FUSE

Fungal Systematics and Evolution

VOLUME 9
JUNE 2022
PAGES 161–200

doi.org/10.3114/fuse.2022.09.08

Fusarium and allied fusarioid taxa (FUSA). 1

P.W. Crous[1,2*], M. Sandoval-Denis[1], M.M. Costa[1], J.Z. Groenewald[1], A.L. van Iperen[1], M. Starink-Willemse[1], M. Hernández-Restrepo[1], H. Kandemir[1], B. Ulaszewski[3], W. de Boer[4,5], A.M. Abdel-Azeem[6], J. Abdollahzadeh[7], A. Akulov[8], M. Bakhshi[9], J.D.P. Bezerra[10], C.S. Bhunjun[11], M.P.S. Câmara[12], P. Chaverri[13], W.A.S. Vieira[12], C.A. Decock[14], E. Gaya[15], J. Gené[16], J. Guarro[16], D. Gramaje[17], M. Grube[18], V.K. Gupta[19,20], V. Guarnaccia[21], R. Hill[15], Y. Hirooka[22], K.D. Hyde[11], R.S. Jayawardena[11], R. Jeewon[23], Ž. Jurjević[24], L. Korsten[25], S.C. Lamprecht[26], L. Lombard[27], S.S.N. Maharachchikumbura[28], G. Polizzi[29], K.C. Rajeshkumar[30], C. Salgado-Salazar[31], Q.-J. Shang[11, 28], R.G. Shivas[32], R.C. Summerbell[33,34], G.Y. Sun[35], W.J. Swart[36], Y.P. Tan[32,37], A. Vizzini[38], J.W. Xia[39], R. Zare[9], C.D. González[40], T. Iturriaga[41], O. Savary[42], M. Coton[42], E. Coton[42], J.-L. Jany[42], C. Liu[43], Z.-Q. Zeng[43,44], W.-Y. Zhuang[44], Z.-H. Yu[43], M. Thines[3,45,46]

[1]Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands
[2]Wageningen University and Research Centre (WUR), Laboratory of Phytopathology, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands
[3]Senckenberg Biodiversity and Climate Research Center, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany
[4]Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands
[5]Soil Biology Group, Wageningen University, Wageningen, Netherlands
[6]Systematic Mycology Lab., Botany and Microbiology Department, Faculty of Science, Suez Canal University, Ismailia 41522, Egypt
[7]Department of Plant Protection, Faculty of Agriculture, University of Kurdistan, P.O. Box 416, Sanandaj, Iran
[8]Department of Mycology and Plant Resistance, V. N. Karazin Kharkiv National University, Maidan Svobody 4, 61022 Kharkiv, Ukraine
[9]Iranian Research Institute of Plant Protection, Agricultural Research, Education and Extension Organization (AREEO), P.O. Box 19395-1454, Tehran, Iran
[10]Setor de Micologia / Departamento de Biociências e Tecnologia, Instituto de Patologia Tropical e Saúde Pública, Rua 235 - s/n – Setor Universitário - CEP: 74605-050, Universidade Federal de Goiás / Federal University of Goiás, Goiânia, Brasil / Goiânia, Brazil
[11]Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
[12]Departamento de Agronomia, Universidade Federal Rural de Pernambuco, Recife, 52171-900, PE, Brazil
[13]Escuela de Biología and Centro de Investigaciones en Productos Naturales, Universidad de Costa Rica, San Pedro, Costa Rica
[14]Mycothèque de l'Université catholique de Louvain (MUCL, BCCMTM), Earth and Life Institute – ELIM – Mycology, Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, B-1348 Louvain-la-Neuve, Belgium
[15]Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK
[16]Unitat de Micologia, Facultat de Medicina i Ciències de la Salut i Institut d'Investigació Sanitària Pere Virgili (IISPV), Universitat Rovira i Virgili, 43201 Reus, Spain
[17]Institute of Grapevine and Wine Sciences (ICVV), Spanish National Research Council (CSIC)-University of La Rioja-Government of La Rioja, Logroño 26007, Spain
[18]Institut für Biologie, Karl-Franzens-Universität Graz, Holteigasse 6, 8010 Graz, Austria
[19]Center for Safe and Improved Food, Scotland's Rural College (SRUC), Kings Buildings, West Mains Road, Edinburgh, EH9 3JG, UK
[20]Biorefining and Advanced Materials Research Center, Scotland's Rural College (SRUC), Kings Buildings, West Mains Road, Edinburgh, EH9 3JG, UK
[21]Department of Agricultural, Forestry and Food Sciences (DISAFA), University of Torino, Largo P. Braccini 2, 10095 Grugliasco (TO), Italy
[22]Department of Clinical Plant Science, Faculty of Bioscience, Hosei University3-7-2 Kajino-cho, Koganei, Tokyo 184-8584, Japan
[23]Department of Health Sciences, Faculty of Medicine and Health Sciences, University of Mauritius, Reduit, Mauritius
[24]EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077, USA
[25]Department of Plant and Soil Sciences, University of Pretoria, P. Bag X20 Hatfield, Pretoria 0002, South Africa
[26]ARC-Plant Health and Protection, Private Bag X5017, Stellenbosch 7599, Western Cape, South Africa
[27]Dutch General Inspection Service for agricultural seeds and seed potatoes (NAK), Randweg 14, 8304 AS, Emmeloord, The Netherlands
[28]School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu 611731, People's Republic of China
[29]Dipartimento di Agricoltura, Alimentazione e Ambiente, sez. Patologia vegetale, University of Catania, Via S. Sofia 100, 95123 Catania, Italy
[30]National Fungal Culture Collection of India (NFCCI), Biodiversity and Palaeobiology (Fungi) Group, Agharkar Research Institute, Pune, Maharashtra 411 004, India
[31]USDA-ARS Mycology & Nematology Genetic Diversity & Biology Laboratory, Bldg. 010A, Rm. 212, BARC-West, 10300 Baltimore Ave. Beltsville, MD 20705, USA
[32]Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia
[33]Sporometrics, Toronto, ON, Canada
[34]Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada
[35]College of Plant Protection, Northwest A&F University, Yangling, Shaanxi, China
[36]Faculty of Natural and Agricultural Sciences, Department of Plant Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa
[37]Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Dutton Park, Queensland 4102, Australia
[38]Department of Life Sciences and Systems Biology, University of Torino and Institute for Sustainable Plant Protection (IPSP-SS Turin), C.N.R, Viale P.A. Mattioli, 25, I-10125 Torino, Italy
[39]Shandong Provincial Key Laboratory for Biology of Vegetable Diseases and Insect Pests, College of Plant Protection, Shandong Agricultural University, Taian, 271018, China
[40]Lab. Salud de Bosques, Fac. de Ciencias Forestales y RRNN, Universidad Austral de Chile, Chile

[41]Curator, Cornell University Plant Pathology Herbarium, Ithaca, NY, USA
[42]Univ Brest, Laboratoire Universitaire de Biodiversité et Écologie Microbienne, F-29280 Plouzané, France
[43]College of Life Sciences, Yangtze University, Jingzhou, Hubei 434025, China
[44]State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China
[45]Goethe-University Frankfurt am Main, Department of Biological Sciences, Institute of Ecology, Evolution and Diversity, Max-von-Laue Str. 13, D-60438 Frankfurt am Main, Germany
[46]LOEWE Centre for Translational Biodiversity Genomics, Georg-Voigt-Str. 14-16, D-60325 Frankfurt am Main, Germany

*Corresponding author: p.crous@wi.knaw.nl

Key words:
Longinectria
multi-gene phylogeny
Nectriaceae
Neocosmospora
new taxa
systematics
typification

Abstract: Seven *Fusarium* species complexes are treated, namely *F. aywerte* species complex (FASC) (two species), *F. buharicum* species complex (FBSC) (five species), *F. burgessii* species complex (FBURSC) (three species), *F. camptoceras* species complex (FCAMSC) (three species), *F. chlamydosporum* species complex (FCSC) (eight species), *F. citricola* species complex (FCCSC) (five species) and the *F. concolor* species complex (FCOSC) (four species). New species include *Fusicolla elongata* from soil (Zimbabwe), and *Neocosmospora geoasparagicola* from soil associated with *Asparagus officinalis* (Netherlands). New combinations include *Neocosmospora akasia, N. awan, N. drepaniformis, N. duplosperma, N. geoasparagicola, N. mekan, N. papillata, N. variasi* and *N. warna.* Newly validated taxa include *Longinectria gen. nov.*, *L. lagenoides*, *L. verticilliforme*, *Fusicolla gigas* and *Fusicolla guangxiensis*. Furthermore, *Fusarium rosicola* is reduced to synonymy under *N. brevis.* Finally, the genome assemblies of *Fusarium secorum* (CBS 175.32), *Microcera coccophila* (CBS 310.34), *Rectifusarium robinianum* (CBS 430.91), *Rugonectria rugulosa* (CBS 126565), and *Thelonectria blattea* (CBS 952.68) are also announced here.

Citation: Crous PW, Sandoval-Denis M, Costa MM, Groenewald JZ, van Iperen AL, Starink-Willemse M, Hernández-Restrepo M, Kandemir H, Ulaszewski B, de Boer W, Abdel-Azeem AM, Abdollahzadeh J, Akulov A, Bakhshi M, Bezerra JDP, Bhunjun CS, Câmara MPS, Chaverri P, Vieira WAS, Decock CA, Gaya E, Gené J, Guarro J, Gramaje D, Grube M, Gupta VK, Guarnaccia V, Hill R, Hirooka Y, Hyde KD, Jayawardena RS, Jeewon R, Jurjević Ž, Korsten L, Lamprecht SC, Lombard L, Maharachchikumbura SSN, Polizzi G, Rajeshkumar KC, Salgado-Salazar C, Shang Q-J, Shivas RG, Summerbell RC, Sun GY, Swart WJ, Tan YP, Vizzini A, Xia JW, Zare R, González CD, Iturriaga T, Savary O, Coton M, Coton E, Jany J-L, Liu C, Zeng Z-Q, Zhuang W-Y, Yu Z-H, Thines M (2022). *Fusarium* and allied fusarioid taxa (FUSA). 1. *Fungal Systematics and Evolution* **9**: 161–200. doi: 10.3114/fuse.2022.09.08
Received: 21 March 2022; **Accepted:** 14 June 2022; **Effectively published online:** 23 June 2022
Corresponding editor: A.J.L. Phillips

INTRODUCTION

Several initiatives in recent years have addressed problems that face contemporary fungal taxonomy. The Fungal Planet series was launched to overcome the reluctance of most mycology journals to publish single new species descriptions (Crous *et al.* 2011). The Genera of Fungi (GoF) project facilitated the application of fungal generic names through the re-collection of generic types and the designation of epitypes or neotypes (Kirk *et al.* 2013, Crous *et al*. 2014). The Fungal Systematics and Evolution (FUSE) series allowed the effective combination of molecular phylogenetic data with phenotypic data to link sexual, asexual and synasexual morphs to known or newly described taxa following the end of the dual nomenclatural system (Crous *et al.* 2015). Finally, the Genera of Phytopathogenic Fungi (GOPHY) project was introduced to stabilize the taxonomy of fungal phytopathogens at generic and species levels, coupled with biological information about host distribution, pathogenicity, disease symptomatology and DNA barcodes for accepted species (Marin-Felix *et al.* 2017). The aforementioned publication series inspired other similar initiatives worldwide, such as Fungal Biodiversity Notes (Liu *et al.* 2015), Fungal Biodiversity Profiles (Adamčík *et al.* 2015), Mycosphere Notes (Thambugala *et al*. 2017), and the more recent New and Interesting Fungi (Crous *et al.* 2018). With an average of 10 to more than 100 new taxa per issue, these publications have become valuable tools for the description of new fungal families, genera and species, as well as for the dissemination of knowledge about the world's fungal diversity.

In FUSA we introduce a new series of specialised papers focusing on the taxonomy, phylogeny, systematics, ecology and pathogenicity of known and novel *Fusarium* and allied fusarioid taxa. *Fusarium* (*F.*) and related genera are globally distributed fungi, found in diverse substrates, although most commonly in soil, living and dead plant material, air and water (Nelson *et al.* 1994, Leslie & Summerell 2006, Aoki *et al.* 2014, Leslie & Summerell 2011). Much of the historical importance of these fungi is based on the economically impactful of plant pathogenic species that infect a wide spectrum of crops inducing cankers, dieback, dry rot of roots and seeds, scab and wilt diseases (Booth 1971, Summerell *et al.* 2003); as well as numerous mycotoxigenic species endanger animal and human health (Nelson *et al.* 1994, O'Donnell *et al.* 2018). Nevertheless, in the last decade several taxa have gained importance as opportunistic human and animal pathogens, particularly members of *Neocosmospora* (formerly the *Fusarium solani* species complex), *Bisifusarium* (formerly the *Fusarium dimerum* species complex) and members of at least five species complexes of *Fusarium sensu stricto* (van Diepeningen *et al.* 2014, Lombard *et al.* 2015, Sandoval-Denis *et al*. 2018, 2019, Crous *et al.* 2021b).

The main goal of FUSA is to publish modern diagnoses of fusarioid taxa, based on multilocus phylogenies, ideally accompanied by genomic data, morphological descriptions, as well as physiological and ecological data. These data will subsequently be placed in an online database, www.fusarium.org, linked to the fusarioid-ID database, which aims to provide a stable, regularly updated, and user-friendly platform for the identification of *Fusarium* and other fusarioid genera and species through advanced BLASTn queries of well-curated DNA sequences.

