	1	
4	Sunco	1	5	1	LS3	2	0	0	0	0	0	
4	Sunco	1	5	1	LS4	1	0	0	0	0	0	
4	Sunco	1	5	1	LS5	1	0	0	0	0	0	
4	Sunco	1	5	1	LS6	0	0	0	0	0	0	
4	Sunco	1	5	1	LS7	0	0	0	0	0	0	
4	Sunco	1	5	1	I1	0	0	0	0	0	0	
4	Sunco	1	5	2	LS1	4	0	0	0	0	0	
4	Sunco	1	5	2	LS2	4	0	0	0	0	0	
4	Sunco	1	5	2	LS3	3	0	0	0	0	0	
4	Sunco	1	5	2	LS4	1	0	0	0	0	0	
4	Sunco	1	5	2	LS5	0	0	0	0	0	0	
4	Sunco	1	5	2	LS6	0	0	0	0	0	0	
4	Sunco	1	5	2	I1	0	0	0	0	0	0	
4	Sunco	1	5	3	LS1	2	0	0	0	0	0	
4	Sunco	1	5	3	LS2	2	0	0	0	0	0	
4	Sunco	1	5	3	LS3	1	0	0	0	0	0	
4	Sunco	1	5	3	LS4	0	0	0	0	0	0	
4	Sunco	1	5	3	LS5	0	0	0	0	0	0	
4	Sunco	1	5	3	I1	0	0	0	0	0	0	
4	Sunco	1	5	4	LS1	2	12	3	3	3	3	

4	Sunco	1	5	4	LS2	1	1	1	0	0	0	
4	Sunco	1	5	4	LS3	0	0	0	0	0	0	
4	Sunco	1	5	4	LS4	0	0	0	0	0	0	
4	Sunco	2	1	1	LS1	4	9	3	2	3	1	
4	Sunco	2	1	1	LS2	4	8	3	1	2	2	
4	Sunco	2	1	1	LS3	4	10	3	3	3	1	
4	Sunco	2	1	1	LS4	4	4	3	1	0	0	
4	Sunco	2	1	1	LS5	2	0	0	0	0	0	
4	Sunco	2	1	1	LS6	1	0	0	0	0	0	
4	Sunco	2	1	1	LS7	0	0	0	0	0	0	
4	Sunco	2	1	1	LS8	0	0	0	0	0	0	
4	Sunco	2	1	1	I1	1	0	0	0	0	0	
4	Sunco	2	1	1	I2	0	6	2	2	1	1	
4	Sunco	2	1	2	LS1	4	6	2	1	2	1	
4	Sunco	2	1	2	LS2	2	7	2	2	2	1	
4	Sunco	2	1	2	LS3	1	4	3	1	0	0	
4	Sunco	2	1	2	LS4	1	3	3	0	0	0	
4	Sunco	2	1	2	LS5	0	0	0	0	0	0	
4	Sunco	2	1	3	LS1	4	7	4	3	0	0	
4	Sunco	2	1	3	LS2	1	5	3	2	0	0	
4	Sunco	2	1	3	LS3	0	3	3	0	0	0	
4	Sunco	2	2	1	LS1	4	12	4	1	3	4	
4	Sunco	2	2	1	LS2	4	7	2	1	2	2	
4	Sunco	2	2	1	LS3	4	11	4	2	3	2	
4	Sunco	2	2	1	LS4	1	8	4	3	1	0	
4	Sunco	2	2	1	LS5	1	6	5	1	0	0	
4	Sunco	2	2	1	LS6	0	0	0	0	0	0	
4	Sunco	2	2	1	LS7	0	0	0	0	0	0	
4	Sunco	2	2	1	LS8	0	0	0	0	0	0	
4	Sunco	2	2	2	LS1	4	6	2	0	1	3	
4	Sunco	2	2	2	LS2	3	4	1	3	0	0	
4	Sunco	2	2	2	LS3	2	0	0	0	0	0	
4	Sunco	2	2	2	LS4	0	0	0	0	0	0	
4	Sunco	2	2	2	LS5	0	0	0	0	0	0	
4	Sunco	2	2	3	LS1	1	0	0	0	0	0	
4	Sunco	2	2	3	LS2	1	0	0	0	0	0	

4	Sunco	2	2	3	LS3	0	0	0	0	0	0	
4	Sunco	2	2	3	LS4	0	0	0	0	0	0	
4	Sunco	2	2	4	LS1	1	0	0	0	0	0	
4	Sunco	2	2	4	LS2	0	0	0	0	0	0	
4	Sunco	2	2	4	LS3	0	0	0	0	0	0	
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4	Sunco	2	3	1	LS4	4	9	3	3	3	0	
4	Sunco	2	3	1	LS5	2	0	0	0	0	0	
4	Sunco	2	3	1	LS6	1	0	0	0	0	0	
4	Sunco	2	3	1	LS7	0	0	0	0	0	0	
4	Sunco	2	3	1	I1	1	0	0	0	0	0	
4	Sunco	2	3	2	LS1	4	5	2	2	1	0	
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4	Sunco	2	3	2	LS3	2	5	2	3	0	0	
4	Sunco	2	3	2	LS4	2	0	0	0	0	0	
4	Sunco	2	3	2	LS5	0	0	0	0	0	0	
4	Sunco	2	3	2	LS6	0	0	0	0	0	0	
4	Sunco	2	3	2	I1	0	0	0	0	0	0	
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4	Sunco	2	3	3	LS2	3	0	0	0	0	0	
4	Sunco	2	3	3	LS3	1	0	0	0	0	0	
4	Sunco	2	3	3	LS4	0	0	0	0	0	0	
4	Sunco	2	3	3	LS5	0	0	0	0	0	0	
4	Sunco	2	4	1	LS1	4	14	3	4	4	3	
4	Sunco	2	4	1	LS2	4	6	3	3			
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4	Sunco	2	4	1	LS4	1	2	1	1	0	0	
4	Sunco	2	4	1	LS5	1	0	0	0	0	0	
4	Sunco	2	4	1	LS6	1	0	0	0	0	0	
4	Sunco	2	4	1	LS7	0	0	0	0	0	0	
4	Sunco	2	4	2	LS1	4	6	3	1	2	0	
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4	Sunco	2	4	2	LS3	1	3	3	0	0	0	
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4	Sunco	2	4	2	LS5	0	0	0	0	0	0	
4	Sunco	2	4	2	LS6	0	0	0	0	0	0	
4	Sunco	2	5	1	LS1	4	0	0	0	0	0	
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4	Sunco	2	5	1	LS5	2	0	0	0	0	0	
4	Sunco	2	5	1	LS6	1	0	0	0	0	0	
4	Sunco	2	5	1	LS7	0	0	0	0	0	0	
4	Sunco	2	5	1	LS8	0	0	0	0	0	0	
4	Sunco	2	5	1	I1	0	0	0	0	0	0	
4	Sunco	2	5	2	LS1	4	8	2	2	2	2	
4	Sunco	2	5	2	LS2	2						
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4	Sunco	2	5	2	LS4	0	0	0	0	0	0	
4	Sunco	2	5	2	LS5	0	0	0	0	0	0	
4	Sunco	2	5	3	LS1	4	7	3	3	1	0	
4	Sunco	2	5	3	LS2	2	0	0	0	0	0	
4	Sunco	2	5	3	LS3	1	0	0	0	0	0	
4	Sunco	2	5	3	LS4	0	0	0	0	0	0	
4	Sunco	2	5	3	LS5	0	0	0	0	0	0	
4	Sunco	3	1	1	LS1	4						
4	Sunco	3	1	1	LS2	4						
4	Sunco	3	1	1	LS3	4						
4	Sunco	3	1	1	LS4	4						
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4	Sunco	3	1	1	LS6	0						
4	Sunco	3	1	1	LS7	0						
4	Sunco	3	1	1	I1	1						
4	Sunco	3	1	2	LS1	4						
4	Sunco	3	1	2	LS2	4						
4	Sunco	3	1	2	LS3	2						
4	Sunco	3	1	2	LS4	1						
4	Sunco	3	1	2	LS5	0						

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4	Sunco	3	1	3	LS3	0						
4	Sunco	3	1	3	LS4	0						
4	Sunco	3	1	4	LS1	2						
4	Sunco	3	1	4	LS2	0						
4	Sunco	3	1	4	LS3	0						
4	Sunco	3	1	4	LS4	0						
4	Sunco	3	1	5	LS1	0						
4	Sunco	3	1	5	LS2	0						
4	Sunco	3	1	5	LS3	0						
4	Sunco	3	2	1	LS1	4						
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4	Sunco	3	2	1	LS5	0						
4	Sunco	3	2	1	LS6	0						
4	Sunco	3	2	1	LS7	0						
4	Sunco	3	2	1	LS8	0						
4	Sunco	3	2	1	I1	0						
4	Sunco	3	2	2	LS1	4						
4	Sunco	3	2	2	LS2	2						
4	Sunco	3	2	2	LS3	1						
4	Sunco	3	2	2	LS4	0						
4	Sunco	3	2	2	LS5	0						
4	Sunco	3	2	2	LS6	0						
4	Sunco	3	2	2	I1	0						
4	Sunco	3	2	3	LS1	4						
4	Sunco	3	2	3	LS2	2						
4	Sunco	3	2	3	LS3	1						
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4	Sunco	3	2	3	LS5	0						
4	Sunco	3	2	4	LS1	1						
4	Sunco	3	2	4	LS2	0						
4	Sunco	3	2	4	LS3	0						
4	Sunco	3	2	5	LS1	0						

4	Sunco	3	2	5	LS2	0						
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4	Sunco	3	3	1	LS2	4						
4	Sunco	3	3	1	LS3	2						
4	Sunco	3	3	1	LS4	1						
4	Sunco	3	3	1	LS5	0						
4	Sunco	3	3	1	LS6	0						
4	Sunco	3	3	1	LS7	0						
4	Sunco	3	3	1	LS8	0						
4	Sunco	3	3	2	LS1	3						
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4	Sunco	3	3	3	LS3	0						
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4	Sunco	3	4	1	I1	0						
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4	Sunco	3	4	2	LS5	0						
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4	Sunco	3	4	3	LS3	0						
4	Sunco	3	5	1	LS1	4						
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4	Sunco	3	5	1	LS3	2						

4	Sunco	3	5	1	LS4	1						
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4	Sunco	3	5	1	LS6	0						
4	Sunco	3	5	1	LS7	0						
4	Sunco	3	5	1	LS8	0						
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4	Sunco	3	5	2	LS2	1						
4	Sunco	3	5	2	LS3	1						
4	Sunco	3	5	2	LS4	0						
4	Sunco	3	5	2	LS5	0						
5	Puseas	1	1	1	I1	4	4	1	1	1	1	
5	Puseas	1	1	1	I2	1	2	2	0	0	0	
5	Puseas	1	1	1	I3	0	0	0	0	0	0	
5	Puseas	1	1	1	I4	0	0	0	0	0	0	
5	Puseas	1	1	2	I1	4	6	2	1	1	2	
5	Puseas	1	1	2	I2	1	0	0	0	0	0	
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5	Puseas	1	1	3	I2	1	0	0	0	0	0	
5	Puseas	1	1	3	I3	0	0	0	0	0	0	
5	Puseas	1	1	4	I1	0	0	0	0	0	0	
5	Puseas	1	1	4	I2	0	0	0	0	0	0	
5	Puseas	1	1	5	I1	2	0	0	0	0	0	
5	Puseas	1	2	1	I1	4	4	1	1	1	1	
5	Puseas	1	2	1	I2	3	6	4	1	0	1	
5	Puseas	1	2	1	I3	1	0	0	0	0	0	
5	Puseas	1	2	1	I4	0	0	0	0	0	0	
5	Puseas	1	2	2	I1	4	4	1	1	1	1	
5	Puseas	1	2	2	I2	1	4	3	1	0	0	
5	Puseas	1	2	2	I3	0	0	0	0	0	0	
5	Puseas	1	2	3	I1	4	4	4	0	0	0	
5	Puseas	1	2	3	I2	0	0	0	0	0	0	
5	Puseas	1	2	4	I1	2	6	3	3	0	0	
5	Puseas	1	2	4	I2	0	0	0	0	0	0	
5	Puseas	1	2	5	I1	2	3	0	0	1	2	
5	Puseas	1	3	1	I1	4	4	1	1	1	1	
5	Puseas	1	3	1	I2	4	8	2	2	2	2	

5	Puseas	1	3	1	I3	2	3	3	0	0	0	
5	Puseas	1	3	1	I4	0	0	0	0	0	0	
5	Puseas	1	3	2	I1	4	4	1	1	1	1	
5	Puseas	1	3	2	I2	2	4	4	0	0	0	
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5	Puseas	2	3	2	I2	3	0	0	0	0	0	
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5	Puseas	3	1	3	I2	0						
5	Puseas	3	1	4	I1	0						
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5	Puseas	3	3	1	I4	0						
5	Puseas	3	3	2	I1	2						
5	Puseas	3	3	2	I2	2						
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5	Puseas	3	3	3	I2	1						
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5	Vasco	1	1	2	I1	3	6	1	2	1	2	
5	Vasco	1	1	2	I2	2	9	4	2	3	0	
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5	Vasco	3	5	2	I2	0						
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5	2-49	2	3	2	I1	0	0	0	0	0	0	
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5	2-49	2	3	4	I2	0	0	0	0	0	0	
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5	2-49	3	1	1	I3	0						
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5	2-49	3	1	2	I3	0						
5	2-49	3	1	3	I1	0						
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5	2-49	3	1	4	I1	0						
5	2-49	3	1	4	I2	0						
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5	2-49	3	2	2	I2	0						
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5	2-49	3	3	1	I3	0						
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5	2-49	3	3	4	I2	0						
5	2-49	3	3	5	I1	0						
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5	2-49	3	4	1	I2	0						
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5	2-49	3	5	3	I1	0						
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5	2-49	3	5	4	I1	0						
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5	Sunco	1	1	1	I2	0	0	0	0	0	0	
5	Sunco	1	1	1	I3	0	0	0	0	0	0	
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5	Sunco	1	1	2	I2	1	3	2	1	0	0	
5	Sunco	1	1	2	I3	0	0	0	0	0	0	
5	Sunco	1	1	3	I1	2	4	1	1	1	1	
5	Sunco	1	1	3	I2	0	0	0	0	0	0	

5	Sunco	1	1	3	I3	0	0	0	0	0	0	
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5	Sunco	1	1	4	I2	0	0	0	0	0	0	
5	Sunco	1	1	4	I3	0	0	0	0	0	0	
5	Sunco	1	1	5	I1	0	0	0	0	0	0	
5	Sunco	1	1	5	I2	0	0	0	0	0	0	
5	Sunco	1	1	5	I3	0	0	0	0	0	0	
5	Sunco	1	2	1	I1	1	0	0	0	0	0	
5	Sunco	1	2	1	I2	0	0	0	0	0	0	
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5	Sunco	1	2	2	I1	1	0	0	0	0	0	
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5	Sunco	1	2	2	I3	0	0	0	0	0	0	
5	Sunco	1	2	3	I1	1	0	0	0	0	0	
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5	Sunco	1	2	5	I2	0	0	0	0	0	0	
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5	Sunco	3	5	1	I3	0						

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6	Puseas	3	1	2	I1	4						
6	Puseas	3	1	2	I2	4						
6	Puseas	3	1	2	I3	3						
6	Puseas	3	1	2	I4	0						
6	Puseas	3	1	2	I5	0						
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6	Puseas	3	1	3	I1	4						

6	Puseas	3	1	3	I2	3						
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6	Puseas	3	1	3	P	0						
6	Puseas	3	1	4	I1	4						
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6	Puseas	3	1	4	I3	0						
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6	Puseas	3	1	5	I2	3						
6	Puseas	3	1	5	I3	0						
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6	Puseas	3	2	1	I2	2						
6	Puseas	3	2	1	I3	1						
6	Puseas	3	2	1	I4	0						
6	Puseas	3	2	1	I5	0						
6	Puseas	3	2	1	P	0						
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6	Puseas	3	2	2	I2	1						
6	Puseas	3	2	2	I3	0						
6	Puseas	3	2	2	I4	0						
6	Puseas	3	2	2	I5	0						
6	Puseas	3	2	2	P	0						
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6	Puseas	3	2	3	I2	2						
6	Puseas	3	2	3	I3	0						
6	Puseas	3	2	3	I4	0						
6	Puseas	3	2	3	I5	0						
6	Puseas	3	2	3	P	0						
6	Puseas	3	2	4	I1	4						
6	Puseas	3	2	4	I2	3						
6	Puseas	3	2	4	I3	1						
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6	Puseas	3	2	4	I5	0						

6	Puseas	3	2	5	I1	3						
6	Puseas	3	2	5	I2	0						
6	Puseas	3	2	5	I3	0						
6	Puseas	3	3	1	I1	4						
6	Puseas	3	3	1	I2	3						
6	Puseas	3	3	1	I3	1						
6	Puseas	3	3	1	I4	0						
6	Puseas	3	3	1	I5	0						
6	Puseas	3	3	1	P	0						
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6	Puseas	3	3	2	I2	2						
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6	Puseas	3	3	3	I2	3						
6	Puseas	3	3	3	I3	0						
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6	Puseas	3	3	4	I1	4						
6	Puseas	3	3	4	I2	1						
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6	Puseas	3	3	5	I1	4						
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6	Puseas	3	4	1	I4	1						
6	Puseas	3	4	1	I5	0						
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6	Puseas	3	4	2	I2	3						
6	Puseas	3	4	2	I3	3						
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6	Puseas	3	4	3	I2	3						
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6	Puseas	3	4	5	I2	2						
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6	Puseas	3	5	1	I2	4						
6	Puseas	3	5	1	I3	2						
6	Puseas	3	5	1	I4	2						
6	Puseas	3	5	1	I5	1						
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6	Puseas	3	5	2	I2	3						
6	Puseas	3	5	2	I3	0						
6	Puseas	3	5	2	I4	0						
6	Puseas	3	5	2	I5	0						
6	Puseas	3	5	2	P	0						
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6	Puseas	3	5	3	I2	4						
6	Puseas	3	5	3	I3	1						
6	Puseas	3	5	3	I4	0						
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6	Puseas	3	5	4	I2	3						
6	Puseas	3	5	4	I3	0						
6	Puseas	3	5	4	I4	0						
6	Puseas	3	5	4	I5	0						
6	Puseas	3	5	4	P	0						

6	Puseas	3	5	5	I1	4						
6	Puseas	3	5	5	I2	3						
6	Puseas	3	5	5	I3	1						
6	Puseas	3	5	5	I4	0						
6	Puseas	3	5	5	I5	0						
6	Puseas	3	5	5	P	0						
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6	Vasco	1	1	1	I2	0	0	0	0	0	0	
6	Vasco	1	1	1	I3	0	0	0	0	0	0	
6	Vasco	1	1	1	I4	0	0	0	0	0	0	
6	Vasco	1	1	1	I5	0	0	0	0	0	0	
6	Vasco	1	1	1	P	0	0	0	0	0	0	
6	Vasco	1	1	2	I1	1	4	1	1	1	1	
6	Vasco	1	1	2	I2	0	0	0	0	0	0	
6	Vasco	1	1	2	I3	0	0	0	0	0	0	
6	Vasco	1	1	2	I4	0	0	0	0	0	0	
6	Vasco	1	1	2	P	0	0	0	0	0	0	
6	Vasco	1	1	3	I1	0	0	0	0	0	0	
6	Vasco	1	1	3	I2	0	0	0	0	0	0	
6	Vasco	1	1	3	I3	0	0	0	0	0	0	
6	Vasco	1	1	3	I4	0	0	0	0	0	0	
6	Vasco	1	1	3	P	0	0	0	0	0	0	
6	Vasco	1	1	4	I1	0	0	0	0	0	0	
6	Vasco	1	1	4	I2	0	0	0	0	0	0	
6	Vasco	1	1	4	I3	0	0	0	0	0	0	
6	Vasco	1	2	1	I1	3	0	0	0	0	0	
6	Vasco	1	2	1	I2	0	0	0	0	0	0	
6	Vasco	1	2	1	I3	0	0	0	0	0	0	
6	Vasco	1	2	1	I4	0	0	0	0	0	0	
6	Vasco	1	2	1	I5	0	0	0	0	0	0	
6	Vasco	1	2	1	P	0	0	0	0	0	0	
6	Vasco	1	2	2	I1	1	0	0	0	0	0	
6	Vasco	1	2	2	I2	0	0	0	0	0	0	
6	Vasco	1	2	2	I3	0	0	0	0	0	0	
6	Vasco	1	2	2	I4	0	0	0	0	0	0	
6	Vasco	1	2	2	I5	0	0	0	0	0	0	

6	Vasco	1	2	2	P	0	0	0	0	0	0	
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6	Vasco	1	2	3	I2	0	0	0	0	0	0	
6	Vasco	1	2	3	I3	0	0	0	0	0	0	
6	Vasco	1	2	3	I4	0	0	0	0	0	0	
6	Vasco	1	2	3	I5	0	0	0	0	0	0	
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6	Vasco	1	3	1	I2	0	0	0	0	0	0	
6	Vasco	1	3	1	I3	0	0	0	0	0	0	
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6	Vasco	1	3	1	I5	0	0	0	0	0	0	
6	Vasco	1	3	1	P	0	0	0	0	0	0	
6	Vasco	1	3	2	I1	1	0	0	0	0	0	
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6	Vasco	1	3	2	I3	0	0	0	0	0	0	
6	Vasco	1	3	2	I4	0	0	0	0	0	0	
6	Vasco	1	3	2	P	0	0	0	0	0	0	
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6	Vasco	1	3	3	I3	0	0	0	0	0	0	
6	Vasco	1	3	3	I4	0	0	0	0	0	0	
6	Vasco	1	3	3	P	0	0	0	0	0	0	
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6	Vasco	1	3	4	I3	0	0	0	0	0	0	
6	Vasco	1	3	4	I4	0						
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6	Vasco	1	4	1	I1	4	5	1	1	1	2	
6	Vasco	1	4	1	I2	3	12	4	5	0	3	
6	Vasco	1	4	1	I3	1	1	1	0	0	0	
6	Vasco	1	4	1	I4	0	0	0	0	0	0	
6	Vasco	1	4	1	I5	0	0	0	0	0	0	
6	Vasco	1	4	1	P	0	0	0	0	0	0	
6	Vasco	1	4	2	I1	1	4	1	1	1	1	
6	Vasco	1	4	2	I2	0	0	0	0	0	0	
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6	Vasco	1	4	2	I4	0	0	0	0	0	0	
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6	Vasco	1	4	2	P	0	0	0	0	0	0	
6	Vasco	1	4	3	I1	0	0	0	0	0	0	
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6	Vasco	1	4	3	I3	0	0	0	0	0	0	
6	Vasco	1	4	3	I4	0	0	0	0	0	0	
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6	Vasco	1	4	4	I2	0	0	0	0	0	0	
6	Vasco	1	4	4	I3	0	0	0	0	0	0	
6	Vasco	1	4	4	I4	0	0	0	0	0	0	
6	Vasco	1	4	5	I1	1	0	0	0	0	0	
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6	Vasco	1	4	5	I3	0	0	0	0	0	0	
6	Vasco	1	5	1	I1	4	4	1	1	1	1	
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6	Vasco	1	5	1	I3	4	14	5	4	3	2	
6	Vasco	1	5	1	I4	1	0	0	0	0	0	
6	Vasco	1	5	1	I5	0	0	0	0	0	0	
6	Vasco	1	5	1	P	0	0	0	0	0	0	
6	Vasco	1	5	2	I1	4	8	2	2	2	2	
6	Vasco	1	5	2	I2	2	12	4	3	3	2	
6	Vasco	1	5	2	I3	1	0	0	0	0	0	
6	Vasco	1	5	2	I4	0	0	0	0	0	0	
6	Vasco	1	5	2	P	0	0	0	0	0	0	
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6	Vasco	1	5	3	I2	1	2	2	0	0	0	
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6	Vasco	1	5	3	I4	0	0	0	0	0	0	
6	Vasco	1	5	3	I5	0	0	0	0	0	0	
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6	Vasco	1	5	4	I3	0	0	0	0	0	0	
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6	Vasco	1	5	4	I5	0	0	0	0	0	0	
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6	Vasco	1	5	5	I2	0	0	0	0	0	0	
6	Vasco	1	5	5	I3	0	0	0	0	0	0	
6	Vasco	1	5	5	I4	0	0	0	0	0	0	
6	Vasco	1	5	5	P	0	0	0	0	0	0	
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6	Vasco	2	1	1	I3	0	0	0	0	0	0	
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6	Vasco	2	1	1	I5	0	0	0	0	0	0	
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6	Vasco	2	1	2	I3	0	0	0	0	0	0	
6	Vasco	2	1	2	I4	0	0	0	0	0	0	
6	Vasco	2	1	2	I5	0	0	0	0	0	0	
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6	Vasco	2	1	4	I4	0	0	0	0	0	0	
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6	Vasco	2	2	1	I4	0	0	0	0	0	0	
6	Vasco	2	2	1	I5	0	0	0	0	0	0	
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6	Vasco	2	2	1	P	0	0	0	0	0	0	
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6	Vasco	2	2	2	I3	3	12	3	3	3	3	
6	Vasco	2	2	2	I4	0	0	0	0	0	0	
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6	Vasco	2	2	2	I6	0	0	0	0	0	0	
6	Vasco	2	2	2	P	0	0	0	0	0	0	
6	Vasco	2	2	3	I1	4	4	1	1	1	1	
6	Vasco	2	2	3	I2	4	8	2	2	2	2	
6	Vasco	2	2	3	I3	2	14	4	4	4	2	
6	Vasco	2	2	3	I4	0	0	0	0	0	0	
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6	Vasco	2	2	4	I3	0	0	0	0	0	0	
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6	Vasco	2	2	4	I5	0	0	0	0	0	0	
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6	Vasco	2	3	2	I4	1	4	4	0	0	0	
6	Vasco	2	3	2	I5	0	0	0	0	0	0	
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6	Vasco	2	3	3	I1	4	4	1	1	1	1	
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6	Vasco	2	3	3	I3	0	0	0	0	0	0	
6	Vasco	2	3	3	I4	0	0	0	0	0	0	
6	Vasco	2	3	3	I5	0	0	0	0	0	0	
6	Vasco	2	3	3	P	0	0	0	0	0	0	
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6	Vasco	2	3	4	I2	1	10	4	1	1	4	
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6	Vasco	2	3	4	I5	0	0	0	0	0	0	
6	Vasco	2	3	4	P	0	0	0	0	0	0	
6	Vasco	2	3	5	I1	4	8	2	2	2	2	
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6	Vasco	2	3	5	I5	0	0	0	0	0	0	
6	Vasco	2	3	5	P	0	0	0	0	0	0	
6	Vasco	2	4	1	I1	4	4	1	1	1	1	
6	Vasco	2	4	1	I2	4	8	2	2	2	2	
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6	Vasco	2	4	1	I4	3	10	6	4	0	0	
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6	Vasco	2	4	2	I3	1	7	4	3	0	0	
6	Vasco	2	4	2	I4	0	0	0	0	0	0	
6	Vasco	2	4	2	I5	0	0	0	0	0	0	
6	Vasco	2	4	2	P	0	0	0	0	0	0	
6	Vasco	2	4	3	I1	2	4	1	1	1	1	
6	Vasco	2	4	3	I2	1	4	3	1	0	0	
6	Vasco	2	4	3	I3	0	0	0	0	0	0	
6	Vasco	2	4	3	I4	0	0	0	0	0	0	
6	Vasco	2	4	3	I5	0	0	0	0	0	0	
6	Vasco	2	4	3	P	0	0	0	0	0	0	

6	Vasco	2	4	4	I1	3	4	1	1	1	1	
6	Vasco	2	4	4	I2	2	9	3	3	2	1	
6	Vasco	2	4	4	I3	0	0	0	0	0	0	
6	Vasco	2	4	4	I4	0	0	0	0	0	0	
6	Vasco	2	4	4	I5	0	0	0	0	0	0	
6	Vasco	2	4	4	P	0	0	0	0	0	0	
6	Vasco	2	4	5	I1	4	10	3	2	3	2	
6	Vasco	2	4	5	I2	4	16	4	4	4	4	
6	Vasco	2	4	5	I3	4	16	6	4	2	4	
6	Vasco	2	4	5	I4	1	0	0	0	0	0	
6	Vasco	2	4	5	P	1	0	0	0	0	0	
6	Vasco	2	5	1	I1	2	4	1	1	1	1	
6	Vasco	2	5	1	I2	0	4	2	2	0	0	
6	Vasco	2	5	1	I3	0	0	0	0	0	0	
6	Vasco	2	5	1	I4	0	0	0	0	0	0	
6	Vasco	2	5	1	I5	0	0	0	0	0	0	
6	Vasco	2	5	1	P	0	0	0	0	0	0	
6	Vasco	2	5	2	I1	4	4	1	1	1	1	
6	Vasco	2	5	2	I2	1	3	3	0	0	0	
6	Vasco	2	5	2	I3	0	0	0	0	0	0	
6	Vasco	2	5	2	I4	0	0	0	0	0	0	
6	Vasco	2	5	2	I5	0	0	0	0	0	0	
6	Vasco	2	5	2	P	0	0	0	0	0	0	
6	Vasco	2	5	3	I1	1	4	3	1	0	0	
6	Vasco	2	5	3	I2	0	0	0	0	0	0	
6	Vasco	2	5	3	I3	0	0	0	0	0	0	
6	Vasco	2	5	3	I4	0	0	0	0	0	0	
6	Vasco	2	5	4	I1	1	1	1	0	0	0	
6	Vasco	2	5	4	I2	0	0	0	0	0	0	
6	Vasco	2	5	4	I3	0	0	0	0	0	0	
6	Vasco	3	1	1	I1	4						
6	Vasco	3	1	1	I2	2						
6	Vasco	3	1	1	I3	1						
6	Vasco	3	1	1	I4	1						
6	Vasco	3	1	1	I5	0						
6	Vasco	3	1	1	IP	0						

6	Vasco	3	1	2	I1	4						
6	Vasco	3	1	2	I2	2						
6	Vasco	3	1	2	I3	1						
6	Vasco	3	1	2	I4	0						
6	Vasco	3	1	2	I5	0						
6	Vasco	3	1	2	P	0						
6	Vasco	3	1	3	I1	4						
6	Vasco	3	1	3	I2	3						
6	Vasco	3	1	3	I3	1						
6	Vasco	3	1	3	I4	0						
6	Vasco	3	1	3	I5	0						
6	Vasco	3	1	3	P	0						
6	Vasco	3	1	4	I1	4						
6	Vasco	3	1	4	I2	3						
6	Vasco	3	1	4	I3	1						
6	Vasco	3	1	4	I4	0						
6	Vasco	3	1	4	I5	0						
6	Vasco	3	1	4	P	0						
6	Vasco	3	1	5	I1	4						
6	Vasco	3	1	5	I2	3						
6	Vasco	3	1	5	I3	0						
6	Vasco	3	1	5	I4	0						
6	Vasco	3	1	5	P	0						
6	Vasco	3	2	1	I1	4						
6	Vasco	3	2	1	I2	4						
6	Vasco	3	2	1	I3	1						
6	Vasco	3	2	1	I4	1						
6	Vasco	3	2	1	I5	0						
6	Vasco	3	2	1	P	0						
6	Vasco	3	2	2	I1	1						
6	Vasco	3	2	2	I2	1						
6	Vasco	3	2	2	I3	0						
6	Vasco	3	2	2	I4	0						
6	Vasco	3	2	2	I5	0						
6	Vasco	3	2	2	P	0						
6	Vasco	3	2	3	I1	1						

6	Vasco	3	2	3	I2	1						
6	Vasco	3	2	3	I3	0						
6	Vasco	3	2	3	I4	0						
6	Vasco	3	2	3	I5	0						
6	Vasco	3	2	3	P	0						
6	Vasco	3	2	4	I1	3						
6	Vasco	3	2	4	I2	0						
6	Vasco	3	2	4	I3	0						
6	Vasco	3	2	4	I4	0						
6	Vasco	3	2	5	I1	1						
6	Vasco	3	2	5	I2	0						
6	Vasco	3	2	5	I3	0						
6	Vasco	3	2	5	I4	0						
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6	Vasco	3	3	1	I2	4						
6	Vasco	3	3	1	I3	1						
6	Vasco	3	3	1	I4	1						
6	Vasco	3	3	1	I5	0						
6	Vasco	3	3	1	P	0						
6	Vasco	3	3	2	I1	4						
6	Vasco	3	3	2	I2	4						
6	Vasco	3	3	2	I3	1						
6	Vasco	3	3	2	I4	0						
6	Vasco	3	3	3	I1	4						
6	Vasco	3	3	3	I2	4						
6	Vasco	3	3	3	I3	4						
6	Vasco	3	3	3	I4	4						
6	Vasco	3	3	4	I1	4						
6	Vasco	3	3	4	I2	4						
6	Vasco	3	3	4	I3	4						
6	Vasco	3	3	5	I1	4						
6	Vasco	3	3	5	I2	1						
6	Vasco	3	3	5	I3	0						
6	Vasco	3	4	1	I1	2						
6	Vasco	3	4	1	I2	1						
6	Vasco	3	4	1	I3	0						

6	Vasco	3	4	1	I4	0						
6	Vasco	3	4	1	I5	0						
6	Vasco	3	4	1	P	0						
6	Vasco	3	4	2	I1	1						
6	Vasco	3	4	2	I2	1						
6	Vasco	3	4	2	I3	0						
6	Vasco	3	4	2	I4	0						
6	Vasco	3	4	2	I5	0						
6	Vasco	3	4	2	P	0						
6	Vasco	3	4	3	I1	3						
6	Vasco	3	4	3	I2	1						
6	Vasco	3	4	3	I3	0						
6	Vasco	3	4	3	I4	0						
6	Vasco	3	4	3	I5	0						
6	Vasco	3	4	3	P	0						
6	Vasco	3	4	4	I1	1						
6	Vasco	3	4	4	I2	1						
6	Vasco	3	4	4	I3	0						
6	Vasco	3	4	4	I4	0						
6	Vasco	3	4	4	I5	0						
6	Vasco	3	4	4	P	0						
6	Vasco	3	4	5	I1	3						
6	Vasco	3	4	5	I2	2						
6	Vasco	3	4	5	I3	0						
6	Vasco	3	4	5	I4	0						
6	Vasco	3	5	1	I1	4						
6	Vasco	3	5	1	I2	3						
6	Vasco	3	5	1	I3	3						
6	Vasco	3	5	1	I4	1						
6	Vasco	3	5	1	I5	0						
6	Vasco	3	5	1	P	0						
6	Vasco	3	5	2	I1	4						
6	Vasco	3	5	2	I2	3						
6	Vasco	3	5	2	I3	2						
6	Vasco	3	5	2	I4	0						
6	Vasco	3	5	2	I5	0						

6	Vasco	3	5	2	P	0						
6	Vasco	3	5	3	I1	4						
6	Vasco	3	5	3	I2	3						
6	Vasco	3	5	3	I3	1						
6	Vasco	3	5	3	I4	1						
6	Vasco	3	5	3	I5	0						
6	Vasco	3	5	3	P	0						
6	Vasco	3	5	4	I1	3						
6	Vasco	3	5	4	I2	1						
6	Vasco	3	5	4	I3	0						
6	Vasco	3	5	4	I4	0						
6	Vasco	3	5	5	I1	3						
6	Vasco	3	5	5	I2	1						
6	Vasco	3	5	5	I3	0						
6	Vasco	3	5	5	I4	0						
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6	2-49	1	1	1	I2	0	0	0	0	0	0	
6	2-49	1	1	1	I3	0	0	0	0	0	0	
6	2-49	1	1	1	I4	0	0	0	0	0	0	
6	2-49	1	1	1	I5	0	0	0	0	0	0	
6	2-49	1	1	1	P	0	0	0	0	0	0	
6	2-49	1	1	2	I1	0	0	0	0	0	0	
6	2-49	1	1	2	I2	0	0	0	0	0	0	
6	2-49	1	1	2	I3	0	0	0	0	0	0	
6	2-49	1	1	2	I4	0	0	0	0	0	0	
6	2-49	1	1	2	P	0	0	0	0	0	0	
6	2-49	1	1	3	I1	0	0	0	0	0	0	
6	2-49	1	1	3	I2	0	0	0	0	0	0	
6	2-49	1	1	3	I3	0	0	0	0	0	0	
6	2-49	1	1	3	I4	0	0	0	0	0	0	
6	2-49	1	1	4	I1	0	0	0	0	0	0	
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6	2-49	1	1	4	I4	0	0	0	0	0	0	
6	2-49	1	1	5	I1	0	0	0	0	0	0	
6	2-49	1	1	5	I2	0	0	0	0	0	0	

6	2-49	1	1	5	I3	0	0	0	0	0	0	
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6	2-49	1	2	1	I2	0	0	0	0	0	0	
6	2-49	1	2	1	I3	0	0	0	0	0	0	
6	2-49	1	2	1	I4	0	0	0	0	0	0	
6	2-49	1	2	1	I5	0	0	0	0	0	0	
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6	2-49	1	2	2	I1	0	0	0	0	0	0	
6	2-49	1	2	2	I2	0	0	0	0	0	0	
6	2-49	1	2	2	I3	0	0	0	0	0	0	
6	2-49	1	2	2	I4	0	0	0	0	0	0	
6	2-49	1	2	2	I5	0	0	0	0	0	0	
6	2-49	1	2	2	P	0	0	0	0	0	0	
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6	2-49	1	2	3	I4	0	0	0	0	0	0	
6	2-49	1	2	3	I5	0	0	0	0	0	0	
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6	2-49	1	2	4	I1	0	3	1	1	1	0	
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6	2-49	1	2	4	I4	0	0	0	0	0	0	
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6	2-49	1	3	1	I3	0	0	0	0	0	0	
6	2-49	1	3	1	I4	0	0	0	0	0	0	
6	2-49	1	3	1	I5	0	0	0	0	0	0	
6	2-49	1	3	1	P	0	0	0	0	0	0	
6	2-49	1	3	2	I1	0	0	0	0	0	0	

6	2-49	1	3	2	I2	0	0	0	0	0	0	
6	2-49	1	3	2	I3	0	0	0	0	0	0	
6	2-49	1	3	2	I4	0	0	0	0	0	0	
6	2-49	1	3	2	P	0	0	0	0	0	0	
6	2-49	1	3	3	I1	0	0	0	0	0	0	
6	2-49	1	3	3	I2	0	0	0	0	0	0	
6	2-49	1	3	3	I3	0	0	0	0	0	0	
6	2-49	1	3	3	I4	0	0	0	0	0	0	
6	2-49	1	3	3	I5	0						
6	2-49	1	3	4	I1	0	0	0	0	0	0	
6	2-49	1	3	4	I2	0	0	0	0	0	0	
6	2-49	1	3	4	I3	0	0	0	0	0	0	
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6	2-49	1	4	1	I2	0	0	0	0	0	0	
6	2-49	1	4	1	I3	0	0	0	0	0	0	
6	2-49	1	4	1	I4	0	0	0	0	0	0	
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6	2-49	1	4	1	P	0	0	0	0	0	0	
6	2-49	1	4	2	I1	0	0	0	0	0	0	
6	2-49	1	4	2	I2	0	0	0	0	0	0	
6	2-49	1	4	2	I3	0	0	0	0	0	0	
6	2-49	1	4	2	I4	0	0	0	0	0	0	
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6	2-49	1	5	4	I3	0	0	0	0	0	0	
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6	2-49	1	5	5	I3	0	0	0	0	0	0	
6	2-49	1	5	5	I4	0	0	0	0	0	0	
6	2-49	1	5	5	I5	0	0	0	0	0	0	
6	2-49	1	5	5	P	0	0	0	0	0	0	

6	2-49	2	1	1	I1	1	0	0	0	0	0	
6	2-49	2	1	1	I2	0	0	0	0	0	0	
6	2-49	2	1	1	I3	0	0	0	0	0	0	
6	2-49	2	1	1	I4	0	0	0	0	0	0	
6	2-49	2	1	1	I5	0	0	0	0	0	0	
6	2-49	2	1	1	P	0	0	0	0	0	0	
6	2-49	2	1	2	I1	0	3	3	0	0	0	
6	2-49	2	1	2	I2	0	0	0	0	0	0	
6	2-49	2	1	2	I3	0	0	0	0	0	0	
6	2-49	2	1	2	I4	0	0	0	0	0	0	
6	2-49	2	1	2	I5	0	0	0	0	0	0	
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6	2-49	2	1	3	I2	0	0	0	0	0	0	
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6	2-49	2	1	5	I3	0	0	0	0	0	0	
6	2-49	2	1	5	I4	0	0	0	0	0	0	
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6	2-49	2	2	1	I2	0	0	0	0	0	0	
6	2-49	2	2	1	I3	0	0	0	0	0	0	
6	2-49	2	2	1	I4	0	0	0	0	0	0	
6	2-49	2	2	1	I5	0	0	0	0	0	0	
6	2-49	2	2	1	P	0	0	0	0	0	0	
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6	2-49	2	2	5	I3	0	0	0	0	0	0	
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6	2-49	2	2	5	I5	0	0	0	0	0	0	
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6	2-49	2	4	5	I3	0	0	0	0	0	0	
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6	2-49	3	1	3	I2	0						
6	2-49	3	1	3	I3	0						
6	2-49	3	1	3	I4	0						
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6	Sunco	1	1	1	I3	0	0	0	0	0	0	
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6	Sunco	1	1	1	I5	0	0	0	0	0	0	
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6	Sunco	1	1	2	I1	2	4	1	1	1	1	
6	Sunco	1	1	2	I2	0	0	0	0	0	0	
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6	Sunco	1	1	2	I4	0	0	0	0	0	0	

6	Sunco	1	1	2	I5	0	0	0	0	0	0	
6	Sunco	1	1	2	P	0	0	0	0	0	0	
6	Sunco	1	1	3	I1	3	6	2	1	1	2	
6	Sunco	1	1	3	I2	0	0	0	0	0	0	
6	Sunco	1	1	3	I3	0	0	0	0	0	0	
6	Sunco	1	1	3	I4	0	0	0	0	0	0	
6	Sunco	1	1	3	I5	0	0	0	0	0	0	
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6	Sunco	1	1	4	I1	2	0	0	0	0	0	
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6	Sunco	1	1	4	I3	0	0	0	0	0	0	
6	Sunco	1	1	4	I4	0	0	0	0	0	0	
6	Sunco	1	1	4	I5	0	0	0	0	0	0	
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6	Sunco	1	1	5	I2	1	1	1	0	0	0	
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6	Sunco	1	1	5	I4	0	0	0	0	0	0	
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6	Sunco	1	2	1	I2	0	2	2	0	0	0	
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6	Sunco	1	2	1	I4	0	0	0	0	0	0	
6	Sunco	1	2	1	I5	0	0	0	0	0	0	
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6	Sunco	1	2	3	I3	0	0	0	0	0	0	
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6	Sunco	1	3	2	I3	0	0	0	0	0	0	
6	Sunco	1	3	2	I4	0	0	0	0	0	0	
6	Sunco	1	3	2	I5	0	0	0	0	0	0	
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6	Sunco	1	3	4	I5	0	0	0	0	0	0	
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6	Sunco	1	3	5	I3	0	0	0	0	0	0	
6	Sunco	1	3	5	I4	0	0	0	0	0	0	
6	Sunco	1	3	5	I5	0	0	0	0	0	0	
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6	Sunco	1	4	1	I4	0	0	0	0	0	0	
6	Sunco	1	4	1	I5	0	0	0	0	0	0	
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6	Sunco	1	4	2	I1	1	2	1	1	0	0	
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6	Sunco	1	4	2	I3	0	0	0	0	0	0	
6	Sunco	1	4	2	I4	0	0	0	0	0	0	
6	Sunco	1	4	2	I5	0	0	0	0	0	0	
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6	Sunco	1	4	3	I4	0	0	0	0	0	0	
6	Sunco	1	4	3	I5	0	0	0	0	0	0	
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6	Sunco	1	4	4	I2	0	0	0	0	0	0	
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6	Sunco	1	4	4	I4	0	0	0	0	0	0	
6	Sunco	1	4	4	I5	0	0	0	0	0	0	
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6	Sunco	1	4	5	I1	4	6	2	2	1	1	
6	Sunco	1	4	5	I2	1	2	2	0	0	0	
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6	Sunco	1	4	5	I4	0	0	0	0	0	0	
6	Sunco	1	4	5	I5	0	0	0	0	0	0	
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6	Sunco	1	5	1	I1	4	4	1	1	1	1	
6	Sunco	1	5	1	I2	4	8	2	2	2	2	
6	Sunco	1	5	1	I3	1	0	0	0	0	0	
6	Sunco	1	5	1	I4	0	0	0	0	0	0	
6	Sunco	1	5	1	I5	0	0	0	0	0	0	

6	Sunco	1	5	1	I6	0	0	0	0	0	0	
6	Sunco	1	5	1	P	0	0	0	0	0	0	
6	Sunco	1	5	2	I1	4	4	1	1	1	1	
6	Sunco	1	5	2	I2	0	3	3	0	0	0	
6	Sunco	1	5	2	I3	0	0	0	0	0	0	
6	Sunco	1	5	2	I4	0	0	0	0	0	0	
6	Sunco	1	5	2	I5	0	0	0	0	0	0	
6	Sunco	1	5	2	I6	0	0	0	0	0	0	
6	Sunco	1	5	2	P	0	0	0	0	0	0	
6	Sunco	1	5	3	I1	1	4	1	1	1	1	
6	Sunco	1	5	3	I2	0	0	0	0	0	0	
6	Sunco	1	5	3	I3	0	0	0	0	0	0	
6	Sunco	1	5	3	I4	0	0	0	0	0	0	
6	Sunco	1	5	3	I5	0	0	0	0	0	0	
6	Sunco	1	5	3	I6	0	0	0	0	0	0	
6	Sunco	1	5	3	P	0	0	0	0	0	0	
6	Sunco	1	5	4	I1	1	0	0	0	0	0	
6	Sunco	1	5	4	I2	0	0	0	0	0	0	
6	Sunco	1	5	4	I3	0	0	0	0	0	0	
6	Sunco	1	5	4	I4	0	0	0	0	0	0	
6	Sunco	1	5	4	I5	0	0	0	0	0	0	
6	Sunco	1	5	4	I6	0	0	0	0	0	0	
6	Sunco	1	5	4	P	0	0	0	0	0	0	
6	Sunco	1	5	5	I1	1	4	1	1	1	1	
6	Sunco	1	5	5	I2	0	0	0	0	0	0	
6	Sunco	1	5	5	I3	0	0	0	0	0	0	
6	Sunco	1	5	5	I4	0	0	0	0	0	0	
6	Sunco	1	5	5	I5	0	0	0	0	0	0	
6	Sunco	1	5	5	I6	0	0	0	0	0	0	
6	Sunco	1	5	5	P	0	0	0	0	0	0	
6	Sunco	2	1	1	I1	1	4	1	1	1	1	
6	Sunco	2	1	1	I2	0	0	0	0	0	0	
6	Sunco	2	1	1	I3	0	0	0	0	0	0	
6	Sunco	2	1	1	I4	0	0	0	0	0	0	
6	Sunco	2	1	1	I5	0	0	0	0	0	0	
6	Sunco	2	1	1	P	0	0	0	0	0	0	

6	Sunco	2	1	2	I1	1	4	1	1	1	1	
6	Sunco	2	1	2	I2	0	0	0	0	0	0	
6	Sunco	2	1	2	I3	0	0	0	0	0	0	
6	Sunco	2	1	2	I4	0	0	0	0	0	0	
6	Sunco	2	1	2	I5	0	0	0	0	0	0	
6	Sunco	2	1	2	P	0	0	0	0	0	0	
6	Sunco	2	1	3	I1	0	7	3	1	1	2	
6	Sunco	2	1	3	I2	0	0	0	0	0	0	
6	Sunco	2	1	3	I3	0	0	0	0	0	0	
6	Sunco	2	1	3	I4	0	0	0	0	0	0	
6	Sunco	2	1	3	P	0	0	0	0	0	0	
6	Sunco	2	1	4	I1	1	8	2	2	2	2	
6	Sunco	2	1	4	I2	0	0	0	0	0	0	
6	Sunco	2	1	4	I3	0	0	0	0	0	0	
6	Sunco	2	1	4	I4	0	0	0	0	0	0	
6	Sunco	2	1	4	P	0	0	0	0	0	0	
6	Sunco	2	1	5	I1	0	4	0	0	0	4	
6	Sunco	2	1	5	I2	0	1	1	0	0	0	
6	Sunco	2	1	5	I3	0	0	0	0	0	0	
6	Sunco	2	1	5	I4	0	0	0	0	0	0	
6	Sunco	2	1	5	P	0	0	0	0	0	0	
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6	Sunco	2	2	1	I2	0	6	4	2	0	0	
6	Sunco	2	2	1	I3	0	0	0	0	0	0	
6	Sunco	2	2	1	I4	0	0	0	0	0	0	
6	Sunco	2	2	1	P	0	0	0	0	0	0	
6	Sunco	2	2	2	I1	4	4	1	1	1	1	
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6	Sunco	2	2	2	I3	1	0	0	0	0	0	
6	Sunco	2	2	2	I4	0	0	0	0	0	0	
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6	Sunco	2	2	3	I2	1	3	1	1	1	0	
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6	Sunco	2	2	3	I4	0	0	0	0	0	0	
6	Sunco	2	2	4	I1	4	5	2	1	1	1	
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6	Sunco	2	3	1	I2	1	0	0	0	0	0	
6	Sunco	2	3	1	I3	0	0	0	0	0	0	
6	Sunco	2	3	1	I4	0	0	0	0	0	0	
6	Sunco	2	3	1	I5	0	0	0	0	0	0	
6	Sunco	2	3	1	I6	0	0	0	0	0	0	
6	Sunco	2	3	1	P	0	0	0	0	0	0	
6	Sunco	2	3	2	I1	2	2	1	1	0	0	
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6	Sunco	2	3	2	I3	0	0	0	0	0	0	
6	Sunco	2	3	2	I4	0	0	0	0	0	0	
6	Sunco	2	3	2	I5	0	0	0	0	0	0	
6	Sunco	2	3	2	P	0	0	0	0	0	0	
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6	Sunco	2	3	3	I3	0	2	2	0	0	0	
6	Sunco	2	3	3	I4	0	0	0	0	0	0	
6	Sunco	2	3	3	I5	0	0	0	0	0	0	
6	Sunco	2	3	3	P	0	0	0	0	0	0	
6	Sunco	2	3	4	I1	1	4	1	1	1	1	
6	Sunco	2	3	4	I2	0	4	2	2	0	0	
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6	Sunco	2	3	4	I4	0	0	0	0	0	0	
6	Sunco	2	3	4	I5	0	0	0	0	0	0	
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6	Sunco	2	3	5	I4	0	0	0	0	0	0	
6	Sunco	2	3	5	P	0	0	0	0	0	0	
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6	Sunco	2	4	1	I3	0	0	0	0	0	0	
6	Sunco	2	4	1	I4	0	0	0	0	0	0	
6	Sunco	2	4	1	I5	0	0	0	0	0	0	

6	Sunco	2	4	1	P	0	0	0	0	0	0	
6	Sunco	2	4	2	I1	1	5	1	2	1	1	
6	Sunco	2	4	2	I2	0	2	2	0	0	0	
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6	Sunco	2	4	3	I4	0	0	0	0	0	0	
6	Sunco	2	4	3	I5	0	0	0	0	0	0	
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6	Sunco	2	4	5	I5	0	0	0	0	0	0	
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6	Sunco	2	5	2	I4	0	0	0	0	0	0	
6	Sunco	2	5	2	I5	0	0	0	0	0	0	

6	Sunco	2	5	2	P	0	0	0	0	0	0	
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6	Sunco	2	5	3	I3	0	0	0	0	0	0	
6	Sunco	2	5	3	I4	0	0	0	0	0	0	
6	Sunco	2	5	3	I5	0	0	0	0	0	0	
6	Sunco	2	5	3	P	0	0	0	0	0	0	
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6	Sunco	2	5	4	I3	0	0	0	0	0	0	
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6	Sunco	2	5	4	I5	0	0	0	0	0	0	
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6	Sunco	2	5	5	I2	0	0	0	0	0	0	
6	Sunco	2	5	5	I3	0	0	0	0	0	0	
6	Sunco	2	5	5	I4	0	0	0	0	0	0	
6	Sunco	2	5	5	P	0	0	0	0	0	0	
6	Sunco	3	1	1	I1	1						
6	Sunco	3	1	1	I2	0						
6	Sunco	3	1	1	I3	0						
6	Sunco	3	1	1	I4	0						
6	Sunco	3	1	1	I5	0						
6	Sunco	3	1	1	P	0						
6	Sunco	3	1	2	I1	2						
6	Sunco	3	1	2	I2	1						
6	Sunco	3	1	2	I3	0						
6	Sunco	3	1	2	I4	0						
6	Sunco	3	1	2	I5	0						
6	Sunco	3	1	2	P	0						
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6	Sunco	3	1	3	I2	0						
6	Sunco	3	1	3	I3	0						
6	Sunco	3	1	3	I4	0						
6	Sunco	3	1	3	I5	0						
6	Sunco	3	1	3	P	0						

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6	Sunco	3	1	4	I2	0						
6	Sunco	3	1	4	I3	0						
6	Sunco	3	1	4	I4	0						
6	Sunco	3	1	4	P	0						
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6	Sunco	3	1	5	I2	1						
6	Sunco	3	1	5	I3	0						
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6	Sunco	3	1	5	P	0						
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6	Sunco	3	2	1	I2	0						
6	Sunco	3	2	1	I3	0						
6	Sunco	3	2	1	I4	0						
6	Sunco	3	2	1	I5	0						
6	Sunco	3	2	1	P	0						
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6	Sunco	3	2	2	I3	0						
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6	Sunco	3	2	2	I5	0						
6	Sunco	3	2	2	P	0						
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6	Sunco	3	2	3	I4	0						
6	Sunco	3	2	3	I5	0						
6	Sunco	3	2	3	P	0						
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6	Sunco	3	2	4	I4	0						
6	Sunco	3	2	4	P	0						
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6	Sunco	3	2	5	I3	0						

6	Sunco	3	2	5	I4	0						
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6	Sunco	3	3	4	I4	0						
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6	Sunco	3	4	1	I3	0						
6	Sunco	3	4	1	I4	0						
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6	Sunco	3	4	2	I3	0						
6	Sunco	3	4	2	I4	0						
6	Sunco	3	4	2	I5	0						
6	Sunco	3	4	2	P	0						
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6	Sunco	3	4	3	I2	3						

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6	Sunco	3	4	3	I5	0						
6	Sunco	3	4	3	P	0						
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6	Sunco	3	4	4	P	0						
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6	Sunco	3	4	5	I2	4						
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6	Sunco	3	5	1	I2	0						
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6	Sunco	3	5	2	I5	0						
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6	Sunco	3	5	3	I2	0						
6	Sunco	3	5	3	I3	0						
6	Sunco	3	5	3	I4	0						
6	Sunco	3	5	3	P	0						
6	Sunco	3	5	4	I1	1						
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6	Sunco	3	5	4	I3	0						

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6	Sunco	3	5	5	I2	0						
6	Sunco	3	5	5	I3	0						
6	Sunco	3	5	5	I4	0						
6	Sunco	3	5	5	P	0						
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7	Puseas	1	1	1	I2	4	11	3	3	3	2	
7	Puseas	1	1	1	I3	4	14	4	3	4	3	
7	Puseas	1	1	1	I4	1	2	2	0	0	0	
7	Puseas	1	1	1	I5	1	0	0	0	0	0	
7	Puseas	1	1	1	P	0	0	0	0	0	0	
7	Puseas	1	1	2	I1	4	6	1.5	1.5	1.5	1.5	
7	Puseas	1	1	2	I2	4	11	3	3	3	2	
7	Puseas	1	1	2	I3	4	14	5	6	2	1	
7	Puseas	1	1	2	I4	2	16	6	6	4	0	
7	Puseas	1	1	2	I5	1	0	0	0	0	0	
7	Puseas	1	1	2	P	0	0	0	0	0	0	
7	Puseas	1	1	3	I1	4	4	1	1	1	1	
7	Puseas	1	1	3	I2	4	10	3	2	3	2	
7	Puseas	1	1	3	I3	4	15	5	3	3	4	
7	Puseas	1	1	3	I4	1	10	4	6	0	0	
7	Puseas	1	1	3	I5	1	0	0	0	0	0	
7	Puseas	1	1	3	P	1	0	0	0	0	0	
7	Puseas	1	1	4	I1	4	4	1	1	1	1	
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7	Puseas	1	1	4	I3	4	15	4	4	3	4	
7	Puseas	1	1	4	I4	1	2	2	0	0	0	
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7	Puseas	1	2	1	I3	4	12	3	3	3	3	
7	Puseas	1	2	1	I4	1	0	0	0	0	0	
7	Puseas	1	2	1	I5	0	0	0	0	0	0	
7	Puseas	1	2	1	P	0	0	0	0	0	0	
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7	Puseas	1	2	2	I2	4	16	5	4	3	4	
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7	Puseas	1	2	2	I4	1	0	0	0	0	0	
7	Puseas	1	2	2	I5	0	0	0	0	0	0	
7	Puseas	1	2	2	P	0	0	0	0	0	0	
7	Puseas	1	2	3	I1	4	4	1	1	1	1	
7	Puseas	1	2	3	I2	4	13	4	4	2	3	
7	Puseas	1	2	3	I3	1	20	7	6	6	1	
7	Puseas	1	2	3	I4	0	0	0	0	0	0	
7	Puseas	1	2	3	I5	0	0	0	0	0	0	
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7	Puseas	3	4	4	P	0						
7	Puseas	3	4	5	I1	3						
7	Puseas	3	4	5	I2	1						
7	Puseas	3	4	5	I3	0						
7	Puseas	3	4	5	I4	0						
7	Puseas	3	5	1	I1	4						
7	Puseas	3	5	1	I2	4						
7	Puseas	3	5	1	I3	3						
7	Puseas	3	5	1	I4	1						
7	Puseas	3	5	1	I5	0						
7	Puseas	3	5	1	P	0						
7	Puseas	3	5	2	I1	4						
7	Puseas	3	5	2	I2	4						
7	Puseas	3	5	2	I3	4						
7	Puseas	3	5	2	I4	2						
7	Puseas	3	5	2	I5	0						
7	Puseas	3	5	2	P	0						
7	Puseas	3	5	3	I1	4						
7	Puseas	3	5	3	I2	3						
7	Puseas	3	5	3	I3	2						
7	Puseas	3	5	3	I4	1						
7	Puseas	3	5	3	I5	0						
7	Puseas	3	5	3	P	0						
7	Puseas	3	5	4	I1	4						
7	Puseas	3	5	4	I2	1						
7	Puseas	3	5	4	I3	1						
7	Puseas	3	5	4	I4	0						
7	Puseas	3	5	4	I5	0						
7	Puseas	3	5	5	I1	4						
7	Puseas	3	5	5	I2	1						
7	Puseas	3	5	5	I3	0						
7	Puseas	3	5	5	I4	0						
7	Vasco	1	1	1	I1	1	9	4	4	1	0	
7	Vasco	1	1	1	I2	0	0	0	0	0	0	

7	Vasco	1	1	1	I3	0	0	0	0	0	0	
7	Vasco	1	1	1	I4	0	0	0	0	0	0	
7	Vasco	1	1	2	P	0	0	0	0	0	0	
7	Vasco	1	1	2	I1	1	8	4	4	0	0	
7	Vasco	1	1	2	I2	0	0	0	0	0	0	
7	Vasco	1	1	2	I3	0	0	0	0	0	0	
7	Vasco	1	1	2	I4	0	0	0	0	0	0	
7	Vasco	1	1	3	I1	1	3	3	0	0	0	
7	Vasco	1	1	3	I2	0	0	0	0	0	0	
7	Vasco	1	1	3	I3	0	0	0	0	0	0	
7	Vasco	1	1	3	I4	0	0	0	0	0	0	
7	Vasco	1	1	3	P	0	0	0	0	0	0	
7	Vasco	1	2	1	I1	4	4	1	1	1	1	
7	Vasco	1	2	1	I2	1	5	4	1	0	0	
7	Vasco	1	2	1	I3	0	0	0	0	0	0	
7	Vasco	1	2	1	I4	0	0	0	0	0	0	
7	Vasco	1	2	1	I5	0	0	0	0	0	0	
7	Vasco	1	2	1	P	0	0	0	0	0	0	
7	Vasco	1	2	2	I1	4	4	1	1	1	1	
7	Vasco	1	2	2	I2	1	4	3	1	0	0	
7	Vasco	1	2	2	I3	0	0	0	0	0	0	
7	Vasco	1	2	2	I4	0	0	0	0	0	0	
7	Vasco	1	2	2	I5	0	0	0	0	0	0	
7	Vasco	1	2	2	P	0	0	0	0	0	0	
7	Vasco	1	2	3	I1	4	4	1	1	1	1	
7	Vasco	1	2	3	I2	1	3	3	0	0	0	
7	Vasco	1	2	3	I3	0	0	0	0	0	0	
7	Vasco	1	2	3	I4	0	0	0	0	0	0	
7	Vasco	1	2	3	I5	0	0	0	0	0	0	
7	Vasco	1	2	3	P	0	0	0	0	0	0	
7	Vasco	1	2	4	I1	4	4	1	1	1	1	
7	Vasco	1	2	4	I2	2	5	4	1	0	0	
7	Vasco	1	2	4	I3	0	0	0	0	0	0	
7	Vasco	1	2	4	I4	0	0	0	0	0	0	
7	Vasco	1	2	4	I5	0	0	0	0	0	0	
7	Vasco	1	2	4	P	0	0	0	0	0	0	

7	Vasco	1	2	5	I1	4	4	1	1	1	1	
7	Vasco	1	2	5	I2	1	11	3	3	3	2	
7	Vasco	1	2	5	I3	0	0	0	0	0	0	
7	Vasco	1	2	5	I4	0	0	0	0	0	0	
7	Vasco	1	2	5	I5	0	0	0	0	0	0	
7	Vasco	1	2	5	P	0	0	0	0	0	0	
7	Vasco	1	3	1	I1	4	4	1	1	1	1	
7	Vasco	1	3	1	I2	3	8	3	2	2	1	
7	Vasco	1	3	1	I3	1	0	0	0	0	0	
7	Vasco	1	3	1	I4	0	0	0	0	0	0	
7	Vasco	1	3	1	I5	0	0	0	0	0	0	
7	Vasco	1	3	1	P	0	0	0	0	0	0	
7	Vasco	1	3	2	I1	4	4	1	1	1	1	
7	Vasco	1	3	2	I2	1	0	0	0	0	0	
7	Vasco	1	3	2	I3	0	0	0	0	0	0	
7	Vasco	1	3	2	I4	0	0	0	0	0	0	
7	Vasco	1	3	2	I5	0	0	0	0	0	0	
7	Vasco	1	3	2	P	0	0	0	0	0	0	
7	Vasco	1	3	3	I1	3	5	2	1	1	1	
7	Vasco	1	3	3	I2	1	0	0	0	0	0	
7	Vasco	1	3	3	I3	0	0	0	0	0	0	
7	Vasco	1	3	3	I4	0	0	0	0	0	0	
7	Vasco	1	3	3	P	0	0	0	0	0	0	
7	Vasco	1	3	4	I1	4	4	1	1	1	1	
7	Vasco	1	3	4	I2	1	4	3	1	0	0	
7	Vasco	1	3	4	I3	0	0	0	0	0	0	
7	Vasco	1	3	4	I4	0	0	0	0	0	0	
7	Vasco	1	3	4	I5	0	0	0	0	0	0	
7	Vasco	1	3	4	P	0	0	0	0	0	0	
7	Vasco	1	3	5	I1	3	0	0	0	0	0	
7	Vasco	1	3	5	I2	1	0	0	0	0	0	
7	Vasco	1	4	1	I1	4	4	1	1	1	1	
7	Vasco	1	4	1	I2	4	16	4	4	4	4	
7	Vasco	1	4	1	I3	4	17	5	5	3	4	
7	Vasco	1	4	1	I4	1	3	3	0	0	0	
7	Vasco	1	4	1	I5	0	0	0	0	0	0	

7	Vasco	1	4	1	P	0	0	0	0	0	0	
7	Vasco	1	4	2	I1	4	4	1	1	1	1	
7	Vasco	1	4	2	I2	4	11	4	2	2	3	
7	Vasco	1	4	2	I3	1	3	3	0	0	0	
7	Vasco	1	4	2	I4	0	0	0	0	0	0	
7	Vasco	1	4	2	I5	0	0	0	0	0	0	
7	Vasco	1	4	2	P	0	0	0	0	0	0	
7	Vasco	1	4	3	I1	4	4	1	1	1	1	
7	Vasco	1	4	3	I2	1	0	0	0	0	0	
7	Vasco	1	4	3	I3	0	0	0	0	0	0	
7	Vasco	1	4	3	I4	0	0	0	0	0	0	
7	Vasco	1	5	1	I1	4	4	1	1	1	1	
7	Vasco	1	5	1	I2	4	12	3	3	3	3	
7	Vasco	1	5	1	I3	1	3	3	0	0	0	
7	Vasco	1	5	1	I4	0	0	0	0	0	0	
7	Vasco	1	5	1	I5	0	0	0	0	0	0	
7	Vasco	1	5	1	P	0	0	0	0	0	0	
7	Vasco	1	5	2	I1	4	4	1	1	1	1	
7	Vasco	1	5	2	I2	4	16	4	4	4	4	
7	Vasco	1	5	2	I3	2	3	3	0	0	0	
7	Vasco	1	5	2	I4	0	0	0	0	0	0	
7	Vasco	1	5	2	I5	0	0	0	0	0	0	
7	Vasco	1	5	2	P	0	0	0	0	0	0	
7	Vasco	1	5	3	I1	4	4	1	1	1	1	
7	Vasco	1	5	3	I2	4	13	4	3	3	3	
7	Vasco	1	5	3	I3	4	20	5	5	5	5	
7	Vasco	1	5	3	I4	3	20	5	5	5	5	
7	Vasco	1	5	3	I5	0	0	0	0	0	0	
7	Vasco	1	5	3	P	0	0	0	0	0	0	
7	Vasco	1	5	4	I1	4	4	1	1	1	1	
7	Vasco	1	5	4	I2	2	8	3	2	1	2	
7	Vasco	1	5	4	I3	1	1	1	0	0	0	
7	Vasco	1	5	4	I4	0	0	0	0	0	0	
7	Vasco	1	5	4	I5	0	0	0	0	0	0	
7	Vasco	1	5	4	P	0	0	0	0	0	0	
7	Vasco	1	5	5	I1	4	4	1	1	1	1	

7	Vasco	1	5	5	I2	4	12	3	3	3	3	
7	Vasco	1	5	5	I3	1	5	4	1	0	0	
7	Vasco	1	5	5	I4	0	0	0	0	0	0	
7	Vasco	1	5	5	I5	0	0	0	0	0	0	
7	Vasco	1	5	5	P	0	0	0	0	0	0	
7	Vasco	2	1	1	I1	4	4	1	1	1	1	
7	Vasco	2	1	1	I2	2	10	4	2	1	3	
7	Vasco	2	1	1	I3	1	4	4	0	0	0	
7	Vasco	2	1	1	I4	0	0	0	0	0	0	
7	Vasco	2	1	1	I5	0	0	0	0	0	0	
7	Vasco	2	1	1	P	0	0	0	0	0	0	
7	Vasco	2	1	2	I1	4	4	1	1	1	1	
7	Vasco	2	1	2	I2	4	12	3	3	3	3	
7	Vasco	2	1	2	I3	4	12	4	3	2	3	
7	Vasco	2	1	2	I4	3	20	5	5	5	5	
7	Vasco	2	1	2	I5	1	0	0	0	0	0	
7	Vasco	2	1	2	P	0	0	0	0	0	0	
7	Vasco	2	1	3	I1	4	5	2	1	1	1	
7	Vasco	2	1	3	I2	4	13	4	3	3	3	
7	Vasco	2	1	3	I3	1	8	4	4	0	0	
7	Vasco	2	1	3	I4	0	0	0	0	0	0	
7	Vasco	2	1	3	I5	0	0	0	0	0	0	
7	Vasco	2	1	3	P	0	0	0	0	0	0	
7	Vasco	2	1	4	I1	4	4	1	1	1	1	
7	Vasco	2	1	4	I2	4	11	3	3	2	3	
7	Vasco	2	1	4	I3	3	9	3	3	2	1	
7	Vasco	2	1	4	I4	1	2	2	0	0	0	
7	Vasco	2	1	4	I5	0	0	0	0	0	0	
7	Vasco	2	1	4	P	0	0	0	0	0	0	
7	Vasco	2	1	5	I1	4	5	2	1	1	1	
7	Vasco	2	1	5	I2	1	7	3	2	1	1	
7	Vasco	2	1	5	I3	0	0	0	0	0	0	
7	Vasco	2	1	5	I4	0	0	0	0	0	0	
7	Vasco	2	1	5	P	0	0	0	0	0	0	
7	Vasco	2	2	1	I1	4	4	1	1	1	1	
7	Vasco	2	2	1	I2	4	11	4	3	1	3	

7	Vasco	2	2	1	I3	1	2	2	0	0	0	
7	Vasco	2	2	1	I4	0	0	0	0	0	0	
7	Vasco	2	2	1	I5	0	0	0	0	0	0	
7	Vasco	2	2	1	P	0	0	0	0	0	0	
7	Vasco	2	2	2	I1	4	6	1.5	1.5	1.5	1.5	
7	Vasco	2	2	2	I2	4	12	4	3	2	3	
7	Vasco	2	2	2	I3	1	7	5	2	0	0	
7	Vasco	2	2	2	I4	0	0	0	0	0	0	
7	Vasco	2	2	2	I5	0	0	0	0	0	0	
7	Vasco	2	2	2	P	0	0	0	0	0	0	
7	Vasco	2	2	3	I1	4	4	1	1	1	1	
7	Vasco	2	2	3	I2	1	4	1	1	1	1	
7	Vasco	2	2	3	I3	0	0	0	0	0	0	
7	Vasco	2	2	3	I4	0	0	0	0	0	0	
7	Vasco	2	2	3	I5	0	0	0	0	0	0	
7	Vasco	2	2	3	P	0	0	0	0	0	0	
7	Vasco	2	2	4	I1	4	12	3	3	3	3	
7	Vasco	2	2	4	I2	1	10	4	3	2	1	
7	Vasco	2	2	4	I3	0	0	0	0	0	0	
7	Vasco	2	2	4	I4	0	0	0	0	0	0	
7	Vasco	2	2	4	P	0	0	0	0	0	0	
7	Vasco	2	3	1	I1	4	6	2	1	2	1	
7	Vasco	2	3	1	I2	4	8	2	2	2	2	
7	Vasco	2	3	1	I3	4	8	3	3	0	2	
7	Vasco	2	3	1	I4	4	20	5	5	5	5	
7	Vasco	2	3	1	I5	1	4	4	0	0	0	
7	Vasco	2	3	1	I6	0	0	0	0	0	0	
7	Vasco	2	3	1	P	0	0	0	0	0	0	
7	Vasco	2	3	2	I1	4	4	1	1	1	1	
7	Vasco	2	3	2	I2	4	9	3	2	2	2	
7	Vasco	2	3	2	I3	3	13	4	4	3	2	
7	Vasco	2	3	2	I4	1	0	0	0	0	0	
7	Vasco	2	3	2	I5	0	0	0	0	0	0	
7	Vasco	2	3	2	P	0	0	0	0	0	0	
7	Vasco	2	3	3	I1	4	4	1	1	1	1	
7	Vasco	2	3	3	I2	4	12	3	3	3	3	

7	Vasco	2	3	3	I3	4	14	4	4	3	3	
7	Vasco	2	3	3	I4	4	18	5	5	4	4	
7	Vasco	2	3	3	I5	4	19	6	5	4	4	
7	Vasco	2	3	4	I1	4	4	1	1	1	1	
7	Vasco	2	3	4	I2	4	4	1	1	1	1	
7	Vasco	2	3	4	I3	4	9	3	2	2	2	
7	Vasco	2	3	4	I4	4	18	5	5	5	3	
7	Vasco	2	3	4	I5	4	20	5	5	5	5	
7	Vasco	2	3	5	I1	4	8	2	2	2	2	
7	Vasco	2	3	5	I2	4	10	3	2	2	3	
7	Vasco	2	3	5	I3	4	14	4	3	4	3	
7	Vasco	2	3	5	I4	4	15	5	4	4	2	
7	Vasco	2	4	1	I1	4	4	1	1	1	1	
7	Vasco	2	4	1	I2	3	12	3	3	3	3	
7	Vasco	2	4	1	I3	1	3	3	0	0	0	
7	Vasco	2	4	1	I4	0	0	0	0	0	0	
7	Vasco	2	4	1	I5	0	0	0	0	0	0	
7	Vasco	2	4	1	P	0	0	0	0	0	0	
7	Vasco	2	4	2	I1	1	4	1	1	1	1	
7	Vasco	2	4	2	I2	0	0	0	0	0	0	
7	Vasco	2	4	2	I3	0	0	0	0	0	0	
7	Vasco	2	4	2	I4	0	0	0	0	0	0	
7	Vasco	2	4	2	I5	0	0	0	0	0	0	
7	Vasco	2	4	2	P	0	0	0	0	0	0	
7	Vasco	2	4	3	I1	4	4	1	1	1	1	
7	Vasco	2	4	3	I2	1	6	4	2	0	0	
7	Vasco	2	4	4	I1	4	4	1	1	1	1	
7	Vasco	2	4	4	I2	0	12	3	3	3	3	
7	Vasco	2	5	1	I1	4	4	1	1	1	1	
7	Vasco	2	5	1	I2	1	8	2	2	2	2	
7	Vasco	2	5	1	I3	0	1	1	0	0	0	
7	Vasco	2	5	1	I4	0	0	0	0	0	0	
7	Vasco	2	5	1	I5	0	0	0	0	0	0	
7	Vasco	2	5	1	P	0	0	0	0	0	0	
7	Vasco	2	5	2	I1	4	4	1	1	1	1	
7	Vasco	2	5	2	I2	4	11	3	3	2	3	

7	Vasco	2	5	2	I3	2	13	6	3	2	2	
7	Vasco	2	5	2	I4	0	0	0	0	0	0	
7	Vasco	2	5	2	I5	0	0	0	0	0	0	
7	Vasco	2	5	2	P	0	0	0	0	0	0	
7	Vasco	2	5	3	I1	4	4	1	1	1	1	
7	Vasco	2	5	3	I2	1	11	3	3	2	3	
7	Vasco	2	5	3	I3	0	0	0	0	0	0	
7	Vasco	2	5	3	I4	0	0	0	0	0	0	
7	Vasco	2	5	3	I5	0	0	0	0	0	0	
7	Vasco	2	5	3	P	0	0	0	0	0	0	
7	Vasco	2	5	4	I1	2	8	2	2	2	2	
7	Vasco	2	5	4	I2	1	0	0	0	0	0	
7	Vasco	2	5	4	I3	0	0	0	0	0	0	
7	Vasco	2	5	4	I4	0	0	0	0	0	0	
7	Vasco	2	5	4	P	0	0	0	0	0	0	
7	Vasco	2	5	5	I1	4	6	2	2	1	1	
7	Vasco	2	5	5	I2	4	14	4	4	3	3	
7	Vasco	2	5	5	I3	1	12	5	6	1	0	
7	Vasco	2	5	5	I4	0	0	0	0	0	0	
7	Vasco	2	5	5	P	0	0	0	0	0	0	
7	Vasco	3	1	1	I1	4						
7	Vasco	3	1	1	I2	4						
7	Vasco	3	1	1	I3	4						
7	Vasco	3	1	1	I4	1						
7	Vasco	3	1	1	I5	0						
7	Vasco	3	1	1	P	0						
7	Vasco	3	1	2	I1	4						
7	Vasco	3	1	2	I2	4						
7	Vasco	3	1	2	I3	2						
7	Vasco	3	1	2	I4	0						
7	Vasco	3	1	2	I5	0						
7	Vasco	3	1	2	P	0						
7	Vasco	3	1	3	I1	4						
7	Vasco	3	1	3	I2	4						
7	Vasco	3	1	3	I3	1						
7	Vasco	3	1	3	I4	0						

7	Vasco	3	1	3	I5	0						
7	Vasco	3	1	3	P	0						
7	Vasco	3	1	4	I1	4						
7	Vasco	3	1	4	I2	4						
7	Vasco	3	1	4	I3	1						
7	Vasco	3	1	4	I4	0						
7	Vasco	3	1	4	I5	0						
7	Vasco	3	1	4	P	0						
7	Vasco	3	1	5	I1	4						
7	Vasco	3	1	5	I2	2						
7	Vasco	3	1	5	I3	0						
7	Vasco	3	1	5	I4	0						
7	Vasco	3	1	5	I5	0						
7	Vasco	3	1	5	P	0						
7	Vasco	3	2	1	I1	4						
7	Vasco	3	2	1	I2	3						
7	Vasco	3	2	1	I3	1						
7	Vasco	3	2	1	I4	0						
7	Vasco	3	2	1	I5	0						
7	Vasco	3	2	1	P	0						
7	Vasco	3	2	2	I1	4						
7	Vasco	3	2	2	I2	1						
7	Vasco	3	2	2	I3	0						
7	Vasco	3	2	2	I4	0						
7	Vasco	3	2	2	I5	0						
7	Vasco	3	2	2	P	0						
7	Vasco	3	2	3	I1	3						
7	Vasco	3	2	3	I2	1						
7	Vasco	3	2	3	I3	0						
7	Vasco	3	2	3	I4	0						
7	Vasco	3	3	1	I1	4						
7	Vasco	3	3	1	I2	4						
7	Vasco	3	3	1	I3	1						
7	Vasco	3	3	1	I4	0						
7	Vasco	3	3	1	I5	0						
7	Vasco	3	3	1	P	0						

7	Vasco	3	3	2	I1	4						
7	Vasco	3	3	2	I2	4						
7	Vasco	3	3	2	I3	1						
7	Vasco	3	3	2	I4	0						
7	Vasco	3	3	2	I5	0						
7	Vasco	3	3	2	P	0						
7	Vasco	3	3	3	I1	4						
7	Vasco	3	3	3	I2	4						
7	Vasco	3	3	3	I3	2						
7	Vasco	3	3	3	I4	0						
7	Vasco	3	3	3	I5	0						
7	Vasco	3	3	3	P	0						
7	Vasco	3	3	4	I1	3						
7	Vasco	3	3	4	I2	2						
7	Vasco	3	3	4	I3	0						
7	Vasco	3	3	4	I4	0						
7	Vasco	3	3	4	P	0						
7	Vasco	3	3	5	I1	3						
7	Vasco	3	3	5	I2	1						
7	Vasco	3	3	5	I3	0						
7	Vasco	3	3	5	I4	0						
7	Vasco	3	3	5	P	0						
7	Vasco	3	4	1	I1	4						
7	Vasco	3	4	1	I2	2						
7	Vasco	3	4	1	I3	0						
7	Vasco	3	4	1	I4	0						
7	Vasco	3	4	1	I5	0						
7	Vasco	3	4	1	P	0						
7	Vasco	3	4	2	I1	4						
7	Vasco	3	4	2	I2	4						
7	Vasco	3	4	2	I3	4						
7	Vasco	3	4	2	I4	1						
7	Vasco	3	4	2	I5	0						
7	Vasco	3	4	2	P	0						
7	Vasco	3	4	3	I1	4						
7	Vasco	3	4	3	I2	4						

7	Vasco	3	4	3	I3	1						
7	Vasco	3	4	3	I4	0						
7	Vasco	3	4	3	I5	0						
7	Vasco	3	4	3	P	0						
7	Vasco	3	4	4	I1	4						
7	Vasco	3	4	4	I2	4						
7	Vasco	3	4	4	I3	1						
7	Vasco	3	4	4	I4	0						
7	Vasco	3	4	4	I5	0						
7	Vasco	3	4	4	P	0						
7	Vasco	3	4	5	I1	4						
7	Vasco	3	4	5	I2	1						
7	Vasco	3	4	5	I3	1						
7	Vasco	3	4	5	I4	0						
7	Vasco	3	4	5	P	0						
7	Vasco	3	5	1	I1	4						
7	Vasco	3	5	1	I2	1						
7	Vasco	3	5	1	I3	0						
7	Vasco	3	5	1	I4	0						
7	Vasco	3	5	1	I5	0						
7	Vasco	3	5	1	P	0						
7	Vasco	3	5	2	I1	2						
7	Vasco	3	5	2	I2	1						
7	Vasco	3	5	2	I3	0						
7	Vasco	3	5	2	I4	0						
7	Vasco	3	5	2	I5	0						
7	Vasco	3	5	2	P	0						
7	Vasco	3	5	3	I1	2						
7	Vasco	3	5	3	I2	0						
7	Vasco	3	5	3	I3	0						
7	Vasco	3	5	3	I4	0						
7	Vasco	3	5	3	I5	0						
7	Vasco	3	5	3	P	0						
7	Vasco	3	5	4	I1	1						
7	Vasco	3	5	4	I2	0						
7	Vasco	3	5	4	I3	0						

7	Vasco	3	5	4	I4	0						
7	Vasco	3	5	4	I5	0						
7	Vasco	3	5	4	P	0						
7	Vasco	3	5	5	I1	1						
7	Vasco	3	5	5	I2	0						
7	Vasco	3	5	5	I3	0						
7	2-49	1	1	1	I1	1	4	1	1	1	1	
7	2-49	1	1	1	I2	0	1	1	0	0	0	
7	2-49	1	1	1	I3	0	0	0	0	0	0	
7	2-49	1	1	1	I4	0	0	0	0	0	0	
7	2-49	1	1	1	I5	0	0	0	0	0	0	
7	2-49	1	1	1	P	0	0	0	0	0	0	
7	2-49	1	1	2	I1	1	4	1	1	1	1	
7	2-49	1	1	2	I2	0	0	0	0	0	0	
7	2-49	1	1	2	I3	0	0	0	0	0	0	
7	2-49	1	1	2	I4	0	0	0	0	0	0	
7	2-49	1	1	2	I5	0	0	0	0	0	0	
7	2-49	1	1	2	P	0	0	0	0	0	0	
7	2-49	1	1	3	I1	0	0	0	0	0	0	
7	2-49	1	1	3	I2	0	0	0	0	0	0	
7	2-49	1	1	3	I3	0	0	0	0	0	0	
7	2-49	1	1	3	I4	0	0	0	0	0	0	
7	2-49	1	1	3	P	0	0	0	0	0	0	
7	2-49	1	1	4	I1	0	3	1	1	1	0	
7	2-49	1	1	4	I2	0	0	0	0	0	0	
7	2-49	1	1	4	I3	0	0	0	0	0	0	
7	2-49	1	1	4	I4	0	0	0	0	0	0	
7	2-49	1	1	4	P	0	0	0	0	0	0	
7	2-49	1	1	5	I1	0	0	0	0	0	0	
7	2-49	1	1	5	I2	0	0	0	0	0	0	
7	2-49	1	1	5	I3	0	0	0	0	0	0	
7	2-49	1	1	5	I4	0	0	0	0	0	0	
7	2-49	1	1	5	P	0	0	0	0	0	0	
7	2-49	1	2	1	I1	4	4	1	1	1	1	
7	2-49	1	2	1	I2	1	8	2	2	2	2	
7	2-49	1	2	1	I3	0	6	3	3	0	0	

7	2-49	1	2	1	I4	0	0	0	0	0	0	
7	2-49	1	2	1	I5	0	0	0	0	0	0	
7	2-49	1	2	1	I6	0	0	0	0	0	0	
7	2-49	1	2	1	P	0	0	0	0	0	0	
7	2-49	1	2	2	I1	4	4	1	1	1	1	
7	2-49	1	2	2	I2	4	9	3	2	2	2	
7	2-49	1	2	2	I3	1	13	6	2	5	0	
7	2-49	1	2	2	I4	0	0	0	0	0	0	
7	2-49	1	2	2	I5	0	0	0	0	0	0	
7	2-49	1	2	2	I6	0	0	0	0	0	0	
7	2-49	1	2	2	P	0	0	0	0	0	0	
7	2-49	1	2	3	I1	1	4	1	1	1	1	
7	2-49	1	2	3	I2	0	2	2	0	0	0	
7	2-49	1	2	3	I3	0	0	0	0	0	0	
7	2-49	1	2	3	I4	0	0	0	0	0	0	
7	2-49	1	2	3	I5	0	0	0	0	0	0	
7	2-49	1	2	3	P	0	0	0	0	0	0	
7	2-49	1	2	4	I1	1	5	1	1	2	1	
7	2-49	1	2	4	I2	0	0	0	0	0	0	
7	2-49	1	2	4	I3	0	0	0	0	0	0	
7	2-49	1	2	4	I4	0	0	0	0	0	0	
7	2-49	1	2	4	I5	0	0	0	0	0	0	
7	2-49	1	2	4	P	0	0	0	0	0	0	
7	2-49	1	2	5	I1	1	8	2	2	2	2	
7	2-49	1	2	5	I2	0	0	0	0	0	0	
7	2-49	1	2	5	I3	0	0	0	0	0	0	
7	2-49	1	2	5	I4	0	0	0	0	0	0	
7	2-49	1	2	5	I5	0	0	0	0	0	0	
7	2-49	1	2	5	P	0	0	0	0	0	0	
7	2-49	1	3	1	I1	3	4	1	1	1	1	
7	2-49	1	3	1	I2	0	0	0	0	0	0	
7	2-49	1	3	1	I3	0	0	0	0	0	0	
7	2-49	1	3	1	I4	0	0	0	0	0	0	
7	2-49	1	3	1	I5	0	0	0	0	0	0	
7	2-49	1	3	1	P	0	0	0	0	0	0	
7	2-49	1	3	2	I1	2	4	1	1	1	1	

