Estimating numbers of resistance genes to root-lesion nematodes from synthetic hexaploid wheat lines

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Introduction

Two species of root-lesion nematodes (*Pratylenchus thornei* and *P. neglectus*) reduce the value of Australian wheat production by AUD$123 million per year (1). Five accessions of synthetic hexaploid wheat (SHW) with resistance to both *P. thornei* and *P. neglectus* have been identified (2). To further investigate inheritance of resistance, doubled haploid (DH) populations between these SHW lines and the susceptible Australian bread wheat cv. Janz were tested and the numbers of genes segregating for resistance were calculated.

Material and Methods

Glasshouse resistance experiments:

Each DH population was tested for resistance to *P. thornei* and *P. neglectus* in separate experiments of 6 replicates in row-column designs. Single plants in pots of 330 g of pasteurised vertosol inoculated with 3,300 nematodes were grown at constant soil temperature (22^oC) and water tension (-2 cm) for 16 weeks. Nematodes were extracted from the soil plus roots by the Whitehead tray method, then counted under a compound microscope, and expressed as number/kg soil.

Numerical analyses:

A linear mixed model was fitted to nematode counts transformed by ln(*Pratylenchus* sp./kg soil + c) where c was a normalising constant. A separable autoregressive process was fitted to the residuals, and all design (that is blocking) and genotype effects were considered as random terms, with a fixed factor included to model the contrast between DH and parental lines. The estimated genetic variance of the DH lines (σ^2_{dh}), and the predicted performance of all entries with corresponding estimates of prediction error variances were obtained from the analysis. Heritability (h^2) on a line mean basis (3) was estimated as $\hat{h}^2 = 1 - PEV/\sigma^2_{dh}$ where PEV is the average prediction error variance of the DH lines (4). Minimum number of effective resistance genes (5; 6) was calculated as (n) = $(Ra)^2/4*\sigma^2_g$ where Ra = predicted range.

Results and Discussion

Heritability for the five DH populations ranged 0.89–0.93 for *P. thornei* (Table 1) and 0.63–0.87 for *P. neglectus* resistance (Table 2). The minimum number of resistance genes segregating in the various populations was 3-4 for *P. thornei* (Table 1) and 3-5 for *P. neglectus* (Table 2). There was no correlation between *P. thornei* and *P. neglectus* densities for four of the DH populations, and a low correlation for one (TAMD870167/AUS18913 x Janz DHs, r = 0.28, P < 0.01). Some individual DHs with moderate resistance to both *P. thornei* and *P. neglectus* were obtained from all populations, and these are valuable parents for pre-breeding dual resistance.

These results confirm that the genes conditioning resistance are mainly additive in action as concluded from diallel analysis of *P. thornei* resistance with F_1 and F_2 populations (7).

These new results with DH populations further indicate that up to 5 genes acting independently for each nematode species contribute quantitatively to the levels of resistance obtained in these crosses.

Table 1. *Pratylenchus thornei*: parameters of resistance in DH populations from SHW/Janz crosses

Parameter	Resistant SHW parent of DHs with susceptible parent Janz				
	(Yallaroi/ AUS24152)	(TAMD870167/ AUS18913)	CPI 133842	CPI 133 859	CPI 133872
Number of DHs	102	114	90	102	120
Predicted mean of DHs	10.76	10.35	10.95	10.78	9.56
Pred. mid-parent value	10.66	10.20	10.89	10.45	9.31
Predicted minimum	9.45	8.85	9.98	9.30	7.65
Predicted maximum	12.27	12.11	12.25	12.44	11.51
Predicted range (Ra)	2.82	3.26	2.27	3.14	3.86
Genetic variance (σ^2_g)	0.464	0.634	0.397	0.660	0.960
Error variance (σ^2_e)	0.282	0.397	0.150	0.286	0.404
Heritability (h^2)	0.89	0.89	0.93	0.92	0.92
Minimum no. of effective genes (n)	4	4	3	4	4

Note: Calculations based on ln(*P. thornei*/kg soil + c) where c = 5300, 1800, 12000, 4900 and 400 for the respective 5 crosses, with c selected to normalise the data

Table 2. *Pratylenchus neglectus*: parameters of resistance in DH populations from SHW/Janz crosses

Parameter	Resistant SHW parent of DHs with susceptible parent Janz				
	(Yallaroi/ AUS24152)	(TAMD870167/ AUS18913)	CPI 133842	CPI 133859	CPI 133 872
Number of DHs	106	106	100	100	99
Predicted mean of DHs	11.20	10.39	10.67	10.41	11.25
Pred. mid-parent value	10.96	10.73	10.34	10.45	10.79
Predicted minimum	10.40	9.42	9.53	9.60	9.04
Predicted maximum	11.77	11.28	11.66	11.18	12.89
Predicted range (Ra)	1.37	1.86	2.14	1.59	3.86
Genetic variance(σ^2_g)	0.160	0.199	0.251	0.169	0.658
Error variance (σ^2_e)	0.377	0.365	0.323	0.232	0.451
Heritability (h^2)	0.63	0.70	0.78	0.77	0.87
Minimum no. of effective genes (n)	3	4	5	4	5

Note: Calculations based on ln(*P. neglectus*/kg soil + c) where c = 300, 2000, 5200, 8500 and 500 for the respective 5 crosses, with c selected to normalise the data

Conclusions

• Five SHWs are a source of polygenic resistance to both *P. thornei* and *P. neglectus*

• Analysis of DH populations from SHW/Janz crosses:
  • Confirmed that inheritance is quantitative for both *P. thornei* and *P. neglectus*
  • Indicated that *P. thornei* resistance is inherited independently of *P. neglectus* resistance
  • Determined a minimum of 3-4 and 4-5 resistance genes for *P. thornei and P. neglectus* respectively in the various DH populations

More information

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