Contributors are encouraged to use FUSE as an instrument for typification events to stabilise the application of names by designating accurate lectotypes, epitypes and neotypes;

proposing taxonomic novelties such as new combinations and replacement names; and publishing undescribed morphologies for known taxa (asexual/sexual-morph connections). The selection of culture media, culture conditions and the morphological treatment must be based on standardised fusarioid laboratory protocols, as outlined in Crous *et al.* (2021b); fungal descriptions must be standardised and follow given examples; description of new species should be accompanied by a brief, comprehensive taxonomic discussion; all taxonomic novelties must be registered in MycoBank and ex-type or ex-isotype strains should be deposited in the CBS collection if possible (hosted in the Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands). Mycologists and other researchers wishing to contribute to future issues of FUSA are encouraged to contact the Editor-in-Chief (p.crous@wi.knaw.nl).

MATERIALS AND METHODS

Methods, media, protocols and molecular analyses follow guidelines as outlined by Crous *et al.* (2021b). Sequences derived in this study were deposited in GenBank (Table 1), alignments and phylogenetic trees in Figshare (www.figshare.com; doi identifier 10.6084/m9.figshare.20076044), and taxonomic novelties in MycoBank (www.MycoBank.org; Crous *et al*. 2004). Alignments composition and evolutionary models are summarized in Table 2.

Genome assembly

DNA was extracted from mycelium grown on SAM (Kruse *et al*. 2017) culture plates as described earlier (Mishra *et al*. 2018). Library construction and short-read sequencing was done by a commercial sequencing provider (BGI, Hongkong, PRC). Pair-end reads (150 bp, 400 bp insert) were cleaned with *Trimmomatic* v. 0.39 (Bolger *et al.* 2014) with the following settings: remove leading and trailing low quality (< 3) or N bases; cutting when the average quality per base dropped below 15 in a 4-base sliding window; Illumina adaptor removal; removing reads shorter than 70 bp. Cleaned reads were used to assemble genomes with *velvet* v. 1.2.10 (Zerbino & Birney, 2008) using a k-mer value of 93. Assembly statistics were obtained using the stats.sh script of the BBTools package (Bushnell 2021). The assembly quality was evaluated with BUSCO v. 5.2.2 against the fungi_odb10 library (Manni *et al.* 2021). Genome annotation was done with maker v. 3.01.03 (Cantarel *et al.* 2008) for gene prediction using the protein sequences of *Fusarium oxysporum* from the UniProt database as reference. All genomes were submitted to GenBank (see Table 3 for details).

RESULTS

Phylogeny

For this study, three multilocus analyses were carried out. The datasets were analysed using IQ-TREE v. 2.1.3 (Nguyen *et al*. 2015, Minh *et al*. 2020) and MrBayes v. 3.2.7 (Ronquist & Huelsenbeck 2003) as indicated in Crous *et al.* (2021b).

An overview of currently accepted taxa in *Fusarium* species complexes treated in this study is shown in a phylogeny constructed from combined *rpb1*, *rpb2* and *tef1* data of 62 strains, encompassing eight species complexes *i.e.*, *Fusarium aywerte* (FASC), *F. buharicum* (FBSC), *F. burgessii* (FBURSC), *F. camptoceras* (FCAMSC), *F. chlamydosporum* (FCSC), *F. citricola* (FCCSC), and *F. concolor* (FCOSC), including the outgroup taxa (*F. lateritium* NRRL 13622 and *F. stilboides* NRRL 20429, both species belonging to the *F. lateritium* species complex) (Fig. 1). IQ-TREE best tree (log-likelihood -26203.881) was found after 102 iterations. Bayesian analysis lasted for 235 000 generations and recovered 472 trees from which 354 where sampled. The phylogeny resolved all the treated species complexes with high statistical support. Thirty species are recognised (two in FASC, three each in FBURSC and FCAMSC, five each in FCCSC, and FBSC; eight in FCSC, and four in FCOSC). Additionally, three phylogenetic species awaiting formal description were found, of which one resolved in FCSC (*Fusarium* sp. FCSC 9) and two in the FBSC (clades *Fusarium* sp. 1, and *Fusarium* sp. 2)

Fusicolla: A phylogeny was constructed using combined *acl1*, ITS, LSU, *rpb2* and *tub2* sequences of 23 strains representing 18 species of *Fusicolla* (*Fu.*), plus two outgroup taxa (*Macroconia leptosphaeriae* CBS 10001 and *Scolecofusarium ciliatum* CBS 148938) (Fig. 2). IQ-TREE best tree (log-likelihood -15164.779) was found after 117 iterations. Bayesian analysis lasted for 1 535 000 generations and recovered 3 072 trees from which 2 304 where sampled. Two strains obtained from soil in Zimbabwe (MUCL 58143, 58144) are formally described below as the novel species *Fusicolla elongata*. Sequence data from additional *Fusicolla* species known from culture (*Fu*. *gigas*, *Fu*. *hughesii*, *Fu*. *guangxiensis*) or sequenced from fungarium specimens (*Fu*. *reyesiana*) were initially included in the phylogenies and later removed from the final analyses due to their incomplete datasets (nrDNA or only ITS1 and ITS2 sequences available). Two species recently invalidly published *i.e*., *Fu*. *gigas* and *Fu*. *guangxiensis* are re-validated here based on the original protologue (Liu *et al*. 2022).

Neocosmospora: A combined alignment was built including ITS, *rpb1*, *rpb2*, and *tef1* sequences from 73 strains representing the known species diversity of the Ambrosia Clade (Kasson *et al.* 2013) and close relatives from Clades 1, 2 and 3 of *Neocosmospora* (O'Donnell 2000) (Fig. 3). IQ-TREE best tree (log-likelihood -20219.033) was found after 103 iterations. Bayesian analysis lasted for 480 000 generations and recovered 962 trees from which 722 where sampled. The Ambrosia Clade was found to encompass 23 phylogenetic species (AF 1-23), 15 of which have been formally described to date. *Fusarium* species are recombined in *Neocosmospora* including seven species in the Ambrosia Clade (*N. akasia*, *N. drepaniformis*, *N. duplosperma*, *N. mekan*, *N. papillata*, *N. variasi*, and *N. warna*) and the distantly related although ecologically similar *N. awan*. The ex-type of *F. rosicola* (YJ1) clustered with *N. brevis*, and the former is synonymised under the latter. A previously undescribed, phylogenetically well-differentiated clade composed of seven soil isolates obtained from different asparagus (*Asparagus officinalis*) fields, formed a basal lineage in Clade 2. This lineage is formally proposed below as the novel species *N. geoasparagicola*.

Table 1. Collection details and GenBank accession numbers of isolates treated in this study.

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
Fusarium abutilonis	NRRL 66737[T]	Canada, *Abutilon theophrasti*				JAJJWN010000057[†]	JAJJWN010000064[†]	JAJJWN010000135[†]	
Fusarium aconidiale	CBS 147772[T]	France, *Triticum aestivum*	-	-	-	MZ078192	MZ078218	MZ078246	-
Fusarium algeriense	CBS 142638[T]	Algeria, *Triticum durum*	-	-	-	MF120488	MF120499	MF120510	-
Fusarium anguioides	LC7240	China, bamboo	-	-	-	MW024433	MW474388	MW580442	-
	NRRL 25385	China, bamboo	-	-	-	JX171511	JX171624	MH742689	-
Fusarium atrovinosum	CBS 445.67[T]	Australia, *Triticum aestivum*	-	-	-	MN120713	MW928822	MN120752	-
	CBS 130394	USA, human leg	-	-	-	MN120714	MN120734	MN120753	-
	NRRL 13444	Australia, corn soil	-	-	-	JX171454	JX171568	GQ505403	-
	NRRL 34013	USA, human toe nail	-	-	-	-	GQ505472	GQ505408	-
	NRRL 34016	USA, human leg	-	-	-	HM347170	GQ505475	GQ505411	-
Fusarium austroafricanum	NRRL 66741[T]	South Africa, *Pennisetum clandestinum*	-	-	-	MH742537	MH742616	MH742616	-
	NRRL 66742	South Africa, *Pennisetum clandestinum*	-	-	-	MH742538	MH742617	MH742688	-
Fusarium aywerte	NRRL 25410[T]	Australia, soil	-	-	-	JX171513	JX171626	JABCQV010000336[†]	-
Fusarium bambusarum	CGMCC 3.20820[T]	China, bamboo	-	-	-	MW024434	MW474389	MW580443	-
	LC7187	China, bamboo	-	-	-	MW024435	MW474390	MW580444	-
Fusarium beomiforme	CBS 100160[T]	Australia, soil	-	-	-	MF120485	MF120496	MF120507	-
Fusarium buharicum	CBS 178.35[ET]	Uzbekistan, *Gossypium herbaceum*	-	-	-	KX302920	KX302928	KX302912	-
	CBS 796.70	Iran, *Hibiscus cannabinus*	-	-	-	JX171449	JX171563	-	-
Fusarium burgessii	CBS 125537[T]	Australia, soil	-	-	-	MT409440	HQ646393	HQ667148	-
Fusarium camptoceras	CBS 193.65[ET]	Costa Rica, *Theobroma cacao*	-	-	-	MW928800	MN170383	AB820706	-
Fusarium celtidicola	MFLUCC 16-0526[T]	Italy, *Celtis australis*	-	-	-	MH576579	**ON759296**	**ON745620**	-
Fusarium chlamydosporum	CBS 145.25[NT]	Honduras, *Musa sapientum*	-	-	-	MN120715	MN120735	MN120754	-
	CBS 615.87	Cuba, *Colocasia esculenta*	-	-	-	JX171526	GQ505469	GQ505405	-
	CBS 677.77	Solomon Islands, soil	-	-	-	MN120716	GQ505486	GQ505422	-
	NRRL 34019	USA, human eye	-	-	-	-	GQ505478	GQ505414	-
	NRRL 43633	USA, human sinus	-	-	-	-	GQ505493	GQ505429	-
Fusarium citricola	CBS 142421[T]	Italy, *Citrus reticulata*	-	-	-	LT746290	LT746310	LT746197	-

Table 1. (Continued).

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
	CPC 27067	Italy, *Citrus limon*	-	-	-	LT746287	LT746307	LT746194	-
Fusarium concolor	CBS 183.34^{T}	Uruguay, *Hordeum vulgare*	-	-	-	MH742492	MH742569	MH742650	-
	CBS 677.94	South Africa, soil	-	-	-	MH742503	MH742580	MH742660	-
Fusarium convolutans	CBS 144207^{T}	South Africa, *Kyphocarpa angustifolia* rhizosphere	-	-	-	LT996193	LT996141	LT996094	-
	CBS 144208	South Africa, *Kyphocarpa angustifolia* rhizosphere	-	-	-	LT996194	LT996142	LT996095	-
Fusarium guadeloupense	CBS 102302^{T}	Guadeloupe, soil				JAJJWL010000373[†]	JAJJWL010000322[†]	JAJJWL010000221[†]	
	NRRL 66743	USA, human blood				JAJJWM010000272[†]	JAJJWM010000096[†]	JAJJWM010000091[†]	
Fusarium humicola	CBS 124.73^{T}	Pakistan, soil	-	-	-	MN120718	MN120738	MN120757	-
Fusarium juglandicola	CBS 147773^{T}	France, *Juglans regia*	-	-	-	MZ078190	MZ078215	MZ078243	-
	CBS 147775	France, *Juniperus* sp.	-	-	-	MZ078191	MZ078217	MK034341	-
Fusarium kotabaruense	InaCC F963^{T}	Indonesia, *Musa* sp.	-	-	-	LS479875	LS479859	LS479445	-
Fusarium lateritium	NRRL 13622	USA, *Ulmus* sp.	-	-	-	JX171457	JX171571	JAAVTZ000000000[†]	-
Fusarium microconidium	CBS 119843^{T}	Unknown	-	-	-	MN120721	-	MN120759	-
Fusarium nelsonii	CBS 119876^{T}	South Africa, plant debris	-	-	-	MN120722	GQ505468	GQ505404	-
	CBS 119877	Unknown	-	-	-	MN120721	MN120741	MN120759	-
Fusarium neosemitectum	CBS 189.60^{T}	Congo, *Musa sapientum*	-	-	-	-	MN170422	MN170489	-
	CBS 190.60	Congo, *Musa sapientum*	-	-	-	-	MN170423	MN170490	-
Fusarium peruvianum	CBS 511.75^{T}	Peru, *Gossypium* sp.	-	-	-	MN120728	MN120746	MN120767	-
Fusarium salinense	CBS 142420^{T}	Italy, *Citrus sinensis*	-	-	-	LT746286	LT746306	LT746193	-
	CPC 26403	Italy, *Citrus sinensis*	-	-	-	LT746304	LT746191	LT746284	-
Fusarium sp. (FCSC9)	NRRL 13338	Australia, soil	-	-	-	JX171447	JX171561	GQ505402	-
Fusarium sp. 1	NRRL 66179	USA, *Hibiscus moscheutos*	-	-	-	KX302921	KX302929	KX302913	-
	NRRL 66180	USA, *Hibiscus moscheutos*	-	-	-	KX302922	KX302930	KX302914	-
	NRRL 66181	USA, *Hibiscus moscheutos*	-	-	-	KX302923	KX302931	KX302915	-
	NRRL 66182	USA, *Hibiscus moscheutos*	-	-	-	KX302924	KX302932	KX302916	-
	NRRL 66183	USA, *Hibiscus moscheutos*	-	-	-	KX302925	KX302933	KX302917	-

Table 1. (Continued).