7	2-49	1	3	2	I2	1	8	4	4	0	0	
7	2-49	1	3	2	I3	0	0	0	0	0	0	
7	2-49	1	3	2	I4	0	0	0	0	0	0	
7	2-49	1	3	2	I5	0	0	0	0	0	0	
7	2-49	1	3	2	P	0	0	0	0	0	0	
7	2-49	1	3	3	I1	2	4	1	1	1	1	
7	2-49	1	3	3	I2	0	0	0	0	0	0	
7	2-49	1	3	3	I3	0	0	0	0	0	0	
7	2-49	1	3	3	I4	0	0	0	0	0	0	
7	2-49	1	3	3	I5	0	0	0	0	0	0	
7	2-49	1	3	3	P	0	0	0	0	0	0	
7	2-49	1	3	4	I1	0	0	0	0	0	0	
7	2-49	1	3	4	I2	0	0	0	0	0	0	
7	2-49	1	3	4	I3	0	0	0	0	0	0	
7	2-49	1	3	4	I4	0	0	0	0	0	0	
7	2-49	1	3	4	P	0	0	0	0	0	0	
7	2-49	1	3	5	I1	1	7	1	2	2	2	
7	2-49	1	3	5	I2	0	0	0	0	0	0	
7	2-49	1	3	5	I3	0	0	0	0	0	0	
7	2-49	1	3	5	I4	0	0	0	0	0	0	
7	2-49	1	3	5	P	0	0	0	0	0	0	
7	2-49	1	4	1	I1	1	3	2	1	0	0	
7	2-49	1	4	1	I2	0	0	0	0	0	0	
7	2-49	1	4	1	I3	0	0	0	0	0	0	
7	2-49	1	4	1	I4	0	0	0	0	0	0	
7	2-49	1	4	1	I5	0	0	0	0	0	0	
7	2-49	1	4	1	P	0	0	0	0	0	0	
7	2-49	1	4	2	I1	3	4	1	1	1	1	
7	2-49	1	4	2	I2	0	2	2	0	0	0	
7	2-49	1	4	2	I3	0	0	0	0	0	0	
7	2-49	1	4	2	I4	0	0	0	0	0	0	
7	2-49	1	4	2	I5	0	0	0	0	0	0	
7	2-49	1	4	2	P	0	0	0	0	0	0	
7	2-49	1	4	3	I1	0	3	3	0	0	0	
7	2-49	1	4	3	I2	0	0	0	0	0	0	
7	2-49	1	4	3	I3	0	0	0	0	0	0	

7	2-49	1	4	3	I4	0	0	0	0	0	0	
7	2-49	1	4	3	P	0	0	0	0	0	0	
7	2-49	1	4	4	I1	1	3	3	0	0	0	
7	2-49	1	4	4	I2	1	0	0	0	0	0	
7	2-49	1	4	4	I3	0	0	0	0	0	0	
7	2-49	1	5	1	I1	1	7	4	1	1	1	
7	2-49	1	5	1	I2	0	3	3	0	0	0	
7	2-49	1	5	1	I3	0	0	0	0	0	0	
7	2-49	1	5	1	I4	0	0	0	0	0	0	
7	2-49	1	5	1	I5	0	0	0	0	0	0	
7	2-49	1	5	1	P	0	0	0	0	0	0	
7	2-49	1	5	2	I1	1	3	1	1	1	0	
7	2-49	1	5	2	I2	0	0	0	0	0	0	
7	2-49	1	5	2	I3	0	0	0	0	0	0	
7	2-49	1	5	2	I4	0	0	0	0	0	0	
7	2-49	1	5	2	I5	0	0	0	0	0	0	
7	2-49	1	5	2	P	0	0	0	0	0	0	
7	2-49	1	5	3	I1	0	3	1	0	1	1	
7	2-49	1	5	3	I2	0	0	0	0	0	0	
7	2-49	1	5	3	I3	0	0	0	0	0	0	
7	2-49	1	5	3	I4	0	0	0	0	0	0	
7	2-49	1	5	3	I5	0	0	0	0	0	0	
7	2-49	1	5	3	P	0	0	0	0	0	0	
7	2-49	1	5	4	I1	0	3	3	0	0	0	
7	2-49	1	5	4	I2	0	0	0	0	0	0	
7	2-49	1	5	4	I3	0	0	0	0	0	0	
7	2-49	1	5	4	I4	0	0	0	0	0	0	
7	2-49	1	5	4	P	0	0	0	0	0	0	
7	2-49	1	5	5	I1	0	0	0	0	0	0	
7	2-49	1	5	5	I2	0	0	0	0	0	0	
7	2-49	1	5	5	I3	0	0	0	0	0	0	
7	2-49	1	5	5	I4	0	0	0	0	0	0	
7	2-49	1	5	5	P	0	0	0	0	0	0	
7	2-49	2	1	1	I1	2	4	1	1	1	1	
7	2-49	2	1	1	I2	1	4	4	0	0	0	
7	2-49	2	1	1	I3	0	0	0	0	0	0	

7	2-49	2	1	1	I4	0	0	0	0	0	0	
7	2-49	2	1	1	I5	0	0	0	0	0	0	
7	2-49	2	1	1	I6	0	0	0	0	0	0	
7	2-49	2	1	1	P	0	0	0	0	0	0	
7	2-49	2	1	2	I1	2	4	1	1	1	1	
7	2-49	2	1	2	I2	1	5	3	2	0	0	
7	2-49	2	1	2	I3	0	0	0	0	0	0	
7	2-49	2	1	2	I4	0	0	0	0	0	0	
7	2-49	2	1	2	I5	0	0	0	0	0	0	
7	2-49	2	1	2	I6	0	0	0	0	0	0	
7	2-49	2	1	2	P	0	0	0	0	0	0	
7	2-49	2	1	3	I1	1	6	2	2	1	1	
7	2-49	2	1	3	I2	0	3	3	0	0	0	
7	2-49	2	1	3	I3	0	0	0	0	0	0	
7	2-49	2	1	3	I4	0	0	0	0	0	0	
7	2-49	2	1	3	I5	0	0	0	0	0	0	
7	2-49	2	1	3	P	0	0	0	0	0	0	
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7	2-49	2	1	4	I2	0	3	3	0	0	0	
7	2-49	2	1	4	I3	0	0	0	0	0	0	
7	2-49	2	1	4	I4	0	0	0	0	0	0	
7	2-49	2	1	4	I5	0	0	0	0	0	0	
7	2-49	2	1	4	P	0	0	0	0	0	0	
7	2-49	2	1	5	I1	1	2	2	0	0	0	
7	2-49	2	1	5	I2	0	0	0	0	0	0	
7	2-49	2	1	5	I3	0	0	0	0	0	0	
7	2-49	2	1	5	I4	0	0	0	0	0	0	
7	2-49	2	1	5	P	0	0	0	0	0	0	
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7	2-49	2	2	1	I2	0	1	1	0	0	0	
7	2-49	2	2	1	I3	0	0	0	0	0	0	
7	2-49	2	2	1	I4	0	0	0	0	0	0	
7	2-49	2	2	1	I5	0	0	0	0	0	0	
7	2-49	2	2	1	P	0	0	0	0	0	0	
7	2-49	2	2	2	I1	1	8	2	2	2	2	
7	2-49	2	2	2	I2	0	1	1	0	0	0	

7	2-49	2	2	2	I3	0	0	0	0	0	0	
7	2-49	2	2	2	I4	0	0	0	0	0	0	
7	2-49	2	2	2	I5	0	0	0	0	0	0	
7	2-49	2	2	2	P	0	0	0	0	0	0	
7	2-49	2	2	3	I1	1	7	4	3	0	0	
7	2-49	2	2	3	I2	0	0	0	0	0	0	
7	2-49	2	2	3	I3	0	0	0	0	0	0	
7	2-49	2	2	3	I4	0	0	0	0	0	0	
7	2-49	2	2	3	P	0	0	0	0	0	0	
7	2-49	2	2	4	I1	0	1	1	0	0	0	
7	2-49	2	2	4	I2	0	0	0	0	0	0	
7	2-49	2	2	4	I3	0	0	0	0	0	0	
7	2-49	2	2	4	I4	0	0	0	0	0	0	
7	2-49	2	2	4	P	0	0	0	0	0	0	
7	2-49	2	3	1	I1	4	4	1	1	1	1	
7	2-49	2	3	1	I2	1	4	3	1	0	0	
7	2-49	2	3	1	I3	0	0	0	0	0	0	
7	2-49	2	3	1	I4	0	0	0	0	0	0	
7	2-49	2	3	1	I5	0	0	0	0	0	0	
7	2-49	2	3	1	I6	0	0	0	0	0	0	
7	2-49	2	3	1	P	0	0	0	0	0	0	
7	2-49	2	3	2	I1	3	5	2	1	1	1	
7	2-49	2	3	2	I2	0	4	2	2	0	0	
7	2-49	2	3	2	I3	0	0	0	0	0	0	
7	2-49	2	3	2	I4	0	0	0	0	0	0	
7	2-49	2	3	2	I5	0	0	0	0	0	0	
7	2-49	2	3	2	P	0	0	0	0	0	0	
7	2-49	2	3	3	I1	0	0	0	0	0	0	
7	2-49	2	3	3	I2	0	0	0	0	0	0	
7	2-49	2	3	3	I3	0	0	0	0	0	0	
7	2-49	2	3	3	I4	0	0	0	0	0	0	
7	2-49	2	3	3	P	0	0	0	0	0	0	
7	2-49	2	3	4	I1	1	4	3	1	0	0	
7	2-49	2	3	4	I2	1	0	0	0	0	0	
7	2-49	2	3	4	I3	0	0	0	0	0	0	
7	2-49	2	3	4	I4	0	0	0	0	0	0	

7	2-49	2	3	4	P	0	0	0	0	0	0	
7	2-49	2	3	5	I1	0	0	0	0	0	0	
7	2-49	2	3	5	I2	0	0	0	0	0	0	
7	2-49	2	3	5	I3	0	0	0	0	0	0	
7	2-49	2	3	5	I4	0	0	0	0	0	0	
7	2-49	2	3	5	P	0	0	0	0	0	0	
7	2-49	2	4	1	I1	2	4	1	1	1	1	
7	2-49	2	4	1	I2	0	2	2	0	0	0	
7	2-49	2	4	1	I3	0	0	0	0	0	0	
7	2-49	2	4	1	I4	0	0	0	0	0	0	
7	2-49	2	4	1	I5	0	0	0	0	0	0	
7	2-49	2	4	1	P	0	0	0	0	0	0	
7	2-49	2	4	2	I1	2	8	3	1	2	2	
7	2-49	2	4	2	I2	0	0	0	0	0	0	
7	2-49	2	4	2	I3	0	0	0	0	0	0	
7	2-49	2	4	2	I4	0	0	0	0	0	0	
7	2-49	2	4	2	I5	0	0	0	0	0	0	
7	2-49	2	4	2	P	0	0	0	0	0	0	
7	2-49	2	4	3	I1	1	7	5	2	0	0	
7	2-49	2	4	3	I2	0	0	0	0	0	0	
7	2-49	2	4	3	I3	0	0	0	0	0	0	
7	2-49	2	4	3	I4	0	0	0	0	0	0	
7	2-49	2	4	3	P	0	0	0	0	0	0	
7	2-49	2	4	4	I1	1	4	1	1	1	1	
7	2-49	2	4	4	I2	1	0	0	0	0	0	
7	2-49	2	4	4	I3	0	0	0	0	0	0	
7	2-49	2	4	4	I4	0	0	0	0	0	0	
7	2-49	2	4	4	I5	0	0	0	0	0	0	
7	2-49	2	4	4	P	0	0	0	0	0	0	
7	2-49	2	4	5	I1	1	4	1	1	1	1	
7	2-49	2	4	5	I2	1	0	0	0	0	0	
7	2-49	2	4	5	I3	0	0	0	0	0	0	
7	2-49	2	4	5	I4	0	0	0	0	0	0	
7	2-49	2	4	5	P	0	0	0	0	0	0	
7	2-49	2	5	1	I1	2	4	1	1	1	1	
7	2-49	2	5	1	I2	0	0	0	0	0	0	

7	2-49	2	5	1	I3	0	0	0	0	0	0	
7	2-49	2	5	1	I4	0	0	0	0	0	0	
7	2-49	2	5	1	I5	0	0	0	0	0	0	
7	2-49	2	5	1	I6	0	0	0	0	0	0	
7	2-49	2	5	1	P	0	0	0	0	0	0	
7	2-49	2	5	2	I1	1	4	1	1	1	1	
7	2-49	2	5	2	I2	0	10	5	3	1	1	
7	2-49	2	5	2	I3	0	1	1	0	0	0	
7	2-49	2	5	2	I4	0	0	0	0	0	0	
7	2-49	2	5	2	I5	0	0	0	0	0	0	
7	2-49	2	5	2	I6	0	0	0	0	0	0	
7	2-49	2	5	2	P	0	0	0	0	0	0	
7	2-49	2	5	3	I1	3	7	2	2	1.5	1.5	
7	2-49	2	5	3	I2	1	2	2	0	0	0	
7	2-49	2	5	3	I3	0	0	0	0	0	0	
7	2-49	2	5	3	I4	0	0	0	0	0	0	
7	2-49	2	5	3	I5	0	0	0	0	0	0	
7	2-49	2	5	3	I6	0	0	0	0	0	0	
7	2-49	2	5	3	P	0	0	0	0	0	0	
7	2-49	2	5	4	I1	1	3	3	0	0	0	
7	2-49	2	5	4	I2	0	0	0	0	0	0	
7	2-49	2	5	4	I3	0	0	0	0	0	0	
7	2-49	2	5	4	I4	0	0	0	0	0	0	
7	2-49	2	5	4	I5	0	0	0	0	0	0	
7	2-49	2	5	4	P	0	0	0	0	0	0	
7	2-49	2	5	5	I1	1	4	3	1	0	0	
7	2-49	2	5	5	I2	0	0	0	0	0	0	
7	2-49	2	5	5	I3	0	0	0	0	0	0	
7	2-49	2	5	5	I4	0	0	0	0	0	0	
7	2-49	2	5	5	I5	0	0	0	0	0	0	
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7	2-49	3	1	1	I1	2						
7	2-49	3	1	1	I2	0						
7	2-49	3	1	1	I3	0						
7	2-49	3	1	1	I4	0						
7	2-49	3	1	1	I5	0						

7	2-49	3	1	1	P	0						
7	2-49	3	1	2	I1	1						
7	2-49	3	1	2	I2	0						
7	2-49	3	1	2	I3	0						
7	2-49	3	1	2	I4	0						
7	2-49	3	1	2	I5	0						
7	2-49	3	1	2	P	0						
7	2-49	3	1	3	I1	1						
7	2-49	3	1	3	I2	0						
7	2-49	3	1	3	I3	0						
7	2-49	3	1	3	I4	0						
7	2-49	3	1	3	I5	0						
7	2-49	3	1	3	P	0						
7	2-49	3	1	4	I1	1						
7	2-49	3	1	4	I2	0						
7	2-49	3	1	4	I3	0						
7	2-49	3	1	4	I4	0						
7	2-49	3	1	4	I5	0						
7	2-49	3	1	4	P	0						
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7	2-49	3	1	5	I2	0						
7	2-49	3	1	5	I3	0						
7	2-49	3	1	5	I4	0						
7	2-49	3	1	5	P	0						
7	2-49	3	2	1	I1	3						
7	2-49	3	2	1	I2	1						
7	2-49	3	2	1	I3	0						
7	2-49	3	2	1	I4	0						
7	2-49	3	2	1	I5	0						
7	2-49	3	2	1	P	0						
7	2-49	3	2	2	I1	2						
7	2-49	3	2	2	I2	0						
7	2-49	3	2	2	I3	0						
7	2-49	3	2	2	I4	0						
7	2-49	3	2	2	I5	0						
7	2-49	3	2	2	P	0						

7	2-49	3	2	3	I1	1						
7	2-49	3	2	3	I2	0						
7	2-49	3	2	3	I3	0						
7	2-49	3	2	3	I4	0						
7	2-49	3	2	3	I5	0						
7	2-49	3	2	3	P	0						
7	2-49	3	2	4	I1	0						
7	2-49	3	2	4	I2	0						
7	2-49	3	2	4	I3	0						
7	2-49	3	2	4	I4	0						
7	2-49	3	2	4	I5	0						
7	2-49	3	2	4	P	0						
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7	2-49	3	2	5	P	0						
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7	2-49	3	3	1	I2	0						
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7	2-49	3	3	1	I4	0						
7	2-49	3	3	1	I5	0						
7	2-49	3	3	1	I6	0						
7	2-49	3	3	1	P	0						
7	2-49	3	3	2	I1	3						
7	2-49	3	3	2	I2	0						
7	2-49	3	3	2	I3	0						
7	2-49	3	3	2	I4	0						
7	2-49	3	3	2	I5	0						
7	2-49	3	3	2	I6	0						
7	2-49	3	3	2	P	0						
7	2-49	3	3	3	I1	3						
7	2-49	3	3	3	I2	0						
7	2-49	3	3	3	I3	0						
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7	2-49	3	3	3	I5	0						

7	2-49	3	3	3	I6	0						
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7	2-49	3	3	4	I2	0						
7	2-49	3	3	4	I3	0						
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7	2-49	3	3	4	I5	0						
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7	2-49	3	3	5	I3	0						
7	2-49	3	3	5	I4	0						
7	2-49	3	3	5	I5	0						
7	2-49	3	3	5	P	0						
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7	2-49	3	4	1	I3	0						
7	2-49	3	4	1	I4	0						
7	2-49	3	4	1	I5	0						
7	2-49	3	4	1	P	0						
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7	2-49	3	4	2	I2	1						
7	2-49	3	4	2	I3	0						
7	2-49	3	4	2	I4	0						
7	2-49	3	4	2	I5	0						
7	2-49	3	4	2	P	0						
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7	2-49	3	4	3	I2	0						
7	2-49	3	4	3	I3	0						
7	2-49	3	4	3	I4	0						
7	2-49	3	4	3	I5	0						
7	2-49	3	4	3	P	0						
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7	2-49	3	4	4	I2	0						
7	2-49	3	4	4	I3	0						
7	2-49	3	4	4	I4	0						

7	2-49	3	4	4	P	0						
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7	2-49	3	4	5	I2	0						
7	2-49	3	4	5	I3	0						
7	2-49	3	4	5	I4	0						
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7	2-49	3	5	1	I2	0						
7	2-49	3	5	1	I3	0						
7	2-49	3	5	1	I4	0						
7	2-49	3	5	1	I5	0						
7	2-49	3	5	1	P	0						
7	2-49	3	5	2	I1	1						
7	2-49	3	5	2	I2	0						
7	2-49	3	5	2	I3	0						
7	2-49	3	5	2	I4	0						
7	2-49	3	5	2	I5	0						
7	2-49	3	5	2	P	0						
7	2-49	3	5	3	I1	1						
7	2-49	3	5	3	I2	0						
7	2-49	3	5	3	I3	0						
7	2-49	3	5	3	I4	0						
7	2-49	3	5	3	I5	0						
7	2-49	3	5	3	P	0						
7	2-49	3	5	4	I1	1						
7	2-49	3	5	4	I2	0						
7	2-49	3	5	4	I3	0						
7	2-49	3	5	4	I4	0						
7	2-49	3	5	4	I5	0						
7	2-49	3	5	4	P	0						
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7	Sunco	1	1	1	I2	1	5	3	2	0	0	
7	Sunco	1	1	1	I3	0	0	0	0	0	0	
7	Sunco	1	1	1	I4	0	0	0	0	0	0	
7	Sunco	1	1	1	I5	0	0	0	0	0	0	
7	Sunco	1	1	1	P	0	0	0	0	0	0	

7	Sunco	1	1	2	I1	2	4	1	1	1	1	
7	Sunco	1	1	2	I2	0	4	2	2	0	0	
7	Sunco	1	1	2	I3	0	0	0	0	0	0	
7	Sunco	1	1	2	I4	0	0	0	0	0	0	
7	Sunco	1	1	2	I5	0	0	0	0	0	0	
7	Sunco	1	1	2	P	0	0	0	0	0	0	
7	Sunco	1	1	3	I1	2	4	1	1	1	1	
7	Sunco	1	1	3	I2	0	5	3	2	0	0	
7	Sunco	1	1	3	I3	0	0	0	0	0	0	
7	Sunco	1	1	3	I4	0	0	0	0	0	0	
7	Sunco	1	1	3	I5	0	0	0	0	0	0	
7	Sunco	1	1	3	P	0	0	0	0	0	0	
7	Sunco	1	1	4	I1	2	4	1	1	1	1	
7	Sunco	1	1	4	I2	0	3	2	1	0	0	
7	Sunco	1	1	4	I3	0	0	0	0	0	0	
7	Sunco	1	1	4	I4	0	0	0	0	0	0	
7	Sunco	1	1	4	I5	0	0	0	0	0	0	
7	Sunco	1	1	4	P	0	0	0	0	0	0	
7	Sunco	1	1	5	I1	3	4	1	1	1	1	
7	Sunco	1	1	5	I2	1	1	1	0	0	0	
7	Sunco	1	1	5	I3	0	0	0	0	0	0	
7	Sunco	1	1	5	I4	0	0	0	0	0	0	
7	Sunco	1	1	5	I5	0	0	0	0	0	0	
7	Sunco	1	1	5	P	0	0	0	0	0	0	
7	Sunco	1	2	1	I1	4	5	1	1	1	2	
7	Sunco	1	2	1	I2	2	6	2	2	1	1	
7	Sunco	1	2	1	I3	1	3	3	0	0	0	
7	Sunco	1	2	1	I4	0	0	0	0	0	0	
7	Sunco	1	2	1	I5	0	0	0	0	0	0	
7	Sunco	1	2	1	I6	0	0	0	0	0	0	
7	Sunco	1	2	1	P	0	0	0	0	0	0	
7	Sunco	1	2	2	I1	4	4	1	1	1	1	
7	Sunco	1	2	2	I2	1	3	3	0	0	0	
7	Sunco	1	2	2	I3	0	0	0	0	0	0	
7	Sunco	1	2	2	I4	0	0	0	0	0	0	
7	Sunco	1	2	2	I5	0	0	0	0	0	0	

7	Sunco	1	2	2	P	0	0	0	0	0	0	
7	Sunco	1	2	3	I1	4	4	1	1	1	1	
7	Sunco	1	2	3	I2	4	12	2	3	3	4	
7	Sunco	1	2	3	I3	3	4	3	1	0	0	
7	Sunco	1	2	3	I4	1	0	0	0	0	0	
7	Sunco	1	2	3	I5	0	0	0	0	0	0	
7	Sunco	1	2	3	I6	0	0	0	0	0	0	
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7	Sunco	1	2	4	I2	3	4	1	1	1	1	
7	Sunco	1	2	4	I3	1	3	0	0	0	3	
7	Sunco	1	2	4	I4	0	4	4	0	0	0	
7	Sunco	1	2	4	I5	0	0	0	0	0	0	
7	Sunco	1	2	4	I6	0	0	0	0	0	0	
7	Sunco	1	2	4	P	0	0	0	0	0	0	
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7	Sunco	1	2	5	I3	0	0	0	0	0	0	
7	Sunco	1	2	5	I4	0	0	0	0	0	0	
7	Sunco	1	2	5	I5	0	0	0	0	0	0	
7	Sunco	1	2	5	I6	0	0	0	0	0	0	
7	Sunco	1	2	5	P	0	0	0	0	0	0	
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7	Sunco	1	3	1	I2	1	3	2	1	0	0	
7	Sunco	1	3	1	I3	0	0	0	0	0	0	
7	Sunco	1	3	1	I4	0	0	0	0	0	0	
7	Sunco	1	3	1	I5	0	0	0	0	0	0	
7	Sunco	1	3	1	I6	0	0	0	0	0	0	
7	Sunco	1	3	1	P	0	0	0	0	0	0	
7	Sunco	1	3	2	I1	4	4	1	1	1	1	
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7	Sunco	1	3	2	I3	3	2	2	0	0	0	
7	Sunco	1	3	2	I4	1	0	0	0	0	0	
7	Sunco	1	3	2	I5	1	0	0	0	0	0	
7	Sunco	1	3	2	I6	0	0	0	0	0	0	
7	Sunco	1	3	2	P	0	0	0	0	0	0	

7	Sunco	1	3	3	I1	4	8	2	2	2	2	
7	Sunco	1	3	3	I2	3	10	3	1	3	3	
7	Sunco	1	3	3	I3	2	4	4	0	0	0	
7	Sunco	1	3	3	I4	1	0	0	0	0	0	
7	Sunco	1	3	3	I5	0	0	0	0	0	0	
7	Sunco	1	3	3	P	0	0	0	0	0	0	
7	Sunco	1	3	4	I1	4	5	1	1	1	2	
7	Sunco	1	3	4	I2	1	3	3	0	0	0	
7	Sunco	1	3	4	I3	0	0	0	0	0	0	
7	Sunco	1	3	4	I4	0	0	0	0	0	0	
7	Sunco	1	3	4	I5	0	0	0	0	0	0	
7	Sunco	1	3	4	P	0	0	0	0	0	0	
7	Sunco	1	3	5	I1	4	6	2	1	1	2	
7	Sunco	1	3	5	I2	2	9	3	2	2	2	
7	Sunco	1	3	5	I3	1	2	2	0	0	0	
7	Sunco	1	3	5	I4	1	0	0	0	0	0	
7	Sunco	1	3	5	I5	0	0	0	0	0	0	
7	Sunco	1	3	5	P	0	0	0	0	0	0	
7	Sunco	1	4	1	I1	4	4	1	1	1	1	
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7	Sunco	1	4	1	I3	0	0	0	0	0	0	
7	Sunco	1	4	1	I4	0	0	0	0	0	0	
7	Sunco	1	4	1	I5	0	0	0	0	0	0	
7	Sunco	1	4	1	P	0	0	0	0	0	0	
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7	Sunco	1	4	2	I3	0	0	0	0	0	0	
7	Sunco	1	4	2	I4	0	0	0	0	0	0	
7	Sunco	1	4	2	I5	0	0	0	0	0	0	
7	Sunco	1	4	2	P	0	0	0	0	0	0	
7	Sunco	1	4	3	I1	1	4	1	1	1	1	
7	Sunco	1	4	3	I2	0	0	0	0	0	0	
7	Sunco	1	4	3	I3	0	0	0	0	0	0	
7	Sunco	1	4	3	I4	0	0	0	0	0	0	
7	Sunco	1	4	3	I5	0	0	0	0	0	0	
7	Sunco	1	4	3	P	0	0	0	0	0	0	

7	Sunco	1	4	4	I1	4	4	1	1	1	1	
7	Sunco	1	4	4	I2	4	9	3	2	2	2	
7	Sunco	1	4	4	I3	4	3	3	0	0	0	
7	Sunco	1	4	4	I4	1	0	0	0	0	0	
7	Sunco	1	4	4	I5	0	0	0	0	0	0	
7	Sunco	1	4	4	P	0	0	0	0	0	0	
7	Sunco	1	4	5	I1	1	6	2	2	1	1	
7	Sunco	1	4	5	I2	1	0	0	0	0	0	
7	Sunco	1	4	5	I3	0	0	0	0	0	0	
7	Sunco	1	4	5	I4	0	0	0	0	0	0	
7	Sunco	1	4	5	P	0	0	0	0	0	0	
7	Sunco	1	5	1	I1	2	4	1	1	1	1	
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7	Sunco	1	5	1	I3	0	0	0	0	0	0	
7	Sunco	1	5	1	I4	0	0	0	0	0	0	
7	Sunco	1	5	1	I5	0	0	0	0	0	0	
7	Sunco	1	5	1	I6	0	0	0	0	0	0	
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7	Sunco	1	5	2	I1	2	4	1	1	1	1	
7	Sunco	1	5	2	I2	1	7	4	3	0	0	
7	Sunco	1	5	2	I3	0	0	0	0	0	0	
7	Sunco	1	5	2	I4	0	0	0	0	0	0	
7	Sunco	1	5	2	I5	0	0	0	0	0	0	
7	Sunco	1	5	2	P	0	0	0	0	0	0	
7	Sunco	1	5	3	I1	4	4	1	1	1	1	
7	Sunco	1	5	3	I2	4	8	2	2	2	2	
7	Sunco	1	5	3	I3	1	0	0	0	0	0	
7	Sunco	1	5	3	I4	0	0	0	0	0	0	
7	Sunco	1	5	3	I5	0	0	0	0	0	0	
7	Sunco	1	5	3	P	0	0	0	0	0	0	
7	Sunco	1	5	4	I1	4	4	1	1	1	1	
7	Sunco	1	5	4	I2	4	4	1	1	1	1	
7	Sunco	1	5	4	I3	2	10	3	3	3	1	
7	Sunco	1	5	4	I4	0	0	0	0	0	0	
7	Sunco	1	5	4	I5	0	0	0	0	0	0	
7	Sunco	2	1	1	I1	4	6	1.5	1.5	1.5	1.5	

7	Sunco	2	1	1	I2	1	6	1	2	2	1	
7	Sunco	2	1	1	I3	0	1	1	0	0	0	
7	Sunco	2	1	1	I4	0	0	0	0	0	0	
7	Sunco	2	1	1	I5	0	0	0	0	0	0	
7	Sunco	2	1	1	I6	0	0	0	0	0	0	
7	Sunco	2	1	1	P	0	0	0	0	0	0	
7	Sunco	2	1	2	I1	4	4	1	1	1	1	
7	Sunco	2	1	2	I2	1	7	2	2	2	1	
7	Sunco	2	1	2	I3	0	2	2	0	0	0	
7	Sunco	2	1	2	I4	0	0	0	0	0	0	
7	Sunco	2	1	2	I5	0	0	0	0	0	0	
7	Sunco	2	1	2	I6	0	0	0	0	0	0	
7	Sunco	2	1	2	P	0	0	0	0	0	0	
7	Sunco	2	1	3	I1	4	4	1	1	1	1	
7	Sunco	2	1	3	I2	3	4	1	1	1	1	
7	Sunco	2	1	3	I3	1	7	4	3	0	0	
7	Sunco	2	1	3	I4	0	0	0	0	0	0	
7	Sunco	2	1	3	I5	0	0	0	0	0	0	
7	Sunco	2	1	3	I6	0	0	0	0	0	0	
7	Sunco	2	1	3	P	0	0	0	0	0	0	
7	Sunco	2	1	4	I1	4	4	1	1	1	1	
7	Sunco	2	1	4	I2	0	8	4	4	0	0	
7	Sunco	2	1	4	I3	0	0	0	0	0	0	
7	Sunco	2	1	4	I4	0	0	0	0	0	0	
7	Sunco	2	1	4	I5	0	0	0	0	0	0	
7	Sunco	2	1	4	P	0	0	0	0	0	0	
7	Sunco	2	1	5	I1	4	4	1	1	1	1	
7	Sunco	2	1	5	I2	1	9	4	3	2	0	
7	Sunco	2	1	5	I3	0	0	0	0	0	0	
7	Sunco	2	1	5	I4	0	0	0	0	0	0	
7	Sunco	2	1	5	I5	0	0	0	0	0	0	
7	Sunco	2	1	5	P	0	0	0	0	0	0	
7	Sunco	2	2	1	I1	4	5	1	1	1	2	
7	Sunco	2	2	1	I2	1	6	2	1	2	1	
7	Sunco	2	2	1	I3	0	2	2	0	0	0	
7	Sunco	2	2	1	I4	0	0	0	0	0	0	

7	Sunco	2	2	1	I5	0	0	0	0	0	0	
7	Sunco	2	2	1	I6	0	0	0	0	0	0	
7	Sunco	2	2	1	P	0	0	0	0	0	0	
7	Sunco	2	2	2	I1	2	5	2	1	1	1	
7	Sunco	2	2	2	I2	1	4	1	1	1	1	
7	Sunco	2	2	2	I3	0	7	4	3	0	0	
7	Sunco	2	2	2	I4	0	0	0	0	0	0	
7	Sunco	2	2	2	I5	0	0	0	0	0	0	
7	Sunco	2	2	2	I6	0	0	0	0	0	0	
7	Sunco	2	2	2	P	0	0	0	0	0	0	
7	Sunco	2	2	3	I1	4	4	1	1	1	1	
7	Sunco	2	2	3	I2	4	5	2	1	1	1	
7	Sunco	2	2	3	I3	3	12	4	4	3	1	
7	Sunco	2	2	3	I4	0	0	0	0	0	0	
7	Sunco	2	2	3	I5	0	0	0	0	0	0	
7	Sunco	2	2	3	I6	0	0	0	0	0	0	
7	Sunco	2	2	3	P	0	0	0	0	0	0	
7	Sunco	2	2	4	I1	4	4	1	1	1	1	
7	Sunco	2	2	4	I2	2	11	4	3	3	1	
7	Sunco	2	2	4	I3	0	0	0	0	0	0	
7	Sunco	2	2	4	I4	0	0	0	0	0	0	
7	Sunco	2	2	4	I5	0	0	0	0	0	0	
7	Sunco	2	2	4	P	0	0	0	0	0	0	
7	Sunco	2	2	5	I1	2	8	2	2	2	2	
7	Sunco	2	2	5	I2	1	6	4	2	0	0	
7	Sunco	2	2	5	I3	0	0	0	0	0	0	
7	Sunco	2	2	5	I4	0	0	0	0	0	0	
7	Sunco	2	2	5	I5	0	0	0	0	0	0	
7	Sunco	2	2	5	P	0	0	0	0	0	0	
7	Sunco	2	3	1	I1	4	4	1	1	1	1	
7	Sunco	2	3	1	I2	1	6	2	1	1	2	
7	Sunco	2	3	1	I3	0	3	3	0	0	0	
7	Sunco	2	3	1	I4	0	0	0	0	0	0	
7	Sunco	2	3	1	I5	0	0	0	0	0	0	
7	Sunco	2	3	1	I6	0	0	0	0	0	0	
7	Sunco	2	3	1	P	0	0	0	0	0	0	

7	Sunco	2	3	2	I1	4	4	1	1	1	1	
7	Sunco	2	3	2	I2	1	7	2	1	2	2	
7	Sunco	2	3	2	I3	0	1	1	0	0	0	
7	Sunco	2	3	2	I4	0	0	0	0	0	0	
7	Sunco	2	3	2	I5	0	0	0	0	0	0	
7	Sunco	2	3	2	P	0	0	0	0	0	0	
7	Sunco	2	3	3	I1	4	4	1	1	1	1	
7	Sunco	2	3	3	I2	2	12	4	3	2	3	
7	Sunco	2	3	3	I3	0	0	0	0	0	0	
7	Sunco	2	3	3	I4	0	0	0	0	0	0	
7	Sunco	2	3	3	I5	0	0	0	0	0	0	
7	Sunco	2	3	3	P	0	0	0	0	0	0	
7	Sunco	2	3	4	I1	2	4	1	1	1	1	
7	Sunco	2	3	4	I2	1	5	4	1	0	0	
7	Sunco	2	3	4	I3	0	0	0	0	0	0	
7	Sunco	2	3	4	I4	0	0	0	0	0	0	
7	Sunco	2	3	4	I5	0	0	0	0	0	0	
7	Sunco	2	3	4	P	0	0	0	0	0	0	
7	Sunco	2	3	5	I1	1	0	0	0	0	0	
7	Sunco	2	3	5	I2	0	0	0	0	0	0	
7	Sunco	2	3	5	I3	0	0	0	0	0	0	
7	Sunco	2	3	5	I4	0	0	0	0	0	0	
7	Sunco	2	3	5	I5	0	0	0	0	0	0	
7	Sunco	2	3	5	P	0	0	0	0	0	0	
7	Sunco	2	4	1	I1	4	4	1	1	1	1	
7	Sunco	2	4	1	I2	4	5	1	1	1	2	
7	Sunco	2	4	1	I3	3	9	2	1	3	3	
7	Sunco	2	4	1	I4	1	15	5	4	3	3	
7	Sunco	2	4	1	I5	0	3	3	0	0	0	
7	Sunco	2	4	1	I6	0	0	0	0	0	0	
7	Sunco	2	4	1	P	0	0	0	0	0	0	
7	Sunco	2	4	2	I1	4	6	2	2	1	1	
7	Sunco	2	4	2	I2	4	8	3	2	1	2	
7	Sunco	2	4	2	I3	3	14	4	4	4	2	
7	Sunco	2	4	2	I4	1	8	6	2	0	0	
7	Sunco	2	4	2	I5	0	0	0	0	0	0	

7	Sunco	2	4	2	P	0	0	0	0	0	0	
7	Sunco	2	4	3	I1	4	7	2	2	2	1	
7	Sunco	2	4	3	I2	1	13	4	4	3	2	
7	Sunco	2	4	3	I3	0	0	0	0	0	0	
7	Sunco	2	4	3	I4	0	0	0	0	0	0	
7	Sunco	2	4	3	I5	0	0	0	0	0	0	
7	Sunco	2	4	3	P	0	0	0	0	0	0	
7	Sunco	2	4	4	I1	4	4	1	1	1	1	
7	Sunco	2	4	4	I2	1	7	3	2	0	2	
7	Sunco	2	4	4	I3	0	2	2	0	0	0	
7	Sunco	2	4	4	I4	0	0	0	0	0	0	
7	Sunco	2	4	4	I5	0	0	0	0	0	0	
7	Sunco	2	4	4	P	0	0	0	0	0	0	
7	Sunco	2	4	5	I1	2	8	2	2	2	2	
7	Sunco	2	4	5	I2	1	3	3	0	0	0	
7	Sunco	2	4	5	I3	0	0	0	0	0	0	
7	Sunco	2	4	5	I4	0	0	0	0	0	0	
7	Sunco	2	4	5	P	0	0	0	0	0	0	
7	Sunco	2	5	1	I1	4	4	1	1	1	1	
7	Sunco	2	5	1	I2	2	6	1.5	1.5	1.5	1.5	
7	Sunco	2	5	1	I3	0	3	3	0	0	0	
7	Sunco	2	5	1	I4	0	0	0	0	0	0	
7	Sunco	2	5	1	I5	0	0	0	0	0	0	
7	Sunco	2	5	1	I6	0	0	0	0	0	0	
7	Sunco	2	5	1	P	0	0	0	0	0	0	
7	Sunco	2	5	2	I1	4	4	1	1	1	1	
7	Sunco	2	5	2	I2	4	9	3	2	2	2	
7	Sunco	2	5	2	I3	2	13	4	2	2	5	
7	Sunco	2	5	2	I4	0	2	2	0	0	0	
7	Sunco	2	5	2	I5	0	0	0	0	0	0	
7	Sunco	2	5	2	I6	0	0	0	0	0	0	
7	Sunco	2	5	2	P	0	0	0	0	0	0	
7	Sunco	2	5	3	I1	4	4	1	1	1	1	
7	Sunco	2	5	3	I2	2	8	2	2	2	2	
7	Sunco	2	5	3	I3	1	11	5	3	2	1	
7	Sunco	2	5	3	I4	0	0	0	0	0	0	

7	Sunco	2	5	3	I5	0	0	0	0	0	0	
7	Sunco	2	5	3	I6	0	0	0	0	0	0	
7	Sunco	2	5	3	P	0	0	0	0	0	0	
7	Sunco	2	5	4	I1	4	5	2	1	1	1	
7	Sunco	2	5	4	I2	2	6	2	2	1	1	
7	Sunco	2	5	4	I3	0	3	3	0	0	0	
7	Sunco	2	5	4	I4	0	0	0	0	0	0	
7	Sunco	2	5	4	I5	0	0	0	0	0	0	
7	Sunco	2	5	4	I6	0	0	0	0	0	0	
7	Sunco	2	5	4	P	0	0	0	0	0	0	
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7	Sunco	2	5	5	I2	2	9	4	3	2	0	
7	Sunco	2	5	5	I3	0	0	0	0	0	0	
7	Sunco	2	5	5	I4	0	0	0	0	0	0	
7	Sunco	2	5	5	I5	0	0	0	0	0	0	
7	Sunco	2	5	5	P	0	0	0	0	0	0	
7	Sunco	3	1	1	I1	4						
7	Sunco	3	1	1	I2	1						
7	Sunco	3	1	1	I3	0						
7	Sunco	3	1	1	I4	0						
7	Sunco	3	1	1	I5	0						
7	Sunco	3	1	1	P	0						
7	Sunco	3	1	2	I1	4						
7	Sunco	3	1	2	I2	2						
7	Sunco	3	1	2	I3	1						
7	Sunco	3	1	2	I4	0						
7	Sunco	3	1	2	I5	0						
7	Sunco	3	1	2	P	0						
7	Sunco	3	1	3	I1	4						
7	Sunco	3	1	3	I2	3						
7	Sunco	3	1	3	I3	2						
7	Sunco	3	1	3	I4	0						
7	Sunco	3	1	3	I5	0						
7	Sunco	3	1	3	P	0						
7	Sunco	3	1	4	I1	4						
7	Sunco	3	1	4	I2	1						

7	Sunco	3	1	4	I3	0						
7	Sunco	3	1	4	I4	0						
7	Sunco	3	1	4	I5	0						
7	Sunco	3	1	4	P	0						
7	Sunco	3	1	5	I1	4						
7	Sunco	3	1	5	I2	1						
7	Sunco	3	1	5	I3	0						
7	Sunco	3	1	5	I4	0						
7	Sunco	3	1	5	I5	0						
7	Sunco	3	1	5	P	0						
7	Sunco	3	2	1	I1	4						
7	Sunco	3	2	1	I2	2						
7	Sunco	3	2	1	I3	1						
7	Sunco	3	2	1	I4	0						
7	Sunco	3	2	1	I5	0						
7	Sunco	3	2	1	I6	0						
7	Sunco	3	2	1	P	0						
7	Sunco	3	2	2	I1	2						
7	Sunco	3	2	2	I2	0						
7	Sunco	3	2	2	I3	0						
7	Sunco	3	2	2	I4	0						
7	Sunco	3	2	2	I5	0						
7	Sunco	3	2	2	I6	0						
7	Sunco	3	2	2	P	0						
7	Sunco	3	2	3	I1	4						
7	Sunco	3	2	3	I2	2						
7	Sunco	3	2	3	I3	0						
7	Sunco	3	2	3	I4	0						
7	Sunco	3	2	3	I5	0						
7	Sunco	3	2	3	I6	0						
7	Sunco	3	2	3	P	0						
7	Sunco	3	2	4	I1	4						
7	Sunco	3	2	4	I2	4						
7	Sunco	3	2	4	I3	3						
7	Sunco	3	2	4	I4	0						
7	Sunco	3	2	4	I5	0						

7	Sunco	3	2	4	P	0						
7	Sunco	3	2	5	I1	2						
7	Sunco	3	2	5	I2	1						
7	Sunco	3	2	5	I3	0						
7	Sunco	3	2	5	I4	0						
7	Sunco	3	2	5	I5	0						
7	Sunco	3	2	5	P	0						
7	Sunco	3	3	1	I1	4						
7	Sunco	3	3	1	I2	1						
7	Sunco	3	3	1	I3	0						
7	Sunco	3	3	1	I4	0						
7	Sunco	3	3	1	I5	0						
7	Sunco	3	3	1	I6	0						
7	Sunco	3	3	1	P	0						
7	Sunco	3	3	2	I1	3						
7	Sunco	3	3	2	I2	1						
7	Sunco	3	3	2	I3	0						
7	Sunco	3	3	2	I4	0						
7	Sunco	3	3	2	I5	0						
7	Sunco	3	3	2	I6	0						
7	Sunco	3	3	2	P	0						
7	Sunco	3	3	3	I1	2						
7	Sunco	3	3	3	I2	0						
7	Sunco	3	3	3	I3	0						
7	Sunco	3	3	3	I4	0						
7	Sunco	3	3	3	I5	0						
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7	Sunco	3	3	3	P	0						
7	Sunco	3	3	4	I1	4						
7	Sunco	3	3	4	I2	1						
7	Sunco	3	3	4	I3	0						
7	Sunco	3	3	4	I4	0						
7	Sunco	3	3	4	I5	0						
7	Sunco	3	3	4	I6	0						
7	Sunco	3	3	4	P	0						
7	Sunco	3	3	5	I1	1						

7	Sunco	3	3	5	I2	0						
7	Sunco	3	3	5	I3	0						
7	Sunco	3	3	5	I4	0						
7	Sunco	3	3	5	I5	0						
7	Sunco	3	3	5	P	0						
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7	Sunco	3	4	1	I2	1						
7	Sunco	3	4	1	I3	0						
7	Sunco	3	4	1	I4	0						
7	Sunco	3	4	1	I5	0						
7	Sunco	3	4	1	I6	0						
7	Sunco	3	4	1	P	0						
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7	Sunco	3	4	2	I2	0						
7	Sunco	3	4	2	I3	0						
7	Sunco	3	4	2	I4	0						
7	Sunco	3	4	2	I5	0						
7	Sunco	3	4	2	P	0						
7	Sunco	3	4	3	I1	4						
7	Sunco	3	4	3	I2	1						
7	Sunco	3	4	3	I3	0						
7	Sunco	3	4	3	I4	0						
7	Sunco	3	4	3	I5	0						
7	Sunco	3	4	3	P	0						
7	Sunco	3	4	4	I1	2						
7	Sunco	3	4	4	I2	0						
7	Sunco	3	4	4	I3	0						
7	Sunco	3	4	4	I4	0						
7	Sunco	3	4	4	I5	0						
7	Sunco	3	4	4	P	0						
7	Sunco	3	4	5	I1	1						
7	Sunco	3	4	5	I2	0						
7	Sunco	3	4	5	I3	0						
7	Sunco	3	4	5	I4	0						
7	Sunco	3	4	5	P	0						
7	Sunco	3	5	1	I1	4						

7	Sunco	3	5	1	I2	2						
7	Sunco	3	5	1	I3	1						
7	Sunco	3	5	1	I4	0						
7	Sunco	3	5	1	I5	0						
7	Sunco	3	5	1	P	0						
7	Sunco	3	5	2	I1	4						
7	Sunco	3	5	2	I2	1						
7	Sunco	3	5	2	I3	0						
7	Sunco	3	5	2	I4	0						
7	Sunco	3	5	2	I5	0						
7	Sunco	3	5	2	P	0						
7	Sunco	3	5	3	I1	4						
7	Sunco	3	5	3	I2	2						
7	Sunco	3	5	3	I3	1						
7	Sunco	3	5	3	I4	0						
7	Sunco	3	5	3	I5	0						
7	Sunco	3	5	3	P	0						
7	Sunco	3	5	4	I1	4						
7	Sunco	3	5	4	I2	2						
7	Sunco	3	5	4	I3	0						
7	Sunco	3	5	4	I4	0						
7	Sunco	3	5	4	I5	0						
7	Sunco	3	5	4	P	0						
7	Sunco	3	5	5	I1	4						
7	Sunco	3	5	5	I2	1						
7	Sunco	3	5	5	I3	0						
7	Sunco	3	5	5	I4	0						
7	Sunco	3	5	5	I5	0						
7	Sunco	3	5	5	P	0						
8	Puseas	1	1	1	I1	4	4	1	1	1	1	
8	Puseas	1	1	1	I2	4	6	1	2	1	2	
8	Puseas	1	1	1	I3	2	16	5	4	4	3	
8	Puseas	1	1	1	I4	0	3	3	0	0	0	
8	Puseas	1	1	1	I5	0	0	0	0	0	0	
8	Puseas	1	1	1	I6	0	0	0	0	0	0	
8	Puseas	1	1	1	P	0	0	0	0	0	0	

8	Puseas	1	1	2	I1	4	4	1	1	1	1	
8	Puseas	1	1	2	I2	4	8	2	2	2	2	
8	Puseas	1	1	2	I3	2	18	8	6	2	2	
8	Puseas	1	1	2	I4	0	2	2	0	0	0	
8	Puseas	1	1	2	I5	0	0	0	0	0	0	
8	Puseas	1	1	2	I6	0	0	0	0	0	0	
8	Puseas	1	1	3	I1	4	6	2	2	1	1	
8	Puseas	1	1	3	I2	4	10	2	3	3	2	
8	Puseas	1	1	3	I3	1	21	7	5	5	4	
8	Puseas	1	1	3	I4	1	7	7	0	0	0	
8	Puseas	1	1	3	I5	0	0	0	0	0	0	
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9	Puseas	3	1	5	I5	0						
8	Puseas	3	1	5	P	0						
8	Puseas	3	2	1	I1	4						
8	Puseas	3	2	1	I2	4						
8	Puseas	3	2	1	I3	3						
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8	Puseas	3	2	1	I5	0						
8	Puseas	3	2	1	I6	0						
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8	Puseas	3	2	2	I2	4						
8	Puseas	3	2	2	I3	2						
8	Puseas	3	2	2	I4	0						
8	Puseas	3	2	2	I5	0						
8	Puseas	3	2	2	I6	0						
8	Puseas	3	2	2	P	0						
8	Puseas	3	2	3	I1	4						
8	Puseas	3	2	3	I2	4						
8	Puseas	3	2	3	I3	3						
8	Puseas	3	2	3	I4	0						
8	Puseas	3	2	3	I5	0						
8	Puseas	3	2	3	I6	0						

8	Puseas	3	2	3	P	0						
8	Puseas	3	2	4	I1	4						
8	Puseas	3	2	4	I2	4						
8	Puseas	3	2	4	I3	2						
8	Puseas	3	2	4	I4	0						
8	Puseas	3	2	4	I5	0						
9	Puseas	3	2	4	I6	0						
8	Puseas	3	2	4	P	0						
8	Puseas	3	2	5	I1	4						
8	Puseas	3	2	5	I2	4						
8	Puseas	3	2	5	I3	1						
8	Puseas	3	2	5	I4	0						
9	Puseas	3	2	5	I5	0						
8	Puseas	3	2	5	P	0						
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8	Puseas	3	3	1	I2	4						
8	Puseas	3	3	1	I3	4						
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8	Puseas	3	3	1	I5	1						
8	Puseas	3	3	1	I6	0						
8	Puseas	3	3	1	P	0						
8	Puseas	3	3	2	I1	4						
8	Puseas	3	3	2	I2	4						
8	Puseas	3	3	2	I3	4						
8	Puseas	3	3	2	I4	3						
8	Puseas	3	3	2	I5	1						
8	Puseas	3	3	2	I6	0						
8	Puseas	3	3	2	P	0						
8	Puseas	3	3	3	I1	4						
8	Puseas	3	3	3	I2	4						
8	Puseas	3	3	3	I3	4						
8	Puseas	3	3	3	I4	2						
8	Puseas	3	3	3	I5	0						
8	Puseas	3	3	3	I6	0						
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8	Puseas	3	3	4	I2	4						
8	Puseas	3	3	4	I3	3						
8	Puseas	3	4	1	I1	4						
8	Puseas	3	4	1	I2	4						
8	Puseas	3	4	1	I3	4						
8	Puseas	3	4	1	I4	2						
8	Puseas	3	4	1	I5	0						
8	Puseas	3	4	1	P	0						
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8	Puseas	3	4	2	I2	4						
8	Puseas	3	4	2	I3	4						
8	Puseas	3	4	2	I4	1						
8	Puseas	3	4	2	I5	0						
8	Puseas	3	4	2	P	0						
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8	Puseas	3	4	3	I2	4						
8	Puseas	3	4	3	I3	2						
8	Puseas	3	4	3	I4	1						
8	Puseas	3	4	3	I5	0						
8	Puseas	3	4	3	P	0						
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8	Puseas	3	4	4	I2	2						
8	Puseas	3	4	4	I3	0						
8	Puseas	3	4	4	I4	0						
8	Puseas	3	4	4	I5	0						
8	Puseas	3	4	4	P	0						
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8	Puseas	3	4	5	I2	1						
8	Puseas	3	4	5	I3	0						
8	Puseas	3	4	5	I4	0						
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8	Puseas	3	5	1	I1	4						
8	Puseas	3	5	1	I2	4						
8	Puseas	3	5	1	I3	4						
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8	Puseas	3	5	1	I5	0						

8	Puseas	3	5	1	P	0						
8	Puseas	3	5	2	I1	4						
8	Puseas	3	5	2	I2	4						
8	Puseas	3	5	2	I3	4						
8	Puseas	3	5	2	I4	2						
8	Puseas	3	5	2	I5	0						
8	Puseas	3	5	2	P	0						
8	Puseas	3	5	3	I1	4						
8	Puseas	3	5	3	I2	4						
8	Puseas	3	5	3	I3	1						
8	Puseas	3	5	3	I4	0						
8	Puseas	3	5	3	I5	0						
8	Puseas	3	5	3	P	0						
8	Puseas	3	5	4	I1	4						
8	Puseas	3	5	4	I2	4						
8	Puseas	3	5	4	I3	0						
8	Puseas	3	5	4	I4	0						
8	Puseas	3	5	4	I5	0						
8	Puseas	3	5	4	P	0						
8	Puseas	3	5	5	I1	4						
8	Puseas	3	5	5	I2	4						
8	Puseas	3	5	5	I3	0						
8	Puseas	3	5	5	I4	0						
8	Puseas	3	5	5	I5	0						
8	Puseas	3	5	5	P	0						
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8	Vasco	1	1	1	I2	4	6	2	1	1	2	
8	Vasco	1	1	1	I3	1	9	5	2	0	2	
8	Vasco	1	1	1	I4	0	0	0	0	0	0	
8	Vasco	1	1	1	I5	0	0	0	0	0	0	
8	Vasco	1	1	1	I6	0	0	0	0	0	0	
8	Vasco	1	1	1	P	0	0	0	0	0	0	
8	Vasco	1	1	2	I1	4	4	1	1	1	1	
8	Vasco	1	1	2	I2	4	6	2	1	1	2	
8	Vasco	1	1	2	I3	1	15	5	3	3	4	
8	Vasco	1	1	2	I4	1	4	4	0	0	0	

8	Vasco	1	1	2	I5	0	0	0	0	0	0	
8	Vasco	1	1	2	P	0	0	0	0	0	0	
8	Vasco	1	1	3	I1	4	4	1	1	1	1	
8	Vasco	1	1	3	I2	3	9	3	2	2	2	
8	Vasco	1	1	3	I3	0	0	0	0	0	0	
8	Vasco	1	1	3	I4	0	0	0	0	0	0	
8	Vasco	1	1	3	I5	0	0	0	0	0	0	
8	Vasco	1	1	3	P	0	0	0	0	0	0	
8	Vasco	1	2	1	I1	4	4	1	1	1	1	
8	Vasco	1	2	1	I2	1	6	2	2	1	1	
8	Vasco	1	2	1	I3	0	2	2	0	0	0	
8	Vasco	1	2	1	I4	0	0	0	0	0	0	
8	Vasco	1	2	1	I5	0	0	0	0	0	0	
8	Vasco	1	2	1	P	0	0	0	0	0	0	
8	Vasco	1	2	2	I1	4	4	1	1	1	1	
8	Vasco	1	2	2	I2	1	12	3	3	3	3	
8	Vasco	1	2	2	I3	0	1	1	0	0	0	
8	Vasco	1	2	2	I4	0	0	0	0	0	0	
8	Vasco	1	2	2	I5	0	0	0	0	0	0	
8	Vasco	1	2	2	P	0	0	0	0	0	0	
8	Vasco	1	2	3	I1	4	4	1	1	1	1	
8	Vasco	1	2	3	I2	4	4	1	1	1	1	
8	Vasco	1	2	3	I3	4	12	3	3	3	3	
8	Vasco	1	2	3	I4	4	13	4	4	2	3	
8	Vasco	1	2	3	I5	4	19	6	5	4	4	
8	Vasco	1	2	3	P	1	20	8	8	4	0	
8	Vasco	1	3	1	I1	4	4	1	1	1	1	
8	Vasco	1	3	1	I2	4	4	1	1	1	1	
8	Vasco	1	3	1	I3	1	6	5	1	0	0	
8	Vasco	1	3	1	I4	0	0	0	0	0	0	
8	Vasco	1	3	1	I5	0	0	0	0	0	0	
8	Vasco	1	3	1	I6	0	0	0	0	0	0	
8	Vasco	1	3	1	P	0	0	0	0	0	0	
8	Vasco	1	3	2	I1	4	4	1	1	1	1	
8	Vasco	1	3	2	I2	2	6	2	1	1	2	
8	Vasco	1	3	2	I3	1	8	5	3	0	0	

8	Vasco	1	3	2	I4	0	0	0	0	0	0	
8	Vasco	1	3	2	I5	0	0	0	0	0	0	
8	Vasco	1	3	2	I6	0	0	0	0	0	0	
8	Vasco	1	3	2	P	0	0	0	0	0	0	
8	Vasco	1	3	3	I1	4	4	1	1	1	1	
8	Vasco	1	3	3	I2	2	6	2	2	1	1	
8	Vasco	1	3	3	I3	1	9	7	2	0	0	
8	Vasco	1	3	3	I4	0	0	0	0	0	0	
8	Vasco	1	3	3	I5	0	0	0	0	0	0	
8	Vasco	1	3	3	I6	0	0	0	0	0	0	
8	Vasco	1	3	3	P	0	0	0	0	0	0	
8	Vasco	1	3	4	I1	4	4	1	1	1	1	
8	Vasco	1	3	4	I2	2	8	3	2	2	1	
8	Vasco	1	3	4	I3	1	8	6	2	0	0	
8	Vasco	1	3	4	I4	0	0	0	0	0	0	
8	Vasco	1	3	4	I5	0	0	0	0	0	0	
8	Vasco	1	3	4	P	0	0	0	0	0	0	
8	Vasco	1	4	1	I1	4	4	1	1	1	1	
8	Vasco	1	4	1	I2	4	6	2	1	1	2	
8	Vasco	1	4	1	I3	3	12	3	3	2	4	
8	Vasco	1	4	1	I4	1	4	4	0	0	0	
8	Vasco	1	4	1	I5	0	0	0	0	0	0	
8	Vasco	1	4	1	P	0	0	0	0	0	0	
8	Vasco	1	4	2	I1	4	4	1	1	1	1	
8	Vasco	1	4	2	I2	4	6	2	1	1	2	
8	Vasco	1	4	2	I3	1	4	3	1	0	0	
8	Vasco	1	4	2	I4	0	0	0	0	0	0	
8	Vasco	1	4	2	I5	0	0	0	0	0	0	
8	Vasco	1	4	2	P	0	0	0	0	0	0	
8	Vasco	1	4	3	I1	4	4	1	1	1	1	
8	Vasco	1	4	3	I2	4	6	1	1	1	3	
8	Vasco	1	4	3	I3	3	12	4	4	2	2	
8	Vasco	1	4	3	I4	2	2	2	0	0	0	
8	Vasco	1	4	3	I5	0	0	0	0	0	0	
9	Vasco	1	4	3	I6	0	0	0	0	0	0	
8	Vasco	1	4	3	P	0	0	0	0	0	0	

8	Vasco	1	4	4	I1	4	4	1	1	1	1	
8	Vasco	1	4	4	I2	4	6	1	2	2	1	
8	Vasco	1	4	4	I3	3	12	4	3	3	2	
8	Vasco	1	4	4	I4	1	0	0	0	0	0	
8	Vasco	1	4	4	I5	0	0	0	0	0	0	
8	Vasco	1	4	4	P	0	0	0	0	0	0	
8	Vasco	1	4	5	I1	4	6	2	1	1	2	
8	Vasco	1	4	5	I2	1	7	3	1	1	2	
8	Vasco	1	4	5	I3	1	3	3	0	0	0	
8	Vasco	1	4	5	I4	0	0	0	0	0	0	
8	Vasco	1	4	5	I5	0	0	0	0	0	0	
8	Vasco	1	5	1	I1	4	4	1	1	1	1	
8	Vasco	1	5	1	I2	4	4	1	1	1	1	
8	Vasco	1	5	1	I3	3	8	3	2	1	2	
8	Vasco	1	5	1	I4	0	4	1	3	0	0	
8	Vasco	1	5	1	I5	0	0	0	0	0	0	
8	Vasco	1	5	1	I6	0	0	0	0	0	0	
8	Vasco	1	5	1	P	0	0	0	0	0	0	
8	Vasco	1	5	2	I1	4	4	1	1	1	1	
8	Vasco	1	5	2	I2	4	6	1	1.5	1.5	2	
8	Vasco	1	5	2	I3	4	14	5	4	1	4	
8	Vasco	1	5	2	I4	1	1	1	0	0	0	
8	Vasco	1	5	2	I5	0	0	0	0	0	0	
8	Vasco	1	5	2	I6	0	0	0	0	0	0	
8	Vasco	1	5	2	P	0	0	0	0	0	0	
8	Vasco	1	5	3	I1	4	4	1	1	1	1	
8	Vasco	1	5	3	I2	4	4	1	1	1	1	
8	Vasco	1	5	3	I3	2	9	3	2	2	2	
8	Vasco	1	5	3	I4	0	1	1	0	0	0	
8	Vasco	1	5	3	I5	0	0	0	0	0	0	
8	Vasco	1	5	3	I6	0	0	0	0	0	0	
8	Vasco	1	5	3	P	0	0	0	0	0	0	
8	Vasco	1	5	4	I1	4	4	1	1	1	1	
8	Vasco	1	5	4	I2	1	9	2	3	2	2	
8	Vasco	1	5	4	I3	1	4	4	0	0	0	
8	Vasco	1	5	4	I4	0	0	0	0	0	0	

8	Vasco	1	5	4	I5	0	0	0	0	0	0	
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8	Vasco	2	1	1	I1	4	4	1	1	1	1	
8	Vasco	2	1	1	I2	3	9	2	3	2	2	
8	Vasco	2	1	1	I3	1	4	1	1	1	1	
8	Vasco	2	1	1	I4	0	0	0	0	0	0	
8	Vasco	2	1	1	I5	0	0	0	0	0	0	
8	Vasco	2	1	1	P	0	0	0	0	0	0	
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8	Vasco	2	1	2	I2	2	15	4	4	4	3	
8	Vasco	2	1	2	I3	1	6	3	2	1	0	
8	Vasco	2	1	2	I4	0	0	0	0	0	0	
8	Vasco	2	1	2	I5	0	0	0	0	0	0	
8	Vasco	2	1	2	P	0	0	0	0	0	0	
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8	Vasco	2	1	3	I2	3	10	3	1	2	4	
8	Vasco	2	1	3	I3	1	9	2	2	2	3	
8	Vasco	2	1	3	I4	0	0	0	0	0	0	
8	Vasco	2	1	3	I5	0	0	0	0	0	0	
8	Vasco	2	1	3	P	0	0	0	0	0	0	
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8	Vasco	2	2	1	I5	0	3	3	0	0	0	
8	Vasco	2	2	1	I6	0	0	0	0	0	0	
8	Vasco	2	2	1	P	0	0	0	0	0	0	
8	Vasco	2	2	2	I1	4	4	1	1	1	1	
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8	Vasco	2	2	2	I5	0	0	0	0	0	0	
8	Vasco	2	2	2	I6	0	0	0	0	0	0	
8	Vasco	2	2	2	P	0	0	0	0	0	0	
8	Vasco	2	2	3	I1	4	4	1	1	1	1	
8	Vasco	2	2	3	I2	2	9	3	3	0	3	

8	Vasco	2	2	3	I3	1	9	3	2	1	3	
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8	Vasco	2	2	3	I5	0	0	0	0	0	0	
8	Vasco	2	2	3	P	0	0	0	0	0	0	
8	Vasco	2	3	1	I1	4	4	1	1	1	1	
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8	Vasco	2	3	1	I3	1	12	4	4	1	3	
8	Vasco	2	3	1	I4	1	3	3	0	0	0	
8	Vasco	2	3	1	I5	0	0	0	0	0	0	
8	Vasco	2	3	1	I6	0	0	0	0	0	0	
8	Vasco	2	3	1	P	0	0	0	0	0	0	
8	Vasco	2	3	2	I1	4	8	2	2	2	2	
8	Vasco	2	3	2	I2	4	8	2	2	2	2	
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8	Vasco	2	3	2	I4	1	0	0	0	0	0	
8	Vasco	2	3	2	I5	0	0	0	0	0	0	
8	Vasco	2	3	2	I6	0	0	0	0	0	0	
8	Vasco	2	3	2	P	0	0	0	0	0	0	
8	Vasco	2	3	3	I1	4	6	2	1	1	2	
8	Vasco	2	3	3	I2	4	12	4	3	2	3	
8	Vasco	2	3	3	I3	3	13	5	4	3	1	
8	Vasco	2	3	3	I4	1	11	7	4	0	0	
8	Vasco	2	3	3	I5	0	0	0	0	0	0	
8	Vasco	2	3	3	P	0	0	0	0	0	0	
8	Vasco	2	3	4	I1	4	8	2	2	2	2	
8	Vasco	2	3	4	I2	4	12	3	3	3	3	
8	Vasco	2	3	4	I3	2	8	3	1	1	3	
8	Vasco	2	3	4	I4	0	24	7	7	6	4	
8	Vasco	2	3	4	I5	0	0	0	0	0	0	
8	Vasco	2	3	4	P	0	0	0	0	0	0	
8	Vasco	2	3	5	I1	4	8	2	2	2	2	
8	Vasco	2	3	5	I2	4	9	3	2	2	2	
8	Vasco	2	3	5	I3	4	19	6	5	4	4	
8	Vasco	2	3	5	I4	4	19	6	6	5	2	
8	Vasco	2	3	5	I5	1	0	0	0	0	0	
8	Vasco	2	3	5	P	0	0	0	0	0	0	

8	Vasco	2	4	1	I1	4	4	1	1	1	1	
8	Vasco	2	4	1	I2	4	4	1	1	1	1	
8	Vasco	2	4	1	I3	1	14	5	4	2	3	
8	Vasco	2	4	1	I4	0	2	2	0	0	0	
8	Vasco	2	4	1	I5	0	0	0	0	0	0	
8	Vasco	2	4	1	I6	0	0	0	0	0	0	
8	Vasco	2	4	1	P	0	0	0	0	0	0	
8	Vasco	2	4	2	I1	4	4	1	1	1	1	
8	Vasco	2	4	2	I2	4	8	2	2	2	2	
8	Vasco	2	4	2	I3	1	11	4	3	2	2	
8	Vasco	2	4	2	I4	0	2	2	0	0	0	
8	Vasco	2	4	2	I5	0	0	0	0	0	0	
8	Vasco	2	4	2	I6	0	0	0	0	0	0	
8	Vasco	2	4	2	P	0	0	0	0	0	0	
8	Vasco	2	4	3	I1	4	4	1	1	1	1	
8	Vasco	2	4	3	I2	3	7	2	2	2	1	
8	Vasco	2	4	3	I3	0	3	3	0	0	0	
8	Vasco	2	4	3	I4	0	0	0	0	0	0	
8	Vasco	2	4	3	I5	0	0	0	0	0	0	
8	Vasco	2	4	3	I6	0	0	0	0	0	0	
8	Vasco	2	4	3	P	0	0	0	0	0	0	
8	Vasco	2	4	4	I1	4	4	1	1	1	1	
8	Vasco	2	4	4	I2	4	8	2	2	2	2	
8	Vasco	2	4	4	I3	2	13	4	4	2	3	
8	Vasco	2	4	4	I4	0	1	1	0	0	0	
8	Vasco	2	4	4	I5	0	0	0	0	0	0	
8	Vasco	2	4	4	P	0	0	0	0	0	0	
8	Vasco	2	5	1	I1	4	4	1	1	1	1	
8	Vasco	2	5	1	I2	4	5	1	1.5	1.5	1	
8	Vasco	2	5	1	I3	4	15	5	4	4	2	
8	Vasco	2	5	1	I4	3	19	7	4	4	4	
8	Vasco	2	5	1	I5	1	1	1	0	0	0	
8	Vasco	2	5	1	I6	0	0	0	0	0	0	
8	Vasco	2	5	1	P	0	0	0	0	0	0	
8	Vasco	2	5	2	I1	4	4	1	1	1	1	
8	Vasco	2	5	2	I2	4	8	2	2	2	2	

8	Vasco	2	5	2	I3	4	11	4	2	2	3	
8	Vasco	2	5	2	I4	3	15	4	3	5	3	
8	Vasco	2	5	2	I5	1	3	3	0	0	0	
8	Vasco	2	5	2	I6	0	0	0	0	0	0	
8	Vasco	2	5	2	P	0	0	0	0	0	0	
8	Vasco	2	5	3	I1	4	4	1	1	1	1	
8	Vasco	2	5	3	I2	4	8	2	2	2	2	
8	Vasco	2	5	3	I3	2	17	5	4	4	4	
8	Vasco	2	5	3	I4	0	1	1	0	0	0	
8	Vasco	2	5	3	I5	0	0	0	0	0	0	
8	Vasco	2	5	3	P	0	0	0	0	0	0	
8	Vasco	2	5	4	I1	4	4	1	1	1	1	
8	Vasco	2	5	4	I2	4	8	2	2	2	2	
8	Vasco	2	5	4	I3	3	14	4	3	4	3	
8	Vasco	2	5	4	I4	1	4	2	1	1	0	
8	Vasco	2	5	4	I5	0	0	0	0	0	0	
8	Vasco	2	5	4	P	0	0	0	0	0	0	
8	Vasco	2	5	5	I1	4	7	2	1	2	2	
8	Vasco	2	5	5	I2	4	12	3	3	3	3	
8	Vasco	2	5	5	I3	3	13	3	4	2	4	
8	Vasco	2	5	5	I4	1	1	1	0	0	0	
8	Vasco	2	5	5	I5	0	0	0	0	0	0	
8	Vasco	2	5	5	P	0	0	0	0	0	0	
8	Vasco	3	1	1	I1	4						
8	Vasco	3	1	1	I2	4						
8	Vasco	3	1	1	I3	4						
8	Vasco	3	1	1	I4	1						
8	Vasco	3	1	1	I5	0						
8	Vasco	3	1	1	P	0						
8	Vasco	3	1	2	I1	4						
8	Vasco	3	1	2	I2	4						
8	Vasco	3	1	2	I3	4						
8	Vasco	3	1	2	I4	1						
8	Vasco	3	1	2	I5	0						
8	Vasco	3	1	2	P	0						
8	Vasco	3	1	3	I1	4						

8	Vasco	3	1	3	I2	4						
8	Vasco	3	1	3	I3	2						
8	Vasco	3	1	3	I4	1						
8	Vasco	3	1	3	I5	0						
8	Vasco	3	1	3	P	0						
8	Vasco	3	1	4	I1	4						
8	Vasco	3	1	4	I2	4						
8	Vasco	3	1	4	I3	3						
8	Vasco	3	1	4	I4	1						
8	Vasco	3	1	4	I5	0						
8	Vasco	3	1	4	P	0						
8	Vasco	3	2	1	I1	4						
8	Vasco	3	2	1	I2	2						
8	Vasco	3	2	1	I3	1						
8	Vasco	3	2	1	I4	0						
8	Vasco	3	2	1	I5	0						
8	Vasco	3	2	1	I6	0						
8	Vasco	3	2	1	P	0						
8	Vasco	3	2	2	I1	4						
8	Vasco	3	2	2	I2	1						
8	Vasco	3	2	2	I3	0						
8	Vasco	3	2	2	I4	0						
8	Vasco	3	2	2	I5	0						
8	Vasco	3	2	2	I6	0						
8	Vasco	3	2	2	P	0						
8	Vasco	3	2	3	I1	4						
8	Vasco	3	2	3	I2	1						
8	Vasco	3	2	3	I3	0						
8	Vasco	3	2	3	I4	0						
8	Vasco	3	2	3	I5	0						
8	Vasco	3	2	3	P	0						
8	Vasco	3	2	4	I1	4						
8	Vasco	3	2	4	I2	1						
8	Vasco	3	2	4	I3	0						
8	Vasco	3	2	4	I4	0						
8	Vasco	3	2	4	I5	0						

8	Vasco	3	2	4	P	0						
8	Vasco	3	2	5	I1	4						
8	Vasco	3	2	5	I2	1						
8	Vasco	3	2	5	I3	0						
8	Vasco	3	2	5	I4	0						
8	Vasco	3	2	5	I5	0						
8	Vasco	3	2	5	P	0						
8	Vasco	3	3	1	I1	4						
8	Vasco	3	3	1	I2	3						
8	Vasco	3	3	1	I3	0						
8	Vasco	3	3	1	I4	0						
8	Vasco	3	3	1	I5	0						
8	Vasco	3	3	1	P	0						
8	Vasco	3	3	2	I1	4						
8	Vasco	3	3	2	I2	4						
8	Vasco	3	3	2	I3	1						
8	Vasco	3	3	2	I4	0						
8	Vasco	3	3	2	I5	0						
8	Vasco	3	3	2	P	0						
8	Vasco	3	3	3	I1	4						
8	Vasco	3	3	3	I2	3						
8	Vasco	3	3	3	I3	2						
8	Vasco	3	3	3	I4	1						
8	Vasco	3	3	3	I5	0						
8	Vasco	3	3	3	P	0						
8	Vasco	3	4	1	I1	4						
8	Vasco	3	4	1	I2	4						
8	Vasco	3	4	1	I3	1						
8	Vasco	3	4	1	I4	0						
8	Vasco	3	4	1	I5	0						
8	Vasco	3	4	1	I6	0						
8	Vasco	3	4	1	P	0						
8	Vasco	3	4	2	I1	4						
8	Vasco	3	4	2	I2	2						
8	Vasco	3	4	2	I3	2						
8	Vasco	3	4	2	I4	1						

8	Vasco	3	4	2	I5	0						
8	Vasco	3	4	2	I6	0						
8	Vasco	3	4	2	P	0						
8	Vasco	3	4	3	I1	4						
8	Vasco	3	4	3	I2	2						
8	Vasco	3	4	3	I3	1						
8	Vasco	3	4	3	I4	0						
8	Vasco	3	4	3	I5	0						
8	Vasco	3	4	3	I6	0						
8	Vasco	3	4	3	P	0						
8	Vasco	3	4	4	I1	4						
8	Vasco	3	4	4	I2	4						
8	Vasco	3	4	4	I3	1						
8	Vasco	3	4	4	I4	0						
8	Vasco	3	4	5	I1	4						
8	Vasco	3	4	5	I2	2						
8	Vasco	3	4	5	I3	0						
8	Vasco	3	4	5	I4	0						
8	Vasco	3	5	1	I1	4						
8	Vasco	3	5	1	I2	4						
8	Vasco	3	5	1	I3	2						
8	Vasco	3	5	1	I4	1						
8	Vasco	3	5	1	I5	0						
8	Vasco	3	5	1	I6	0						
8	Vasco	3	5	1	P	0						
8	Vasco	3	5	2	I1	4						
8	Vasco	3	5	2	I2	4						
8	Vasco	3	5	2	I3	3						
8	Vasco	3	5	2	I4	0						
8	Vasco	3	5	2	I5	0						
8	Vasco	3	5	2	I6	0						
8	Vasco	3	5	2	P	0						
8	Vasco	3	5	3	I1	4						
8	Vasco	3	5	3	I2	4						
8	Vasco	3	5	3	I3	3						
8	Vasco	3	5	3	I4	0						

8	Vasco	3	5	3	I5	0						
8	Vasco	3	5	3	P	0						
8	Vasco	3	5	4	I1	4						
8	Vasco	3	5	4	I2	2						
8	Vasco	3	5	4	I3	1						
8	Vasco	3	5	4	I4	0						
8	2-49	1	1	1	I1	4	4	1	1	1	1	
8	2-49	1	1	1	I2	2	7	2	2	1	2	
8	2-49	1	1	1	I3	0	13	7	3	3	0	
8	2-49	1	1	1	I4	0	0	0	0	0	0	
8	2-49	1	1	1	I5	0	0	0	0	0	0	
8	2-49	1	1	1	I6	0	0	0	0	0	0	
8	2-49	1	1	1	P	0	0	0	0	0	0	
8	2-49	1	1	2	I1	4	4	1	1	1	1	
8	2-49	1	1	2	I2	4	4	1	1	1	1	
8	2-49	1	1	2	I3	1	13	7	3	2	1	
8	2-49	1	1	2	I4	0	6	1	3	2	0	
8	2-49	1	1	2	I5	0	0	0	0	0	0	
8	2-49	1	1	2	I6	0	0	0	0	0	0	
8	2-49	1	1	2	P	0	0	0	0	0	0	
8	2-49	1	1	3	I1	4	4	1	1	1	1	
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8	2-49	1	1	3	I3	1	3	3	0	0	0	
8	2-49	1	1	3	I4	0	0	0	0	0	0	
8	2-49	1	1	3	I5	0	0	0	0	0	0	
8	2-49	1	1	3	I6	0	0	0	0	0	0	
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8	2-49	1	1	4	I3	0	0	0	0	0	0	
8	2-49	1	1	4	I4	0	0	0	0	0	0	
8	2-49	1	1	4	I5	0	0	0	0	0	0	
8	2-49	1	1	4	I6	0	0	0	0	0	0	
8	2-49	1	1	4	P	0	0	0	0	0	0	
8	2-49	1	1	5	I1	4	4	1	1	1	1	
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8	2-49	1	1	5	I3	0	0	0	0	0	0	
8	2-49	1	1	5	I4	0	0	0	0	0	0	
8	2-49	1	1	5	I5	0	0	0	0	0	0	
8	2-49	1	1	5	P	0	0	0	0	0	0	
8	2-49	1	2	1	I1	4	4	1	1	1	1	
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8	2-49	1	2	1	I3	1	6	5	1	0	0	
8	2-49	1	2	1	I4	0	0	0	0	0	0	
8	2-49	1	2	1	I5	0	0	0	0	0	0	
8	2-49	1	2	1	I6	0	0	0	0	0	0	
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8	2-49	1	2	2	I4	0	0	0	0	0	0	
8	2-49	1	2	2	I5	0	0	0	0	0	0	
8	2-49	1	2	2	I6	0	0	0	0	0	0	
8	2-49	1	2	2	P	0	0	0	0	0	0	
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8	2-49	1	2	3	I4	0	0	0	0	0	0	
8	2-49	1	2	3	I5	0	0	0	0	0	0	
8	2-49	1	2	3	P	0	0	0	0	0	0	
8	2-49	1	2	4	I1	4	4	1	1	1	1	
8	2-49	1	2	4	I2	1	4	4	0	0	0	
8	2-49	1	2	4	I3	0	0	0	0	0	0	
8	2-49	1	2	4	I4	0	0	0	0	0	0	
8	2-49	1	2	4	I5	0	0	0	0	0	0	
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8	2-49	1	2	5	I3	0	0	0	0	0	0	
8	2-49	1	2	5	I4	0	0	0	0	0	0	
8	2-49	1	2	5	I5	0	0	0	0	0	0	
8	2-49	1	2	5	P	0	0	0	0	0	0	

8	2-49	1	3	1	I1	4	4	1	1	1	1	
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8	2-49	1	3	1	I3	0	2	2	0	0	0	
8	2-49	1	3	1	I4	0	0	0	0	0	0	
8	2-49	1	3	1	I5	0	0	0	0	0	0	
8	2-49	1	3	1	P	0	0	0	0	0	0	
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8	2-49	1	3	2	I3	0	8	2	3	3	0	
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8	2-49	1	3	2	I5	0	0	0	0	0	0	
8	2-49	1	3	2	P	0	0	0	0	0	0	
8	2-49	1	3	3	I1	4	4	1	1	1	1	
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8	2-49	1	3	3	I3	0	12	2	3	6	1	
8	2-49	1	3	3	I4	0	0	0	0	0	0	
8	2-49	1	3	3	I5	0	0	0	0	0	0	
8	2-49	1	3	3	P	0	0	0	0	0	0	
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8	2-49	1	3	4	I5	0	0	0	0	0	0	
8	2-49	1	3	4	P	0	0	0	0	0	0	
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8	2-49	1	4	3	I3	0	0	0	0	0	0	
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8	2-49	1	4	3	I5	0	0	0	0	0	0	
8	2-49	1	4	3	P	0	0	0	0	0	0	
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8	2-49	1	4	4	I2	1	8	5	3	0	0	
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8	2-49	1	4	4	I4	0	0	0	0	0	0	
8	2-49	1	4	4	I5	0	0	0	0	0	0	
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8	2-49	1	4	5	I5	0	0	0	0	0	0	
8	2-49	1	4	5	P	0	0	0	0	0	0	
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8	2-49	1	5	1	I3	0	5	4	1	0	0	
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8	2-49	1	5	1	I5	0	0	0	0	0	0	
8	2-49	1	5	1	I6	0	0	0	0	0	0	
8	2-49	1	5	1	P	0	0	0	0	0	0	
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8	2-49	1	5	2	I3	0	3	3	0	0	0	
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8	2-49	1	5	2	I5	0	0	0	0	0	0	
8	2-49	1	5	2	P	0	0	0	0	0	0	
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8	2-49	1	5	3	I3	0	1	1	0	0	0	
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8	2-49	1	5	3	I5	0	0	0	0	0	0	
8	2-49	1	5	3	P	0	0	0	0	0	0	
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8	2-49	1	5	4	I3	0	7	7	0	0	0	
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8	2-49	1	5	4	I5	0	0	0	0	0	0	
8	2-49	1	5	4	P	0	0	0	0	0	0	
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8	2-49	1	5	5	I4	0	0	0	0	0	0	
8	2-49	1	5	5	I5	0	0	0	0	0	0	
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8	2-49	2	1	1	I2	2	15	4	4	3	4	
8	2-49	2	1	1	I3	0	6	3	0	0	3	
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8	2-49	2	1	3	I4	0	0	0	0	0	0	
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8	2-49	2	1	4	I2	0	4	4	0	0	0	
8	2-49	2	1	4	I3	0	0	0	0	0	0	
8	2-49	2	1	4	I4	0	0	0	0	0	0	

8	2-49	2	1	4	I5	0	0	0	0	0	0	
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8	2-49	2	1	5	I4	0	0	0	0	0	0	
8	2-49	2	1	5	I5	0	0	0	0	0	0	
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8	2-49	2	2	1	I4	0	0	0	0	0	0	
8	2-49	2	2	1	I5	0	0	0	0	0	0	
8	2-49	2	2	1	I6	0	0	0	0	0	0	
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8	2-49	2	2	2	I3	0	3	3	0	0	0	
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8	2-49	2	2	2	I5	0	0	0	0	0	0	
8	2-49	2	2	2	I6	0	0	0	0	0	0	
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8	2-49	2	2	3	I5	0	0	0	0	0	0	
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8	2-49	2	4	3	I5	0	0	0	0	0	0	
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8	2-49	2	4	4	I4	0	0	0	0	0	0	
8	2-49	2	4	4	I5	0	0	0	0	0	0	
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8	2-49	3	1	1	P	0						
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8	2-49	3	1	2	I3	0						
8	2-49	3	1	2	I4	0						
8	2-49	3	1	2	I5	0						
8	2-49	3	1	2	P	0						
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8	2-49	3	1	3	I3	0						
8	2-49	3	1	3	I4	0						
8	2-49	3	1	3	I5	0						
8	2-49	3	1	3	P	0						
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8	2-49	3	1	4	I2	1						

8	2-49	3	1	4	I3	0						
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8	2-49	3	5	3	I2	1						
8	2-49	3	5	3	I3	0						
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8	2-49	3	5	3	I5	0						
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8	2-49	3	5	4	I4	0						
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8	Sunco	1	1	1	I2	1	4	1	1	1	1	
8	Sunco	1	1	1	I3	0	4	3	1	0	0	
8	Sunco	1	1	1	I4	0	0	0	0	0	0	
8	Sunco	1	1	1	I5	0	0	0	0	0	0	
8	Sunco	1	1	1	I6	0	0	0	0	0	0	
8	Sunco	1	1	1	P	0	0	0	0	0	0	
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8	Sunco	1	1	2	I3	0	4	4	0	0	0	
8	Sunco	1	1	2	I4	0	0	0	0	0	0	
8	Sunco	1	1	2	I5	0	0	0	0	0	0	
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8	Sunco	1	1	3	I1	4	4	1	1	1	1	
8	Sunco	1	1	3	I2	1	9	3	2	1	3	
8	Sunco	1	1	3	I3	0	0	0	0	0	0	
8	Sunco	1	1	3	I4	0	0	0	0	0	0	

8	Sunco	1	1	3	I5	0	0	0	0	0	0	
8	Sunco	1	1	3	P	0	0	0	0	0	0	
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8	Sunco	1	1	4	I3	0	0	0	0	0	0	
8	Sunco	1	1	4	I4	0	0	0	0	0	0	
8	Sunco	1	1	4	I5	0	0	0	0	0	0	
8	Sunco	1	1	4	P	0	0	0	0	0	0	
8	Sunco	1	1	5	I1	4	4	1	1	1	1	
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8	Sunco	1	1	5	I3	0	0	0	0	0	0	
8	Sunco	1	1	5	I4	0	0	0	0	0	0	
8	Sunco	1	2	1	I1	4	4	1	1	1	1	
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8	Sunco	1	2	2	I5	0	0	0	0	0	0	
8	Sunco	1	2	2	I6	0	0	0	0	0	0	
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8	Sunco	1	2	4	I4	0	0	0	0	0	0	
8	Sunco	1	2	4	I5	0	0	0	0	0	0	
8	Sunco	1	2	4	P	0	0	0	0	0	0	
8	Sunco	1	2	5	I1	4	4	1	1	1	1	

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8	Sunco	1	2	5	I3	0	0	0	0	0	0	
8	Sunco	1	2	5	I4	0	0	0	0	0	0	
8	Sunco	1	3	1	I1	4	4	1	1	1	1	
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8	Sunco	1	3	1	I4	0	2	2	0	0	0	
8	Sunco	1	3	1	I5	0	0	0	0	0	0	
8	Sunco	1	3	1	I6	0	0	0	0	0	0	
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8	Sunco	1	3	2	I4	1	0	0	0	0	0	
8	Sunco	1	3	2	I5	0	0	0	0	0	0	
8	Sunco	1	3	2	I6	0	0	0	0	0	0	
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8	Sunco	1	3	3	I3	0	0	0	0	0	0	
8	Sunco	1	3	3	I4	0	0	0	0	0	0	
8	Sunco	1	3	3	I5	0	0	0	0	0	0	
8	Sunco	1	3	3	P	0	0	0	0	0	0	
8	Sunco	1	3	4	I1	4	4	1	1	1	1	
8	Sunco	1	3	4	I2	1	0	0	0	0	0	
8	Sunco	1	3	4	I3	0	0	0	0	0	0	
8	Sunco	1	3	4	I4	0	0	0	0	0	0	
8	Sunco	1	3	4	I5	0	0	0	0	0	0	
8	Sunco	1	3	4	P	0	0	0	0	0	0	
8	Sunco	1	4	1	I1	4	4	1	1	1	1	
8	Sunco	1	4	1	I2	4	4	1	1	1	1	
8	Sunco	1	4	1	I3	1	14	4	4	4	2	
8	Sunco	1	4	1	I4	0	0	0	0	0	0	
8	Sunco	1	4	1	I5	0	0	0	0	0	0	
8	Sunco	1	4	1	I6	0	0	0	0	0	0	
8	Sunco	1	4	1	P	0	0	0	0	0	0	

8	Sunco	1	4	2	I1	4	4	1	1	1	1	
8	Sunco	1	4	2	I2	4	8	2	2	2	2	
8	Sunco	1	4	2	I3	4	19	5	5	4	5	
8	Sunco	1	4	2	I4	3	11	2	0	3	6	
8	Sunco	1	4	2	I5	0	3	3	0	0	0	
8	Sunco	1	4	2	I6	0	0	0	0	0	0	
8	Sunco	1	4	2	P	0	0	0	0	0	0	
8	Sunco	1	4	3	I1	4	8	2	2	2	2	
8	Sunco	1	4	3	I2	1	9	5	4	0	0	
8	Sunco	1	4	3	I3	0	0	0	0	0	0	
8	Sunco	1	4	3	I4	0	0	0	0	0	0	
8	Sunco	1	4	3	I5	0	0	0	0	0	0	
8	Sunco	1	4	3	P	0	0	0	0	0	0	
8	Sunco	1	4	4	I1	4	4	1	1	1	1	
8	Sunco	1	4	4	I2	3	10	3	2	2	3	
8	Sunco	1	4	4	I3	0	1	1	0	0	0	
8	Sunco	1	4	4	I4	0	0	0	0	0	0	
8	Sunco	1	4	5	I1	4	4	1	1	1	1	
8	Sunco	1	4	5	I2	2	14	5	4	3	2	
8	Sunco	1	4	5	I3	1	0	0	0	0	0	
8	Sunco	1	4	5	I4	0	0	0	0	0	0	
8	Sunco	1	5	1	I1	4	4	1	1	1	1	
8	Sunco	1	5	1	I2	4	8	3	1	3	1	
8	Sunco	1	5	1	I3	2	18	5	5	4	4	
8	Sunco	1	5	1	I4	1	13	5	2	3	3	
8	Sunco	1	5	1	I5	0	8	4	3	1	0	
8	Sunco	1	5	1	I6	0	0	0	0	0	0	
8	Sunco	1	5	1	P	0	0	0	0	0	0	
8	Sunco	1	5	2	I1	4	4	1	1	1	1	
8	Sunco	1	5	2	I2	4	9	3	2	2	2	
8	Sunco	1	5	2	I3	1	11	6	3	1	1	
8	Sunco	1	5	2	I4	0	8	5	3	0	0	
8	Sunco	1	5	2	I5	0	0	0	0	0	0	
8	Sunco	1	5	2	I6	0	0	0	0	0	0	
8	Sunco	1	5	2	P	0	0	0	0	0	0	
8	Sunco	1	5	3	I1	4	4	1	1	1	1	

8	Sunco	1	5	3	I2	4	2	0	0	1	1	
8	Sunco	1	5	3	I3	2	8	2	2	2	2	
8	Sunco	1	5	3	I4	0	6	4	1	1	0	
8	Sunco	1	5	3	I5	0	0	0	0	0	0	
8	Sunco	1	5	3	I6	0	0	0	0	0	0	
8	Sunco	1	5	3	P	0	0	0	0	0	0	
8	Sunco	1	5	4	I1	4	4	1	1	1	1	
8	Sunco	1	5	4	I2	4	8	2	2	2	2	
8	Sunco	1	5	4	I3	1	13	4	4	2	3	
8	Sunco	1	5	4	I4	0	0	0	0	0	0	
8	Sunco	1	5	4	I5	0	0	0	0	0	0	
8	Sunco	1	5	4	I6	0	0	0	0	0	0	
8	Sunco	1	5	4	P	0	0	0	0	0	0	
8	Sunco	1	5	5	I1	4	5	1	2	1	1	
8	Sunco	1	5	5	I2	4	11	3	3	2	3	
8	Sunco	1	5	5	I3	0	8	5	3	0	0	
8	Sunco	1	5	5	I4	0	0	0	0	0	0	
8	Sunco	1	5	5	I5	0	0	0	0	0	0	
8	Sunco	1	5	5	P	0	0	0	0	0	0	
8	Sunco	2	1	1	I1	4	4	1	1	1	1	
8	Sunco	2	1	1	I2	4	4	1	1	1	1	
8	Sunco	2	1	1	I3	1	9	3	2	2	2	
8	Sunco	2	1	1	I4	1	13	5	5	2	1	
8	Sunco	2	1	1	I5	0	0	0	0	0	0	
8	Sunco	2	1	1	I6	0	0	0	0	0	0	
8	Sunco	2	1	1	P	0	0	0	0	0	0	
8	Sunco	2	1	2	I1	4	3	0	1	1	1	
8	Sunco	2	1	2	I2	4	6	2	1	1	2	
8	Sunco	2	1	2	I3	1	10	4	3	1	2	
8	Sunco	2	1	2	I4	0	1	1	0	0	0	
8	Sunco	2	1	2	I5	0	0	0	0	0	0	
8	Sunco	2	1	2	I6	0	0	0	0	0	0	
8	Sunco	2	1	2	P	0	0	0	0	0	0	
8	Sunco	2	1	3	I1	4	4	1	1	1	1	
8	Sunco	2	1	3	I2	2	7	2	2	2	1	
8	Sunco	2	1	3	I3	0	4	4	0	0	0	

8	Sunco	2	1	3	I4	0	0	0	0	0	0	
8	Sunco	2	1	3	I5	0	0	0	0	0	0	
8	Sunco	2	1	3	I6	0	0	0	0	0	0	
8	Sunco	2	1	3	P	0	0	0	0	0	0	
8	Sunco	2	1	4	I1	4	4	1	1	1	1	
8	Sunco	2	1	4	I2	2	11	4	2	3	2	
8	Sunco	2	1	4	I3	0	0	0	0	0	0	
8	Sunco	2	1	4	I4	0	0	0	0	0	0	
8	Sunco	2	1	4	I5	0	0	0	0	0	0	
8	Sunco	2	1	4	P	0	0	0	0	0	0	
8	Sunco	2	1	5	I1	3	6	1.5	1.5	1.5	1.5	
8	Sunco	2	1	5	I2	1	6	3	2	1	0	
8	Sunco	2	1	5	I3	0	2	1	0	1	0	
8	Sunco	2	1	5	I4	0	0	0	0	0	0	
8	Sunco	2	1	5	I5	0	0	0	0	0	0	
8	Sunco	2	1	5	P	0	0	0	0	0	0	
8	Sunco	2	2	1	I1	4	4	1	1	1	1	
8	Sunco	2	2	1	I2	4	4	1	1	1	1	
8	Sunco	2	2	1	I3	3	8	2	2	2	2	
8	Sunco	2	2	1	I4	1	7	3	1	1	2	
8	Sunco	2	2	1	I5	0	0	0	0	0	0	
8	Sunco	2	2	1	I6	0	0	0	0	0	0	
8	Sunco	2	2	1	P	0	0	0	0	0	0	
8	Sunco	2	2	2	I1	4	4	1	1	1	1	
8	Sunco	2	2	2	I2	4	4	1	1	1	1	
8	Sunco	2	2	2	I3	1	9	3	2	1	3	
8	Sunco	2	2	2	I4	0	1	1	0	0	0	
8	Sunco	2	2	2	I5	0	0	0	0	0	0	
8	Sunco	2	2	2	I6	0	0	0	0	0	0	
8	Sunco	2	2	2	P	0	0	0	0	0	0	
8	Sunco	2	2	3	I1	4	4	1	1	1	1	
8	Sunco	2	2	3	I2	4	5	1	1	1	2	
8	Sunco	2	2	3	I3	1	4	3	1	0	0	
8	Sunco	2	2	3	I4	0	0	0	0	0	0	
8	Sunco	2	2	3	I5	0	0	0	0	0	0	
8	Sunco	2	2	3	I6	0	0	0	0	0	0	

8	Sunco	2	2	3	P	0	0	0	0	0	0	
8	Sunco	2	2	4	I1	3	4	1	1	1	1	
8	Sunco	2	2	4	I2	0	1	1	0	0	0	
8	Sunco	2	2	4	I3	0	0	0	0	0	0	
8	Sunco	2	2	4	I4	0	0	0	0	0	0	
8	Sunco	2	2	4	I5	0	0	0	0	0	0	
8	Sunco	2	2	4	P	0	0	0	0	0	0	
8	Sunco	2	2	5	I1	2	4	1	1	1	1	
8	Sunco	2	2	5	I2	0	1	1	0	0	0	
8	Sunco	2	2	5	I3	0	0	0	0	0	0	
8	Sunco	2	2	5	I4	0	0	0	0	0	0	
8	Sunco	2	3	1	I1	4	6	1.5	1.5	1.5	1.5	
8	Sunco	2	3	1	I2	3	6	1.5	1.5	1.5	1.5	
8	Sunco	2	3	1	I3	1	6	4	2	0	0	
8	Sunco	2	3	1	I4	0	0	0	0	0	0	
8	Sunco	2	3	1	I5	0	0	0	0	0	0	
8	Sunco	2	3	1	P	0	0	0	0	0	0	
8	Sunco	2	3	2	I1	4	4	1	1	1	1	
8	Sunco	2	3	2	I2	4	4	1	1	1	1	
8	Sunco	2	3	2	I3	1	11	3	3	2	3	
8	Sunco	2	3	2	I4	0	0	0	0	0	0	
8	Sunco	2	3	2	I5	0	0	0	0	0	0	
8	Sunco	2	3	2	I6	0	0	0	0	0	0	
8	Sunco	2	3	2	P	0	0	0	0	0	0	
8	Sunco	2	3	3	I1	3	4	1	1	1	1	
8	Sunco	2	3	3	I2	1	8	2	2	2	2	
8	Sunco	2	3	3	I3	0	0	0	0	0	0	
8	Sunco	2	3	3	I4	0	0	0	0	0	0	
8	Sunco	2	3	3	I5	0	0	0	0	0	0	
8	Sunco	2	3	3	P	0	0	0	0	0	0	
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8	Sunco	2	4	1	I3	0	0	0	0	0	0	
8	Sunco	2	4	1	I4	0	0	0	0	0	0	
8	Sunco	2	4	1	I5	0	0	0	0	0	0	
8	Sunco	2	4	1	P	0	0	0	0	0	0	

8	Sunco	2	4	2	I1	4	4	1	1	1	1	
8	Sunco	2	4	2	I2	1	11	3	3	2	3	
8	Sunco	2	4	2	I3	1	6	4	2	0	0	
8	Sunco	2	4	2	I4	0	0	0	0	0	0	
8	Sunco	2	4	2	I5	0	0	0	0	0	0	
8	Sunco	2	4	2	P	0	0	0	0	0	0	
8	Sunco	2	4	3	I1	4	4	1	1	1	1	
8	Sunco	2	4	3	I2	1	7	2	2	1	2	
8	Sunco	2	4	3	I3	0	3	3	0	0	0	
8	Sunco	2	4	3	I4	0	0	0	0	0	0	
8	Sunco	2	4	3	I5	0	0	0	0	0	0	
8	Sunco	2	4	3	P	0	0	0	0	0	0	
8	Sunco	2	4	4	I1	4	4	1	1	1	1	
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8	Sunco	2	4	4	I3	0	2	2	0	0	0	
8	Sunco	2	4	4	I4	0	0	0	0	0	0	
8	Sunco	2	4	4	I5	0	0	0	0	0	0	
8	Sunco	2	4	4	P	0	0	0	0	0	0	
8	Sunco	2	4	5	I1	4	4	1	1	1	1	
8	Sunco	2	4	5	I2	1	8	2	2	2	2	
8	Sunco	2	4	5	I3	1	11	6	5	0	0	
8	Sunco	2	4	5	I4	0	0	0	0	0	0	
8	Sunco	2	4	5	I5	0	0	0	0	0	0	
8	Sunco	2	4	5	P	0	0	0	0	0	0	
8	Sunco	2	5	1	I1	4	6	2	1	2	1	
8	Sunco	2	5	1	I2	1	9	3	2	1	3	
8	Sunco	2	5	1	I3	1	8	5	1	1	1	
8	Sunco	2	5	1	I4	0	0	0	0	0	0	
8	Sunco	2	5	1	I5	0	0	0	0	0	0	
8	Sunco	2	5	1	P	0	0	0	0	0	0	
8	Sunco	2	5	2	I1	4	4	1	1	1	1	
8	Sunco	2	5	2	I2	1	7	3	4	0	0	
8	Sunco	2	5	2	I3	0	0	0	0	0	0	
8	Sunco	2	5	2	I4	0	0	0	0	0	0	
8	Sunco	2	5	2	I5	0	0	0	0	0	0	
8	Sunco	2	5	2	P	0	0	0	0	0	0	

8	Sunco	2	5	3	I1	4	4	1	1	1	1	
8	Sunco	2	5	3	I2	1	8	2	2	2	2	
8	Sunco	2	5	3	I3	0	3	3	0	0	0	
8	Sunco	2	5	3	I4	0	0	0	0	0	0	
8	Sunco	2	5	3	I5	0	0	0	0	0	0	
8	Sunco	2	5	3	P	0	0	0	0	0	0	
8	Sunco	2	5	4	I1	4	4	1	1	1	1	
8	Sunco	2	5	4	I2	2	9	3	2	2	2	
8	Sunco	2	5	4	I3	0	4	4	0	0	0	
8	Sunco	2	5	4	I4	0	0	0	0	0	0	
8	Sunco	2	5	4	I5	0	0	0	0	0	0	
8	Sunco	2	5	4	P	0	0	0	0	0	0	
8	Sunco	2	5	5	I1	4	4	1	1	1	1	
8	Sunco	2	5	5	I2	1	12	3	3	3	3	
8	Sunco	2	5	5	I3	0	0	0	0	0	0	
8	Sunco	2	5	5	I4	0	0	0	0	0	0	
8	Sunco	2	5	5	I5	0	0	0	0	0	0	
8	Sunco	2	5	5	P	0	0	0	0	0	0	
8	Sunco	3	1	1	I1	4						
8	Sunco	3	1	1	I2	4						
8	Sunco	3	1	1	I3	2						
8	Sunco	3	1	1	I4	0						
8	Sunco	3	1	1	I5	0						
8	Sunco	3	1	1	P	0						
8	Sunco	3	1	2	I1	4						
8	Sunco	3	1	2	I2	4						
8	Sunco	3	1	2	I3	1						
8	Sunco	3	1	2	I4	0						
8	Sunco	3	1	2	I5	0						
8	Sunco	3	1	2	P	0						
8	Sunco	3	1	3	I1	4						
8	Sunco	3	1	3	I2	3						
8	Sunco	3	1	3	I3	0						
8	Sunco	3	1	3	I4	0						
8	Sunco	3	1	3	I5	0						
8	Sunco	3	1	3	P	0						

8	Sunco	3	1	4	I1	4						
8	Sunco	3	1	4	I2	1						
8	Sunco	3	1	4	I3	0						
8	Sunco	3	1	4	I4	0						
8	Sunco	3	1	4	I5	0						
8	Sunco	3	1	4	P	0						
8	Sunco	3	1	5	I1	4						
8	Sunco	3	1	5	I2	1						
8	Sunco	3	1	5	I3	0						
8	Sunco	3	1	5	I4	0						
8	Sunco	3	1	5	I5	0						
8	Sunco	3	1	5	P	0						
8	Sunco	3	2	1	I1	4						
8	Sunco	3	2	1	I2	3						
8	Sunco	3	2	1	I3	1						
8	Sunco	3	2	1	I4	0						
8	Sunco	3	2	1	I5	0						
8	Sunco	3	2	1	P	0						
8	Sunco	3	2	2	I1	4						
8	Sunco	3	2	2	I2	4						
8	Sunco	3	2	2	I3	1						
8	Sunco	3	2	2	I4	0						
8	Sunco	3	2	2	I5	0						
8	Sunco	3	2	2	P	0						
8	Sunco	3	2	3	I1	4						
8	Sunco	3	2	3	I2	2						
8	Sunco	3	2	3	I3	0						
8	Sunco	3	2	3	I4	0						
8	Sunco	3	2	3	I5	0						
8	Sunco	3	2	3	P	0						
8	Sunco	3	2	4	I1	4						
8	Sunco	3	2	4	I2	0						
8	Sunco	3	2	4	I3	0						
8	Sunco	3	2	4	I4	0						
8	Sunco	3	2	4	I5	0						
8	Sunco	3	2	4	P	0						

8	Sunco	3	2	5	I1	3						
8	Sunco	3	2	5	I2	0						
8	Sunco	3	2	5	I3	0						
8	Sunco	3	2	5	I4	0						
8	Sunco	3	2	5	I5	0						
8	Sunco	3	2	5	P	0						
8	Sunco	3	3	1	I1	4						
8	Sunco	3	3	1	I2	4						
8	Sunco	3	3	1	I3	3						
8	Sunco	3	3	1	I4	1						
8	Sunco	3	3	1	I5	0						
8	Sunco	3	3	1	I6	0						
8	Sunco	3	3	1	P	0						
8	Sunco	3	3	2	I1	4						
8	Sunco	3	3	2	I2	4						
8	Sunco	3	3	2	I3	2						
8	Sunco	3	3	2	I4	1						
8	Sunco	3	3	2	I5	0						
8	Sunco	3	3	2	I6	0						
8	Sunco	3	3	2	P	0						
8	Sunco	3	3	3	I1	4						
8	Sunco	3	3	3	I2	4						
8	Sunco	3	3	3	I3	1						
8	Sunco	3	3	3	I4	0						
8	Sunco	3	3	3	I5	0						
8	Sunco	3	3	3	I6	0						
8	Sunco	3	3	3	P	0						
8	Sunco	3	3	4	I1	4						
8	Sunco	3	3	4	I2	4						
8	Sunco	3	3	4	I3	1						
8	Sunco	3	3	4	I4	0						
8	Sunco	3	3	4	I5	0						
8	Sunco	3	3	4	I6	0						
8	Sunco	3	3	4	P	0						
8	Sunco	3	3	5	I1	4						
8	Sunco	3	3	5	I2	4						

8	Sunco	3	3	5	I3	0						
8	Sunco	3	3	5	I4	0						
8	Sunco	3	3	5	I5	0						
8	Sunco	3	3	5	P	0						
8	Sunco	3	4	1	I1	4						
8	Sunco	3	4	1	I2	4						
8	Sunco	3	4	1	I3	1						
8	Sunco	3	4	1	I4	0						
8	Sunco	3	4	1	I5	0						
8	Sunco	3	4	1	I6	0						
8	Sunco	3	4	1	P	0						
8	Sunco	3	4	2	I1	4						
8	Sunco	3	4	2	I2	4						
8	Sunco	3	4	2	I3	1						
8	Sunco	3	4	2	I4	0						
8	Sunco	3	4	2	I5	0						
8	Sunco	3	4	2	I6	0						
8	Sunco	3	4	2	P	0						
8	Sunco	3	4	3	I1	4						
8	Sunco	3	4	3	I2	1						
8	Sunco	3	4	3	I3	0						
8	Sunco	3	4	3	I4	0						
8	Sunco	3	4	3	I5	0						
8	Sunco	3	4	3	I6	0						
8	Sunco	3	4	3	P	0						
8	Sunco	3	4	4	I1	4						
8	Sunco	3	4	4	I2	1						
8	Sunco	3	4	4	I3	0						
8	Sunco	3	4	4	I4	0						
8	Sunco	3	5	1	I1	4						
8	Sunco	3	5	1	I2	1						
8	Sunco	3	5	1	I3	0						
8	Sunco	3	5	1	I4	0						
8	Sunco	3	5	1	I5	0						
8	Sunco	3	5	1	P	0						
8	Sunco	3	5	2	I1	4						

8	Sunco	3	5	2	I2	1						
8	Sunco	3	5	2	I3	0						
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8	Sunco	3	5	3	I3	0						
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8	Sunco	3	5	3	I5	0						
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8	Sunco	3	5	5	I2	1						
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9	Puseas	3	3	2	I2	4						
9	Puseas	3	3	2	I3	2						
9	Puseas	3	3	2	I4	0						
9	Puseas	3	3	2	I5	0						
9	Puseas	3	3	2	I6	0						
9	Puseas	3	3	2	P	0						
9	Puseas	3	3	3	I1	4						
9	Puseas	3	3	3	I2	4						
9	Puseas	3	3	3	I3	1						
9	Puseas	3	3	3	I4	0						
9	Puseas	3	3	3	I5	0						
9	Puseas	3	3	3	P	0						
9	Puseas	3	3	4	I1	4						
9	Puseas	3	3	4	I2	4						
9	Puseas	3	3	4	I3	1						
9	Puseas	3	3	4	I4	0						

9	Puseas	3	3	5	I1	4						
9	Puseas	3	3	5	I2	4						
9	Puseas	3	3	5	I3	2						
9	Puseas	3	3	5	I4	0						
9	Puseas	3	3	5	P	0						
9	Puseas	3	4	1	I1	4						
9	Puseas	3	4	1	I2	4						
9	Puseas	3	4	1	I3	4						
9	Puseas	3	4	1	I4	1						
9	Puseas	3	4	1	I5	0						
9	Puseas	3	4	1	I6	0						
9	Puseas	3	4	1	P	0						
9	Puseas	3	4	2	I1	4						
9	Puseas	3	4	2	I2	3						
9	Puseas	3	4	2	I3	1						
9	Puseas	3	4	2	I4	0						
9	Puseas	3	4	2	I5	0						
9	Puseas	3	4	2	I6	0						
9	Puseas	3	4	2	P	0						
9	Puseas	3	4	3	I1	4						
9	Puseas	3	4	3	I2	4						
9	Puseas	3	4	3	I3	1						
9	Puseas	3	4	3	I4	0						
9	Puseas	3	4	3	I5	0						
9	Puseas	3	4	3	P	0						
9	Puseas	3	4	4	I1	4						
9	Puseas	3	4	4	I2	4						
9	Puseas	3	4	4	I3	1						
9	Puseas	3	4	4	I4	0						
9	Puseas	3	4	4	I5	0						
9	Puseas	3	4	4	P	0						
9	Puseas	3	4	5	I1	4						
9	Puseas	3	4	5	I2	4						
9	Puseas	3	4	5	I3	1						
9	Puseas	3	4	5	I4	0						
9	Puseas	3	4	5	I5	0						

9	Puseas	3	4	5	P	0						
9	Puseas	3	5	1	I1	4						
9	Puseas	3	5	1	I2	4						
9	Puseas	3	5	1	I3	4						
9	Puseas	3	5	1	I4	3						
9	Puseas	3	5	1	I5	1						
9	Puseas	3	5	1	I6	0						
9	Puseas	3	5	1	P	0						
9	Puseas	3	5	2	I1	4						
9	Puseas	3	5	2	I2	4						
9	Puseas	3	5	2	I3	3						
9	Puseas	3	5	2	I4	2						
9	Puseas	3	5	2	I5	1						
9	Puseas	3	5	2	I6	0						
9	Puseas	3	5	2	P	0						
9	Puseas	3	5	3	I1	4						
9	Puseas	3	5	3	I2	4						
9	Puseas	3	5	3	I3	3						
9	Puseas	3	5	3	I4	1						
9	Puseas	3	5	3	I5	0						
9	Puseas	3	5	3	P	0						
9	Puseas	3	5	4	I1	4						
9	Puseas	3	5	4	I2	4						
9	Puseas	3	5	4	I3	4						
9	Puseas	3	5	4	I4	3						
9	Puseas	3	5	5	I1	4						
9	Puseas	3	5	5	I2	4						
9	Puseas	3	5	5	I3	4						
9	Puseas	3	5	5	I4	4						
9	Vasco	1	1	1	I1	4	4	1	1	1	1	
10	Vasco	1	1	1	I2	4	8	2	2	2	2	
9	Vasco	1	1	1	I3	4	17	4	5	4	4	
9	Vasco	1	1	1	I4	1	21	7	5	5	4	
9	Vasco	1	1	1	I5	1	26	8	6	6	6	
9	Vasco	1	1	1	I6	0	5	5	0	0	0	
9	Vasco	1	1	1	P	0	0	0	0	0	0	

9	Vasco	1	1	2	I1	4	4	1	1	1	1	
9	Vasco	1	1	2	I2	4	12	3	3	3	3	
9	Vasco	1	1	2	I3	3	19	5	5	5	4	
9	Vasco	1	1	2	I4	2	25	8	7	7	3	
9	Vasco	1	1	2	I5	1	0	0	0	0	0	
9	Vasco	1	1	2	P	0	0	0	0	0	0	
9	Vasco	1	1	3	I1	4	4	1	1	1	1	
9	Vasco	1	1	3	I2	4	8	2	2	2	2	
9	Vasco	1	1	3	I3	3	17	6	4	3	4	
9	Vasco	1	1	3	I4	1	3	3	0	0	0	
9	Vasco	1	1	3	I5	0	0	0	0	0	0	
9	Vasco	1	1	3	P	0	0	0	0	0	0	
9	Vasco	1	1	4	I1	4	4	1	1	1	1	
9	Vasco	1	1	4	I2	4	6	2	2	1	1	
9	Vasco	1	1	4	I3	3	13	4	4	3	2	
9	Vasco	1	1	4	I4	1	7	5	1	1	0	
9	Vasco	1	1	4	I5	0	3	3	0	0	0	
9	Vasco	1	1	4	P	0	0	0	0	0	0	
9	Vasco	1	1	5	I1	4	6	1.5	1.5	1.5	1.5	
9	Vasco	1	1	5	I2	4	11	3	2	3	3	
9	Vasco	1	1	5	I3	2	23	6	5	6	6	
9	Vasco	1	1	5	I4	1	1	1	0	0	0	
9	Vasco	1	1	5	I5	0	0	0	0	0	0	
9	Vasco	1	1	5	P	0	6	6	0	0	0	
9	Vasco	1	2	1	I1	4	8	2	2	2	2	
9	Vasco	1	2	1	I2	4	6	2	2	1	1	
9	Vasco	1	2	1	I3	4	10	3	2	2	3	
9	Vasco	1	2	1	I4	4	13	3	4	2	4	
9	Vasco	1	2	1	I5	3	0	0	0	0	0	
9	Vasco	1	2	1	I6	1	0	0	0	0	0	
9	Vasco	1	2	1	P	0	0	0	0	0	0	
9	Vasco	1	2	2	I1	4	6	1.5	1.5	1.5	1.5	
9	Vasco	1	2	2	I2	4	8	2	2	2	2	
9	Vasco	1	2	2	I3	3	13	4	3	3	3	
9	Vasco	1	2	2	I4	2	16	4	4	4	4	
9	Vasco	1	2	2	I5	3	20	6	6	4	4	

9	Vasco	1	2	2	I6	1	11	7	4	0	0	
9	Vasco	1	2	2	P	0	0	0	0	0	0	
9	Vasco	1	2	3	I1	4	4	1	1	1	1	
9	Vasco	1	2	3	I2	4	6	2	1	1	2	
9	Vasco	1	2	3	I3	4	9	3	2	2	2	
9	Vasco	1	2	3	I4	1	14	4	4	2	4	
9	Vasco	1	2	3	I5	0	3	3	0	0	0	
9	Vasco	1	2	3	I6	0	0	0	0	0	0	
9	Vasco	1	2	3	P	0	0	0	0	0	0	
9	Vasco	1	2	4	I1	4	4	1	1	1	1	
9	Vasco	1	2	4	I2	3	8	2	2	2	2	
9	Vasco	1	2	4	I3	1	12	3	3	3	3	
9	Vasco	1	2	4	I4	0	1	0	1	0	0	
9	Vasco	1	2	4	I5	0	0	0	0	0	0	
9	Vasco	1	2	4	P	0	0	0	0	0	0	
9	Vasco	1	3	1	I1	4	5	2	1	1	1	
9	Vasco	1	3	1	I2	4	9	3	3	1	2	
9	Vasco	1	3	1	I3	4	20	5	5	5	5	
9	Vasco	1	3	1	I4	1	18	5	4	4	5	
9	Vasco	1	3	1	I5	0	12	9	3	0	0	
9	Vasco	1	3	1	P	0	0	0	0	0	0	
9	Vasco	1	3	2	I1	4	8	2	2	2	2	
9	Vasco	1	3	2	I2	2	14	4	3	3	4	
9	Vasco	1	3	2	I3	1	18	4	5	4	5	
9	Vasco	1	3	2	I4	0	3	3	0	0	0	
9	Vasco	1	3	2	I5	0	0	0	0	0	0	
9	Vasco	1	3	2	P	0	0	0	0	0	0	
9	Vasco	1	3	3	I1	4	10	3	1	3	3	
9	Vasco	1	3	3	I2	4	12	3	3	3	3	
9	Vasco	1	3	3	I3	1	16	4	4	4	4	
9	Vasco	1	3	3	I4	0	4	4	0	0	0	
9	Vasco	1	3	3	P	0	0	0	0	0	0	
9	Vasco	1	4	1	I1	4	4	1	1	1	1	
9	Vasco	1	4	1	I2	4	11	3	3	2	3	
9	Vasco	1	4	1	I3	4	16	4	4	4	4	
9	Vasco	1	4	1	I4	3	24	6	6	6	6	

9	Vasco	1	4	1	I5	1	16	10	6	0	0	
9	Vasco	1	4	1	P	0	0	0	0	0	0	
9	Vasco	1	4	2	I1	4	8	2	2	2	2	
9	Vasco	1	4	2	I2	4	17	5	4	4	4	
9	Vasco	1	4	2	I3	2	11	6	5	0	0	
9	Vasco	1	4	2	I4	1	0	0	0	0	0	
9	Vasco	1	4	2	I5	0	0	0	0	0	0	
9	Vasco	1	4	2	P	0	0	0	0	0	0	
9	Vasco	1	4	3	I1	4	4	1	1	1	1	
9	Vasco	1	4	3	I2	3	8	2	2	2	2	
9	Vasco	1	4	3	I3	2	10	4	4	2	0	
9	Vasco	1	4	3	I4	2	0	0	0	0	0	
9	Vasco	1	4	3	I5	0	0	0	0	0	0	
9	Vasco	1	4	3	P	0	0	0	0	0	0	
9	Vasco	1	4	4	I1	4	9	2	2	3	2	
9	Vasco	1	4	4	I2	2	14	4	4	3	3	
9	Vasco	1	4	4	I3	2	2	2	0	0	0	
9	Vasco	1	4	4	I4	0	0	0	0	0	0	
9	Vasco	1	5	1	I1	4	5	2	1	1	1	
9	Vasco	1	5	1	I2	4	11	3	3	2	3	
9	Vasco	1	5	1	I3	4	17	5	4	4	4	
9	Vasco	1	5	1	I4	2	19	6	5	4	4	
9	Vasco	1	5	1	I5	1	7	7	0	0	0	
9	Vasco	1	5	1	P	0	0	0	0	0	0	
9	Vasco	1	5	2	I1	4	8	2	2	2	2	
9	Vasco	1	5	2	I2	4	11	3	3	2	3	
9	Vasco	1	5	2	I3	3	15	5	3	3	4	
9	Vasco	1	5	2	I4	1	20	6	5	5	4	
9	Vasco	1	5	2	I5	0	8	8	0	0	0	
9	Vasco	1	5	2	P	0	0	0	0	0	0	
9	Vasco	1	5	3	I1	4	4	1	1	1	1	
9	Vasco	1	5	3	I2	4	10	2.5	2.5	2	3	
9	Vasco	1	5	3	I3	2	17	4	5	4	4	
9	Vasco	1	5	3	I4	1	14	5	3	2	4	
9	Vasco	1	5	3	I5	0	11	10	1	0	0	
9	Vasco	1	5	3	P	0	0	0	0	0	0	

9	Vasco	2	1	1	I1	4	4	1	1	1	1	
9	Vasco	2	1	1	I2	4	8	3	1	2	2	
9	Vasco	2	1	1	I3	4	15	4	4	3	4	
9	Vasco	2	1	1	I4	2	22	7	5	6	4	
9	Vasco	2	1	1	I5	1	3	3	0	0	0	
9	Vasco	2	1	1	P	0	0	0	0	0	0	
9	Vasco	2	1	2	I1	4	5	1	1	1	2	
9	Vasco	2	1	2	I2	4	10	4	0	3	3	
9	Vasco	2	1	2	I3	1	14	4	4	3	3	
9	Vasco	2	1	2	I4	0	9	2	1	3	3	
9	Vasco	2	1	2	I5	0	21	13	8	0	0	
9	Vasco	2	1	2	P	0	0	0	0	0	0	
9	Vasco	2	1	3	I1	4	5	1	1	2	1	
9	Vasco	2	1	3	I2	4	8	2	2	2	2	
9	Vasco	2	1	3	I3	1	18	5	5	4	4	
9	Vasco	2	1	3	I4	0	20	5	5	5	5	
9	Vasco	2	1	3	I5	0	0	0	0	0	0	
9	Vasco	2	1	3	P	0	0	0	0	0	0	
9	Vasco	2	1	4	I1	4	5	1	1	1	2	
9	Vasco	2	1	4	I2	1	13	3	3	3	4	
9	Vasco	2	1	4	I3	0	20	6	5	4	5	
9	Vasco	2	1	4	I4	0	14	8	6	0	0	
9	Vasco	2	1	4	I5	0	0	0	0	0	0	
9	Vasco	2	1	4	P	0	0	0	0	0	0	
9	Vasco	2	1	5	I1	4	4	1	1	1	1	
9	Vasco	2	1	5	I2	4	10	2	2	3	3	
9	Vasco	2	1	5	I3	3	15	5	4	5	1	
9	Vasco	2	1	5	I4	1	17	6	4	2	5	
9	Vasco	2	1	5	I5	0	0	0	0	0	0	
9	Vasco	2	1	5	P	0	0	0	0	0	0	
9	Vasco	2	2	1	I1	4	8	2	2	2	2	
9	Vasco	2	2	1	I2	4	8	2	2	2	2	
9	Vasco	2	2	1	I3	1	11	4	3	3	1	
9	Vasco	2	2	1	I4	0	18	5	4	4	5	
9	Vasco	2	2	1	I5	0	16	8	8	0	0	
9	Vasco	2	2	1	I6	0	0	0	0	0	0	

9	Vasco	2	2	1	P	0	0	0	0	0	0	
9	Vasco	2	2	2	I1	4	5	2	1	1	1	
9	Vasco	2	2	2	I2	4	5	2	1	1	1	
9	Vasco	2	2	2	I3	1	19	5	4	5	5	
9	Vasco	2	2	2	I4	0	17	6	5	3	3	
9	Vasco	2	2	2	I5	0	2	2	0	0	0	
9	Vasco	2	2	2	I6	0	0	0	0	0	0	
9	Vasco	2	2	2	P	0	0	0	0	0	0	
9	Vasco	2	2	3	I1	4	6	1	1	2	2	
9	Vasco	2	2	3	I2	3	9	3	2	2	2	
9	Vasco	2	2	3	I3	0	17	5	3	4	5	
9	Vasco	2	2	3	I4	0	10	6	4	0	0	
9	Vasco	2	2	3	I5	0	0	0	0	0	0	
9	Vasco	2	2	3	P	0	0	0	0	0	0	
9	Vasco	2	2	4	I1	4	8	2	2	2	2	
9	Vasco	2	2	4	I2	2	14	3	4	4	3	
9	Vasco	2	2	4	I3	0	5	3	2	0	0	
9	Vasco	2	2	4	I4	0	13	6	4	3	0	
9	Vasco	2	2	4	I5	0	0	0	0	0	0	
9	Vasco	2	2	4	P	0	0	0	0	0	0	
9	Vasco	2	2	5	I1	4	8	2	2	2	2	
9	Vasco	2	2	5	I2	4	17	4	4	4	5	
9	Vasco	2	2	5	I3	1	5	3	2	0	0	
9	Vasco	2	2	5	I4	0	0	0	0	0	0	
9	Vasco	2	2	5	P	0	0	0	0	0	0	
9	Vasco	2	3	1	I1	4	7	2	2	1	2	
9	Vasco	2	3	1	I2	4	6	2	1	1	2	
9	Vasco	2	3	1	I3	2	17	5	4	4	4	
9	Vasco	2	3	1	I4	0	7	6	1	0	0	
9	Vasco	2	3	1	I5	0	0	0	0	0	0	
9	Vasco	2	3	1	I6	0	0	0	0	0	0	
9	Vasco	2	3	1	P	0	0	0	0	0	0	
9	Vasco	2	3	2	I1	4	4	1	1	1	1	
9	Vasco	2	3	2	I2	4	6	2	1	1	2	
9	Vasco	2	3	2	I3	4	13	4	3	2	4	
9	Vasco	2	3	2	I4	1	24	6	7	6	5	

9	Vasco	2	3	2	I5	0	16	10	6	0	0	
9	Vasco	2	3	2	P	0	0	0	0	0	0	
9	Vasco	2	3	3	I1	4	4	1	1	1	1	
9	Vasco	2	3	3	I2	4	10	3	2	2	3	
9	Vasco	2	3	3	I3	4	18	4	4	4	6	
9	Vasco	2	3	3	I4	0	2	2	0	0	0	
9	Vasco	2	3	3	I5	0	0	0	0	0	0	
9	Vasco	2	3	3	P	0	0	0	0	0	0	
9	Vasco	2	4	1	I1	4	4	1	1	1	1	
9	Vasco	2	4	1	I2	4	7	2	2	2	1	
9	Vasco	2	4	1	I3	4	9	2	2	2	3	
9	Vasco	2	4	1	I4	1	19	5	5	5	4	
9	Vasco	2	4	1	I5	0	15	8	7	0	0	
9	Vasco	2	4	1	I6	0	0	0	0	0	0	
9	Vasco	2	4	1	P	0	0	0	0	0	0	
9	Vasco	2	4	2	I1	4	2	1	0	0	1	
9	Vasco	2	4	2	I2	4	10	2	3	2	3	
9	Vasco	2	4	2	I3	4	16	4	4	3	5	
9	Vasco	2	4	2	I4	1	28	7	7	7	7	
9	Vasco	2	4	2	I5	0	23	12	11	0	0	
9	Vasco	2	4	2	P	0	0	0	0	0	0	
9	Vasco	2	4	3	I1	4	6	2	2	1	1	
9	Vasco	2	4	3	I2	4	6	2	1	1.5	1.5	
9	Vasco	2	4	3	I3	4	14	3	4	3	4	
9	Vasco	2	4	3	I4	4	16	4	5	4	3	
9	Vasco	2	4	3	I5	1	23	5	5	7	6	
9	Vasco	2	4	3	I6	0	10	9	1	0	0	
9	Vasco	2	4	3	P	0	0	0	0	0	0	
9	Vasco	2	4	4	I1	4	4	1	1	1	1	
9	Vasco	2	4	4	I2	4	10	3	2	2	3	
9	Vasco	2	4	4	I3	4	19	6	5	3	5	
9	Vasco	2	4	4	I4	3	27	8	6	6	7	
9	Vasco	2	4	4	I5	0	18	12	6	0	0	
9	Vasco	2	4	4	P	0	0	0	0	0	0	
9	Vasco	2	4	5	I1	4	4	1	1	1	1	
9	Vasco	2	4	5	I2	4	6	1	1	2	2	

9	Vasco	2	4	5	I3	4	18	5	5	4	4	
9	Vasco	2	4	5	I4	2	18	6	4	4	4	
9	Vasco	2	4	5	I5	0	18	15	3	0	0	
9	Vasco	2	4	5	P	0	0	0	0	0	0	
9	Vasco	2	5	1	I1	4	4	1	1	1	1	
9	Vasco	2	5	1	I2	4	11	3	2	3	3	
9	Vasco	2	5	1	I3	4	22	5	5	6	6	
9	Vasco	2	5	1	I4	1	24	7	6	5	6	
9	Vasco	2	5	1	I5	0	11	11	0	0	0	
9	Vasco	2	5	1	P	0	0	0	0	0	0	
9	Vasco	2	5	2	I1	4	1	0	0	0	1	
9	Vasco	2	5	2	I2	4	13	4	3	3	3	
9	Vasco	2	5	2	I3	4	15	3	4	3	5	
9	Vasco	2	5	2	I4	1	23	7	6	5	5	
9	Vasco	2	5	2	I5	0	17	10	5	2	0	
9	Vasco	2	5	2	P	0	0	0	0	0	0	
9	Vasco	2	5	3	I1	4	8	2	2	2	2	
9	Vasco	2	5	3	I2	4	16	4	4	4	4	
9	Vasco	2	5	3	I3	4	19	5	4	5	5	
9	Vasco	2	5	3	I4	3	25	6	6	6	7	
9	Vasco	2	5	3	I5	0	13	9	4	0	0	
9	Vasco	2	5	3	P	0	0	0	0	0	0	
9	Vasco	2	5	4	I1	4	0	0	0	0	0	
9	Vasco	2	5	4	I2	4	11	3	3	3	2	
9	Vasco	2	5	4	I3	4	14	3	3	3	5	
9	Vasco	2	5	4	I4	1	23	7	6	5	5	
9	Vasco	2	5	4	I5	0	16	10	6	0	0	
9	Vasco	2	5	4	P	0	0	0	0	0	0	
9	Vasco	2	5	5	I1	4	11	3	2	2	4	
9	Vasco	2	5	5	I2	4	15	4	4	4	3	
9	Vasco	2	5	5	I3	4	16	4	4	4	4	
9	Vasco	2	5	5	I4	0	15	7	7	1	0	
9	Vasco	2	5	5	P	0	0	0	0	0	0	
9	Vasco	3	1	1	I1	4						
9	Vasco	3	1	1	I2	4						
9	Vasco	3	1	1	I3	4						

9	Vasco	3	1	1	I4	1						
9	Vasco	3	1	1	I5	0						
9	Vasco	3	1	1	P	0						
9	Vasco	3	1	2	I1	4						
9	Vasco	3	1	2	I2	4						
9	Vasco	3	1	2	I3	4						
9	Vasco	3	1	2	I4	1						
9	Vasco	3	1	2	I5	0						
9	Vasco	3	1	2	P	0						
9	Vasco	3	1	3	I1	4						
9	Vasco	3	1	3	I2	4						
9	Vasco	3	1	3	I3	3						
9	Vasco	3	1	3	I4	0						
9	Vasco	3	1	3	I5	0						
9	Vasco	3	1	3	P	0						
9	Vasco	3	1	4	I1	4						
9	Vasco	3	1	4	I2	4						
9	Vasco	3	1	4	I3	2						
9	Vasco	3	1	4	I4	0						
9	Vasco	3	1	4	I5	0						
9	Vasco	3	1	4	P	0						
9	Vasco	3	2	1	I1	4						
9	Vasco	3	2	1	I2	4						
9	Vasco	3	2	1	I3	4						
9	Vasco	3	2	1	I4	4						
9	Vasco	3	2	1	I5	2						
9	Vasco	3	2	1	I6	0						
9	Vasco	3	2	1	P	0						
9	Vasco	3	2	2	I1	4						
9	Vasco	3	2	2	I2	4						
9	Vasco	3	2	2	I3	4						
9	Vasco	3	2	2	I4	3						
9	Vasco	3	2	2	I5	1						
9	Vasco	3	2	2	I6	0						
9	Vasco	3	2	2	P	0						
9	Vasco	3	2	3	I1	4						

9	Vasco	3	2	3	I2	4						
9	Vasco	3	2	3	I3	4						
9	Vasco	3	2	3	I4	1						
9	Vasco	3	2	3	I5	0						
9	Vasco	3	2	3	I6	0						
9	Vasco	3	2	3	P	0						
9	Vasco	3	3	1	I1	4						
9	Vasco	3	3	1	I2	4						
9	Vasco	3	3	1	I3	1						
9	Vasco	3	3	1	I4	0						
9	Vasco	3	3	1	I5	0						
9	Vasco	3	3	1	I6	0						
9	Vasco	3	3	1	P	0						
9	Vasco	3	3	2	I1	4						
9	Vasco	3	3	2	I2	3						
9	Vasco	3	3	2	I3	1						
9	Vasco	3	3	2	I4	0						
9	Vasco	3	3	2	I5	0						
9	Vasco	3	3	2	I6	0						
9	Vasco	3	3	2	P	0						
9	Vasco	3	3	3	I1	4						
9	Vasco	3	3	3	I2	3						
9	Vasco	3	3	3	I3	2						
9	Vasco	3	3	3	I4	0						
9	Vasco	3	3	3	I5	0						
9	Vasco	3	3	3	I6	0						
9	Vasco	3	3	3	P	0						
9	Vasco	3	3	4	I1	4						
9	Vasco	3	3	4	I2	4						
9	Vasco	3	3	4	I3	1						
9	Vasco	3	3	4	I4	0						
9	Vasco	3	3	4	I5	0						
9	Vasco	3	3	4	P	0						
9	Vasco	3	3	5	I1	4						
9	Vasco	3	3	5	I2	3						
9	Vasco	3	3	5	I3	2						

9	Vasco	3	3	5	I4	0						
9	Vasco	3	3	5	I5	0						
9	Vasco	3	3	5	P	0						
9	Vasco	3	4	1	I1	4						
9	Vasco	3	4	1	I2	4						
9	Vasco	3	4	1	I3	3						
9	Vasco	3	4	1	I4	1						
9	Vasco	3	4	1	I5	0						
9	Vasco	3	4	1	P	0						
9	Vasco	3	4	2	I1	4						
9	Vasco	3	4	2	I2	4						
9	Vasco	3	4	2	I3	2						
9	Vasco	3	4	2	I4	0						
9	Vasco	3	4	2	I5	0						
9	Vasco	3	4	2	P	0						
9	Vasco	3	4	3	I1	4						
9	Vasco	3	4	3	I2	4						
9	Vasco	3	4	3	I3	1						
9	Vasco	3	4	3	I4	0						
9	Vasco	3	4	3	I5	0						
9	Vasco	3	4	3	P	0						
9	Vasco	3	4	4	I1	4						
9	Vasco	3	4	4	I2	3						
9	Vasco	3	4	4	I3	0						
9	Vasco	3	4	4	I4	0						
9	Vasco	3	4	4	I5	0						
9	Vasco	3	4	4	P	0						
9	Vasco	3	4	5	I1	4						
9	Vasco	3	4	5	I2	1						
9	Vasco	3	4	5	I3	0						
9	Vasco	3	4	5	I4	0						
9	Vasco	3	4	5	P	0						
9	Vasco	3	5	1	I1	4						
9	Vasco	3	5	1	I2	4						
9	Vasco	3	5	1	I3	4						
9	Vasco	3	5	1	I4	2						

9	Vasco	3	5	1	I5	0						
9	Vasco	3	5	1	P	0						
9	Vasco	3	5	2	I1	4						
9	Vasco	3	5	2	I2	4						
9	Vasco	3	5	2	I3	3						
9	Vasco	3	5	2	I4	1						
9	Vasco	3	5	2	I5	0						
9	Vasco	3	5	2	P	0						
9	Vasco	3	5	3	I1	4						
9	Vasco	3	5	3	I2	4						
9	Vasco	3	5	3	I3	4						
9	Vasco	3	5	3	I4	1						
9	Vasco	3	5	3	I5	0						
9	Vasco	3	5	3	P	0						
9	Vasco	3	5	4	I1	4						
9	Vasco	3	5	4	I2	4						
9	Vasco	3	5	4	I3	2						
9	Vasco	3	5	4	I4	0						
9	Vasco	3	5	4	I5	0						
9	Vasco	3	5	4	P	0						
9	Vasco	3	5	5	I1	4						
9	Vasco	3	5	5	I2	1						
9	Vasco	3	5	5	I3	0						
9	Vasco	3	5	5	I4	0						
9	Vasco	3	5	5	P	0						
9	2-49	1	1	1	I1	4	4	1	1	1	1	
9	2-49	1	1	1	I2	1	12	3	4	3	2	
9	2-49	1	1	1	I3	0	0	0	0	0	0	
9	2-49	1	1	1	I4	0	0	0	0	0	0	
9	2-49	1	1	1	I5	0	0	0	0	0	0	
9	2-49	1	1	1	P	0	0	0	0	0	0	
9	2-49	1	1	2	I1	4	4	1	1	1	1	
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9	2-49	1	1	2	I3	0	4	4	0	0	0	
9	2-49	1	1	2	I4	0	0	0	0	0	0	
9	2-49	1	1	2	I5	0	0	0	0	0	0	

9	2-49	1	1	2	P	0	0	0	0	0	0	
9	2-49	1	1	3	I1	3	8	2	2	2	2	
9	2-49	1	1	3	I2	1	17	5	5	5	2	
9	2-49	1	1	3	I3	0	2	2	0	0	0	
9	2-49	1	1	3	I4	0	0	0	0	0	0	
9	2-49	1	1	3	I5	0	0	0	0	0	0	
9	2-49	1	1	3	P	0	0	0	0	0	0	
9	2-49	1	1	4	I1	4	2	0.5	0.5	0.5	0.5	
9	2-49	1	1	4	I2	1	10	3	3	1	3	
9	2-49	1	1	4	I3	0	7	7	0	0	0	
9	2-49	1	1	4	I4	0	0	0	0	0	0	
9	2-49	1	1	4	I5	0	0	0	0	0	0	
9	2-49	1	1	4	P	0	0	0	0	0	0	
9	2-49	1	1	5	I1	4	4	1	1	1	1	
9	2-49	1	1	5	I2	1	23	6	6	5	6	
9	2-49	1	1	5	I3	0	2	2	0	0	0	
9	2-49	1	1	5	I4	0	0	0	0	0	0	
9	2-49	1	1	5	I5	0	0	0	0	0	0	
9	2-49	1	1	5	P	0	0	0	0	0	0	
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9	2-49	1	2	1	I3	0	18	10	6	2	0	
9	2-49	1	2	1	I4	0	0	0	0	0	0	
9	2-49	1	2	1	I5	0	0	0	0	0	0	
9	2-49	1	2	1	I6	0	0	0	0	0	0	
9	2-49	1	2	1	P	0	0	0	0	0	0	
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9	2-49	1	2	2	I3	0	1	1	0	0	0	
9	2-49	1	2	2	I4	0	0	0	0	0	0	
9	2-49	1	2	2	I5	0	0	0	0	0	0	
9	2-49	1	2	2	P	0	0	0	0	0	0	
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9	2-49	1	2	3	I2	1	17	6	4	3	4	
9	2-49	1	2	3	I3	0	8	2	4	0	2	
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9	2-49	1	2	3	I5	0	0	0	0	0	0	
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9	2-49	1	2	4	I3	0	13	8	4	1	0	
9	2-49	1	2	4	I4	0	0	0	0	0	0	
9	2-49	1	2	4	I5	0	0	0	0	0	0	
9	2-49	1	2	4	P	0	0	0	0	0	0	
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9	2-49	1	3	1	I2	1	0	0	0	0	0	
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9	2-49	1	3	1	I4	0	0	0	0	0	0	
9	2-49	1	3	1	I5	0	0	0	0	0	0	
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9	2-49	1	3	1	P	0	0	0	0	0	0	
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9	2-49	1	3	2	I2	1	0	0	0	0	0	
9	2-49	1	3	2	I3	0	0	0	0	0	0	
9	2-49	1	3	2	I4	0	0	0	0	0	0	
9	2-49	1	3	2	I5	0	0	0	0	0	0	
9	2-49	1	3	2	P	0	0	0	0	0	0	
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9	2-49	1	3	3	I2	2	11	5	3	0	3	
9	2-49	1	3	3	I3	0	0	0	0	0	0	
9	2-49	1	3	3	I4	0	0	0	0	0	0	
9	2-49	1	3	3	I5	0	0	0	0	0	0	
9	2-49	1	3	3	P	0	0	0	0	0	0	
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9	2-49	1	3	4	I4	0	0	0	0	0	0	
9	2-49	1	3	4	I5	0	0	0	0	0	0	
9	2-49	1	3	4	P	0	0	0	0	0	0	
9	2-49	1	4	1	I1	4	4	1	1	1	1	
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9	2-49	1	4	2	I5	0	0	0	0	0	0	
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9	2-49	1	4	4	I5	0	0	0	0	0	0	
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9	2-49	1	4	5	I3	0	6	3	3	0	0	
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9	2-49	1	5	4	P	0	0	0	0	0	0	
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9	2-49	1	5	5	I3	0	0	0	0	0	0	
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9	2-49	1	5	5	I5	0	0	0	0	0	0	
9	2-49	1	5	5	P	0	0	0	0	0	0	
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9	2-49	2	1	1	I3	0	13	5	4	4	0	
9	2-49	2	1	1	I4	0	0	0	0	0	0	
9	2-49	2	1	1	I5	0	0	0	0	0	0	
9	2-49	2	1	1	P	0	0	0	0	0	0	
9	2-49	2	1	2	I1	3	4	1	1	1	1	
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9	2-49	2	1	2	I4	0	0	0	0	0	0	
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9	2-49	2	1	2	P	0	0	0	0	0	0	
9	2-49	2	1	3	I1	3	4	1	1	1	1	
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9	2-49	2	1	3	P	0	0	0	0	0	0	
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9	2-49	2	1	4	I2	1	11	3	2	3	3	
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9	2-49	2	1	4	I5	0	0	0	0	0	0	
9	2-49	2	1	4	P	0	0	0	0	0	0	
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9	2-49	2	2	3	I5	0	0	0	0	0	0	
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9	2-49	2	2	4	I4	0	0	0	0	0	0	
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9	2-49	2	2	5	I5	0	0	0	0	0	0	
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9	2-49	3	1	2	I2	1						
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9	2-49	3	1	2	I4	0						
9	2-49	3	1	2	I5	0						
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9	2-49	3	5	5	I5	0						
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9	Sunco	1	1	1	I3	1	8	4	3	1	0	
9	Sunco	1	1	1	I4	0	0	0	0	0	0	
9	Sunco	1	1	1	I5	0	0	0	0	0	0	
9	Sunco	1	1	1	I6	0	0	0	0	0	0	
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9	Sunco	1	1	2	I5	0	2	2	0	0	0	
9	Sunco	1	1	2	I6	0	0	0	0	0	0	
9	Sunco	1	1	2	P	0	0	0	0	0	0	
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9	Sunco	1	1	3	I4	0	1	1	0	0	0	
9	Sunco	1	1	3	I5	0	0	0	0	0	0	
9	Sunco	1	1	3	I6	0	0	0	0	0	0	
9	Sunco	1	1	3	P	0	0	0	0	0	0	
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9	Sunco	1	1	4	I3	0	5	5	0	0	0	
9	Sunco	1	1	4	I4	0	0	0	0	0	0	

9	Sunco	1	1	4	I5	0	0	0	0	0	0	
9	Sunco	1	1	4	P	0	0	0	0	0	0	
9	Sunco	1	1	5	I1	1	9	2	2.5	2.5	2	
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9	Sunco	1	2	2	I5	0	0	0	0	0	0	
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9	Sunco	1	3	3	I6	0	0	0	0	0	0	
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9	Sunco	1	3	4	I4	0	0	0	0	0	0	
9	Sunco	1	4	1	I1	4	4	1	1	1	1	
9	Sunco	1	4	1	I2	2	8	2	2	2	2	
9	Sunco	1	4	1	I3	0	13	5	4	3	1	
9	Sunco	1	4	1	I4	0	0	0	0	0	0	
9	Sunco	1	4	1	I5	0	0	0	0	0	0	
9	Sunco	1	4	1	P	0	0	0	0	0	0	
9	Sunco	1	4	2	I1	4	4	1	1	1	1	
9	Sunco	1	4	2	I2	2	14	4	4	3	3	
9	Sunco	1	4	2	I3	0	15	4	5	5	1	
9	Sunco	1	4	2	I4	0	0	0	0	0	0	
9	Sunco	1	4	2	I5	0	0	0	0	0	0	
9	Sunco	1	4	2	P	0	0	0	0	0	0	
9	Sunco	1	4	3	I1	4	4	1	1	1	1	
9	Sunco	1	4	3	I2	1	3	2	1	0	0	
9	Sunco	1	4	3	I3	0	0	0	0	0	0	
9	Sunco	1	4	3	I4	0	0	0	0	0	0	

9	Sunco	1	4	3	I5	0	0	0	0	0	0	
9	Sunco	1	4	3	P	0	0	0	0	0	0	
9	Sunco	1	4	4	I1	4	4	1	1	1	1	
9	Sunco	1	4	4	I2	1	8	2	2	2	2	
9	Sunco	1	4	4	I3	0	11	5	3	3	0	
9	Sunco	1	4	4	I4	0	0	0	0	0	0	
9	Sunco	1	4	4	I5	0	0	0	0	0	0	
9	Sunco	1	4	4	P	0	0	0	0	0	0	
9	Sunco	1	4	5	I1	3	6	2	1	1	2	
9	Sunco	1	4	5	I2	1	8	2	3	2	1	
9	Sunco	1	4	5	I3	0	0	0	0	0	0	
9	Sunco	1	4	5	I4	0	0	0	0	0	0	
9	Sunco	1	4	5	I5	0	0	0	0	0	0	
9	Sunco	1	4	5	P	0	0	0	0	0	0	
9	Sunco	1	5	1	I1	4	8	2	2	2	2	
9	Sunco	1	5	1	I2	4	4	1	1	1	1	
9	Sunco	1	5	1	I3	2	7	2	2	2	1	
9	Sunco	1	5	1	I4	1	0	0	0	0	0	
9	Sunco	1	5	1	I5	0	0	0	0	0	0	
9	Sunco	1	5	1	I6	0	0	0	0	0	0	
9	Sunco	1	5	1	P	0	0	0	0	0	0	
9	Sunco	1	5	2	I1	4	4	1	1	1	1	
9	Sunco	1	5	2	I2	3	8	2	2	2	2	
9	Sunco	1	5	2	I3	1	19	6	5	5	3	
9	Sunco	1	5	2	I4	0	0	0	0	0	0	
9	Sunco	1	5	2	I5	0	0	0	0	0	0	
9	Sunco	1	5	2	I6	0	0	0	0	0	0	
9	Sunco	1	5	2	P	0	0	0	0	0	0	
9	Sunco	1	5	3	I1	4	4	1	1	1	1	
9	Sunco	1	5	3	I2	4	5	2	1	1	1	
9	Sunco	1	5	3	I3	2	12	4	3	3	2	
9	Sunco	1	5	3	I4	0	0	0	0	0	0	
9	Sunco	1	5	3	I5	0	0	0	0	0	0	
9	Sunco	1	5	3	I6	0	0	0	0	0	0	
9	Sunco	1	5	3	P	0	0	0	0	0	0	
9	Sunco	2	1	1	I1	4	4	1	1	1	1	

9	Sunco	2	1	1	I2	4	8	2	2	2	2	
9	Sunco	2	1	1	I3	3	18	4	4	5	5	
9	Sunco	2	1	1	I4	0	2	2	0	0	0	
9	Sunco	2	1	1	I5	0	0	0	0	0	0	
9	Sunco	2	1	1	I6	0	0	0	0	0	0	
9	Sunco	2	1	1	P	0	0	0	0	0	0	
9	Sunco	2	1	2	I1	4	6	1	2	1	2	
9	Sunco	2	1	2	I2	4	10	2	3	2	3	
9	Sunco	2	1	2	I3	1	16	5	4	4	3	
9	Sunco	2	1	2	I4	0	12	5	3	4	0	
9	Sunco	2	1	2	I5	0	0	0	0	0	0	
9	Sunco	2	1	2	P	0	0	0	0	0	0	
9	Sunco	2	1	3	I1	4	6	2	1	2	1	
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9	Sunco	2	1	3	I3	0	15	5	3	2	5	
9	Sunco	2	1	3	I4	0	8	6	2	0	0	
9	Sunco	2	1	3	I5	0	0	0	0	0	0	
9	Sunco	2	1	3	P	0	0	0	0	0	0	
9	Sunco	2	1	4	I1	4	9	2	2	2	3	
9	Sunco	2	1	4	I2	3	6	4	2	0	0	
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9	Sunco	2	1	4	I4	0	9	3	6	0	0	
9	Sunco	2	1	4	I5	0	0	0	0	0	0	
9	Sunco	2	1	4	P	0	0	0	0	0	0	
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9	Sunco	2	1	5	I4	0	1	1	0	0	0	
9	Sunco	2	1	5	I5	0	0	0	0	0	0	
9	Sunco	2	1	5	P	0	0	0	0	0	0	
9	Sunco	2	2	1	I1	4	7	2	2	1	2	
9	Sunco	2	2	1	I2	4	8	2	2	2	2	
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9	Sunco	2	2	1	I4	1	11	6	5	0	0	
9	Sunco	2	2	1	I5	0	0	0	0	0	0	
9	Sunco	2	2	1	I6	0	0	0	0	0	0	

9	Sunco	2	2	1	P	0	0	0	0	0	0	
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9	Sunco	2	2	2	I2	4	0	0	0	0	0	
9	Sunco	2	2	2	I3	3	0	0	0	0	0	
9	Sunco	2	2	2	I4	1	14	0	4	5	5	
9	Sunco	2	2	2	I5	0	10	7	3	0	0	
9	Sunco	2	2	2	I6	0	0	0	0	0	0	
9	Sunco	2	2	2	P	0	0	0	0	0	0	
9	Sunco	2	2	3	I1	4	4	1	1	1	1	
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9	Sunco	2	2	3	I3	2	19	5	5	5	4	
9	Sunco	2	2	3	I4	0	6	6	0	0	0	
9	Sunco	2	2	3	I5	0	0	0	0	0	0	
9	Sunco	2	2	3	I6	0	0	0	0	0	0	
9	Sunco	2	2	3	P	0	0	0	0	0	0	
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9	Sunco	2	2	4	I5	0	0	0	0	0	0	
9	Sunco	2	2	4	I6	0	0	0	0	0	0	
9	Sunco	2	2	4	P	0	0	0	0	0	0	
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9	Sunco	2	2	5	I3	0	3	3	0	0	0	
9	Sunco	2	2	5	I4	0	0	0	0	0	0	
9	Sunco	2	2	5	I5	0	0	0	0	0	0	
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9	Sunco	2	3	1	I6	0	0	0	0	0	0	
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9	Sunco	2	3	2	I4	0	13	6	0	3	4	
9	Sunco	2	3	2	I5	0	5	5	0	0	0	
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9	Sunco	2	3	4	I5	0	0	0	0	0	0	
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9	Sunco	2	4	2	I6	0	0	0	0	0	0	
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9	Sunco	2	4	3	I5	0	0	0	0	0	0	
9	Sunco	2	4	3	I6	0	0	0	0	0	0	
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9	Sunco	2	4	4	I6	0	0	0	0	0	0	
9	Sunco	2	4	4	P	0	0	0	0	0	0	
9	Sunco	2	4	5	I1	4	4	1	1	1	1	
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9	Sunco	2	4	5	I5	0	0	0	0	0	0	
9	Sunco	2	4	5	I6	0	0	0	0	0	0	
9	Sunco	2	4	5	P	0	0	0	0	0	0	
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9	Sunco	2	5	1	I2	4	6	2	1	2	1	
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9	Sunco	2	5	1	I4	1	15	4	4	4	3	
9	Sunco	2	5	1	I5	0	6	5	1	0	0	
9	Sunco	2	5	1	I6	0	0	0	0	0	0	
9	Sunco	2	5	1	P	0	0	0	0	0	0	
9	Sunco	2	5	2	I1	4	6	2	1	1.5	1.5	
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9	Sunco	2	5	3	P	0	0	0	0	0	0	
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9	Sunco	2	5	4	I5	0	0	0	0	0	0	
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9	Sunco	2	5	5	I5	0	0	0	0	0	0	
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9	Sunco	3	1	1	I3	4						
9	Sunco	3	1	1	I4	2						
9	Sunco	3	1	1	I5	0						
9	Sunco	3	1	1	I6	0						
9	Sunco	3	1	1	P	0						
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9	Sunco	3	1	2	I2	4						
9	Sunco	3	1	2	I3	3						
9	Sunco	3	1	2	I4	1						
9	Sunco	3	1	2	I5	0						
9	Sunco	3	1	2	I6	0						
9	Sunco	3	1	2	P	0						
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9	Sunco	3	1	3	I2	4						

9	Sunco	3	1	3	I3	3						
9	Sunco	3	1	3	I4	0						
9	Sunco	3	1	3	I5	0						
9	Sunco	3	1	3	I6	0						
9	Sunco	3	1	3	P	0						
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9	Sunco	3	1	4	I2	4						
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9	Sunco	3	1	5	I2	3						
9	Sunco	3	1	5	I3	1						
9	Sunco	3	1	5	I4	0						
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9	Sunco	3	1	5	I6	0						
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9	Sunco	3	2	1	I2	4						
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9	Sunco	3	2	3	I4	0						

9	Sunco	3	2	3	I5	0						
9	Sunco	3	2	3	P	0						
9	Sunco	3	2	4	I1	4						
9	Sunco	3	2	4	I2	1						
9	Sunco	3	2	4	I3	0						
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9	Sunco	3	2	4	I5	0						
9	Sunco	3	2	4	P	0						
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9	Sunco	3	3	2	I4	0						
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9	Sunco	3	3	2	I6	0						
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9	Sunco	3	3	3	I4	0						
9	Sunco	3	3	3	I5	0						
9	Sunco	3	3	3	I6	0						
9	Sunco	3	3	3	P	0						
9	Sunco	3	3	4	I1	4						

9	Sunco	3	3	4	I2	2						
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9	Sunco	3	3	4	I4	0						
9	Sunco	3	3	4	I5	0						
9	Sunco	3	3	4	I6	0						
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9	Sunco	3	4	1	I6	0						
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9	Sunco	3	4	2	I5	0						
9	Sunco	3	4	2	I6	0						
9	Sunco	3	4	2	P	0						
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9	Sunco	3	4	3	I2	4						
9	Sunco	3	4	3	I3	1						
9	Sunco	3	4	3	I4	0						
9	Sunco	3	4	3	I5	0						
9	Sunco	3	4	3	I6	0						
9	Sunco	3	4	3	P	0						
9	Sunco	3	4	4	I1	4						
9	Sunco	3	4	4	I2	4						

9	Sunco	3	4	4	I3	1						
9	Sunco	3	4	4	I4	0						
9	Sunco	3	4	4	I5	0						
9	Sunco	3	4	4	I6	0						
9	Sunco	3	4	4	P	0						
9	Sunco	3	4	5	I1	3						
9	Sunco	3	4	5	I2	0						
9	Sunco	3	4	5	I3	0						
9	Sunco	3	4	5	I4	0						
9	Sunco	3	4	5	P	0						
9	Sunco	3	5	1	I1	4						
9	Sunco	3	5	1	I2	4						
9	Sunco	3	5	1	I3	2						
9	Sunco	3	5	1	I4	1						
9	Sunco	3	5	1	I5	0						
9	Sunco	3	5	1	I6	0						
9	Sunco	3	5	1	P	0						
9	Sunco	3	5	2	I1	4						
9	Sunco	3	5	2	I2	4						
9	Sunco	3	5	2	I3	2						
9	Sunco	3	5	2	I4	0						
9	Sunco	3	5	2	I5	0						
9	Sunco	3	5	2	P	0						
9	Sunco	3	5	3	I1	4						
9	Sunco	3	5	3	I2	4						
9	Sunco	3	5	3	I3	1						
9	Sunco	3	5	3	I4	0						
9	Sunco	3	5	3	I5	0						
9	Sunco	3	5	3	P	0						
9	Sunco	3	5	4	I1	4						
9	Sunco	3	5	4	I2	1						
9	Sunco	3	5	4	I3	0						
9	Sunco	3	5	4	I4	0						
9	Sunco	3	5	4	I5	0						
9	Sunco	3	5	4	P	0						
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9	CPI133814	1	1	1	I2	4	4	1	1	1	1	
9	CPI133814	1	1	1	I3	1	15	6	4	3	2	
9	CPI133814	1	1	1	I4	0	0	0	0	0	0	
9	CPI133814	1	1	1	I5	0	0	0	0	0	0	
9	CPI133814	1	1	1	I6	0	0	0	0	0	0	
9	CPI133814	1	1	1	P	0	0	0	0	0	0	
9	CPI133814	1	1	2	I1	4	9	2	3	2	2	
9	CPI133814	1	1	2	I2	1	13	6	2	5	0	
9	CPI133814	1	1	2	I3	0	2	2	0	0	0	
9	CPI133814	1	1	2	I4	0	0	0	0	0	0	
9	CPI133814	1	1	2	I5	0	0	0	0	0	0	
9	CPI133814	1	1	2	P	0	0	0	0	0	0	
9	CPI133814	1	1	3	I1	4	4	1	1	1	1	
9	CPI133814	1	1	3	I2	1	7	6	1	0	0	
9	CPI133814	1	1	3	I3	0	0	0	0	0	0	
9	CPI133814	1	1	3	I4	0	0	0	0	0	0	
9	CPI133814	1	1	3	I5	0	0	0	0	0	0	
9	CPI133814	1	1	3	P	0	0	0	0	0	0	
9	CPI133814	1	1	4	I1	4	4	1	1	1	1	
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9	CPI133814	1	1	4	I3	0	2	2	0	0	0	
9	CPI133814	1	1	4	I4	0	0	0	0	0	0	
9	CPI133814	1	1	4	I5	0	0	0	0	0	0	
9	CPI133814	1	1	4	P	0	0	0	0	0	0	
9	CPI133814	1	1	5	I1	4	4	1	1	1	1	
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9	CPI133814	1	1	5	I3	0	1	1	0	0	0	
9	CPI133814	1	1	5	I4	0	0	0	0	0	0	
9	CPI133814	1	1	5	I5	0	0	0	0	0	0	
9	CPI133814	1	1	5	P	0	0	0	0	0	0	
9	CPI133814	1	2	1	I1	4	6	2	1	1	2	
9	CPI133814	1	2	1	I2	4	5	2	1	0	2	
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9	CPI133814	1	2	1	I4	0	3	2	0	0	1	
9	CPI133814	1	2	1	I5	0	0	0	0	0	0	
9	CPI133814	1	2	1	I6	0	0	0	0	0	0	

9	CPI133814	1	2	1	P	0	0	0	0	0	0	
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9	CPI133814	1	2	2	I2	4	7	2	2	1	2	
9	CPI133814	1	2	2	I3	1	14	3	3	5	3	
9	CPI133814	1	2	2	I4	0	15	4	6	2	3	
9	CPI133814	1	2	2	I5	0	4	2	2	0	0	
9	CPI133814	1	2	2	I6	0	0	0	0	0	0	
9	CPI133814	1	2	2	P	0	0	0	0	0	0	
9	CPI133814	1	2	3	I1	4	4	1	1	1	1	
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9	CPI133814	1	2	3	I4	0	0	0	0	0	0	
9	CPI133814	1	2	3	I5	0	0	0	0	0	0	
9	CPI133814	1	2	3	I6	0	0	0	0	0	0	
9	CPI133814	1	2	3	P	0	0	0	0	0	0	
9	CPI133814	1	3	1	I1	4	4	1	1	1	1	
9	CPI133814	1	3	1	I2	4	4	1	1	1	1	
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9	CPI133814	1	3	1	I4	1	0	0	0	0	0	
9	CPI133814	1	3	1	I5	0	0	0	0	0	0	
9	CPI133814	1	3	1	I6	0	0	0	0	0	0	
9	CPI133814	1	3	1	P	0	0	0	0	0	0	
9	CPI133814	1	3	2	I1	4	4	1	1	1	1	
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9	CPI133814	1	3	2	I4	0	0	0	0	0	0	
9	CPI133814	1	3	2	I5	0	0	0	0	0	0	
9	CPI133814	1	3	2	I6	0	0	0	0	0	0	
9	CPI133814	1	3	2	P	0	0	0	0	0	0	
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9	CPI133814	1	3	3	I5	0	0	0	0	0	0	
9	CPI133814	1	3	3	P	0	0	0	0	0	0	
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9	CPI133814	1	3	4	I2	4	8	3	2	1	2	
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9	CPI133814	1	3	4	I4	0	4	4	0	0	0	
9	CPI133814	1	3	4	I5	0	0	0	0	0	0	
9	CPI133814	1	3	4	P	0	0	0	0	0	0	
9	CPI133814	1	3	5	I1	4	6	1.5	1.5	1.5	1.5	
9	CPI133814	1	3	5	I2	2	15	4	1	5	5	
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9	CPI133814	1	3	5	I4	0	1	1	0	0	0	
9	CPI133814	1	3	5	I5	0	0	0	0	0	0	
9	CPI133814	1	3	5	P	0	0	0	0	0	0	
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9	CPI133814	1	4	1	I6	0	0	0	0	0	0	
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9	CPI133814	1	4	2	I4	0	0	0	0	0	0	
9	CPI133814	1	4	2	I5	0	0	0	0	0	0	
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9	CPI133814	1	4	4	I3	0	6	5	1	0	0	
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9	CPI133814	1	4	5	I3	4	7	1	4	1	1	
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9	CPI133814	1	4	5	P	2	10	4	3	3	0	
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9	CPI133814	1	5	1	I2	1	13	5	4	3	1	
9	CPI133814	1	5	1	I3	0	0	0	0	0	0	
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9	CPI133814	1	5	2	I5	0	0	0	0	0	0	
9	CPI133814	1	5	2	P	0	0	0	0	0	0	
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9	CPI133814	1	5	3	I5	0	0	0	0	0	0	
9	CPI133814	1	5	3	P	0	0	0	0	0	0	
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9	CPI133814	1	5	4	I5	0	0	0	0	0	0	
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9	CPI133814	1	5	5	I4	0	0	0	0	0	0	
9	CPI133814	1	5	5	P	0	0	0	0	0	0	
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9	CPI133814	2	1	1	I4	0	7	5	2	0	0	
9	CPI133814	2	1	1	I5	0	0	0	0	0	0	
9	CPI133814	2	1	1	I6	0	0	0	0	0	0	
9	CPI133814	2	1	1	P	0	0	0	0	0	0	
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9	CPI133814	2	1	2	I2	1	8	4	0	2	2	
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9	CPI133814	2	1	2	I4	0	0	0	0	0	0	
9	CPI133814	2	1	2	I5	0	0	0	0	0	0	
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9	CPI133814	2	1	3	I3	0	2	2	0	0	0	
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9	CPI133814	2	1	3	P	0	0	0	0	0	0	
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9	CPI133814	2	1	4	I3	0	1	1	0	0	0	
9	CPI133814	2	1	4	I4	0	0	0	0	0	0	
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9	CPI133814	2	1	4	P	0	0	0	0	0	0	
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9	CPI133814	2	2	1	I5	0	0	0	0	0	0	
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9	CPI133814	2	2	2	I3	1	12	6	4	2	0	
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9	CPI133814	2	2	2	I5	0	0	0	0	0	0	
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9	CPI133814	2	2	3	I2	1	6	1	2	1	2	

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9	CPI133814	2	2	3	I5	0	0	0	0	0	0	
9	CPI133814	2	2	3	I6	0	0	0	0	0	0	
9	CPI133814	2	2	3	P	0	0	0	0	0	0	
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9	CPI133814	2	2	4	I5	0	0	0	0	0	0	
9	CPI133814	2	2	4	P	0	0	0	0	0	0	
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9	CPI133814	2	2	5	I2	1	6	1	2	1	2	
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9	CPI133814	2	3	1	I4	0	8	7	1	0	0	
9	CPI133814	2	3	1	I5	0	0	0	0	0	0	
9	CPI133814	2	3	1	I6	0	0	0	0	0	0	
9	CPI133814	2	3	2	I1	4	5	2	1	1	1	
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9	CPI133814	2	3	2	I5	0	0	0	0	0	0	
9	CPI133814	2	3	2	I6	0	0	0	0	0	0	
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9	CPI133814	2	3	3	I2	1	7	2	2	0	3	
9	CPI133814	2	3	3	I3	0	7	7	0	0	0	
9	CPI133814	2	3	3	I4	0	0	0	0	0	0	
9	CPI133814	2	3	3	I5	0	0	0	0	0	0	
9	CPI133814	2	3	4	I1	4	5	1	1	2	1	
9	CPI133814	2	3	4	I2	1	13	4	3	3	3	
9	CPI133814	2	3	4	I3	0	21	6	6	5	4	

9	CPI133814	2	3	4	I4	0	0	0	0	0	0	
9	CPI133814	2	3	5	I1	4	4	1	1	1	1	
9	CPI133814	2	3	5	I2	1	9	4	2	0	3	
9	CPI133814	2	3	5	I3	0	8	3	1	0	4	
9	CPI133814	2	3	5	I4	0	6	4	2	0	0	
9	CPI133814	2	3	5	I5	0	0	0	0	0	0	
9	CPI133814	2	3	5	P	0	0	0	0	0	0	
9	CPI133814	2	4	1	I1	4	5	2	1	1	1	
9	CPI133814	2	4	1	I2	1	6	2	1	2	1	
9	CPI133814	2	4	1	I3	0	13	5	4	4	0	
9	CPI133814	2	4	1	I4	0	0	0	0	0	0	
9	CPI133814	2	4	1	I5	0	0	0	0	0	0	
9	CPI133814	2	4	1	I6	0	0	0	0	0	0	
9	CPI133814	2	4	1	P	0	0	0	0	0	0	
9	CPI133814	2	4	2	I1	4	4	1	1	1	1	
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9	CPI133814	2	4	2	I4	0	1	1	0	0	0	
9	CPI133814	2	4	2	I5	0	0	0	0	0	0	
9	CPI133814	2	4	2	P	0	0	0	0	0	0	
9	CPI133814	2	4	3	I1	4	5	1	1	1	2	
9	CPI133814	2	4	3	I2	3	15	4	4	3	4	
9	CPI133814	2	4	3	I3	0	13	5	4	3	1	
9	CPI133814	2	4	3	I4	0	5	5	0	0	0	
9	CPI133814	2	4	3	I5	0	0	0	0	0	0	
9	CPI133814	2	4	3	P	0	0	0	0	0	0	
9	CPI133814	2	4	4	I1	4	4	1	1	1	1	
9	CPI133814	2	4	4	I2	2	9	2	3	0	4	
9	CPI133814	2	4	4	I3	0	0	0	0	0	0	
9	CPI133814	2	4	4	I4	0	0	0	0	0	0	
9	CPI133814	2	4	4	I5	0	0	0	0	0	0	
9	CPI133814	2	4	4	P	0	0	0	0	0	0	
9	CPI133814	2	5	1	I1	4	6	2	1	1.5	1.5	
9	CPI133814	2	5	1	I2	2	11	3	2	3	3	
9	CPI133814	2	5	1	I3	0	4	4	0	0	0	
9	CPI133814	2	5	1	I4	0	0	0	0	0	0	

9	CPI133814	2	5	1	I5	0	0	0	0	0	0	
9	CPI133814	2	5	1	P	0	0	0	0	0	0	
9	CPI133814	2	5	2	I1	4	4	1	1	1	1	
9	CPI133814	2	5	2	I2	2	7	1	2	2	2	
9	CPI133814	2	5	2	I3	1	12	4	3	3	2	
9	CPI133814	2	5	2	I4	0	0	0	0	0	0	
9	CPI133814	2	5	2	I5	0	0	0	0	0	0	
9	CPI133814	2	5	2	P	0	0	0	0	0	0	
9	CPI133814	2	5	3	I1	4	4	1	1	1	1	
9	CPI133814	2	5	3	I2	3	10	3	3	2	2	
9	CPI133814	2	5	3	I3	0	9	6	3	0	0	
9	CPI133814	2	5	3	I4	0	0	0	0	0	0	
9	CPI133814	2	5	3	I5	0	0	0	0	0	0	
9	CPI133814	2	5	3	P	0	0	0	0	0	0	
9	CPI133814	2	5	4	I1	4	4	1	1	1	1	
9	CPI133814	2	5	4	I2	1	6	2	1	1	2	
9	CPI133814	2	5	4	I3	0	11	5	2	1	3	
9	CPI133814	2	5	4	I4	0	2	2	0	0	0	
9	CPI133814	2	5	4	I5	0	0	0	0	0	0	
9	CPI133814	2	5	4	P	0	0	0	0	0	0	
9	CPI133814	2	5	5	I1	4	4	1	1	1	1	
9	CPI133814	2	5	5	I2	4	7	2	2	1	2	
9	CPI133814	2	5	5	I3	1	15	6	3	5	1	
9	CPI133814	2	5	5	I4	0	0	0	0	0	0	
9	CPI133814	2	5	5	I5	0	0	0	0	0	0	
9	CPI133814	2	5	5	P	0	0	0	0	0	0	
9	CPI133814	3	1	1	I1	4						
9	CPI133814	3	1	1	I2	4						
9	CPI133814	3	1	1	I3	2						
9	CPI133814	3	1	1	I4	1						
9	CPI133814	3	1	1	I5	0						
9	CPI133814	3	1	1	I6	0						
9	CPI133814	3	1	1	P	0						
9	CPI133814	3	1	2	I1	4						
9	CPI133814	3	1	2	I2	4						
9	CPI133814	3	1	2	I3	1						

9	CPI133814	3	1	2	I4	0						
9	CPI133814	3	1	2	I5	0						
9	CPI133814	3	1	2	P	0						
9	CPI133814	3	1	3	I1	4						
9	CPI133814	3	1	3	I2	1						
9	CPI133814	3	1	3	I3	0						
9	CPI133814	3	1	3	I4	0						
9	CPI133814	3	1	3	I5	0						
9	CPI133814	3	1	3	P	0						
9	CPI133814	3	1	4	I1	4						
9	CPI133814	3	1	4	I2	1						
9	CPI133814	3	1	4	I3	0						
9	CPI133814	3	1	4	I4	0						
9	CPI133814	3	1	4	I5	0						
9	CPI133814	3	1	4	P	0						
9	CPI133814	3	1	5	I1	4						
9	CPI133814	3	1	5	I2	1						
9	CPI133814	3	1	5	I3	0						
9	CPI133814	3	1	5	I4	0						
9	CPI133814	3	1	5	I5	0						
9	CPI133814	3	1	5	P	0						
9	CPI133814	3	2	1	I1	4						
9	CPI133814	3	2	1	I2	3						
9	CPI133814	3	2	1	I3	1						
9	CPI133814	3	2	1	I4	0						
9	CPI133814	3	2	1	I5	0						
9	CPI133814	3	2	1	P	0						
9	CPI133814	3	2	2	I1	4						
9	CPI133814	3	2	2	I2	2						
9	CPI133814	3	2	2	I3	0						
9	CPI133814	3	2	2	I4	0						
9	CPI133814	3	2	2	I5	0						
9	CPI133814	3	2	2	P	0						
9	CPI133814	3	2	3	I1	4						
9	CPI133814	3	2	3	I2	1						
9	CPI133814	3	2	3	I3	0						