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
	NRRL 66184	USA, *Hibiscus moscheutos*	-	-	-	KX302926	KX302934	KX302918	-
Fusarium sp. 2	NRRL 66739	China, unknown				JAJJWO010000055[†]	JAJJWO010000203[†]	JAJJWO010000256[†]	
Fusarium spinosum	CBS 122438[T]	Brazil, *Cucumis melo*	-	-	-	MN120729	MN120747	MN120768	-
	NRRL 43631	USA, human leg	-	-	-	HM347187	GQ505491	GQ505427	-
Fusarium sporodochiale	CBS 220.61[T]	South Africa, soil	-	-	-	MN120731	MN120749	MN120770	-
Fusarium stilboides	NRRL 20429	Nyasaland, *Coffea* sp.	-	-	-	JX171468	JX171582	-	-
Fusarium sublunatum	CBS 189.34[T]	Costa Rica, soil	-	-	-	JX171451	JX171565	-	-
	CBS 190.34	Costa Rica, soil	-	-	-	KX302927	KX302935	KX302919	-
Fusarium tjaynera	NRRL 66246[T]	Australia, *Triodia microstachya*	-	-	-	KP083268	KP083279	EF107152	-
Fusicolla acetilerea	BBA 63789[T]	Japan, polluted soil	HQ897839	HQ897790	U88108	-	HQ897701	-	-
Fusicolla aquaeductuum	CBS 268.53	Netherlands, rubber tubing	-	MH857190	MH868728	-	-	-	-
	CBS 837.85[ET]	Germany, plug in water tap	-	KM231823	KM231699	-	-	-	KM232094
Fusicolla betae	BBA 64317[ET]	Germany, *Triticum aestivum*	HQ897917	-	-	-	HQ897781	-	-
Fusicolla bharatavarshae	NFCCI 4423[T]	India, *Avicennia marina*	-	MK152510	MK152511	-	MK157022	-	MK376462
Fusicolla cassiae-fistulae	MFLUCC 19-0318[T]	Thailand, *Cassia fistula*	-	MT215497	MT215549	-	-	-	-
Fusicolla elongata	CBS 148934[T]	Zimbabwe, soil	**ON759286**	**ON763203**	**ON763200**	-	**ON759297**	-	**ON745628**
	CBS 148935	Zimbabwe, soil	**ON759287**	**ON763204**	**ON763201**	-	**ON759298**	-	**ON745629**
Fusicolla epistroma	BBA 62201[ET]	UK, *Diatrypella* sp., on *Betula* sp.	HQ897901	-	AF228352	-	HQ897765	-	-
Fusicolla gigantispora	HKAS 101990	Thailand, *Bruguiera* sp.	-	MN047106	MN017870	-	-	-	-
	MFLU 16-1206[T]	Thailand, *Avicennia marina*	-	MN047105	MN017876	-	-	-	-
Fusicolla gigas	CGMCC 3.20680	China, soil	-	OK465362	OK465449	-	-	-	-
Fusicolla guangxiensis	CGMCC 3.20679	China, rotten twig	-	OK465363	OK465450	-	-	-	-
Fusicolla matuoi	CBS 581.78	Japan, *Albizzia julibrissin*	HQ897858	KM231822	KM231698	-	HQ897720	-	KM232093
Fusicolla melogrammae	CBS 141092[T]	UK, *Melogramma campylosporum* on *Carpinus* sp.	-	KX897140	KY092489	-	HQ897720	-	MW834305
Fusicolla meniscoidea	CBS 110189[T]	Australia, soil	MW834043	MW827613	MW827654	-	MW834010	-	MW834306
	CBS 186.34	Germany, *Acer* sp.	-	MH855482	MH866963	-	-	-	-

Table 1. (Continued).

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
Fusicolla ossicola	CBS 140161[T]	Belgium, bone of wild boar	-	MF628022	MF628021	-	MW834011	-	MW834307
Fusicolla quarantenae	CBS 141541[T]	Brazil, *Melocactus zehntneri*	MW834044	MW553789	MW553788	-	MW556626	-	MW556624
Fusicolla septimanifiniscientiae	CBS 144935[T]	Netherlands, soil	-	MK069422	MK069418	-	-	-	MK069408
Fusicolla siamensis	MFLUCC 17-2577[T]	Thailand, *Cassia fistula*	-	MT215498	MT215550	-	-	-	-
Fusicolla sporellula	CBS 110191[T]	South Africa, soil	MW834044	MW827614	MW827655	-	MW834012	-	MW834308
Fusicolla violacea	CBS 634.76[T]	Iran, *Quadraspidiotus perniciosus*	-	KM231824	U88112	-	HQ897696	-	KM232095
Geejayessia atrofusca	NRRL 22316	USA, *Staphylea trifolia*	-	AF178423	-	JX171496	EU329502	AF178361	-
Geejayessia cicatricum	CBS 125552	Slovenia, dead twig	-	HQ728145	-	-	HQ728153	HM626644	-
Macroconia leptosphaeriae	CBS 100001	Netherlands, *Leptosphaeria* sp.	HQ897891	HQ897810	HQ897755	MW834203	HQ728164	-	KM232097
Neocosmospora acutispora	CBS 145461[T]	Guatemala, *Coffea arabica*	-	LR583700	-	MW834210	LR583814	LR583593	-
Neocosmospora akasia	CBS 146880[T]	Indonesia, *Euwallacea perbrevis*	-	MN954357	-	-	MT009931, MT010011	MT009971	-
	CMW52865	Indonesia, *Acacia crassicarpa*	-	MN954330	-	-	MT009904, MT009984	MT009943	-
Neocosmospora ambrosia	CBS 571.94[ET]	India, *Euwallacea fornicatus*	-	EU329669	-	MW834211	EU329503	FJ240350	-
	NRRL 62942	Sri Lanka, *Camellia sinensis*	-	KM406631	-	KM406638	KM406638, KM406645	KM406624	-
Neocosmospora awan	CBS 146882[T]	Indonesia, *Acacia crassicarpa*	-	MN954345	-	-	MT009919, MT009999	MT009973	-
	CBS 146884	Indonesia, *Acacia crassicarpa*	-	JQ038014	-	-	JQ038028	JQ038007	-
Neocosmospora brevis	CBS 144387[T]	Belgium, soil-water	-	LR583708	-	MW834214	LR583822	LR583601	-
	CPC 27191	Italy, *Citrus sinensis*	-	LT746248	-	-	LT746313	LT746200	-
	YJ1	China, *Rosa chinensis*	-	MW724816	-	-	MW795356	MW795357	-
	YJ2	China, *Rosa chinensis*	-	MW724817	-	-	MW795358	MW795359	-
Neocosmospora cryptoseptata	CBS 145463[T]	French Guiana, bark	-	AF178414	-	MW834215	EU329510	AF178351	-
Neocosmospora drepaniformis	NRRL 62941[T]	Singapore, unknown	-	KM406633	-	JAALXN000000000[†]	KM406640, KM406647	KM406626	-

Table 1. (Continued).

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
Neocosmospora duplosperma	NRRL 62583[T]	USA, *Euwallacea fornicatus*	-	KC691581	-	KC691611	KC691642, KC691671	KC691553	-
	NRRL 62585	USA, *Euwallacea fornicatus*	-	KC691577	-	KC691607	KC691638, KC691667	KC691549	-
Neocosmospora euwallaceae	CBS 135854[T]	Israel, *Euwallacea* sp.	-	JQ038014	-	JQ038021	JQ038028	JQ038007	-
	NRRL 62626	USA, *Euwallacea* sp.	-	KC691560	-	KC691590	KC691621, KC691650	KC691532	-
Neocosmospora floridana	NRRL 62608	USA, Boxelder tree infested with *Euwallacea interjectus*	-	KC691562	-	KC691592	KC691623, KC691652	KC691534	-
	NRRL 62628[T]	USA, *Euwallacea interjectus*	-	KC691563	-	KC691593	KC691624, KC691653	KC691535	-
Neocosmospora geoasparagicola	CBS 148936	Netherlands, soil	-	**ON763206**	-	**ON759289**	**ON759300**	**ON745621**	-
	CBS 148937[T]	Netherlands, soil	-	**ON763207**	-	**ON759290**	**ON759301**	**ON745622**	-
	CPC 39931	Netherlands, soil	-	**ON763208**	-	**ON759291**	**ON759302**	**ON745623**	-
	CPC 39932	Netherlands, soil	-	**ON763209**	-	**ON759292**	**ON759303**	**ON745624**	-
	CPC 40571	Netherlands, soil	-	**ON763210**	-	**ON759293**	**ON759304**	**ON745625**	-
	CPC 40579	Netherlands, soil	-	**ON763211**	-	**ON759294**	**ON759305**	**ON745626**	-
	CPC 40628	Netherlands, soil	-	**ON763212**	-	**ON759295**	**ON759306**	**ON745627**	-
Neocosmospora illudens	CBS 147303	New Zealand, *Beilschmiedia tawa*	-	AF178393	-	JX171488	JX171601	AF178326	-
Neocosmospora kuroshio	CBS 142642[T]	USA, *Euwallacea* sp. gallery	-	LR583723	-	KX262236	KX262256	KX262216	-
	NRRL 62946	USA, *Platanus racemosa*	-	KM406637	-	KM406644	KM406650	KM406630	-
Neocosmospora kurunegalensis	CBS 119599[T]	Sri Lanka, recently cut tree	-	JF433036	-	MW834228	LR583838	DQ247511	-
Neocosmospora lichenicola	CBS 623.92[ET]	Germany, human	-		-	-	LR583845	LR583620	-
Neocosmospora mahasenii	CBS 119594[T]	Sri Lanka, unknown tree	-	JF433045	-	MW834231	LT960563	DQ247513	-
Neocosmospora mekan	CBS 146885[T]	Indonesia, *Euwallacea similis*	-	MN954342	-	-	MT009916, MT009996	MT009956	-
	CBS 146886	Indonesia, *Acacia crassicarpa* infested with *Euwallaceae* spp.	-	MN954335	-	-	MT009909, MT009989	MT009962	-
Neocosmospora nirenbergiana	CBS 145469[T]	French Guiana, Bark	-	AF178403	-	-	EU329505	AF178339	-
Neocosmospora obliquiseptata	NRRL 62610	Australia, *Euwallacea* sp. gallery	-	KC691575	-	KC691605	KC691636, KC691665	KC691547	-

Table 1. (Continued).

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
	NRRL 62611[T]	Australia, *Euwallacea* sp. gallery	-	KC691576	-	KC691606	KC691637, KC691666	KC691535	-
Neocosmospora oligoseptata	CBS 143241[T]	USA, *Euwallacea validus*	-	KC691566	-	KC691596	LR583854	KC691538	-
	NRRL 62582	USA, *Ailanthus* sp.	-	KC691569	-	KC691599	KC691630, KC691659	KC691541	-
Neocosmospora papillata	NRRL 62943[T]	Sri Lanka, *Camellia sinensis*	-	KM406635	-	KM406642	S24402*	KM406628	-
	NRRL 62944	Sri Lanka, *Euwallaceae* sp. on *Camellia sinensis*	-	KM406634	-	KM406641	KM406648	KM406627	-
Neocosmospora phaseoli	CBS 265.50	USA, *Phaseolus* sp.	-	LR583750	-	-	KJ511278	FJ919464	-
Neocosmospora plagianthi	NRRL 22632	New Zealand, *Hoheria glabrata*	-	AF178417	-	JX171501	JX171614	AF178354	-
Neocosmospora rectiphora	CBS 125726	Sri Lanka, dead tree	-	JF433043	-	MW834248	MW834028	JF433026	-
	CBS 125727[T]	Sri Lanka, dead tree	-	JF433034	-	MW834249	LR583871	DQ247509	-
Neocosmospora rekana	CMW53690	Indonesia, *Euwallacea fornicatus*	-	MN249098	-	-	MN249141, MN249112	MN249155	-
	CMW52862[T]	Indonesia, *Euwallacea perbrevis*	-	MN249094	-	-	MN249137, MN249108	MN249151	-
Neocosmospora robusta	CBS 145473[T]	Venezuela, bark	-	AF178405	-	MW834251	EU329507	AF178341	-
Neocosmospora samuelsii	CBS 114067[T]	Guyana, bark	-	LR583764	-	MW834252	LR583874	LR583644	-
Neocosmospora sp. (AF-6)	NRRL 62590	USA, *Euwallacea fornicatus* gallery	-	KC691574	-	KC691604	KC691635, KC691664	KC691546	-
	NRRL 62591	USA, *Euwallacea fornicatus* gallery	-	KC691573	-	KC691603	KC691634, KC691663	KC691545	-
Neocosmospora sp. (AF-9)	NRRL 22643	Costa Rica, *Xyleborus ferrugineus*	-	KC691583	-	KC691613	KC691644, KC691673	DQ247628	-
	NRRL 66088	USA, *Delonix regia*	-	KM406632	-	KM406639	KM406646	KM406625	-
Neocosmospora sp. (AF-13)	UCR4674	Taiwan, *Euwallacea* sp.	-	KX262208	-	KX262248	KX262268	KX262228	-
	UCR4675	Taiwan, *Euwallacea* sp.	-	KX262209	-	KX262249	KX262269	KX262229	-
Neocosmospora sp. (AF-14)	UCR4672	Taiwan, *Euwallacea* sp.	-	KX262206	-	KX262246	KX262266	KX262226	-
	UCR4681	Taiwan, *Euwallacea* sp.	-	KX262215	-	KX262255	KX262275	KX262235	-
Neocosmospora sp. (AF-15)	UCR4679	Taiwan, *Euwallacea* sp.	-	KX262213	-	KX262253	KX262273	KX262233	-
Neocosmospora sp. (AF-16)	UCR4673	Taiwan, *Euwallacea* sp.	-	KX262207	-	KX262247	KX262267	KX262227	-
	UCR4678	Taiwan, *Euwallacea* sp.	-	KX262212	-	KX262252	KX262272	KX262232	-
Neocosmospora sp. (AF-17)	UCR4676	Taiwan, *Euwallacea* sp.	-	KX262210	-	KX262250	KX262270	KX262230	-
	UCR4680	Taiwan, *Euwallacea* sp.	-	KX262214	-	KX262254	KX262274	KX262234	-

Table 1. (Continued).

Species	Strain[1]	Country and substrate/ host	GenBank accession number[2]						
			acl1	ITS	LSU	*rpb1*	*rpb2*	*tef1*	*tub2*
Neocosmospora sp. (AF-18)	UCR4677	Taiwan, *Euwallacea* sp.	-	KX262211	-	KX262251	KX262271	KX262231	-
Neocosmospora tuaranensis	NRRL 22231^{T}	Malaysia, *Hevea brasiliensis*	-	KC691570	-	KC691600	KC691660, KC691631	KC691542	-
	NRRL 46519	Malaysia, beetle on *Hevea brasiliensis*	-	KC691572	-	KC691602	KC691633	KC691544	-
Neocosmospora variasi	CBS 146888^{T}	Indonesia, *Acacia crassicarpa* infested with *E. perbrevis*	-	MN954356	-	-	MT009913, MT009993	MT009967	-
	CBS 146889	Indonesia, *Acacia crassicarpa* infested with *E. perbrevis*	-	MN954357	-	-	MT009914, MT009994	MT009968	-
Neocosmospora vasinfecta	NRRL 22166^{ET}	USA, *Gossypium* sp.	-	DQ094319	-	SSHR01002742†	EU329497	AF178350	-
	NRRL 43467	USA, human eye	-	EF453092	-	HM347178	EF469979	EF452940	-
Neocosmospora warna	CBS 146891^{T}	Indonesia, *Euwallacea perbrevis*	-	MN954346	-	-	MT009920, MT010000	MT009955	-
	CBS 146893	Indonesia, *Euwallacea perbrevis*	-	MN954351	-	-	MT009925, MT010005	MT009958	-
Scolecofusarium ciliatum	CBS 148938	Ukraine, *Peniophora rufomarginata*	**ON759288**	**ON763205**	**ON763202**	-	**ON759299**	-	**ON745630**

[1] CBS: Westerdijk Fungal Biodiverity Institute (WI), Utrecht, The Netherlands; CGMCC: China General Microbiological Culture Collection Centre, Beijing, China. CMW: Culture collection at the FABI, University of Pretoria, South Africa; CPC: Collection of P.W. Crous, held at WI; HKAS: Herbarium of Cryptogams, Kunming Institute of Botany, Kunming, China; InaCC: Indonesian Culture Collection, Cibinong, Indonesia; LC: Collection of Lei Cai, held at the Institute of Microbiology, Chinese Academy of Sciences, Beijing, China. MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NFCCI; National Fungal Culture Collection of India, Pune, India; NRRL: Agricultural Research Service Culture Collection, National Center for Agricultural Utilization Research, USDA, Peoria, USA; UCR: collection of the University of California, Riverside, USA; YJ: Pathology Laboratory, Nanjing Forestry University, Nanjing, China. ^{ET}: Ex-epitype; ^{NT}: Ex-neotype; ^{T}: Ex-type.

[2] *acl1*: partial ATP citrate lyase gene; ITS: internal transcribed spacer regions with intervening 5.8S nrRNA gene; LSU: 28S large subunit of the nrDNA; *rpb1*: partial DNA-directed RNA polymerase II largest subunit gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene, two accession numbers refer to two non-contiguous fragments; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial beta-tubulin gene. †: sequences extracted from full genome sequences; *: sequence available at TreeBASE (study number); sequences generated in this study are shown in **bold**.

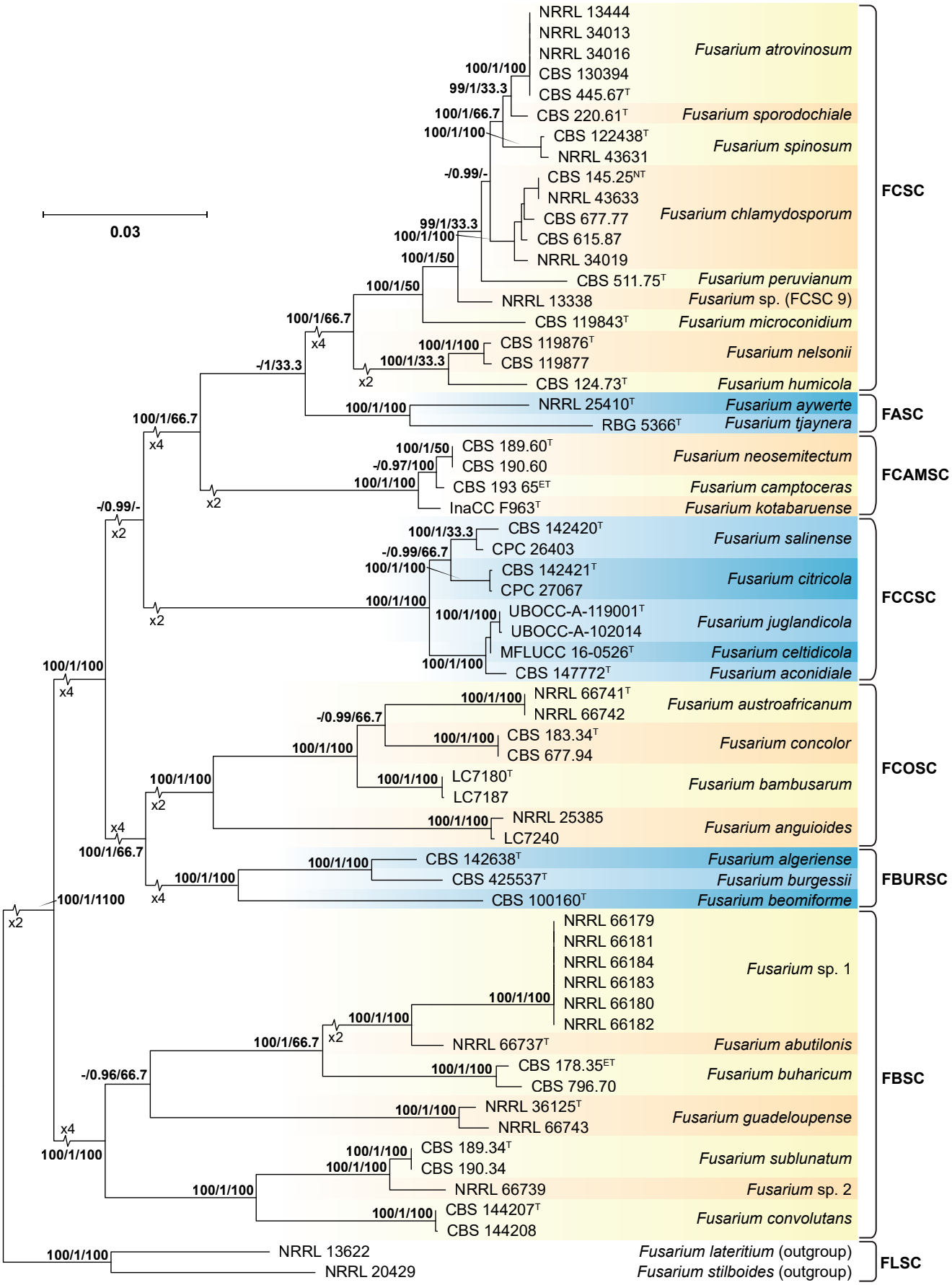

Fig. 1. IQ-TREE phylogeny inferred from the combined *rpb1*, *rpb2* and *tef1* sequences of currently accepted species belonging to seven species complexes (SC) of *Fusarium i.e.*, *F. aywerte* (FASC), *F. buharicum* (FBSC), *F. burgessii* (FBURSC), *F. camptoceras* (FCAMSC), *F. chlamydosporum* (FCSC), *F. citricola* (FCCSC), and *F. concolor* (FCOSC). Numbers at the nodes correspond to IQ-TREE bootstrap values ≥ 95 % followed by Bayesian posterior probabilities ≥ 0.95, and IQ-TREE gene concordance factors. The tree is rooted to *F. lateritium* NRRL 13622 and *F. stilboides* NRRL 20429 (FLSC). The scale bar indicates the expected number of nucleotide substitutions per site. Species complexes are indicated on the right and highlighted with coloured blocks. Ex-epitype, ex-neotype, and ex-type strains are indicated with ET, NT, and T, respectively.

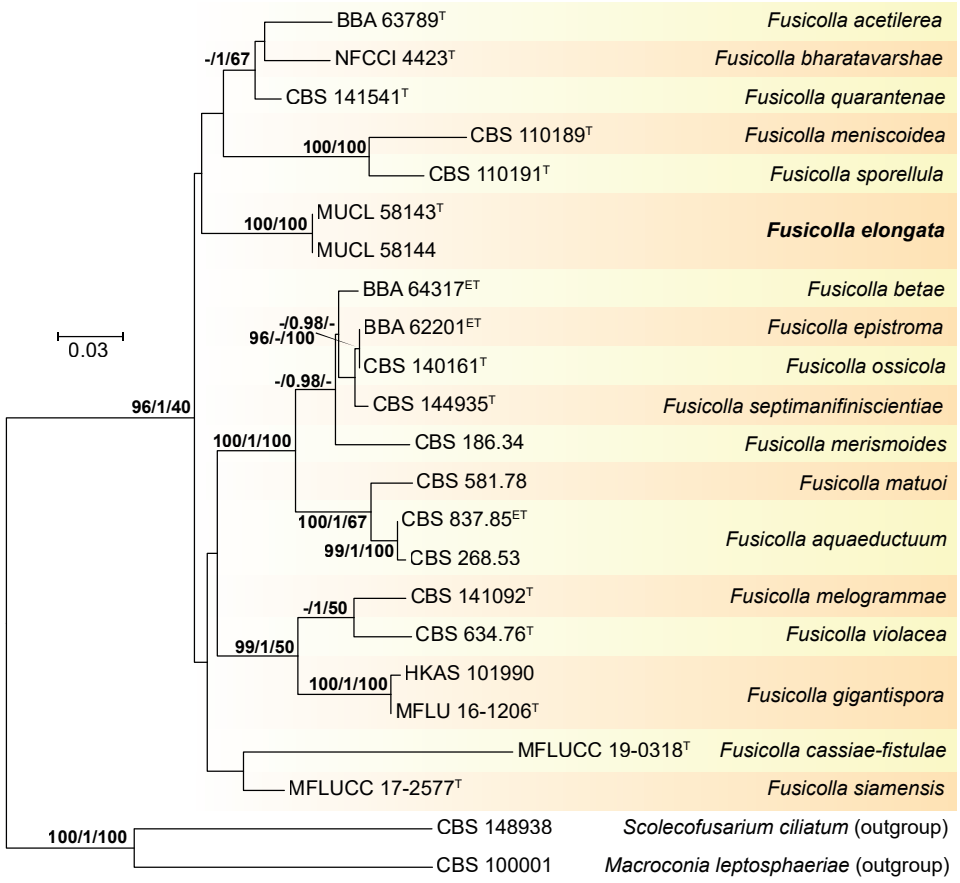

Fig. 2. IQ-TREE phylogeny inferred from the combined *acl1*, ITS, LSU, *rpb2* and *tub2* sequences of *Fusicolla* spp. Numbers at the nodes correspond to IQ-TREE bootstrap values ≥ 95 % followed by Bayesian posterior probabilities ≥ 0.95, and IQ-TREE gene concordance factors. The tree is rooted to *Macroconia leptosphaeriae* CBS 10001 and *Scolecofusarium ciliatum* CBS 148938. The scale bar indicates the expected number of nucleotide substitutions per site. Novel taxa are indicated in **bold**. Ex-epitype and ex-type strains are indicated with ET and T, respectively.

Table 2. Summary of phylogenetic information for the different analyses in this study.