9	CPI133814	3	2	3	I4	0						
9	CPI133814	3	2	3	I5	0						
9	CPI133814	3	2	3	P	0						
9	CPI133814	3	2	4	I1	3						
9	CPI133814	3	2	4	I2	0						
9	CPI133814	3	2	4	I3	0						
9	CPI133814	3	2	4	I4	0						
9	CPI133814	3	2	4	I5	0						
9	CPI133814	3	2	4	P	0						
9	CPI133814	3	2	5	I1	4						
9	CPI133814	3	2	5	I2	0						
9	CPI133814	3	2	5	I3	0						
9	CPI133814	3	2	5	I4	0						
9	CPI133814	3	2	5	I5	0						
9	CPI133814	3	2	5	P	0						
9	CPI133814	3	3	1	I1	4						
9	CPI133814	3	3	1	I2	1						
9	CPI133814	3	3	1	I3	0						
9	CPI133814	3	3	1	I4	0						
9	CPI133814	3	3	1	I5	0						
9	CPI133814	3	3	2	I1	4						
9	CPI133814	3	3	2	I2	1						
9	CPI133814	3	3	2	I3	0						
9	CPI133814	3	3	2	I4	0						
9	CPI133814	3	3	2	I5	0						
9	CPI133814	3	3	2	I6	0						
9	CPI133814	3	3	2	P	0						
9	CPI133814	3	3	3	I1	4						
9	CPI133814	3	3	3	I2	1						
9	CPI133814	3	3	3	I3	0						
9	CPI133814	3	3	3	I4	0						
9	CPI133814	3	3	3	I5	0						
9	CPI133814	3	3	3	I6	0						
9	CPI133814	3	3	3	P	0						
9	CPI133814	3	3	4	I1	4						
9	CPI133814	3	3	4	I2	2						

9	CPI133814	3	3	4	I3	0						
9	CPI133814	3	3	4	I4	0						
9	CPI133814	3	3	4	I5	0						
9	CPI133814	3	3	4	I6	0						
9	CPI133814	3	3	4	P	0						
9	CPI133814	3	3	5	I1	4						
9	CPI133814	3	3	5	I2	1						
9	CPI133814	3	3	5	I3	0						
9	CPI133814	3	3	5	I4	0						
9	CPI133814	3	3	5	I5	0						
9	CPI133814	3	3	5	P	0						
9	CPI133814	3	4	1	I1	4						
9	CPI133814	3	4	1	I2	4						
9	CPI133814	3	4	1	I3	1						
9	CPI133814	3	4	1	I4	0						
9	CPI133814	3	4	1	I5	0						
9	CPI133814	3	4	1	I6	0						
9	CPI133814	3	4	1	P	0						
9	CPI133814	3	4	2	I1	4						
9	CPI133814	3	4	2	I2	2						
9	CPI133814	3	4	2	I3	0						
9	CPI133814	3	4	2	I4	0						
9	CPI133814	3	4	2	I5	0						
9	CPI133814	3	4	2	I6	0						
9	CPI133814	3	4	2	P	0						
9	CPI133814	3	4	3	I1	4						
9	CPI133814	3	4	3	I2	1						
9	CPI133814	3	4	3	I3	0						
9	CPI133814	3	4	3	I4	0						
9	CPI133814	3	4	3	I5	0						
9	CPI133814	3	4	3	I6	0						
9	CPI133814	3	4	3	P	0						
9	CPI133814	3	4	4	I1	4						
9	CPI133814	3	4	4	I2	1						
9	CPI133814	3	4	4	I3	0						
9	CPI133814	3	4	4	I4	0						

9	CPI133814	3	4	4	I5	0						
9	CPI133814	3	4	4	I6	0						
9	CPI133814	3	4	4	P	0						
9	CPI133814	3	4	5	I1	4						
9	CPI133814	3	4	5	I2	4						
9	CPI133814	3	4	5	I3	0						
9	CPI133814	3	4	5	I4	0						
9	CPI133814	3	5	1	I1	4						
9	CPI133814	3	5	1	I2	4						
9	CPI133814	3	5	1	I3	2						
9	CPI133814	3	5	1	I4	0						
9	CPI133814	3	5	2	I1	4						
9	CPI133814	3	5	2	I2	4						
9	CPI133814	3	5	2	I3	1						
9	CPI133814	3	5	2	I4	0						
9	CPI133814	3	5	2	I5	0						
9	CPI133814	3	5	2	P	0						
9	CPI133814	3	5	3	I1	4						
9	CPI133814	3	5	3	I2	4						
9	CPI133814	3	5	3	I3	1						
9	CPI133814	3	5	3	I4	0						

Appendix 3C
Jondaryan Field Trial Analysis Output

```
GenStat Release 6.1  (PC/Windows 2000)           03 February 2004 14:01:36
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                 ________________________________________

                 GenStat Sixth Edition
                 GenStat Procedure Library Release PL14
                 ________________________________________

   1  %CD 'C:/KerryBell/Biometry'
   2  "Cassandra Percy (UQ) and Graham Wildermuth (supervisor)
file=Jondaryan2000.gen
  -3  Jondaryan Inoculated Field Trial 2000
  -4
  -5  3 reps x 5 Genotypes / 5 Harvest times / 5 plants / up to 4 tillers /
plant part
  -6
  -7  Approximately every fortnight (harvest times), 5 plants were taken from
each plot.
  -8
  -9  Each plant was divided into its tillers (tiller 1 being the main tiller),
 -10  and each node was given a disease rating (0-4) and
 -11  then divided into 4 parts (for rep 1 & 2 only), these was placed out on
agar
 -12  and the number of 'infections' were counted. The sum of the infections
 -13  across these parts were analysed (=isolation counts).
 -14
 -15  Genotypes:
 -16  2-49
 -17  CPI133814
 -18  Puseas
 -19  Sunco
 -20  Vasco
 -21
 -22  Plant parts:
 -23  level 1: C (Coleoptile)
 -24  levels 2...6:   I1 to I5 (Internode)
 -25  levels 7...16:   LS1 to LS10 (Leaf Sheath)
 -26  level 17:   P (Peduncle)
 -27  level 18: SCI (Sub crown internode)
 -28
 -29  ANALYSES: An ar(1) parameter was attempted to be fitted across harvests,
 -30  but many times the REML analysis did not converge or produce sensible
results
 -31  so this parameter was dropped in these instances. If the parameter was
non-significant
 -32  (by comparing change in deviance to 2.8) then it was also dropped out.
 -33
 -34  Plant parts analysed across tillers and harvest times
 -35  {Each tiller not analysed separately as doesn't give much extra value}
 -36  - Disease Rating: I1 (H3,4); I2 (H3,4,5); I3 (H3,4,5); LS2 (H2), LS3 (H2),
LS4 (H2); SC1 (H1,2, tiller 1 only)
 -37  - Isolation Counts: I1 (H3,4,5); I2 (H3,4,5); I3 (H3,4,5); I4 (H4,5); LS1
(H2), LS2 (H2), LS3 (H2)
 -38  other parts were not analysed due to lack of values or high proportion of
zeros or the same value.
 -39  "
  40
  41  set [outprint=dot]
  42  import file='C:/KerryBell/Biometry/CassandraPercy(UQ)/Jondaryan 2000.xls';
\
  43    sheetname='original data'
```

```
 *** Loading Spreadsheet File ***

Catalogue of file C:\DOCUME~1\BELLK\LOCALS~1\TEMP\GENSTAT\G61D40.GSH

Sheet Title:
Data read from C:\KerryBell\Biometry\CassandraPercy(UQ)\Jondaryan 2000.xls
[ORIGINAL DATA]A1:L6921

Sheet Type: vector
Index       Type    Nval   Name
    1    variate    6920   Harvest
    3       text    6920   Genotype
    4    variate    6920   Rep
    5    variate    6920   Plant
    6    variate    6920   Tiller
    8       text    6920   Part
    9    variate    6920   Disease_Rating
   10    variate    6920   Infection_total
   11    variate    6920   Infection_1_4
   12    variate    6920   Infection_2_4
   13    variate    6920   Infection_3_4
   14    variate    6920   Infection_4_4

Missing indices are used by unnamed or system structures. These store ancillary
information, for example factor labels.
  44  group [redefine=yes] Harvest, Genotype, Rep, Plant, Tiller, Part
  45  facproduct factors=!P(Rep, Genotype); product=plot
  46  page
```

```
  47
  48  "=========================================================================
 -49      PART = I1 (Disease Rating: harvest 6, 7 & 8; Isolation Counts: harvest
5, 6, 7 & 8)
 -50  ========================================================================="
  51
  52  "**** I1 Disease Rating (Harvests 6, 7 & 8, only tillers 1, 2 & 3) ****"
  53
  54  subset
[condition=(Part.eq.2).and.(Harvest.ge.6).and.(Harvest.le.8).and.(Tiller.ge.1).a
nd.(Tiller.le.3); setlevel=yes] \
  55   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
  56   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
  57
  58  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
  59  reml [print=means, wald, comp, mod,dev] ndr

59.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 533

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0000       BOUND
nplot                        0.0145      0.0288
nplot.nharv                  0.0000       BOUND
nplot.nharv.nplant           0.5388      0.0718


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.352    0.0296


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     398.51   484

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***
```

```
   Fixed term               Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                         66.85             2        33.43      <0.001
   ngeno                        193.67             4        48.42      <0.001
   ntill                         78.30             2        39.15      <0.001
   nharv.ngeno                    9.60             8         1.20       0.294
   nharv.ntill                   16.10             4         4.03       0.003
   ngeno.ntill                   12.86             8         1.61       0.117
   nharv.ngeno.ntill             25.62            15         1.71       0.042

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill             25.62            15         1.71       0.042

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.627    Standard error:  0.0663



*** Table of predicted means for nharv ***

   nharv    6.000    7.000    8.000
                *    1.497    2.284

Standard error of differences:      0.1382



*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                    0.837            *        3.301        1.025        1.932

Standard error of differences:     Average       0.2063
                                   Maximum       0.2097
                                   Minimum       0.2028

Average variance of differences:              0.04256


*** Table of predicted means for ntill ***

   ntill    1.000    2.000    3.000
            1.971    1.566        *

Standard error of differences:     0.06140



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        6.000        0.356            *        3.048        0.749        1.086
        7.000        0.658        0.924        3.164        0.552        2.189
        8.000        1.498        1.937        3.690        1.775        2.520

Standard error of differences:     Average       0.3251
                                   Maximum       0.3537
```

```
                                   Minimum       0.3004

Average variance of differences:                 0.1058

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.3267      0.3129
Maximum          0.3464      0.3340
Minimum          0.3164      0.3004
Average variance of differences:
                 0.1068     0.09803



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000    3.000
        nharv
        6.000    1.528    1.026        *
        7.000    1.640    1.535    1.317
        8.000    2.747    2.137    1.969

Standard error of differences:     Average       0.1533
                                   Maximum       0.1838
                                   Minimum       0.1015

Average variance of differences:                0.02408

Standard error of differences for same level of factor:

                  nharv       ntill
Average          0.1144      0.1636
Maximum          0.1270      0.1838
Minimum          0.1015      0.1541
Average variance of differences:
                0.01316     0.02688



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000    3.000
        ngeno
         2-49    1.178    0.768    0.566
    CPI133814    1.489    1.148        *
       Puseas    3.444    3.249    3.208
        Sunco    1.467    0.938    0.672
        Vasco    2.280    1.725    1.790

Standard error of differences:     Average       0.2270
                                   Maximum       0.2770
                                   Minimum       0.1287

Average variance of differences:                0.05264

Standard error of differences for same level of factor:

                  ngeno       ntill
Average          0.1525      0.2373
Maximum          0.1794      0.2770
Minimum          0.1287      0.2219
Average variance of differences:
                0.02350     0.05661



*** Table of predicted means for nharv.ngeno.ntill ***
```

```
                 ntill    1.000    2.000    3.000
        nharv    ngeno
        6.000     2-49    0.867    0.353   -0.151
             CPI133814    0.867    0.441        *
                Puseas    3.200    2.853    3.092
                 Sunco    1.200    0.535    0.512
                 Vasco    1.506    0.946    0.808
        7.000     2-49    0.733    0.733    0.508
             CPI133814    1.067    1.141    0.565
                Puseas    3.400    3.022    3.069
                 Sunco    0.933    0.561    0.161
                 Vasco    2.067    2.217    2.283
        8.000     2-49    1.933    1.218    1.342
             CPI133814    2.533    1.862    1.416
                Puseas    3.733    3.872    3.463
                 Sunco    2.267    1.718    1.342
                 Vasco    3.267    2.013    2.281

Standard error of differences:     Average       0.3827
                                   Maximum       0.5020
                                   Minimum       0.2165

Average variance of differences:                 0.1480

Standard error of differences for same level of factor:

                   nharv       ngeno       ntill
Average           0.3716      0.3488      0.3871
Maximum           0.4956      0.4739      0.5020
Minimum           0.2165      0.2165      0.3445
Average variance of differences:
                  0.1410      0.1252      0.1511


  60
  61  "REML wouldn't converge with code below"
  62  \vcomp [fixed=ngeno*nharv*ntill]
random="nrep+"nplot+nplot.nharv+nplot.nharv.nplant; const=pos
  63  \vstruct [nplot.nharv] factor=nharv; model="ar "uniform
  64  \reml [print=means, wald, comp, mod,dev] ndr
  65  page
```

```
  66
  67  "**** I1 Isolation counts (total) (Harvests 5, 6, 7 & 8, only tillers 1 &
2, no data collected for rep 3) ****"
  68
  69  subset
[condition=(Part.eq.2).and.(Harvest.ge.5).and.(Harvest.le.8).and.(Rep.le.2).and.
(Tiller.ge.1).and.(Tiller.le.2); setlevel=yes] \
  70   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
  71   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
  72
  73  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
  74  reml [print=means, wald, comp, mod,dev] sqrt(ntotal)

74...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 322

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term                Component        S.e.

nrep                          0.0347      0.0580
nplot                         0.0018      0.0247
nplot.nharv                   0.0269      0.0430
nplot.nharv.nplant            0.1441      0.0569


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.429    0.0564


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     205.74   278

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term               Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

   nharv                         129.72            3         43.24      <0.001
   ngeno                          71.36            4         17.84      <0.001
   ntill                           2.44            1          2.44       0.118
   nharv.ngeno                    13.44           12          1.12       0.338
   nharv.ntill                     9.43            3          3.14       0.024
   ngeno.ntill                    10.35            4          2.59       0.035
   nharv.ngeno.ntill              15.27           11          1.39       0.170

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill              15.27           11          1.39       0.170

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.328    Standard error:  0.1466



*** Table of predicted means for nharv ***

   nharv    5.000    6.000    7.000    8.000
                *    0.842    1.386    2.220

Standard error of differences:     Average       0.1480
                                   Maximum       0.1500
                                   Minimum       0.1459


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                    0.877            *        2.100        1.146        1.604

Standard error of differences:     Average       0.1847
                                   Maximum       0.1879
                                   Minimum       0.1817

Average variance of differences:                0.03412


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
            1.338        *

* SEDs not available


*** Table of predicted means for nharv.ngeno ***

        ngeno          2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        5.000         0.043            *        1.735        0.777        0.964
        6.000         0.268        0.203        1.914        0.508        1.319
        7.000         1.064        0.951        2.116        1.162        1.636
        8.000         2.132        1.698        2.637        2.139        2.496

Standard error of differences:     Average       0.3548
                                   Maximum       0.4629
                                   Minimum       0.3164

Average variance of differences:                 0.1270
```

```
Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.3499      0.3542
Maximum          0.4629      0.4096
Minimum          0.3193      0.3164
Average variance of differences:
                 0.1240      0.1264



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        5.000    0.643        *
        6.000    0.910    0.774
        7.000    1.434    1.337
        8.000    2.363    2.078

Standard error of differences:     Average       0.1745
                                   Maximum       0.1977
                                   Minimum       0.1382

Average variance of differences:                0.03066

Standard error of differences for same level of factor:

                  nharv       ntill
Average          0.1464      0.1771
Maximum          0.1545      0.1977
Minimum          0.1382      0.1682
Average variance of differences:
                0.02149     0.03148



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49    0.831    0.923
    CPI133814    0.941        *
       Puseas    2.228    1.973
        Sunco    1.255    1.038
        Vasco    1.434    1.774

Standard error of differences:     Average       0.2198
                                   Maximum       0.2683
                                   Minimum       0.1751

Average variance of differences:                0.04891

Standard error of differences for same level of factor:

                  ngeno       ntill
Average          0.1903      0.2185
Maximum          0.1986      0.2683
Minimum          0.1751      0.1940
Average variance of differences:
                0.03629     0.04869



*** Table of predicted means for nharv.ngeno.ntill ***

                     ntill    1.000    2.000
```

```
        nharv         ngeno
        5.000          2-49    0.011    0.076
                  CPI133814    0.728        *
                     Puseas    1.477    1.994
                      Sunco    0.345    1.210
                      Vasco    0.656    1.273
        6.000          2-49    0.373    0.163
                  CPI133814    0.141    0.265
                     Puseas    2.245    1.584
                      Sunco    0.848    0.167
                      Vasco    0.944    1.694
        7.000          2-49    0.688    1.439
                  CPI133814    1.139    0.763
                     Puseas    2.236    1.995
                      Sunco    1.493    0.831
                      Vasco    1.615    1.657
        8.000          2-49    2.251    2.014
                  CPI133814    1.757    1.638
                     Puseas    2.956    2.317
                      Sunco    2.333    1.944
                      Vasco    2.519    2.474

Standard error of differences:     Average       0.4332
                                   Maximum       0.7661
                                   Minimum       0.2930

Average variance of differences:                 0.1935

Standard error of differences for same level of factor:

                 nharv       ngeno       ntill
Average         0.4237      0.4241      0.4324
Maximum         0.7661      0.6466      0.7661
Minimum         0.2930      0.2930      0.3762
Average variance of differences:
                0.1862      0.1863      0.1936


  75
  76  "REML wouldn't converge with code below"
  77  \vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
  78  \vstruct [nplot.nharv] factor=nharv; model=ar "uniform"
  79  \reml [print=means, wald, comp, mod,dev] (ntotal)
  80
  81  vkeep means=htmean; term=nharv.ntill
  82  vkeep means=gtmean; term=ngeno.ntill
  83  print 'Back-transformed means' & htmean**2 & gtmean**2


 Back-transformed means


              htmean** 2
        ntill       1.000       2.000
        nharv
        5.000       0.414           *
        6.000       0.829       0.600
        7.000       2.056       1.788
        8.000       5.584       4.316


              gtmean** 2
        ntill       1.000       2.000
        ngeno
         2-49       0.690       0.852
    CPI133814       0.886           *
       Puseas       4.965       3.891
```

```
      Sunco       1.574       1.078
      Vasco       2.055       3.148

  84  delete [redefine=yes] htmean, gtmean
  85  page
```

```
  86
  87  "==========================================================================
 -88                     PART = I2 (Disease rating: no analysis; Infection
count: harvest 7 & 8)
 -89  =========================================================================="
  90
  91  "**** I2 Disease Rating ****"
  92  "No analysis as too many zeros's"
  93
  94  "**** I2 Isolation counts (total) (Harvests 7 & 8, only tillers 1, 2 & 3,
no data collected for rep 3) ****"
  95
  96  subset
[condition=(Part.eq.3).and.(Harvest.ge.7).and.(Harvest.le.8).and.(Rep.le.2).and.
(Tiller.ge.1).and.(Tiller.le.3); setlevel=yes] \
  97   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
  98   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
  99
 100  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 101  reml [print=means, wald, comp, mod,dev] sqrt(ntotal)

101..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 226

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0291      0.0746
nplot                        0.0435      0.0817
nplot.nharv                  0.0000       BOUND
nplot.nharv.nplant           0.3415      0.1108


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.706    0.0950


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     252.18   191

Note: deviance omits constants which depend on fixed model fitted.
```

```
*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                         52.95            1        52.95      <0.001
   ngeno                         10.25            4         2.56       0.036
   ntill                         13.66            2         6.83       0.001
   nharv.ngeno                   14.42            4         3.61       0.006
   nharv.ntill                    3.09            2         1.55       0.213
   ngeno.ntill                    5.31            8         0.66       0.724
   nharv.ngeno.ntill              5.71            8         0.71       0.680

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill              5.71            8         0.71       0.680

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.9852    Standard error: 0.16365



*** Table of predicted means for nharv ***

   nharv    7.000    8.000
           0.4020   1.5684

Standard error of differences:      0.1769



*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.8491       0.4544       1.2462       0.9768       1.3994

Standard error of differences:     Average       0.3493
                                   Maximum       0.3686
                                   Minimum       0.3319

Average variance of differences:                 0.1221


*** Table of predicted means for ntill ***

   ntill    1.000    2.000    3.000
           1.2562   0.9134   0.7860

Standard error of differences:     Average       0.1569
                                   Maximum       0.1715
                                   Minimum       0.1318

Average variance of differences:                0.02495


*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
```

```
        nharv
        7.000      -0.0027       0.0333       1.1240      -0.0474       0.9028
        8.000       1.7008       0.8754       1.3684       2.0011       1.8960

Standard error of differences:     Average       0.4410
                                   Maximum       0.5153
                                   Minimum       0.3608

Average variance of differences:                 0.1954

Standard error of differences for same level of factor:

                 nharv       ngeno
Average         0.4467      0.3944
Maximum         0.5153      0.4322
Minimum         0.4141      0.3608
Average variance of differences:
                0.2003      0.1564



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000    3.000
        nharv
        7.000   0.5349   0.3422   0.3290
        8.000   1.9775   1.4846   1.2430

Standard error of differences:     Average       0.2391
                                   Maximum       0.3108
                                   Minimum       0.1777

Average variance of differences:                0.05860

Standard error of differences for same level of factor:

                 nharv       ntill
Average         0.2205      0.2498
Maximum         0.2704      0.3108
Minimum         0.1777      0.2047
Average variance of differences:
               0.04978     0.06440



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000    3.000
        ngeno
         2-49   1.0598   0.6735   0.8138
    CPI133814   0.8316   0.4816   0.0499
       Puseas   1.6224   1.3370   0.7792
        Sunco   1.2396   0.8120   0.8789
        Vasco   1.5274   1.2627   1.4082

Standard error of differences:     Average       0.4351
                                   Maximum       0.6153
                                   Minimum       0.2705

Average variance of differences:                 0.1937

Standard error of differences for same level of factor:

                 ngeno       ntill
Average         0.3480      0.4478
Maximum         0.4546      0.6153
Minimum         0.2705      0.3850
Average variance of differences:
```

```
                 0.1246      0.2052



*** Table of predicted means for nharv.ngeno.ntill ***

                     ntill    1.000    2.000    3.000
        nharv        ngeno
        7.000         2-49    0.000    0.000   -0.008
                 CPI133814    0.173   -0.027   -0.047
                    Puseas    1.588    1.060    0.724
                     Sunco    0.200   -0.078   -0.264
                     Vasco    0.714    0.755    1.240
        8.000         2-49    2.120    1.347    1.636
                 CPI133814    1.490    0.990    0.146
                    Puseas    1.657    1.614    0.834
                     Sunco    2.279    1.702    2.022
                     Vasco    2.341    1.770    1.576

Standard error of differences:     Average       0.5860
                                   Maximum       0.9870
                                   Minimum       0.3757

Average variance of differences:                 0.3535

Standard error of differences for same level of factor:

                  nharv       ngeno       ntill
Average          0.5816      0.5304      0.5904
Maximum          0.9870      0.8368      0.9870
Minimum          0.3757      0.3757      0.4576
Average variance of differences:
                 0.3494      0.2928      0.3612


 102  vkeep means=hgmean; term=nharv.ngeno
 103  vkeep means=tmean; term=ntill
 104  print 'Back-transformed means' & hgmean**2 & tmean**2


 Back-transformed means


               hgmean** 2
        nharv       7.000       8.000
        ngeno
         2-49       0.000       2.893
    CPI133814       0.001       0.766
       Puseas       1.263       1.872
        Sunco       0.002       4.004
        Vasco       0.815       3.595


                tmean** 2
        ntill
        1.000       1.578
        2.000       0.834
        3.000       0.618

 105  delete [redefine=yes] hgmean, tmean
 106  page
```

```
 107
 108  "=========================================================================
-109                      PART = I3 (Disease rating: no analysis; Infection
count: harvest 8)
-110  ========================================================================"
 111
 112  "**** I3 Disease Rating ****"
 113  "No analysis as too many zeros's"
 114
 115  "**** I3 Isolation counts (total) (Harvests 8, only tiller 1, no data
collected for rep 3) ****"
 116
 117  subset
[condition=(Part.eq.4).and.(Harvest.ge.8).and.(Harvest.le.8).and.(Rep.le.2).and.
(Tiller.ge.1).and.(Tiller.le.1); setlevel=yes] \
 118   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 119   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 120
 121  vcomp [fixed=ngeno] random=nrep+nplot+nplot.nharv.nplant; const=pos
 122  reml [print=means, wald, comp, mod,dev] sqrt(ntotal)

122.....................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+ngeno
Random model     : nrep+nplot+nplot.nharv.nplant

Number of units  : 50

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                        0.0000       BOUND
nplot                       0.0000       BOUND


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

nplot.nharv.nplant             Identity      Sigma2              0.771    0.1626


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                      44.83    42

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***
```

```
   Fixed term               Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   ngeno                             6.39             4         1.60       0.172

* Dropping individual terms from full fixed model

   ngeno                             6.39             4         1.60       0.172

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.4326    Standard error: 0.12421



*** Table of predicted means for ngeno ***

       ngeno          2-49    CPI133814       Puseas         Sunco         Vasco
                    0.5146       0.1414       0.2000        0.3000        1.0068

Standard error of differences:      0.3928


 123  vkeep means=gmean; term=ngeno
 124  print 'Back-transformed means' & gmean**2


 Back-transformed means


                 gmean** 2
        ngeno
         2-49      0.2648
    CPI133814      0.0200
       Puseas      0.0400
        Sunco      0.0900
        Vasco      1.0137

 125  delete [redefine=yes] gmean
 126  page
```

```
 127
 128  "===========================================================================
-129                      PART = I4 (No analysis - too many zero's)
-130  ==========================================================================="
 131
 132  "===========================================================================
-133                      PART = I5 (No analysis - too many zero's)
-134  ==========================================================================="
 135
 136  "===========================================================================
-137                      PART = LS1 (Disease rating: harvest 3, 4, 5 & 6;
Infection count: harvest 4, 5 & 6)
-138  ==========================================================================="
 139
 140  "**** LS1 Disease Rating (Harvests 3, 4, 5 & 6, only tillers 1 & 2) ****"
 141
 142  subset
[condition=(Part.eq.7).and.(Harvest.ge.3).and.(Harvest.le.6).and.(Tiller.ge.1).a
nd.(Tiller.le.2); setlevel=yes] \
 143   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 144   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 145
 146  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 147  reml [print=means, wald, comp, mod,dev] ndr

147.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 519 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0004      0.0062
nplot                        0.0000       BOUND
nplot.nharv                  0.0000       BOUND
nplot.nharv.nplant           0.2024      0.0599


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.620    0.0612


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.
```

```
                      474.16   474

Note: deviance omits constants which depend on fixed model fitted.


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                         24.08            3         8.03      <0.001
   ngeno                         13.12            4         3.28       0.011
   ntill                         51.51            1        51.51      <0.001
   nharv.ngeno                   22.91           12         1.91       0.028
   nharv.ntill                    8.31            3         2.77       0.040
   ngeno.ntill                   33.80            4         8.45      <0.001
   nharv.ngeno.ntill             16.57           12         1.38       0.167

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill             16.57           12         1.38       0.167

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.098    Standard error:  0.0464



*** Table of predicted means for nharv ***

   nharv    3.000    4.000    5.000    6.000
            0.705    1.089    1.444    1.152

Standard error of differences:     Average       0.1267
                                   Maximum       0.1316
                                   Minimum       0.1218

Average variance of differences:               0.01607


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                    1.184        1.030        1.425        0.924        0.924

Standard error of differences:     Average       0.1417
                                   Maximum       0.1477
                                   Minimum       0.1363

Average variance of differences:               0.02009


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
            1.374    0.821

Standard error of differences:     0.07307
```

```
*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        3.000        0.905        0.360        0.870        0.625        0.764
        4.000        1.006        1.115        1.416        1.064        0.844
        5.000        1.448        1.313        2.149        1.257        1.055
        6.000        1.378        1.333        1.265        0.750        1.033

Standard error of differences:     Average       0.2831
                                   Maximum       0.3354
                                   Minimum       0.2631

Average variance of differences:                0.08037

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.2830      0.2831
Maximum          0.3354      0.3191
Minimum          0.2631      0.2668
Average variance of differences:
                0.08037     0.08037



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        3.000    1.087    0.322
        4.000    1.476    0.703
        5.000    1.560    1.329
        6.000    1.373    0.930

Standard error of differences:     Average       0.1605
                                   Maximum       0.1910
                                   Minimum       0.1341

Average variance of differences:                0.02598

Standard error of differences for same level of factor:

                  nharv       ntill
Average          0.1457      0.1628
Maximum          0.1632      0.1910
Minimum          0.1341      0.1481
Average variance of differences:
                0.02135     0.02675



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49    1.083    1.285
    CPI133814    1.411    0.649
       Puseas    1.637    1.213
        Sunco    1.367    0.481
        Vasco    1.372    0.476

Standard error of differences:     Average       0.1802
                                   Maximum       0.2158
                                   Minimum       0.1528

Average variance of differences:                0.03269
```

```
Standard error of differences for same level of factor:

                  ngeno       ntill
Average          0.1631      0.1820
Maximum          0.1787      0.2158
Minimum          0.1528      0.1651
Average variance of differences:
                0.02669     0.03344



*** Table of predicted means for nharv.ngeno.ntill ***

                     ntill    1.000    2.000
        nharv        ngeno
        3.000         2-49    1.067    0.744
                 CPI133814    0.467    0.253
                    Puseas    1.214    0.526
                     Sunco    1.267   -0.017
                     Vasco    1.423    0.105
        4.000         2-49    0.933    1.079
                 CPI133814    1.778    0.451
                    Puseas    1.667    1.166
                     Sunco    1.667    0.461
                     Vasco    1.333    0.355
        5.000         2-49    1.000    1.896
                 CPI133814    1.667    0.959
                    Puseas    2.400    1.899
                     Sunco    1.533    0.981
                     Vasco    1.200    0.909
        6.000         2-49    1.333    1.422
                 CPI133814    1.733    0.933
                    Puseas    1.267    1.263
                     Sunco    1.000    0.500
                     Vasco    1.533    0.534

Standard error of differences:     Average       0.3628
                                   Maximum       0.5382
                                   Minimum       0.2874

Average variance of differences:                 0.1331

Standard error of differences for same level of factor:

                  nharv       ngeno       ntill
Average          0.3594      0.3582      0.3633
Maximum          0.5382      0.4968      0.5382
Minimum          0.2874      0.2874      0.3278
Average variance of differences:
                 0.1307      0.1299      0.1337
```

```
 149
 150  "**** LS1 Isolation counts (total) (Harvests 4, 5 & 6, only tillers 1 & 2,
no data collected for rep 3) ****"
 151
 152  subset
[condition=(Part.eq.7).and.(Harvest.ge.4).and.(Harvest.le.6).and.(Rep.le.2).and.
(Tiller.ge.1).and.(Tiller.le.2); setlevel=yes] \
 153   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 154   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 155
 156  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 157  reml [print=means, wald, comp, mod,dev] sqrt(ntotal)

157.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 268 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term                Component        S.e.

nrep                          0.0000       BOUND
nplot                         0.0077       BOUND
nplot.nharv                   0.0947      0.0938
nplot.nharv.nplant            0.3854      0.1078


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.612    0.0850


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     293.72   233

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term               Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

   nharv                          2.89            2         1.45       0.235
   ngeno                          4.39            4         1.10       0.355
   ntill                         77.32            1        77.32      <0.001
   nharv.ngeno                    8.26            8         1.03       0.409
   nharv.ntill                    4.01            2         2.01       0.135
   ngeno.ntill                    3.08            4         0.77       0.544
   nharv.ngeno.ntill              9.42            8         1.18       0.308

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill              9.42            8         1.18       0.308

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.216    Standard error:  0.0920



*** Table of predicted means for nharv ***

   nharv    4.000    5.000    6.000
            1.064    1.412    1.172

Standard error of differences:     Average       0.2248
                                   Maximum       0.2257
                                   Minimum       0.2239


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                    1.129        1.047        1.539        1.060        1.305

Standard error of differences:     Average       0.2911
                                   Maximum       0.2936
                                   Minimum       0.2888


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
            1.653    0.779

Standard error of differences:     0.09951



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        4.000        1.233        0.798        1.052        0.987        1.251
        5.000        0.946        1.297        2.030        1.656        1.132
        6.000        1.209        1.047        1.535        0.537        1.532

Standard error of differences:     Average       0.5030
                                   Maximum       0.5189
                                   Minimum       0.4922

Average variance of differences:                 0.2531

Standard error of differences for same level of factor:
```

```
                 nharv       ngeno
Average          0.5031      0.5026
Maximum          0.5156      0.5137
Minimum          0.4927      0.4922
Average variance of differences:
                 0.2532      0.2526



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        4.000    1.546    0.582
        5.000    1.948    0.876
        6.000    1.465    0.879

Standard error of differences:     Average       0.2389
                                   Maximum       0.2681
                                   Minimum       0.1671

Average variance of differences:                0.05825

Standard error of differences for same level of factor:

                 nharv       ntill
Average          0.1723      0.2555
Maximum          0.1776      0.2681
Minimum          0.1671      0.2454
Average variance of differences:
                0.02971     0.06538



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49    1.450    0.808
    CPI133814    1.635    0.459
       Puseas    1.935    1.143
        Sunco    1.516    0.604
        Vasco    1.731    0.879

Standard error of differences:     Average       0.3187
                                   Maximum       0.3520
                                   Minimum       0.2159

Average variance of differences:                 0.1028

Standard error of differences for same level of factor:

                 ngeno       ntill
Average          0.2224      0.3306
Maximum          0.2322      0.3520
Minimum          0.2159      0.3176
Average variance of differences:
                0.04951      0.1095



*** Table of predicted means for nharv.ngeno.ntill ***

                    ntill    1.000    2.000
        nharv       ngeno
        4.000        2-49    1.359    1.107
                CPI133814    1.564    0.031
```

```
                 Puseas    1.356    0.748
                  Sunco    1.474    0.500
                  Vasco    1.979    0.523
       5.000       2-49    1.595    0.297
              CPI133814    1.764    0.829
                 Puseas    2.708    1.352
                  Sunco    2.150    1.161
                  Vasco    1.524    0.739
       6.000       2-49    1.396    1.021
              CPI133814    1.575    0.518
                 Puseas    1.740    1.330
                  Sunco    0.925    0.150
                  Vasco    1.689    1.375

Standard error of differences:     Average       0.5653
                                   Maximum       0.6459
                                   Minimum       0.3498

Average variance of differences:                 0.3212

Standard error of differences for same level of factor:

                  nharv       ngeno       ntill
Average          0.5510      0.5341      0.5716
Maximum          0.6312      0.6304      0.6459
Minimum          0.3498      0.3498      0.5486
Average variance of differences:
                 0.3075      0.2912      0.3274


 158  vkeep means=tmean; term=ntill
 159  print 'Back-transformed means' & tmean**2


 Back-transformed means


                tmean** 2
       ntill
       1.000       2.733
       2.000       0.606

 160  delete [redefine=yes] tmean
 161  page
```

```
 162
 163  "=========================================================================
-164                      PART = LS2 (Disease rating: harvest 4, 5 & 6;
Infection count: harvest 4, 5 & 6)
-165  ========================================================================="
 166
 167  "**** LS2 Disease Rating (Harvests 4, 5 & 6, only tillers 1 & 2) ****"
 168
 169  subset
[condition=(Part.eq.9).and.(Harvest.ge.4).and.(Harvest.le.6).and.(Tiller.ge.1).a
nd.(Tiller.le.2); setlevel=yes] \
 170   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 171   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 172
 173  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 174  reml [print=means, wald, comp, mod,dev] ndr

174.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 403

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0010      0.0066
nplot                        0.0040      0.0130
nplot.nharv                  0.0000       BOUND
nplot.nharv.nplant           0.1584      0.0372


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.284    0.0314


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     126.25   368

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***
```

```
   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                         31.86            2        15.93      <0.001
   ngeno                         31.25            4         7.81      <0.001
   ntill                         89.81            1        89.81      <0.001
   nharv.ngeno                   19.57            8         2.45       0.012
   nharv.ntill                    5.55            2         2.77       0.062
   ngeno.ntill                   13.07            4         3.27       0.011
   nharv.ngeno.ntill              7.94            8         0.99       0.439

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill              7.94            8         0.99       0.439

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.8427    Standard error: 0.04530



*** Table of predicted means for nharv ***

   nharv    4.000    5.000    6.000
           0.5483   1.1025   0.8773

Standard error of differences:     Average      0.09363
                                   Maximum      0.09465
                                   Minimum      0.09264


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.7496       0.8814       1.2867       0.5882       0.7077

Standard error of differences:     Average       0.1316
                                   Maximum       0.1335
                                   Minimum       0.1297


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
           1.0978   0.5877

Standard error of differences:     0.05507


*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        4.000       0.5218       0.5302       0.7639       0.4394       0.4865
        5.000       0.8369       0.9808       1.9605       0.8478       0.8863
        6.000       0.8900       1.1333       1.1356       0.4773       0.7504

Standard error of differences:     Average       0.2148
                                   Maximum       0.2243
                                   Minimum       0.2038
```

```
Average variance of differences:                0.04614

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.2157      0.2093
Maximum          0.2243      0.2182
Minimum          0.2079      0.2038
Average variance of differences:
                0.04653     0.04383



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        4.000   0.8933   0.2034
        5.000   1.2800   0.9249
        6.000   1.1200   0.6347

Standard error of differences:     Average       0.1113
                                   Maximum       0.1248
                                   Minimum      0.09120

Average variance of differences:                0.01247

Standard error of differences for same level of factor:

                  nharv       ntill
Average         0.09529      0.1152
Maximum         0.09911      0.1248
Minimum         0.09120      0.1086
Average variance of differences:
               0.009090     0.01331



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49   0.9778   0.5214
    CPI133814   1.2889   0.4740
       Puseas   1.4222   1.1511
        Sunco   0.8889   0.2874
        Vasco   0.9111   0.5044

Standard error of differences:     Average       0.1538
                                   Maximum       0.1717
                                   Minimum       0.1183

Average variance of differences:                0.02380

Standard error of differences for same level of factor:

                  ngeno       ntill
Average          0.1230      0.1575
Maximum          0.1306      0.1717
Minimum          0.1183      0.1495
Average variance of differences:
                0.01515     0.02488



*** Table of predicted means for nharv.ngeno.ntill ***
```

```
                ntill        1.000        2.000
        nharv           ngeno
        4.000            2-49       0.8000       0.2435
                    CPI133814       0.9333       0.1270
                       Puseas       1.0667       0.4611
                        Sunco       0.9333      -0.0545
                        Vasco       0.7333       0.2396
        5.000            2-49       1.0667       0.6072
                    CPI133814       1.2667       0.6949
                       Puseas       2.0667       1.8544
                        Sunco       1.0000       0.6955
                        Vasco       1.0000       0.7727
        6.000            2-49       1.0667       0.7134
                    CPI133814       1.6667       0.6000
                       Puseas       1.1333       1.1379
                        Sunco       0.7333       0.2213
                        Vasco       1.0000       0.5009

Standard error of differences:     Average       0.2604
                                   Maximum       0.3031
                                   Minimum       0.1947

Average variance of differences:                0.06805

Standard error of differences for same level of factor:

                   nharv       ngeno       ntill
Average           0.2572      0.2486      0.2619
Maximum           0.3031      0.2985      0.3031
Minimum           0.1947      0.1947      0.2429
Average variance of differences:
                 0.06660     0.06233     0.06886
```

```
 176
 177  "**** LS2 Isolation counts (total) (Harvests 4, 5 & 6, only tillers 1 & 2,
no data collected for rep 3) ****"
 178
 179  subset
[condition=(Part.eq.9).and.(Harvest.ge.4).and.(Harvest.le.6).and.(Rep.le.2).and.
(Tiller.ge.1).and.(Tiller.le.2); setlevel=yes] \
 180   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 181   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 182
 183  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 184  reml [print=means, wald, comp, mod,dev] sqrt(ntotal)

184.................................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 269

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0000       BOUND
nplot                        0.0000       BOUND
nplot.nharv                  0.0747      0.0720
nplot.nharv.nplant           0.3282      0.0840


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.451    0.0623


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     231.72   234

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term               Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

   nharv                          7.40            2         3.70        0.025
   ngeno                          6.43            4         1.61        0.169
   ntill                         64.24            1        64.24       <0.001
   nharv.ngeno                    8.32            8         1.04        0.403
   nharv.ntill                    0.58            2         0.29        0.747
   ngeno.ntill                    1.55            4         0.39        0.817
   nharv.ngeno.ntill              7.92            8         0.99        0.442

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill              7.92            8         0.99        0.442

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.8124    Standard error: 0.08061



*** Table of predicted means for nharv ***

   nharv    4.000    5.000    6.000
           0.6175   1.1119   0.7079

Standard error of differences:     Average       0.1974
                                   Maximum       0.1982
                                   Minimum       0.1968


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.7863       0.5740       1.1278       0.6649       0.9091

Standard error of differences:     Average       0.2549
                                   Maximum       0.2572
                                   Minimum       0.2528


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
           1.1522   0.4727

Standard error of differences:     0.08531



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        4.000       0.7327       0.3901       0.4515       0.5936       0.9197
        5.000       0.9316       0.9746       1.6173       1.1460       0.8900
        6.000       0.6946       0.3573       1.3147       0.2551       0.9177

Standard error of differences:     Average       0.4415
                                   Maximum       0.4552
                                   Minimum       0.4327

Average variance of differences:                 0.1949

Standard error of differences for same level of factor:
```

```
                  nharv       ngeno
Average          0.4415      0.4415
Maximum          0.4512      0.4512
Minimum          0.4327      0.4327
Average variance of differences:
                 0.1949      0.1949



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        4.000   0.9479   0.2871
        5.000   1.4924   0.7315
        6.000   1.0163   0.3995

Standard error of differences:     Average       0.2082
                                   Maximum       0.2343
                                   Minimum       0.1437

Average variance of differences:                0.04429

Standard error of differences for same level of factor:

                  nharv       ntill
Average          0.1477      0.2232
Maximum          0.1514      0.2343
Minimum          0.1437      0.2147
Average variance of differences:
                0.02183     0.04990



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49   1.1629   0.4097
    CPI133814   0.9876   0.1604
       Puseas   1.4497   0.8059
        Sunco   0.9275   0.4023
        Vasco   1.2331   0.5851

Standard error of differences:     Average       0.2774
                                   Maximum       0.3069
                                   Minimum       0.1846

Average variance of differences:                0.07797

Standard error of differences for same level of factor:

                  ngeno       ntill
Average          0.1907      0.2882
Maximum          0.1999      0.3069
Minimum          0.1846      0.2772
Average variance of differences:
                0.03639     0.08317



*** Table of predicted means for nharv.ngeno.ntill ***

                     ntill        1.000        2.000
        nharv        ngeno
        4.000         2-49       1.0114       0.4540
                 CPI133814       0.8196      -0.0394
```

```
                 Puseas       0.6182       0.2848
                  Sunco       0.8878       0.2994
                  Vasco       1.4025       0.4369
       5.000       2-49       1.4341       0.4291
              CPI133814       1.4287       0.5206
                 Puseas       2.2364       0.9983
                  Sunco       1.3564       0.9356
                  Vasco       1.0063       0.7738
       6.000       2-49       1.0432       0.3460
              CPI133814       0.7146       0.0000
                 Puseas       1.4946       1.1348
                  Sunco       0.5382      -0.0280
                  Vasco       1.2906       0.5447

Standard error of differences:     Average       0.4933
                                   Maximum       0.5637
                                   Minimum       0.3003

Average variance of differences:                 0.2447

Standard error of differences for same level of factor:

                  nharv       ngeno       ntill
Average          0.4804      0.4653      0.4990
Maximum          0.5505      0.5505      0.5637
Minimum          0.3003      0.3003      0.4801
Average variance of differences:
                 0.2339      0.2214      0.2495


 185  vkeep means=tmean; term=ntill
 186  vkeep means=hmean; term=nharv
 187  print 'Back-transformed means' & tmean**2 & hmean**2


 Back-transformed means


                tmean** 2
        ntill
        1.000      1.3275
        2.000      0.2234


                hmean** 2
        nharv
        4.000      0.3813
        5.000      1.2364
        6.000      0.5011

 188  delete [redefine=yes] tmean, hmean
 189  page
```

```
 190
 191  "==========================================================================
-192                       PART = LS3 (Disease rating: harvest 5 & 6; Infection
count: harvest 4, 5 & 6)
-193  =========================================================================="
 194
 195  "**** LS3 Disease Rating (Harvests 5 & 6, only tillers 1 & 2) ****"
 196
 197  subset
[condition=(Part.eq.10).and.(Harvest.ge.5).and.(Harvest.le.6).and.(Tiller.ge.1).
and.(Tiller.le.2); setlevel=yes] \
 198   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 199   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 200
 201  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 202  reml [print=means, wald, comp, mod,dev] ndr

202.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 268

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0023      0.0104
nplot                        0.0000       BOUND
nplot.nharv                  0.0000       BOUND
nplot.nharv.nplant           0.2274      0.0560


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.308    0.0424


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     123.56   243

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***
```

```
   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                             2.50            1         2.50       0.114
   ngeno                            24.69            4         6.17      <0.001
   ntill                            59.69            1        59.69      <0.001
   nharv.ngeno                       6.53            4         1.63       0.163
   nharv.ntill                       0.34            1         0.34       0.561
   ngeno.ntill                       4.84            4         1.21       0.304
   nharv.ngeno.ntill                 5.83            4         1.46       0.212

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill                 5.83            4         1.46       0.212

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.7295    Standard error: 0.05935



*** Table of predicted means for nharv ***

   nharv    5.000    6.000
           0.7962   0.6628

Standard error of differences:      0.1052



*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.6093       0.6789       1.2420       0.5817       0.5356

Standard error of differences:     Average       0.1663
                                   Maximum       0.1691
                                   Minimum       0.1638

Average variance of differences:               0.02767


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
           0.9933   0.4657

Standard error of differences:     0.07077



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        5.000       0.6364       0.5578       1.4434       0.8218       0.5215
        6.000       0.5822       0.8000       1.0406       0.3417       0.5496

Standard error of differences:     Average       0.2352
                                   Maximum       0.2437
                                   Minimum       0.2266
```

```
Average variance of differences:                0.05534

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.2352      0.2352
Maximum          0.2436      0.2437
Minimum          0.2266      0.2313
Average variance of differences:
                0.05534     0.05534



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        5.000   1.0400   0.5524
        6.000   0.9467   0.3790

Standard error of differences:     Average       0.1178
                                   Maximum       0.1337
                                   Minimum      0.09562

Average variance of differences:                0.01406

Standard error of differences for same level of factor:

                  nharv       ntill
Average         0.09998      0.1266
Maximum          0.1043      0.1337
Minimum         0.09562      0.1195
Average variance of differences:
                0.01002     0.01608



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49   0.9000   0.3187
    CPI133814   1.0667   0.2912
       Puseas   1.4667   1.0173
        Sunco   0.7667   0.3968
        Vasco   0.7667   0.3045

Standard error of differences:     Average       0.1956
                                   Maximum       0.2200
                                   Minimum       0.1523

Average variance of differences:                0.03850

Standard error of differences for same level of factor:

                  ngeno       ntill
Average          0.1581      0.2001
Maximum          0.1705      0.2200
Minimum          0.1523      0.1889
Average variance of differences:
                0.02503     0.04018



*** Table of predicted means for nharv.ngeno.ntill ***

                     ntill    1.000    2.000
```

```
        nharv         ngeno
        5.000          2-49   1.0000   0.2729
                  CPI133814   0.8000   0.3157
                     Puseas   1.7333   1.1535
                      Sunco   0.9333   0.7103
                      Vasco   0.7333   0.3097
        6.000          2-49   0.8000   0.3645
                  CPI133814   1.3333   0.2667
                     Puseas   1.2000   0.8812
                      Sunco   0.6000   0.0833
                      Vasco   0.8000   0.2993

Standard error of differences:     Average       0.2799
                                   Maximum       0.3248
                                   Minimum       0.2026

Average variance of differences:                0.07877

Standard error of differences for same level of factor:

                 nharv       ngeno       ntill
Average         0.2764      0.2631      0.2829
Maximum         0.3248      0.3248      0.3248
Minimum         0.2026      0.2026      0.2671
Average variance of differences:
               0.07700     0.07026     0.08036
```

```
 204
 205  "**** LS3 Isolation counts (total) (Harvests 4, 5 & 6, only tillers 1 & 2,
no data collected for rep 3) ****"
 206
 207  subset
[condition=(Part.eq.10).and.(Harvest.ge.4).and.(Harvest.le.6).and.(Rep.le.2).and
.(Tiller.ge.1).and.(Tiller.le.2); setlevel=yes] \
 208   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 209   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 210
 211  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 212  reml [print=means, wald, comp, mod,dev] sqrt(ntotal)

212.................................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 268

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                        0.0000       BOUND
nplot                       0.0232      0.0494
nplot.nharv                 0.0622      0.0639
nplot.nharv.nplant          0.1683      0.0612


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.392    0.0553


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     166.21   233

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

   nharv                          8.68            2         4.34        0.013
   ngeno                          9.04            4         2.26        0.060
   ntill                         32.45            1        32.45       <0.001
   nharv.ngeno                    8.32            8         1.04        0.403
   nharv.ntill                    0.82            2         0.41        0.663
   ngeno.ntill                    2.80            4         0.70        0.593
   nharv.ngeno.ntill             14.14            8         1.77        0.078

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill             14.14            8         1.77        0.078

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.4927    Standard error: 0.08415



*** Table of predicted means for nharv ***

   nharv    4.000    5.000    6.000
           0.2525   0.7393   0.4862

Standard error of differences:     Average       0.1691
                                   Maximum       0.1696
                                   Minimum       0.1685


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.4750       0.3233       0.9525       0.3511       0.3615

Standard error of differences:     Average       0.2661
                                   Maximum       0.2678
                                   Minimum       0.2647


*** Table of predicted means for ntill ***

   ntill    1.000    2.000
           0.7188   0.2666

Standard error of differences:     0.07931



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        4.000       0.4789       0.0343       0.2682       0.3272       0.1540
        5.000       0.6258       0.5543       1.3616       0.6567       0.4982
        6.000       0.3202       0.3813       1.2277       0.0696       0.4322

Standard error of differences:     Average       0.4033
                                   Maximum       0.4192
                                   Minimum       0.3694

Average variance of differences:                 0.1628

Standard error of differences for same level of factor:
```

```
                 nharv       ngeno
Average         0.4075      0.3780
Maximum         0.4157      0.3868
Minimum         0.3995      0.3694
Average variance of differences:
                0.1661      0.1429



*** Table of predicted means for nharv.ntill ***

        ntill    1.000    2.000
        nharv
        4.000   0.4454   0.0597
        5.000   1.0172   0.4614
        6.000   0.6937   0.2787

Standard error of differences:     Average       0.1833
                                   Maximum       0.2048
                                   Minimum       0.1344

Average variance of differences:                0.03417

Standard error of differences for same level of factor:

                 nharv       ntill
Average         0.1373      0.1948
Maximum         0.1401      0.2048
Minimum         0.1344      0.1866
Average variance of differences:
               0.01885     0.03800



*** Table of predicted means for ngeno.ntill ***

        ntill    1.000    2.000
        ngeno
         2-49   0.7228   0.2272
    CPI133814   0.5174   0.1293
       Puseas   1.3040   0.6010
        Sunco   0.5166   0.1857
        Vasco   0.5331   0.1898

Standard error of differences:     Average       0.2811
                                   Maximum       0.3089
                                   Minimum       0.1714

Average variance of differences:                0.08042

Standard error of differences for same level of factor:

                 ngeno       ntill
Average         0.1773      0.2940
Maximum         0.1850      0.3089
Minimum         0.1714      0.2850
Average variance of differences:
               0.03145     0.08655



*** Table of predicted means for nharv.ngeno.ntill ***

                    ntill        1.000        2.000
        nharv       ngeno
        4.000        2-49       0.5650       0.3929
                CPI133814       0.1000      -0.0313
```

```
                    Puseas       0.5914      -0.0549
                     Sunco       0.6293       0.0252
                     Vasco       0.3414      -0.0334
       5.000          2-49       1.1033       0.1484
                 CPI133814       0.6894       0.4191
                    Puseas       1.9945       0.7286
                     Sunco       0.7792       0.5341
                     Vasco       0.5196       0.4767
       6.000          2-49       0.5000       0.1405
                 CPI133814       0.7626       0.0000
                    Puseas       1.3261       1.1293
                     Sunco       0.1414      -0.0023
                     Vasco       0.7382       0.1262

Standard error of differences:     Average       0.4526
                                   Maximum       0.5172
                                   Minimum       0.2799

Average variance of differences:                 0.2059

Standard error of differences for same level of factor:

                 nharv       ngeno       ntill
Average         0.4443      0.4098      0.4576
Maximum         0.5061      0.4823      0.5172
Minimum         0.2799      0.2799      0.4173
Average variance of differences:
                0.2000      0.1709      0.2099


 213  vkeep means=tmean; term=ntill
 214  vkeep means=hmean; term=nharv
 215  print 'Back-transformed means' & tmean**2 & hmean**2


 Back-transformed means


               tmean** 2
       ntill
       1.000      0.5166
       2.000      0.0711


               hmean** 2
       nharv
       4.000      0.0638
       5.000      0.5465
       6.000      0.2364

 216  delete [redefine=yes] tmean, hmean
 217  page
```

```
 218
 219  "=========================================================================
-220                       PART = LS4 (Disease rating: harvest 5 & 6; Infection
count: no analysis)
-221  ========================================================================="
 222
 223  "**** LS4 Disease Rating (Harvests 5 & 6, only tiller 1) ****"
 224
 225  subset
[condition=(Part.eq.11).and.(Harvest.ge.5).and.(Harvest.le.6).and.(Tiller.ge.1).
and.(Tiller.le.1); setlevel=yes] \
 226   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 227   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 228
 229  vcomp [fixed=ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 230  reml [print=means, wald, comp, mod,dev] ndr

230................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+nharv.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 150

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                        0.0000       BOUND
nplot                       0.0000       BOUND
nplot.nharv                 0.0307      0.0388


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

nplot.nharv.nplant             Identity      Sigma2              0.433    0.0559


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                      56.06   136

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***
```

```
   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                          1.14            1         1.14       0.286
   ngeno                         28.34            4         7.09      <0.001
   nharv.ngeno                    6.02            4         1.51       0.197

* Dropping individual terms from full fixed model

   nharv.ngeno                    6.02            4         1.51       0.197

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.6400    Standard error: 0.06254



*** Table of predicted means for nharv ***

   nharv    5.000    6.000
           0.7067   0.5733

Standard error of differences:      0.1251



*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.4000       0.5333       1.3000       0.4667       0.5000

Standard error of differences:      0.1978



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        5.000       0.6000       0.4000       1.5333       0.6000       0.4000
        6.000       0.2000       0.6667       1.0667       0.3333       0.6000

Standard error of differences:      0.2797
```

```
 232
 233  "**** LS4 Isolation counts (total) ****"
 234  " No analysis due to too many zero's"
 235
 236  "===========================================================================
-237                        PART = LS5 (Disease rating: harvest 5 & 6; Infection
count: no analysis)
-238  ==========================================================================="
 239
 240  "**** LS5 Disease Rating (Harvests 5 & 6, only tiller 1) ****"
 241
 242  subset
[condition=(Part.eq.12).and.(Harvest.ge.5).and.(Harvest.le.6).and.(Tiller.ge.1).
and.(Tiller.le.1); setlevel=yes] \
 243   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 244   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 245
 246  vcomp [fixed=ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 247  reml [print=means, wald, comp, mod,dev] ndr

247.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+nharv.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 150

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component        S.e.

nrep                         0.0000       BOUND
nplot                        0.0000       BOUND
nplot.nharv                  0.0073      0.0338


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

nplot.nharv.nplant             Identity      Sigma2              0.463    0.0598


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                      60.90   136

Note: deviance omits constants which depend on fixed model fitted.
```

```
*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                          0.85            1         0.85       0.356
   ngeno                         20.19            4         5.05      <0.001
   nharv.ngeno                    5.68            4         1.42       0.224

* Dropping individual terms from full fixed model

   nharv.ngeno                    5.68            4         1.42       0.224

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.4400    Standard error: 0.05774



*** Table of predicted means for nharv ***

   nharv    5.000    6.000
           0.4933   0.3867

Standard error of differences:      0.1155



*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                   0.3000       0.2667       0.9333       0.2333       0.4667

Standard error of differences:      0.1826



*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        5.000       0.5333       0.2000       1.0000       0.4000       0.3333
        6.000       0.0667       0.3333       0.8667       0.0667       0.6000

Standard error of differences:      0.2582
```

```
 249
 250  "**** LS5 Isolation counts (total) ****"
 251  " No analysis due to too many zero's"
 252
 253  "===========================================================================
-254                       PART = LS6 (No analysis - too many zero's)
-255  ==========================================================================="
 256
 257  "===========================================================================
-258                       PART = LS7 (No analysis - too many zero's)
-259  ==========================================================================="
 260
 261  "===========================================================================
-262                       PART = LS8 (No analysis - too many zero's)
-263  ==========================================================================="
 264
 265  "===========================================================================
-266                       PART = LS9 (No analysis - too many zero's)
-267  ==========================================================================="
 268
 269  "===========================================================================
-270                       PART = LS10 (No analysis - too many zero's)
-271  ==========================================================================="
 272
 273  "===========================================================================
-274                       PART = C (Disease rating: harvest 1, 2 & 3; Infection
count: no analysis)
-275  ==========================================================================="
 276
 277  "**** Coleoptile Disease Rating (Harvests 1, 2 & 3, only tiller 1) ****"
 278
 279  subset
[condition=(Part.eq.1).and.(Harvest.ge.1).and.(Harvest.le.3).and.(Tiller.ge.1).a
nd.(Tiller.le.1); setlevel=yes] \
 280   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 281   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 282
 283  vcomp [fixed=ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 284  reml [print=means, wald, comp, mod,dev] ndr

284.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+nharv.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 225

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term                Component        S.e.

nrep                          0.0000       BOUND
nplot                         0.0207      0.0332
nplot.nharv                   0.0000       BOUND
```

```
nplot.nharv.nplant           0.0000       BOUND

*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.791    0.0791

*** Deviance: -2*Log-Likelihood ***

                   Deviance   d.f.

                     204.67   205

Note: deviance omits constants which depend on fixed model fitted.


*** Wald tests for fixed effects ***

   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                        137.38            2        68.69      <0.001
   ngeno                          8.01            4         2.00       0.091
   nharv.ngeno                   28.24            8         3.53      <0.001

* Dropping individual terms from full fixed model

   nharv.ngeno                   28.24            8         3.53      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.

*** Table of predicted means for Constant ***

            3.031    Standard error:  0.0700


*** Table of predicted means for nharv ***

   nharv    1.000    2.000    3.000
            2.052    3.440    3.600

Standard error of differences:     Average       0.1452
                                   Maximum       0.1452
                                   Minimum       0.1452

*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                    3.000        3.064        2.933        2.778        3.378

Standard error of differences:     Average       0.2213
                                   Maximum       0.2213
                                   Minimum       0.2212

*** Table of predicted means for nharv.ngeno ***
```

```
        ngeno          2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        1.000         2.133        1.593        1.533        2.467        2.533
        2.000         3.133        3.733        3.600        2.867        3.867
        3.000         3.733        3.867        3.667        3.000        3.733

Standard error of differences:     Average       0.3424
                                   Maximum       0.3455
                                   Minimum       0.3247

Average variance of differences:                 0.1173

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.3454      0.3248
Maximum          0.3455      0.3249
Minimum          0.3453      0.3247
```

```
 286
 287  "**** Coleoptile Isolation counts (total) ****"
 288  " No analysis due to too many zero's"
 289
 290  "==========================================================================
-291                       PART = P (No analysis - too many zero's)
-292  =========================================================================="
 293
 294  "==========================================================================
-295                       PART = SCI (Disease rating: harvest 2, 3, 4, 5 & 6;
Infection count: no analysis)
-296  =========================================================================="
 297
 298  "**** SCI Disease Rating (Harvests 2, 3, 4, 5 & 6, only tiller 1) ****"
 299
 300  subset
[condition=(Part.eq.18).and.(Harvest.ge.2).and.(Harvest.le.6).and.(Tiller.ge.1).
and.(Tiller.le.1); setlevel=yes] \
 301   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 302   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 303
 304  vcomp [fixed=ngeno*nharv]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 305  reml [print=means, wald, comp, mod,dev] ndr

305.....................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+nharv.ngeno
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 366

* nplot.nharv.nplant used as residual term

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                         0.003       BOUND
nplot                        0.000       BOUND
nplot.nharv                  0.002       0.068


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

nplot.nharv.nplant             Identity      Sigma2              1.505     0.125


*** Deviance: -2*Log-Likelihood ***


                   Deviance   d.f.

                     548.20   337
```

```
Note: deviance omits constants which depend on fixed model fitted.


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                        335.73            4        83.93      <0.001
   ngeno                         45.45            4        11.36      <0.001
   nharv.ngeno                   16.74           16         1.05       0.403

* Dropping individual terms from full fixed model

   nharv.ngeno                   16.74           16         1.05       0.403

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.723    Standard error:  0.0653



*** Table of predicted means for nharv ***

   nharv    2.000    3.000    4.000    5.000    6.000
            0.495    0.782    1.048    2.884    3.409

Standard error of differences:     Average       0.2046
                                   Maximum       0.2064
                                   Minimum       0.2034


*** Table of predicted means for ngeno ***

       ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
                    1.593        1.178        2.403        1.440        2.004

Standard error of differences:     Average       0.2046
                                   Maximum       0.2064
                                   Minimum       0.2027


*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49    CPI133814       Puseas        Sunco        Vasco
        nharv
        2.000        0.500        0.154        1.067        0.467        0.285
        3.000        0.333        0.067        1.642        0.733        1.133
        4.000        0.333        0.800        1.642        0.667        1.800
        5.000        3.154        2.133        3.667        2.267        3.200
        6.000        3.643        2.733        4.000        3.067        3.600

Standard error of differences:     Average       0.4574
                                   Maximum       0.4846
                                   Minimum       0.4516

Average variance of differences:                 0.2093

Standard error of differences for same level of factor:

                  nharv       ngeno
```

```
Average          0.4574      0.4574
Maximum          0.4760      0.4760
Minimum          0.4516      0.4516
Average variance of differences:
                 0.2093      0.2093


 306  page
```

```

"**** SCI Isolation counts (total) ****"
" No analysis due to too few values"

```

Appendix 3D
Wellcamp Field Trial Analysis Output

```
GenStat Release 6.1  (PC/Windows 2000)           07 April 2003 12:41:07
Copyright 2002, Lawes Agricultural Trust (Rothamsted Experimental Station)


              GenStat Sixth Edition
              GenStat Procedure Library Release PL14


   1  %CD 'C:/KerryBell/Biometry'
   2  "Cassandra Percy (UQ) and Graham Wildermuth (supervisor)
file=WellcampInocTrial2001.gen
  -3  Wellcamp Inoculated Field Trial
  -4
  -5  3 reps x 5 Genotypes / 9 Harvest times / 5 plants / up to 5 tillers / plant part
  -6
  -7  Every two weeks (harvest times), 5 plants were taken from each plot.
  -8
  -9  Each plant was divided into its tillers (tiller 1 being the main tiller),
 -10  and each node was given a disease rating (0-4) and
 -11  then divided into 4 parts (for rep 1 & 2 only), these was placed out on agar
 -12  and the number of 'infections' were counted. The sum of the infections
 -13  across these parts were analysed.
 -14
 -15  Genotypes:
 -16  2-49
 -17  CPI133814 (hardly any data, dropped out of analyses)
 -18  Puseas
 -19  Sunco
 -20  Vasco
 -21
 -22  Plant parts:
 -23  levels 1...7:   I1 to I7 (Internode)
 -24  levels 8...15:   LS1 to LS8 (Leaf Sheath)
 -25  level 16:   P (Peduncle)
 -26
 -27  ANALYSES: An ar(1) parameter was attempted to be fitted across harvests,
 -28  but many times the REML analysis did not converge or produce sensible results
 -29  so this parameter was dropped in these instances. If the parameter was non-
significant
 -30  (by comparing change in deviance to 2.8) then it was also dropped out.
 -31  For each plant part (I1, I2, I3, I4, LS1, LS2, LS3, LS4):
 -32  - Across tillers was analysed
```

```
 -33  - Each tiller analysed separately
 -34  Plant parts I5, I6, LS5, LS6, LS7, LS8 and P were not analysed due to lack of
 -35  values or high proportion of zeros.
 -36  "
  37
  38  set [outprint=dot]
  39  import file='C:/KerryBell/Biometry/CassandraPercy(UQ)/Wellcamp 2a 2001.xls'; \
  40    sheetname='original data'

 *** Loading Spreadsheet File ***

Catalogue of file
C:\DOCUME~1\BELLK.DPI\LOCALS~1\TEMP\GENSTAT\G61DB4.GSH

Sheet Title:
Data read from C:\KerryBell\Biometry\CassandraPercy(UQ)\Wellcamp 2a 2001.xls
[ORIGINAL DATA]A1:L10425

Sheet Type: vector
Index       Type    Nval   Name
    1     factor   10424   Harvest
    4     factor   10424   Genotype
    5     factor   10424   Rep
    6     factor   10424   Plant
    7     factor   10424   Tiller
   10     factor   10424   Part
   11    variate   10424   Disease_Rating
   12    variate   10424   Infection_total
   13    variate   10424   Infection_1_4
   14    variate   10424   Infection_2_4
   15    variate   10424   Infection_3_4
   16    variate   10424   Infection_4_4

Missing indices are used by unnamed or system structures. These store ancillary
information, for example factor labels.
  41  facproduct factors=!P(Rep, Genotype); product=plot
  42
  43
"==========================================================================
===========
 -44                     PART = I1 (harvest 5, 6, & 7)
 -45
==========================================================================
=========="
  46
```

```
  47  "**** Disease Rating (Harvests 5, 6 & 7; harvests 8 & 9 don't have variation; leave
out CPI1338)****"
  48
  49  "### Analysing the tillers together ###"
  50
  51  subset
[condition=(Part.eq.1).and.(Harvest.ge.5).and.(Harvest.le.7).and.(Genotype.ne.2);
setlevel=yes] \
  52   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
  53   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
  54
  55  vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
  56  vstruct [nplot.nharv] factor=nharv; model=ar "uniform"
  57  reml [print=means, wald, comp, mod,dev] ndr

57.................................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot.nharv+nplot.nharv.nplant

Number of units  : 842

* Residual term has been added to model

* Sparse algorithm with AI optimisation

*** Covariance structures defined for random model ***

Covariance structures defined within terms:

Term                  Factor     Model                  Order Nrows
nplot.nharv             nplot      Identity                 1    12
                     nharv      Auto-regressive            1     3



*** Estimated Variance Components ***
```

```
Random term             Component       S.e.

nrep                        0.0000       BOUND
nplot.nharv.nplant          0.4309      0.0669


*** Estimated Parameters for Covariance Models ***

Random term(s)   Factor       Model(order)  Parameter       Estimate      S.e.

nplot.nharv      nplot        Identity      Scalar            0.1253    0.0926
                 nharv        AR(1)         phi_1            -0.4969    0.5691

Note: the covariance matrix for each term is calculated as G or R where
      var(y) = Sigma2( ZGZ'+R ), ie. relative to the residual variance, Sigma2


*** Residual variance model ***

Term             Factor       Model(order)  Parameter       Estimate      S.e.

Residual                      Identity      Sigma2             0.621    0.0354


*** Deviance: -2*Log-Likelihood ***


                 Deviance   d.f.

                   820.14   777

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                          123.10          2        61.55      <0.001
   ngeno                          181.56          3        60.52      <0.001
   ntill                          167.48          4        41.87      <0.001
   nharv.ngeno                     16.88          6         2.81       0.010
```

```
   nharv.ntill              22.06        8      2.76     0.005
   ngeno.ntill              13.76       12      1.15     0.317
   nharv.ngeno.ntill        74.64       24      3.11    <0.001

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill        74.64       24      3.11    <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         2.060    Standard error:  0.0656



*** Table of predicted means for nharv ***

   nharv    5.000    6.000    7.000
         0.993    2.232    2.955

Standard error of differences:     Average       0.1872
                                   Maximum       0.1956
                                   Minimum       0.1713

Average variance of differences:                 0.03518


*** Table of predicted means for ngeno ***

   ngeno     2-49   Puseas    Sunco    Vasco
         0.744    2.972    2.065    2.458

Standard error of differences:     Average       0.1855
                                   Maximum       0.1866
                                   Minimum       0.1844


*** Table of predicted means for ntill ***

   ntill       1        2        3        4        5
         2.594    2.372    1.979    1.708    1.646

Standard error of differences:     Average      0.08768
```

```
                                  Maximum      0.09364
                                  Minimum      0.08306

Average variance of differences:              0.007706


*** Table of predicted means for nharv.ngeno ***

       ngeno     2-49   Puseas    Sunco    Vasco
       nharv
       5.000    0.294    1.731    0.827    1.119
       6.000    0.526    3.627    2.030    2.746
       7.000    1.413    3.559    3.336    3.510

Standard error of differences:     Average       0.3611
                                  Maximum       0.3942
                                  Minimum       0.3397

Average variance of differences:                0.1305

Standard error of differences for same level of factor:

                nharv       ngeno
Average          0.3581      0.3745
Maximum          0.3641      0.3942
Minimum          0.3552      0.3397
Average variance of differences:
                0.1282      0.1407



*** Table of predicted means for nharv.ntill ***

       ntill       1        2        3        4        5
       nharv
       5.000    1.683    1.483    0.936    0.522    0.340
       6.000    2.600    2.500    2.050    1.875    2.135
       7.000    3.500    3.133    2.950    2.727    2.464

Standard error of differences:     Average       0.2087
                                  Maximum       0.2550
                                  Minimum       0.1439

Average variance of differences:               0.04494

Standard error of differences for same level of factor:
```

```
              nharv      ntill
Average         0.1518     0.2314
Maximum          0.1756     0.2550
Minimum          0.1439     0.2126
Average variance of differences:
            0.02312    0.05368



*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49    1.356    1.044    0.600    0.370    0.351
     Puseas    3.578    3.422    2.892    2.445    2.525
      Sunco    2.378    2.422    2.089    1.889    1.546
      Vasco    3.067    2.600    2.333    2.128    2.164

Standard error of differences:     Average       0.2287
                           Maximum       0.2729
                           Minimum       0.1661

Average variance of differences:              0.05312

Standard error of differences for same level of factor:

              ngeno      ntill
Average         0.1753     0.2428
Maximum          0.1999     0.2729
Minimum          0.1661     0.2361
Average variance of differences:
            0.03082    0.05907



*** Table of predicted means for nharv.ngeno.ntill ***

                ntill       1       2       3       4       5
      nharv       ngeno
      5.000          2-49    0.533    0.400    0.200    0.177    0.158
                 Puseas    3.000    2.467    1.542    0.807    0.839
                  Sunco    1.067    1.533    1.000    0.533    0.003
                  Vasco    2.133    1.533    1.000    0.570    0.360
      6.000          2-49    1.000    0.667    0.467    0.200    0.295
                 Puseas    3.867    3.933    3.533    3.333    3.467
```

```
                 Sunco    2.267    2.600    1.733    1.533    2.019
                 Vasco    3.267    2.800    2.467    2.433    2.761
       7.000         2-49    2.533    2.067    1.133    0.733    0.599
                Puseas    3.867    3.867    3.600    3.193    3.270
                 Sunco    3.800    3.133    3.533    3.600    2.615
                 Vasco    3.800    3.467    3.533    3.382    3.370

Standard error of differences:     Average       0.4417
                             Maximum      0.5416
                             Minimum      0.2877

Average variance of differences:               0.1969

Standard error of differences for same level of factor:

               nharv       ngeno       ntill
Average         0.4185      0.4171      0.4517
Maximum         0.5416      0.5411      0.5416
Minimum         0.2877      0.2877      0.4252
Average variance of differences:
              0.1791      0.1798      0.2045



  58
  59  "### Analysing the tillers separately ###"
  60
  61  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
  62      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
  63  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
  64  reml [print=means, wald, comp, mod] t1dr

64..................................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 180

* Residual term has been added to model
```

```
* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term            Component      S.e.

t1rep                   0.0000      BOUND
t1plot                  0.0000      BOUND
t1plot.t1harv             0.0156     0.0645


*** Residual variance model ***

Term         Factor      Model(order)  Parameter      Estimate     S.e.

Residual                 Identity      Sigma2            0.967    0.1139


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                  94.80          2       47.40      <0.001
  t1geno                 119.42          3       39.81      <0.001
  t1harv.t1geno             18.56          6        3.09       0.005

* Dropping individual terms from full fixed model

  t1harv.t1geno             18.56          6        3.09       0.005

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        2.594    Standard error:  0.0762



*** Table of predicted means for t1harv ***
```

```
  t1harv    5.000    6.000    7.000
           1.683    2.600    3.500

Standard error of differences:      0.1866



*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
           1.356    3.578    2.378    3.067

Standard error of differences:      0.2155



*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        5.000    0.533    3.000    1.067    2.133
        6.000    1.000    3.867    2.267    3.267
        7.000    2.533    3.867    3.800    3.800

Standard error of differences:      0.3732


  65
  66  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
  67      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
  68  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
  69  reml [print=means, wald, comp, mod] t2dr

69...................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv
```

```
Number of units  : 180

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t2rep                    0.000       BOUND
t2plot                   0.000       BOUND
t2plot.t2harv              0.122       0.124


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2             1.456     0.172


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                    40.23            2        20.12      <0.001
  t2geno                     63.58            3        21.19      <0.001
  t2harv.t2geno                  4.99            6         0.83       0.545

* Dropping individual terms from full fixed model

  t2harv.t2geno                  4.99            6         0.83       0.545

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         2.372    Standard error:  0.1072
```

```
*** Table of predicted means for t2harv ***

  t2harv    5.000    6.000    7.000
            1.483    2.500    3.133

Standard error of differences:      0.2625



*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
            1.044    3.422    2.422    2.600

Standard error of differences:      0.3031



*** Table of predicted means for t2harv.t2geno ***

       t2geno     2-49   Puseas    Sunco    Vasco
       t2harv
        5.000    0.400    2.467    1.533    1.533
        6.000    0.667    3.933    2.600    2.800
        7.000    2.067    3.867    3.133    3.467

Standard error of differences:      0.5249


  70
  71  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
  72      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
  73  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
  74  reml [print=means, wald, comp, mod] t3dr

74..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t3dr
```

```
Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 179

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                   0.0000      BOUND
t3plot                  0.0000      BOUND
t3plot.t3harv               0.1589     0.1031


*** Residual variance model ***

Term           Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.945    0.1117


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t3harv                    69.97           2       34.98      <0.001
   t3geno                     74.53           3       24.84      <0.001
   t3harv.t3geno                  14.39           6        2.40       0.026

* Dropping individual terms from full fixed model

   t3harv.t3geno                  14.39           6        2.40       0.026

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
            1.980    Standard error:  0.0985



*** Table of predicted means for t3harv ***

  t3harv    5.000    6.000    7.000
            0.941    2.050    2.950

Standard error of differences:     Average       0.2412
                                   Maximum       0.2414
                                   Minimum       0.2408


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
            0.600    2.899    2.089    2.333

Standard error of differences:     Average       0.2785
                                   Maximum       0.2790
                                   Minimum       0.2780


*** Table of predicted means for t3harv.t3geno ***

       t3geno     2-49   Puseas    Sunco    Vasco
       t3harv
        5.000    0.200    1.562    1.000    1.000
        6.000    0.467    3.533    1.733    2.467
        7.000    1.133    3.600    3.533    3.533

Standard error of differences:     Average       0.4824
                                   Maximum       0.4866
                                   Minimum       0.4816

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average          0.4824      0.4824
Maximum          0.4866      0.4866
Minimum          0.4816      0.4816
```

```
  76  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
  77      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
  78  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
  79  reml [print=means, wald, comp, mod] t4dr

79..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 166

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t4rep                   0.0000       BOUND
t4plot                  0.0000       BOUND
t4plot.t4harv               0.0019      0.0626


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate       S.e.

Residual                    Identity      Sigma2             0.881    0.1097


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model
```

```
  t4harv                    145.10          2       72.55     <0.001
  t4geno                     136.59          3       45.53     <0.001
  t4harv.t4geno                 50.29          6        8.38     <0.001

* Dropping individual terms from full fixed model

  t4harv.t4geno                 50.29          6        8.38     <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.738    Standard error:  0.0738



*** Table of predicted means for t4harv ***

  t4harv    5.000    6.000    7.000
          0.561    1.892    2.762

Standard error of differences:     Average       0.1807
                                   Maximum       0.1841
                                   Minimum       0.1764

Average variance of differences:              0.03267


*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.359    2.483    1.889    2.222

Standard error of differences:     Average       0.2086
                                   Maximum       0.2169
                                   Minimum       0.2001

Average variance of differences:              0.04356


*** Table of predicted means for t4harv.t4geno ***

       t4geno     2-49   Puseas    Sunco    Vasco
```

```
     t4harv
      5.000    0.143    0.900    0.533    0.666
      6.000    0.200    3.333    1.533    2.499
      7.000    0.733    3.214    3.600    3.500

Standard error of differences:     Average       0.3611
                                  Maximum       0.4036
                                  Minimum       0.3446

Average variance of differences:                0.1307

Standard error of differences for same level of factor:

               t4harv      t4geno
Average          0.3611      0.3611
Maximum          0.4036      0.3904
Minimum          0.3446      0.3446
Average variance of differences:
               0.1307      0.1307


  80
  81  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
  82      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
  83  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
  84  reml [print=means, wald, comp, mod] t5dr

84.................................................................................


***** REML Variance Components Analysis *****


Response Variate : t5dr

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 137

* Residual term has been added to model

* Sparse algorithm with AI optimisation
```

```
*** Estimated Variance Components ***

Random term             Component       S.e.

t5rep                   0.0000      BOUND
t5plot                  0.0000      BOUND
t5plot.t5harv               0.0582     0.0952


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2             0.967    0.1343


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t5harv                     90.70           2        45.35      <0.001
   t5geno                      95.74           3        31.91      <0.001
   t5harv.t5geno                  22.81           6         3.80      <0.001

* Dropping individual terms from full fixed model

   t5harv.t5geno                  22.81           6         3.80      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.730    Standard error:  0.0963



*** Table of predicted means for t5harv ***

  t5harv    5.000    6.000    7.000
            0.432    2.234    2.524
```

```
Standard error of differences:     Average       0.2356
                                   Maximum       0.2436
                                   Minimum       0.2233

Average variance of differences:                0.05561


*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
           0.345    2.568    1.645    2.364

Standard error of differences:     Average       0.2721
                                   Maximum       0.2879
                                   Minimum       0.2558

Average variance of differences:                0.07414


*** Table of predicted means for t5harv.t5geno ***

       t5geno     2-49   Puseas    Sunco    Vasco
       t5harv
        5.000    0.087    0.964    0.190    0.489
        6.000    0.282    3.467    2.096    3.093
        7.000    0.667    3.274    2.648    3.510

Standard error of differences:     Average       0.4699
                                   Maximum       0.5660
                                   Minimum       0.4153

Average variance of differences:                 0.2224

Standard error of differences for same level of factor:

                 t5harv      t5geno
Average          0.4696      0.4700
Maximum          0.5652      0.5564
Minimum          0.4153      0.4273
Average variance of differences:
                 0.2224      0.2224


  85
  86
```

```
  87  "**** Infection - Total (Harvests 5, 6 & 7; harvests 8 & 9 don't have variation;
leave out Rep 3 & CPI1338)****"
  88
  89  "### Analysing the tillers together ###"
  90
  91  subset
[condition=(Part.eq.1).and.(Harvest.ge.5).and.(Harvest.le.7).and.(Genotype.ne.2).and.(Re
p.le.2);\
  92   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
  93   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
  94
  95  vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
  96  vstruct [nplot.nharv] factor=nharv; model=ar
  97  reml [print=means, wald, comp, mod] sqrt(ntotal)

97..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot.nharv+nplot.nharv.nplant

Number of units  : 559

* Residual term has been added to model

* Sparse algorithm with AI optimisation

*** Covariance structures defined for random model ***

Covariance structures defined within terms:

Term                Factor     Model                 Order Nrows
nplot.nharv           nplot      Identity                1     8
                   nharv      Auto-regressive            1     3



*** Estimated Variance Components ***
```

```
Random term              Component       S.e.

nrep                   0.0077      0.0201
nplot.nharv.nplant          0.1195      0.0358


*** Estimated Parameters for Covariance Models ***

Random term(s)   Factor        Model(order)  Parameter        Estimate      S.e.

nplot.nharv      nplot         Identity      Scalar            0.1255    0.0961
              nharv         AR(1)         phi_1            -0.6107    0.5297

Note: the covariance matrix for each term is calculated as G or R where
     var(y) = Sigma2( ZGZ'+R ), ie. relative to the residual variance, Sigma2


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2            0.556    0.0397


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                     50.78           2        25.39      <0.001
  ngeno                      70.40           3        23.47      <0.001
  ntill                   9.11            4         2.28       0.058
  nharv.ngeno                 7.51            6         1.25       0.276
  nharv.ntill               5.99            8         0.75       0.648
  ngeno.ntill               10.76           12         0.90       0.550
  nharv.ngeno.ntill           21.27           24         0.89       0.623

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill           21.27           24         0.89       0.623

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.
```

```
*** Table of predicted means for Constant ***

           1.579    Standard error:  0.0845



*** Table of predicted means for nharv ***

   nharv    5.000    6.000    7.000
           1.032    1.594    2.112

Standard error of differences:     Average       0.1846
                                   Maximum       0.2008
                                   Minimum       0.1529

Average variance of differences:              0.03458


*** Table of predicted means for ngeno ***

   ngeno     2-49   Puseas    Sunco    Vasco
           0.921    2.146    1.545    1.704

Standard error of differences:     Average       0.1626
                                   Maximum       0.1643
                                   Minimum       0.1609


*** Table of predicted means for ntill ***

   ntill       1        2        3        4        5
           1.662    1.704    1.511    1.598    1.420

Standard error of differences:     Average       0.1016
                                   Maximum       0.1087
                                   Minimum      0.09624

Average variance of differences:              0.01034


*** Table of predicted means for nharv.ngeno ***

        ngeno     2-49   Puseas    Sunco    Vasco
        nharv
```

```
        5.000    0.254    1.579    0.860    1.435
        6.000    0.715    2.401    1.692    1.568
        7.000    1.794    2.460    2.082    2.111

Standard error of differences:     Average       0.3489
                                   Maximum       0.4044
                                   Minimum       0.3017

Average variance of differences:                0.1222

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.3444      0.3692
Maximum          0.3499      0.4044
Minimum          0.3408      0.3017
Average variance of differences:
                 0.1187      0.1383



*** Table of predicted means for nharv.ntill ***

        ntill        1        2        3        4        5
        nharv
        5.000    1.142    1.265    0.839    1.040    0.873
        6.000    1.674    1.560    1.585    1.606    1.543
        7.000    2.170    2.286    2.110    2.149    1.845

Standard error of differences:     Average       0.2239
                                   Maximum       0.2757
                                   Minimum       0.1667

Average variance of differences:                0.05129

Standard error of differences for same level of factor:

                  nharv       ntill
Average          0.1759      0.2430
Maximum          0.1973      0.2757
Minimum          0.1667      0.2116
Average variance of differences:
                0.03103     0.05940
```

```
*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49   1.176   1.025   0.762   0.870   0.772
     Puseas   2.261   2.283   1.917   2.179   2.092
      Sunco   1.436   1.640   1.742   1.523   1.384
      Vasco   1.776   1.867   1.625   1.821   1.433

Standard error of differences:     Average       0.2352
                                   Maximum       0.2859
                                   Minimum       0.1925

Average variance of differences:                 0.05572

Standard error of differences for same level of factor:

                 ngeno      ntill
Average         0.2030     0.2436
Maximum         0.2377     0.2859
Minimum         0.1925     0.2348
Average variance of differences:
               0.04137    0.05954



*** Table of predicted means for nharv.ngeno.ntill ***

             ntill       1       2       3       4       5
      nharv      ngeno
      5.000       2-49   0.400   0.283   0.000   0.407   0.182
                Puseas   2.035   1.742   1.092   1.214   1.811
                 Sunco   0.573   1.245   0.997   0.946   0.539
                 Vasco   1.560   1.790   1.269   1.594   0.961
      6.000       2-49   1.089   0.629   0.500   0.588   0.768
                Puseas   2.344   2.323   2.173   2.698   2.466
                 Sunco   1.642   1.606   2.083   1.575   1.555
                 Vasco   1.624   1.683   1.586   1.562   1.383
      7.000       2-49   2.038   2.162   1.785   1.616   1.368
                Puseas   2.406   2.784   2.486   2.625   1.999
                 Sunco   2.092   2.069   2.147   2.047   2.057
                 Vasco   2.145   2.128   2.020   2.308   1.955

Standard error of differences:     Average       0.4619
                                   Maximum       0.5927
                                   Minimum       0.3334
```

```
Average variance of differences:            0.2149

Standard error of differences for same level of factor:

              nharv     ngeno     ntill
Average       0.4422    0.4475    0.4697
Maximum       0.5599    0.5927    0.5927
Minimum       0.3334    0.3334    0.4231
Average variance of differences:
              0.1982    0.2052    0.2215


  98  vdisp [print=mean; pterm=nharv; pse=alldiff]

98..............................................................................


*** Table of predicted means for nharv ***

   nharv    5.000    6.000    7.000
            1.032    1.594    2.112

Standard errors of differences between pairs

nharv   5   1        *
nharv   6   2    0.201        *
nharv   7   3    0.153    0.200        *

                     1        2        3

Standard error of differences:     Average       0.1846
                                   Maximum       0.2008
                                   Minimum       0.1529

Average variance of differences:              0.03458

  99
 100  "### Analysing the tillers separately ###"
 101
 102  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 103      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 104  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 105  reml [print=means, wald, comp, mod] sqrt(t1total)
```