Genus	Locus[1]	Number of sites (including gaps)[2]					Model selection[3]	
		Total	Conserved	Variable	Informative	BI unique site patterns	IQ-TREE (BIC)	BI (AIC)
Fusarium	*rpb1*	1 774	1 134	639	568	713	TNe+I+G4	SYM+I+G
	rpb2	1 657	1 085	572	535	592	TIM2e+I+G4	SYM+I+G
	tef1	517	217	285	245	348	TIM2e+G4	GTR+G
	Combined	3 948	2 436	1 496	1 348	1 653	-	-
Neocosmospora	ITS	464	333	128	99	180	TNe+R3	GTR+I+G
	rpb1	1 588	1 151	437	319	435	TIM3e+I+G4	GTR+I+G
	rpb2	1 465	1 057	408	336	454	TNe+I+G4	GTR+I+G
	tef1	688	394	283	200	342	TIM2+F+G4	GTR+I+G
	Combined	4 205	2 935	1 256	954	1 411	-	-
Fusicolla	*acl1*	866	454	382	201	298	TNe+G4	GTR+G
	ITS	516	391	110	56	123	TIM2e+G4	GTR+G
	LSU	474	423	50	28	56	K2P+I	GTR+G+I
	rpb2	1 702	1 220	482	290	415	TIM2e+G4	GTR+G+I
	tub2	482	299	175	109	177	K2P+G4	HKY+G
	Combined	4 040	2 787	1 199	684	1 069	-	-

[1] *acl1*: ATP citrate lyase large subunit; LSU: 28S large subunit of the nrDNA; ITS: Internal transcribed spacer region of the nrDNA; *tef1*: partial translation elongation factor 1-alpha gene; *rpb1*: partial DNA-directed RNA polymerase II largest subunit gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tub2*: partial beta-tubulin gene.

[2] BI: Bayesian inference.

[3] BIC: Evolutionary model selected by ModelFinder in IQ-TREE; AIC: Evolutionary model selected by MrModeltest under the Akaike Information Criterion

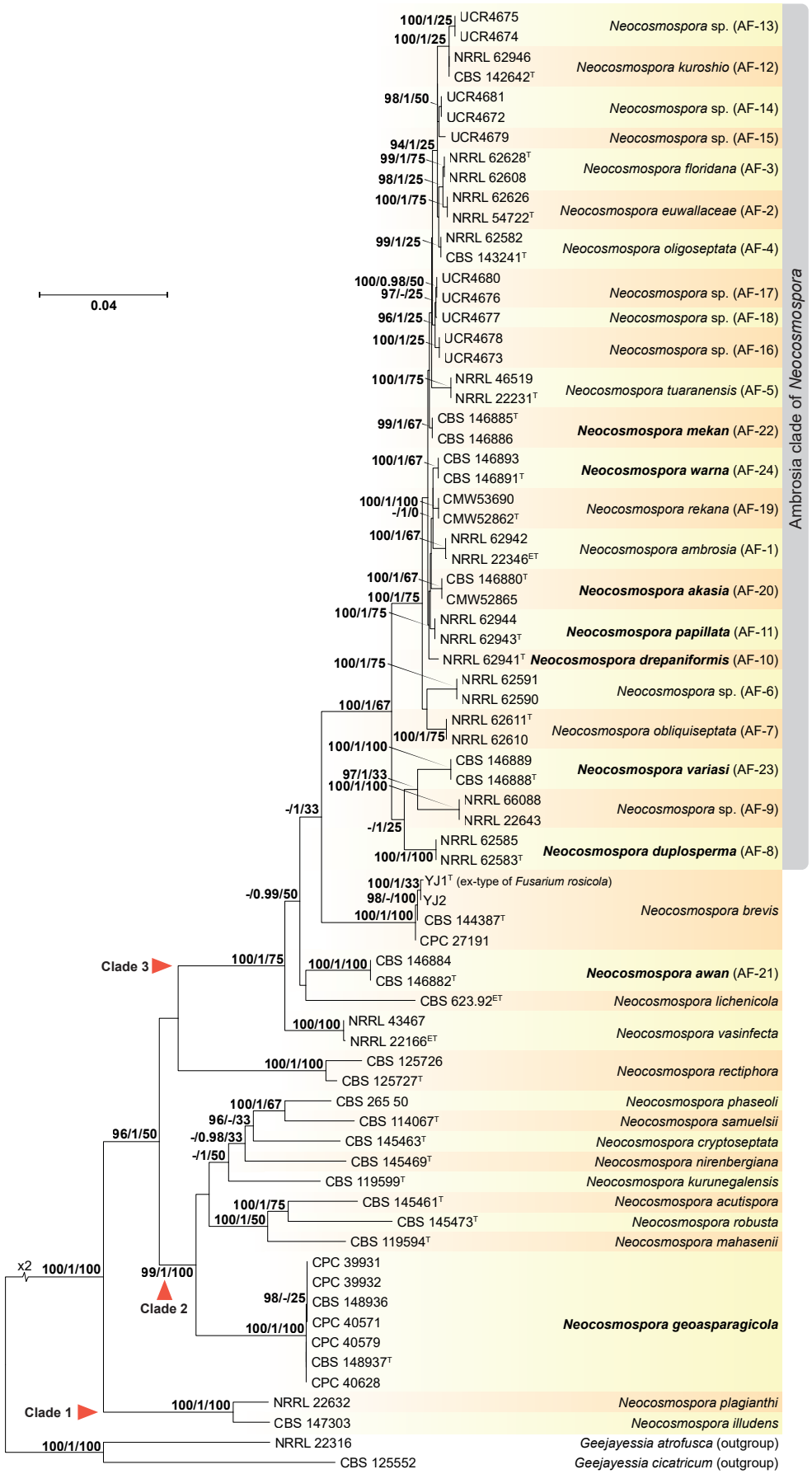

Fig. 3. IQ-TREE phylogeny inferred from the combined ITS, *rpb1*, *rpb2* and *tef1* sequences of representative *Neocosmospora* spp. Numbers at the nodes correspond to IQ-TREE bootstrap values ≥ 95 % followed by Bayesian posterior probabilities ≥ 0.95, and IQ-TREE gene concordance factors. The tree is rooted to *Geejayessia atrofusca* NRRL 22316 and *G. cicatricum* CBS 125552. The scale bar indicates the expected number of nucleotide substitutions per site. New combinations and species are indicated in **bold**. Numbers between parenthesis indicate former phylogenetic species nomenclature. The 'Ambrosia clade' of *Neocosmospora* is indicated on the right. Ex-epitype and ex-type strains are indicated with ET and T, respectively.

Table 3. Basic statistics of the assembled genomes announced in this publication.

Species	Strain[1]	BioProject ID	Complete BUSCOs [%]	Assembly size [Mbp]	No. of scaffolds	Scaff. N50 [kbp]	Longest scaff. [kbp]	Total no. of CDS
Fusarium secorum	CBS 175.32	PRJNA826072	99.1 %	50.5	15 085	17.3	156.3	46 001
Microcera coccophila	CBS 310.34	PRJNA826070	98.7 %	36.7	2 725	27.3	177.9	24 411
Rectifusarium robinianum	CBS 430.91^{T}	PRJNA826068	98.7 %	34.7	2 358	27.4	219.8	25 210
Rugonectria rugulosa	CBS 126565	PRJNA826071	98.8 %	46.9	2 884	56.0	353.8	30 877
Thelonectria blattea	CBS 952.68^{T}	PRJNA826075	98.9 %	38.9	3 001	34.8	221.9	26 348

[1] ^{T} = Ex-type.

TAXONOMY

Fusarium aywerte species complex (FASC)

Fusarium aywerte (Sangal. & L.W. Burgess) Benyon & L.W. Burgess, *Mycol. Res.* **104**: 1171. 2000. MB 466154. Fig. 4.
Basionym: *Fusarium avenaceum* subsp. *aywerte* Sangal. & L.W. Burgess, *Mycol. Res*. **99**: 287. 1995. MB 363513.

Holotypus: DAR 69501 (dried culture).

Ex-type culture: DAR 69501 = F10108 = NRRL 25410.

Type locality: **Australia**, Northern Territory, Deep Well.

Type substrate: Soil (from a depth of 5–10 cm) associated with roots of *Triodia basedowii*.

Descriptions and illustrations: See Sangalang *et al*. (1995a), Benyon *et al.* (2000) and Leslie & Summerell (2006).

Reference culture: **Australia**, Northern Territory, Little Palm Creek, soil under *Plectrachne* sp. (*Poaceae*), 1992, *D. Backhouse*, CBS 395.96 = F 10989.

Diagnostic features: *Colonies* with greyish rose mycelium and red pigment on PDA, having optimal growth at 25 °C; *microconidia* not observed; *sporodochia* with monophialides give rise to long, thin, flexuous, 6–8-septate *macroconidia* with a long tapering apical cell and a well-developed, elongated foot-shaped basal cell; *chlamydospores* absent (Sangalang *et al*. 1995a, Leslie & Summerell 2006).

Notes: *Fusarium aywerte* was initially described as a subspecies of *F. avenaceum* (Sangalang *et al.* 1995b), later to be recognised as a distinct species (Benyon *et al*. 2000). Besides the molecular differences, there are morphological, physiological and ecological differences between *F. aywerte* and *F. nurragi*. *Fusarium aywerte* has longer macroconidia and a faster growth rate than those of *F. nurragi*. Further, *F. aywerte* occurs in the rhizosphere of tussock-forming grasses (*Plectrachne*, *Triodia*) in arid tropical regions in northern Australia, while *F. nurragi* occurs in the rhizosphere of coastal heathland plants (*Kunzea ambigua*, *Banksia serrata*, *Allocasuarina paradoxa*) in temperate regions in southern Australia (Sangalang *et al*. 1995a, b).

Fusarium tjaynera J.L. Walsh *et al*., *Fungal Diversity* **77**: 361. 2015. MB 812309. Fig. 5.

Holotypus: RBG 5367 (metabolically inactive and dried culture).

Ex-type culture: NRRL 66246 = RBG 5367.

Type locality: **Australia**, Northern Territory, Litchfield National Park.

Type substrate: *Triodia microstachya*.

Description and illustrations: See Laurence *et al.* (2016).

Diagnostic features: *Colonies* with white to greyish rose aerial mycelium and red to burgundy reverse on PDA; mono- to polyphialides give rise to oval, 0–1-septate *microconidia* in false heads (*1-septate, subcylindrical mesoconidia also present); orange *sporodochia* give rise to falcate, slender, parallel dorse-ventral sides, (4–)5(–7)-septate *macroconidia* with a tapering, curved apical cell and well-developed, foot-shaped basal cell; *chlamydospores* absent (*emended from Laurence *et al.* 2016).

Notes: *Fusarium tjaynera* has been isolated from soil as well as from *Triodia macrostachya*, *Sorghum interjectum* and *S. intrans* in northern Australia (Laurence *et al.* 2016). *Fusarium tjaynera* is considered endemic to Australia. *Fusarium tjaynera* resembles *F. aywerte*, but can be distinguished by the production of microconidia [described as oval, but illustrated as subcylindrical; figs 47, 48 in Laurence *et al.* (2016)] and red pigmentation on PDA. Compared to *F. longipes* (distinctly notched basal cell), *F. tjaynera* has an indistinctly notched basal cell, and a less prominently elongated whip-like apical cell (Burgess *et al.* 1994, Laurence *et al.* 2016).

Fusarium buharicum species complex (FBSC)

Fusarium abutilonis Gräfenhan, Nirenberg & Seifert, *Mycologia* DOI: 10.1080/00275514.2022.2071563 [7]. 2022.

Holotypus: BPI 924391, dried culture of NRRL 66737.

Ex-type culture: NRRL 66737 = DAOMC 213370.

Type locality: **Canada**, Ontario.

Type substrate: On *Abutilon theophrasti*.

Descriptions and illustrations: O'Donnell *et al*. (2022).