105...

```
***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 120

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t1rep                   0.0207      0.0463
t1plot                  0.0000       BOUND
t1plot.t1harv                0.0500      0.0622


*** Residual variance model ***

Term            Factor        Model(order)  Parameter       Estimate      S.e.

Residual                   Identity      Sigma2            0.462    0.0666


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                    29.72           2        14.86      <0.001
   t1geno                     27.82           3         9.27      <0.001
   t1harv.t1geno                10.38           6         1.73       0.109

* Dropping individual terms from full fixed model
```

```
  t1harv.t1geno              10.38          6        1.73      0.109

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.662    Standard error:  0.1276



*** Table of predicted means for t1harv ***

  t1harv    5.000    6.000    7.000
          1.142    1.674    2.170

Standard error of differences:      0.1887



*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
          1.176    2.261    1.436    1.776

Standard error of differences:      0.2179



*** Table of predicted means for t1harv.t1geno ***

      t1geno     2-49   Puseas    Sunco    Vasco
      t1harv
       5.000    0.400    2.035    0.573    1.560
       6.000    1.089    2.344    1.642    1.624
       7.000    2.038    2.406    2.092    2.145

Standard error of differences:      0.3773


 106
 107  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 108      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
```

```
 109  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 110  reml [print=means, wald, comp, mod] sqrt(t2total)

110..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 120

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t2rep                   0.0000      BOUND
t2plot                  0.0000      BOUND
t2plot.t2harv              0.1184     0.0910


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.508    0.0733


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                     20.06           2       10.03      <0.001
   t2geno                      22.55           3        7.52      <0.001
```

```
  t2harv.t2geno              7.16          6        1.19      0.306

* Dropping individual terms from full fixed model

  t2harv.t2geno              7.16          6        1.19      0.306

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.704    Standard error:  0.0957



*** Table of predicted means for t2harv ***

 t2harv    5.000    6.000    7.000
          1.265    1.560    2.286

Standard error of differences:      0.2345



*** Table of predicted means for t2geno ***

 t2geno     2-49   Puseas    Sunco    Vasco
          1.025    2.283    1.640    1.867

Standard error of differences:      0.2708



*** Table of predicted means for t2harv.t2geno ***

     t2geno     2-49   Puseas    Sunco    Vasco
     t2harv
      5.000    0.283    1.742    1.245    1.790
      6.000    0.629    2.323    1.606    1.683
      7.000    2.162    2.784    2.069    2.128

Standard error of differences:      0.4690
```

```
 112  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 113      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 114  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 115  reml [print=means, wald, comp, mod] sqrt(t3total)

115..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 119

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t3rep                   0.0000       BOUND
t3plot                  0.0026      0.0353
t3plot.t3harv               0.0000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2             0.688    0.0959


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model
```

```
   t3harv                    47.54          2        23.77      <0.001
   t3geno                     32.45          3        10.82      <0.001
   t3harv.t3geno                9.15          6         1.52       0.165

* Dropping individual terms from full fixed model

   t3harv.t3geno                9.15          6         1.52       0.165

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           1.510    Standard error:  0.0782



*** Table of predicted means for t3harv ***

  t3harv    5.000    6.000    7.000
           0.834    1.585    2.110

Standard error of differences:     Average       0.1864
                                   Maximum       0.1868
                                   Minimum       0.1855


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
           0.762    1.910    1.742    1.625

Standard error of differences:     Average       0.2211
                                   Maximum       0.2220
                                   Minimum       0.2201


*** Table of predicted means for t3harv.t3geno ***

      t3geno     2-49   Puseas    Sunco    Vasco
      t3harv
       5.000    0.000    1.070    0.997    1.269
       6.000    0.500    2.173    2.083    1.586
       7.000    1.785    2.486    2.147    2.020
```

```
Standard error of differences:     Average       0.3755
                                   Maximum       0.3846
                                   Minimum       0.3710

Average variance of differences:                 0.1410

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average          0.3762      0.3727
Maximum          0.3846      0.3812
Minimum          0.3745      0.3710
Average variance of differences:
                 0.1415      0.1389


 116
 117  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 118      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 119  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 120  reml [print=means, wald, comp, mod] sqrt(t4total)

120..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t4total)

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 111

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.
```

```
t4rep                 0.0000    BOUND
t4plot                0.0000    BOUND
t4plot.t4harv            0.1126    0.1193


*** Residual variance model ***

Term          Factor      Model(order)  Parameter       Estimate     S.e.

Residual                  Identity     Sigma2          0.774    0.1175


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t4harv                   16.88          2        8.44      <0.001
  t4geno                   20.35          3        6.78      <0.001
  t4harv.t4geno               5.50          6        0.92       0.481

* Dropping individual terms from full fixed model

  t4harv.t4geno               5.50          6        0.92       0.481

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.606    Standard error:  0.1086



*** Table of predicted means for t4harv ***

  t4harv    5.000    6.000    7.000
        1.052    1.616    2.149

Standard error of differences:     Average       0.2659
                                Maximum      0.2685
                                Minimum      0.2634
```

```
*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.880    2.185    1.523    1.835

Standard error of differences:     Average       0.3070
                                   Maximum       0.3137
                                   Minimum       0.3003

Average variance of differences:               0.09429


*** Table of predicted means for t4harv.t4geno ***

       t4geno     2-49   Puseas    Sunco    Vasco
       t4harv
        5.000    0.435    1.192    0.946    1.634
        6.000    0.588    2.698    1.575    1.604
        7.000    1.616    2.664    2.047    2.266

Standard error of differences:     Average       0.5317
                                   Maximum       0.5575
                                   Minimum       0.5172

Average variance of differences:                0.2829

Standard error of differences for same level of factor:

                t4harv      t4geno
Average          0.5317      0.5317
Maximum           0.5575      0.5575
Minimum          0.5172      0.5172
Average variance of differences:
                0.2829      0.2829


 121
 122  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 123      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 124  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 125  reml [print=means, wald, comp, mod] sqrt(t5total)

125.............................................................................
```

```
***** REML Variance Components Analysis *****


Response Variate : SQRT(t5total)

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 89

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t5rep                   0.000       BOUND
t5plot                  0.000       BOUND
t5plot.t5harv               0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            1.093     0.176


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t5harv                    16.64           2         8.32      <0.001
   t5geno                     18.29           3         6.10      <0.001
   t5harv.t5geno                3.84           6         0.64       0.699

* Dropping individual terms from full fixed model

   t5harv.t5geno                3.84           6         0.64       0.699
```

```
* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.427    Standard error:  0.1137



*** Table of predicted means for t5harv ***

  t5harv    5.000    6.000    7.000
            0.837    1.606    1.838

Standard error of differences:     Average       0.2784
                                   Maximum       0.2839
                                   Minimum       0.2701

Average variance of differences:               0.07753


*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
            0.754    2.050    1.388    1.516

Standard error of differences:     Average       0.3211
                                   Maximum       0.3443
                                   Minimum       0.2970

Average variance of differences:                0.1034


*** Table of predicted means for t5harv.t5geno ***

       t5geno     2-49   Puseas    Sunco    Vasco
       t5harv
        5.000    0.143    1.676    0.500    1.030
        6.000    0.759    2.466    1.601    1.598
        7.000    1.361    2.010    2.062    1.919

Standard error of differences:     Average       0.5552
                                   Maximum       0.6612
                                   Minimum       0.4804
```

```
Average variance of differences:            0.3101

Standard error of differences for same level of factor:

           t5harv     t5geno
Average        0.5552     0.5546
Maximum        0.6331     0.6331
Minimum        0.4804     0.4928
Average variance of differences:
           0.3101     0.3101


 126
 127
 128
"===============================================================
===========
-129                  PART = I2 (harvest 6, 7, 8 & 9)
-130
===============================================================
=========="
 131
 132  "**** Disease Rating (Harvests 6, 7, 8 & 9; leave out CPI1338)****"
 133
 134  "### Analysing the tillers together ###"
 135
 136  subset [condition=(Part.eq.2).and.(Harvest.ge.6).and.(Genotype.ne.2); setlevel=yes]
\
 137   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
 138   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 139
 140  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-141  vstruct [nplot.nharv] factor=nharv; model=ar "
 142  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 143  reml [print=means, wald, comp, mod, dev; mvincl=yvar, expl] ndr

143..............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr
```

```
Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 1104

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                     0.0000      BOUND
nplot                    0.0177      0.0249
nplot.nharv                  0.0093      0.0353
nplot.nharv.nplant           0.3843      0.0546


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.656    0.0328


*** Deviance: -2*Log-Likelihood ***


               Deviance   d.f.

                1097.57  1019

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

  nharv                     226.46        3      75.49     <0.001
  ngeno                     244.02        3      81.34     <0.001
  ntill                   137.27        4      34.32     <0.001
  nharv.ngeno                 22.50         9       2.50      0.007
  nharv.ntill               11.98        12       1.00      0.447
  ngeno.ntill               21.43        12       1.79      0.044
  nharv.ngeno.ntill          105.78        36       2.94     <0.001

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill          105.78        36       2.94     <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
 (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        2.041    Standard error:  0.0626



*** Table of predicted means for nharv ***

  nharv    6.000    7.000    8.000    9.000
        1.047    1.678    2.561    2.877

Standard error of differences:     Average       0.1397
                          Maximum      0.1411
                          Minimum      0.1382


*** Table of predicted means for ngeno ***

  ngeno     2-49   Puseas    Sunco    Vasco
        0.606    3.189    1.824    2.544

Standard error of differences:     Average       0.1769
                          Maximum      0.1778
                          Minimum      0.1761


*** Table of predicted means for ntill ***
```

```
  ntill       1       2       3       4       5
          2.441   2.280   2.071   1.767   1.645

Standard error of differences:    Average      0.07913
                                  Maximum      0.08572
                                  Minimum      0.07412

Average variance of differences:               0.006282


*** Table of predicted means for nharv.ngeno ***

     ngeno     2-49  Puseas   Sunco   Vasco
     nharv
     6.000    0.013   2.291   0.490   1.394
     7.000    0.224   2.767   1.527   2.194
     8.000    1.170   3.820   2.236   3.018
     9.000    1.019   3.877   3.042   3.572

Standard error of differences:    Average       0.2956
                                  Maximum       0.3093
                                  Minimum       0.2749

Average variance of differences:                0.08745

Standard error of differences for same level of factor:

             nharv       ngeno
Average        0.2997      0.2793
Maximum        0.3093      0.2888
Minimum        0.2950      0.2749
Average variance of differences:
             0.08981     0.07802



*** Table of predicted means for nharv.ntill ***

     ntill       1       2       3       4       5
     nharv
     6.000    1.433   1.167   1.017   0.763   0.856
     7.000    2.050   2.017   1.750   1.418   1.156
     8.000    3.046   2.938   2.584   2.228   2.008
     9.000    3.233   3.000   2.933   2.659   2.562

Standard error of differences:    Average       0.1902
```

```
                       Maximum     0.2334
                       Minimum     0.1479

Average variance of differences:          0.03656

Standard error of differences for same level of factor:

            nharv     ntill
Average        0.1581    0.1986
Maximum        0.1823    0.2334
Minimum        0.1479    0.1903
Average variance of differences:
          0.02513   0.03960



*** Table of predicted means for ngeno.ntill ***

     ntill      1      2      3      4      5
     ngeno
      2-49   0.846  0.688  0.518  0.519  0.461
    Puseas   3.700  3.483  3.250  2.762  2.749
     Sunco   2.183  2.117  1.933  1.555  1.332
     Vasco   3.033  2.833  2.583  2.233  2.040

Standard error of differences:    Average      0.2121
                       Maximum     0.2579
                       Minimum     0.1479

Average variance of differences:          0.04587

Standard error of differences for same level of factor:

            ngeno     ntill
Average        0.1581    0.2264
Maximum        0.1924    0.2579
Minimum        0.1479    0.2192
Average variance of differences:
          0.02513   0.05140



*** Table of predicted means for nharv.ngeno.ntill ***

             ntill      1      2      3      4      5
     nharv     ngeno
```

```
    6.000       2-49   0.067   0.000   0.000   0.000  -0.002
              Puseas   3.067   2.600   2.400   1.867   1.524
               Sunco   0.600   0.400   0.333   0.267   0.851
               Vasco   2.000   1.667   1.333   0.918   1.052
    7.000       2-49   0.333   0.467   0.067   0.200   0.051
              Puseas   3.733   3.533   2.800   1.809   1.960
               Sunco   1.467   1.400   2.067   1.733   0.971
               Vasco   2.667   2.667   2.067   1.929   1.640
    8.000       2-49   1.851   1.351   1.137   0.860   0.649
              Puseas   4.000   4.000   4.000   3.570   3.530
               Sunco   2.867   3.200   2.067   1.569   1.477
               Vasco   3.467   3.200   3.133   2.914   2.375
    9.000       2-49   1.133   0.933   0.867   1.015   1.145
              Puseas   4.000   3.800   3.800   3.801   3.983
               Sunco   3.800   3.467   3.267   2.649   2.030
               Vasco   4.000   3.800   3.800   3.169   3.091

Standard error of differences:     Average       0.4042
                                   Maximum       0.5535
                                   Minimum       0.2958

Average variance of differences:                 0.1644

Standard error of differences for same level of factor:

                 nharv       ngeno       ntill
Average         0.3916      0.3801      0.4087
Maximum         0.5297      0.5425      0.5535
Minimum         0.2958      0.2958      0.3807
Average variance of differences:
                0.1555      0.1462      0.1679


 144
 145
 146  "### Analysing the tillers separately ###"
 147
 148  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 149     t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 150  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 151  reml [print=means, wald, comp, mod] t1dr

151.............................................................................
```

```
***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 239

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t1rep                  0.0000      BOUND
t1plot                 0.0000      BOUND
t1plot.t1harv              0.0000      BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                   Identity      Sigma2            0.781    0.0739


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                   167.71           3        55.90      <0.001
   t1geno                   347.34           3       115.78      <0.001
   t1harv.t1geno               44.49           9         4.94      <0.001

* Dropping individual terms from full fixed model

   t1harv.t1geno               44.49           9         4.94      <0.001
```

```
* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          2.441    Standard error:  0.0572



*** Table of predicted means for t1harv ***

  t1harv    6.000    7.000    8.000    9.000
          1.433    2.050    3.048    3.233

Standard error of differences:     Average       0.1617
                                   Maximum       0.1620
                                   Minimum       0.1613


*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
          0.848    3.700    2.183    3.033

Standard error of differences:     Average       0.1617
                                   Maximum       0.1620
                                   Minimum       0.1613


*** Table of predicted means for t1harv.t1geno ***

      t1geno     2-49   Puseas    Sunco    Vasco
      t1harv
       6.000    0.067    3.067    0.600    2.000
       7.000    0.333    3.733    1.467    2.667
       8.000    1.857    4.000    2.867    3.467
       9.000    1.133    4.000    3.800    4.000

Standard error of differences:     Average       0.3234
                                   Maximum       0.3284
                                   Minimum       0.3227

Standard error of differences for same level of factor:

              t1harv      t1geno
```

```
Average          0.3234      0.3234
Maximum          0.3284      0.3284
Minimum          0.3227      0.3227


 152
 153  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 154      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 155  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 156  reml [print=means, wald, comp, mod] t2dr

156..................................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 239

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t2rep                    0.000       BOUND
t2plot                   0.051       0.051
t2plot.t2harv            0.000       BOUND


*** Residual variance model ***

Term           Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2          1.015     0.098
```

```
*** Wald tests for fixed effects ***


   Fixed term             Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                     134.24          3        44.75      <0.001
   t2geno                     126.65          3        42.22      <0.001
   t2harv.t2geno               30.26          9         3.36      <0.001

* Dropping individual terms from full fixed model

   t2harv.t2geno               30.26          9         3.36      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           2.280    Standard error:  0.0922



*** Table of predicted means for t2harv ***

  t2harv    6.000    7.000    8.000    9.000
           1.167    2.017    2.938    3.000

Standard error of differences:     Average       0.1843
                                  Maximum       0.1847
                                  Minimum       0.1839


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
           0.688    3.483    2.117    2.833

Standard error of differences:     Average       0.2607
                                  Maximum       0.2610
                                  Minimum       0.2604


*** Table of predicted means for t2harv.t2geno ***
```

```
      t2geno    2-49   Puseas    Sunco    Vasco
      t2harv
       6.000    0.000    2.600    0.400    1.667
       7.000    0.467    3.533    1.400    2.667
       8.000    1.351    4.000    3.200    3.200
       9.000    0.933    3.800    3.467    3.800

Standard error of differences:     Average       0.4035
                                   Maximum       0.4174
                                   Minimum       0.3678

Average variance of differences:                 0.1631

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.4122      0.3687
Maximum          0.4174      0.3745
Minimum          0.4114      0.3678


 157
 158  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 159      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 160  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 161  reml [print=means, wald, comp, mod] t3dr

161...............................................................................


***** REML Variance Components Analysis *****


Response Variate : t3dr

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 239

* Residual term has been added to model

* Sparse algorithm with AI optimisation
```

```
*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                  0.000       BOUND
t3plot                 0.010       0.032
t3plot.t3harv              0.000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2             1.066     0.103


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t3harv                    126.07           3        42.02      <0.001
   t3geno                    190.71           3        63.57      <0.001
   t3harv.t3geno                 26.26           9         2.92       0.002

* Dropping individual terms from full fixed model

   t3harv.t3geno                 26.26           9         2.92       0.002

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            2.071    Standard error:  0.0730



*** Table of predicted means for t3harv ***

  t3harv    6.000    7.000    8.000    9.000
            1.017    1.750    2.585    2.933
```

```
Standard error of differences:     Average       0.1889
                                   Maximum       0.1893
                                   Minimum       0.1885


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
           0.519    3.250    1.933    2.583

Standard error of differences:     Average       0.2065
                                   Maximum       0.2069
                                   Minimum       0.2062


*** Table of predicted means for t3harv.t3geno ***

       t3geno     2-49   Puseas    Sunco    Vasco
       t3harv
        6.000    0.000    2.400    0.333    1.333
        7.000    0.067    2.800    2.067    2.067
        8.000    1.141    4.000    2.067    3.133
        9.000    0.867    3.800    3.267    3.800

Standard error of differences:     Average       0.3851
                                   Maximum       0.3927
                                   Minimum       0.3769

Average variance of differences:                 0.1483

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average          0.3869      0.3778
Maximum          0.3927      0.3837
Minimum          0.3861      0.3769


 162
 163  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 164      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 165  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 166  reml [print=means, wald, comp, mod] t4dr
```

```
166.................................................................


***** REML Variance Components Analysis *****


Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 215

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term             Component       S.e.

t4rep                  0.000       BOUND
t4plot                 0.000       BOUND
t4plot.t4harv              0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            1.261     0.126


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                    81.32            3        27.11      <0.001
   t4geno                   121.75            3        40.58      <0.001
   t4harv.t4geno                18.16            9         2.02       0.033

* Dropping individual terms from full fixed model
```

```
  t4harv.t4geno              18.16         9       2.02     0.033

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.794    Standard error:  0.0773



*** Table of predicted means for t4harv ***

  t4harv    6.000    7.000    8.000    9.000
          0.783    1.468    2.266    2.656

Standard error of differences:     Average       0.2185
                                   Maximum       0.2269
                                   Minimum       0.2100

Average variance of differences:              0.04779


*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.531    2.774    1.554    2.316

Standard error of differences:     Average       0.2185
                                   Maximum       0.2272
                                   Minimum       0.2097

Average variance of differences:              0.04779


*** Table of predicted means for t4harv.t4geno ***

      t4geno     2-49   Puseas    Sunco    Vasco
      t4harv
       6.000    0.000    1.867    0.267    1.000
       7.000    0.200    1.857    1.733    2.083
       8.000    0.923    3.571    1.571    3.000
       9.000    1.000    3.800    2.643    3.182
```

```
Standard error of differences:     Average       0.4367
                                   Maximum      0.5021
                                   Minimum      0.4100

Average variance of differences:               0.1912

Standard error of differences for same level of factor:

                t4harv      t4geno
Average          0.4366      0.4365
Maximum          0.4906      0.4906
Minimum          0.4100      0.4100
Average variance of differences:
                0.1912      0.1912


 167
 168  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 169      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 170  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 171  reml [print=means, wald, comp, mod] t5dr

171..........................................................................


***** REML Variance Components Analysis *****


Response Variate : t5dr

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 172

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t5rep                   0.0000       BOUND
```

```
t5plot                    0.1297      0.1385
t5plot.t5harv             0.2386      0.1540


*** Residual variance model ***

Term            Factor      Model(order)  Parameter      Estimate     S.e.

Residual                    Identity      Sigma2            0.957    0.1215


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t5harv                    32.98           3        10.99       <0.001
  t5geno                    34.42           3        11.47       <0.001
  t5harv.t5geno              6.82           9         0.76        0.656

* Dropping individual terms from full fixed model

  t5harv.t5geno              6.82           9         0.76        0.656

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.682    Standard error:  0.1483



*** Table of predicted means for t5harv ***

 t5harv    6.000    7.000    8.000    9.000
        0.947    1.251    2.023    2.506

Standard error of differences:     Average       0.2984
                            Maximum       0.3116
                            Minimum       0.2848

Average variance of differences:             0.08909
```

```
*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
           0.479    2.766    1.280    2.202

Standard error of differences:     Average       0.4194
                                   Maximum       0.4297
                                   Minimum       0.4089

Average variance of differences:                0.1759


*** Table of predicted means for t5harv.t5geno ***

       t5geno    2-49   Puseas    Sunco    Vasco
       t5harv
        6.000   -0.001    1.473    0.833    1.481
        7.000    0.083    2.015    0.939    1.967
        8.000    0.711    3.565    1.500    2.318
        9.000    1.121    4.013    1.848    3.041

Standard error of differences:     Average       0.6511
                                   Maximum       0.7602
                                   Minimum       0.5547

Average variance of differences:                0.4258

Standard error of differences for same level of factor:

                t5harv      t5geno
Average          0.6649      0.5956
Maximum          0.7325      0.6987
Minimum          0.6190      0.5547
Average variance of differences:
                0.4432      0.3563


 172
 173
 174  "**** Infection - Total (Harvests 6, 7, 8 & 9; leave out CPI1338 & Rep 3)****"
 175
 176  "### Analysing the tillers together ###"
 177
```

```
 178  subset
[condition=(Part.eq.2).and.(Harvest.ge.6).and.(Genotype.ne.2).and.(Rep.le.2);\
 179   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 180   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 181
 182  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
constr=pos
-183  vstruct [nplot.nharv] factor=nharv; model=ar "
 184  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; constr=pos
 185  reml [print=means, wald, comp, mod, dev] sqrt(ntotal)

185..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 723

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                         0.0000       BOUND
nplot                        0.0370      0.0493
nplot.nharv                      0.0446      0.0505
nplot.nharv.nplant            0.2153      0.0483


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.
```

```
Residual                  Identity     Sigma2           0.715    0.0452


*** Deviance: -2*Log-Likelihood ***


             Deviance   d.f.

              734.24    638

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                     151.56          3       50.52      <0.001
  ngeno                      36.87          3       12.29      <0.001
  ntill                      7.68           4        1.92       0.104
  nharv.ngeno                26.81          9        2.98       0.002
  nharv.ntill                45.90         12        3.82      <0.001
  ngeno.ntill                12.51         12        1.04       0.405
  nharv.ngeno.ntill          43.61         36        1.21       0.179

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill          43.61         36        1.21       0.179

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        2.249    Standard error:  0.0919



*** Table of predicted means for nharv ***

  nharv    6.000    7.000    8.000    9.000
```

```
         1.077    2.087    2.756    3.075

Standard error of differences:     Average       0.1750
                                   Maximum       0.1772
                                   Minimum       0.1728


*** Table of predicted means for ngeno ***

  ngeno     2-49   Puseas    Sunco    Vasco
         1.514    3.013    2.049    2.418

Standard error of differences:     Average       0.2600
                                   Maximum       0.2613
                                   Minimum       0.2587


*** Table of predicted means for ntill ***

  ntill       1        2        3        4        5
         2.318    2.360    2.186    2.153    2.226

Standard error of differences:     Average       0.1029
                                   Maximum       0.1136
                                   Minimum      0.09489

Average variance of differences:               0.01064


*** Table of predicted means for nharv.ngeno ***

      ngeno     2-49   Puseas    Sunco    Vasco
      nharv
      6.000    0.087    2.159    0.674    1.387
      7.000    0.667    2.975    2.329    2.377
      8.000    2.323    3.406    2.537    2.755
      9.000    2.978    3.512    2.657    3.153

Standard error of differences:     Average       0.3894
                                   Maximum       0.4142
                                   Minimum       0.3428

Average variance of differences:                0.1521

Standard error of differences for same level of factor:
```

```
               nharv      ngeno
Average          0.3993     0.3499
Maximum          0.4119     0.3632
Minimum          0.3924     0.3428
Average variance of differences:
                 0.1595     0.1225



*** Table of predicted means for nharv.ntill ***

      ntill       1       2       3       4       5
      nharv
      6.000   1.440   1.242   0.788   0.953   0.960
      7.000   2.413   2.518   2.056   1.752   1.696
      8.000   2.549   2.674   2.839   2.813   2.904
      9.000   2.871   3.005   3.062   3.093   3.345

Standard error of differences:     Average       0.2437
                                   Maximum       0.3067
                                   Minimum       0.1891

Average variance of differences:                 0.06002

Standard error of differences for same level of factor:

               nharv      ntill
Average          0.2056     0.2536
Maximum          0.2433     0.3067
Minimum          0.1891     0.2402
Average variance of differences:
                0.04256    0.06467



*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49   1.689   1.656   1.573   1.248   1.404
     Puseas   3.063   3.276   3.064   2.830   2.832
      Sunco   2.099   2.039   1.948   2.099   2.062
      Vasco   2.422   2.467   2.160   2.434   2.607

Standard error of differences:     Average       0.2948
                                   Maximum       0.3665
```

```
                       Minimum      0.1891

Average variance of differences:             0.08921

Standard error of differences for same level of factor:

              ngeno      ntill
Average         0.2055     0.3184
Maximum         0.2586     0.3665
Minimum         0.1891     0.3077
Average variance of differences:
             0.04256     0.1017



*** Table of predicted means for nharv.ngeno.ntill ***

              ntill       1        2        3        4        5
      nharv       ngeno
      6.000        2-49    0.300    0.141    0.000    0.000   -0.006
                 Puseas    2.795    2.570    1.790    1.768    1.873
                  Sunco    1.052    0.638    0.456    0.734    0.492
                  Vasco    1.612    1.619    0.907    1.312    1.483
      7.000        2-49    1.197    1.564    0.456    0.173   -0.057
                 Puseas    3.312    3.773    3.168    2.238    2.387
                  Sunco    2.328    2.479    2.583    2.394    1.860
                  Vasco    2.813    2.256    2.017    2.202    2.596
      8.000        2-49    2.702    2.223    2.501    2.106    2.085
                 Puseas    2.784    3.146    3.610    3.788    3.702
                  Sunco    2.344    2.540    2.543    2.409    2.850
                  Vasco    2.365    2.786    2.700    2.950    2.977
      9.000        2-49    2.555    2.695    3.336    2.712    3.593
                 Puseas    3.359    3.617    3.686    3.528    3.368
                  Sunco    2.673    2.497    2.209    2.859    3.048
                  Vasco    2.898    3.209    3.017    3.271    3.371

Standard error of differences:     Average      0.5291
                       Maximum      0.7635
                       Minimum      0.3782

Average variance of differences:             0.2823

Standard error of differences for same level of factor:

              nharv      ngeno      ntill
Average         0.5146     0.4867     0.5350
```

```
Maximum          0.7040      0.7106      0.7635
Minimum          0.3782      0.3782      0.4804
Average variance of differences:
                 0.2693      0.2401      0.2883


 186
 187  "### Analysing the tillers separately ###"
 188
 189  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 190      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 191  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 192  reml [print=means, wald, comp, mod] sqrt(t1total)

192..................................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 159

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t1rep                    0.0000       BOUND
t1plot                   0.0672      0.0784
t1plot.t1harv            0.0214      0.0695


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.
```

```
Residual                    Identity     Sigma2            0.713    0.0894


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                    55.43           3        18.48      <0.001
   t1geno                     18.83           3         6.28      <0.001
   t1harv.t1geno                27.57           9         3.06       0.001

* Dropping individual terms from full fixed model

   t1harv.t1geno                27.57           9         3.06       0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            2.320    Standard error:  0.1164



*** Table of predicted means for t1harv ***

  t1harv    6.000    7.000    8.000    9.000
            1.440    2.413    2.558    2.871

Standard error of differences:     Average       0.2031
                                   Maximum       0.2037
                                   Minimum       0.2025


*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
            1.698    3.063    2.099    2.422

Standard error of differences:     Average       0.3292
                                   Maximum       0.3296
                                   Minimum       0.3289
```

```
*** Table of predicted means for t1harv.t1geno ***

      t1geno    2-49   Puseas    Sunco    Vasco
      t1harv
       6.000    0.300    2.795    1.052    1.612
       7.000    1.197    3.312    2.328    2.813
       8.000    2.738    2.784    2.344    2.365
       9.000    2.555    3.359    2.673    2.898

Standard error of differences:     Average       0.4667
                                   Maximum       0.4892
                                   Minimum       0.4050

Average variance of differences:                 0.2187

Standard error of differences for same level of factor:

               t1harv      t1geno
Average          0.4818      0.4062
Maximum          0.4892      0.4149
Minimum          0.4808      0.4050
Average variance of differences:
               0.2322      0.1650


 193
 194  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 195      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 196  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 197  reml [print=means, wald, comp, mod] sqrt(t2total)

197..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 159
```

```
* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term            Component      S.e.

t2rep                  0.0000      BOUND
t2plot                 0.0000      BOUND
t2plot.t2harv             0.0447     0.0886


*** Residual variance model ***

Term          Factor       Model(order)  Parameter       Estimate      S.e.

Residual                   Identity      Sigma2            0.969    0.1217


*** Wald tests for fixed effects ***


   Fixed term            Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                   60.17          3        20.06      <0.001
   t2geno                    48.43          3        16.14      <0.001
   t2harv.t2geno                12.24          9        1.36       0.200

* Dropping individual terms from full fixed model

   t2harv.t2geno                12.24          9        1.36       0.200

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            2.360    Standard error:  0.0866
```

```
*** Table of predicted means for t2harv ***

  t2harv    6.000    7.000    8.000    9.000
           1.242    2.518    2.676    3.005

Standard error of differences:     Average       0.2449
                                   Maximum       0.2456
                                   Minimum       0.2442


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
           1.658    3.276    2.039    2.467

Standard error of differences:     Average       0.2449
                                   Maximum       0.2456
                                   Minimum       0.2442


*** Table of predicted means for t2harv.t2geno ***

       t2geno     2-49   Puseas    Sunco    Vasco
       t2harv
        6.000    0.141    2.570    0.638    1.619
        7.000    1.564    3.773    2.479    2.256
        8.000    2.233    3.146    2.540    2.786
        9.000    2.695    3.617    2.497    3.209

Standard error of differences:     Average       0.4898
                                   Maximum       0.4996
                                   Minimum       0.4884

Average variance of differences:                0.2399

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.4898      0.4898
Maximum          0.4996      0.4996
Minimum          0.4884      0.4884
Average variance of differences:
                 0.2399      0.2399
```

```
 198
 199  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 200      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 201  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 202  reml [print=means, wald, comp, mod] sqrt(t3total)

202..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 159

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                  0.0605      0.1244
t3plot                 0.0610      0.0855
t3plot.t3harv              0.0000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.860    0.1032


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

  t3harv                146.91       3      48.97     <0.001
  t3geno                 23.10       3       7.70     <0.001
  t3harv.t3geno              35.18       9       3.91     <0.001

* Dropping individual terms from full fixed model

  t3harv.t3geno              35.18       9       3.91     <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        2.188    Standard error:  0.2081



*** Table of predicted means for t3harv ***

  t3harv    6.000    7.000    8.000    9.000
        0.788    2.056    2.844    3.062

Standard error of differences:     Average       0.2081
                                   Maximum       0.2088
                                   Minimum       0.2074


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
        1.579    3.064    1.948    2.160

Standard error of differences:     Average       0.3230
                                   Maximum       0.3235
                                   Minimum       0.3225


*** Table of predicted means for t3harv.t3geno ***

      t3geno     2-49   Puseas    Sunco    Vasco
      t3harv
       6.000    0.000    1.790    0.456    0.907
       7.000    0.456    3.168    2.583    2.017
```

```
      8.000    2.523    3.610    2.543    2.700
      9.000    3.336    3.686    2.209    3.017

Standard error of differences:     Average       0.4704
                                   Maximum       0.4927
                                   Minimum       0.4148

Average variance of differences:                0.2221

Standard error of differences for same level of factor:

                t3harv      t3geno
Average          0.4840      0.4162
Maximum          0.4927      0.4263
Minimum          0.4828      0.4148
Average variance of differences:
                0.2343      0.1732


 203
 204  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 205      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 206  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 207  reml [print=means, wald, comp, mod] sqrt(t4total)

207...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t4total)

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 139

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***
```

```
Random term              Component       S.e.

t4rep                    0.0000      BOUND
t4plot                   0.0152      0.0794
t4plot.t4harv                0.1103      0.1419


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.970    0.1324


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                    67.29           3        22.43      <0.001
   t4geno                    29.76           3         9.92      <0.001
   t4harv.t4geno                 11.06           9         1.23       0.272

* Dropping individual terms from full fixed model

   t4harv.t4geno                 11.06           9         1.23       0.272

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            2.165    Standard error:  0.1121



*** Table of predicted means for t4harv ***

  t4harv    6.000    7.000    8.000    9.000
            0.970    1.802    2.806    3.081

Standard error of differences:     Average       0.2922
                                   Maximum       0.3027
```

```
                              Minimum      0.2813

Average variance of differences:              0.08540


*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
           1.247    2.836    2.103    2.474

Standard error of differences:     Average       0.3171
                              Maximum      0.3258
                              Minimum      0.3083

Average variance of differences:               0.1006


*** Table of predicted means for t4harv.t4geno ***

      t4geno     2-49   Puseas    Sunco    Vasco
      t4harv
       6.000    0.000    1.768    0.734    1.378
       7.000    0.173    2.273    2.394    2.368
       8.000    2.119    3.787    2.417    2.900
       9.000    2.694    3.515    2.866    3.250

Standard error of differences:     Average       0.5942
                              Maximum      0.6738
                              Minimum      0.5517

Average variance of differences:               0.3538

Standard error of differences for same level of factor:

              t4harv      t4geno
Average          0.5967      0.5838
Maximum          0.6571      0.6414
Minimum          0.5653      0.5517
Average variance of differences:
              0.3568      0.3416


 208
 209  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 210      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
```

```
 211  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 212  reml [print=means, wald, comp, mod] sqrt(t5total)

212..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t5total)

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 107

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t5rep                    0.000       BOUND
t5plot                   0.123       0.201
t5plot.t5harv                0.192       0.233


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate       S.e.

Residual                      Identity      Sigma2            1.086     0.177


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t5harv                    53.20           3        17.73      <0.001
   t5geno                     11.32           3         3.77       0.010
```

```
  t5harv.t5geno              14.07           9         1.56       0.120

* Dropping individual terms from full fixed model

  t5harv.t5geno              14.07           9         1.56       0.120

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         2.243    Standard error:  0.1816



*** Table of predicted means for t5harv ***

 t5harv    6.000    7.000    8.000    9.000
         1.022    1.734    2.911    3.305

Standard error of differences:     Average       0.3743
                                  Maximum       0.3954
                                  Minimum       0.3525

Average variance of differences:               0.1402


*** Table of predicted means for t5geno ***

 t5geno     2-49   Puseas    Sunco    Vasco
         1.425    2.806    2.055    2.686

Standard error of differences:     Average       0.5134
                                  Maximum       0.5328
                                  Minimum       0.4936

Average variance of differences:               0.2638


*** Table of predicted means for t5harv.t5geno ***

     t5geno     2-49   Puseas    Sunco    Vasco
     t5harv
      6.000   -0.012    1.846    0.427    1.826
      7.000    0.000    2.351    1.862    2.722
```

```
        8.000    2.037    3.759    2.904    2.945
        9.000    3.674    3.266    3.028    3.252

Standard error of differences:     Average       0.8097
                                   Maximum       0.9922
                                   Minimum       0.6705

Average variance of differences:                0.6598

Standard error of differences for same level of factor:

                 t5harv      t5geno
Average          0.8254      0.7457
Maximum          0.9292      0.8992
Minimum          0.7473      0.6705
Average variance of differences:
                 0.6845      0.5609



 213
 214
 215
"=========================================================================
===========
-216                      PART = I3 (harvest 6, 7, 8 & 9)
-217
=========================================================================
=========="
 218
 219  "**** Disease Rating (Harvests 6, 7, 8 & 9; leave out CPI1338)****"
 220
 221  "### Analysing the tillers together ###"
 222
 223  subset [condition=(Part.eq.3).and.(Harvest.ge.7).and.(Genotype.ne.2); setlevel=yes]
\
 224   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
 225   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 226
 227  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 228  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-229  vstruct [nplot.nharv] factor=nharv; model=ar"
 230  reml [print=means, wald, comp, mod; mvincl=yvar, expl; maxcyc=100] ndr

230.............................................................................
```

```
***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 811

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                    0.0000       BOUND
nplot                   0.0000       BOUND
nplot.nharv                 0.0000       BOUND
nplot.nharv.nplant          0.4339      0.0634


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2             0.627    0.0367


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      45.40           2        22.70      <0.001
  ngeno                      282.26           3        94.09      <0.001
  ntill                   140.59           4        35.15      <0.001
```

```
  nharv.ngeno                26.17         6        4.36     <0.001
  nharv.ntill               24.23          8        3.03      0.002
  ngeno.ntill                60.98         12        5.08     <0.001
  nharv.ngeno.ntill          45.78         24        1.91      0.005

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill          45.78         24        1.91      0.005

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.259    Standard error:  0.0573



*** Table of predicted means for nharv ***

  nharv    7.000    8.000    9.000
        0.795    1.265    1.717

Standard error of differences:     Average       0.1400
                           Maximum      0.1407
                           Minimum      0.1394


*** Table of predicted means for ngeno ***

  ngeno     2-49   Puseas    Sunco    Vasco
        0.041    2.486    0.808    1.702

Standard error of differences:     Average       0.1617
                           Maximum      0.1633
                           Minimum      0.1601


*** Table of predicted means for ntill ***

  ntill       1        2        3        4        5
        1.779    1.501    1.203    0.948    0.863

Standard error of differences:     Average      0.09082
                           Maximum     0.09976
```

```
                              Minimum      0.08373

Average variance of differences:             0.008284


*** Table of predicted means for nharv.ngeno ***

       ngeno    2-49   Puseas    Sunco    Vasco
       nharv
       7.000    0.013    1.676    0.535    0.954
       8.000    0.110    2.753    0.564    1.633
       9.000    0.000    3.027    1.324    2.518

Standard error of differences:     Average       0.2801
                              Maximum       0.2889
                              Minimum       0.2742

Average variance of differences:              0.07846

Standard error of differences for same level of factor:

               nharv       ngeno
Average          0.2801      0.2801
Maximum          0.2889      0.2876
Minimum          0.2742      0.2746
Average variance of differences:
             0.07846     0.07846



*** Table of predicted means for nharv.ntill ***

       ntill       1        2        3        4        5
       nharv
       7.000    1.133    0.983    0.857    0.660    0.339
       8.000    1.705    1.687    1.118    0.986    0.828
       9.000    2.500    1.833    1.633    1.199    1.421

Standard error of differences:     Average       0.1867
                              Maximum       0.2301
                              Minimum       0.1446

Average variance of differences:              0.03531

Standard error of differences for same level of factor:
```

```
                nharv      ntill
Average         0.1572     0.1983
Maximum         0.1784     0.2301
Minimum         0.1446     0.1881
Average variance of differences:
              0.02485    0.03950



*** Table of predicted means for ngeno.ntill ***

       ntill        1        2        3        4        5
       ngeno
        2-49    0.095    0.094    0.024   -0.003   -0.006
      Puseas    3.511    2.889    2.244    1.971    1.812
       Sunco    1.400    1.044    0.822    0.479    0.292
       Vasco    2.111    1.978    1.721    1.347    1.353

Standard error of differences:     Average       0.2190
                                   Maximum       0.2768
                                   Minimum       0.1670

Average variance of differences:                 0.04855

Standard error of differences for same level of factor:

                ngeno      ntill
Average         0.1813     0.2288
Maximum         0.2280     0.2768
Minimum         0.1670     0.2172
Average variance of differences:
              0.03314    0.05266



*** Table of predicted means for nharv.ngeno.ntill ***

                 ntill        1        2        3        4        5
       nharv       ngeno
       7.000        2-49    0.000    0.067    0.000    0.000   -0.003
                  Puseas    2.867    1.933    1.600    1.200    0.782
                   Sunco    0.400    0.600    0.933    0.667    0.077
                   Vasco    1.267    1.333    0.895    0.775    0.501
       8.000        2-49    0.286    0.214    0.071   -0.010   -0.014
                  Puseas    3.733    3.533    2.400    2.330    1.768
                   Sunco    1.133    1.067    0.333    0.134    0.152
```

```
                Vasco    1.667    1.933    1.667    1.490    1.408
      9.000         2-49    0.000    0.000    0.000    0.000    0.000
               Puseas    3.933    3.200    2.733    2.382    2.888
                Sunco    2.667    1.467    1.200    0.638    0.648
                Vasco    3.400    2.667    2.600    1.775    2.150

Standard error of differences:     Average       0.3910
                             Maximum       0.5343
                             Minimum       0.2892

Average variance of differences:               0.1540

Standard error of differences for same level of factor:

              nharv       ngeno       ntill
Average         0.3791      0.3729      0.3962
Maximum         0.5109      0.5341      0.5343
Minimum         0.2892      0.2892      0.3761
Average variance of differences:
              0.1457      0.1413      0.1580


 231
 232
 233  "### Analysing the tillers separately ###"
 234
 235  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 236      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 237  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 238  reml [print=means, wald, comp, mod] t1dr

238..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 179

* Residual term has been added to model
```

```
* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term            Component       S.e.

t1rep                 0.0000      BOUND
t1plot                0.0122     0.0363
t1plot.t1harv             0.0000      BOUND


*** Residual variance model ***

Term          Factor       Model(order)  Parameter       Estimate      S.e.

Residual                  Identity      Sigma2            0.883    0.0991


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                   63.81           2        31.91      <0.001
  t1geno                  255.61           3        85.20      <0.001
  t1harv.t1geno               36.85           6         6.14      <0.001

* Dropping individual terms from full fixed model

  t1harv.t1geno               36.85           6         6.14      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         1.779    Standard error:  0.0772



*** Table of predicted means for t1harv ***
```

```
  t1harv    7.000    8.000    9.000
            1.133    1.705    2.500

Standard error of differences:     Average       0.1721
                                   Maximum       0.1724
                                   Minimum       0.1716


*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
            0.095    3.511    1.400    2.111

Standard error of differences:     Average       0.2182
                                   Maximum       0.2188
                                   Minimum       0.2177


*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        7.000    0.000    2.867    0.400    1.267
        8.000    0.285    3.733    1.133    1.667
        9.000    0.000    3.933    2.667    3.400

Standard error of differences:     Average       0.3537
                                   Maximum       0.3608
                                   Minimum       0.3432

Average variance of differences:                 0.1252

Standard error of differences for same level of factor:

                 t1harv      t1geno
Average          0.3558      0.3442
Maximum          0.3608      0.3493
Minimum          0.3549      0.3432


 239
 240  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 241      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 242  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
```

```
 243  reml [print=means, wald, comp, mod] t2dr

243..................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 179

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t2rep                    0.000       BOUND
t2plot                   0.006       0.041
t2plot.t2harv                0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            1.123     0.126


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                    22.51           2        11.25      <0.001
   t2geno                   160.09           3        53.36      <0.001
   t2harv.t2geno                 14.23           6         2.37       0.027
```

```
* Dropping individual terms from full fixed model

  t2harv.t2geno            14.23      6     2.37     0.027

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.501   Standard error:  0.0821



*** Table of predicted means for t2harv ***

  t2harv   7.000   8.000   9.000
          0.983   1.687   1.833

Standard error of differences:    Average     0.1941
                                  Maximum     0.1943
                                  Minimum     0.1935


*** Table of predicted means for t2geno ***

  t2geno    2-49   Puseas   Sunco   Vasco
          0.094   2.889   1.044   1.978

Standard error of differences:    Average     0.2323
                                  Maximum     0.2330
                                  Minimum     0.2317


*** Table of predicted means for t2harv.t2geno ***

      t2geno    2-49   Puseas   Sunco   Vasco
      t2harv
       7.000   0.067   1.933   0.600   1.333
       8.000   0.214   3.533   1.067   1.933
       9.000   0.000   3.200   1.467   2.667

Standard error of differences:    Average     0.3921
                                  Maximum     0.3986
                                  Minimum     0.3870
```

```
Average variance of differences:              0.1537

Standard error of differences for same level of factor:

               t2harv     t2geno
Average         0.3929     0.3881
Maximum         0.3986     0.3938
Minimum         0.3918     0.3870


 244
 245  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 246     t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 247  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 248  reml [print=means, wald, comp, mod] t3dr

248.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t3dr

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 178

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t3rep                      0.000       BOUND
t3plot                     0.000       BOUND
t3plot.t3harv                 0.000       BOUND


*** Residual variance model ***
```

```
Term           Factor       Model(order)  Parameter       Estimate      S.e.

Residual                  Identity      Sigma2           1.202     0.132


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t3harv                   15.07           2         7.54      <0.001
  t3geno                  107.79           3        35.93      <0.001
  t3harv.t3geno            15.44           6         2.57       0.017

* Dropping individual terms from full fixed model

  t3harv.t3geno            15.44           6         2.57       0.017

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.206    Standard error:  0.0822



*** Table of predicted means for t3harv ***

 t3harv    7.000    8.000    9.000
          0.865    1.118    1.633

Standard error of differences:     Average       0.2014
                                   Maximum       0.2020
                                   Minimum       0.2011


*** Table of predicted means for t3geno ***

 t3geno     2-49   Puseas    Sunco    Vasco
          0.024    2.244    0.822    1.732
```

```
Standard error of differences:     Average       0.2325
                                   Maximum       0.2339
                                   Minimum       0.2312


*** Table of predicted means for t3harv.t3geno ***

       t3geno     2-49   Puseas    Sunco    Vasco
       t3harv
        7.000    0.000    1.600    0.933    0.929
        8.000    0.071    2.400    0.333    1.667
        9.000    0.000    2.733    1.200    2.600

Standard error of differences:     Average       0.4028
                                   Maximum       0.4144
                                   Minimum       0.4004

Average variance of differences:                 0.1622

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average          0.4028      0.4028
Maximum          0.4075      0.4075
Minimum          0.4004      0.4004
Average variance of differences:
                 0.1622      0.1622



 249
 250  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 251      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 252  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 253  reml [print=means, wald, comp, mod] t4dr

253..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv
```

```
Number of units  : 154

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term               Component       S.e.

t4rep                      0.011       0.035
t4plot                     0.000       0.055
t4plot.t4harv                 0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            1.154     0.141


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t4harv                     4.06           2         2.03       0.131
  t4geno                    78.93           3        26.31      <0.001
  t4harv.t4geno                 10.97           6         1.83       0.089

* Dropping individual terms from full fixed model

  t4harv.t4geno                 10.97           6         1.83       0.089

* Message: chi-square distribution for Wald tests is an asymptotic approximation
 (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.9764    Standard error: 0.10632
```

```
*** Table of predicted means for t4harv ***

  t4harv    7.000    8.000    9.000
          0.7039   1.0534   1.1720

Standard error of differences:     Average       0.2144
                                   Maximum       0.2173
                                   Minimum       0.2118

Average variance of differences:              0.04597


*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.0017   1.9679   0.4857   1.4504

Standard error of differences:     Average       0.2477
                                   Maximum       0.2611
                                   Minimum       0.2338

Average variance of differences:              0.06143


*** Table of predicted means for t4harv.t4geno ***

       t4geno     2-49   Puseas    Sunco    Vasco
       t4harv
        7.000   0.0000   1.2360   0.6667   0.9131
        8.000   0.0035   2.3588   0.1444   1.7068
        9.000   0.0016   2.3090   0.6461   1.7313

Standard error of differences:     Average       0.4283
                                   Maximum       0.4808
                                   Minimum       0.3925

Average variance of differences:               0.1839

Standard error of differences for same level of factor:

                 t4harv      t4geno
Average          0.4284      0.4278
Maximum          0.4697      0.4695
```

```
Minimum          0.3925      0.3993
Average variance of differences:
                 0.1839      0.1838


 254
 255  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 256      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 257  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 258  reml [print=means, wald, comp, mod] t5dr

258..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t5dr

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 121

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t5rep                    0.0850      0.1689
t5plot                   0.2375      0.1852
t5plot.t5harv                 0.0098      0.0846


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2              0.700    0.1069
```

```
*** Wald tests for fixed effects ***


  Fixed term              Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t5harv                      18.41           2         9.20      <0.001
  t5geno                      21.05           3         7.02      <0.001
  t5harv.t5geno               15.55           6         2.59       0.016

* Dropping individual terms from full fixed model

  t5harv.t5geno               15.55           6         2.59       0.016

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.8918    Standard error: 0.23424



*** Table of predicted means for t5harv ***

  t5harv    7.000    8.000    9.000
         0.4434   0.8881   1.3441

Standard error of differences:     Average       0.1983
                                   Maximum       0.2058
                                   Minimum       0.1937

Average variance of differences:               0.03936


*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
         0.0028   1.8581   0.2851   1.4214

Standard error of differences:     Average       0.4605
                                   Maximum       0.4722
                                   Minimum       0.4488
```

```
Average variance of differences:              0.2122


*** Table of predicted means for t5harv.t5geno ***

      t5geno        2-49      Puseas       Sunco       Vasco
      t5harv
       7.000      0.0000      0.8520      0.0715      0.8500
       8.000      0.0037      1.8119      0.1667      1.5700
       9.000      0.0046      2.9103      0.6172      1.8442

Standard error of differences:     Average       0.5318
                                   Maximum       0.6322
                                   Minimum       0.3391

Average variance of differences:              0.2880

Standard error of differences for same level of factor:

                t5harv      t5geno
Average         0.5624      0.3940
Maximum         0.6117      0.4858
Minimum         0.5228      0.3391
Average variance of differences:
                0.3170      0.1573



 259
 260
 261  "**** Infection - Total (Harvests 6, 7, 8 & 9; leave out CPI1338 & Rep 3)****"
 262
 263  "### Analysing the tillers together ###"
 264
 265  subset
[condition=(Part.eq.3).and.(Harvest.ge.6).and.(Genotype.ne.2).and.(Rep.le.2);\
 266   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 267   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 268
 269  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
cons=pos
-270  vstruct [nplot.nharv] factor=nharv; model=ar"
 271  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; cons=pos
 272  reml [print=means, wald, comp, mod] sqrt(ntotal)
```

```
272...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 716 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                    0.000       BOUND
nplot                   0.021       0.050
nplot.nharv                 0.052       0.074
nplot.nharv.nplant              0.369       0.079


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate       S.e.

Residual                    Identity      Sigma2            1.072     0.068


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                     204.04           3        68.01      <0.001
   ngeno                      61.47           3        20.49      <0.001
   ntill                    74.68           4        18.67      <0.001
```

```
  nharv.ngeno              9.85        9       1.09     0.363
  nharv.ntill             9.49        12       0.79     0.661
  ngeno.ntill             14.29        12       1.19     0.283
  nharv.ngeno.ntill        46.07        36       1.28     0.121

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill        46.07        36       1.28     0.121

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

       1.746    Standard error:  0.0908



*** Table of predicted means for nharv ***

  nharv    6.000    7.000    8.000    9.000
       0.405    1.142    2.307    3.130

Standard error of differences:     Average       0.2116
                         Maximum      0.2140
                         Minimum      0.2092


*** Table of predicted means for ngeno ***

  ngeno     2-49   Puseas    Sunco    Vasco
       0.795    2.636    1.397    2.156

Standard error of differences:     Average       0.2567
                         Maximum      0.2589
                         Minimum      0.2545


*** Table of predicted means for ntill ***

  ntill       1        2        3        4        5
       2.236    1.999    1.723    1.409    1.364

Standard error of differences:     Average       0.1269
                         Maximum      0.1405
```

```
                              Minimum      0.1164

Average variance of differences:             0.01618


*** Table of predicted means for nharv.ngeno ***

       ngeno    2-49   Puseas   Sunco   Vasco
       nharv
       6.000   0.000   1.007   0.027   0.585
       7.000   0.136   2.101   0.978   1.355
       8.000   1.061   3.514   1.724   2.930
       9.000   1.983   3.921   2.861   3.755

Standard error of differences:     Average      0.4425
                              Maximum      0.4665
                              Minimum      0.4130

Average variance of differences:              0.1960

Standard error of differences for same level of factor:

                nharv      ngeno
Average          0.4474      0.4231
Maximum          0.4638      0.4398
Minimum          0.4378      0.4130
Average variance of differences:
               0.2002      0.1791



*** Table of predicted means for nharv.ntill ***

       ntill       1        2        3        4        5
       nharv
       6.000   0.789   0.570   0.352   0.129   0.184
       7.000   1.587   1.440   1.133   0.880   0.673
       8.000   2.971   2.754   2.185   1.903   1.724
       9.000   3.597   3.233   3.221   2.725   2.875

Standard error of differences:     Average      0.2982
                              Maximum      0.3741
                              Minimum      0.2315

Average variance of differences:             0.08982
```

```
Standard error of differences for same level of factor:

               nharv      ntill
Average         0.2535     0.3097
Maximum          0.2981     0.3741
Minimum         0.2315     0.2917
Average variance of differences:
             0.06470    0.09652



*** Table of predicted means for ngeno.ntill ***

      ntill       1        2        3        4        5
      ngeno
       2-49    1.280    0.939    0.883    0.511    0.363
     Puseas    3.473    2.813    2.489    2.252    2.152
      Sunco    1.805    1.868    1.435    1.091    0.789
      Vasco    2.386    2.377    2.084    1.783    2.151

Standard error of differences:     Average       0.3237
                             Maximum       0.4120
                             Minimum       0.2315

Average variance of differences:               0.1065

Standard error of differences for same level of factor:

               ngeno      ntill
Average         0.2532     0.3422
Maximum          0.3225     0.4120
Minimum         0.2315     0.3259
Average variance of differences:
             0.06470     0.1177



*** Table of predicted means for nharv.ngeno.ntill ***

                 ntill       1        2        3        4        5
      nharv       ngeno
      6.000        2-49    0.000    0.000    0.000    0.000    0.000
                 Puseas    1.967    1.258    0.893    0.577    0.341
                  Sunco    0.000    0.000    0.141   -0.001   -0.005
                  Vasco    1.190    1.023    0.374   -0.060    0.399
      7.000        2-49    0.245    0.461    0.000    0.000   -0.026
```

```
                 Puseas   3.559    2.238    1.979    1.667    1.064
                  Sunco   1.061    1.382    1.343    0.977    0.125
                  Vasco   1.483    1.679    1.210    0.875    1.528
        8.000        2-49    2.188    1.487    1.214    0.442   -0.025
                 Puseas   3.960    3.828    3.376    3.345    3.062
                  Sunco   2.752    2.790    1.312    0.870    0.896
                  Vasco   2.984    2.910    2.839    2.954    2.961
        9.000        2-49    2.686    1.807    2.320    1.603    1.501
                 Puseas   4.407    3.929    3.708    3.420    4.141
                  Sunco   3.405    3.300    2.943    2.516    2.140
                  Vasco   3.888    3.898    3.912    3.362    3.716

Standard error of differences:     Average       0.6265
                            Maximum       0.9150
                            Minimum       0.4631

Average variance of differences:                0.3957

Standard error of differences for same level of factor:

               nharv       ngeno       ntill
Average          0.6088      0.5954      0.6322
Maximum          0.8401      0.8684      0.9150
Minimum          0.4631      0.4631      0.5834
Average variance of differences:
              0.3760      0.3593      0.4030


 273
 274  "### Analysing the tillers separately ###"
 275
 276  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 277      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 278  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 279  reml [print=means, wald, comp, mod] sqrt(t1total)

279.................................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
```

```
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 159

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t1rep                    0.000       BOUND
t1plot                   0.000       BOUND
t1plot.t1harv               0.102       0.122


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate       S.e.

Residual                    Identity      Sigma2            1.150     0.144


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                    118.37           3        39.46      <0.001
   t1geno                     63.59           3        21.20      <0.001
   t1harv.t1geno                 8.43           9         0.94       0.491

* Dropping individual terms from full fixed model

   t1harv.t1geno                 8.43           9         0.94       0.491

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
           2.236    Standard error:  0.1022



*** Table of predicted means for t1harv ***

  t1harv    6.000    7.000    8.000    9.000
           0.789    1.587    2.972    3.597

Standard error of differences:     Average       0.2890
                                   Maximum       0.2897
                                   Minimum       0.2883


*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
           1.281    3.473    1.805    2.386

Standard error of differences:     Average       0.2890
                                   Maximum       0.2897
                                   Minimum       0.2883


*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        6.000    0.000    1.967    0.000    1.190
        7.000    0.245    3.559    1.061    1.483
        8.000    2.192    3.960    2.752    2.984
        9.000    2.686    4.407    3.405    3.888

Standard error of differences:     Average       0.5780
                                   Maximum       0.5879
                                   Minimum       0.5765

Average variance of differences:                0.3340

Standard error of differences for same level of factor:

                t1harv      t1geno
Average          0.5780      0.5780
Maximum          0.5879      0.5879
Minimum          0.5765      0.5765
Average variance of differences:
```

```
          0.3340     0.3340


 280
 281  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 282      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 283  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 284  reml [print=means, wald, comp, mod] sqrt(t2total)

284.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 158 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term             Component       S.e.

t2rep                      0.000       BOUND
t2plot                     0.039       0.142
t2plot.t2harv                 0.274       0.239


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            1.483     0.187


*** Wald tests for fixed effects ***
```

```
  Fixed term            Wald statistic    d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                   62.17        3      20.72     <0.001
  t2geno                   21.40        3       7.13     <0.001
  t2harv.t2geno             3.36        9       0.37      0.948

* Dropping individual terms from full fixed model

  t2harv.t2geno             3.36        9       0.37      0.948

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         1.999   Standard error:  0.1512



*** Table of predicted means for t2harv ***

 t2harv   6.000   7.000   8.000   9.000
          0.570   1.440   2.745   3.239

Standard error of differences:    Average      0.3792
                                  Maximum      0.3807
                                  Minimum      0.3778


*** Table of predicted means for t2geno ***

 t2geno    2-49  Puseas   Sunco   Vasco
          0.930   2.813   1.873   2.377

Standard error of differences:    Average      0.4275
                                  Maximum      0.4288
                                  Minimum      0.4263


*** Table of predicted means for t2harv.t2geno ***

     t2geno    2-49  Puseas   Sunco   Vasco
```

```
     t2harv
      6.000    0.000    1.258    0.000    1.023
      7.000    0.461    2.238    1.382    1.679
      8.000    1.454    3.828    2.790    2.910
      9.000    1.807    3.929    3.321    3.898

Standard error of differences:     Average       0.7787
                                   Maximum       0.8030
                                   Minimum       0.7556

Average variance of differences:                 0.6065

Standard error of differences for same level of factor:

                t2harv      t2geno
Average          0.7837      0.7585
Maximum          0.7921      0.7671
Minimum          0.7810      0.7556
Average variance of differences:
                0.6143      0.5753


 285
 286  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 287      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 288  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 289  reml [print=means, wald, comp, mod] sqrt(t3total)

289.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 158

* Residual term has been added to model

* Sparse algorithm with AI optimisation
```

```
*** Estimated Variance Components ***

Random term             Component       S.e.

t3rep                   0.031       0.077
t3plot                  0.000       BOUND
t3plot.t3harv               0.000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2             1.830     0.218


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t3harv                    102.63           3        34.21      <0.001
  t3geno                     32.28           3        10.76      <0.001
  t3harv.t3geno                 8.83           9         0.98       0.454

* Dropping individual terms from full fixed model

  t3harv.t3geno                 8.83           9         0.98       0.454

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           1.726    Standard error:  0.1652



*** Table of predicted means for t3harv ***

  t3harv    6.000    7.000    8.000    9.000
           0.352    1.140    2.192    3.221
```

```
Standard error of differences:     Average       0.3045
                                   Maximum       0.3066
                                   Minimum       0.3025


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
          0.891    2.489    1.435    2.091

Standard error of differences:     Average       0.3045
                                   Maximum       0.3066
                                   Minimum       0.3025


*** Table of predicted means for t3harv.t3geno ***

       t3geno     2-49   Puseas    Sunco    Vasco
       t3harv
        6.000    0.000    0.893    0.141    0.374
        7.000    0.000    1.979    1.343    1.237
        8.000    1.243    3.376    1.312    2.839
        9.000    2.320    3.708    2.943    3.912

Standard error of differences:     Average       0.6091
                                   Maximum       0.6376
                                   Minimum       0.6049

Average variance of differences:                0.3710

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average          0.6091      0.6091
Maximum          0.6215      0.6215
Minimum          0.6049      0.6049
Average variance of differences:
                 0.3710      0.3710


 290
 291  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 292      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 293  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
```

```
 294  reml [print=means, wald, comp, mod] sqrt(t4total)

294.................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t4total)

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 136

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t4rep                   0.000       BOUND
t4plot                  0.000       BOUND
t4plot.t4harv               0.000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate       S.e.

Residual                     Identity      Sigma2             1.368     0.177


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                    88.63           3        29.54      <0.001
   t4geno                     43.45           3        14.48      <0.001
   t4harv.t4geno                19.21           9         2.13       0.023
```

```
* Dropping individual terms from full fixed model

   t4harv.t4geno               19.21          9        2.13      0.023

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.448    Standard error:  0.1017



*** Table of predicted means for t4harv ***

  t4harv    6.000    7.000    8.000    9.000
            0.144    0.952    1.974    2.720

Standard error of differences:     Average       0.2876
                                   Maximum       0.2990
                                   Minimum       0.2759

Average variance of differences:               0.08276


*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
            0.544    2.302    1.093    1.851

Standard error of differences:     Average       0.2875
                                   Maximum       0.3019
                                   Minimum       0.2727

Average variance of differences:               0.08276


*** Table of predicted means for t4harv.t4geno ***

       t4geno     2-49   Puseas    Sunco    Vasco
       t4harv
        6.000    0.000    0.577    0.000    0.000
        7.000    0.000    1.832    0.977    1.000
        8.000    0.547    3.378    0.891    3.078
```

```
        9.000    1.630    3.420    2.503    3.328

Standard error of differences:     Average       0.5743
                                   Maximum       0.6753
                                   Minimum       0.5231

Average variance of differences:                 0.3310

Standard error of differences for same level of factor:

                t4harv      t4geno
Average          0.5742      0.5740
Maximum          0.6507      0.6507
Minimum          0.5231      0.5231
Average variance of differences:
                 0.3310      0.3310


 295
 296  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 297      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 298  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 299  reml [print=means, wald, comp, mod] sqrt(t5total)

299.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t5total)

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 105

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.
```

```
t5rep                   0.107      0.191
t5plot                  0.000      BOUND
t5plot.t5harv              0.083      0.180


*** Residual variance model ***

Term           Factor       Model(order)  Parameter       Estimate     S.e.

Residual                  Identity      Sigma2            1.098     0.183


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t5harv                   62.03           3        20.68      <0.001
  t5geno                    49.32           3        16.44      <0.001
  t5harv.t5geno               14.20           9        1.58       0.116

* Dropping individual terms from full fixed model

  t5harv.t5geno               14.20           9        1.58       0.116

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.454    Standard error:  0.2602



*** Table of predicted means for t5harv ***

 t5harv    6.000    7.000    8.000    9.000
        0.318    0.789    1.835    2.875

Standard error of differences:     Average       0.3379
                             Maximum       0.3577
                             Minimum       0.3178
```

```
Average variance of differences:                0.1143


*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
           0.444    2.257    0.748    2.368

Standard error of differences:     Average       0.3373
                                   Maximum       0.3677
                                   Minimum       0.3058

Average variance of differences:                0.1142


*** Table of predicted means for t5harv.t5geno ***

       t5geno     2-49   Puseas    Sunco    Vasco
       t5harv
        6.000    0.017    0.511    0.000    0.745
        7.000    0.000    1.179    0.145    1.834
        8.000    0.023    3.235    0.945    3.136
        9.000    1.736    4.104    1.901    3.758

Standard error of differences:     Average       0.6721
                                   Maximum       0.8585
                                   Minimum       0.5726

Average variance of differences:                0.4558

Standard error of differences for same level of factor:

                t5harv      t5geno
Average         0.6719      0.6705
Maximum         0.7879      0.8285
Minimum         0.5852      0.5852
Average variance of differences:
                0.4555      0.4556


 300
 301
 302
"==============================================================
===========
```

```
-303                     PART = I4 (harvest 6, 7, 8 & 9)
-304
============================================================
=========="
 305
 306  "**** Disease Rating (Harvests 6, 7, 8 & 9; leave out CPI1338)****"
 307
 308  "### Analysing the tillers together ###"
 309
 310  subset [condition=(Part.eq.4).and.(Harvest.ge.7).and.(Genotype.ne.2); setlevel=yes]
\
 311   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
 312   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 313
 314  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 315  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-316  vstruct [nplot.nharv] factor=nharv; model=ar"
 317  reml [print=means, wald, comp, mod; mvincl=yvar, expl; maxcyc=100] ndr

317...........................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 804

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                       0.0000       BOUND
```

```
nplot                    0.0000      BOUND
nplot.nharv                 0.0000      BOUND
nplot.nharv.nplant          0.1848     0.0298


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.371    0.0218


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      16.63            2         8.31      <0.001
  ngeno                     115.89            3        38.63      <0.001
  ntill                   44.72            4        11.18      <0.001
  nharv.ngeno                  19.00            6         3.17       0.004
  nharv.ntill                22.07            8         2.76       0.005
  ngeno.ntill                42.58           12         3.55      <0.001
  nharv.ngeno.ntill            24.69           24         1.03       0.423

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill            24.69           24         1.03       0.423

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.4362    Standard error: 0.03920



*** Table of predicted means for nharv ***

  nharv    7.000    8.000    9.000
        0.2360   0.4805   0.5919
```

```
Standard error of differences:     Average      0.09602
                                   Maximum      0.09639
                                   Minimum      0.09562


*** Table of predicted means for ngeno ***

   ngeno     2-49   Puseas    Sunco    Vasco
          0.0000   0.9954   0.1346   0.6146

Standard error of differences:     Average       0.1109
                                   Maximum       0.1125
                                   Minimum       0.1093


*** Table of predicted means for ntill ***

   ntill        1         2         3         4         5
          0.6902   0.4889   0.4161   0.2995   0.2861

Standard error of differences:     Average      0.07013
                                   Maximum      0.07720
                                   Minimum      0.06447

Average variance of differences:              0.004940


*** Table of predicted means for nharv.ngeno ***

        ngeno         2-49       Puseas        Sunco        Vasco
        nharv
        7.000       0.0000       0.4668       0.0933       0.3840
        8.000       0.0000       1.2321       0.1187       0.5714
        9.000       0.0000       1.2871       0.1919       0.8886

Standard error of differences:     Average       0.1920
                                   Maximum       0.1986
                                   Minimum       0.1871

Average variance of differences:               0.03688

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.1920      0.1920
Maximum          0.1983      0.1985
```

```
Minimum          0.1871      0.1873
Average variance of differences:
              0.03688     0.03688



*** Table of predicted means for nharv.ntill ***

       ntill       1        2        3        4        5
       nharv
       7.000   0.3000   0.2333   0.3149   0.2151   0.1169
       8.000   0.7038   0.6167   0.4333   0.3528   0.2961
       9.000   1.0667   0.6167   0.5000   0.3307   0.4455

Standard error of differences:     Average       0.1382
                              Maximum      0.1695
                              Minimum      0.1111

Average variance of differences:              0.01929

Standard error of differences for same level of factor:

                nharv       ntill
Average          0.1214      0.1447
Maximum          0.1373      0.1695
Minimum          0.1111      0.1361
Average variance of differences:
              0.01482     0.02108



*** Table of predicted means for ngeno.ntill ***

       ntill       1        2        3        4        5
       ngeno
        2-49   0.0000   0.0000   0.0000   0.0000   0.0000
      Puseas   1.6222   1.1333   0.9242   0.7747   0.5223
       Sunco   0.3162   0.2000   0.0667   0.0441   0.0462
       Vasco   0.8222   0.6222   0.6734   0.3794   0.5760

Standard error of differences:     Average       0.1615
                              Maximum      0.2061
                              Minimum      0.1283

Average variance of differences:              0.02635
```

```
Standard error of differences for same level of factor:

                ngeno      ntill
Average          0.1400      0.1670
Maximum           0.1769      0.2061
Minimum           0.1283      0.1571
Average variance of differences:
              0.01976     0.02810



*** Table of predicted means for nharv.ngeno.ntill ***

                  ntill          1           2           3           4
       nharv       ngeno
       7.000        2-49      0.0000      0.0000      0.0000      0.0000
                 Puseas      0.7333      0.4667      0.6393      0.4043
                  Sunco      0.0667      0.1333      0.1333      0.0667
                  Vasco      0.4000      0.3333      0.4869      0.3896
       8.000        2-49      0.0000      0.0000      0.0000      0.0000
                 Puseas      2.0000      1.5333      1.1333      1.1333
                  Sunco      0.2820      0.3333      0.0000     -0.0088
                  Vasco      0.5333      0.6000      0.6000      0.2867
       9.000        2-49      0.0000      0.0000      0.0000      0.0000
                 Puseas      2.1333      1.4000      1.0000      0.7866
                  Sunco      0.6000      0.1333      0.0667      0.0743
                  Vasco      1.5333      0.9333      0.9333      0.4618


                  ntill          5
       nharv       ngeno
       7.000        2-49      0.0000
                 Puseas      0.0906
                  Sunco      0.0667
                  Vasco      0.3102
       8.000        2-49      0.0000
                 Puseas      0.3606
                  Sunco     -0.0132
                  Vasco      0.8368
       9.000        2-49      0.0000
                 Puseas      1.1157
                  Sunco      0.0851
                  Vasco      0.5811

Standard error of differences:     Average       0.2863
                              Maximum       0.3972
```

```
                        Minimum       0.2223

Average variance of differences:              0.08261

Standard error of differences for same level of factor:

             nharv      ngeno      ntill
Average         0.2796     0.2760     0.2892
Maximum         0.3785     0.3971     0.3972
Minimum         0.2223     0.2223     0.2721
Average variance of differences:
            0.07904    0.07715    0.08430



 318
 319  "### Analysing the tillers separately ###"
 320
 321  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 322     t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 323  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 324  reml [print=means, wald, comp, mod] t1dr

324.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 178

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t1rep                    0.0000       BOUND
```

```
t1plot                0.0000     BOUND
t1plot.t1harv            0.0310     0.0482


*** Residual variance model ***

Term          Factor       Model(order)  Parameter      Estimate     S.e.

Residual                   Identity      Sigma2            0.635    0.0753


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                   22.39            2        11.20      <0.001
  t1geno                    84.80            3        28.27      <0.001
  t1harv.t1geno              17.63            6         2.94       0.007

* Dropping individual terms from full fixed model

  t1harv.t1geno              17.63            6         2.94       0.007

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.6904    Standard error: 0.06657



*** Table of predicted means for t1harv ***

 t1harv    7.000    8.000    9.000
        0.3000   0.7047   1.0667

Standard error of differences:     Average       0.1631
                                   Maximum       0.1635
                                   Minimum       0.1623
```

```
*** Table of predicted means for t1geno ***

 t1geno     2-49   Puseas    Sunco    Vasco
         0.0000   1.6222   0.3173   0.8222

Standard error of differences:     Average       0.1883
                                   Maximum      0.1892
                                   Minimum      0.1874


*** Table of predicted means for t1harv.t1geno ***

     t1geno        2-49      Puseas       Sunco       Vasco
     t1harv
      7.000      0.0000      0.7333      0.0667      0.4000
      8.000      0.0000      2.0000      0.2853      0.5333
      9.000      0.0000      2.1333      0.6000      1.5333

Standard error of differences:     Average       0.3261
                                   Maximum      0.3340
                                   Minimum      0.3245

Standard error of differences for same level of factor:

              t1harv      t1geno
Average         0.3261      0.3261
Maximum          0.3340      0.3293
Minimum         0.3245      0.3245
Average variance of differences:
              0.1064      0.1064


 325
 326  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 327      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 328  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 329  reml [print=means, wald, comp, mod] t2dr

329.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr
```

```
Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 179

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t2rep                   0.0000       BOUND
t2plot                  0.0000       BOUND
t2plot.t2harv               0.0000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2             0.513    0.0562


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                     11.73           2         5.87       0.003
   t2geno                     65.51           3        21.84      <0.001
   t2harv.t2geno                 14.32           6         2.39       0.026

* Dropping individual terms from full fixed model

   t2harv.t2geno                 14.32           6         2.39       0.026

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.
```

```
*** Table of predicted means for Constant ***

           0.4889    Standard error: 0.05356



*** Table of predicted means for t2harv ***

  t2harv    7.000    8.000    9.000
           0.2333   0.6167   0.6167

Standard error of differences:     Average       0.1312
                                   Maximum       0.1314
                                   Minimum       0.1308


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
           0.0000   1.1333   0.2000   0.6222

Standard error of differences:     Average       0.1515
                                   Maximum       0.1519
                                   Minimum       0.1511


*** Table of predicted means for t2harv.t2geno ***

       t2geno     2-49   Puseas    Sunco    Vasco
       t2harv
        7.000   0.0000   0.4667   0.1333   0.3333
        8.000   0.0000   1.5333   0.3333   0.6000
        9.000   0.0000   1.4000   0.1333   0.9333

Standard error of differences:     Average       0.2624
                                   Maximum       0.2663
                                   Minimum       0.2616

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.2624      0.2624
Maximum          0.2663      0.2663
Minimum          0.2616      0.2616
```

```
 330
 331  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 332      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 333  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 334  reml [print=means, wald, comp, mod] t3dr

334.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t3dr

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 177

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t3rep                    0.0048      0.0158
t3plot                   0.0000       BOUND
t3plot.t3harv                0.0000       BOUND


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                     Identity      Sigma2             0.649    0.0719


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

  t3harv                1.69        2      0.85     0.429
  t3geno               42.81        3     14.27    <0.001
  t3harv.t3geno         3.92        6      0.65     0.687

* Dropping individual terms from full fixed model

  t3harv.t3geno         3.92        6      0.65     0.687

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.4177    Standard error: 0.07255



*** Table of predicted means for t3harv ***

  t3harv    7.000    8.000    9.000
          0.3198   0.4335   0.5000

Standard error of differences:     Average       0.1484
                                   Maximum       0.1490
                                   Minimum       0.1477


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
          0.0002   0.9262   0.0667   0.6780

Standard error of differences:     Average       0.1713
                                   Maximum       0.1719
                                   Minimum       0.1708


*** Table of predicted means for t3harv.t3geno ***

      t3geno     2-49   Puseas    Sunco    Vasco
      t3harv
       7.000   0.0000   0.6453   0.1333   0.5005
       8.000   0.0005   1.1333   0.0000   0.6000
```

```
     9.000   0.0000   1.0000   0.0667   0.9333

Standard error of differences:     Average       0.2968
                                   Maximum       0.3045
                                   Minimum       0.2942

Average variance of differences:              0.08808

Standard error of differences for same level of factor:

             t3harv      t3geno
Average          0.2968      0.2968
Maximum          0.3045      0.2994
Minimum          0.2942      0.2942
Average variance of differences:
             0.08808     0.08808



 335
 336  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 337      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 338  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 339  reml [print=means, wald, comp, mod] t4dr

339..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 150

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.
```

```
t4rep                 0.0000      BOUND
t4plot                0.0115     0.0241
t4plot.t4harv             0.0000      BOUND


*** Residual variance model ***

Term           Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.421    0.0523


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t4harv                    0.86           2        0.43       0.649
  t4geno                   24.74            3         8.25      <0.001
  t4harv.t4geno                5.43           6         0.91       0.490

* Dropping individual terms from full fixed model

  t4harv.t4geno                5.43           6         0.91       0.490

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          0.2986    Standard error: 0.06185



*** Table of predicted means for t4harv ***

  t4harv    7.000    8.000    9.000
          0.2429   0.3454   0.3076

Standard error of differences:     Average       0.1311
                                   Maximum       0.1318
                                   Minimum       0.1303
```

```
*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.0000   0.7447   0.0464   0.4035

Standard error of differences:     Average       0.1749
                                   Maximum       0.1828
                                   Minimum       0.1667

Average variance of differences:                0.03060


*** Table of predicted means for t4harv.t4geno ***

       t4geno        2-49       Puseas       Sunco       Vasco
       t4harv
        7.000      0.0000       0.4536      0.0667      0.4513
        8.000      0.0000       1.0747     -0.0010      0.3079
        9.000      0.0000       0.7059      0.0734      0.4513

Standard error of differences:     Average       0.2736
                                   Maximum       0.3035
                                   Minimum       0.2411

Average variance of differences:                0.07505

Standard error of differences for same level of factor:

                t4harv      t4geno
Average          0.2763      0.2617
Maximum          0.2971      0.2841
Minimum          0.2565      0.2411
Average variance of differences:
                0.07644     0.06876


 340
 341  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 342      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 343  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 344  reml [print=means, wald, comp, mod] t5dr

344..............................................................................
```

```
***** REML Variance Components Analysis *****


Response Variate : t5dr

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 120

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t5rep                   0.0000       BOUND
t5plot                  0.1062      0.0797
t5plot.t5harv               0.0029      0.0537


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.425    0.0662


*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t5harv                     1.78           2        0.89       0.411
   t5geno                     4.43           3        1.48       0.219
   t5harv.t5geno                 10.90           6        1.82       0.092

* Dropping individual terms from full fixed model
```

```
 t5harv.t5geno           10.90        6      1.82     0.092

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.2885    Standard error: 0.11341



*** Table of predicted means for t5harv ***

  t5harv    7.000    8.000    9.000
          0.1631   0.3152   0.3871

Standard error of differences:     Average       0.1535
                                   Maximum       0.1583
                                   Minimum       0.1502

Average variance of differences:              0.02356


*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
          0.0000   0.4842   0.0568   0.6129

Standard error of differences:     Average       0.3207
                                   Maximum       0.3309
                                   Minimum       0.3103

Average variance of differences:               0.1029


*** Table of predicted means for t5harv.t5geno ***

      t5geno        2-49      Puseas       Sunco       Vasco
      t5harv
       7.000      0.0000      0.0991      0.0743      0.4790
       8.000      0.0000      0.2947      0.0000      0.9662
       9.000      0.0000      1.0587      0.0961      0.3934

Standard error of differences:     Average       0.3880
                                   Maximum       0.4635
```

```
                         Minimum      0.2604

Average variance of differences:              0.1527

Standard error of differences for same level of factor:

              t5harv      t5geno
Average          0.4065      0.3047
Maximum          0.4463      0.3755
Minimum          0.3723      0.2604
Average variance of differences:
              0.1657     0.09424



 345
 346
 347  "**** Infection - Total (Harvests 6, 7, 8 & 9; leave out CPI1338 & Rep 3)****"
 348
 349  "### Analysing the tillers together ###"
 350
 351  subset
[condition=(Part.eq.4).and.(Harvest.ge.6).and.(Genotype.ne.2).and.(Rep.le.2);\
 352   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 353   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 354
 355  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
cons=pos
-356  vstruct [nplot.nharv] factor=nharv; model=ar "
 357  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; cons=pos
 358  reml [print=means, wald, comp, mod, dev] sqrt(ntotal)

358..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 698 (1 units excluded due to zero weights or missing values)
```

```
* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                    0.0422      0.0899
nplot                   0.0293      0.0698
nplot.nharv                 0.0914      0.0856
nplot.nharv.nplant          0.3556      0.0734


*** Residual variance model ***

Term            Factor        Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.928    0.0601


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                893.60   613

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      77.31           3        25.77      <0.001
  ngeno                      34.01           3        11.34      <0.001
  ntill                    59.43           4        14.86      <0.001
  nharv.ngeno                   33.58           9         3.73      <0.001
  nharv.ntill                 36.00          12         3.00      <0.001
```

```
  ngeno.ntill               38.56        12       3.21     <0.001
  nharv.ngeno.ntill             32.18        36       0.89      0.651

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill             32.18        36       0.89      0.651

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.8052    Standard error: 0.17708



*** Table of predicted means for nharv ***

  nharv    6.000    7.000    8.000    9.000
         0.0598   0.3913   0.9632   1.8064

Standard error of differences:     Average       0.2296
                               Maximum       0.2304
                               Minimum       0.2288


*** Table of predicted means for ngeno ***

  ngeno     2-49   Puseas    Sunco    Vasco
         0.0809   1.3860   0.4632   1.2906

Standard error of differences:     Average       0.2864
                               Maximum       0.2887
                               Minimum       0.2841


*** Table of predicted means for ntill ***

  ntill       1        2        3        4        5
         1.3254   0.8699   0.7751   0.6280   0.4274

Standard error of differences:     Average       0.1204
                               Maximum       0.1351
                               Minimum       0.1085
```

```
Average variance of differences:          0.01459


*** Table of predicted means for nharv.ngeno ***

     ngeno      2-49     Puseas     Sunco     Vasco
     nharv
     6.000     0.0000     0.1865     0.0011     0.0515
     7.000    -0.0005     0.7305     0.1976     0.6377
     8.000     0.0923     2.0337     0.4368     1.2903
     9.000     0.2317     2.5936     1.2171     3.1829

Standard error of differences:    Average      0.4838
                              Maximum     0.5032
                              Minimum     0.4492

Average variance of differences:          0.2343

Standard error of differences for same level of factor:

            nharv      ngeno
Average       0.4900     0.4591
Maximum       0.5015     0.4732
Minimum       0.4807     0.4492
Average variance of differences:
            0.2401     0.2108



*** Table of predicted means for nharv.ntill ***

     ntill        1          2          3          4          5
     nharv
     6.000     0.2725     0.0596     0.0736    -0.0330    -0.0740
     7.000     0.5583     0.3791     0.4595     0.4245     0.1351
     8.000     1.6720     0.9670     0.7039     0.7026     0.7708
     9.000     2.7987     2.0739     1.8634     1.4180     0.8778

Standard error of differences:    Average      0.2991
                              Maximum     0.3673
                              Minimum     0.2154

Average variance of differences:          0.09074

Standard error of differences for same level of factor:
```

```
               nharv      ntill
Average         0.2407     0.3143
Maximum         0.2775     0.3673
Minimum         0.2154     0.2950
Average variance of differences:
               0.05834    0.09938



*** Table of predicted means for ngeno.ntill ***

       ntill          1          2          3          4          5
       ngeno
        2-49     0.2193     0.0943     0.0879    -0.0056     0.0086
      Puseas     2.5684     1.1895     1.3618     0.9408     0.8697
       Sunco     0.8354     0.8110     0.3772     0.3819    -0.0897
       Vasco     1.6785     1.3847     1.2735     1.1951     0.9212

Standard error of differences:    Average      0.3334
                              Maximum      0.4248
                              Minimum      0.2154

Average variance of differences:            0.1139

Standard error of differences for same level of factor:

               ngeno      ntill
Average         0.2402     0.3580
Maximum         0.3103     0.4248
Minimum         0.2154     0.3411
Average variance of differences:
               0.05834     0.1287



*** Table of predicted means for nharv.ngeno.ntill ***

                  ntill          1          2          3          4
       nharv       ngeno
       6.000        2-49     0.0000     0.0000     0.0000     0.0000
                  Puseas     0.7739     0.0383     0.2944    -0.0459
                   Sunco     0.0000     0.0000     0.0000     0.0047
                   Vasco     0.3162     0.2000     0.0000    -0.0906
       7.000        2-49     0.0000     0.0000     0.0000    -0.0024
                  Puseas     1.2256     0.6449     0.8772     0.7996
                   Sunco     0.3873     0.4243     0.0000     0.2000
```

```
            Vasco     0.6204     0.4472     0.9607     0.7009
    8.000     2-49     0.1974     0.2772     0.0050    -0.0025
           Puseas     3.7305     1.6158     1.3589     1.5752
            Sunco     1.2353     0.8145     0.2449    -0.0442
            Vasco     1.5247     1.1604     1.2068     1.2817
    9.000     2-49     0.6796     0.1000     0.3464    -0.0177
           Puseas     4.5436     2.4588     2.9169     1.4345
            Sunco     1.7191     2.0054     1.2637     1.3669
            Vasco     4.2525     3.7314     2.9264     2.8883


            ntill        5
    nharv      ngeno
    6.000     2-49     0.0000
           Puseas    -0.1284
            Sunco     0.0007
            Vasco    -0.1681
    7.000     2-49    -0.0004
           Puseas     0.1050
            Sunco    -0.0235
            Vasco     0.4593
    8.000     2-49    -0.0157
           Puseas     1.8879
            Sunco    -0.0667
            Vasco     1.2777
    9.000     2-49     0.0504
           Puseas     1.6143
            Sunco    -0.2694
            Vasco     2.1159

Standard error of differences:    Average      0.6387
                                  Maximum     0.8901
                                  Minimum     0.4308

Average variance of differences:             0.4114

Standard error of differences for same level of factor:

               nharv      ngeno      ntill
Average          0.6156     0.5973     0.6464
Maximum          0.8234     0.8734     0.8901
Minimum          0.4308     0.4308     0.5900
Average variance of differences:
                 0.3861     0.3629     0.4209
```

```
 359
 360  "### Analysing the tillers separately ###"
 361
 362  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 363      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 364  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 365  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-366  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 367  reml [print=means, wald, comp, mod] sqrt(t1total)

367.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 158

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t1rep                    0.092       0.169
t1plot                   0.000       BOUND
t1plot.t1harv                0.134       0.161


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2             1.461     0.184


*** Wald tests for fixed effects ***
```

```
  Fixed term            Wald statistic    d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                    75.39          3       25.13      <0.001
  t1geno                    57.91          3       19.30      <0.001
  t1harv.t1geno             28.54          9        3.17      <0.001

* Dropping individual terms from full fixed model

  t1harv.t1geno             28.54          9        3.17      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.327    Standard error:  0.2441



*** Table of predicted means for t1harv ***

 t1harv    6.000    7.000    8.000    9.000
           0.273    0.558    1.677    2.799

Standard error of differences:     Average       0.3278
                                   Maximum       0.3294
                                   Minimum       0.3262


*** Table of predicted means for t1geno ***

 t1geno     2-49   Puseas    Sunco    Vasco
           0.223    2.568    0.836    1.678

Standard error of differences:     Average       0.3279
                                   Maximum       0.3295
                                   Minimum       0.3262


*** Table of predicted means for t1harv.t1geno ***
```

```
      t1geno     2-49   Puseas    Sunco    Vasco
      t1harv
       6.000    0.000    0.774    0.000    0.316
       7.000    0.000    1.226    0.387    0.620
       8.000    0.214    3.730    1.237    1.525
       9.000    0.680    4.544    1.719    4.253

Standard error of differences:     Average       0.6557
                                Maximum      0.6780
                                Minimum      0.6525

Average variance of differences:                0.4300

Standard error of differences for same level of factor:

               t1harv      t1geno
Average          0.6557      0.6557
Maximum          0.6780      0.6653
Minimum          0.6525      0.6525
Average variance of differences:
               0.4300      0.4300



 368
 369  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 370      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 371  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 372  reml [print=means, wald, comp, mod] sqrt(t2total)

372.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 158

* Residual term has been added to model

* Sparse algorithm with AI optimisation
```

```
*** Estimated Variance Components ***

Random term            Component      S.e.

t2rep                  0.013      0.063
t2plot                 0.041      0.092
t2plot.t2harv            0.000      BOUND


*** Residual variance model ***

Term          Factor       Model(order)  Parameter       Estimate      S.e.

Residual                   Identity      Sigma2           1.390     0.167


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                 67.63          3       22.54      <0.001
  t2geno                  17.40          3        5.80      <0.001
  t2harv.t2geno              29.68          9        3.30      <0.001

* Dropping individual terms from full fixed model

  t2harv.t2geno              29.68          9        3.30      <0.001

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.8671    Standard error: 0.14356



*** Table of predicted means for t2harv ***

 t2harv    6.000    7.000    8.000    9.000
```

```
          0.0494   0.3791   0.9662   2.0739

Standard error of differences:     Average       0.2655
                                   Maximum       0.2673
                                   Minimum       0.2637


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
          0.0935   1.1793   0.8110   1.3847

Standard error of differences:     Average       0.3345
                                   Maximum       0.3359
                                   Minimum       0.3330


*** Table of predicted means for t2harv.t2geno ***

       t2geno        2-49      Puseas       Sunco       Vasco
       t2harv
        6.000      0.0000     -0.0025      0.0000      0.2000
        7.000      0.0000      0.6449      0.4243      0.4472
        8.000      0.2742      1.6158      0.8145      1.1604
        9.000      0.1000      2.4588      2.0054      3.7314

Standard error of differences:     Average       0.5611
                                   Maximum       0.5923
                                   Minimum       0.5273

Average variance of differences:                 0.3151

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.5686      0.5310
Maximum          0.5789      0.5419
Minimum          0.5652      0.5273
Average variance of differences:
                 0.3234      0.2820


 373
 374  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 375      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
```

```
 376  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 377  reml [print=means, wald, comp, mod] sqrt(t3total)

377...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 156

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                    0.014       0.044
t3plot                   0.000       BOUND
t3plot.t3harv               0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            1.340     0.161


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t3harv                    52.82           3       17.61      <0.001
   t3geno                     36.39           3       12.13      <0.001
```

```
  t3harv.t3geno              16.85          9        1.87      0.051

* Dropping individual terms from full fixed model

  t3harv.t3geno              16.85          9        1.87      0.051

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.7791    Standard error: 0.12489



*** Table of predicted means for t3harv ***

  t3harv    6.000    7.000    8.000    9.000
         0.0801   0.4688   0.7042   1.8634

Standard error of differences:     Average       0.2625
                             Maximum       0.2642
                             Minimum       0.2607


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
         0.0882   1.3742   0.3772   1.2769

Standard error of differences:     Average       0.2625
                             Maximum       0.2642
                             Minimum       0.2607


*** Table of predicted means for t3harv.t3geno ***

      t3geno        2-49       Puseas       Sunco        Vasco
      t3harv
       6.000      0.0000       0.3205      0.0000       0.0000
       7.000      0.0000       0.9007      0.0000       0.9745
       8.000      0.0062       1.3589      0.2449       1.2068
       9.000      0.3464       2.9169      1.2637       2.9264

Standard error of differences:     Average       0.5249
```

```
                    Maximum     0.5460
                    Minimum     0.5178

Average variance of differences:          0.2756

Standard error of differences for same level of factor:

          t3harv     t3geno
Average        0.5249     0.5249
Maximum        0.5460     0.5460
Minimum        0.5178     0.5178
Average variance of differences:
          0.2756     0.2756


 378
 379  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 380      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 381  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 382  reml [print=means, wald, comp, mod] sqrt(t4total)

382.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t4total)

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 128 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term            Component       S.e.

t4rep                  0.2170     0.4086
t4plot                 0.1284     0.2384
```

```
t4plot.t4harv              0.3521      0.2493


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2             0.943    0.1362


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                     12.29           3         4.10       0.006
   t4geno                      6.29           3         2.10       0.098
   t4harv.t4geno                 11.40           9         1.27       0.249

* Dropping individual terms from full fixed model

   t4harv.t4geno                 11.40           9         1.27       0.249

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.6331    Standard error: 0.37854



*** Table of predicted means for t4harv ***

      t4harv        6.000        7.000        8.000        9.000
                -0.0155       0.4541       0.7488       1.3451

Standard error of differences:     Average       0.3874
                                   Maximum       0.3896
                                   Minimum       0.3851


*** Table of predicted means for t4geno ***
```

```
 t4geno     2-49   Puseas    Sunco    Vasco
         0.0039   0.9315   0.4031   1.1940

Standard error of differences:     Average       0.5277
                                   Maximum       0.5367
                                   Minimum       0.5186

Average variance of differences:                 0.2785


*** Table of predicted means for t4harv.t4geno ***

       t4geno        2-49       Puseas       Sunco       Vasco
       t4harv
        6.000       0.0000       0.0200       0.0119     -0.0940
        7.000      -0.0063       0.9065       0.2000      0.7161
        8.000       0.0157       1.6512       0.0119      1.3165
        9.000       0.0063       1.1482       1.3886      2.8375

Standard error of differences:     Average       0.8376
                                   Maximum       0.9036
                                   Minimum       0.7430

Average variance of differences:                 0.7030

Standard error of differences for same level of factor:

                 t4harv      t4geno
Average          0.8535      0.7743
Maximum          0.8862      0.8231
Minimum          0.8249      0.7430
Average variance of differences:
                 0.7287      0.6002


 383
 384  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 385      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 386  vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
 387  reml [print=means, wald, comp, mod] sqrt(t5total)

387.............................................................................
```

```
***** REML Variance Components Analysis *****


Response Variate : SQRT(t5total)

Fixed model      : Constant+t5harv+t5geno+t5harv.t5geno
Random model     : t5rep+t5plot+t5plot.t5harv

Number of units  : 98

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t5rep                   0.0000       BOUND
t5plot                  0.3292      0.3055
t5plot.t5harv              0.0000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.935    0.1500


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t5harv                     15.80           3         5.27       0.001
   t5geno                      4.22           3         1.41       0.239
   t5harv.t5geno                 21.03           9         2.34       0.013

* Dropping individual terms from full fixed model

   t5harv.t5geno                 21.03           9         2.34       0.013
```

```
* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.4980    Standard error: 0.22822



*** Table of predicted means for t5harv ***

     t5harv       6.000       7.000       8.000       9.000
               -0.0895      0.1675      0.8574      1.0567

Standard error of differences:     Average       0.2902
                                   Maximum       0.3007
                                   Minimum       0.2810

Average variance of differences:               0.08431


*** Table of predicted means for t5geno ***

  t5geno     2-49   Puseas    Sunco    Vasco
           0.0428   0.8239   0.0336   1.0918

Standard error of differences:     Average       0.6454
                                   Maximum       0.6627
                                   Minimum       0.6279

Average variance of differences:                0.4167


*** Table of predicted means for t5harv.t5geno ***

       t5geno        2-49      Puseas       Sunco       Vasco
       t5harv
        6.000      0.0000     -0.1004      0.0000     -0.2575
        7.000      0.0000      0.0000     -0.0017      0.6716
        8.000      0.0044      1.8108      0.0000      1.6146
        9.000      0.1667      1.5853      0.1361      2.3387

Standard error of differences:     Average       0.7688
                                   Maximum       0.9431
                                   Minimum       0.4703
```

```
Average variance of differences:              0.6031

Standard error of differences for same level of factor:

               t5harv      t5geno
Average          0.8171      0.5752
Maximum          0.8870      0.7395
Minimum          0.7418      0.4703
Average variance of differences:
               0.6696      0.3372



 388
 389
"=============================================================
===========
-390                    PART = LS1 (harvest 1, 2, 3 & 4)
-391
=============================================================
=========="
 392
 393  "**** Disease Rating (Harvests 1, 2, 3 & 4; leave out CPI1338)****"
 394
 395  "### Analysing the tillers together ###"
 396
 397  subset [condition=(Part.eq.8).and.(Harvest.le.4).and.(Genotype.ne.2); setlevel=yes]
\
 398   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
 399   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 400
 401  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 402  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-403  vstruct [nplot.nharv] factor=nharv; model=ar "
 404  reml [print=means, wald, comp, mod, dev; mvincl=yvar, expl; maxcyc=100] ndr

404.............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr
```

```
Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 676

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                       0.0000       BOUND
nplot                      0.0159      0.0283
nplot.nharv                    0.0160      0.0442
nplot.nharv.nplant             0.3237      0.0667


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2             0.787    0.0548


*** Deviance: -2*Log-Likelihood ***


                  Deviance   d.f.

                    771.40   612

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model
```

```
  nharv                    179.60          3       59.87     <0.001
  ngeno                      4.72          3        1.57      0.193
  ntill                  715.44          4      178.86     <0.001
  nharv.ngeno                24.92          9        2.77      0.003
  nharv.ntill              48.43          8        6.05     <0.001
  ngeno.ntill              20.08         12        1.67      0.066
  nharv.ngeno.ntill           33.19         19        1.75      0.023

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill           33.19         19        1.75      0.023

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         1.499    Standard error:  0.1183



*** Table of predicted means for nharv ***

  nharv    1.000    2.000    3.000    4.000
              *        *        *    2.546

* SEDs not available


*** Table of predicted means for ngeno ***

      ngeno        2-49      Puseas       Sunco       Vasco
                  *           *           *           *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ntill ***

  ntill       1       2       3       4       5
         3.175       *       *       *       *

* SEDs not available
```

```
*** Table of predicted means for nharv.ngeno ***

      ngeno    2-49   Puseas    Sunco    Vasco
      nharv
      1.000       *        *        *        *
      2.000   1.782        *        *        *
      3.000   3.113        *    2.284    2.003
      4.000   2.473    2.511    2.233    2.965

Standard error of differences:     Average       0.3378
                                   Maximum       0.4167
                                   Minimum       0.2823

Average variance of differences:                 0.1152

Standard error of differences for same level of factor:

                nharv       ngeno
Average          0.3248      0.3276
Maximum          0.3672      0.3535
Minimum          0.3015      0.2823
Average variance of differences:
                0.1060      0.1082



*** Table of predicted means for nharv.ntill ***

      ntill       1        2        3        4        5
      nharv
      1.000   0.933        *        *        *        *
      2.000   3.800    2.937    1.361        *        *
      3.000   3.983    3.580    3.139    1.358        *
      4.000   3.983    3.587    2.452    1.535    1.171

Standard error of differences:     Average       0.2149
                                   Maximum       0.2782
                                   Minimum       0.1652

Average variance of differences:                 0.04680

Standard error of differences for same level of factor:

                nharv       ntill
```

```
Average          0.1927      0.2109
Maximum          0.2377      0.2498
Minimum          0.1652      0.1992
Average variance of differences:
                0.03764     0.04474



*** Table of predicted means for ngeno.ntill ***

        ntill       1       2       3       4       5
        ngeno
         2-49   2.950       *       *       *       *
       Puseas   3.133       *       *       *       *
        Sunco   3.267       *       *       *       *
        Vasco   3.350       *       *       *       *

Standard error of differences:      0.2243



*** Table of predicted means for nharv.ngeno.ntill ***

                 ntill       1       2       3       4       5
        nharv       ngeno
        1.000        2-49   0.333       *       *       *       *
                   Puseas   0.800       *       *       *       *
                    Sunco   1.067       *       *       *       *
                    Vasco   1.533       *       *       *       *
        2.000        2-49   3.533   2.933   1.333   0.269   0.839
                   Puseas   3.733   2.494   1.193   1.203       *
                    Sunco   4.000   3.482   2.064   0.214       *
                    Vasco   3.933   2.840   0.853       *       *
        3.000        2-49   3.933   3.644   3.858   2.072   2.055
                   Puseas   4.000   3.927   3.502   1.226       *
                    Sunco   4.000   3.467   2.733   1.336  -0.117
                    Vasco   4.000   3.284   2.462   0.797  -0.527
        4.000        2-49   4.000   3.733   2.267   1.250   1.113
                   Puseas   4.000   3.417   2.333   1.458   1.349
                    Sunco   4.000   3.400   2.408   1.317   0.041
                    Vasco   3.933   3.800   2.800   2.114   2.179

Standard error of differences:     Average       0.5252
                                   Maximum        1.380
                                   Minimum       0.3239
```

```
Average variance of differences:              0.3097

Standard error of differences for same level of factor:

               nharv      ngeno      ntill
Average         0.5167     0.5050     0.4968
Maximum          1.380      1.098      1.371
Minimum         0.3239     0.3239     0.3984
Average variance of differences:
               0.3012     0.2898     0.2766


 405
 406  "### Analysing the tillers separately ###"
 407
 408  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 409     t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 410  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 411  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-412  vstruct [t1plot.t1harv] factor=t1harv; model=ar "
 413  reml [print=means, wald, comp, mod, dev] t1dr

413...............................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 240

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term             Component       S.e.

t1rep                      0.0000      BOUND
```

```
t1plot                    0.0233      0.0320
t1plot.t1harv                0.0812      0.0434


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2             0.335    0.0342


*** Deviance: -2*Log-Likelihood ***


               Deviance   d.f.

                 51.93   220

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                    543.84           3       181.28      <0.001
  t1geno                      4.54           3         1.51       0.209
  t1harv.t1geno              10.72           9         1.19       0.295

* Dropping individual terms from full fixed model

  t1harv.t1geno              10.72           9         1.19       0.295

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         3.175    Standard error:  0.0710
```

```
*** Table of predicted means for t1harv ***

  t1harv    1.000    2.000    3.000    4.000
            0.933    3.800    3.983    3.983

Standard error of differences:      0.1572



*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
            2.950    3.133    3.267    3.350

Standard error of differences:      0.2007



*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        1.000    0.333    0.800    1.067    1.533
        2.000    3.533    3.733    4.000    3.933
        3.000    3.933    4.000    4.000    4.000
        4.000    4.000    4.000    4.000    3.933

Standard error of differences:     Average       0.3335
                                   Maximum       0.3383
                                   Minimum       0.3145

Average variance of differences:                0.1113

Standard error of differences for same level of factor:

                 t1harv      t1geno
Average          0.3383      0.3145
Maximum          0.3383      0.3145
Minimum          0.3383      0.3145


 414
 415  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 416      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
```

```
 417  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 418  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-419  vstruct [t2plot.t2harv] factor=t2harv; model=ar "
 420  reml [print=means, wald, comp, mod, dev] t2dr

420..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 164

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t2rep                   0.000       BOUND
t2plot                  0.031       0.066
t2plot.t2harv              0.030       0.096


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2            1.041     0.130


*** Deviance: -2*Log-Likelihood ***


             Deviance   d.f.

               194.77   148
```

```
Note: deviance omits constants which depend on fixed model fitted.


*** Wald tests for fixed effects ***

  Fixed term           Wald statistic   d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                  11.68          2       5.84       0.003
  t2geno                   0.27          3       0.09       0.965
  t2harv.t2geno            8.09          6       1.35       0.231

* Dropping individual terms from full fixed model

  t2harv.t2geno            8.09          6       1.35       0.231

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         3.374   Standard error:  0.0994



*** Table of predicted means for t2harv ***

 t2harv    2.000    3.000    4.000
           2.950    3.583    3.587

Standard error of differences:     Average       0.2091
                                   Maximum       0.2114
                                   Minimum       0.2050

Average variance of differences:                 0.04375


*** Table of predicted means for t2geno ***

 t2geno     2-49   Puseas    Sunco    Vasco
           3.438    3.294    3.444    3.319
```

```
Standard error of differences:     Average       0.2810
                                   Maximum       0.2877
                                   Minimum       0.2742

Average variance of differences:               0.07899


*** Table of predicted means for t2harv.t2geno ***

       t2geno     2-49   Puseas    Sunco    Vasco
       t2harv
        2.000    2.933    2.534    3.466    2.868
        3.000    3.647    3.932    3.467    3.288
        4.000    3.733    3.417    3.400    3.800

Standard error of differences:     Average       0.4377
                                   Maximum       0.4843
                                   Minimum       0.3982

Average variance of differences:                0.1919

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.4420      0.4178
Maximum          0.4843      0.4603
Minimum          0.4233      0.3982
Average variance of differences:
                 0.1956      0.1750



 421
 422  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 423      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 424  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 425  "vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot.t3harv ; const=pos
-426  vstruct [t3plot.t3harv] factor=t3harv; model=ar"
 427  reml [print=means, wald, comp, mod, dev] t3dr

427..............................................................................


***** REML Variance Components Analysis *****
```

```
Response Variate : t3dr

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 146

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term            Component       S.e.

t3rep                  0.031       0.071
t3plot                 0.000       BOUND
t3plot.t3harv              0.004       BOUND


*** Residual variance model ***

Term          Factor       Model(order)  Parameter       Estimate      S.e.

Residual                   Identity      Sigma2            1.855     0.228


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                247.62   130

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model
```

```
  t3harv                 37.86        2      18.93     <0.001
  t3geno                  1.37        3       0.46      0.712
  t3harv.t3geno             12.51        6       2.09      0.051

* Dropping individual terms from full fixed model

  t3harv.t3geno             12.51        6       2.09      0.051

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          2.342    Standard error:  0.1552



*** Table of predicted means for t3harv ***

  t3harv    2.000    3.000    4.000
          1.422    3.155    2.449

Standard error of differences:     Average       0.2852
                               Maximum       0.2972
                               Minimum       0.2658

Average variance of differences:              0.08154


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
          2.488    2.371    2.439    2.070

Standard error of differences:     Average       0.3297
                               Maximum       0.3524
                               Minimum       0.3063

Average variance of differences:               0.1090


*** Table of predicted means for t3harv.t3geno ***

      t3geno     2-49   Puseas    Sunco    Vasco
      t3harv
```

```
     2.000    1.333    1.280    2.154    0.921
     3.000    3.865    3.500    2.768    2.488
     4.000    2.267    2.333    2.394    2.800

Standard error of differences:     Average       0.5686
                                   Maximum       0.7222
                                   Minimum       0.4975

Average variance of differences:               0.3267

Standard error of differences for same level of factor:

                t3harv      t3geno
Average          0.5680      0.5683
Maximum          0.7222      0.6833
Minimum          0.4975      0.4975
Average variance of differences:
                 0.3268      0.3266


 428
 429  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 430      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 431  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 432  "vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot.t4harv ; const=pos
-433  vstruct [t4plot.t4harv] factor=t4harv; model=ar "
 434  reml [print=means, wald, comp, mod, dev] t4dr

434.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 85

* Residual term has been added to model

* Sparse algorithm with AI optimisation
```

```
*** Estimated Variance Components ***

Random term            Component      S.e.

t4rep                  0.000      BOUND
t4plot                 0.024      0.186
t4plot.t4harv              0.063      0.266


*** Residual variance model ***

Term          Factor       Model(order)  Parameter       Estimate      S.e.

Residual                   Identity      Sigma2            1.677     0.307


*** Deviance: -2*Log-Likelihood ***


            Deviance   d.f.

              134.96    70

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                     3.74           2        1.87       0.154
   t4geno                      0.75           3        0.25       0.860
   t4harv.t4geno                   6.22           5        1.24       0.286

* Dropping individual terms from full fixed model

   t4harv.t4geno                   6.22           5        1.24       0.286

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.
```

```
*** Table of predicted means for Constant ***

          1.166    Standard error:  0.2305



*** Table of predicted means for t4harv ***

  t4harv    2.000    3.000    4.000
                *    1.466    1.578

Standard error of differences:      0.3285



*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          1.233    1.631    1.056        *

Standard error of differences:     Average       0.5592
                             Maximum       0.6075
                             Minimum       0.4648

Average variance of differences:              0.3172


*** Table of predicted means for t4harv.t4geno ***

      t4geno     2-49   Puseas    Sunco    Vasco
      t4harv
       2.000    0.331    1.985    0.458        *
       3.000    2.057    1.343    1.441    1.021
       4.000    1.309    1.564    1.270    2.171

Standard error of differences:     Average       0.8701
                             Maximum        1.539
                             Minimum       0.5400

Average variance of differences:              0.8395

Standard error of differences for same level of factor:

              t4harv      t4geno
Average          0.8048      0.8830
```

```
Maximum           1.539       1.435
Minimum         0.5754      0.5400
Average variance of differences:
                0.7371      0.8612



 435
 436  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 437      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 438  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
-439  reml [print=means, wald, comp, mod, dev] t5dr"
 440  "NOT ENOUGH INFORMATION TO ANALYSE ADEQUATELY"
 441
 442
 443  "**** Infection - Total (Harvests 6, 7, 8 & 9; leave out CPI1338 & Rep 3)****"
 444
 445  "### Analysing the tillers together ###"
 446
 447  subset
[condition=(Part.eq.8).and.(Harvest.le.4).and.(Genotype.ne.2).and.(Rep.le.2);\
 448   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 449   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 450
 451  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; cons=pos
 452  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
cons=pos
-453  vstruct [nplot.nharv] factor=nharv; model=ar "
 454  reml [print=means, wald, comp, mod, dev] sqrt(ntotal)

454..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 449 (9 units excluded due to zero weights or missing values)
```

```
* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

nrep                     0.0000       BOUND
nplot                    0.1085      0.1308
nplot.nharv                  0.1237      0.1154
nplot.nharv.nplant          0.4398      0.0967


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.783    0.0687


*** Deviance: -2*Log-Likelihood ***


                 Deviance   d.f.

                   545.97   386

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                      13.21           3         4.40       0.004
   ngeno                        1.33           3         0.44       0.722
   ntill                    160.23           4        40.06      <0.001
   nharv.ngeno                    7.69           9         0.85       0.565
   nharv.ntill                  4.85           8         0.61       0.774
   ngeno.ntill                  21.25          12         1.77       0.047
```

```
  nharv.ngeno.ntill          11.59        18        0.64     0.868

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill          11.59        18        0.64     0.868

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.8537    Standard error: 0.18523



*** Table of predicted means for nharv ***

  nharv    1.000    2.000    3.000    4.000
              *        *        *    1.162

* SEDs not available


*** Table of predicted means for ngeno ***

      ngeno        2-49       Puseas       Sunco       Vasco
                     *           *           *           *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ntill ***

  ntill       1       2       3       4       5
         1.896       *       *       *       *

* SEDs not available


*** Table of predicted means for nharv.ngeno ***

       ngeno    2-49   Puseas    Sunco    Vasco
       nharv
       1.000       *       *       *       *
```

```
     2.000   0.967       *       *       *
     3.000   1.570       *   1.494       *
     4.000   1.237   0.719   1.443   1.250

Standard error of differences:    Average     0.6036
                                  Maximum     0.6556
                                  Minimum     0.5021

Average variance of differences:              0.3659

Standard error of differences for same level of factor:

             nharv     ngeno
Average     0.6138    0.5305
Maximum     0.6257    0.5521
Minimum     0.6041    0.5021
Average variance of differences:
            0.3768    0.2818



*** Table of predicted means for nharv.ntill ***

     ntill       1       2       3       4       5
     nharv
     1.000   0.814       *       *       *       *
     2.000   1.868   1.401   0.861       *       *
     3.000   2.538   2.009   1.498   0.965       *
     4.000   2.364   1.428   1.053   0.468   0.498

Standard error of differences:    Average     0.3125
                                  Maximum     0.4135
                                  Minimum     0.2048

Average variance of differences:              0.09997

Standard error of differences for same level of factor:

             nharv     ntill
Average     0.2462    0.3198
Maximum     0.3170    0.3606
Minimum     0.2048    0.3034
Average variance of differences:
           0.06190    0.1027
```

```
*** Table of predicted means for ngeno.ntill ***

      ntill      1       2       3       4       5
      ngeno
       2-49   1.588      *       *       *       *
     Puseas   1.836      *       *       *       *
      Sunco   2.174      *       *       *       *
      Vasco   1.985      *       *       *       *

Standard error of differences:    Average     0.4489
                                  Maximum     0.4493
                                  Minimum     0.4486

Standard error of differences for same level of factor:

              ngeno     ntill
Average          *     0.4489
Maximum          *     0.4493
Minimum          *     0.4486



*** Table of predicted means for nharv.ngeno.ntill ***

              ntill      1       2       3       4       5
      nharv      ngeno
      1.000       2-49   0.173      *       *       *       *
                Puseas   0.797      *       *       *       *
                 Sunco   0.820      *       *       *       *
                 Vasco   1.464      *       *       *       *
      2.000       2-49   1.722   1.459   0.397   0.501   0.755
                Puseas   2.146   1.346   1.217   1.245      *
                 Sunco   2.015   1.696   1.387   0.775      *
                 Vasco   1.591   1.101   0.443      *       *
      3.000       2-49   2.052   1.949   1.355   1.180   1.315
                Puseas   2.548   2.097   2.109   1.381      *
                 Sunco   3.014   2.197   1.145   1.122  -0.010
                 Vasco   2.537   1.793   1.383   0.179      *
      4.000       2-49   2.406   1.096   0.838   0.537   1.307
                Puseas   1.853   1.100   0.548   0.130  -0.038
                 Sunco   2.848   1.974   1.265   1.093   0.036
                 Vasco   2.349   1.544   1.559   0.113   0.688

Standard error of differences:    Average     0.7596
                                  Maximum      1.484
```

```
                           Minimum     0.3956

Average variance of differences:            0.6000

Standard error of differences for same level of factor:

             nharv     ngeno     ntill
Average        0.7364    0.6698    0.7487
Maximum          1.484     1.274     1.320
Minimum        0.3956    0.3956    0.6068
Average variance of differences:
             0.5724    0.4774    0.5791



 455
 456  "### Analysing the tillers separately ###"
 457
 458  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 459     t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 460  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 461  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-462  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 463  reml [print=means, wald, comp, mod, dev] sqrt(t1total)

463.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 157 (3 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term             Component       S.e.
```

```
t1rep                    0.000      BOUND
t1plot                   0.246      0.258
t1plot.t1harv               0.227      0.187


*** Residual variance model ***

Term           Factor       Model(order)  Parameter       Estimate      S.e.

Residual                  Identity      Sigma2             1.102     0.139


*** Deviance: -2*Log-Likelihood ***


               Deviance   d.f.

                 207.05   137

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                    30.90           3        10.30      <0.001
   t1geno                     0.99           3         0.33       0.804
   t1harv.t1geno                  5.45           9         0.61       0.793

* Dropping individual terms from full fixed model

   t1harv.t1geno                  5.45           9         0.61       0.793

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.884    Standard error:  0.2119
```

```
*** Table of predicted means for t1harv ***

  t1harv    1.000    2.000    3.000    4.000
            0.814    1.868    2.491    2.364

Standard error of differences:     Average       0.3363
                                   Maximum       0.3382
                                   Minimum       0.3345


*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
            1.591    1.799    2.162    1.985

Standard error of differences:     Average       0.5992
                                   Maximum       0.5996
                                   Minimum       0.5989


*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        1.000    0.173    0.797    0.820    1.464
        2.000    1.722    2.146    2.015    1.591
        3.000    2.064    2.399    2.964    2.537
        4.000    2.406    1.853    2.848    2.349

Standard error of differences:     Average       0.8031
                                   Maximum       0.8484
                                   Minimum       0.6690

Average variance of differences:                0.6493

Standard error of differences for same level of factor:

                 t1harv      t1geno
Average          0.8357      0.6727
Maximum          0.8484      0.6787
Minimum          0.8328      0.6690
Average variance of differences:
                 0.6985      0.4525
```

```
 464
 465  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 466      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 467  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 468  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-469  vstruct [t2plot.t2harv] factor=t2harv; model=ar"
 470  reml [print=means, wald, comp, mod, dev] sqrt(t2total)

470.............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 110 (3 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t2rep                   0.000       BOUND
t2plot                  0.110       0.212
t2plot.t2harv               0.184       0.242


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                     Identity      Sigma2            1.279     0.195


*** Deviance: -2*Log-Likelihood ***
```

```
              Deviance   d.f.

                156.65    94

Note: deviance omits constants which depend on fixed model fitted.


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                     3.95           2        1.97       0.139
  t2geno                      1.22           3        0.41       0.747
  t2harv.t2geno                  1.91           6        0.32       0.927

* Dropping individual terms from full fixed model

  t2harv.t2geno                  1.91           6        0.32       0.927

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         1.608    Standard error:  0.1833



*** Table of predicted means for t2harv ***

  t2harv    2.000    3.000    4.000
         1.437    2.005    1.381

Standard error of differences:     Average       0.3446
                                   Maximum       0.3496
                                   Minimum       0.3417

Average variance of differences:               0.1188
```

```
*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
           1.486    1.511    1.956    1.479

Standard error of differences:     Average       0.5184
                                Maximum       0.5297
                                Minimum       0.5069

Average variance of differences:               0.2688


*** Table of predicted means for t2harv.t2geno ***

      t2geno     2-49   Puseas    Sunco    Vasco
      t2harv
       2.000    1.459    1.493    1.696    1.101
       3.000    1.949    2.083    2.197    1.793
       4.000    1.049    0.956    1.974    1.544

Standard error of differences:     Average       0.7509
                                Maximum       0.8454
                                Minimum       0.6632

Average variance of differences:               0.5654

Standard error of differences for same level of factor:

               t2harv      t2geno
Average          0.7648      0.6885
Maximum          0.8075      0.7527
Minimum          0.7418      0.6632
Average variance of differences:
               0.5855      0.4750


 471
 472  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 473     t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 474  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 475  "vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot.t3harv ; const=pos
-476  vstruct [t3plot.t3harv] factor=t3harv; model=ar"
 477  reml [print=means, wald, comp, mod, dev] sqrt(t3total)
```

```
477..............................................................................

***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 97 (2 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                     0.000       BOUND
t3plot                    0.000       BOUND
t3plot.t3harv                0.230       0.244


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2            1.321     0.219


*** Deviance: -2*Log-Likelihood ***


                 Deviance   d.f.

                   139.13    81

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***
```

```
   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

 * Sequentially adding terms to fixed model

   t3harv                     4.48          2        2.24       0.106
   t3geno                      1.16          3        0.39       0.763
   t3harv.t3geno                   6.50          6        1.08       0.369

 * Dropping individual terms from full fixed model

   t3harv.t3geno                   6.50          6        1.08       0.369

 * Message: chi-square distribution for Wald tests is an asymptotic approximation
   (i.e. for large samples) and underestimates the probabilities in other cases.


 *** Table of predicted means for Constant ***

            1.161    Standard error:  0.1620



 *** Table of predicted means for t3harv ***

  t3harv    2.000    3.000    4.000
            0.895    1.579    1.008

 Standard error of differences:     Average       0.3963
                                    Maximum       0.4129
                                    Minimum       0.3674

 Average variance of differences:               0.1575


 *** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
            0.858    1.295    1.245    1.246

 Standard error of differences:     Average       0.4571
                                    Maximum       0.4922
                                    Minimum       0.4215

 Average variance of differences:               0.2100
```

```
*** Table of predicted means for t3harv.t3geno ***

      t3geno    2-49   Puseas    Sunco    Vasco
      t3harv
       2.000    0.397    1.414    1.377    0.393
       3.000    1.355    2.066    1.110    1.785
       4.000    0.821    0.405    1.249    1.559

Standard error of differences:     Average       0.7863
                                   Maximum       1.046
                                   Minimum       0.7029

Average variance of differences:               0.6299

Standard error of differences for same level of factor:

              t3harv      t3geno
Average         0.7860      0.7860
Maximum           1.046       1.027
Minimum         0.7138      0.7029
Average variance of differences:
              0.6299      0.6299



 478
 479  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 480      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 481  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 482  "vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot.t4harv ; const=pos
-483  vstruct [t4plot.t4harv] factor=t4harv; model=ar"
 484  reml [print=means, wald, comp, mod, dev] sqrt(t4total)

484..................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t4total)

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv
```

```
Number of units  : 59 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t4rep                  0.000       BOUND
t4plot                 0.013       0.136
t4plot.t4harv              0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            1.281     0.271


*** Deviance: -2*Log-Likelihood ***


                 Deviance   d.f.

                   76.64    44

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                      5.31           2        2.65       0.070
   t4geno                      1.18           3        0.39       0.757
   t4harv.t4geno                   2.65           5        0.53       0.754

* Dropping individual terms from full fixed model
```

```
  t4harv.t4geno              2.65        5      0.53     0.754

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.7571    Standard error: 0.23429



*** Table of predicted means for t4harv ***

  t4harv    2.000    3.000    4.000
                *   1.0852   0.4631

Standard error of differences:      0.3385



*** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.7426   1.2634   0.9211        *

Standard error of differences:     Average       0.5179
                             Maximum       0.5563
                             Minimum       0.4521

Average variance of differences:               0.2704


*** Table of predicted means for t4harv.t4geno ***

      t4geno     2-49   Puseas    Sunco    Vasco
      t4harv
       2.000   0.5306   2.0025   0.7735        *
       3.000   1.1798   1.5527   1.1369   0.4713
       4.000   0.5172   0.2349   0.8529   0.2475

Standard error of differences:     Average       0.8372
                             Maximum        1.395
                             Minimum       0.5201
```

```
Average variance of differences:           0.7543

Standard error of differences for same level of factor:

              t4harv     t4geno
Average        0.7894     0.8416
Maximum         1.395      1.243
Minimum        0.5489     0.5201
Average variance of differences:
              0.6806     0.7572



 485
 486  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 487     t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 488  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
-489  reml [print=means, wald, comp, mod, dev] sqrt(t5total)"
 490  "NOT ENOUGH INFORMATION TO ANALYSE ADEQUATELY"
 491
 492
 493
"============================================================
===========
-494                  PART = LS2 (harvest 1, 2, 3 & 4)
-495
============================================================
=========="
 496
 497  "**** Disease Rating (Harvests 1, 2, 3 & 4; leave out CPI1338)****"
 498
 499  "### Analysing the tillers together ###"
 500
 501  subset [condition=(Part.eq.9).and.(Harvest.le.4).and.(Genotype.ne.2); setlevel=yes]
\
 502   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
 503   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 504
 505  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 506  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-507  vstruct [nplot.nharv] factor=nharv; model=ar"
 508  reml [print=means, wald, comp, mod; mvincl=yvar, expl; maxcyc=100] ndr

508.............................................................................
```

```
***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 675

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***

Random term             Component       S.e.

nrep                    0.0000      BOUND
nplot                   0.0046      0.0166
nplot.nharv                 0.0000      BOUND
nplot.nharv.nplant          0.2887      0.0524


*** Residual variance model ***

Term            Factor      Model(order)  Parameter      Estimate      S.e.

Residual                    Identity      Sigma2            0.617    0.0427


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                    164.88          3        54.96      <0.001
  ngeno                     12.42          3         4.14       0.006
  ntill                   1671.65          4       417.91      <0.001
```

```
  nharv.ngeno                 8.95          9        0.99      0.442
  nharv.ntill                14.09          8        1.76      0.079
  ngeno.ntill                 8.63         12        0.72      0.734
  nharv.ngeno.ntill          18.69         19        0.98      0.477

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill          18.69         19        0.98      0.477

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.4030    Standard error: 0.10118



*** Table of predicted means for nharv ***

  nharv    1.000    2.000    3.000    4.000
               *        *        *    1.566

* SEDs not available


*** Table of predicted means for ngeno ***

     ngeno        2-49       Puseas        Sunco        Vasco
                     *            *            *            *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ntill ***

  ntill        1        2        3        4        5
           2.775        *        *        *        *

* SEDs not available


*** Table of predicted means for nharv.ngeno ***
```

```
     ngeno     2-49   Puseas    Sunco    Vasco
     nharv
     1.000        *        *        *        *
     2.000    1.025        *        *        *
     3.000    1.449        *    1.286    1.076
     4.000    1.532    1.478    1.468    1.785

Standard error of differences:     Average       0.2857
                                   Maximum       0.3573
                                   Minimum       0.2426

Average variance of differences:                 0.08249

Standard error of differences for same level of factor:

                nharv       ngeno
Average        0.2719      0.2839
Maximum        0.3115      0.3075
Minimum        0.2496      0.2426
Average variance of differences:
              0.07431     0.08130



*** Table of predicted means for nharv.ntill ***

     ntill        1        2        3        4        5
     nharv
     1.000    0.167        *        *        *        *
     2.000    3.333    1.024    0.294        *        *
     3.000    3.733    2.015    0.879    0.181        *
     4.000    3.867    2.165    1.184    0.346    0.269

Standard error of differences:     Average       0.1893
                                   Maximum       0.2449
                                   Minimum       0.1463

Average variance of differences:                 0.03629

Standard error of differences for same level of factor:

                nharv       ntill
Average        0.1712      0.1850
Maximum        0.2106      0.2194
Minimum        0.1463      0.1737
Average variance of differences:
```

```
         0.02972   0.03443



*** Table of predicted means for ngeno.ntill ***

      ntill      1      2      3      4      5
      ngeno
       2-49    2.633      *      *      *      *
     Puseas    2.817      *      *      *      *
      Sunco    2.833      *      *      *      *
      Vasco    2.817      *      *      *      *

Standard error of differences:      0.1823



*** Table of predicted means for nharv.ngeno.ntill ***

              ntill      1      2      3      4      5
      nharv      ngeno
      1.000       2-49   0.000      *      *      *      *
                Puseas   0.267      *      *      *      *
                 Sunco   0.133      *      *      *      *
                 Vasco   0.267      *      *      *      *
      2.000       2-49   3.267   0.867   0.200   0.068   0.721
                Puseas   3.200   0.606   0.005  -0.612      *
                 Sunco   3.333   1.800   0.756  -0.366      *
                 Vasco   3.533   0.823   0.215      *      *
      3.000       2-49   3.533   2.085   0.871   0.513   0.243
                Puseas   3.933   2.518   1.008   0.127      *
                 Sunco   3.933   1.733   0.820   0.133  -0.188
                 Vasco   3.533   1.725   0.817  -0.048  -0.651
      4.000       2-49   3.733   2.200   1.000   0.326   0.401
                Puseas   3.867   1.927   1.177   0.326   0.094
                 Sunco   3.933   2.267   1.223   0.148  -0.230
                 Vasco   3.933   2.267   1.333   0.581   0.812

Standard error of differences:     Average       0.4577
                                   Maximum        1.222
                                   Minimum       0.2867

Average variance of differences:              0.2369

Standard error of differences for same level of factor:
```

```
              nharv      ngeno      ntill
Average         0.4505     0.4451     0.4313
Maximum          1.222     0.9736      1.213
Minimum         0.2867     0.2867     0.3474
Average variance of differences:
                0.2304     0.2259     0.2102


 509
 510  "### Analysing the tillers separately ###"
 511
 512  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 513     t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 514  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 515  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-516  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 517  reml [print=means, wald, comp, mod] t1dr

517.........................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 240

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t1rep                    0.0075      0.0152
t1plot                   0.0000       BOUND
t1plot.t1harv            0.0000       BOUND
```

```
*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2             0.610    0.0579


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                   907.26          3       302.42      <0.001
  t1geno                     2.65          3         0.88       0.449
  t1harv.t1geno              4.67          9         0.52       0.862

* Dropping individual terms from full fixed model

  t1harv.t1geno              4.67          9         0.52       0.862

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         2.775    Standard error:  0.0711



*** Table of predicted means for t1harv ***

 t1harv    1.000    2.000    3.000    4.000
         0.167    3.333    3.733    3.867

Standard error of differences:      0.1426



*** Table of predicted means for t1geno ***

 t1geno     2-49   Puseas    Sunco    Vasco
         2.633    2.817    2.833    2.817
```

```
Standard error of differences:      0.1426



*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        1.000    0.000    0.267    0.133    0.267
        2.000    3.267    3.200    3.333    3.533
        3.000    3.533    3.933    3.933    3.533
        4.000    3.733    3.867    3.933    3.933

Standard error of differences:      0.2852


 518
 519  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 520      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 521  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 522  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-523  vstruct [t2plot.t2harv] factor=t2harv; model=ar"
 524  reml [print=means, wald, comp, mod] t2dr

524.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 164

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.
```

```
t2rep                   0.000      BOUND
t2plot                  0.000      BOUND
t2plot.t2harv              0.000      BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            1.665     0.191


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                    23.18           2        11.59      <0.001
  t2geno                     1.05           3         0.35      0.789
  t2harv.t2geno                 9.11           6         1.52       0.167

* Dropping individual terms from full fixed model

  t2harv.t2geno                 9.11           6         1.52       0.167

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          1.753    Standard error:  0.1015



*** Table of predicted means for t2harv ***

  t2harv    2.000    3.000    4.000
          1.064    2.032    2.162

Standard error of differences:     Average       0.2487
                                   Maximum       0.2515
                                   Minimum       0.2435
```

```
Average variance of differences:          0.06184


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
           1.737    1.718    1.944    1.613

Standard error of differences:     Average       0.2870
                                   Maximum       0.2971
                                   Minimum       0.2769

Average variance of differences:          0.08245


*** Table of predicted means for t2harv.t2geno ***

      t2geno     2-49   Puseas    Sunco    Vasco
      t2harv
       2.000    0.867    0.700    1.833    0.857
       3.000    2.143    2.538    1.733    1.714
       4.000    2.200    1.917    2.267    2.267

Standard error of differences:     Average       0.4969
                                   Maximum       0.5526
                                   Minimum       0.4712

Average variance of differences:           0.2474

Standard error of differences for same level of factor:

               t2harv      t2geno
Average         0.4969      0.4967
Maximum          0.5526      0.5526
Minimum          0.4712      0.4712
Average variance of differences:
               0.2474      0.2474


 525
 526  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 527      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 528  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 529  "vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot.t3harv ; const=pos
```

```
-530  vstruct [t3plot.t3harv] factor=t3harv; model=ar"
 531  reml [print=means, wald, comp, mod] t3dr

531.............................................................................


***** REML Variance Components Analysis *****


Response Variate : t3dr

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 145

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t3rep                   0.0000       BOUND
t3plot                  0.0308      0.0578
t3plot.t3harv              0.0000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.935    0.1185


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t3harv                    17.34           2         8.67      <0.001
   t3geno                     0.67           3         0.22       0.880
```

```
   t3harv.t3geno                  2.75            6          0.46       0.840

* Dropping individual terms from full fixed model

   t3harv.t3geno                  2.75            6          0.46       0.840

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.8197    Standard error: 0.09827



*** Table of predicted means for t3harv ***

  t3harv    2.000    3.000    4.000
           0.3525   0.9228   1.1838

Standard error of differences:     Average       0.2059
                                   Maximum       0.2161
                                   Minimum       0.1887

Average variance of differences:               0.04254


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
           0.7102   0.7931   0.9547   0.8208

Standard error of differences:     Average       0.2777
                                   Maximum       0.2944
                                   Minimum       0.2605

Average variance of differences:               0.07726


*** Table of predicted means for t3harv.t3geno ***

       t3geno     2-49   Puseas    Sunco    Vasco
       t3harv
        2.000   0.2000   0.2126   0.7965   0.2011
        3.000   0.9306   1.0000   0.8326   0.9279
```

```
       4.000   1.0000   1.1667   1.2351   1.3333

Standard error of differences:     Average       0.4294
                               Maximum       0.5617
                               Minimum       0.3531

Average variance of differences:               0.1870

Standard error of differences for same level of factor:

               t3harv      t3geno
Average          0.4334      0.4090
Maximum          0.5617      0.5171
Minimum          0.3810      0.3531
Average variance of differences:
               0.1907      0.1702


 532
 533  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 534      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 535  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 536  "vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot.t4harv ; const=pos
-537  vstruct [t4plot.t4harv] factor=t4harv; model=ar"
 538  reml [print=means, wald, comp, mod] t4dr

538..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 85

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***
```

```
Random term             Component       S.e.

t4rep                  0.0000       BOUND
t4plot                 0.0024      0.0550
t4plot.t4harv              0.0591      0.0768


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2             0.354    0.0646


*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t4harv                      2.37            2         1.18       0.306
  t4geno                      1.53            3         0.51       0.675
  t4harv.t4geno                   1.89            5         0.38       0.864

* Dropping individual terms from full fixed model

  t4harv.t4geno                   1.89            5         0.38       0.864

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.1939    Standard error: 0.11592



*** Table of predicted means for t4harv ***

  t4harv    2.000    3.000    4.000
                *   0.2771   0.4011

Standard error of differences:      0.1757
```

```
*** Table of predicted means for t4geno ***

 t4geno     2-49   Puseas    Sunco    Vasco
          0.3174   0.1700   0.1413        *

Standard error of differences:     Average       0.2802
                                   Maximum       0.3022
                                   Minimum       0.2378

Average variance of differences:              0.07941


*** Table of predicted means for t4harv.t4geno ***

    t4geno        2-49      Puseas       Sunco       Vasco
    t4harv
     2.000      0.0067     -0.0048     -0.0035           *
     3.000      0.5620      0.1724      0.1762      0.1978
     4.000      0.3834      0.3425      0.2513      0.6271

Standard error of differences:     Average       0.4466
                                   Maximum       0.7531
                                   Minimum       0.3036

Average variance of differences:               0.2166

Standard error of differences for same level of factor:

                t4harv      t4geno
Average         0.4166      0.4548
Maximum         0.7531      0.7044
Minimum         0.3143      0.3036
Average variance of differences:
                0.1924      0.2234


 539
 540  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 541      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 542  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
-543  reml [print=means, wald, comp, mod,dev] t5dr"
 544  "NOT ENOUGH INFORMATION TO ANALYSE ADEQUATELY"
```

```
 545
 546
 547  "**** Infection - Total (Harvests 1, 2, 3 & 4; leave out CPI1338 & Rep 3)****"
 548
 549  "### Analysing the tillers together ###"
 550
 551  subset
[condition=(Part.eq.9).and.(Harvest.le.4).and.(Genotype.ne.2).and.(Rep.le.2);\
 552   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 553   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 554
 555  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; cons=pos
 556  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
cons=pos
-557  vstruct [nplot.nharv] factor=nharv; model=ar"
 558  reml [print=means, wald, comp, mod, dev] sqrt(ntotal)

558...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 453 (5 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                     0.0000       BOUND
nplot                    0.0626      0.0730
nplot.nharv                  0.0022      0.0602
nplot.nharv.nplant           0.4059      0.0883
```

```
*** Residual variance model ***

Term            Factor      Model(order)  Parameter      Estimate     S.e.

Residual                   Identity      Sigma2          0.724    0.0627


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                510.74   390

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      34.77          3       11.59      <0.001
  ngeno                       1.62          3        0.54       0.656
  ntill                     222.51          4       55.63      <0.001
  nharv.ngeno                  7.94          9        0.88       0.540
  nharv.ntill                  3.90          8        0.49       0.866
  ngeno.ntill                 14.28         12        1.19       0.283
  nharv.ngeno.ntill            11.56         18        0.64       0.869

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill            11.56         18        0.64       0.869

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.5511    Standard error: 0.15308
```

```
*** Table of predicted means for nharv ***

   nharv    1.000    2.000    3.000    4.000
                *        *        *   0.9198

* SEDs not available


*** Table of predicted means for ngeno ***

       ngeno        2-49       Puseas        Sunco        Vasco
                       *            *            *            *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ntill ***

   ntill        1        2        3        4        5
          1.617        *        *        *        *

* SEDs not available


*** Table of predicted means for nharv.ngeno ***

        ngeno     2-49   Puseas    Sunco    Vasco
        nharv
        1.000        *        *        *        *
        2.000   0.8837        *        *        *
        3.000   1.2340        *   1.0614        *
        4.000   0.9606   0.6360   0.9356   1.1470

Standard error of differences:     Average       0.4399
                                   Maximum       0.4969
                                   Minimum       0.3462

Average variance of differences:                 0.1948

Standard error of differences for same level of factor:

                 nharv       ngeno
```

```
Average          0.4445      0.3829
Maximum          0.4597      0.4100
Minimum          0.4324      0.3462
Average variance of differences:
                 0.1977      0.1473



*** Table of predicted means for nharv.ntill ***

      ntill       1       2       3       4       5
      nharv
      1.000   0.247       *       *       *       *
      2.000   1.732   1.365   0.396       *       *
      3.000   2.331   1.609   1.025   0.508       *
      4.000   2.158   1.314   0.706   0.154   0.266

Standard error of differences:     Average       0.2627
                                   Maximum       0.3604
                                   Minimum       0.1936

Average variance of differences:                 0.07032

Standard error of differences for same level of factor:

                 nharv       ntill
Average          0.2344      0.2561
Maximum          0.2993      0.2989
Minimum          0.1936      0.2389
Average variance of differences:
                 0.05616     0.06613



*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49   1.447       *       *       *       *
     Puseas   1.521       *       *       *       *
      Sunco   1.750       *       *       *       *
      Vasco   1.750       *       *       *       *

Standard error of differences:     Average       0.3464
                                   Maximum       0.3468
                                   Minimum       0.3460
```

```
Standard error of differences for same level of factor:

              ngeno      ntill
Average           *        0.3464
Maximum           *        0.3468
Minimum           *        0.3460



*** Table of predicted means for nharv.ngeno.ntill ***

                 ntill       1       2       3       4       5
      nharv        ngeno
      1.000         2-49   0.000       *       *       *       *
                  Puseas   0.241       *       *       *       *
                   Sunco   0.200       *       *       *       *
                   Vasco   0.546       *       *       *       *
      2.000         2-49   1.615   0.894   0.300   0.926   0.684
                  Puseas   1.809   1.995   0.046   0.914       *
                   Sunco   1.909   1.709   1.161   0.218       *
                   Vasco   1.595   0.861   0.076       *       *
      3.000         2-49   2.158   1.496   0.967   0.586   0.963
                  Puseas   2.267   1.896   1.595   1.027       *
                   Sunco   2.372   1.565   1.113   0.417  -0.161
                   Vasco   2.527   1.481   0.427   0.002       *
      4.000         2-49   2.015   1.245   0.638   0.265   0.640
                  Puseas   1.766   1.012   0.644  -0.069  -0.172
                   Sunco   2.519   1.573   0.563   0.213  -0.190
                   Vasco   2.333   1.427   0.978   0.208   0.789

Standard error of differences:     Average       0.6275
                           Maximum       1.370
                           Minimum      0.3805

Average variance of differences:              0.4168

Standard error of differences for same level of factor:

              nharv      ngeno      ntill
Average        0.6179     0.5720     0.6069
Maximum         1.370      1.176      1.206
Minimum        0.3805     0.3805     0.4777
Average variance of differences:
             0.4064     0.3532     0.3892
```

```
 559
 560  "### Analysing the tillers separately ###"
 561
 562  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 563      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 564  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 565  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-566  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 567  reml [print=means, wald, comp, mod, dev] sqrt(t1total)

567..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 159 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t1rep                   0.000       BOUND
t1plot                  0.110       0.148
t1plot.t1harv               0.166       0.153


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2            1.003     0.126
```

```
*** Deviance: -2*Log-Likelihood ***


             Deviance   d.f.

               192.88   139

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term           Wald statistic    d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                   59.14          3       19.71      <0.001
  t1geno                    0.68          3        0.23       0.879
  t1harv.t1geno             1.85          9        0.21       0.994

* Dropping individual terms from full fixed model

  t1harv.t1geno             1.85          9        0.21       0.994

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         1.621    Standard error:  0.1589



*** Table of predicted means for t1harv ***

 t1harv    1.000    2.000    3.000    4.000
           0.247    1.732    2.348    2.158

Standard error of differences:     Average       0.3034
                          Maximum       0.3040
                          Minimum       0.3028
```

```
*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
           1.464    1.521    1.750    1.750

Standard error of differences:     Average       0.4494
                                   Maximum       0.4498
                                   Minimum       0.4489


*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        1.000    0.000    0.241    0.200    0.546
        2.000    1.615    1.809    1.909    1.595
        3.000    2.226    2.267    2.372    2.527
        4.000    2.015    1.766    2.519    2.333

Standard error of differences:     Average       0.6744
                                   Maximum       0.6988
                                   Minimum       0.6055

Average variance of differences:                0.4560

Standard error of differences for same level of factor:

                 t1harv      t1geno
Average          0.6914      0.6067
Maximum          0.6988      0.6152
Minimum          0.6903      0.6055


 568
 569  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 570      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 571  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 572  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-573  vstruct [t2plot.t2harv] factor=t2harv; model=ar"
 574  reml [print=means, wald, comp, mod, dev] sqrt(t2total)

574..............................................................................


***** REML Variance Components Analysis *****
```

```
Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 110 (3 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t2rep                   0.000       BOUND
t2plot                  0.000       BOUND
t2plot.t2harv                0.061       0.167


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2             1.479     0.225


*** Deviance: -2*Log-Likelihood ***


                 Deviance   d.f.

                   164.84    94

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob
```

```
* Sequentially adding terms to fixed model

  t2harv                 1.15       2      0.57     0.564
  t2geno                 2.23       3      0.74     0.527
  t2harv.t2geno             4.81       6      0.80     0.568

* Dropping individual terms from full fixed model

  t2harv.t2geno             4.81       6      0.80     0.568

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        1.426   Standard error:  0.1278



*** Table of predicted means for t2harv ***

 t2harv   2.000   3.000   4.000
        1.373   1.602   1.303

Standard error of differences:    Average      0.3129
                        Maximum      0.3183
                        Minimum      0.3098

Average variance of differences:           0.09795


*** Table of predicted means for t2geno ***

 t2geno    2-49  Puseas   Sunco   Vasco
        1.212   1.586   1.649   1.256

Standard error of differences:    Average      0.3612
                        Maximum      0.3748
                        Minimum      0.3475

Average variance of differences:            0.1306


*** Table of predicted means for t2harv.t2geno ***
```

```
        t2geno     2-49   Puseas    Sunco    Vasco
        t2harv
         2.000    0.894    2.027    1.709    0.861
         3.000    1.496    1.867    1.565    1.481
         4.000    1.246    0.864    1.674    1.427

Standard error of differences:     Average       0.6252
                                   Maximum       0.7049
                                   Minimum       0.5972

Average variance of differences:                0.3918

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.6253      0.6249
Maximum          0.6770      0.7038
Minimum          0.5972      0.5972
Average variance of differences:
                 0.3918      0.3918


 575
 576  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 577      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 578  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 579  "vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot.t3harv ; const=pos
-580  vstruct [t3plot.t3harv] factor=t3harv; model=ar"
 581  reml [print=means, wald, comp, mod] sqrt(t3total)

581..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 98 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model
```

```
* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                   0.000       BOUND
t3plot                  0.000       BOUND
t3plot.t3harv              0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2             1.170     0.178


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t3harv                      4.91            2         2.45       0.086
   t3geno                      1.67            3         0.56       0.644
   t3harv.t3geno                   6.82            6         1.14       0.337

* Dropping individual terms from full fixed model

   t3harv.t3geno                   6.82            6         1.14       0.337

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.7286    Standard error: 0.12011



*** Table of predicted means for t3harv ***
```

```
  t3harv    2.000    3.000    4.000
         0.4826   1.0435   0.6596

Standard error of differences:     Average       0.2931
                                   Maximum       0.3117
                                   Minimum       0.2577

Average variance of differences:              0.08656


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
         0.6295   0.8362   0.9254   0.5231

Standard error of differences:     Average       0.3374
                                   Maximum       0.3807
                                   Minimum       0.2931

Average variance of differences:               0.1154


*** Table of predicted means for t3harv.t3geno ***

       t3geno        2-49       Puseas       Sunco        Vasco
       t3harv
        2.000      0.3000      0.5000      1.1305      0.0000
        3.000      0.9668      1.5125      1.1034      0.5914
        4.000      0.6218      0.4960      0.5424      0.9781

Standard error of differences:     Average       0.5753
                                   Maximum       0.8671
                                   Minimum       0.4837

Average variance of differences:               0.3462

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average         0.5749      0.5746
Maximum         0.8671      0.8550
Minimum         0.4969      0.4837
Average variance of differences:
                 0.3462      0.3462
```

```
 582
 583  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 584      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 585  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 586  "vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot.t4harv ; const=pos
-587  vstruct [t4plot.t4harv] factor=t4harv; model=ar"
 588  reml [print=means, wald, comp, mod] sqrt(t4total)

588..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t4total)

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 60

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t4rep                    0.0000       BOUND
t4plot                   0.0763      0.1160
t4plot.t4harv            0.0000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                      Identity      Sigma2             0.615    0.1290


*** Wald tests for fixed effects ***
```

```
   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

 * Sequentially adding terms to fixed model

   t4harv                        5.06           2        2.53       0.080
   t4geno                        1.06           3        0.35       0.787
   t4harv.t4geno                 6.28           5        1.26       0.280

 * Dropping individual terms from full fixed model

   t4harv.t4geno                 6.28           5        1.26       0.280

 * Message: chi-square distribution for Wald tests is an asymptotic approximation
   (i.e. for large samples) and underestimates the probabilities in other cases.


 *** Table of predicted means for Constant ***

          0.5181    Standard error: 0.18862



 *** Table of predicted means for t4harv ***

  t4harv    2.000    3.000    4.000
                *   0.5752   0.1681

 Standard error of differences:      0.2321



 *** Table of predicted means for t4geno ***

  t4geno     2-49   Puseas    Sunco    Vasco
          0.5804   0.9173   0.3544        *

 Standard error of differences:     Average       0.4469
                                    Maximum       0.4695
                                    Minimum       0.4105

 Average variance of differences:                0.2004


 *** Table of predicted means for t4harv.t4geno ***

       t4geno         2-49       Puseas        Sunco        Vasco
```

```
     t4harv
      2.000      0.9314      1.5039      0.4166          *
      3.000      0.5864      1.2778      0.4665     -0.0297
      4.000      0.2235     -0.0299      0.1802      0.2984

Standard error of differences:     Average       0.6317
                               Maximum       1.020
                               Minimum      0.3607

Average variance of differences:               0.4236

Standard error of differences for same level of factor:

               t4harv      t4geno
Average          0.6107      0.5852
Maximum           1.020      0.8786
Minimum          0.4634      0.3607
Average variance of differences:
               0.3985      0.3690


 589
 590  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 591     t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 592  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
-593  reml [print=means, wald, comp, mod] sqrt(t5total)"
 594  "NOT ENOUGH INFORMATION TO ANALYSE ADEQUATELY"
 595
 596
 597
"==============================================================
===========
-598                   PART = LS3 (harvest 2, 3 & 4)
-599
==============================================================
=========="
 600
 601  "**** Disease Rating (Harvests 2, 3 & 4; leave out CPI1338)****"
 602
 603  "### Analysing the tillers together ###"
 604
 605  subset
[condition=(Part.eq.10).and.(Harvest.ne.1).and.(Harvest.le.4).and.(Genotype.ne.2);
setlevel=yes] \
 606   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
```

```
 607   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 608
 609  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 610  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-611  vstruct [nplot.nharv] factor=nharv; model=ar"
 612  reml [print=means, wald, comp, mod; mvincl=yvar, expl; maxcyc=100] ndr

612.............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 512

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***

Random term              Component        S.e.

nrep                       0.0014      0.0154
nplot                      0.0000       BOUND
nplot.nharv                0.0294      0.0516
nplot.nharv.nplant         0.3776      0.0838


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                       Identity      Sigma2           0.643    0.0542
```

```
*** Wald tests for fixed effects ***


  Fixed term            Wald statistic    d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      1.07          2        0.53       0.587
  ngeno                      7.90          3        2.63       0.048
  ntill                    933.00          4      233.25      <0.001
  nharv.ngeno                7.96          6        1.33       0.241
  nharv.ntill                8.03          6        1.34       0.236
  ngeno.ntill               11.78         12        0.98       0.464
  nharv.ngeno.ntill         11.61         16        0.73       0.770

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill         11.61         16        0.73       0.770

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.6050   Standard error: 0.09534



*** Table of predicted means for nharv ***

  nharv   2.000   3.000   4.000
              *       *  0.8952

* SEDs not available


*** Table of predicted means for ngeno ***

     ngeno      2-49     Puseas      Sunco      Vasco
                   *          *          *          *

* All values in table missing: due to missing factor combinations in higher
  order interactions
```

```
*** Table of predicted means for ntill ***

   ntill       1       2       3       4       5
           2.667   0.672   0.143       *       *

Standard error of differences:     Average      0.1291
                                   Maximum      0.1473
                                   Minimum     0.09600

Average variance of differences:             0.01722


*** Table of predicted means for nharv.ngeno ***

        ngeno    2-49   Puseas    Sunco    Vasco
        nharv
        2.000       *        *        *        *
        3.000   0.7077       *   0.8565        *
        4.000   0.7885   0.8041   0.8684   1.1198

Standard error of differences:     Average      0.3389
                                   Maximum      0.3709
                                   Minimum      0.3103

Average variance of differences:              0.1152

Standard error of differences for same level of factor:

                  nharv      ngeno
Average          0.3357     0.3406
Maximum          0.3520     0.3709
Minimum          0.3135     0.3103
Average variance of differences:
                 0.1128     0.1169



*** Table of predicted means for nharv.ntill ***

        ntill          1          2          3          4          5
        nharv
        2.000     2.1667     0.1160    -0.2838          *          *
        3.000     2.6667     0.8774     0.3366    -0.1021          *
        4.000     3.1667     1.0236     0.3761    -0.0689    -0.0216

Standard error of differences:     Average      0.2583
```

```
                              Maximum      0.4426
                              Minimum      0.1495

Average variance of differences:             0.07226

Standard error of differences for same level of factor:

               nharv      ntill
Average          0.2218     0.2575
Maximum          0.3770     0.3961
Minimum          0.1495     0.1973
Average variance of differences:
             0.05340    0.07191



*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49    2.556   0.511   0.215       *       *
     Puseas    2.556   0.803  -0.200       *       *
      Sunco    2.733   0.683   0.360       *       *
      Vasco    2.822   0.693   0.197       *       *

Standard error of differences:    Average      0.2901
                              Maximum      0.4846
                              Minimum      0.1734

Average variance of differences:             0.08920

Standard error of differences for same level of factor:

               ngeno      ntill
Average          0.2527     0.2954
Maximum          0.3636     0.4846
Minimum          0.1734     0.2278
Average variance of differences:
             0.06888    0.09371



*** Table of predicted means for nharv.ngeno.ntill ***

                 ntill           1           2           3           4
      nharv       ngeno
```

```
        2.000      2-49     2.1333    0.2714   -0.0644         *
                 Puseas    1.8000   -0.1913   -0.9245         *
                  Sunco    2.6000    0.1564    0.0292         *
                  Vasco    2.1333    0.2276   -0.1754         *
        3.000      2-49     2.6000    0.5283    0.3855    0.0585
                 Puseas    3.0667    1.5717    0.2078   -0.2416
                  Sunco    2.3333    0.7579    0.6851    0.0154
                  Vasco    2.6667    0.6517    0.0680   -0.2406
        4.000      2-49     2.9333    0.7333    0.3238   -0.1675
                 Puseas    2.8000    1.0277    0.1163   -0.0259
                  Sunco    3.2667    1.1333    0.3671   -0.1866
                  Vasco    3.6667    1.2000    0.6972    0.1043


                  ntill        5
        nharv      ngeno
        2.000      2-49          *
                 Puseas         *
                  Sunco         *
                  Vasco         *
        3.000      2-49    -0.0339
                 Puseas         *
                  Sunco    0.4910
                  Vasco         *
        4.000      2-49     0.1193
                 Puseas    0.1026
                  Sunco   -0.2387
                  Vasco   -0.0694

Standard error of differences:     Average       0.5431
                                   Maximum        1.304
                                   Minimum       0.2927

Average variance of differences:                0.3300

Standard error of differences for same level of factor:

                  nharv      ngeno      ntill
Average          0.5191     0.5233     0.5245
Maximum           1.304      1.128      1.304
Minimum          0.2927     0.2927     0.3945
Average variance of differences:
                 0.3013     0.3111     0.3113
```

```
 614
 615  "### Analysing the tillers separately ###"
 616
 617  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 618      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 619  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 620  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-621  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 622  reml [print=means, wald, comp, mod] t1dr

622..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 180

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t1rep                   0.011       0.049
t1plot                  0.025       0.081
t1plot.t1harv               0.000      BOUND


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.

Residual                     Identity      Sigma2             1.690     0.189


*** Wald tests for fixed effects ***
```

```
  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                      17.75           2         8.88      <0.001
  t1geno                       1.16           3         0.39       0.763
  t1harv.t1geno                7.89           6         1.31       0.246

* Dropping individual terms from full fixed model

  t1harv.t1geno                7.89           6         1.31       0.246

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           2.667    Standard error:  0.1229



*** Table of predicted means for t1harv ***

  t1harv    2.000    3.000    4.000
           2.167    2.667    3.167

Standard error of differences:      0.2373



*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
           2.556    2.556    2.733    2.822

Standard error of differences:      0.3035



*** Table of predicted means for t1harv.t1geno ***

      t1geno     2-49   Puseas    Sunco    Vasco
      t1harv
```

```
     2.000    2.133    1.800    2.600    2.133
     3.000    2.600    3.067    2.333    2.667
     4.000    2.933    2.800    3.267    3.667

Standard error of differences:     Average       0.4891
                                   Maximum      0.4923
                                   Minimum      0.4747

Average variance of differences:                0.2392

Standard error of differences for same level of factor:

               t1harv      t1geno
Average          0.4923      0.4747
Maximum          0.4923      0.4747
Minimum          0.4923      0.4747


 623
 624  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 625      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 626  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 627  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-628  vstruct [t2plot.t2harv] factor=t2harv; model=ar"
 629  reml [print=means, wald, comp, mod, dev] t2dr

629..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 146

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***
```

```
Random term            Component       S.e.

t2rep                  0.0000      BOUND
t2plot                 0.0000      BOUND
t2plot.t2harv              0.0332      0.0739


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2              0.825    0.1109


*** Deviance: -2*Log-Likelihood ***


              Deviance   d.f.

                141.15   130

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


  Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t2harv                    15.27           2         7.64      <0.001
  t2geno                      5.34           3         1.78       0.149
  t2harv.t2geno                   8.14           6        1.36       0.228

* Dropping individual terms from full fixed model

  t2harv.t2geno                   8.14           6        1.36       0.228

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
          0.7075    Standard error: 0.08643



*** Table of predicted means for t2harv ***

  t2harv    2.000    3.000    4.000
          0.2222   0.9044   0.9958

Standard error of differences:     Average       0.2111
                                   Maximum       0.2233
                                   Minimum       0.1876

Average variance of differences:               0.04482


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
          0.4860   0.9541   0.7023   0.6876

Standard error of differences:     Average       0.2439
                                   Maximum       0.2635
                                   Minimum       0.2238

Average variance of differences:               0.05976


*** Table of predicted means for t2harv.t2geno ***

       t2geno     2-49   Puseas    Sunco    Vasco
       t2harv
        2.000   0.1513   0.2547   0.2590   0.2238
        3.000   0.5732   1.6909   0.7146   0.6390
        4.000   0.7333   0.9167   1.1333   1.2000

Standard error of differences:     Average       0.4190
                                   Maximum       0.5780
                                   Minimum       0.3635

Average variance of differences:                0.1793

Standard error of differences for same level of factor:

                t2harv      t2geno
```

```
Average          0.4175      0.4192
Maximum          0.5780      0.5464
Minimum          0.3635      0.3690
Average variance of differences:
                 0.1793      0.1793


 630
 631  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 632      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 633  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 634  "vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot.t3harv ; const=pos
-635  vstruct [t3plot.t3harv] factor=t3harv; model=ar"
 636  reml [print=means, wald, comp, mod] t3dr

636...........................................................................


***** REML Variance Components Analysis *****


Response Variate : t3dr

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 104

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                      0.0000       BOUND
t3plot                     0.0138      0.0383
t3plot.t3harv                0.0000       BOUND


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.
```

```
Residual                  Identity      Sigma2            0.491    0.0757


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t3harv                       2.16           2         1.08       0.339
   t3geno                        2.13           3         0.71       0.545
   t3harv.t3geno                 3.78           6         0.63       0.706

* Dropping individual terms from full fixed model

   t3harv.t3geno                 3.78           6         0.63       0.706

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

           0.2808    Standard error: 0.10981



*** Table of predicted means for t3harv ***

  t3harv    2.000    3.000    4.000
           0.0612   0.3609   0.4203

Standard error of differences:     Average       0.2467
                                   Maximum       0.2965
                                   Minimum       0.1479

Average variance of differences:              0.06572


*** Table of predicted means for t3geno ***

  t3geno     2-49   Puseas    Sunco    Vasco
           0.2516   0.1415   0.4160   0.3140
```

```
Standard error of differences:     Average       0.3076
                                   Maximum       0.3751
                                   Minimum       0.2284

Average variance of differences:              0.09646


*** Table of predicted means for t3harv.t3geno ***

       t3geno        2-49      Puseas       Sunco       Vasco
       t3harv
        2.000      0.0185     -0.0009      0.2005      0.0268
        3.000      0.4297      0.1790      0.6309      0.2038
        4.000      0.3065      0.2465      0.4167      0.7116

Standard error of differences:     Average       0.4791
                                   Maximum        1.003
                                   Minimum       0.2702

Average variance of differences:               0.2701

Standard error of differences for same level of factor:

                 t3harv      t3geno
Average          0.4650      0.4756
Maximum           1.003      0.7525
Minimum          0.2865      0.2702
Average variance of differences:
                 0.2717      0.2629



 637
 638  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 639      t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 640  vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
 641  "vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot.t4harv ; const=pos
-642  vstruct [t4plot.t4harv] factor=t4harv; model=ar"
 643  reml [print=means, wald, comp, mod] t4dr

643..............................................................................


***** REML Variance Components Analysis *****
```

```
Response Variate : t4dr

Fixed model      : Constant+t4harv+t4geno+t4harv.t4geno
Random model     : t4rep+t4plot+t4plot.t4harv

Number of units  : 57

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t4rep                   0.00693     0.01199
t4plot                  0.00000       BOUND
t4plot.t4harv               0.01138     0.01406


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.0519   0.01234


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t4harv                      0.10           1         0.10       0.754
   t4geno                      3.09           3         1.03       0.378
   t4harv.t4geno                   4.86           3         1.62       0.182

* Dropping individual terms from full fixed model

   t4harv.t4geno                   4.86           3         1.62       0.182

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.
```

```
*** Table of predicted means for Constant ***

        0.05458    Standard error:    0.063860



*** Table of predicted means for t4harv ***

     t4harv        3.000        4.000
               0.03171      0.07744

Standard error of differences:     0.08481



*** Table of predicted means for t4geno ***

     t4geno         2-49       Puseas        Sunco        Vasco
               0.08639    -0.00659      0.00287      0.13565

Standard error of differences:     Average       0.1179
                                   Maximum       0.1345
                                   Minimum       0.1003

Average variance of differences:              0.01406


*** Table of predicted means for t4harv.t4geno ***

      t4geno         2-49       Puseas        Sunco        Vasco
      t4harv
       3.000      0.17277     -0.02562     -0.00671     -0.01360
       4.000      0.00000      0.01245      0.01245      0.28489

Standard error of differences:     Average       0.1658
                                   Maximum       0.2216
                                   Minimum       0.1332

Average variance of differences:              0.02822

Standard error of differences for same level of factor:

              t4harv      t4geno
Average         0.1656      0.1656
Maximum         0.2216      0.2125
```

```
Minimum          0.1332      0.1346
Average variance of differences:
               0.02813     0.02829


 644
 645  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 646      t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 647  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos
-648  reml [print=means, wald, comp, mod, dev] t5dr"
 649  "NOT ENOUGH INFORMATION TO ANALYSE ADEQUATELY"
 650
 651
 652  "**** Infection - Total (Harvests 2, 3 & 4; leave out CPI1338 & Rep 3)****"
 653
 654  "### Analysing the tillers together ###"
 655
 656  subset
[condition=(Part.eq.10).and.(Harvest.ne.1).and.(Harvest.le.4).and.(Genotype.ne.2).and.(
Rep.le.2);\
 657   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 658   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 659
 660  vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
cons=pos
 661  vstruct [nplot.nharv] factor=nharv; model=ar
 662  reml [print=means, wald, comp, mod, dev] sqrt(ntotal)

662...............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot.nharv+nplot.nharv.nplant

Number of units  : 348 (2 units excluded due to zero weights or missing values)

* Residual term has been added to model
```

```
* Sparse algorithm with AI optimisation

*** Covariance structures defined for random model ***

Covariance structures defined within terms:

Term                Factor     Model               Order Nrows
nplot.nharv           nplot      Identity              1     8
                 nharv      Auto-regressive            1     3



*** Estimated Variance Components ***

Random term            Component      S.e.

nrep                    0.0000      BOUND
nplot.nharv.nplant          0.1738      0.0727


*** Estimated Parameters for Covariance Models ***

Random term(s)   Factor       Model(order)  Parameter       Estimate      S.e.

nplot.nharv      nplot        Identity      Scalar           0.1503    0.1320
            nharv        AR(1)        phi_1            0.8766    0.3701

Note: the covariance matrix for each term is calculated as G or R where
     var(y) = Sigma2( ZGZ'+R ), ie. relative to the residual variance, Sigma2


*** Residual variance model ***

Term           Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2           0.818    0.0817


*** Deviance: -2*Log-Likelihood ***


             Deviance   d.f.

               383.29   294

Note: deviance omits constants which depend on fixed model fitted.
```

```
*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   nharv                       1.04            2         0.52       0.595
   ngeno                       2.07            3         0.69       0.559
   ntill                     126.82            4        31.70      <0.001
   nharv.ngeno                16.61            6         2.77       0.011
   nharv.ntill                 3.13            6         0.52       0.793
   ngeno.ntill                 4.99           12         0.42       0.958
   nharv.ngeno.ntill           8.74           15         0.58       0.890

* Dropping individual terms from full fixed model

   nharv.ngeno.ntill           8.74           15         0.58       0.890

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

          0.4879    Standard error: 0.15663



*** Table of predicted means for nharv ***

   nharv    2.000    3.000    4.000
                *        *   0.6453

* SEDs not available


*** Table of predicted means for ngeno ***

      ngeno        2-49      Puseas       Sunco       Vasco
                      *           *           *           *

* All values in table missing: due to missing factor combinations in higher
```

```
  order interactions


*** Table of predicted means for ntill ***

   ntill       1       2       3       4       5
          1.558    0.737       *       *       *

Standard error of differences:      0.1292



*** Table of predicted means for nharv.ngeno ***

        ngeno     2-49   Puseas    Sunco    Vasco
        nharv
        2.000       *        *        *        *
        3.000   0.5616       *   0.7108        *
        4.000   0.6613   0.3599   0.6769   0.8832

Standard error of differences:     Average       0.4675
                                   Maximum       0.5121
                                   Minimum       0.3092

Average variance of differences:                0.2210

Standard error of differences for same level of factor:

                  nharv       ngeno
Average          0.4866      0.3549
Maximum          0.5121      0.4006
Minimum          0.4626      0.3092
Average variance of differences:
                 0.2369      0.1280



*** Table of predicted means for nharv.ntill ***

        ntill       1       2       3       4       5
        nharv
        2.000   1.2830   0.6243       *       *       *
        3.000   1.5710   0.7271   0.4449   0.1084       *
        4.000   1.8189   0.8598   0.2257   0.0907   0.2315

Standard error of differences:     Average       0.2891
```

```
                                Maximum      0.4327
                                Minimum      0.2039

Average variance of differences:           0.08694

Standard error of differences for same level of factor:

                nharv      ntill
Average        0.2780     0.2646
Maximum        0.3941     0.3474
Minimum        0.2039     0.2310
Average variance of differences:
              0.08106    0.07143



*** Table of predicted means for ngeno.ntill ***

       ntill       1        2        3        4        5
       ngeno
        2-49  1.4731   0.5096   0.2432        *        *
      Puseas  1.6439   0.8561   0.0690        *        *
       Sunco  1.8771   1.1127   0.6266        *        *
       Vasco  1.2365   0.4699        *        *        *

Standard error of differences:    Average      0.4296
                                Maximum      0.5594
                                Minimum      0.2448

Average variance of differences:            0.1905

Standard error of differences for same level of factor:

                ngeno      ntill
Average        0.2987     0.4521
Maximum        0.4290     0.5594
Minimum        0.2448     0.4196
Average variance of differences:
              0.09299     0.2063



*** Table of predicted means for nharv.ngeno.ntill ***

                ntill          1           2           3           4
       nharv       ngeno
```

```
2.000     2-49    1.1156    0.1031    0.2515        *
        Puseas    1.1797    0.6892   -0.4108        *
         Sunco    1.9250    1.6758    0.8562        *
         Vasco    0.9118    0.0290        *         *
3.000     2-49    1.7367    0.4828    0.1732    0.5081
        Puseas    2.1625    1.2368    0.8254   -0.0924
         Sunco    1.5857    0.8654    0.8058   -0.0004
         Vasco    0.7991    0.3236   -0.0249    0.0184
4.000     2-49    1.5671    0.9429    0.3048    0.3726
        Puseas    1.5894    0.6425   -0.2078   -0.1191
         Sunco    2.1205    0.7968    0.2180    0.0982
         Vasco    1.9986    1.0569    0.5878    0.0112


         ntill        5
nharv     ngeno
2.000     2-49        *
        Puseas        *
         Sunco        *
         Vasco        *
3.000     2-49   -0.0928
        Puseas        *
         Sunco    0.2976
         Vasco        *
4.000     2-49    0.1193
        Puseas   -0.1054
         Sunco    0.1507
         Vasco    0.7613

Standard error of differences:    Average      0.6915
                             Maximum      1.418
                             Minimum     0.4045

Average variance of differences:           0.5109

Standard error of differences for same level of factor:

              nharv     ngeno     ntill
Average       0.6835    0.6177    0.6646
Maximum        1.233     1.369     1.369
Minimum       0.4045    0.4045    0.4621
Average variance of differences:
              0.4993    0.4193    0.4715
```

```
 664  "### Analysing the tillers separately ###"
 665
 666  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 667      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 668  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 669  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-670  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 671  reml [print=means, wald, comp, mod, dev] sqrt(t1total)

671..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 120

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t1rep                    0.000       BOUND
t1plot                   0.345       0.356
t1plot.t1harv                0.197       0.224


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2            1.227     0.177


*** Deviance: -2*Log-Likelihood ***
```

```
                 Deviance   d.f.

                   169.65   104

Note: deviance omits constants which depend on fixed model fitted.



*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                        2.60           2         1.30       0.272
   t1geno                         0.89           3         0.30       0.827
   t1harv.t1geno                      5.17           6         0.86       0.523

* Dropping individual terms from full fixed model

   t1harv.t1geno                      5.17           6         0.86       0.523

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.558    Standard error:  0.2482



*** Table of predicted means for t1harv ***

  t1harv    2.000    3.000    4.000
            1.283    1.571    1.819

Standard error of differences:      0.3325



*** Table of predicted means for t1geno ***

  t1geno     2-49   Puseas    Sunco    Vasco
```

```
          1.473    1.644    1.877    1.236

Standard error of differences:      0.7020



*** Table of predicted means for t1harv.t1geno ***

      t1geno     2-49   Puseas    Sunco    Vasco
      t1harv
       2.000    1.116    1.180    1.925    0.912
       3.000    1.737    2.163    1.586    0.799
       4.000    1.567    1.589    2.121    1.999

Standard error of differences:     Average       0.8470
                                   Maximum       0.8874
                                   Minimum       0.6649

Average variance of differences:              0.7247

Standard error of differences for same level of factor:

              t1harv      t1geno
Average         0.8874      0.6649
Maximum         0.8874      0.6649
Minimum         0.8874      0.6649


 672
 673  subset [condition=ntill.eq.2; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 674      t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 675  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 676  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-677  vstruct [t2plot.t2harv] factor=t2harv; model=ar"
 678  reml [print=means, wald, comp, mod] sqrt(t2total)

678..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t2total)

Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
```

```
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 98 (2 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t2rep                   0.074       0.137
t2plot                  0.000       BOUND
t2plot.t2harv               0.014       0.121


*** Residual variance model ***

Term            Factor        Model(order)  Parameter        Estimate      S.e.

Residual                    Identity      Sigma2            1.027     0.168


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                       1.08            2         0.54       0.582
   t2geno                       4.46            3         1.49       0.216
   t2harv.t2geno                   11.58            6         1.93       0.072

* Dropping individual terms from full fixed model

   t2harv.t2geno                   11.58            6         1.93       0.072

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***
```

```
            0.7489    Standard error: 0.22201



*** Table of predicted means for t2harv ***

  t2harv    2.000    3.000    4.000
            0.6669   0.7162   0.8636

Standard error of differences:     Average       0.2730
                                   Maximum       0.2907
                                   Minimum       0.2424

Average variance of differences:              0.07500


*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
            0.5142   0.8841   1.1191   0.4782

Standard error of differences:     Average       0.3143
                                   Maximum       0.3341
                                   Minimum       0.2944

Average variance of differences:              0.09911


*** Table of predicted means for t2harv.t2geno ***

       t2geno     2-49   Puseas    Sunco    Vasco
       t2harv
        2.000   0.0399   0.8786   1.6952   0.0540
        3.000   0.4828   1.1931   0.8654   0.3236
        4.000   1.0200   0.5807   0.7968   1.0569

Standard error of differences:     Average       0.5405
                                   Maximum       0.7272
                                   Minimum       0.4681

Average variance of differences:               0.2978

Standard error of differences for same level of factor:

                 t2harv      t2geno
Average          0.5382      0.5411
```

```
Maximum          0.7272      0.6973
Minimum          0.4681      0.4681
Average variance of differences:
                 0.2973      0.2980


 679
 680  subset [condition=ntill.eq.3; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 681      t3harv, t3geno, t3rep, t3plot, t3plant, t3till, t3part, t3dr, t3total
 682  vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot+t3plot.t3harv ; const=pos
 683  "vcomp [fixed=t3geno*t3harv] random=t3rep+t3plot.t3harv ; const=pos
-684  vstruct [t3plot.t3harv] factor=t3harv; model=ar"
 685  reml [print=means, wald, comp, mod] sqrt(t3total)

685..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t3total)

Fixed model      : Constant+t3harv+t3geno+t3harv.t3geno
Random model     : t3rep+t3plot+t3plot.t3harv

Number of units  : 72

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t3rep                    0.0000       BOUND
t3plot                   0.0000       BOUND
t3plot.t3harv            0.0000       BOUND


*** Residual variance model ***

Term             Factor        Model(order)  Parameter        Estimate      S.e.
```

```
Residual                Identity     Sigma2          0.750    0.1357


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  t3harv                     0.39          2         0.20        0.822
  t3geno                     2.16          3         0.72        0.539
  t3harv.t3geno              6.58          5         1.32        0.254

* Dropping individual terms from full fixed model

  t3harv.t3geno              6.58          5         1.32        0.254

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.2838    Standard error: 0.14555



*** Table of predicted means for t3harv ***

 t3harv    2.000    3.000    4.000
            *   0.4422   0.2683

Standard error of differences:      0.2222



*** Table of predicted means for t3geno ***

 t3geno     2-49   Puseas    Sunco    Vasco
        0.1509   0.2632   0.5897        *

Standard error of differences:     Average       0.3568
                       Maximum       0.3961
                       Minimum       0.2898
```

```
Average variance of differences:              0.1296


*** Table of predicted means for t3harv.t3geno ***

      t3geno       2-49      Puseas      Sunco      Vasco
      t3harv
       2.000     0.0000      0.0000     0.7464          *
       3.000     0.1732      0.7896     0.8062     0.0000
       4.000     0.2795      0.0000     0.2165     0.5774

Standard error of differences:     Average      0.5649
                                   Maximum      0.9998
                                   Minimum      0.3978

Average variance of differences:              0.3526

Standard error of differences for same level of factor:

                t3harv      t3geno
Average         0.5268      0.5784
Maximum         0.9998      0.9484
Minimum         0.4107      0.4107
Average variance of differences:
                0.3113      0.3689


 686
 687  subset [condition=ntill.eq.4; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 688     t4harv, t4geno, t4rep, t4plot, t4plant, t4till, t4part, t4dr, t4total
 689  "vcomp [fixed=t4geno*t4harv] random=t4rep+t4plot+t4plot.t4harv ; const=pos
-690  reml [print=means, wald, comp, mod] sqrt(t4total)"
 691  "NOT ENOUGH INFORMATION TO ANALYSE ADEQUATELY"
 692
 693  subset [condition=ntill.eq.5; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 694     t5harv, t5geno, t5rep, t5plot, t5plant, t5till, t5part, t5dr, t5total
 695  "*** DATA SET TOO SMALL TO ANALYSE ***"
 696  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot+t5plot.t5harv ; const=pos"
 697  "vcomp [fixed=t5geno*t5harv] random=t5rep+t5plot.t5harv ; const=pos
-698  vstruct [t5plot.t5harv] factor=t5harv; model=ar"
 699  "reml [print=means, wald, comp, mod] t5total"
 700
```

```
 701
"================================================================
===========
-702                    PART = LS4 (harvest 2, 3 & 4)
-703
================================================================
=========="
 704
 705  "**** Disease Rating (Harvests 2, 3 & 4; leave out CPI1338)****"
 706
 707  "### Analysing the tillers together ###"
 708
 709  subset
[condition=(Part.eq.11).and.(Harvest.ne.1).and.(Harvest.le.4).and.(Genotype.ne.2);
setlevel=yes] \
 710   Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating, Infection_total; \
 711   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 712
 713  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 714  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-715  vstruct [nplot.nharv] factor=nharv; model=ar"
 716  reml [print=means, wald, comp, mod; mvincl=yvar, expl; maxcyc=100] ndr

716............................................................................


***** REML Variance Components Analysis *****


Response Variate : ndr

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 375

* Residual term has been added to model

* Sparse algorithm with AI optimisation
* Units with missing factor/covariate values included


*** Estimated Variance Components ***
```

```
Random term           Component      S.e.

nrep                   0.0069     0.0147
nplot                  0.0000      BOUND
nplot.nharv              0.0092     0.0275
nplot.nharv.nplant         0.1285     0.0500


*** Residual variance model ***

Term          Factor      Model(order)  Parameter      Estimate     S.e.

Residual                   Identity     Sigma2          0.496    0.0513


*** Wald tests for fixed effects ***


  Fixed term            Wald statistic     d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                      18.23          2        9.12     <0.001
  ngeno                       7.54          3        2.51      0.057
  ntill                     321.27          4       80.32     <0.001
  nharv.ngeno                  6.09          6        1.01      0.413
  nharv.ntill                 13.21          5        2.64      0.022
  ngeno.ntill                  7.71          9        0.86      0.564
  nharv.ngeno.ntill           10.91         10        1.09      0.364

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill           10.91         10        1.09      0.364

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

     -0.003972    Standard error:   0.1353913



*** Table of predicted means for nharv ***
```

```
    nharv      2.000      3.000      4.000
               *          *          *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ngeno ***

    ngeno       2-49     Puseas      Sunco      Vasco
               *          *          *          *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ntill ***

  ntill      1       2       3       4       5
         1.242       *       *       *       *

* SEDs not available


*** Table of predicted means for nharv.ngeno ***

     ngeno     2-49   Puseas    Sunco    Vasco
     nharv
     2.000        *        *        *        *
     3.000   0.2270        *        *        *
     4.000   0.3061        *        *        *

Standard error of differences:      0.2662



*** Table of predicted means for nharv.ntill ***

     ntill          1           2           3           4           5
     nharv
     2.000     0.4271           *           *           *           *
     3.000     1.3000      0.0898      0.0263           *           *
     4.000     2.0000      0.4997      0.0871     -0.0988           *

Standard error of differences:     Average       0.2067
```

```
                             Maximum      0.3333
                             Minimum      0.1347

Average variance of differences:             0.04581

Standard error of differences for same level of factor:

              nharv      ntill
Average         0.2062     0.1754
Maximum         0.2694     0.2630
Minimum         0.1347     0.1496
Average variance of differences:
             0.04534    0.03272



*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49   1.0444   0.1413       *       *       *
     Puseas   1.2000       *       *       *       *
      Sunco   1.3028   0.1596       *       *       *
      Vasco   1.4222   0.1899       *       *       *

Standard error of differences:     Average      0.2793
                             Maximum      0.3977
                             Minimum      0.1727

Average variance of differences:             0.08353

Standard error of differences for same level of factor:

              ngeno      ntill
Average         0.2932     0.2478
Maximum         0.2943     0.3977
Minimum         0.2927     0.1727
Average variance of differences:
             0.08600    0.07250



*** Table of predicted means for nharv.ngeno.ntill ***

                ntill          1          2          3          4
      nharv       ngeno
```

```
   2.000     2-49     0.4000   -0.0933       *        *
          Puseas    0.3333       *        *        *
           Sunco    0.6416   -0.0596       *        *
           Vasco    0.3333    0.0945       *        *
   3.000     2-49     1.4000    0.0213    0.0139   -0.0478
          Puseas    1.3333    0.2452    0.1338        *
           Sunco    1.2000    0.0717    0.0258    0.0531
           Vasco    1.2667    0.0212   -0.0685   -0.0788
   4.000     2-49     1.3333    0.4959    0.0781   -0.1433
          Puseas    1.9333    0.5822    0.1051   -0.0755
           Sunco    2.0667    0.4667   -0.1145   -0.1033
           Vasco    2.6667    0.4540    0.2796   -0.0732


           ntill        5
   nharv      ngeno
   2.000     2-49        *
          Puseas        *
           Sunco        *
           Vasco        *
   3.000     2-49    -0.2522
          Puseas        *
           Sunco        *
           Vasco        *
   4.000     2-49    -0.2335
          Puseas        *
           Sunco        *
           Vasco        *

Standard error of differences:     Average      0.5333
                                   Maximum       1.104
                                   Minimum      0.2573

Average variance of differences:              0.3423

Standard error of differences for same level of factor:

                 nharv      ngeno      ntill
Average         0.5072     0.5264     0.4842
Maximum          1.104      1.089      1.104
Minimum         0.2573     0.2573     0.2991
Average variance of differences:
                0.3089     0.3327     0.2955
```

```
 718  "### Analysing the tillers separately ###"
 719
 720  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 721     t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 722  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 723  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-724  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 725  reml [print=means, wald, comp, mod, dev] t1dr

725..............................................................................


***** REML Variance Components Analysis *****


Response Variate : t1dr

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 179

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component        S.e.

t1rep                        0.033       0.059
t1plot                       0.029       0.056
t1plot.t1harv                0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            1.011     0.113


*** Deviance: -2*Log-Likelihood ***
```

```
                 Deviance   d.f.

                   205.82   163

Note: deviance omits constants which depend on fixed model fitted.


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t1harv                      73.48            2        36.74      <0.001
   t1geno                       2.38            3         0.79       0.498
   t1harv.t1geno                   11.13            6         1.86       0.084

* Dropping individual terms from full fixed model

   t1harv.t1geno                   11.13            6         1.86       0.084

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

            1.242    Standard error:  0.1386



*** Table of predicted means for t1harv ***

  t1harv    2.000    3.000    4.000
            0.426    1.300    2.000

Standard error of differences:     Average       0.1841
                                   Maximum       0.1844
                                   Minimum       0.1836


*** Table of predicted means for t1geno ***
```

```
 t1geno     2-49   Puseas    Sunco    Vasco
          1.044    1.200    1.301    1.422

Standard error of differences:     Average       0.2538
                                   Maximum       0.2544
                                   Minimum       0.2533


*** Table of predicted means for t1harv.t1geno ***

       t1geno     2-49   Puseas    Sunco    Vasco
       t1harv
        2.000    0.400    0.333    0.637    0.333
        3.000    1.400    1.333    1.200    1.267
        4.000    1.333    1.933    2.067    2.667

Standard error of differences:     Average       0.3889
                                   Maximum       0.3987
                                   Minimum       0.3671

Average variance of differences:                0.1513

Standard error of differences for same level of factor:

                 t1harv      t1geno
Average          0.3935      0.3682
Maximum          0.3987      0.3738
Minimum          0.3925      0.3671


 726
 727  subset [condition=(ntill.eq.2).and.(nharv.ne.2); setlevel=yes] nharv, ngeno, nrep,
nplot, nplant, ntill, npart, ndr, ntotal;\
 728     t2harv, t2geno, t2rep, t2plot, t2plant, t2till, t2part, t2dr, t2total
 729  vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot+t2plot.t2harv ; const=pos
 730  "vcomp [fixed=t2geno*t2harv] random=t2rep+t2plot.t2harv ; const=pos
-731  vstruct [t2plot.t2harv] factor=t2harv; model=ar"
 732  reml [print=means, wald, comp, mod] t2dr

732...............................................................................


***** REML Variance Components Analysis *****


Response Variate : t2dr
```

```
Fixed model      : Constant+t2harv+t2geno+t2harv.t2geno
Random model     : t2rep+t2plot+t2plot.t2harv

Number of units  : 100

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t2rep                   0.0005      0.0114
t2plot                  0.0000       BOUND
t2plot.t2harv                0.0000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            0.359    0.0536


*** Wald tests for fixed effects ***


   Fixed term              Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

   t2harv                     9.25           1         9.25       0.002
   t2geno                      0.87           3         0.29       0.832
   t2harv.t2geno                   0.75           3         0.25       0.861

* Dropping individual terms from full fixed model

   t2harv.t2geno                   0.75           3         0.25       0.861

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.
```

```
*** Table of predicted means for Constant ***

         0.2954    Standard error: 0.06195



*** Table of predicted means for t2harv ***

  t2harv    3.000    4.000
         0.1169   0.4738

Standard error of differences:      0.1212



*** Table of predicted means for t2geno ***

  t2geno     2-49   Puseas    Sunco    Vasco
         0.2500   0.4000   0.2716   0.2598

Standard error of differences:     Average       0.1713
                             Maximum      0.1805
                             Minimum      0.1620

Average variance of differences:             0.02939


*** Table of predicted means for t2harv.t2geno ***

      t2geno         2-49       Puseas        Sunco        Vasco
      t2harv
       3.000      -0.0004       0.3004       0.0765       0.0912
       4.000       0.5004       0.4997       0.4667       0.4285

Standard error of differences:     Average       0.2422
                             Maximum      0.2681
                             Minimum      0.2228

Average variance of differences:             0.05879

Standard error of differences for same level of factor:

              t2harv      t2geno
Average         0.2422      0.2419
Maximum         0.2620      0.2681
Minimum         0.2228      0.2272
```

```
Average variance of differences:
            0.05879     0.05879



 733
 734  "Tillers 3, 4 and 5 are  mainly all zeros, hence no analysis done"
 735
 736  "**** Infection - Total (Harvests 2, 3 & 4; leave out CPI1338 & Rep 3)****"
 737
 738  "### Analysing the tillers together ###"
 739
 740  subset
[condition=(Part.eq.11).and.(Harvest.ne.1).and.(Harvest.le.4).and.(Genotype.ne.2).and.(
Rep.le.2);\
 741   setlevel=yes]  Harvest, Genotype, Rep, plot, Plant, Tiller, Part, Disease_Rating,
Infection_total; \
 742   nharv, ngeno, nrep, nplot, nplant, ntill, npart, ndr, ntotal
 743
 744  vcomp [fixed=ngeno*nharv*ntill]
random=nrep+nplot+nplot.nharv+nplot.nharv.nplant; const=pos
 745  "vcomp [fixed=ngeno*nharv*ntill] random=nrep+nplot.nharv+nplot.nharv.nplant;
const=pos
-746  vstruct [nplot.nharv] factor=nharv; model=ar"
 747  reml [print=means, wald, comp, mod] sqrt(ntotal)

747..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(ntotal)

Fixed model      : Constant+nharv+ngeno+ntill+nharv.ngeno+nharv.ntill+ngeno.ntil
l+nharv.ngeno.ntill
Random model     : nrep+nplot+nplot.nharv+nplot.nharv.nplant

Number of units  : 258 (1 units excluded due to zero weights or missing values)

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***
```

```
Random term              Component       S.e.

nrep                   0.0396      0.0750
nplot                  0.0221      0.0429
nplot.nharv               0.0000       BOUND
nplot.nharv.nplant          0.1303      0.0781


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                     Identity      Sigma2            0.550    0.0771


*** Wald tests for fixed effects ***


  Fixed term             Wald statistic      d.f.    Wald/d.f.    Chi-sq prob

* Sequentially adding terms to fixed model

  nharv                     11.24           2         5.62       0.004
  ngeno                       1.78           3        0.59       0.619
  ntill                   63.05           4        15.76      <0.001
  nharv.ngeno                  11.13           6         1.86       0.084
  nharv.ntill                 2.94           5         0.59       0.709
  ngeno.ntill                  2.41           9         0.27       0.983
  nharv.ngeno.ntill            11.03           9         1.23       0.274

* Dropping individual terms from full fixed model

  nharv.ngeno.ntill            11.03           9         1.23       0.274

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

         0.2320    Standard error: 0.20376



*** Table of predicted means for nharv ***
```

```
      nharv       2.000       3.000       4.000
                      *           *           *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ngeno ***

      ngeno        2-49      Puseas       Sunco       Vasco
                      *           *           *           *

* All values in table missing: due to missing factor combinations in higher
  order interactions


*** Table of predicted means for ntill ***

   ntill        1        2        3        4        5
         0.9246        *        *        *        *

* SEDs not available


*** Table of predicted means for nharv.ngeno ***

       ngeno    2-49  Puseas   Sunco   Vasco
       nharv
       2.000       *       *       *       *
       3.000  0.1772       *       *       *
       4.000  0.1139       *       *       *

Standard error of differences:       0.2900



*** Table of predicted means for nharv.ntill ***

       ntill            1            2            3            4            5
       nharv
       2.000       0.9314            *            *            *            *
       3.000       0.7721       0.0534       0.0838            *            *
       4.000       1.0702       0.2225      -0.0215       0.0840            *

Standard error of differences:      Average        0.2438
                                    Maximum        0.3676
```

```
                              Minimum      0.1780

Average variance of differences:             0.06233

Standard error of differences for same level of factor:

               nharv      ntill
Average         0.2446     0.2112
Maximum         0.3117     0.2927
Minimum         0.1780     0.1845
Average variance of differences:
              0.06247    0.04633



*** Table of predicted means for ngeno.ntill ***

      ntill       1       2       3       4       5
      ngeno
       2-49   0.8077       *       *       *       *
     Puseas   0.9500       *       *       *       *
      Sunco   0.8911   0.2024       *       *       *
      Vasco   1.0495   0.1029       *       *       *

Standard error of differences:     Average      0.3247
                              Maximum      0.4505
                              Minimum      0.2599

Average variance of differences:             0.1089

Standard error of differences for same level of factor:

               ngeno      ntill
Average         0.3238     0.2878
Maximum         0.3244     0.4505
Minimum         0.3231     0.2599
Average variance of differences:
              0.1048    0.08724



*** Table of predicted means for nharv.ngeno.ntill ***

              ntill          1          2          3          4
      nharv       ngeno
      2.000        2-49     0.7914          *          *          *
```

```
          Puseas     0.6882        *          *          *
           Sunco     1.3491     0.4204        *          *
           Vasco     0.8968    -0.0613        *          *
 3.000      2-49      0.9899     0.0540     0.0540     0.0144
          Puseas     1.3511     0.0850     0.2639        *
           Sunco     0.2000     0.0137     0.0538     0.1537
           Vasco     0.5474     0.0611    -0.0365     0.1881
 4.000      2-49      0.6418    -0.0452    -0.0593    -0.0160
          Puseas     0.8106     0.4530    -0.0584     0.1953
           Sunco     1.1243     0.1732    -0.0703     0.1481
           Vasco     1.7042     0.3090     0.1019     0.0086


           ntill          5
 nharv      ngeno
 2.000      2-49          *
          Puseas          *
           Sunco          *
           Vasco          *
 3.000      2-49     -0.2264
          Puseas          *
           Sunco          *
           Vasco          *
 4.000      2-49      0.0481
          Puseas          *
           Sunco          *
           Vasco          *

Standard error of differences:     Average       0.5996
                                   Maximum       1.160
                                   Minimum      0.3316

Average variance of differences:                 0.4072

Standard error of differences for same level of factor:

                nharv       ngeno       ntill
Average        0.5851      0.5733      0.5497
Maximum         1.160       1.136       1.160
Minimum        0.3316      0.3316      0.3689
Average variance of differences:
               0.3852      0.3764      0.3506


 748
 749  "### Analysing the tillers separately ###"
```

```
 750
 751  subset [condition=ntill.eq.1; setlevel=yes] nharv, ngeno, nrep, nplot, nplant, ntill,
npart, ndr, ntotal;\
 752      t1harv, t1geno, t1rep, t1plot, t1plant, t1till, t1part, t1dr, t1total
 753  vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot+t1plot.t1harv ; const=pos
 754  "vcomp [fixed=t1geno*t1harv] random=t1rep+t1plot.t1harv ; const=pos
-755  vstruct [t1plot.t1harv] factor=t1harv; model=ar"
 756  reml [print=means, wald, comp, mod] sqrt(t1total)

756..............................................................................


***** REML Variance Components Analysis *****


Response Variate : SQRT(t1total)

Fixed model      : Constant+t1harv+t1geno+t1harv.t1geno
Random model     : t1rep+t1plot+t1plot.t1harv

Number of units  : 119

* Residual term has been added to model

* Sparse algorithm with AI optimisation


*** Estimated Variance Components ***

Random term              Component       S.e.

t1rep                  0.147       0.252
t1plot                 0.041       0.100
t1plot.t1harv              0.000       BOUND


*** Residual variance model ***

Term            Factor       Model(order)  Parameter       Estimate      S.e.

Residual                    Identity      Sigma2            1.207     0.168


*** Wald tests for fixed effects ***
```

```
  Fixed term            Wald statistic    d.f.   Wald/d.f.   Chi-sq prob

* Sequentially adding terms to fixed model

  t1harv                    1.47          2        0.74       0.479
  t1geno                    0.54          3        0.18       0.910
  t1harv.t1geno            12.79          6        2.13       0.046

* Dropping individual terms from full fixed model

  t1harv.t1geno            12.79          6        2.13       0.046

* Message: chi-square distribution for Wald tests is an asymptotic approximation
  (i.e. for large samples) and underestimates the probabilities in other cases.


*** Table of predicted means for Constant ***

        0.9233   Standard error: 0.29771



*** Table of predicted means for t1harv ***

 t1harv    2.000    3.000    4.000
          0.9277   0.7721   1.0702

Standard error of differences:     Average       0.2468
                                   Maximum       0.2474
                                   Minimum       0.2456


*** Table of predicted means for t1geno ***

 t1geno     2-49   Puseas    Sunco    Vasco
          0.8077   0.9500   0.8862   1.0495

Standard error of differences:     Average       0.3493
                                   Maximum       0.3504
                                   Minimum       0.3482


*** Table of predicted means for t1harv.t1geno ***

     t1geno     2-49   Puseas    Sunco    Vasco
     t1harv
```

```
         2.000   0.7914   0.6882   1.3345   0.8968
         3.000   0.9899   1.3511   0.2000   0.5474
         4.000   0.6418   0.8106   1.1243   1.7042

Standard error of differences:     Average       0.5260
                                   Maximum       0.5438
                                   Minimum       0.4912

Average variance of differences:                 0.2770

Standard error of differences for same level of factor:

                 t1harv      t1geno
Average          0.5333      0.4935
Maximum          0.5438      0.5049
Minimum          0.5311      0.4912
Average variance of differences:
                 0.2844      0.2436


 757
 758  "Tillers 2, 3, 4 and 5 are  mainly all zeros, hence no analysis done"
 759
```