Diagnostic features: *Colonies* reverse orange, sometimes turning greyish brown or greyish blue in the centre; surface smooth or

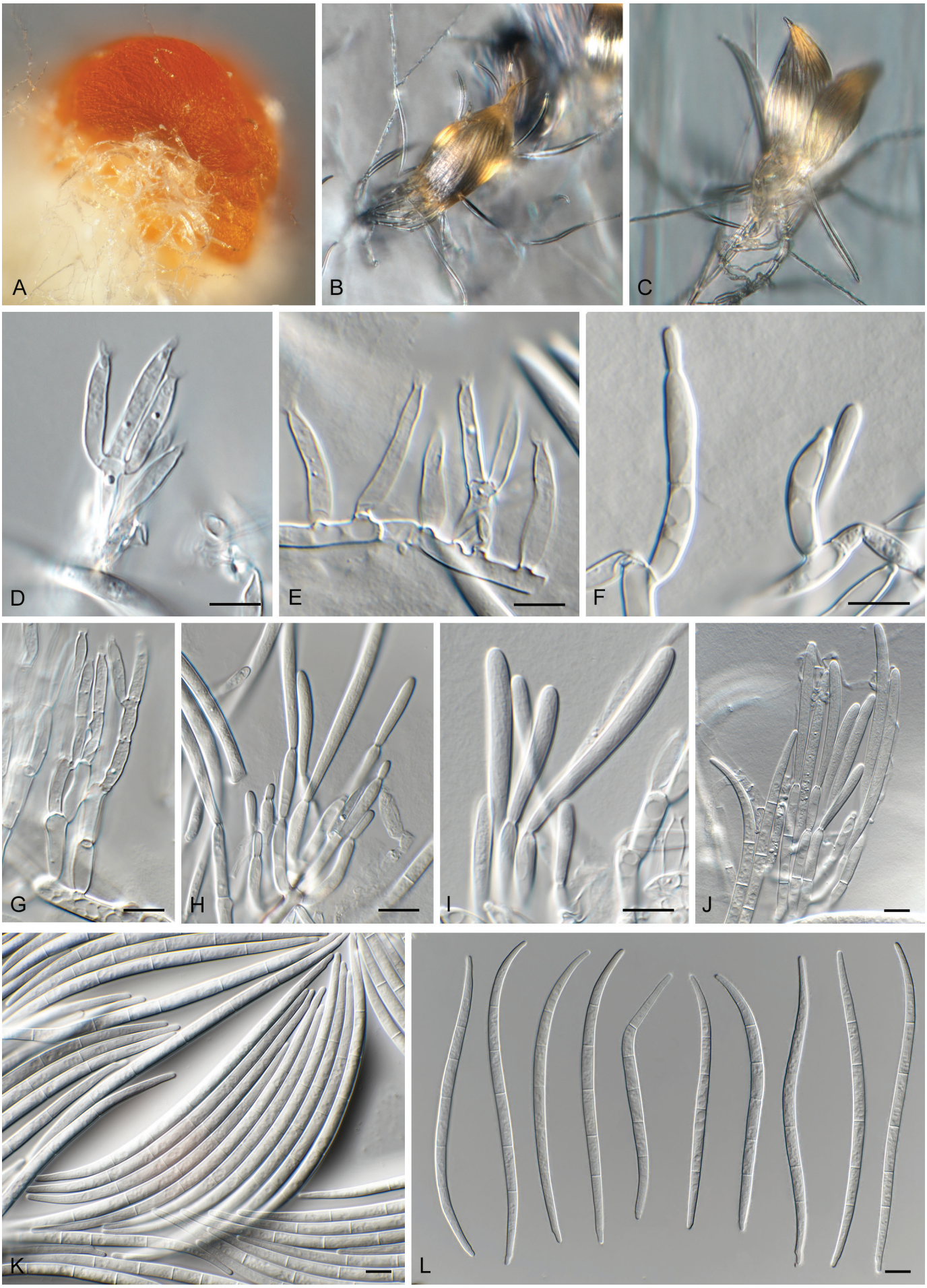

Fig. 4. *Fusarium aywerte* (CBS 395.96). **A.** Sporodochium on CLA. **B, C.** Sporodochia on SNA. **D–G, J.** Aerial conidiophores with monophialides. **H, I.** Sporodochial conidiophores. **K, L.** Macroconidia. Scale bars = 10 µm.

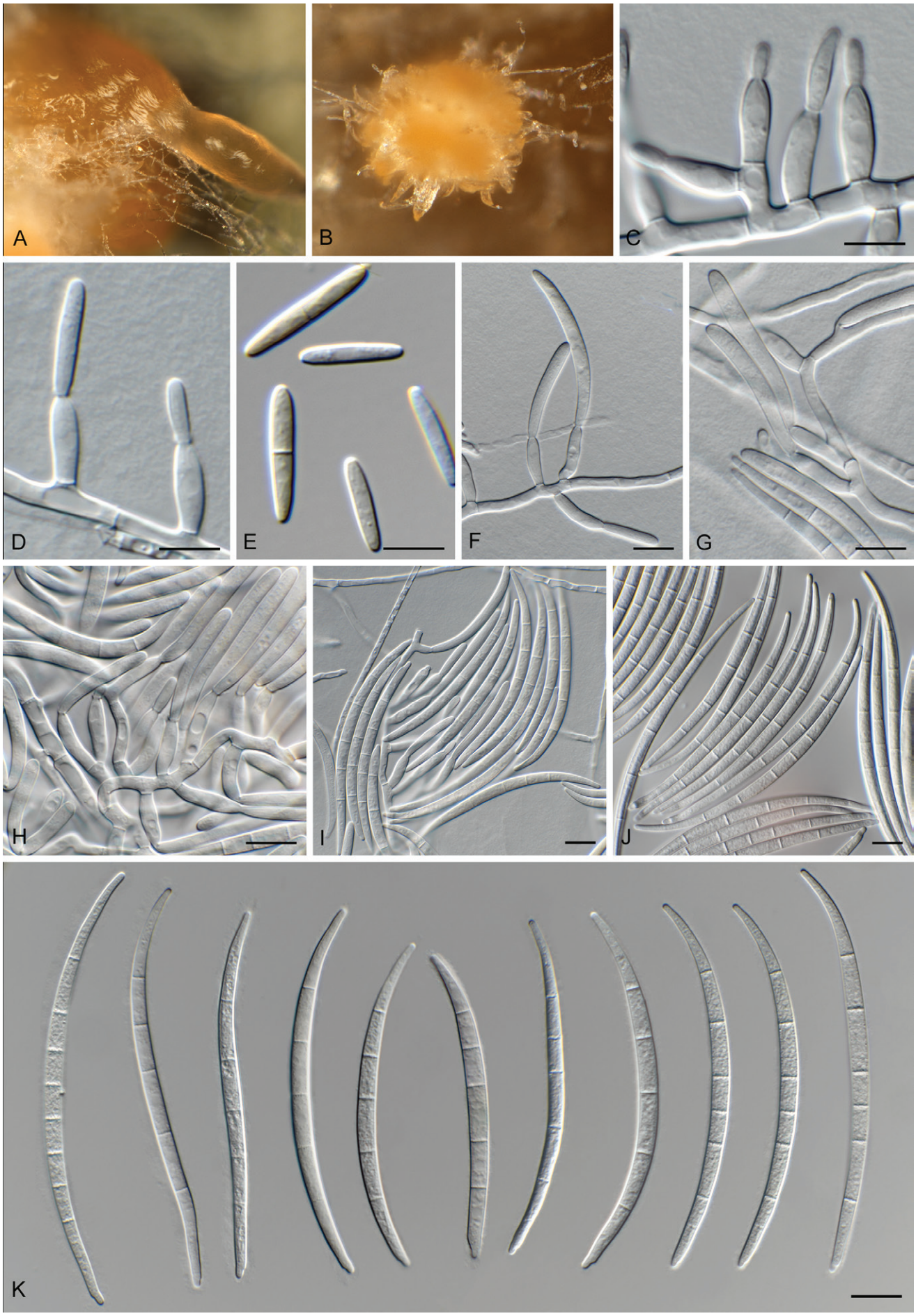

Fig. 5. *Fusarium tjaynera* (NRRL 66246). **A, B.** Sporodochia on CLA. **C, D.** Aerial conidiophores with monophialides giving rise to microconidia. **E.** Microconidia. **F, G.** Aerial conidiophores with monophialides giving rise to macroconidia. **H.** Sporodochial conidiophores. **I–K.** Macroconidia. Scale bars = 10 µm.

slightly mealy, orange, sometimes turning greyish brown in the centre, aerial mycelium white, sparse to slightly lanose to cottony, margin transparent or white on PDA, having optimal growth at 25 °C; aerial conidia 1–3-septate, sparse to absent, from monophialides; *sporodochia* pale orange, with monophialides giving rise to almost straight to curved, walls parallel in the centre, (4–)5(–6)-septate *macroconidia* with a conical and slightly hooked apical cell and well-developed foot-shaped basal cell; *chlamydospores* sparse, single or in chains of up to six, intercalary or terminal, hyaline, globose (O'Donnell *et al*. 2022).

Notes: Under some conditions sporodochial conidia of *F. abutilonis* may appear blue, as reported for *F. buharicum* (Gerlach & Nirenberg 1982). *Fusarium abutilonis* is a putative leaf, stem, and root rot pathogen of some *Malvaceae* and *Fabaceae*, and has also been isolated from soil (O'Donnell *et al*. 2022).

Fusarium buharicum Jacz. *ex* Babajan & Teterevn.-Babajan, *Mater. Mikol. Fitopat. Ross*.: 216. 1929. MB 314210.

Holotypus: LEP 127667.

Epitypus: **Uzbekistan**, Tashkent, on *Gossypium herbaceum*, 1928, *A.I. Raillo*, CBS 178.35 (preserved as metabolically inactive culture, designated by Crous *et al*. 2021b).

Ex-epitype culture: CBS 178.35 = DSM 62166 = IMB 11176 = NRRL 25488.

Descriptions and illustrations: See Gerlach & Nirenberg (1982).

Diagnostic features: *Colonies* pinkish brown, ochraceous to salmon, partly aeruginous, greyish to dark blue or nearly black on PDA, having optimal growth at 25 °C; *microconidia* not observed; sporodochia with monophialides give rise to straight, subcylindrical, (3–)5(–8)-septate *macroconidia* with a short, hooked apical cell and well-developed foot-shaped basal cell; *chlamydospores* in intercalary chains and terminal, in aerial mycelium and especially in conidia (Gerlach & Nirenberg 1982).

Notes: *Fusarium buharicum* was initially described as a pathogen of cotton (*Gossypium*) from the cotton plantations near Bukhara city in Uzbekistan (at that time – the Uzbek Soviet Socialist Republic) on which it induced collar rot symptoms, leading to plant death. With the introduction of resistant and more high yielding varieties of cotton, however, the disease lost its economic significance (Booth 1971). *Fusarium buharicum* was also found to be an important pathogen of kenaf (*Hibiscus cannabinus*) in Iran (CBS 796.70), on which it caused root, crown and stem rot (Gerlach & Sharif 1970). Sandoval-Denis *et al.* (2018b) described *F. convolutans* as a new soil-borne species occurring in South Africa, which is closely related to *F. buharicum* but distinct in that it has by its shorter, less septate and less curved macroconidia, and forms sterile hyphal coils in culture. Booth (1971) mentioned that older cultures of *F. buharicum* form intercalary globose chlamydospores in hyphae or in macroconidial cells, being pale brown, smooth-walled 10–14 µm diam at maturity. Gerlach & Nirenberg (1982) designated CBS 178.35 as neotype of *F. buharicum* as they were unable to locate the type specimen. However, A. Jaczweski did deposit a specimen in LEP, and therefore, CBS 178.35 was retained as epitype for the species (Crous *et al.* 2021b).

Fusarium convolutans Sand.-Den. *et al*., *MycoKeys* **34**: 77. 2018. MB 825102.

Holotypus: CBS H-23495 (dried OA culture).

Ex-type culture: CBS 144207 = CPC 33733.

Type locality: **South Africa**, Kruger National Park, Skukuza, Granite Supersite.

Type substrate: Rhizosphere soil under *Kyphocarpa angustifolia*.

Description and illustrations: See Sandoval-Denis *et al*. (2018b).

Diagnostic features: *Colonies* white to cream coloured on surface, reverse white, with straw to yellow diffusible pigment on PDA, having optimal growth at 30 °C; aerial monophialides giving rise *macroconidia* in false heads, lunate to falcate, curved to somewhat straight, (1–)3-septate, with a blunt to conical apical cell and papillate to distinct foot-shaped basal cell; sporodochia absent; *chlamydospores* abundant, in hyphae or conidia, intercalary or terminal, single or in clumps; sterile, coiled, sometimes branched hyphal projections abundantly formed laterally from the substrate and aerial mycelium (Sandoval-Denis *et al*. 2018b).

Notes: *Fusarium convolutans* is characterised by forming sterile, coiled hyphal projections, similar to structures observed in *F. circinatum*, *F. pseudocircinatum* and *F. sterilihyphosum*. The three latter species, however, are genetically unrelated to *F. convolutans*, being members of the FFSC. Furthermore, they are distinct in that they have microconidia, and lack chlamydospores (Leslie & Summerell 2006).

Fusarium guadeloupense Gräfenhan, Nirenberg & Seifert, *Mycologia* DOI: 10.1080/00275514.2022.2071563 [9]. 2022.

Holotypus: BPI 924391, dried culture of NRRL 36125.

Ex-type culture: NRRL 36125 = CBS 102302 = BBA 70872.

Type locality: **Guadeloupe**.

Type substrate: From soil.

Descriptions and illustrations: O'Donnell *et al*. (2022).

Diagnostic features: *Colonies* reverse orange with greyish brown; surface white to reddish grey, aerial mycelium white to reddish grey, dense, cottony on PDA, fast growing, having optimal growth at 25 °C; *microconidia* absent; *sporodochia* pale to greyish orange, with monophialides giving rise to almost straight to slightly curved, dorsal surface more curved than ventral surface, broadest at or slightly above the centre, 5(–6)-septate *macroconidia* with a conical and slightly bent apical cell and poorly developed foot-shaped basal cell; *chlamydospores* single or in chains, intercalary or terminal, hyaline, mostly globose (O'Donnell *et al*. 2022).

Notes: *Fusarium guadeloupense* is presently known from two strains, one collected from soil in Guadeloupe, and the other from human blood in Texas, USA. The latter isolate was

Fig. 6. *Fusarium sublunatum* (CBS 189.34). **A, B.** Sporodochia on CLA. **C–F.** Sporodochial conidiophores. **G.** Chlamydospores. **H.** Macroconidia. Scale bars = 10 µm.

also able to grow at 37 °C, suggesting that it might be able to infect humans and animals, although this remains to be proven (O'Donnell *et al*. 2022).

Fusarium sublunatum Reinking, *Zentralbl. Bakteriol.,* Abt. 2, **89**: 510. 1934. MB 279278. Fig. 6.
Synonyms: *Fusarium sambucinum* var. *sublunatum* (Reinking) Bilaĭ, *Mikrobiol. Zhurn. (Kiev)* **49**: 6. 1987. MB 346814.

Fusarium elongatum Reinking, *Zentralbl. Bakteriol. Parasitenk.,* Abt. 2, **89**: 511. 1934. MB 263929.
Fusarium sublunatum var. *elongatum* Reinking, *Die Fusarien, ihre Beschreibung, Schadwirkung und Bekämpfung*: 82. 1935. MB 434115.

Authentic material: B 70 0100189.

Lectotypus: **Costa Rica**, Limón, soil from *Musa sapientum* plantation, 1933, *O.A. Reinking*, CBS 189.34 (preserved as metabolically inactive culture, designated by Crous *et al.* 2021b).

Ex-type culture: BBA 62431 = CBS 189.34 = DSM 62431 = IMB 5238 = NRRL 13384 = NRRL 20840.

Descriptions and illustrations: See Reinking (1934), Gerlach & Nirenberg (1982).

Diagnostic features: *Colonies* pale beige, rose to cinnamon on PDA, having optimal growth at 25 °C; *microconidia* not observed; *sporodochia* with monophialides give rise to falcate, inequilaterally curved, (3–)5(–8)-septate *macroconidia* with a hooked apical cell and well-developed foot-shaped basal cell; *chlamydospores* abundant in aerial hyphae and conidia, in pairs, chains or clusters (Gerlach & Nirenberg 1982).

Notes: *Fusarium sublunatum* was described from soil samples collected in a *Musa* plantation in Costa Rica. No holotype specimen could be located for *F. sublunatum* and therefore the metabolically inactive culture CBS 189.34 (= IMB 5238), which represents the ex-type culture (Gerlach & Nirenberg 1982), was designated as lectotype (Crous *et al.* 2021b). *Fusarium sublunatum* var. *elongatum* (original culture CBS 190.34 = NRRL 20897), also described from soil collected in a banana plantation in Costa Rica, proved to be a synonym of *F. sublunatum* (Raillo 1950, Gerlach & Nirenberg 1982).

Fusarium burgessii species complex (FBURSC)

Fusarium algeriense Laraba & O'Donnell, *Mycologia* **109**: 944. 2017 (2018). MB 820565. Fig. 7.

Holotypus: BPI 910347 (dried culture).

Ex-type culture: CBS 142638 = IL-79 = KOD 1247 = NRRL 66647.

Type locality: **Algeria**, Guelma Province, Djeballah Khemissi.

Type substrate: *Triticum durum*.

Description and illustrations: See Laraba *et al*. (2017).

Diagnostic features: *Colonies* reddish orange, brownish grey, yellowish white to purplish grey on PDA, having optimal growth at 25 °C; **microconidia* developing in false heads, on superficial and immersed mycelium, subcylindrical, straight to curved, 0–1-septate; *sporodochia* with monophialides give rise to straight to falcate, slender, 1–3(–4)-septate *macroconidia* with a hooked apical cell and well-developed foot-shaped basal cell; **chlamydospores* intercalary, globose to subglobose, in chains, sparse, hyaline (*emended from Laraba *et al.* 2017).

Notes: *Fusarium algeriense* represents a species within the *F. burgessii* species complex causing crown rot of durum wheat in Algeria (Laraba *et al.* 2017). Following its description, crown rot symptoms of bread wheat in two provinces of Azerbaijan were also attributed to *F. algeriense* (Özer *et al.* 2020).

Morphologically, *F. algeriense* needs to be compared to *F. burgessii* and *F. beomiforme*, which have an optimal growth at 30 °C, and produce abundant chlamydospores. Isolates of *F. algeriense* had an optimal growth at 25 °C, lacked chlamydospore production in culture, and produced monophialides, with reniform or ellipsoidal, mostly aseptate microconidia. In contrast, *F. burgessii* has polyphialides, and *F. beomiforme* has monophialides, but with globose-to-napiform, 0–1-septate microconidia (Laraba *et al.* 2017).

Fusarium beomiforme P.E. Nelson *et al.*, *Mycologia* **79**: 886. 1987. MB 122057. Fig. 8.

Holotypus: DAOM 196987 (dried culture).

Ex-type culture: ATCC 64067 = CBS 100160 = DAOM 196987 = DAR 58880 = F 5759 = FRC M-1425 = IMI 316127 = MRC 4593 = NRRL 13606.

Type locality: **Australia**, Queensland, Rockhampton.

Type substrate: Plant debris in soil.

Descriptions and illustrations: See Nelson *et al.* (1987) and Leslie & Summerell (2006).

Diagnostic features: *Colonies* pale orange to white, with orange red to red-brown pigmentation on PDA; optimal growth at 30 °C; monophialides produce false heads with 0–1-septate napiform to globose *microconidia* in aerial mycelium; *sporodochia* with monophialides giving rise to long falcate, 3–4(–5)-septate *macroconidia* with a slightly curved apical cell and notched basal cell, and slow to form, abundant, intercalary, single to chains of *chlamydospores* in aerial and submerged hyphae (Nelson *et al*. 1987).

Notes: *Fusarium beomiforme* was described from soil and plant debris collected in the Markham Valley of Papua New Guinea (where sorghum had been cultivated), from grassland areas in the vicinity of Rockhampton, Emerald, Longreach, and Boulia along the Tropic of Capricorn in Queensland, Australia, and from Hluhluwe, KwaZulu-Natal, South Africa (Nelson *et al*. 1987). Since then, *F. beomiforme* has also been recovered from Thailand (from soil where previously sorghum had been cultivated; Mohamed Nor *et al*. 2019), though to date, *F. beomiforme* has not been reported to be pathogenic, and is probably a saprobe.

Fusarium burgessii M.H. Laurence *et al*., *Fungal Diversity* **49**: 109. 2011. MB 519216. Fig. 9.

Holotypus: CBS 125537 (preserved as metabolically inactive culture).

Ex-type culture: CBS 125537 = NRRL 66654 = RBG 5315.

Type locality: **Australia**, Queensland, Idalia National Park.

Type substrate: Soil.

Description and illustrations: See Laurence *et al.* (2011).

Diagnostic features: *Colonies* white to yellow with yellow pigmentation on PDA, having optimal growth at 30 °C; mono- to

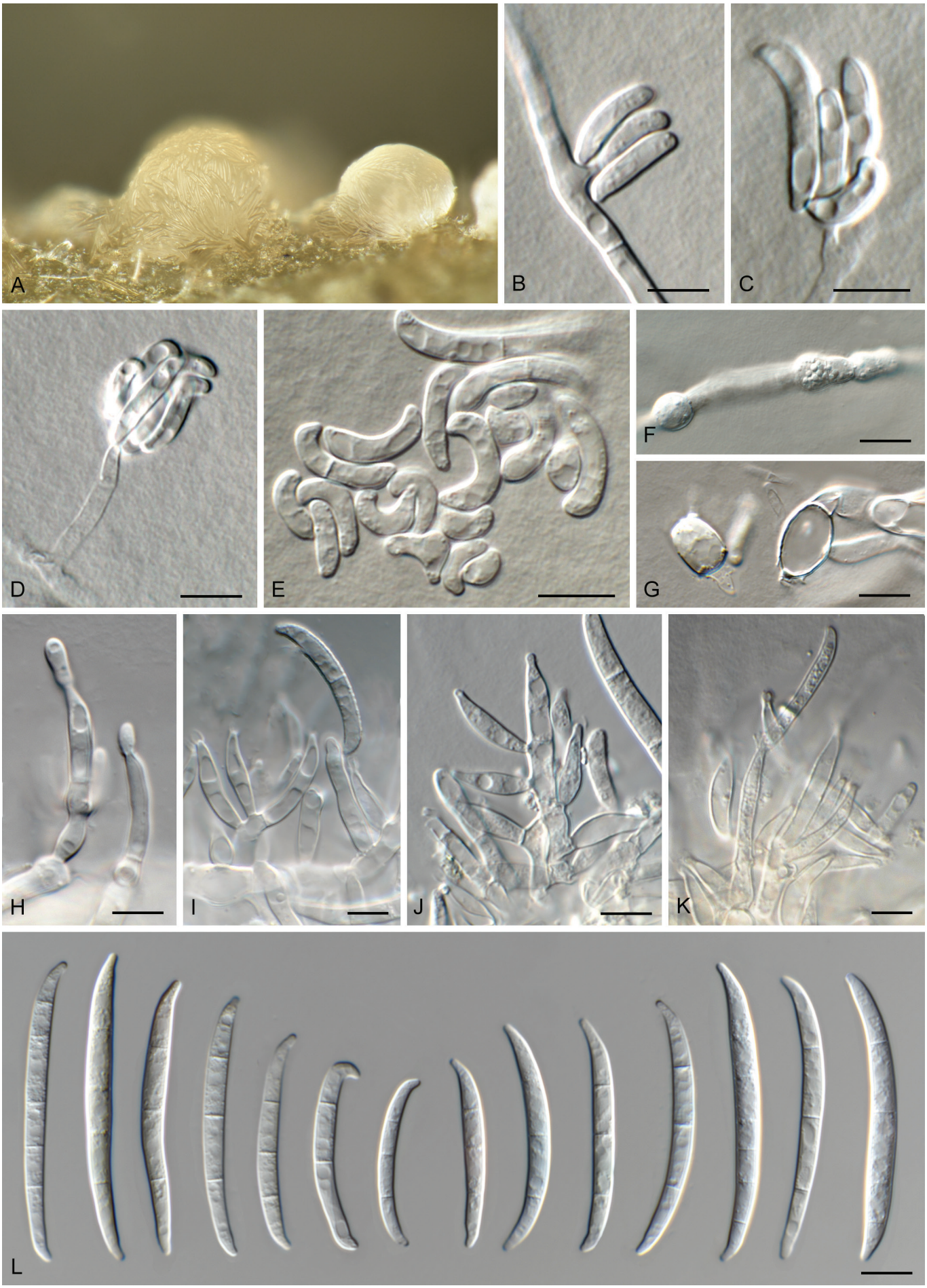

Fig. 7. *Fusarium algeriense* (CBS 142638). **A.** Sporodochium on CLA. **B–D.** Aerial conidiophores with monophialides. **E.** Microconidia. **F, G.** Chlamydospores. **H–K.** Sporodochial conidiophores. **L.** Macroconidia. Scale bars = 10 µm.

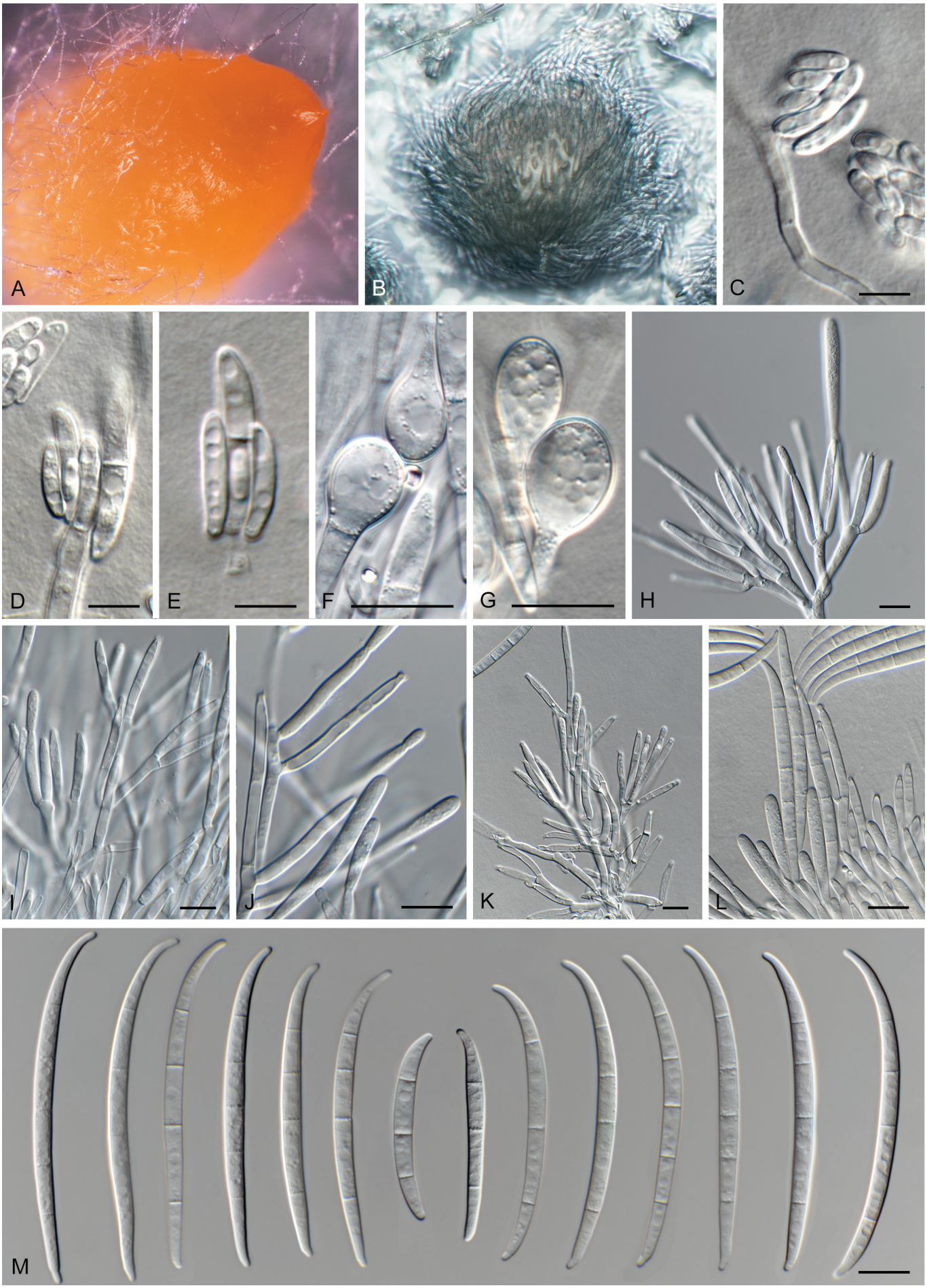

Fig. 8. *Fusarium beomiforme* (CBS 100160). **A, B.** Sporodochia on SNA. **C–E.** Microconidia. **F, G.** Chlamydospores developing in macroconidia. **H–L.** Sporodochial conidiophores. **M.** Macroconidia. Scale bars = 10 µm.