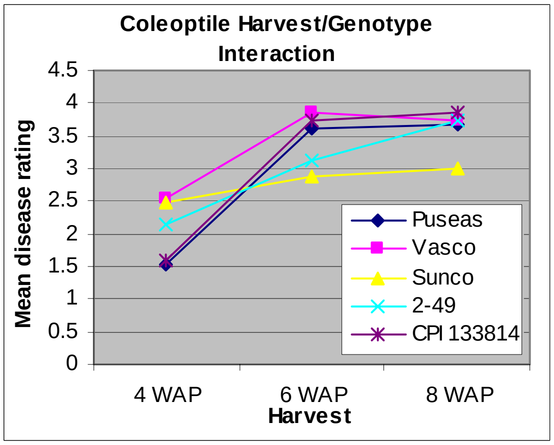
Appendix 3E

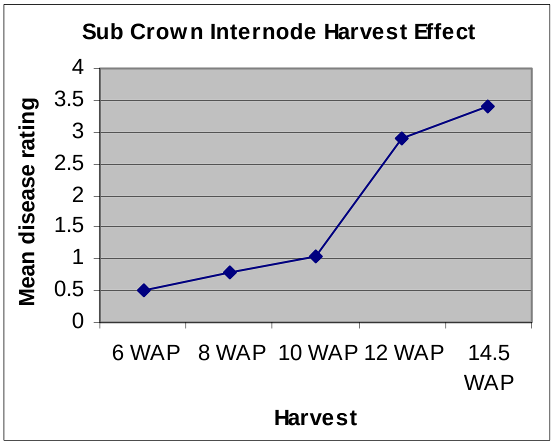
Charts of significant effects and interactions from field trials

(NB: The lines in these charts are for illustration purposes only and do not represent in between measurements).

Figure 3E.1 Mean disease rating line charts of significant effects and interactions from analysis of the coleoptile and sub-crown internode.

Jondaryan Field Trial (2000)





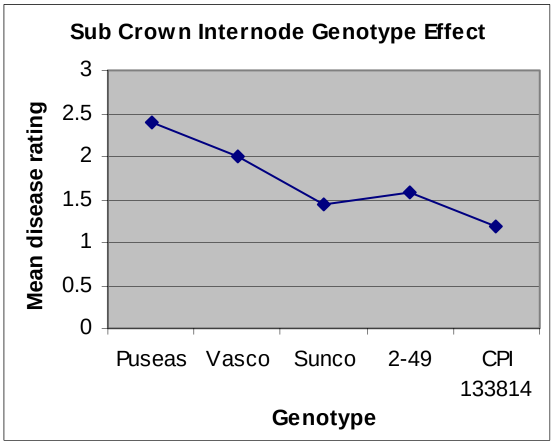
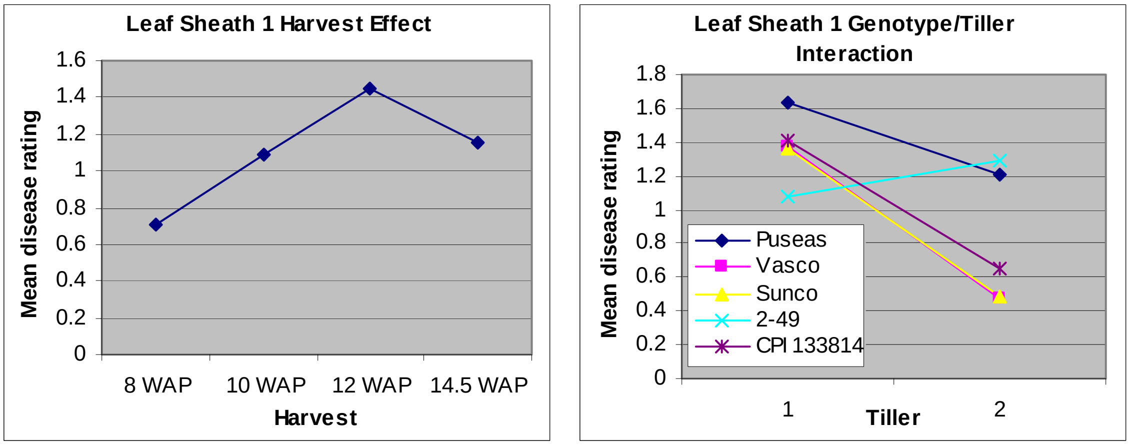


Figure 3E.2 Mean disease rating line charts of significant effects and interactions from analysis of Leaf Sheath 1.

Jondaryan Field Trial (2000)



Wellcamp Field Trial (2001)

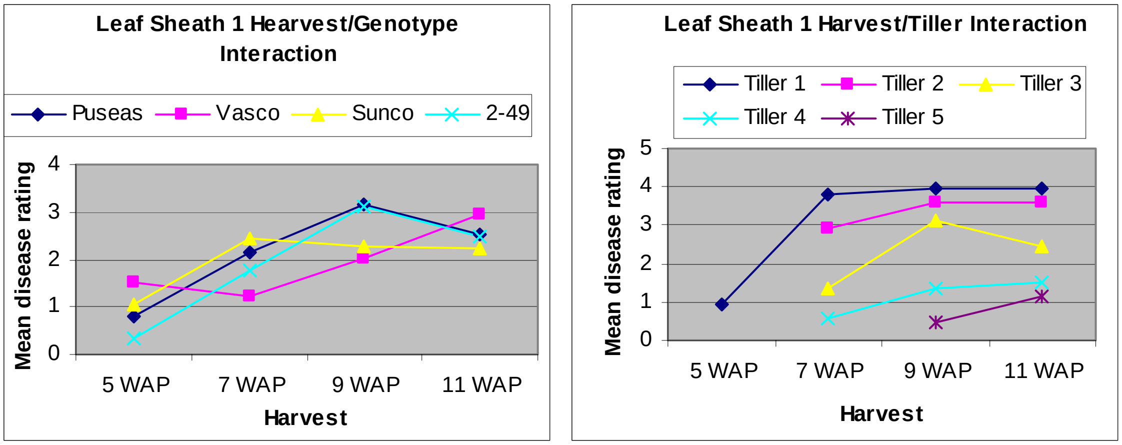
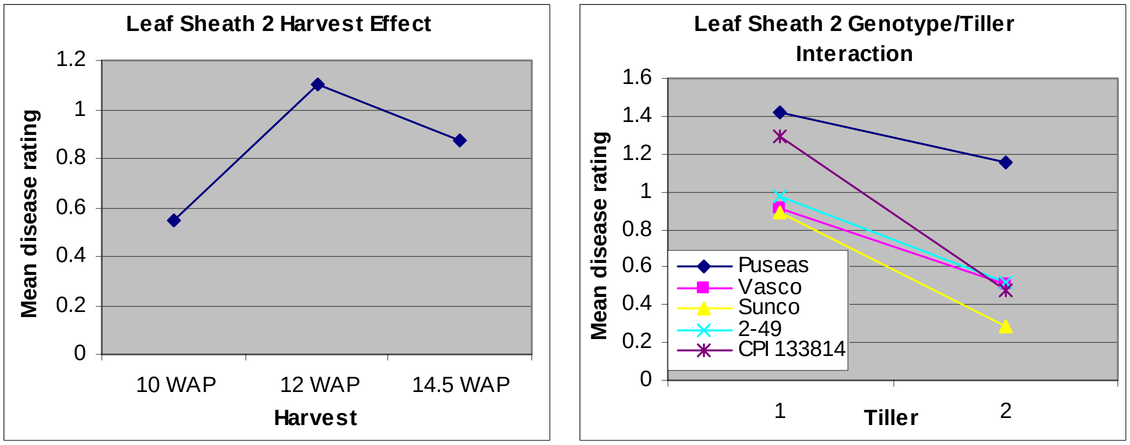


Figure 3E.3 Mean disease rating line charts of significant effects and interactions from analysis of Leaf Sheath 2.

Jondaryan Field Trial (2000)



Wellcamp Field Trial (2001)

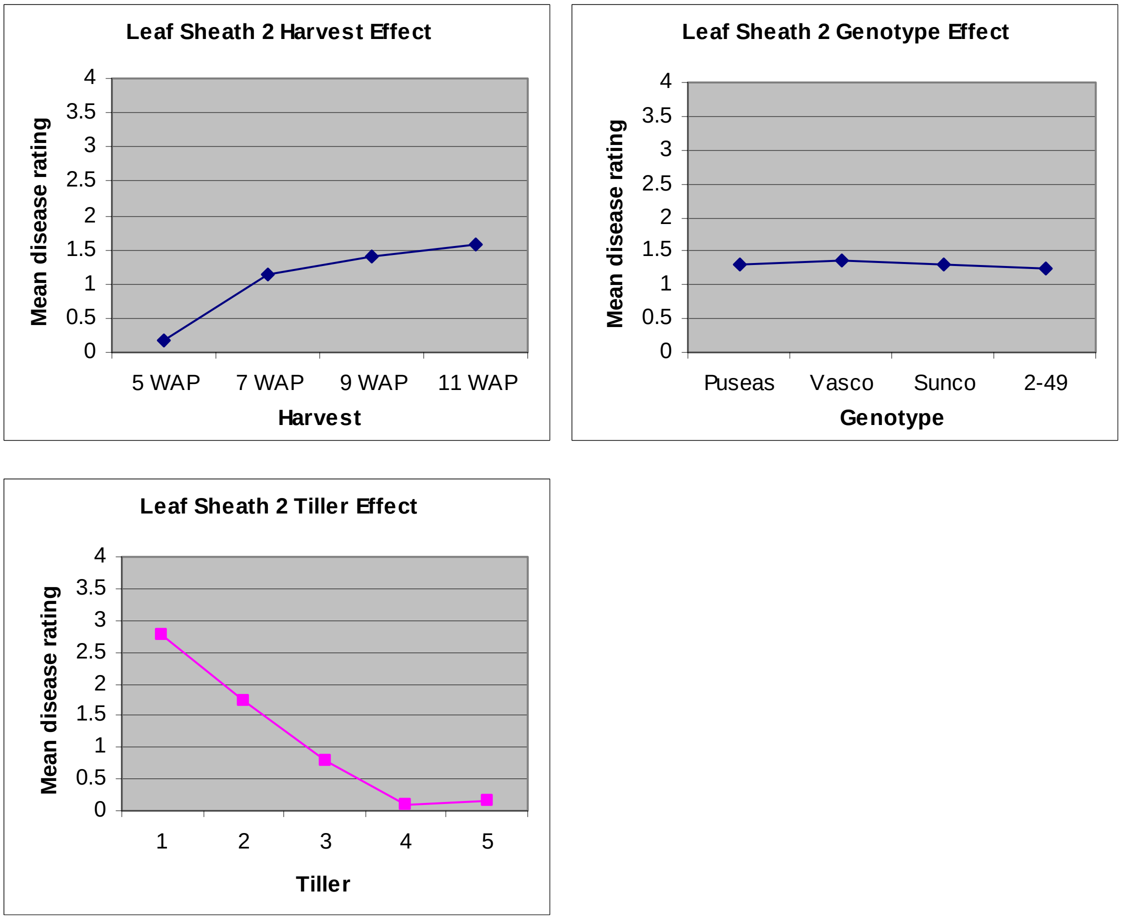
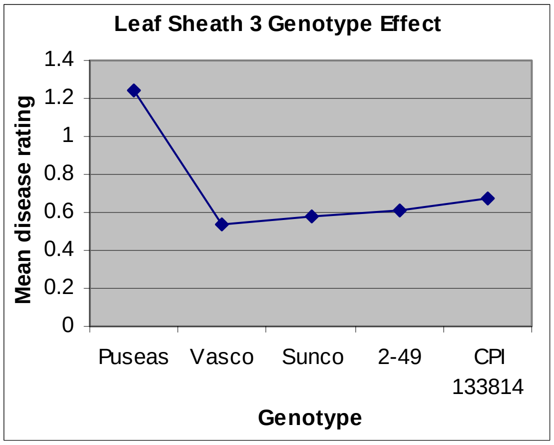
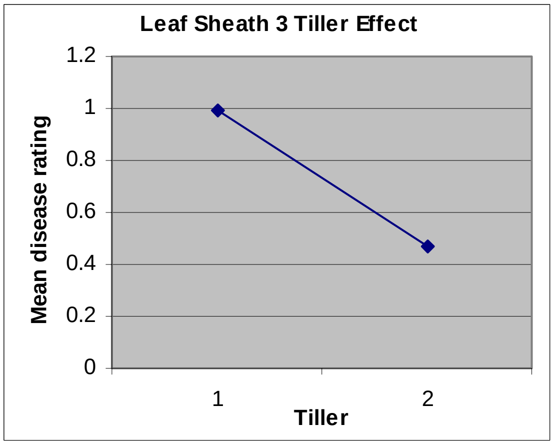


Figure 3E.4 Mean disease rating line charts of significant effects and interactions from analysis of Leaf Sheath 3.

Jondaryan Field Trial (2000)





Wellcamp Field Trial (2001)

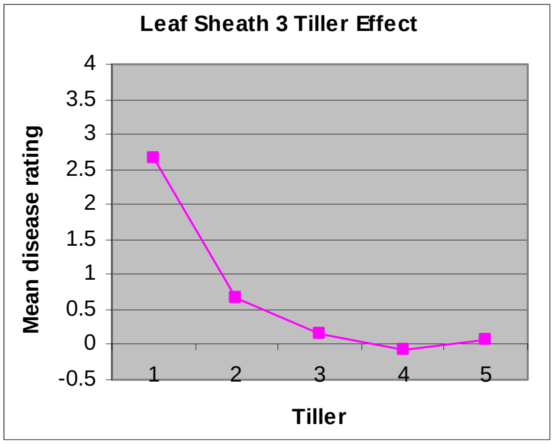
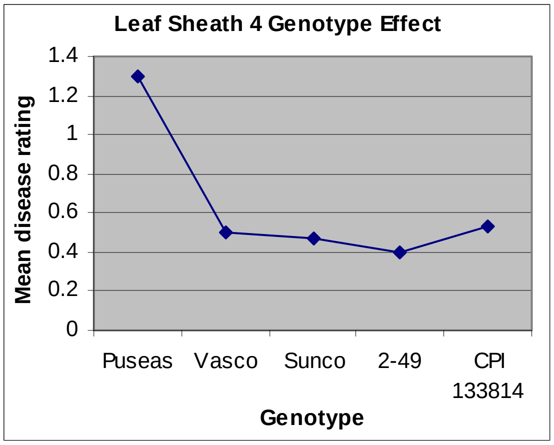
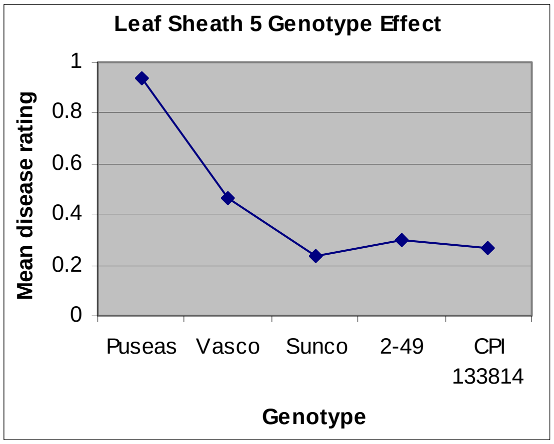


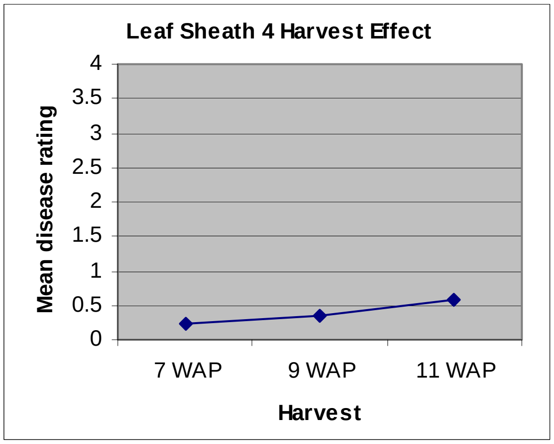
Figure 3E.5 Mean disease rating line charts of significant effects and interactions from analysis of Leaf Sheath 4 (both trials) and 5 (Jondaryan trial only).

Jondaryan Field Trial (2000)





Wellcamp Field Trial (2001)



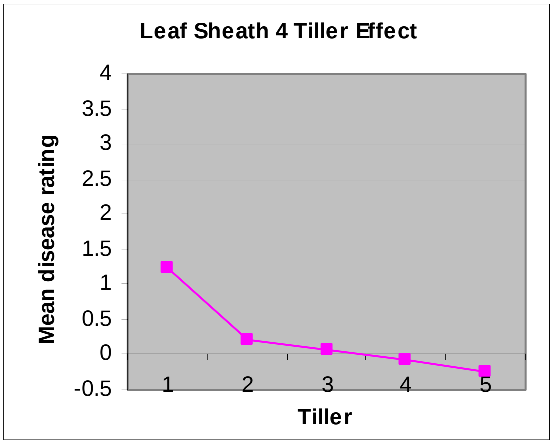
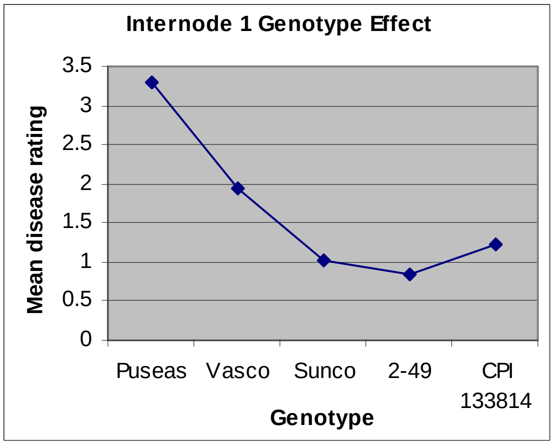
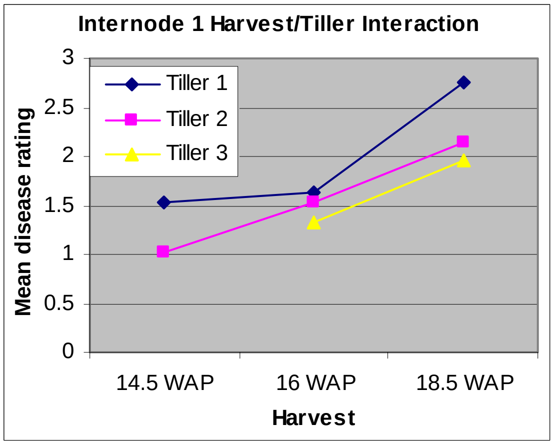


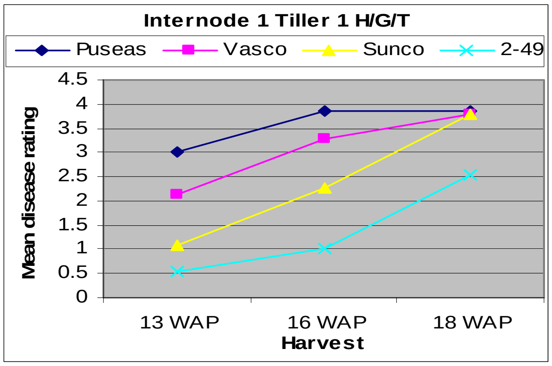
Figure 3E.6 Mean disease rating line charts of significant effects and interactions from analysis of internode 1.

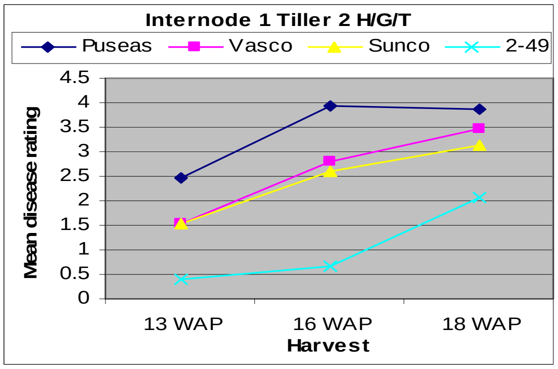
Jondaryan Field Trial (2000)

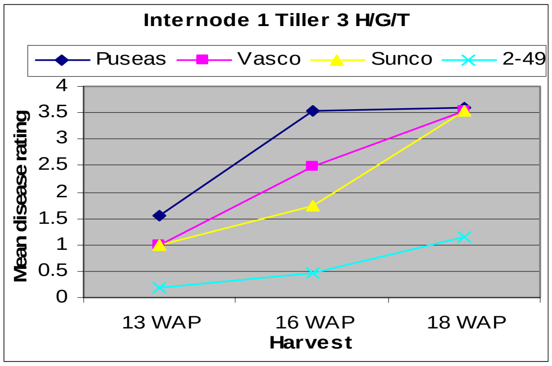


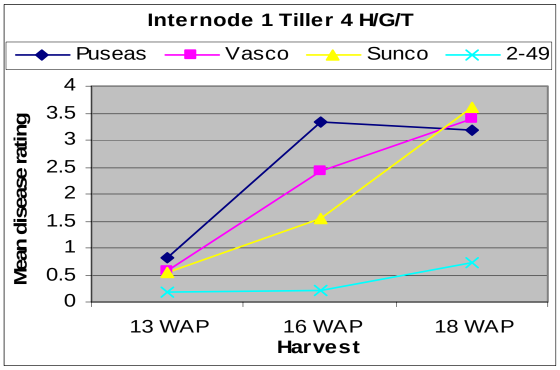


Wellcamp Field Trial (2001) (harvest/genotype/tiller-data presented for each tiller)









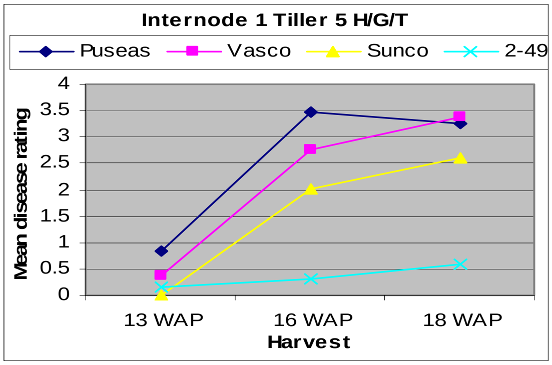


Figure 3E.7 Mean disease rating charts of Internode 1 Wellcamp harvest/genotype/tiller interaction. Data presented for each genotype.

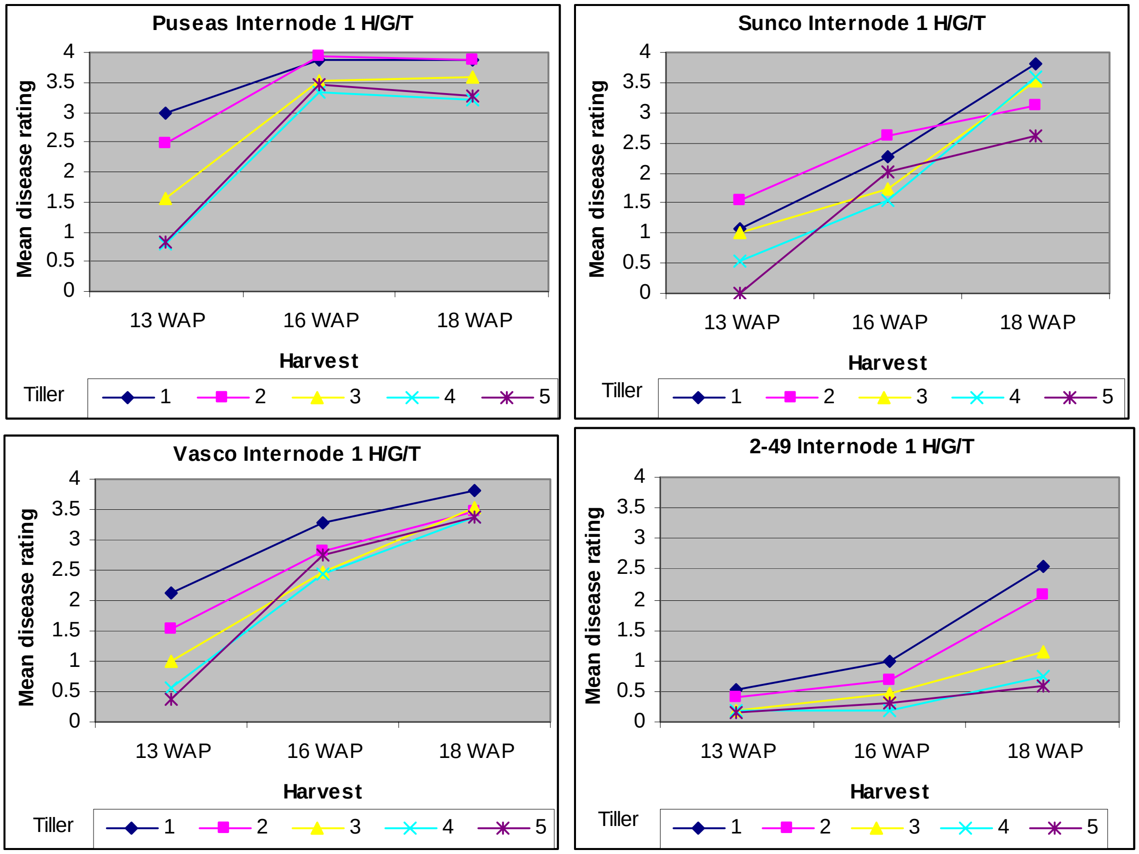


Figure 3E.8 Mean disease rating line charts of harest/genotype/tiller interaction from analysis of internode 2 from Wellcamp trial. Data presented for each tiller

Wellcamp Field Trial (2001)

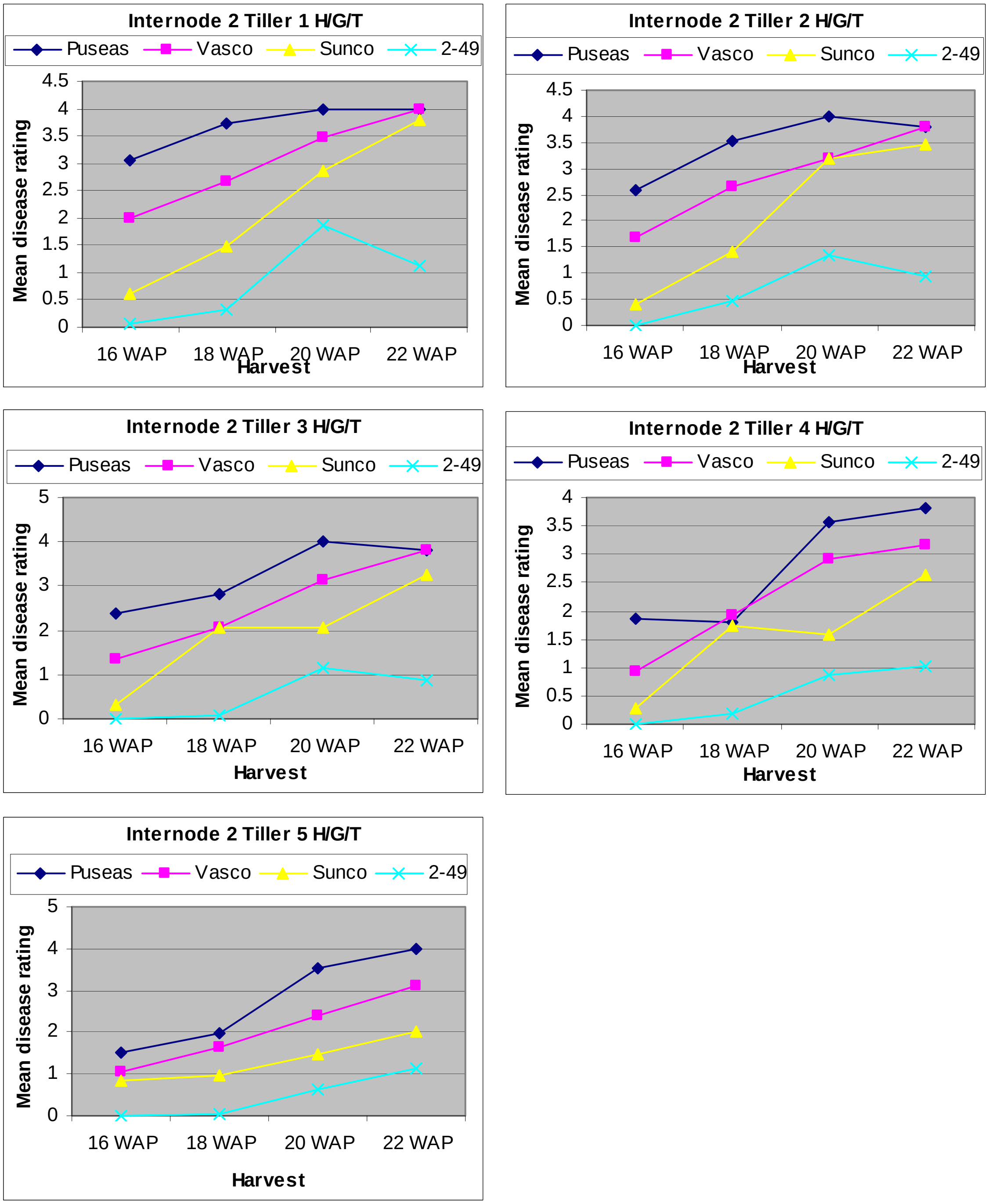


Figure 3E.9 Mean disease rating line charts of Internode 2 Wellcamp harvest/genotype/tiller interaction. Data presented for each genotype.

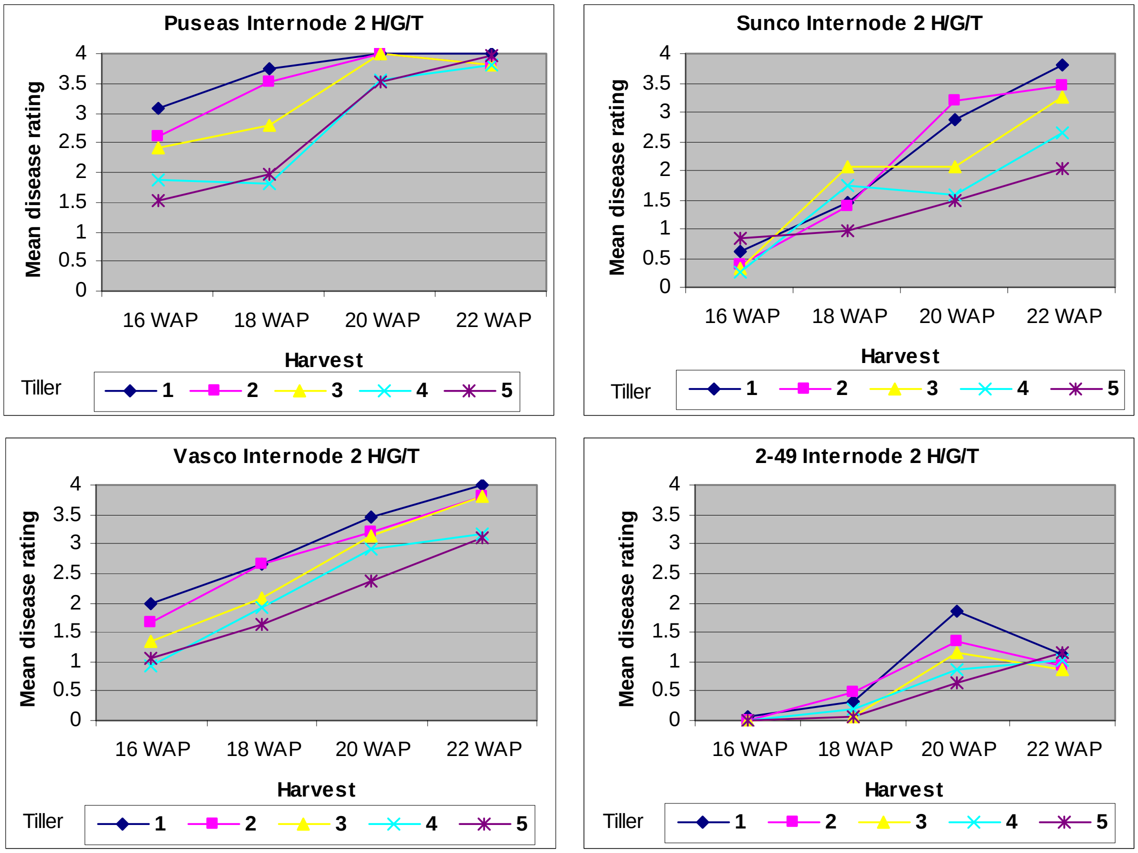


Figure 3E.10 Mean disease rating line charts of harvest/genotype/tiller interaction from analysis of internode 3 from Wellcamp trial. Data presented for each Tiller.

Wellcamp Field Trial (2001)

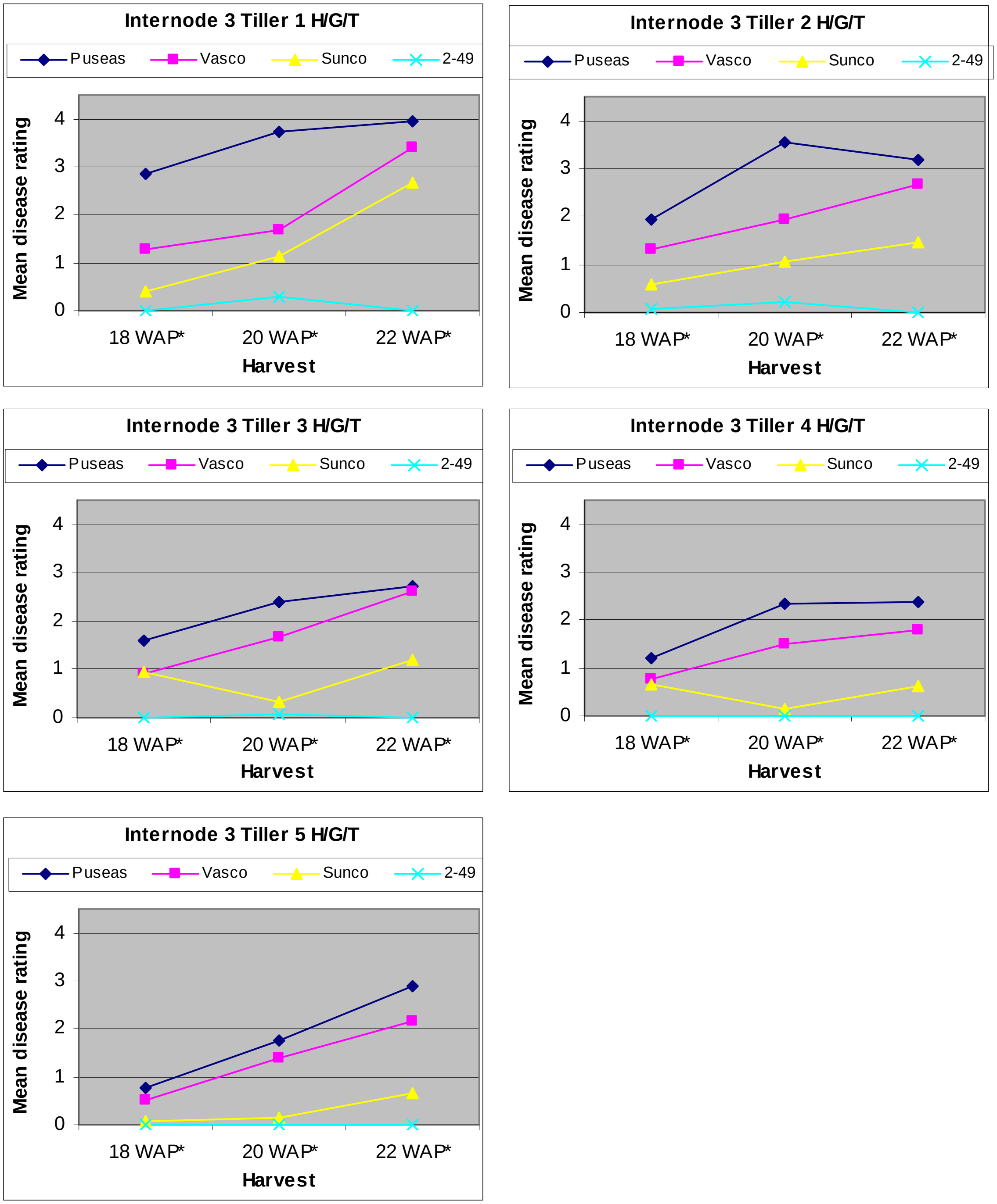


Figure 3E.11 Mean disease rating line charts of harvest/genotype/tiller interaction from analysis of internode 3 in the Wellcamp trial. Data presented for each genotype

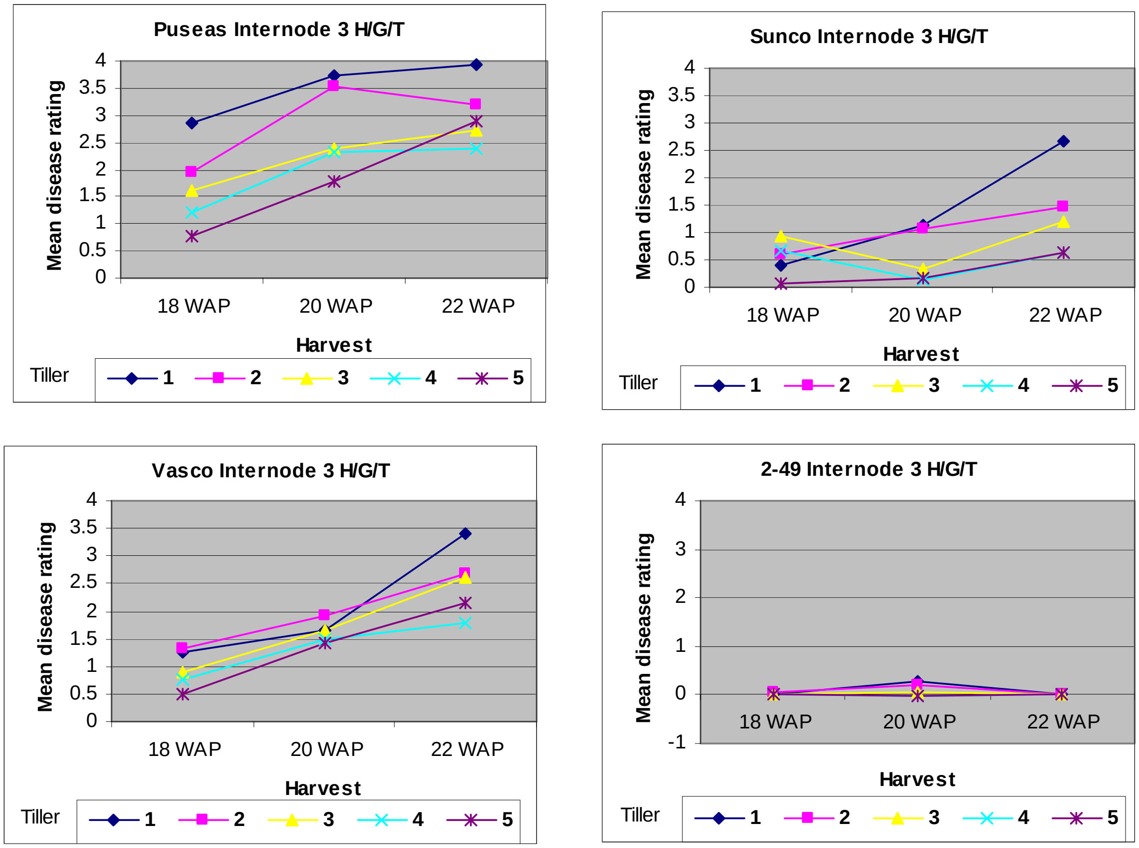
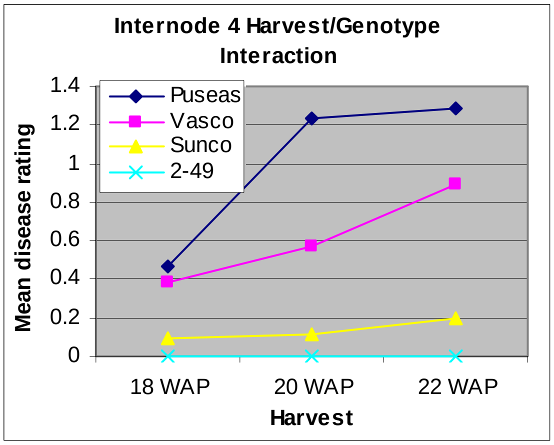
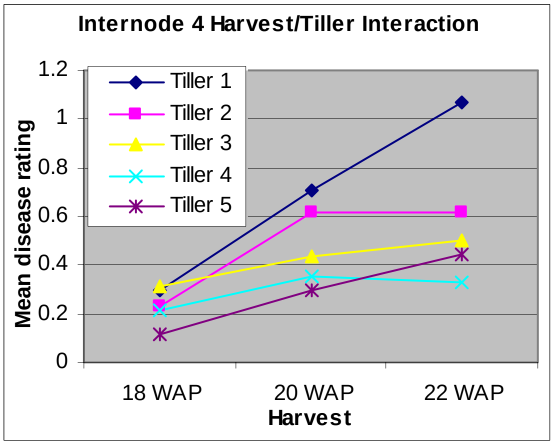


Figure 3E.12 Mean disease rating line charts of significant effects and interactions from analysis of internode 4.

Wellcamp Field Trial (2001)





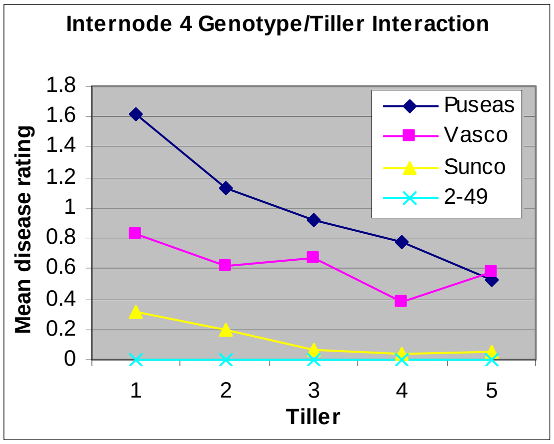
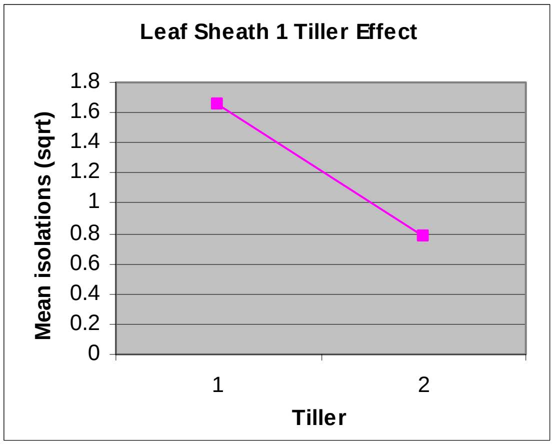
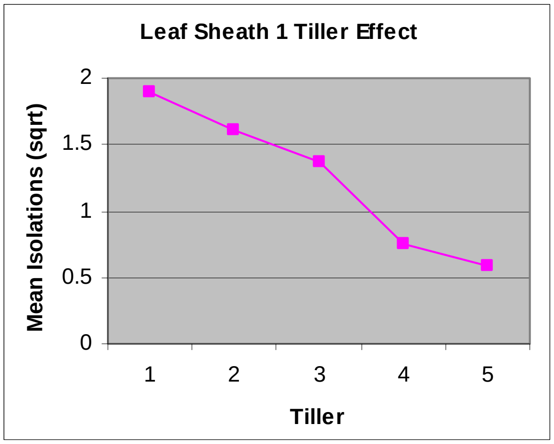


Figure 3E.13 Mean isolation (sqrt of infection counts) line charts of significant effects and interactions from analysis of Leaf Sheath 1.

Jondaryan Field Trial (2000)



Wellcamp Field Trial (2001)



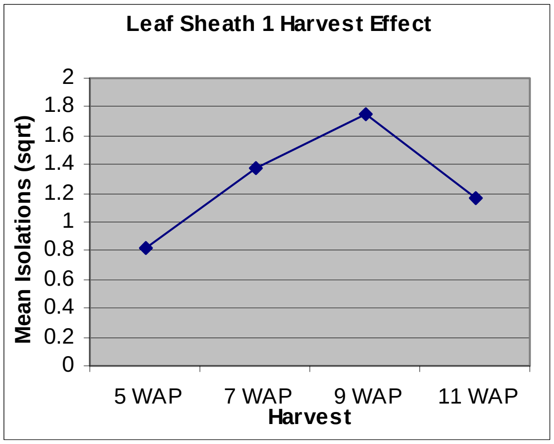
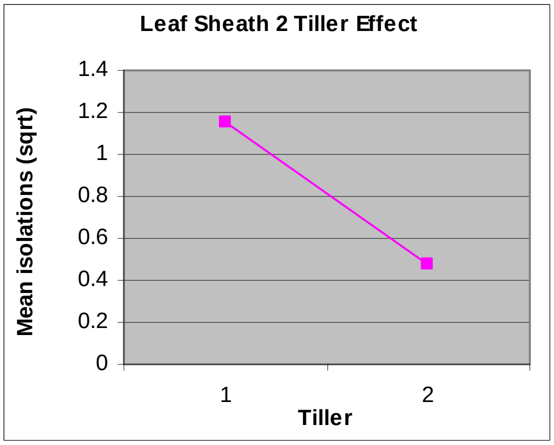
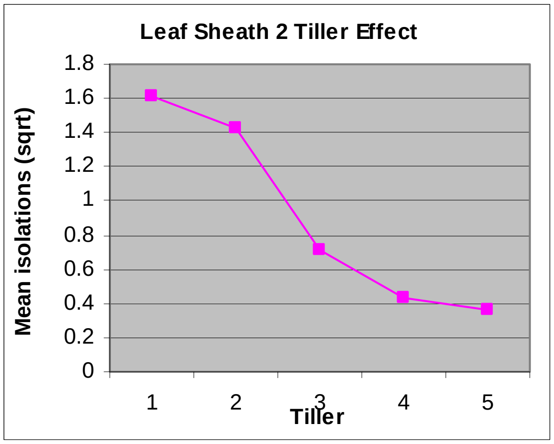


Figure 3E.14 Mean isolation (sqrt of infection counts) line charts of significant effects and interactions from analysis of Leaf Sheath 2.

Jondaryan Field Trial (2000)



Wellcamp Field Trial (2001)



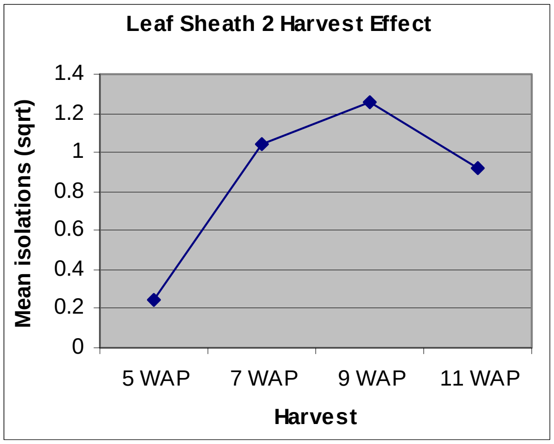
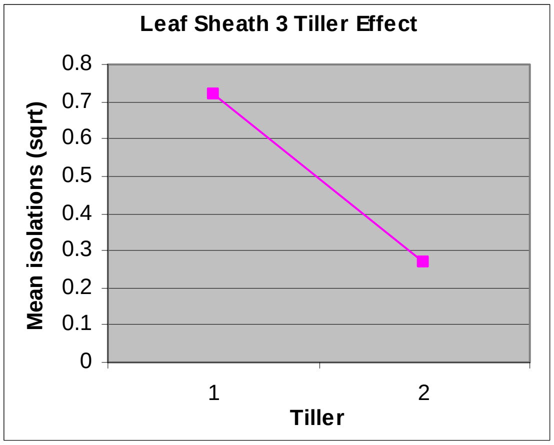
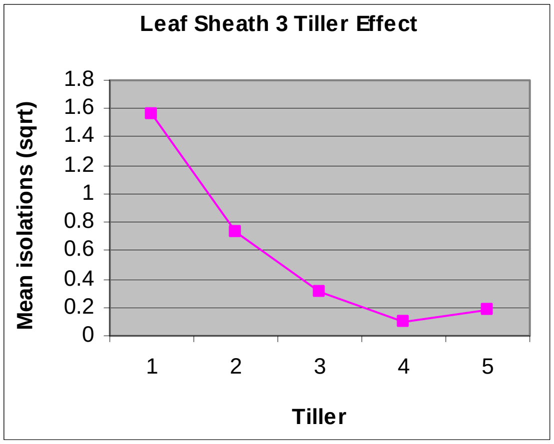


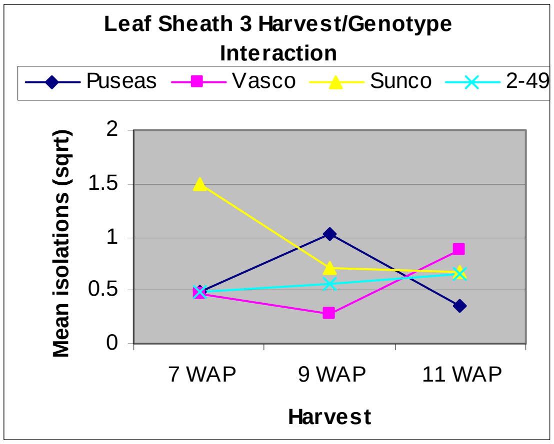
Figure 3E.15 Mean isolation (sqrt of infection counts) line charts of significant effects and interactions from analysis of Leaf Sheath 3 and 4 (Wellcamp only).

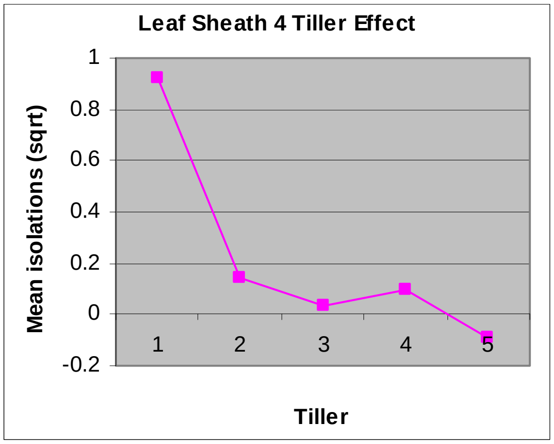
Jondaryan Field Trial (2000)

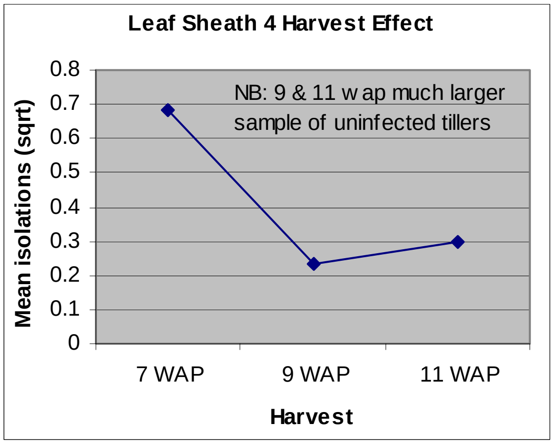


Wellcamp Field Trial (2001)





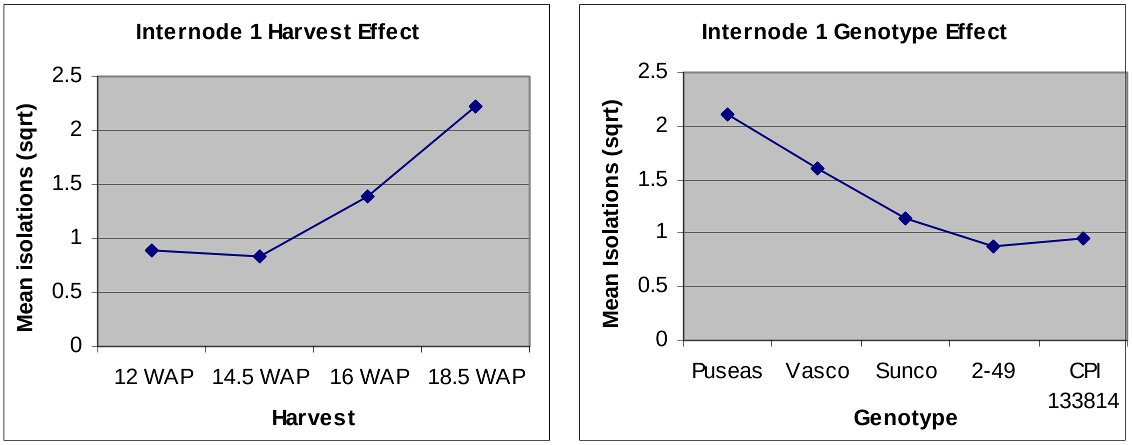




NB: 9 & 11 w ap much larger sample of uninfected tillers

Figure 3E.16 Mean isolation (sqrt of infection counts) line charts of significant effects and interactions from analysis of Internode 1.

Jondaryan Field Trial (2000)



Wellcamp Field Trial (2001)

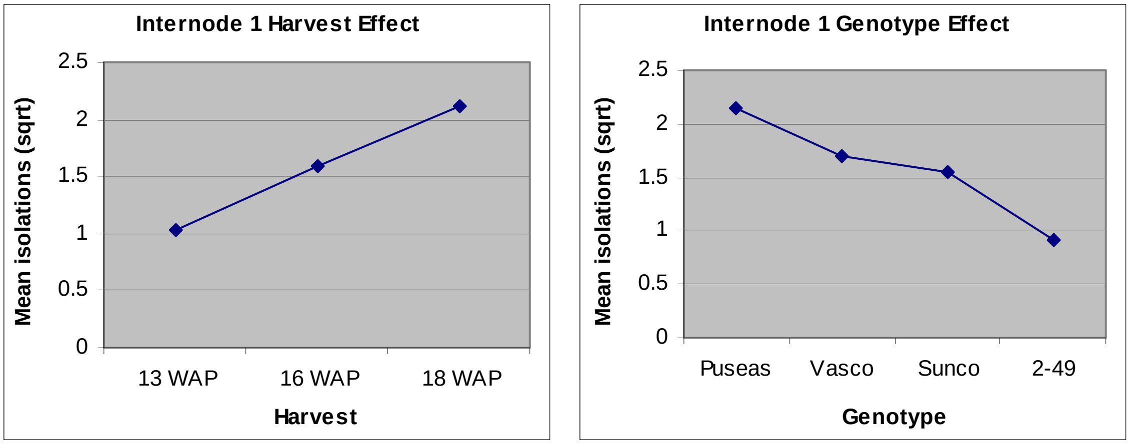
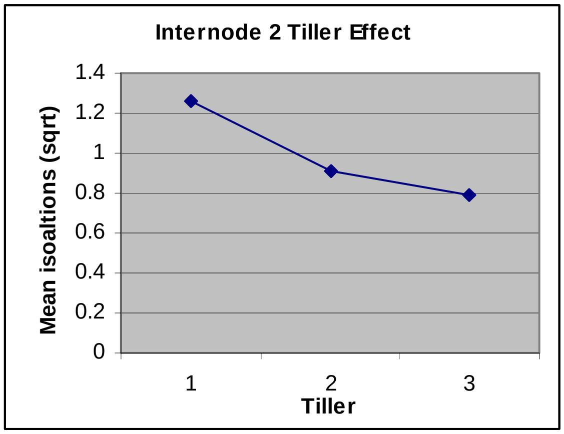
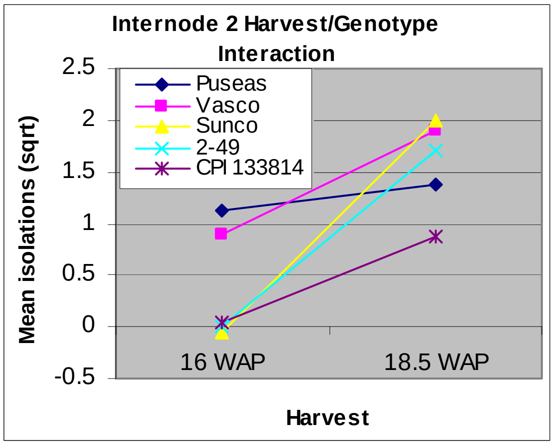


Figure 3E.17 Mean isolation (sqrt of infection counts) line charts of significant effects and interactions from analysis of Internode 2.

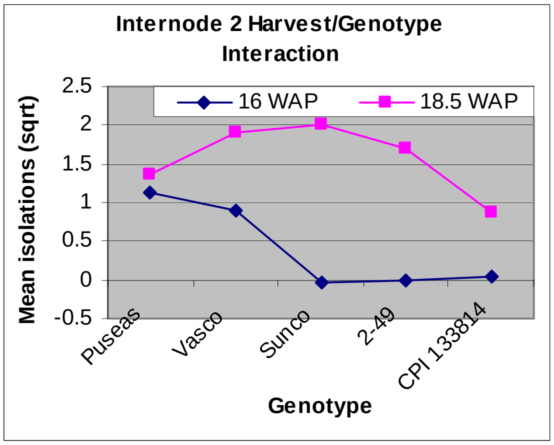
Jondaryan Field Trial (2000)



Internode 2 Tiller Effect



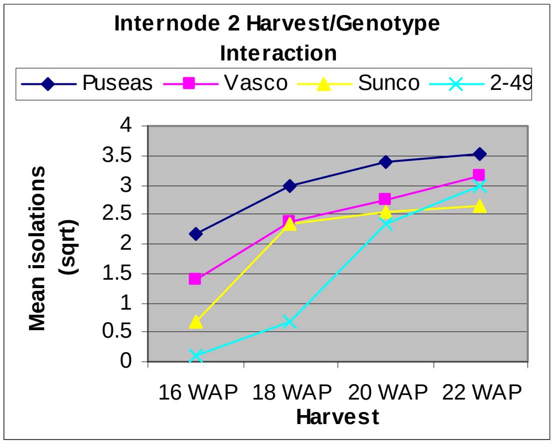
Internode 2 Harvest/Genotype Interaction



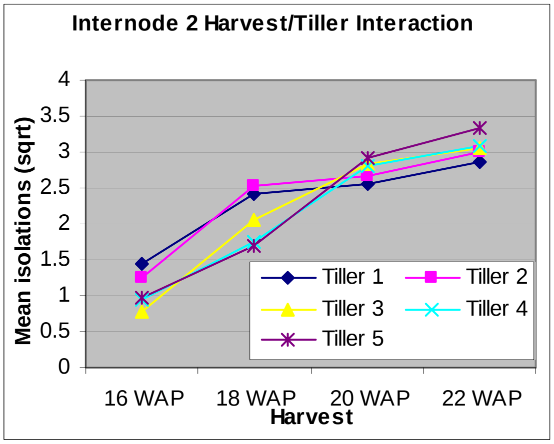
Internode 2 Harvest/Genotype Interaction

NB: Values in the above two charts are the same but presented in a different way.

Wellcamp Field Trial (2001)



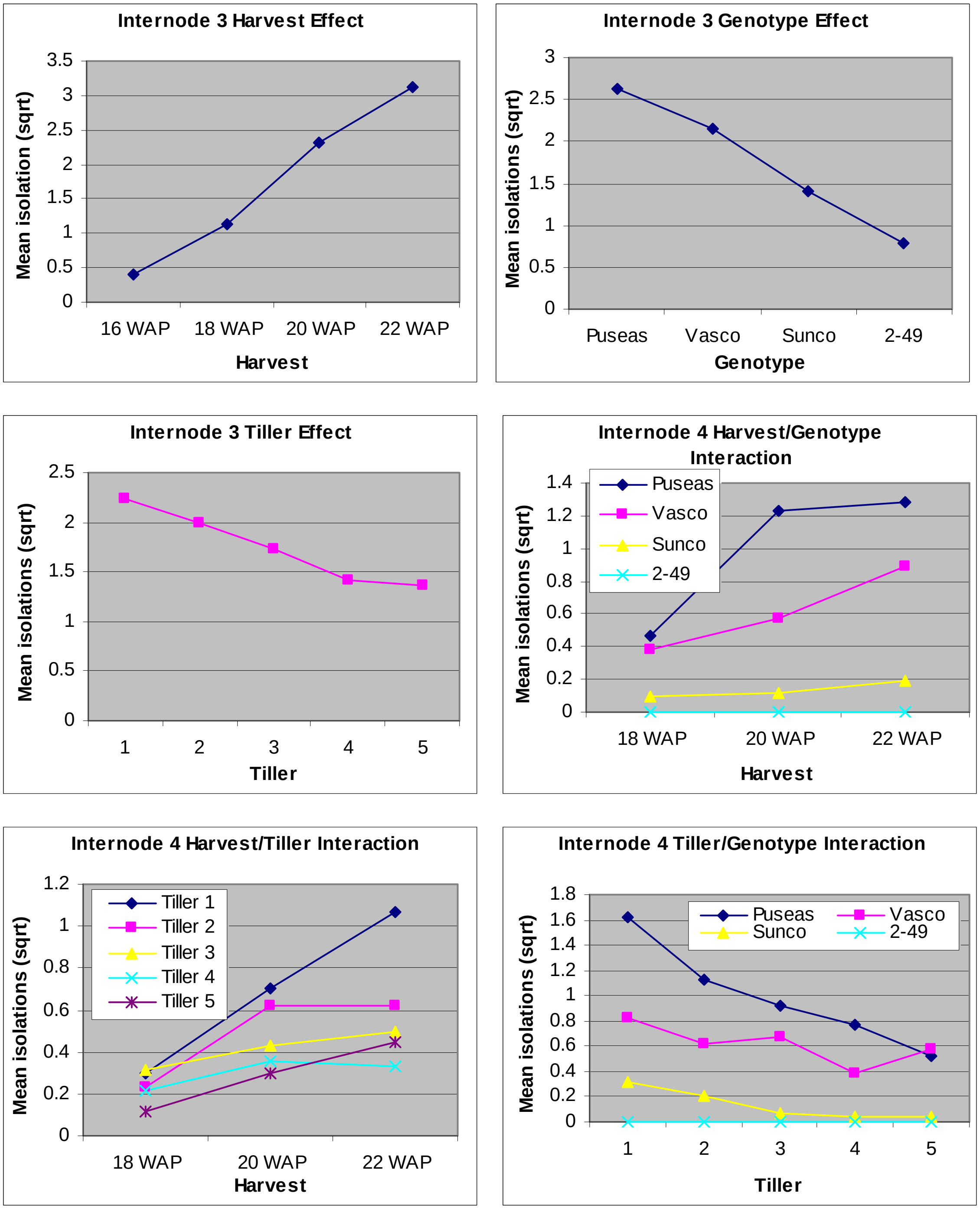
Internode 2 Harvest/Genotype Interaction



Internode 2 Harvest/Tiller Interaction

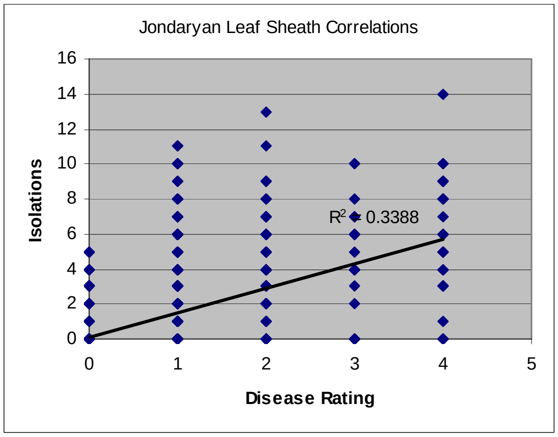
Figure 3E.18 Mean isolation (sqrt of infection counts) line charts of significant effects and interactions from analysis of Internode 3 and Internode 4 (Wellcamp trial only).

Wellcamp Field Trial (2001)



Appendix 3F
Isolation and disease rating data correlations

Figure 3F.1 Jondaryan Field Trial Correlation by plant tissue



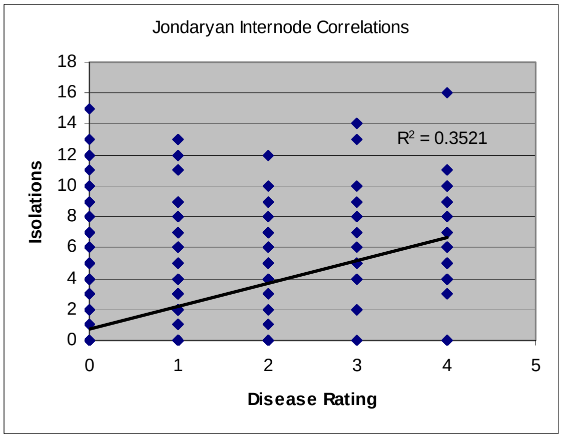
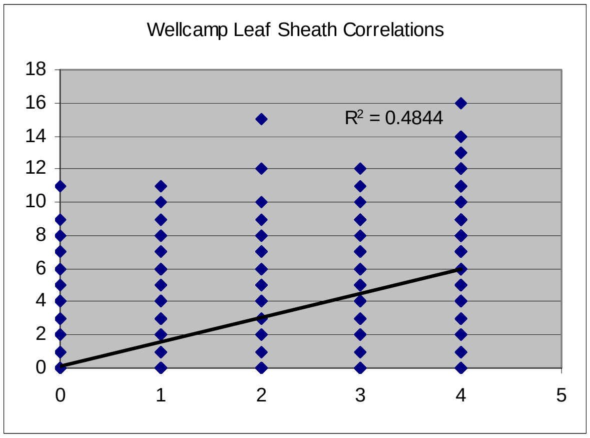


Figure 3F.2 Wellcamp Field Trial Correlation by plant tissue



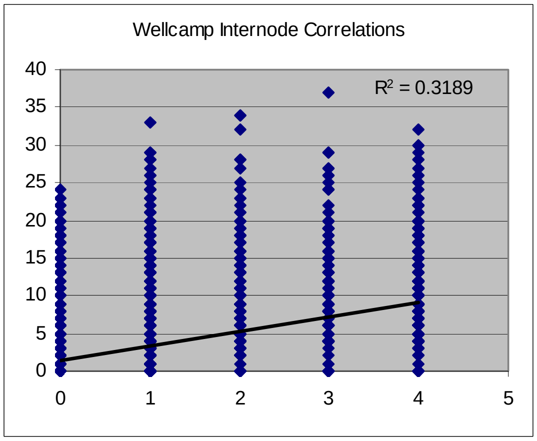


Figure 3F.3 Jondaryan Field Trial Correlations by Harvest

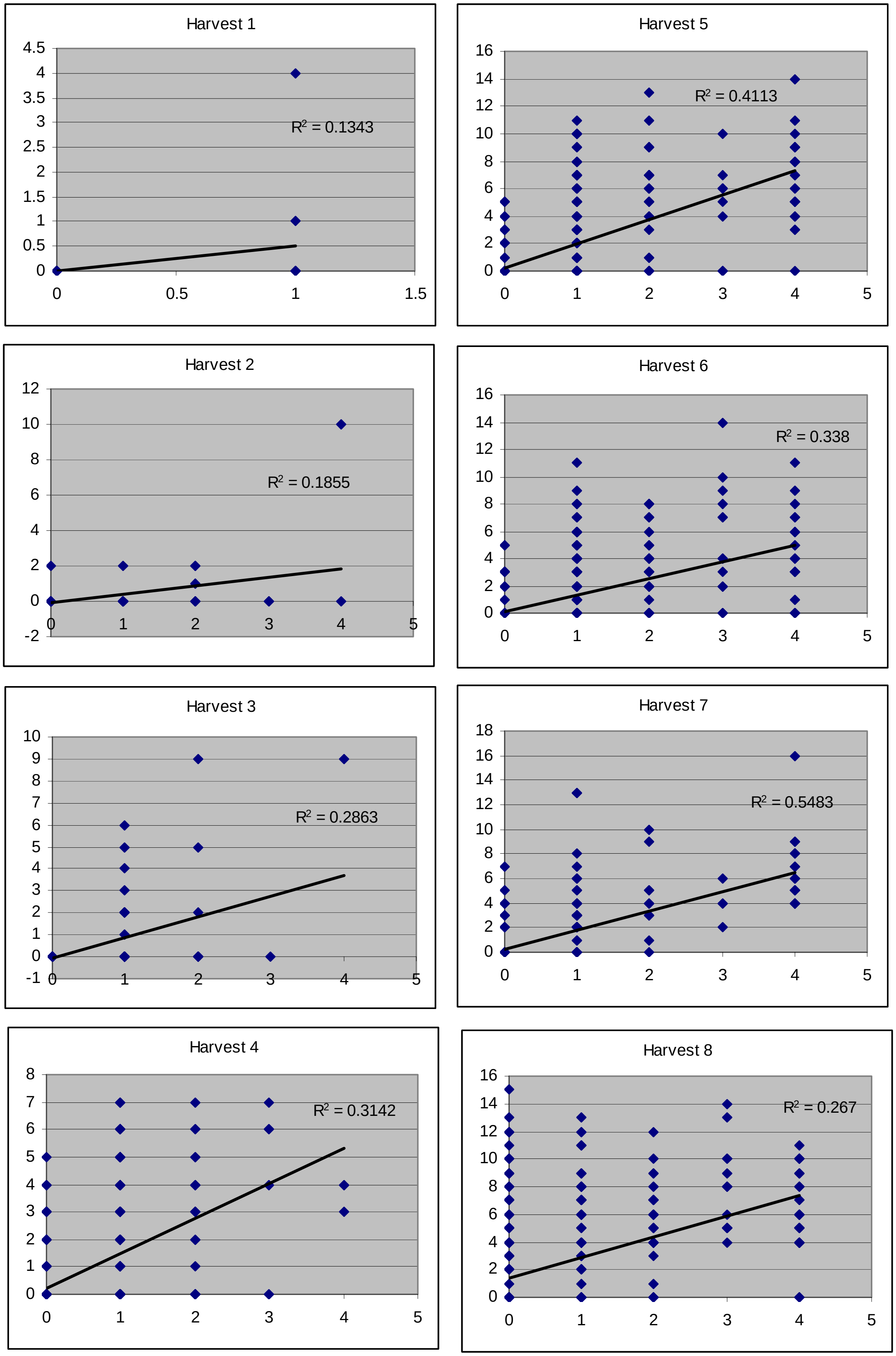


Figure 3F.4 Jondaryan Field Trial Correlation by Genotype

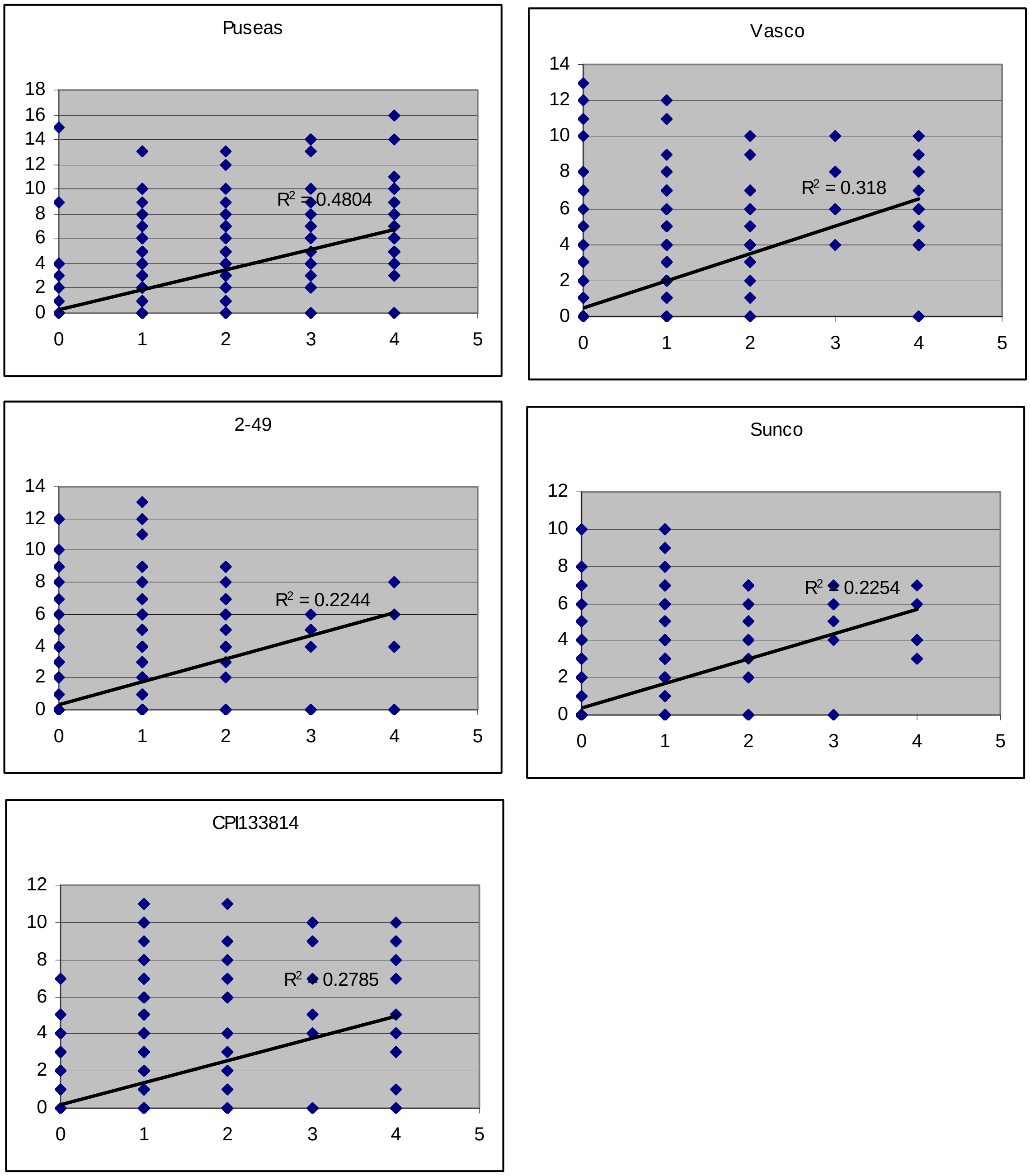


Figure 3F.5 Wellcamp Field Trial Correlations by Harvest

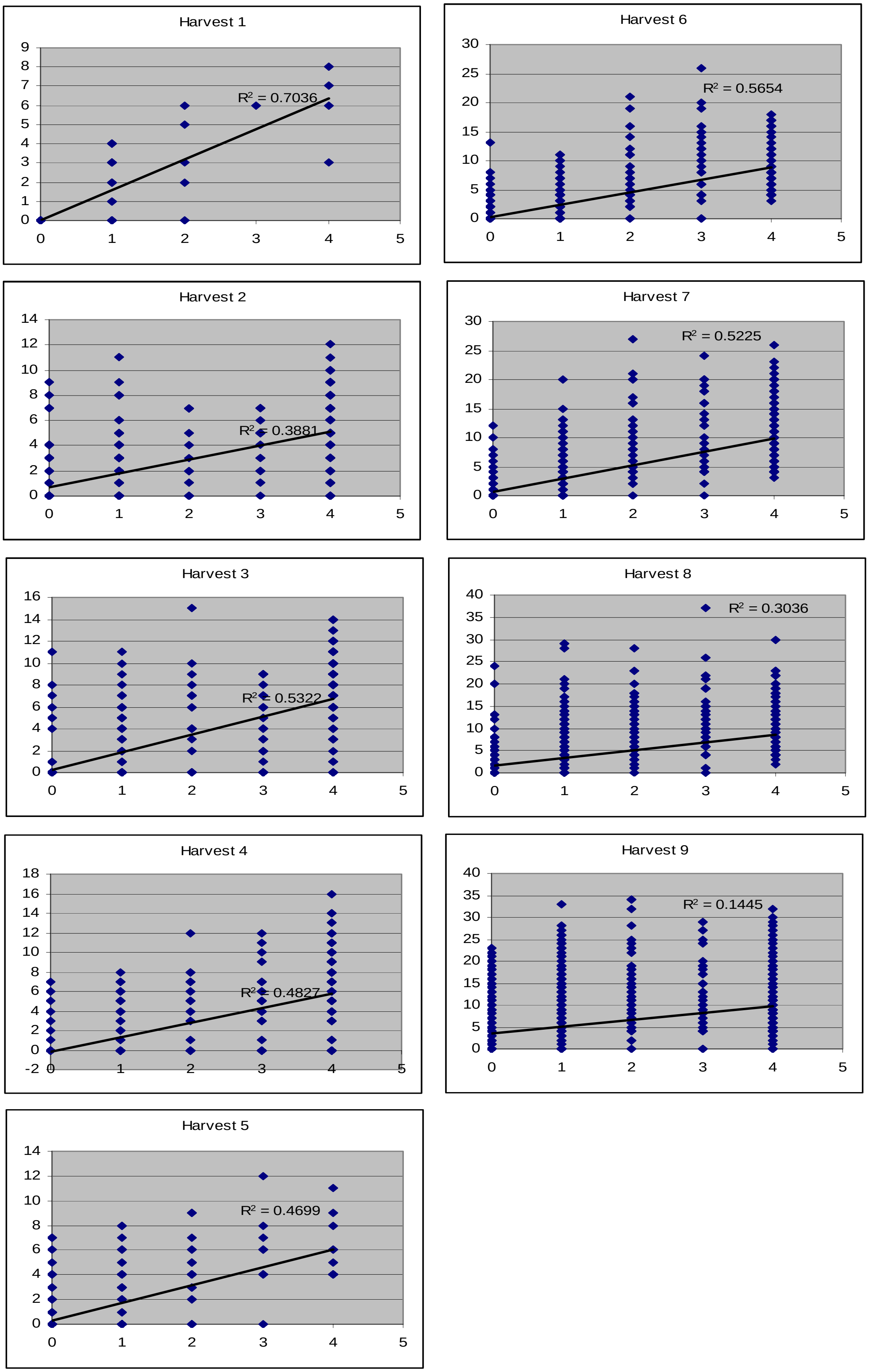
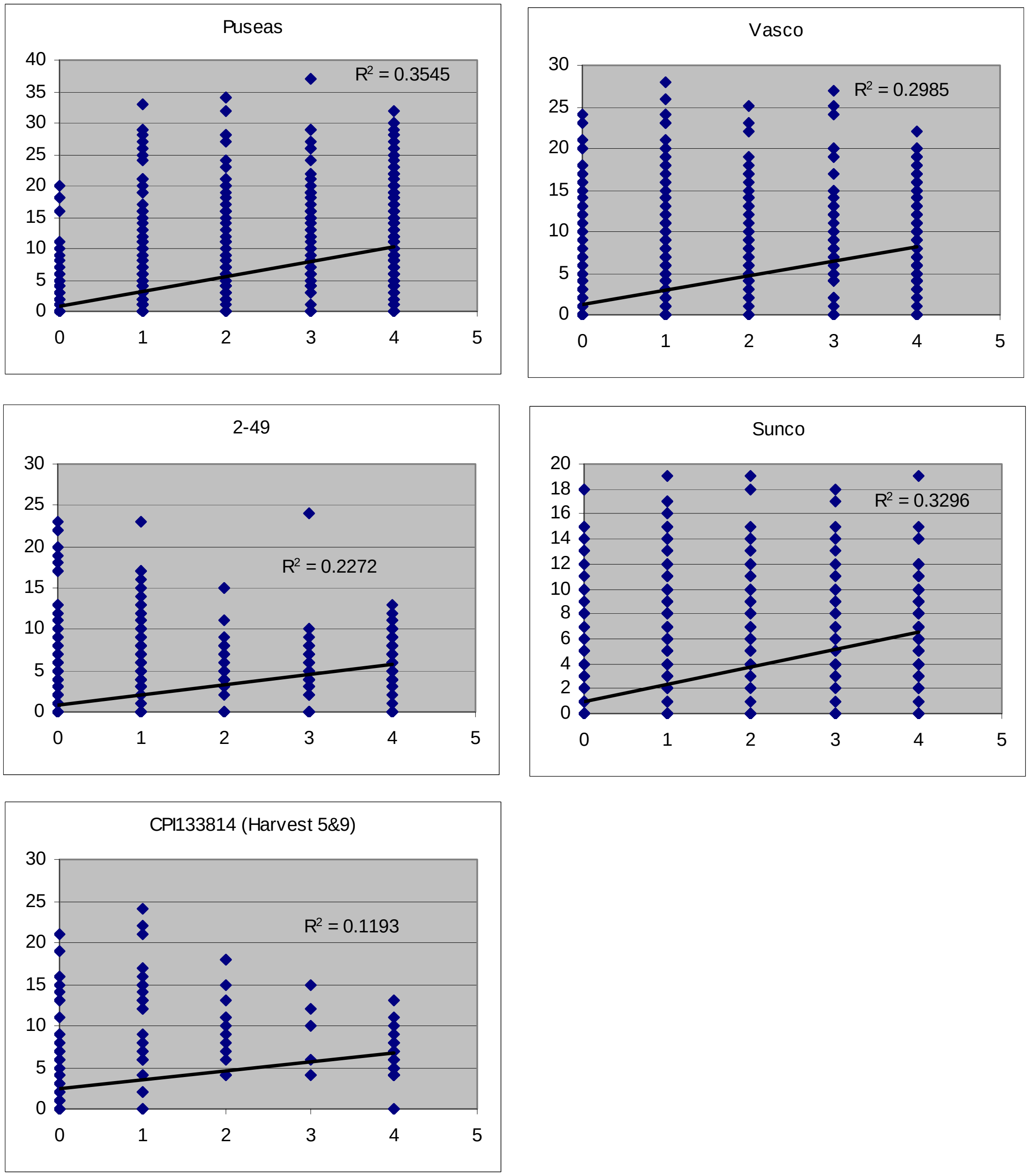


Figure 3F.6 Wellcamp Field Trial Correlation by Genotype



Appendix 4A
Seedling Trial Inoculum Production

Detailed instructions for inoculum production were obtained from the soilborne diseases section of the LRC with technical assistance provided by Sally Coverdale.

Subculture of isolates
A hyphal agar plug of each *Fusarium pseudograminearum* isolate was placed into the centre of CZA_{10+} (Appendix 2C) plates. Two plates were prepared for each isolate and incubated at 25^0C for 7 days.

Grain Preparation
100ml of barley (talon) and 200ml of wheat (Hartog) were placed in 1L flasks using a funnel. 1L of deionised water was put into each flask to cover grain. Flasks were stoppered and shaken well and placed in the coldroom overnight. The following morning the stoppers were removed and the bulk of the water poured off. A piece of muslin was secured over the top of each flask with a rubber band and flasks were turned upside down to continue draining in the sink. Flasks were then righted and restoppered, once the grain was shaken to the bottom. Flasks were autoclaved using a grain cycle which ensures grain remains above 70^0C for 8 mins. Flasks were removed immediately to prevent caramelisation of grain, cooled and left in a cold room overnight.

Inoculation
The following morning flasks were autoclaved for a further 20 mins on a general sterilization cycle and placed inside laminar flow unit to cool. To inoculate, ½ a plate of mycelium was scraped from the agar and dropped onto grain. Each flask was shaken to distribute inoculum around the grain and incubated at 23^0C.

Fungal Growth
After 7 days incubation the clumps formed in each flask were broken by a combination of shaking and tapping. This procedure was repeated daily for 11 days.

Grain Drying and Grinding
Each flask was emptied into an individual tray lined with blotting paper and covered with a second sheet of paper. Only one flask of each isolate was selected based on the extent of visual colonisation, which varied a great deal between isolates and only slightly between the two replicates. One replicate of isolate F14843 had an odour indicating bacterial contamination and therefore the other replicate was used.

Trays were placed in a growth cabinet in the dark at 25^0C. After 4 days clumps in grain were broken up with gloved hands and each tray was shaken every 2nd day thereafter for seventeen days. Inoculated grain was ground in a mill at LRC using a 2mm plate. The mill was cleaned with an air gun between isolates and major components sprayed with 70 % Ethanol. Each isolate was stored in plastic bags in a cold room until required.

Experiment	Genotype	Inoculum	Rep	Disese Rating	Mean
1	1	1	1	5	
1	1	1	1	7	
1	1	1	1	8	
1	1	1	1	6	
1	1	1	1	5	
1	1	1	1	10	
1	1	1	1	12	
1	1	1	1	12	8.125
1	1	1	2	11	
1	1	1	2	5	
1	1	1	2	9	
1	1	1	2	1	
1	1	1	2	12	
1	1	1	2	12	
1	1	1	2	7	
1	1	1	2	9	
1	1	1	2	12	
1	1	1	2	10	8.8
1	1	1	3	12	
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Univariate Analysis of Variance

Notes

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Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
  Mean  BY Genotype Inoculum
Experiment
  /RANDOM = Inoculum Experiment
  /METHOD = SSTYPE(3)
  /INTERCEPT = INCLUDE
  /EMMEANS = TABLES(Genotype)
  /EMMEANS = TABLES(Inoculum)
  /EMMEANS = TABLES(Experiment)
  /EMMEANS =
TABLES(Genotype*Inoculum)
  /EMMEANS =
TABLES(Genotype*Experiment)
  /EMMEANS =
TABLES(Inoculum*Experiment)
  /EMMEANS =
TABLES(Genotype*Inoculum*Experi
ment)
  /PRINT = PARAMETER
  /PLOT = PROFILE(
Genotype*Inoculum )
  /CRITERIA = ALPHA(.05)
  /DESIGN = Genotype Inoculum
Experiment Genotype*Inoculum
Genotype
 *Experiment Inoculum*Experiment
Genotype*Inoculum*Experiment.
```

Resources	Elapsed Time	0:00:02.15

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Between-Subjects Factors

	N

Genotype	1	48
	2	48
	3	48
	4	48
	5	48
	6	48
	7	48
	8	48
	9	48
Inoculum	1	54
	2	54
	3	54
	4	54
	5	54
	6	54
	7	54
	8	54
Experiment	1	216
	2	216

Tests of Between-Subjects Effects

Dependent Variable: Mean

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Hypothesis	6837.810	1	6837.810	35.831	.007
	Error	637.079	3.338	190.833(a)		
Genotype	Hypothesis	628.693	8	78.587	14.944	.000
	Error	71.360	13.569	5.259(b)		
Inoculum	Hypothesis	657.193	7	93.885	35.995	.000
	Error	52.200	20.013	2.608(c)		
Experiment	Hypothesis	98.230	1	98.230	22.878	.001
	Error	36.268	8.447	4.294(d)		
Genotype * Inoculum	Hypothesis	125.821	56	2.247	2.442	.001
	Error	51.531	56	.920(e)		
Genotype * Experiment	Hypothesis	31.458	8	3.932	4.273	.000
	Error	51.531	56	.920(e)		
Inoculum * Experiment	Hypothesis	8.972	7	1.282	1.393	.227
	Error	51.531	56	.920(e)		
Genotype * Inoculum * Experiment	Hypothesis	51.531	56	.920	1.299	.089
	Error	204.044	288	.708(f)		

a 1.000 MS(Inoculum) + 1.000 MS(Experiment) - 1.000 MS(Inoculum * Experiment)
b 1.000 MS(Genotype * Inoculum) + 1.000 MS(Genotype * Experiment) - 1.000 MS(Genotype * Inoculum * Experiment)
c 1.000 MS(Genotype * Inoculum) + 1.000 MS(Inoculum * Experiment) - 1.000 MS(Genotype * Inoculum * Experiment)
d 1.000 MS(Genotype * Experiment) + 1.000 MS(Inoculum * Experiment) - 1.000 MS(Genotype * Inoculum * Experiment)
e MS(Genotype * Inoculum * Experiment)
f MS(Error)

Expected Mean Squares(a,b)

	Variance Component							
Source	Var(Inoculum)	Var(Experiment)	Var(Genotype * Inoculum)	Var(Genotype * Experiment)	Var(Inoculum * Experiment)	Var(Genotype * Inoculum * Experiment)	Var(Error)	Quadratic Term
Intercept	54.000	216.000	6.000	24.000	27.000	3.000	1.000	Intercept, Genotype
Genotype	.000	.000	6.000	24.000	.000	3.000	1.000	Genotype
Inoculum	54.000	.000	6.000	.000	27.000	3.000	1.000	
Experiment	.000	216.000	.000	24.000	27.000	3.000	1.000	
Genotype * Inoculum	.000	.000	6.000	.000	.000	3.000	1.000	
Genotype * Experiment	.000	.000	.000	24.000	.000	3.000	1.000	
Inoculum * Experiment	.000	.000	.000	.000	27.000	3.000	1.000	
Genotype * Inoculum * Experiment	.000	.000	.000	.000	.000	3.000	1.000	
Error	.000	.000	.000	.000	.000	.000	1.000	

a For each source, the expected mean square equals the sum of the coefficients in the cells times the variance components, plus a quadratic term involving effects in the Quadratic Term cell.

b Expected Mean Squares are based on the Type III Sums of Squares.

Parameter Estimates

Dependent Variable: Mean

Parameter	B	Std. Error	t	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Intercept	1.667	.486	3.430	.001	.710	2.623
[Genotype=1]	4.267	.687	6.208	.000	2.914	5.619
[Genotype=2]	2.767	.687	4.026	.000	1.414	4.119
[Genotype=3]	3.200	.687	4.656	.000	1.847	4.553
[Genotype=4]	2.828	.687	4.115	.000	1.475	4.180
[Genotype=5]	3.200	.687	4.656	.000	1.847	4.553
[Genotype=6]	2.933	.687	4.268	.000	1.581	4.286
[Genotype=7]	.533	.687	.776	.438	-.819	1.886
[Genotype=8]	1.000	.687	1.455	.147	-.353	2.353
[Genotype=9]	0(a)	.	.	.	.	.
[Inoculum=1]	-.600	.687	-.873	.383	-1.953	.753
[Inoculum=2]	-.733	.687	-1.067	.287	-2.086	.619
[Inoculum=3]	.367	.687	.534	.594	-.986	1.719
[Inoculum=4]	-.067	.687	-.097	.923	-1.419	1.286
[Inoculum=5]	-.933	.687	-1.358	.176	-2.286	.419
[Inoculum=6]	.200	.687	.291	.771	-1.153	1.553
[Inoculum=7]	1.400	.687	2.037	.043	.047	2.753
[Inoculum=8]	0(a)	.	.	.	.	.
[Experiment=1]	1.800	.687	2.619	.009	.447	3.153
[Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=1]	-1.267	.972	-1.303	.194	-3.180	.646

[Genotype=1] * [Inoculum=2]	-2.400	.972	-2.469	.014	-4.313	-.487
[Genotype=1] * [Inoculum=3]	-.233	.972	-.240	.810	-2.146	1.680
[Genotype=1] * [Inoculum=4]	.944	.972	.972	.332	-.969	2.857
[Genotype=1] * [Inoculum=5]	-3.267	.972	-3.361	.001	-5.180	-1.354
[Genotype=1] * [Inoculum=6]	-1.933	.972	-1.989	.048	-3.846	-.020
[Genotype=1] * [Inoculum=7]	1.000	.972	1.029	.304	-.913	2.913
[Genotype=1] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=1]	2.467	.972	2.538	.012	.554	4.380
[Genotype=2] * [Inoculum=2]	-.167	.972	-.171	.864	-2.080	1.746
[Genotype=2] * [Inoculum=3]	.667	.972	.686	.493	-1.246	2.580
[Genotype=2] * [Inoculum=4]	.915	.972	.941	.347	-.998	2.828
[Genotype=2] * [Inoculum=5]	-2.533	.972	-2.606	.010	-4.446	-.620
[Genotype=2] * [Inoculum=6]	.233	.972	.240	.810	-1.680	2.146
[Genotype=2] * [Inoculum=7]	1.067	.972	1.097	.273	-.846	2.980
[Genotype=2] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=1]	.515	.972	.530	.597	-1.398	2.428
[Genotype=3] * [Inoculum=2]	-.667	.972	-.686	.493	-2.580	1.246
[Genotype=3] * [Inoculum=3]	-.200	.972	-.206	.837	-2.113	1.713
[Genotype=3] * [Inoculum=4]	.100	.972	.103	.918	-1.813	2.013
[Genotype=3] * [Inoculum=5]	-2.567	.972	-2.641	.009	-4.480	-.654
[Genotype=3] * [Inoculum=6]	-.500	.972	-.514	.607	-2.413	1.413
[Genotype=3] * [Inoculum=7]	-.933	.972	-.960	.338	-2.846	.980
[Genotype=3] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=1]	.309	.972	.318	.751	-1.604	2.222
[Genotype=4] * [Inoculum=2]	-1.661	.972	-1.709	.089	-3.574	.252

[Genotype=4] * [Inoculum=3]	-.519	.972	-.534	.593	-2.432	1.394
[Genotype=4] * [Inoculum=4]	-.291	.972	-.299	.765	-2.204	1.622
[Genotype=4] * [Inoculum=5]	-2.794	.972	-2.875	.004	-4.707	-.881
[Genotype=4] * [Inoculum=6]	.111	.972	.114	.909	-1.802	2.024
[Genotype=4] * [Inoculum=7]	-1.141	.972	-1.174	.241	-3.054	.772
[Genotype=4] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=1]	.400	.972	.412	.681	-1.513	2.313
[Genotype=5] * [Inoculum=2]	-1.233	.972	-1.269	.205	-3.146	.680
[Genotype=5] * [Inoculum=3]	-.363	.972	-.373	.709	-2.276	1.550
[Genotype=5] * [Inoculum=4]	-.190	.972	-.196	.845	-2.103	1.723
[Genotype=5] * [Inoculum=5]	-2.533	.972	-2.606	.010	-4.446	-.620
[Genotype=5] * [Inoculum=6]	-.167	.972	-.171	.864	-2.080	1.746
[Genotype=5] * [Inoculum=7]	-1.244	.972	-1.280	.201	-3.157	.669
[Genotype=5] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=1]	-.333	.972	-.343	.732	-2.246	1.580
[Genotype=6] * [Inoculum=2]	-1.567	.972	-1.612	.108	-3.480	.346
[Genotype=6] * [Inoculum=3]	-.800	.972	-.823	.411	-2.713	1.113
[Genotype=6] * [Inoculum=4]	-.067	.972	-.069	.945	-1.980	1.846
[Genotype=6] * [Inoculum=5]	-3.067	.972	-3.155	.002	-4.980	-1.154
[Genotype=6] * [Inoculum=6]	-.559	.972	-.575	.565	-2.472	1.354
[Genotype=6] * [Inoculum=7]	-1.033	.972	-1.063	.289	-2.946	.880
[Genotype=6] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=1]	1.033	.972	1.063	.289	-.880	2.946
[Genotype=7] * [Inoculum=2]	-.033	.972	-.034	.973	-1.946	1.880
[Genotype=7] * [Inoculum=3]	.200	.972	.206	.837	-1.713	2.113

[Genotype=7] * [Inoculum=4]	.667	.972	.686	.493	-1.246	2.580
[Genotype=7] * [Inoculum=5]	-.367	.972	-.377	.706	-2.280	1.546
[Genotype=7] * [Inoculum=6]	.433	.972	.446	.656	-1.480	2.346
[Genotype=7] * [Inoculum=7]	1.233	.972	1.269	.205	-.680	3.146
[Genotype=7] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=1]	-.222	.972	-.229	.819	-2.135	1.691
[Genotype=8] * [Inoculum=2]	-.800	.972	-.823	.411	-2.713	1.113
[Genotype=8] * [Inoculum=3]	-1.708	.972	-1.758	.080	-3.621	.205
[Genotype=8] * [Inoculum=4]	-.774	.972	-.796	.426	-2.687	1.139
[Genotype=8] * [Inoculum=5]	-.733	.972	-.755	.451	-2.646	1.180
[Genotype=8] * [Inoculum=6]	-.615	.972	-.633	.528	-2.528	1.298
[Genotype=8] * [Inoculum=7]	-1.217	.972	-1.252	.212	-3.130	.696
[Genotype=8] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=3]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=4]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=5]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=6]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=7]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=8]	0(a)	.	.	.	.	.
[Genotype=1] * [Experiment=1]	-.100	.972	-.103	.918	-2.013	1.813
[Genotype=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Experiment=1]	.300	.972	.309	.758	-1.613	2.213
[Genotype=2] * [Experiment=2]	0(a)	.	.	.	.	.

[Genotype=3] * [Experiment=1]	-1.367	.972	-1.406	.161	-3.280	.546
[Genotype=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Experiment=1]	-1.492	.972	-1.535	.126	-3.405	.421
[Genotype=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Experiment=1]	-1.508	.972	-1.552	.122	-3.421	.405
[Genotype=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Experiment=1]	-1.700	.972	-1.749	.081	-3.613	.213
[Genotype=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Experiment=1]	.500	.972	.514	.607	-1.413	2.413
[Genotype=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Experiment=1]	-1.220	.972	-1.255	.210	-3.133	.693
[Genotype=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=1] * [Experiment=1]	-.467	.972	-.480	.631	-2.380	1.446
[Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=2] * [Experiment=1]	-.867	.972	-.892	.373	-2.780	1.046
[Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=3] * [Experiment=1]	-1.300	.972	-1.338	.182	-3.213	.613
[Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=4] * [Experiment=1]	.133	.972	.137	.891	-1.780	2.046
[Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=5] * [Experiment=1]	-1.900	.972	-1.955	.052	-3.813	.013
[Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=6] * [Experiment=1]	-1.333	.972	-1.372	.171	-3.246	.580

[Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=7] * [Experiment=1]	-1.167	.972	-1.200	.231	-3.080	.746
[Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=1] * [Experiment=1]	3.342	1.375	2.431	.016	.636	6.047
[Genotype=1] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=2] * [Experiment=1]	.733	1.375	.534	.594	-1.972	3.439
[Genotype=1] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=3] * [Experiment=1]	1.200	1.375	.873	.383	-1.505	3.905
[Genotype=1] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=4] * [Experiment=1]	-.244	1.375	-.178	.859	-2.950	2.461
[Genotype=1] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=5] * [Experiment=1]	.400	1.375	.291	.771	-2.305	3.105
[Genotype=1] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=6] * [Experiment=1]	4.300	1.375	3.128	.002	1.595	7.005
[Genotype=1] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=7] * [Experiment=1]	1.183	1.375	.861	.390	-1.522	3.889
[Genotype=1] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.

[Genotype=1] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=1] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=1] * [Experiment=1]	-1.233	1.375	-.897	.370	-3.939	1.472
[Genotype=2] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=2] * [Experiment=1]	-1.000	1.375	-.728	.467	-3.705	1.705
[Genotype=2] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=3] * [Experiment=1]	.233	1.375	.170	.865	-2.472	2.939
[Genotype=2] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=4] * [Experiment=1]	-1.681	1.375	-1.223	.222	-4.387	1.024
[Genotype=2] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=5] * [Experiment=1]	.900	1.375	.655	.513	-1.805	3.605
[Genotype=2] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=6] * [Experiment=1]	.933	1.375	.679	.498	-1.772	3.639
[Genotype=2] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=7] * [Experiment=1]	-.700	1.375	-.509	.611	-3.405	2.005
[Genotype=2] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=2] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.

[Genotype=2] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=1] * [Experiment=1]	-.300	1.375	-.218	.827	-3.005	2.405
[Genotype=3] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=2] * [Experiment=1]	.800	1.375	.582	.561	-1.905	3.505
[Genotype=3] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=3] * [Experiment=1]	2.593	1.375	1.886	.060	-.113	5.298
[Genotype=3] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=4] * [Experiment=1]	-.933	1.375	-.679	.498	-3.639	1.772
[Genotype=3] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=5] * [Experiment=1]	1.967	1.375	1.431	.154	-.739	4.672
[Genotype=3] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=6] * [Experiment=1]	1.667	1.375	1.213	.226	-1.039	4.372
[Genotype=3] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=7] * [Experiment=1]	1.067	1.375	.776	.438	-1.639	3.772
[Genotype=3] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=3] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.

[Genotype=4] * [Inoculum=1] * [Experiment=1]	.573	1.375	.417	.677	-2.132	3.279
[Genotype=4] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=2] * [Experiment=1]	1.431	1.375	1.041	.299	-1.274	4.137
[Genotype=4] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=3] * [Experiment=1]	1.542	1.375	1.122	.263	-1.164	4.247
[Genotype=4] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=4] * [Experiment=1]	.362	1.375	.263	.792	-2.343	3.067
[Genotype=4] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=5] * [Experiment=1]	1.774	1.375	1.291	.198	-.931	4.480
[Genotype=4] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=6] * [Experiment=1]	1.315	1.375	.956	.340	-1.391	4.020
[Genotype=4] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=7] * [Experiment=1]	.455	1.375	.331	.741	-2.250	3.160
[Genotype=4] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=4] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=1] * [Experiment=1]	.708	1.375	.515	.607	-1.997	3.414

[Genotype=5] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=2] * [Experiment=1]	1.400	1.375	1.019	.309	-1.305	4.105
[Genotype=5] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=3] * [Experiment=1]	1.838	1.375	1.337	.182	-.867	4.543
[Genotype=5] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=4] * [Experiment=1]	.799	1.375	.581	.562	-1.907	3.504
[Genotype=5] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=5] * [Experiment=1]	2.342	1.375	1.704	.090	-.364	5.047
[Genotype=5] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=6] * [Experiment=1]	1.008	1.375	.734	.464	-1.697	3.714
[Genotype=5] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=7] * [Experiment=1]	1.753	1.375	1.275	.203	-.953	4.458
[Genotype=5] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=5] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=1] * [Experiment=1]	.833	1.375	.606	.545	-1.872	3.539
[Genotype=6] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.

[Genotype=6] * [Inoculum=2] * [Experiment=1]	1.167	1.375	.849	.397	-1.539	3.872
[Genotype=6] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=3] * [Experiment=1]	2.675	1.375	1.946	.053	-.030	5.380
[Genotype=6] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=4] * [Experiment=1]	-.133	1.375	-.097	.923	-2.839	2.572
[Genotype=6] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=5] * [Experiment=1]	3.133	1.375	2.280	.023	.428	5.839
[Genotype=6] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=6] * [Experiment=1]	1.793	1.375	1.304	.193	-.913	4.498
[Genotype=6] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=7] * [Experiment=1]	1.393	1.375	1.013	.312	-1.313	4.098
[Genotype=6] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=6] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=1] * [Experiment=1]	-.533	1.375	-.388	.698	-3.239	2.172
[Genotype=7] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=2] * [Experiment=1]	-.467	1.375	-.340	.734	-3.172	2.239

[Genotype=7] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=3] * [Experiment=1]	1.167	1.375	.849	.397	-1.539	3.872
[Genotype=7] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=4] * [Experiment=1]	-1.400	1.375	-1.019	.309	-4.105	1.305
[Genotype=7] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=5] * [Experiment=1]	-.100	1.375	-.073	.942	-2.805	2.605
[Genotype=7] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=6] * [Experiment=1]	1.800	1.375	1.310	.191	-.905	4.505
[Genotype=7] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=7] * [Experiment=1]	-.467	1.375	-.340	.734	-3.172	2.239
[Genotype=7] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=7] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=1] * [Experiment=1]	1.218	1.375	.886	.376	-1.487	3.924
[Genotype=8] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=2] * [Experiment=1]	.835	1.375	.607	.544	-1.870	3.540
[Genotype=8] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.

[Genotype=8] * [Inoculum=3] * [Experiment=1]	2.764	1.375	2.011	.045	.059	5.470
[Genotype=8] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=4] * [Experiment=1]	1.441	1.375	1.048	.295	-1.265	4.146
[Genotype=8] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=5] * [Experiment=1]	1.987	1.375	1.445	.149	-.719	4.692
[Genotype=8] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=6] * [Experiment=1]	1.127	1.375	.820	.413	-1.579	3.832
[Genotype=8] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=7] * [Experiment=1]	1.103	1.375	.803	.423	-1.602	3.809
[Genotype=8] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=8] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=1] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=1] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=2] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=2] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=3] * [Experiment=1]	0(a)	.	.	.	.	.

[Genotype=9] * [Inoculum=3] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=4] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=4] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=5] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=5] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=6] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=6] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=7] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=7] * [Experiment=2]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=8] * [Experiment=1]	0(a)	.	.	.	.	.
[Genotype=9] * [Inoculum=8] * [Experiment=2]	0(a)	.	.	.	.	.

a This parameter is set to zero because it is redundant.

Estimated Marginal Means

1. Genotype

Dependent Variable: Mean

Genotype	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	6.094	.121	5.855	6.333
2	5.178	.121	4.939	5.417
3	4.503	.121	4.264	4.743
4	3.889	.121	3.650	4.128
5	4.485	.121	4.245	4.724
6	3.923	.121	3.684	4.163
7	3.269	.121	3.030	3.508
8	2.376	.121	2.136	2.615

9	2.090	.121	1.850	2.329

2. Inoculum

Dependent Variable: Mean

Inoculum	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	4.249	.115	4.023	4.474
2	2.662	.115	2.436	2.887
3	4.670	.115	4.445	4.896
4	4.549	.115	4.324	4.775
5	1.325	.115	1.100	1.550
6	4.479	.115	4.253	4.704
7	5.390	.115	5.164	5.615
8	4.504	.115	4.278	4.729

3. Experiment

Dependent Variable: Mean

Experiment	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	4.455	.057	4.343	4.568
2	3.502	.057	3.389	3.614

4. Genotype * Inoculum

Dependent Variable: Mean

Genotype	Inoculum	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
1	1	6.354	.344	5.678	7.031
	2	3.583	.344	2.907	4.260
	3	6.867	.344	6.190	7.543
	4	7.606	.344	6.929	8.282
	5	1.833	.344	1.157	2.510
	6	6.533	.344	5.857	7.210
	7	9.192	.344	8.515	9.868
	8	6.783	.344	6.107	7.460
2	1	6.500	.344	5.824	7.176
	2	3.650	.344	2.974	4.326
	3	5.983	.344	5.307	6.660
	4	5.557	.344	4.881	6.234
	5	1.517	.344	.840	2.193
	6	5.717	.344	5.040	6.393
	7	7.017	.344	6.340	7.693
	8	5.483	.344	4.807	6.160
3	1	4.615	.344	3.938	5.291

	2	3.650	.344	2.974	4.326
	3	5.896	.344	5.220	6.573
	4	4.717	.344	4.040	5.393
	5	1.617	.344	.940	2.293
	6	4.950	.344	4.274	5.626
	7	5.500	.344	4.824	6.176
	8	5.083	.344	4.407	5.760
4	1	4.411	.344	3.735	5.087
	2	2.537	.344	1.860	3.213
	3	4.617	.344	3.940	5.293
	4	4.539	.344	3.863	5.215
	5	.859	.344	.182	1.535
	6	4.950	.344	4.274	5.627
	7	4.552	.344	3.875	5.228
	8	4.649	.344	3.972	5.325
5	1	4.933	.344	4.257	5.610
	2	3.313	.344	2.636	3.989
	3	5.285	.344	4.609	5.962
	4	5.221	.344	4.545	5.898
	5	1.767	.344	1.090	2.443
	6	4.883	.344	4.207	5.560
	7	5.461	.344	4.785	6.137
	8	5.013	.344	4.336	5.689
6	1	3.900	.344	3.224	4.576
	2	2.500	.344	1.824	3.176
	3	4.904	.344	4.228	5.581
	4	4.517	.344	3.840	5.193
	5	1.267	.344	.590	1.943
	6	4.520	.344	3.844	5.197
	7	5.130	.344	4.453	5.806
	8	4.650	.344	3.974	5.326
7	1	3.283	.344	2.607	3.960
	2	1.917	.344	1.240	2.593
	3	3.850	.344	3.174	4.526
	4	3.317	.344	2.640	3.993
	5	1.050	.344	.374	1.726
	6	4.217	.344	3.540	4.893
	7	5.167	.344	4.490	5.843
	8	3.350	.344	2.674	4.026
8	1	2.510	.344	1.834	3.187
	2	1.407	.344	.731	2.084
	3	2.347	.344	1.671	3.023
	4	2.903	.344	2.227	3.579
	5	1.333	.344	.657	2.010
	6	2.438	.344	1.762	3.115
	7	3.108	.344	2.432	3.785
	8	2.957	.344	2.280	3.633

9	1	1.733	.344	1.057	2.410
	2	1.400	.344	.724	2.076
	3	2.283	.344	1.607	2.960
	4	2.567	.344	1.890	3.243
	5	.683	.344	.007	1.360
	6	2.100	.344	1.424	2.776
	7	3.383	.344	2.707	4.060
	8	2.567	.344	1.890	3.243

5. Genotype * Experiment

Dependent Variable: Mean

Genotype	Experiment	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
1	1	7.195	.172	6.857	7.533
	2	4.993	.172	4.655	5.331
2	1	5.638	.172	5.299	5.976
	2	4.719	.172	4.380	5.057
3	1	4.718	.172	4.379	5.056
	2	4.289	.172	3.951	4.628
4	1	4.078	.172	3.740	4.416
	2	3.700	.172	3.362	4.039
5	1	4.815	.172	4.476	5.153
	2	4.154	.172	3.816	4.493
6	1	4.221	.172	3.883	4.559
	2	3.626	.172	3.288	3.964
7	1	3.988	.172	3.649	4.326
	2	2.550	.172	2.212	2.888
8	1	2.889	.172	2.551	3.227
	2	1.862	.172	1.524	2.200
9	1	2.558	.172	2.220	2.897
	2	1.621	.172	1.283	1.959

6. Inoculum * Experiment

Dependent Variable: Mean

Inoculum	Experiment	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
1	1	4.806	.162	4.487	5.124
	2	3.692	.162	3.373	4.011
2	1	3.035	.162	2.716	3.354
	2	2.289	.162	1.970	2.608
3	1	5.333	.162	5.014	5.652
	2	4.008	.162	3.689	4.327
4	1	5.050	.162	4.732	5.369
	2	4.048	.162	3.729	4.367
5	1	1.598	.162	1.279	1.917

	2	1.052	.162	.733	1.371
6	1	5.121	.162	4.802	5.440
	2	3.837	.162	3.518	4.156
7	1	5.662	.162	5.343	5.981
	2	5.118	.162	4.799	5.436
8	1	5.038	.162	4.719	5.357
	2	3.970	.162	3.651	4.289

7. Genotype * Inoculum * Experiment

Dependent Variable: Mean

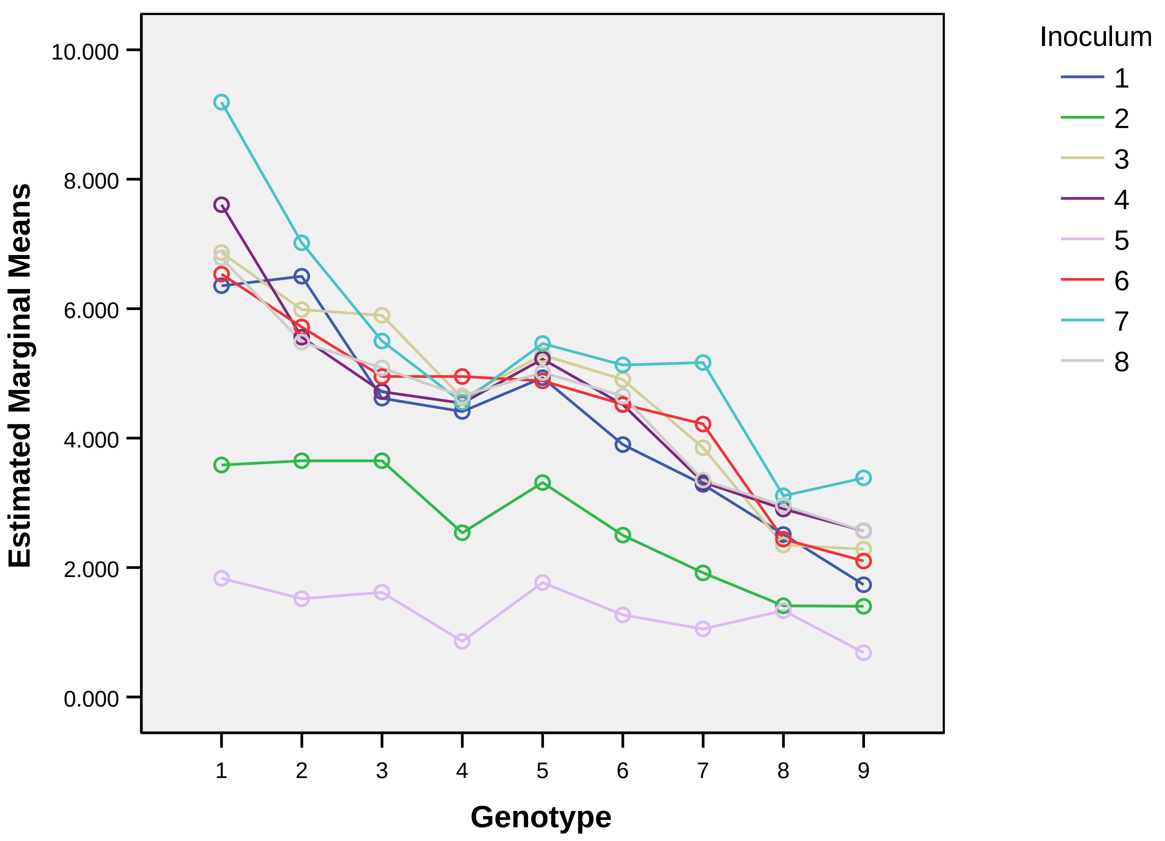
Genotype	Inoculum	Experiment	Mean	Std. Error	95% Confidence Interval	
					Lower Bound	Upper Bound
1	1	1	8.642	.486	7.685	9.598
		2	4.067	.486	3.110	5.023
	2	1	4.367	.486	3.410	5.323
		2	2.800	.486	1.844	3.756
	3	1	7.667	.486	6.710	8.623
		2	6.067	.486	5.110	7.023
	4	1	8.400	.486	7.444	9.356
		2	6.811	.486	5.855	7.768
	5	1	1.933	.486	.977	2.890
		2	1.733	.486	.777	2.690
	6	1	8.867	.486	7.910	9.823
		2	4.200	.486	3.244	5.156
	7	1	10.050	.486	9.094	11.006
		2	8.333	.486	7.377	9.290
	8	1	7.633	.486	6.677	8.590
		2	5.933	.486	4.977	6.890
2	1	1	6.700	.486	5.744	7.656
		2	6.300	.486	5.344	7.256
	2	1	3.767	.486	2.810	4.723
		2	3.533	.486	2.577	4.490
	3	1	6.500	.486	5.544	7.456
		2	5.467	.486	4.510	6.423
	4	1	5.833	.486	4.877	6.790
		2	5.281	.486	4.325	6.238
	5	1	2.067	.486	1.110	3.023
		2	.967	.486	.010	1.923
	6	1	6.567	.486	5.610	7.523
		2	4.867	.486	3.910	5.823
	7	1	7.133	.486	6.177	8.090
		2	6.900	.486	5.944	7.856
	8	1	6.533	.486	5.577	7.490
		2	4.433	.486	3.477	5.390
3	1	1	4.448	.486	3.492	5.405
		2	4.781	.486	3.825	5.738

	2	1	3.833	.486	2.877	4.790
		2	3.467	.486	2.510	4.423
	3	1	6.759	.486	5.803	7.716
		2	5.033	.486	4.077	5.990
	4	1	4.533	.486	3.577	5.490
		2	4.900	.486	3.944	5.856
	5	1	1.867	.486	.910	2.823
		2	1.367	.486	.410	2.323
	6	1	5.333	.486	4.377	6.290
		2	4.567	.486	3.610	5.523
	7	1	5.667	.486	4.710	6.623
		2	5.333	.486	4.377	6.290
	8	1	5.300	.486	4.344	6.256
		2	4.867	.486	3.910	5.823
4	1	1	4.619	.486	3.662	5.575
		2	4.204	.486	3.247	5.160
	2	1	2.973	.486	2.017	3.930
		2	2.100	.486	1.144	3.056
	3	1	4.892	.486	3.935	5.848
		2	4.342	.486	3.385	5.298
	4	1	4.941	.486	3.984	5.897
		2	4.137	.486	3.181	5.094
	5	1	.950	.486	-.006	1.906
		2	.767	.486	-.189	1.724
	6	1	5.095	.486	4.139	6.052
		2	4.806	.486	3.849	5.762
	7	1	4.350	.486	3.394	5.306
		2	4.753	.486	3.797	5.710
	8	1	4.803	.486	3.846	5.759
		2	4.494	.486	3.538	5.451
5	1	1	5.200	.486	4.244	6.156
		2	4.667	.486	3.710	5.623
	2	1	3.725	.486	2.769	4.681
		2	2.900	.486	1.944	3.856
	3	1	5.700	.486	4.744	6.656
		2	4.870	.486	3.914	5.827
	4	1	5.833	.486	4.877	6.790
		2	4.610	.486	3.653	5.566
	5	1	2.133	.486	1.177	3.090
		2	1.400	.486	.444	2.356
	6	1	4.867	.486	3.910	5.823
		2	4.900	.486	3.944	5.856
	7	1	5.900	.486	4.944	6.856
		2	5.022	.486	4.066	5.979
	8	1	5.158	.486	4.202	6.115
		2	4.867	.486	3.910	5.823
6	1	1	4.133	.486	3.177	5.090

		2	3.667	.486	2.710	4.623
	2	1	2.700	.486	1.744	3.656
		2	2.300	.486	1.344	3.256
	3	1	5.642	.486	4.685	6.598
		2	4.167	.486	3.210	5.123
	4	1	4.567	.486	3.610	5.523
		2	4.467	.486	3.510	5.423
	5	1	1.933	.486	.977	2.890
		2	.600	.486	-.356	1.556
	6	1	4.800	.486	3.844	5.756
		2	4.241	.486	3.284	5.197
	7	1	5.293	.486	4.336	6.249
		2	4.967	.486	4.010	5.923
	8	1	4.700	.486	3.744	5.656
		2	4.600	.486	3.644	5.556
7	1	1	3.933	.486	2.977	4.890
		2	2.633	.486	1.677	3.590
	2	1	2.400	.486	1.444	3.356
		2	1.433	.486	.477	2.390
	3	1	4.933	.486	3.977	5.890
		2	2.767	.486	1.810	3.723
	4	1	3.833	.486	2.877	4.790
		2	2.800	.486	1.844	3.756
	5	1	1.200	.486	.244	2.156
		2	.900	.486	-.056	1.856
	6	1	5.600	.486	4.644	6.556
		2	2.833	.486	1.877	3.790
	7	1	5.500	.486	4.544	6.456
		2	4.833	.486	3.877	5.790
	8	1	4.500	.486	3.544	5.456
		2	2.200	.486	1.244	3.156
8	1	1	3.176	.486	2.219	4.132
		2	1.844	.486	.888	2.801
	2	1	1.681	.486	.725	2.638
		2	1.133	.486	.177	2.090
	3	1	3.369	.486	2.413	4.326
		2	1.325	.486	.369	2.281
	4	1	3.980	.486	3.023	4.936
		2	1.826	.486	.869	2.782
	5	1	1.667	.486	.710	2.623
		2	1.000	.486	.044	1.956
	6	1	2.625	.486	1.669	3.581
		2	2.252	.486	1.295	3.208
	7	1	3.367	.486	2.410	4.323
		2	2.850	.486	1.894	3.806
	8	1	3.247	.486	2.290	4.203
		2	2.667	.486	1.710	3.623

9	1	1	2.400	.486	1.444	3.356
		2	1.067	.486	.110	2.023
	2	1	1.867	.486	.910	2.823
		2	.933	.486	-.023	1.890
	3	1	2.533	.486	1.577	3.490
		2	2.033	.486	1.077	2.990
	4	1	3.533	.486	2.577	4.490
		2	1.600	.486	.644	2.556
	5	1	.633	.486	-.323	1.590
		2	.733	.486	-.223	1.690
	6	1	2.333	.486	1.377	3.290
		2	1.867	.486	.910	2.823
	7	1	3.700	.486	2.744	4.656
		2	3.067	.486	2.110	4.023
	8	1	3.467	.486	2.510	4.423
		2	1.667	.486	.710	2.623

Estimated Marginal Means of Mean



Variance Components Estimation

Notes

Output Created		05-JAN-2008 15:52:29
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	4192
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
VARCOMP
  Mean  BY Inoculum Experiment
Genotype
  /RANDOM = Inoculum Experiment
  /METHOD = MINQUE (1)
  /DESIGN = Genotype Inoculum
Experiment  Genotype*Inoculum
Experiment
 *Genotype Experiment*Inoculum
Genotype*Inoculum*Experiment
  /INTERCEPT = INCLUDE .
```

Resources	Elapsed Time	0:00:00.11

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[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Factor Level Information

		N
Inoculum	1	54
	2	54
	3	54
	4	54
	5	54
	6	54
	7	54
	8	54
Experiment	1	216
	2	216
Genotype	1	48
	2	48
	3	48

4	48
5	48
6	48
7	48
8	48
9	48

Dependent Variable: Mean

Variance Estimates

Component	Estimate
Var(Inoculum)	1.690
Var(Experiment)	.435
Var(Inoculum * Genotype)	.221
Var(Experiment * Genotype)	.126
Var(Inoculum * Experiment)	.013
Var(Inoculum * Experiment * Genotype)	.071
Var(Error)	.708

Dependent Variable: Mean
Method: Minimum Norm Quadratic Unbiased Estimation (Weight = 1 for Random Effects and Residual)

Univariate Analysis of Variance

Notes

Output Created		05-JAN-2008 15:52:29
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	4192
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
  Mean  BY Genotype Inoculum
Experiment
  /RANDOM = Inoculum Experiment
  /METHOD = SSTYPE(3)
  /INTERCEPT = INCLUDE
  /PLOT = PROFILE(
Genotype*Inoculum )
  /CRITERIA = ALPHA(.05)
  /DESIGN = Genotype Inoculum
Experiment
Genotype*Inoculum
Experiment*Genotype Experiment
 *Inoculum.
```

Resources	Elapsed Time	0:00:00.78

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[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Between-Subjects Factors

		N
Genotype	1	48
	2	48
	3	48
	4	48
	5	48
	6	48
	7	48
	8	48
	9	48
Inoculum	1	54
	2	54
	3	54
	4	54
	5	54
	6	54
	7	54
	8	54
Experiment	1	216
	2	216

Tests of Between-Subjects Effects

Dependent Variable: Mean

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Hypothesis	6837.810	1	6837.810	35.831	.007
	Error	637.079	3.338	190.833(a)		
Genotype	Hypothesis	628.693	8	78.587	14.456	.000

	Error	79.347	14.596	5.436(b)		
Inoculum	Hypothesis	657.193	7	93.885	33.705	.000
	Error	66.213	23.771	2.785(c)		
Experiment	Hypothesis	98.230	1	98.230	21.971	.001
	Error	41.202	9.216	4.471(d)		
Genotype * Inoculum	Hypothesis	125.821	56	2.247	3.024	.000
	Error	255.574	344	.743(e)		
Genotype * Experiment	Hypothesis	31.458	8	3.932	5.293	.000
	Error	255.574	344	.743(e)		
Inoculum * Experiment	Hypothesis	8.972	7	1.282	1.725	.102
	Error	255.574	344	.743(e)		

a MS(Inoculum) + 1.000 MS(Experiment) - MS(Inoculum * Experiment)
b 1.000 MS(Genotype * Inoculum) + MS(Genotype * Experiment) - MS(Error)
c 1.000 MS(Genotype * Inoculum) + MS(Inoculum * Experiment) - 1.000 MS(Error)
d 1.000 MS(Genotype * Experiment) + 1.000 MS(Inoculum * Experiment) - 1.000 MS(Error)
e MS(Error)

Expected Mean Squares(a,b)

	Variance Component						
Source	Var(Inoculum)	Var(Experiment)	Var(Genotype * Inoculum)	Var(Genotype * Experiment)	Var(Inoculum * Experiment)	Var(Error)	Quadratic Term
Intercept	54.000	216.000	6.000	24.000	27.000	1.000	Intercept, Genotype
Genotype	.000	.000	6.000	24.000	.000	1.000	Genotype
Inoculum	54.000	.000	6.000	.000	27.000	1.000	
Experiment	.000	216.000	.000	24.000	27.000	1.000	
Genotype * Inoculum	.000	.000	6.000	.000	.000	1.000	
Genotype * Experiment	.000	.000	.000	24.000	.000	1.000	
Inoculum * Experiment	.000	.000	.000	.000	27.000	1.000	
Error	.000	.000	.000	.000	.000	1.000	

a For each source, the expected mean square equals the sum of the coefficients in the cells times the variance components, plus a quadratic term involving effects in the Quadratic Term cell.
b Expected Mean Squares are based on the Type III Sums of Squares.

Variance Components Estimation

Notes

Output Created		05-JAN-2008 15:52:30
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	4192

Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
VARCOMP
  Mean  BY Inoculum Experiment
Genotype
  /RANDOM = Inoculum Experiment
  /METHOD = MINQUE (1)
  /DESIGN = Genotype Inoculum
Experiment  Genotype*Inoculum
Experiment
 *Genotype Experiment*Inoculum
Genotype*Inoculum*Experiment
  /INTERCEPT = INCLUDE .
```

Resources	Elapsed Time	0:00:00.13

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[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Factor Level Information

		N
Inoculum	1	54
	2	54
	3	54
	4	54
	5	54
	6	54
	7	54
	8	54
Experiment	1	216
	2	216
Genotype	1	48
	2	48
	3	48
	4	48
	5	48
	6	48
	7	48
	8	48
	9	48

Dependent Variable: Mean

Variance Estimates

Component	Estimate
Var(Inoculum)	1.690
Var(Experiment)	.435

Var(Inoculum * Genotype)	.221
Var(Experiment * Genotype)	.126
Var(Inoculum * Experiment)	.013
Var(Inoculum * Experiment * Genotype)	.071
Var(Error)	.708

Dependent Variable: Mean
Method: Minimum Norm Quadratic Unbiased Estimation (Weight = 1 for Random Effects and Residual)

Univariate Analysis of Variance (Inoculum 2 and 5 removed)

Notes

Output Created		05-JAN-2008 15:52:30
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
UNIANOVA
  Mean  BY Genotype Inoculum
Experiment
  /RANDOM = Inoculum Experiment
  /METHOD = SSTYPE(3)
  /INTERCEPT = INCLUDE
  /PLOT = PROFILE(
Genotype*Inoculum )
  /CRITERIA = ALPHA(.05)
  /DESIGN = Genotype Inoculum
Experiment
Genotype*Inoculum
Experiment*Genotype Experiment
 *Inoculum
Genotype*Inoculum*Experiment   .
```

Resources	Elapsed Time	0:00:02.24

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[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
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Between-Subjects Factors

		N
Genotype	1	36
	2	36
	3	36
	4	36
	5	36
	6	36
	7	36
	8	36
	9	36
Inoculum	1	54
	3	54
	4	54
	6	54
	7	54
	8	54
Experiment	1	162
	2	162

Tests of Between-Subjects Effects

Dependent Variable: Mean

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Hypothesis	6976.061	1	6976.061	71.466	.055
	Error	113.700	1.165	97.614(a)		
Genotype	Hypothesis	658.394	8	82.299	16.115	.000
	Error	43.183	8.456	5.107(b)		
Inoculum	Hypothesis	41.525	5	8.305	6.670	.024
	Error	6.849	5.500	1.245(c)		
Experiment	Hypothesis	90.368	1	90.368	18.060	.003
	Error	38.257	7.645	5.004(d)		
Genotype * Inoculum	Hypothesis	46.487	40	1.162	1.191	.292
	Error	39.042	40	.976(e)		
Genotype * Experiment	Hypothesis	39.367	8	4.921	5.042	.000
	Error	39.042	40	.976(e)		
Inoculum * Experiment	Hypothesis	5.295	5	1.059	1.085	.383
	Error	39.042	40	.976(e)		
Genotype * Inoculum * Experiment	Hypothesis	39.042	40	.976	1.190	.217
	Error	177.205	216	.820(f)		

a 1.000 MS(Inoculum) + 1.000 MS(Experiment) - 1.000 MS(Inoculum * Experiment)
b MS(Genotype * Inoculum) + MS(Genotype * Experiment) - MS(Genotype * Inoculum * Experiment)
c MS(Genotype * Inoculum) + 1.000 MS(Inoculum * Experiment) - 1.000 MS(Genotype * Inoculum * Experiment)
d 1.000 MS(Genotype * Experiment) + MS(Inoculum * Experiment) - MS(Genotype * Inoculum * Experiment)
e MS(Genotype * Inoculum * Experiment)
f MS(Error)

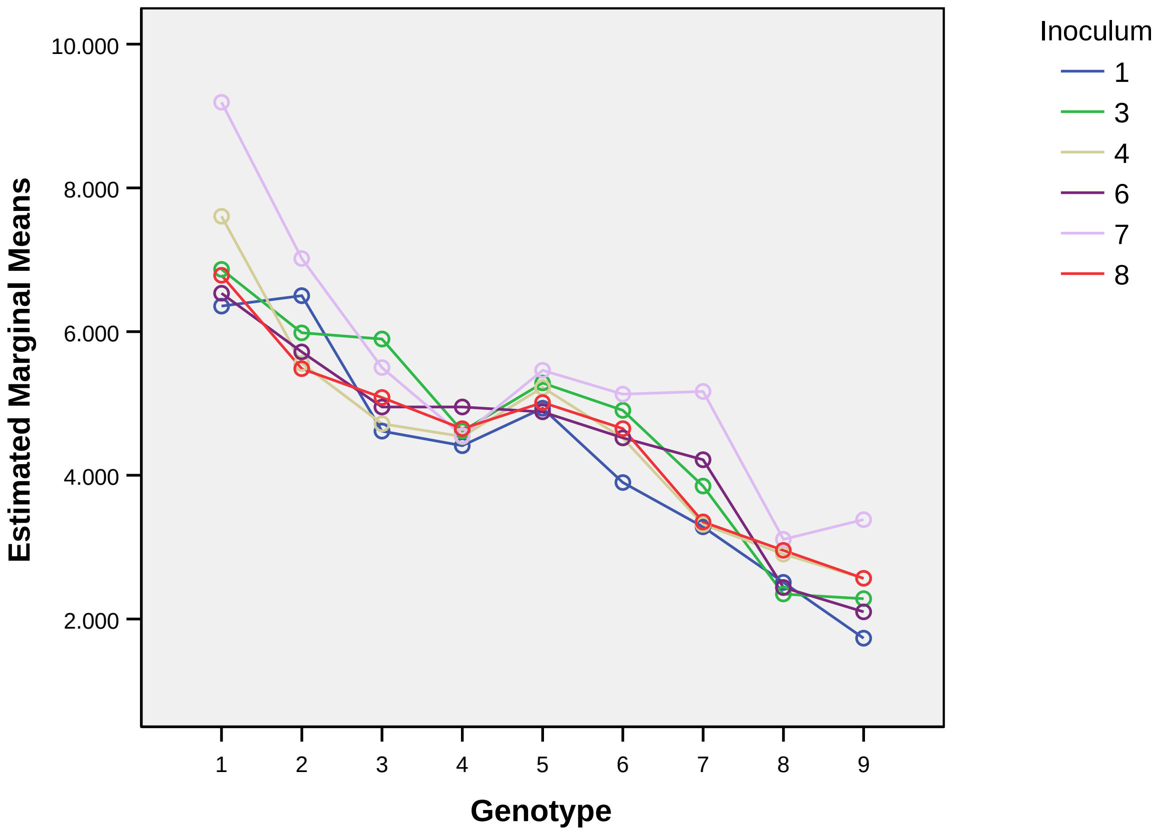
Expected Mean Squares(a,b)

Source	Variance Component							
	Var(Inoculum)	Var(Experiment)	Var(Genotype * Inoculum)	Var(Genotype * Experiment)	Var(Inoculum * Experiment)	Var(Genotype * Inoculum * Experiment)	Var(Error)	Quadratic Term
Intercept	54.000	162.000	6.000	18.000	27.000	3.000	1.000	Intercept, Genotype
Genotype	.000	.000	6.000	18.000	.000	3.000	1.000	Genotype
Inoculum	54.000	.000	6.000	.000	27.000	3.000	1.000	
Experiment	.000	162.000	.000	18.000	27.000	3.000	1.000	
Genotype * Inoculum	.000	.000	6.000	.000	.000	3.000	1.000	
Genotype * Experiment	.000	.000	.000	18.000	.000	3.000	1.000	
Inoculum * Experiment	.000	.000	.000	.000	27.000	3.000	1.000	
Genotype * Inoculum * Experiment	.000	.000	.000	.000	.000	3.000	1.000	
Error	.000	.000	.000	.000	.000	.000	1.000	

a For each source, the expected mean square equals the sum of the coefficients in the cells times the variance components, plus a quadratic term involving effects in the Quadratic Term cell.

b Expected Mean Squares are based on the Type III Sums of Squares.

Estimated Marginal Means of Mean



Variance Components Estimation

Notes

Output Created		05-JAN-2008 15:52:32
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.

	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
VARCOMP
  Mean  BY Inoculum Experiment Rep
Genotype
  /RANDOM = Inoculum Experiment
Rep
  /METHOD = MINQUE (1)
  /DESIGN = Genotype Inoculum
Experiment Genotype*Inoculum
Experiment
 *Genotype Experiment*Inoculum
  /INTERCEPT = INCLUDE .
```

Resources	Elapsed Time	0:00:00.10

```
[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Factor Level Information

		N
Inoculum	1	54
	3	54
	4	54
	6	54
	7	54
	8	54
Experiment	1	162
	2	162
Rep	1	108
	2	108
	3	108
Genotype	1	36
	2	36
	3	36
	4	36
	5	36
	6	36
	7	36
	8	36
	9	36

Dependent Variable: Mean

Variance Estimates

Component	Estimate
Var(Inoculum)	.128
Var(Experiment)	.526
Var(Inoculum * Genotype)	.053

Var(Experiment * Genotype)	.226
Var(Inoculum * Experiment)	.008
Var(Error)	.845

Dependent Variable: Mean
Method: Minimum Norm Quadratic Unbiased Estimation (Weight = 1 for Random Effects and Residual)

Univariate Analysis of Variance

Notes

Output Created		05-JAN-2008 15:52:32
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		
Resources	Elapsed Time	0:00:01.94

Syntax

```
UNIANOVA
  Mean  BY Genotype Inoculum
Experiment
  /RANDOM = Inoculum Experiment
  /METHOD = SSTYPE(3)
  /INTERCEPT = INCLUDE
  /PLOT = PROFILE(
Genotype*Inoculum )
  /PLOT = PROFILE(
Genotype*Inoculum*Experiment)
  /CRITERIA = ALPHA(.05)
  /DESIGN = Genotype Inoculum
Experiment
Genotype*Inoculum
Experiment*Genotype Experiment
 *Inoculum
```

```
[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Between-Subjects Factors

		N
Genotype	1	36
	2	36
	3	36
	4	36
	5	36
	6	36
	7	36
	8	36
	9	36
Inoculum	1	54
	3	54
	4	54
	6	54
	7	54
	8	54
Experiment	1	162
	2	162

Tests of Between-Subjects Effects

Dependent Variable: Mean

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Hypothesis	6976.061	1	6976.061	71.466	.055
	Error	113.700	1.165	97.614(a)		
Genotype	Hypothesis	658.394	8	82.299	15.711	.000
	Error	46.921	8.957	5.238(b)		
Inoculum	Hypothesis	41.525	5	8.305	6.033	.016
	Error	9.998	7.263	1.377(c)		
Experiment	Hypothesis	90.368	1	90.368	17.598	.003
	Error	41.616	8.104	5.135(d)		
Genotype * Inoculum	Hypothesis	46.487	40	1.162	1.376	.076
	Error	216.247	256	.845(e)		
Genotype * Experiment	Hypothesis	39.367	8	4.921	5.825	.000
	Error	216.247	256	.845(e)		
Inoculum * Experiment	Hypothesis	5.295	5	1.059	1.254	.285
	Error	216.247	256	.845(e)		

a 1.000 MS(Inoculum) + 1.000 MS(Experiment) - 1.000 MS(Inoculum * Experiment)
b 1.000 MS(Genotype * Inoculum) + MS(Genotype * Experiment) - MS(Error)
c MS(Genotype * Inoculum) + 1.000 MS(Inoculum * Experiment) - 1.000 MS(Error)
d MS(Genotype * Experiment) + MS(Inoculum * Experiment) - MS(Error)
e MS(Error)

Expected Mean Squares(a,b)

Source	Variance Component

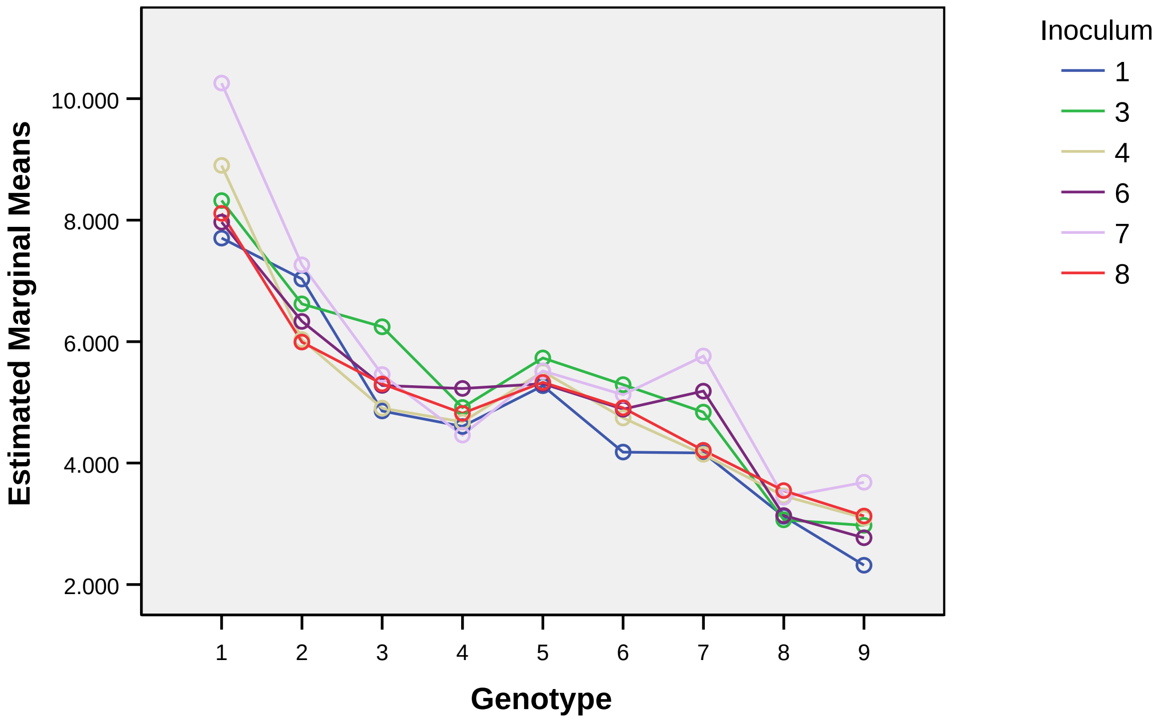
	Var(Inoculum)	Var(Experiment)	Var(Genotype * Inoculum)	Var(Genotype * Experiment)	Var(Inoculum * Experiment)	Var(Error)	Quadratic Term
Intercept	54.000	162.000	6.000	18.000	27.000	1.000	Intercept, Genotype
Genotype	.000	.000	6.000	18.000	.000	1.000	Genotype
Inoculum	54.000	.000	6.000	.000	27.000	1.000	
Experiment	.000	162.000	.000	18.000	27.000	1.000	
Genotype * Inoculum	.000	.000	6.000	.000	.000	1.000	
Genotype * Experiment	.000	.000	.000	18.000	.000	1.000	
Inoculum * Experiment	.000	.000	.000	.000	27.000	1.000	
Error	.000	.000	.000	.000	.000	1.000	

a For each source, the expected mean square equals the sum of the coefficients in the cells times the variance components, plus a quadratic term involving effects in the Quadratic Term cell.

b Expected Mean Squares are based on the Type III Sums of Squares.

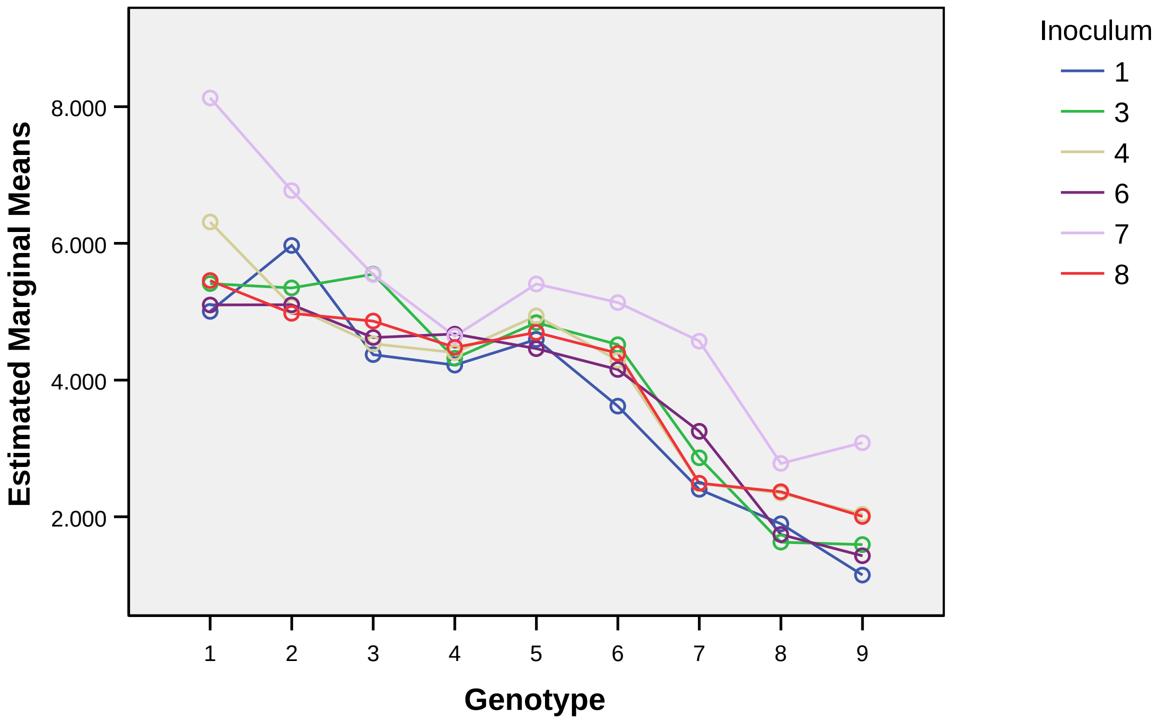
Estimated Marginal Means of Mean

at Experiment = 1



Estimated Marginal Means of Mean

at Experiment = 2



Variance Components Estimation

Notes

Output Created		05-JAN-2008 15:52:34
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.

	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
VARCOMP
  Mean  BY Inoculum Experiment
Genotype
  /RANDOM = Inoculum Experiment
  /METHOD = MINQUE (1)
  /DESIGN = Genotype Inoculum
Experiment Genotype*Inoculum
Experiment
 *Genotype Experiment*Inoculum
  /INTERCEPT = INCLUDE .
```

Resources	Elapsed Time	0:00:00.04

```
[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Factor Level Information

		N
Inoculum	1	54
	3	54
	4	54
	6	54
	7	54
	8	54
Experiment	1	162
	2	162
Genotype	1	36
	2	36
	3	36
	4	36
	5	36
	6	36
	7	36
	8	36
	9	36

Dependent Variable: Mean

Variance Estimates

Component	Estimate
Var(Inoculum)	.128
Var(Experiment)	.526
Var(Inoculum * Genotype)	.053
Var(Experiment * Genotype)	.226
Var(Inoculum * Experiment)	.008

Var(Error)	.845

Dependent Variable: Mean
Method: Minimum Norm Quadratic Unbiased Estimation (Weight = 1 for Random Effects and Residual)

Univariate Analysis of Variance

Notes

Output Created		05-JAN-2008 15:52:34
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		
Resources	Elapsed Time	0:00:00.70

Syntax:

```
UNIANOVA
  Mean  BY Genotype Inoculum
  /RANDOM = Inoculum
  /METHOD = SSTYPE(3)
  /INTERCEPT = INCLUDE
  /PLOT = PROFILE(
Genotype*Inoculum )
  /CRITERIA = ALPHA(.05)
  /DESIGN = Genotype Inoculum
Genotype*Inoculum
```

```
[DataSet1] F:\PhD\Chapter 4\InoculumExpmeansdata.sav
```

Between-Subjects Factors

		N
Genotype	1	36
	2	36
	3	36
	4	36
	5	36
	6	36
	7	36

	8	36
	9	36
Inoculum	1	54
	3	54
	4	54
	6	54
	7	54
	8	54

Tests of Between-Subjects Effects

Dependent Variable: Mean

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Intercept	Hypothesis	6976.061	1	6976.061	839.986	.000
	Error	41.525	5	8.305(a)		
Genotype	Hypothesis	658.394	8	82.299	70.815	.000
	Error	46.487	40	1.162(b)		
Inoculum	Hypothesis	41.525	5	8.305	7.146	.000
	Error	46.487	40	1.162(b)		
Genotype * Inoculum	Hypothesis	46.487	40	1.162	.893	.657
	Error	351.277	270	1.301(c)		

a MS(Inoculum)
b MS(Genotype * Inoculum)
c MS(Error)

Expected Mean Squares(a,b)

	Variance Component			
Source	Var(Inoculum)	Var(Genotype * Inoculum)	Var(Error)	Quadratic Term
Intercept	54.000	6.000	1.000	Intercept, Genotype
Genotype	.000	6.000	1.000	Genotype
Inoculum	54.000	6.000	1.000	
Genotype * Inoculum	.000	6.000	1.000	
Error	.000	.000	1.000	

a For each source, the expected mean square equals the sum of the coefficients in the cells times the variance components, plus a quadratic term involving effects in the Quadratic Term cell.
b Expected Mean Squares are based on the Type III Sums of Squares.

Variance Components Estimation

Notes

Output Created	05-JAN-2008 15:52:35
Comments	

Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
VARCOMP
  Mean  BY Inoculum  Genotype
  /RANDOM = Inoculum
  /METHOD = MINQUE (1)
  /DESIGN = Genotype Inoculum
Genotype*Inoculum
  /INTERCEPT = INCLUDE .
```

Resources	Elapsed Time	0:00:00.06

Factor Level Information

		N
Inoculum	1	54
	3	54
	4	54
	6	54
	7	54
	8	54
Genotype	1	36
	2	36
	3	36
	4	36
	5	36
	6	36
	7	36
	8	36
	9	36

Dependent Variable: Mean

Variance Estimates

Component	Estimate
Var(Inoculum)	.132
Var(Inoculum * Genotype)	-.023(a)

Var(Error)	1.301

Dependent Variable: Mean
Method: Minimum Norm Quadratic Unbiased Estimation (Weight = 1 for Random Effects and Residual)
a For the ANOVA and MINQUE methods, negative variance component estimates may occur. Some possible reasons for their occurrence are: (a) the specified model is not the correct model, or (b) the true value of the variance equals zero.

Notes

Output Created		05-JAN-2008 15:52:35
Comments		
Input	Data	F:\PhD\Chapter 4\InoculumExpmeansdata.sav
	Filter	Inoculum = 1 | Inoculum = 3 | Inoculum = 4 | Inoculum = 6 | Inoculum = 7 | Inoculum = 8 (FILTER)
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	3133
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Mean BY Genotype Inoculum Experiment /RANDOM = Inoculum Experiment /METHOD = SSTYPE(3) /INTERCEPT = INCLUDE
Resources	Elapsed Time	0:00:00.32