Fig. 9. *Fusarium burgessii* (CBS 125537). **A.** Sporodochium on CLA. **B.** Aerial conidiophores with monophialides giving rise to micro- and macroconidia. **C–F.** Microconidia. **G–J.** Sporodochial conidiophores. **K.** Macroconidia. Scale bars = 10 µm.

polyphialides produce false heads with 0–1-septate oval, elliptical or reinform *microconidia* in aerial mycelium; *sporodochia* with mono- to polyphialides produce short to medium length, falcate, 3-septate *macroconidia* with a slightly curved to hooked apical cell and notched to well-developed, foot-shaped basal cell; *chlamydospores* in both aerial and submerged hyphae, terminal and intercalary, solitary or in chains (Laurence *et al.* 2011).

Notes: *Fusarium burgessii* was described from Australia, and is known to occur in soils from Longreach, Queensland, to Finke Gorge National Park, Northern Territory (Laurence *et al*. 2011). Morphologically, it is allied to *F. algeriense* and *F. beomiforme* (see discussion under *F. algeriense*), and morphotype B (isolated from the rhizosphere of indigenous *Gossypium* spp.), which presently still represents an undescribed species (Laurence *et al*. 2011).

Fusarium camptoceras species complex (FCAMSC)

Fusarium camptoceras Wollenw. & Reinking, *Phytopathology* **15**: 158. 1925. MB 259537. Fig. 10.

Neotypus: CBS H-24077, designated in Xia *et al*. (2019).

Ex-neotype culture: ATCC 16065 = ATCC 24364 = BBA 9810 = CBS 193.65 = DSM 62167 = IMB 9810 = IMI 112500 = NRRL 20716 = NRRL 36344.

Neotype locality: **Costa Rica**.

Neotype substrate: Cushion gall of *Theobroma cacao*.

Descriptions and illustrations: See Wollenweber & Reinking (1935), Booth (1971), Gerlach & Nirenberg (1982), Marasas *et al*. (1998) and Leslie & Summerell (2006).

Diagnostic features: *Colonies* brown on PDA, having optimal growth at 25 °C; *microconidia* not observed; aerial polyphialides formed on loosely branched conidiophores giving rise to av. 3–4-septate mesoconidia, and macroconidia; *sporodochia* with monophialides give rise to falcate, 3–5(–7)-septate *macroconidia* with a pointed apical cell and obtuse to well-developed, foot-shaped basal cell; intercalary chains, pairs or clusters of *chlamydospores* in aerial and submerged hyphae, never in terminal pairs (Marasas *et al.* 1998, Leslie & Summerell (2006).

Notes: *Fusarium camptoceras* was described from subtropical and tropical regions (Costa Rica, Ecuador, Honduras, Angola), recovered from decaying *Coffea, Musa* and *Theobroma* spp. (Marasas *et al.* 1998). Reports prior to 1998 could represent two species separated from *F. camptoceras*, namely *F. musarum* and *F. nelsonii*, which differ regarding their red pigmentation on PDA, size and septation of their mesoconidia (*F. musarum* av. 5–6-septate; *F. nelsonii* av. 3-septate), sporodochia (absent in *F. musarum*; present in *F. nelsonii*), and the pattern in which chlamydospores are formed (in terminal pairs in *F. nelsonii*, solitary or chains in *F. camptoceras* and *F. musarum*) (Marasas *et al.* 1998). Further studies are needed to confirm the role of *F. camptoceras* as plant pathogen.

Fusarium kotabaruense Maryani *et al*., *Persoonia* **43**: 65. 2019. MB 828964.

Holotypus: InaCC F963 (preserved as metabolically inactive culture).

Ex-type culture: InaCC F963 = Indo172.

Type locality: **Indonesia**, South Kalimantan, Kota Baru, Kecamatan Pamukan Barat, Desa Sungai Birah.

Type substrate: Infected pseudostem of *Musa* var. Pisang Hawa (ABB).

Description and illustrations: See Maryani *et al*. (2019).

Diagnostic features: *Colonies* rosy buff on PDA, having optimal growth at 25 °C; aerial hyphae and orange *sporodochia* with mono- and polyphialides give rise to macroconidia, falcate, (2–)3–5(–7)-septate, with blunt apical cell and poorly-developed, foot-shaped basal cell; *chlamydospores* not observed (Maryani *et al.* 2019).

Notes: *Fusarium kotabaruense* represents a fast-growing species which clustered basal to the FIESC, and was shown to be better accommodated in the *Fusarium camptoceras* species complex (Xia *et al.* 2019, Crous *et al*. 2021b). Although assumed to lack sporodochia, isolates on CLA incubated under nuv-light did produce orange sporodochia. This species is characterised by its mono- to polyphialides, fast-growing cultures and multiseptate conidia (Maryani *et al.* 2019).

Fusarium neosemitectum L. Lombard *et al*., *Persoonia* **43**: 214. 2019. MB 831845.

Holotypus: CBS H-24067.

Ex-type culture: CBS 189.60.

Type locality: **Democratic Republic of the Congo**.

Type substrate: *Musa sapientum*.

Description and illustrations: See Xia *et al.* (2019).

Diagnostic features: *Colonies* white, felty to velvety on PDA, with abundant aerial mycelium; aerial mono- to polyphialides giving rise to *macroconidia*, ellipsoid to falcate, curved dorsiventrally, (1–)2–4(–5)-septate; blunt, conical to slightly papillate apical cell and blunt to poorly-developed, foot-shaped basal cell; *sporodochia* and *chlamydospores* not observed (Xia *et al.* 2019).

Notes: *Fusarium neosemitectum* can be distinguished from closely related species, such as *F. kotabaruense* and *F. camptoceras*, by the presence of short phialidic pegs on the aerial mycelium, not observed for the latter two species. All three species in FCAMSC appear to be tropical species due to their origins and they also share a mutual host genus, *Musa* (Marasas *et al.* 1998, Maryani *et al*. 2019).

Fusarium chlamydosporum species complex (FCSC)

Fusarium atrovinosum L. Lombard & Crous, *Fungal Syst. Evol*. **4**: 190. 2019. MB 831559.

Holotypus: CBS H-24015.

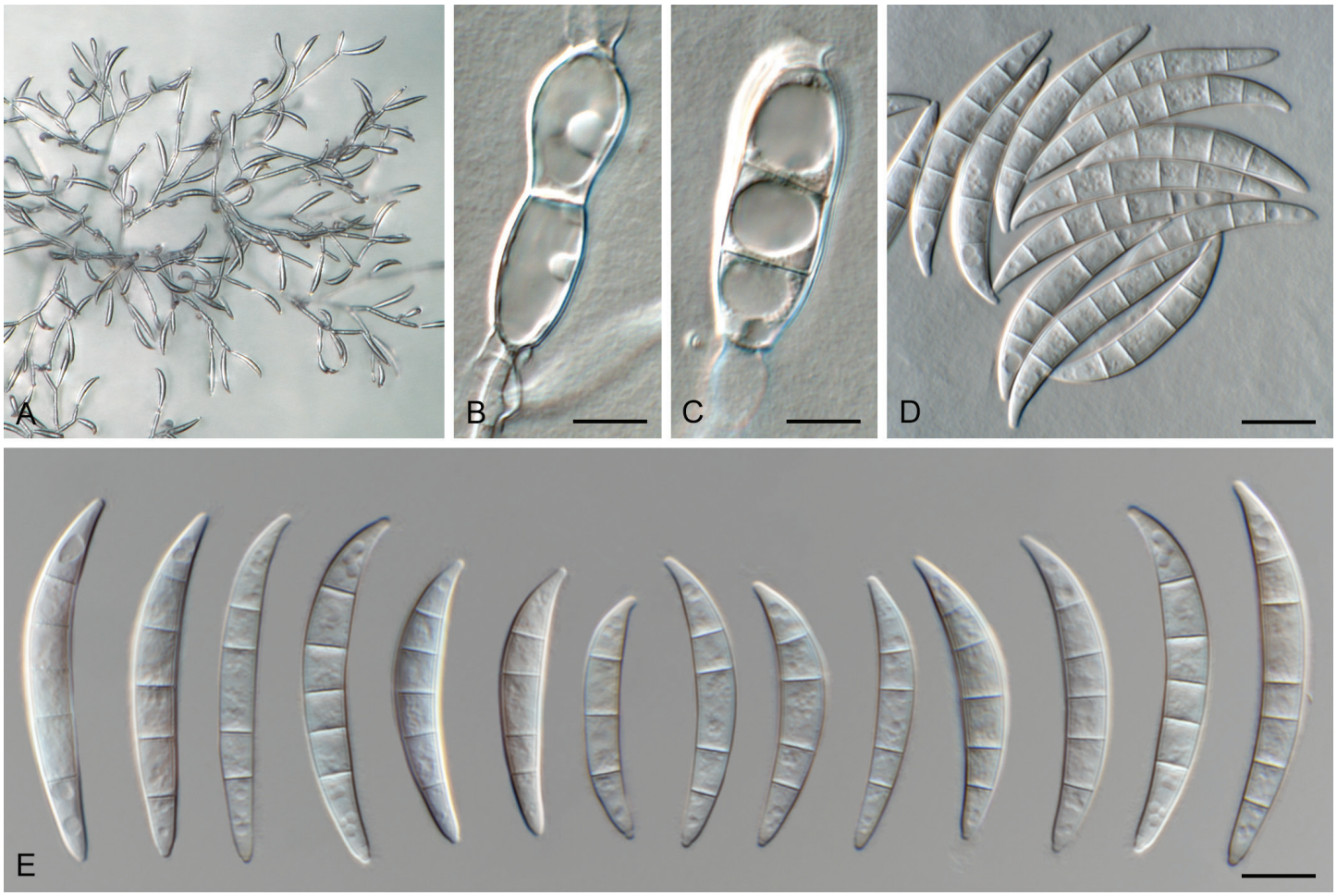

Fig. 10. *Fusarium camptoceras* (CBS 193.65). **A.** Aerial conidiophores with monophialides. **B, C.** Chlamydospores. **D, E.** Macroconidia. Scale bars = 10 µm.

Ex-type culture: BBA 10357 = CBS 445.67 = DSM 62169 = IMB 10357= IMI 096270 = NRRL 26852 = NRRL 26913.

Type locality: **Australia**.

Type substrate: *Triticum aestivum*.

Description and illustrations: See Lombard *et al*. (2019).

Diagnostic features: *Colonies* on the surface greyish rose to vinaceous to buff in the centre, with abundant aerial mycelium, and livid red to dark vinaceous in reverse on PDA; aerial polyphialides giving rise to false heads with fusiform to ellipsoidal to obovoid, 0–1(–2)-septate *microconidia*; *chlamydospores* abundant, globose to subglobose, thick-walled, smooth to slightly verrucose, formed terminally or intercalarily in chains of three or more (Lombard *et al*. 2019).

Notes: *Fusarium atrovinosum* is closely related to *F. chlamydosporum, F. spinosum* and *F. sporodochiale* and can be distinguished from these three species by the lack of monophialides on aerial mycelium, the lack of sporodochia, and abundant chlamydospores.

Fusarium chlamydosporum Wollenw. & Reinking, *Phytopathology* **15**: 156. 1925. MB 260522.
Synonyms: *Fusarium chlamydosporum* var. *chlamydosporum*, *Phytopathology* **15**: 156. 1925. MB 429587.
Fusarium sporotrichioides var. *chlamydosporum* (Wollenw. & Reinking) Joffe, *Mycopathol. Mycol. Appl*. **53**: 211. 1974. MB 348165.
Dactylium fusarioides Gonz. Frag. & Cif., *Bol. Real Soc. Esp. Hist. Nat*. **27**: 280. 1927. MB 265606.
Fusarium fusarioides (Gonz. Frag. & Cif.) C. Booth, *The genus Fusarium*: 88. 1971. MB 314214.
Pseudofusarium purpureum Matsush., *Microfungi of the Solomon Islands and Papua-New Guinea*: 47. 1971. MB 321785.

Neotypus: CBS 145.25 (preserved as metabolically inactive culture), designated in Lombard *et al.* (2019).

Ex-neotype culture: CBS 145.25 = NRRL 26851 = NRRL 26912.

Neotype locality: **Honduras**, Tela.

Neotype substrate: Pseudostem of *Musa sapientum*.

Descriptions and illustrations: See Booth (1971), Gerlach & Nirenberg (1982) and Leslie & Summerell (2006).

Diagnostic features: *Colonies* with white mycelium and greyish rose to burgundy pigment on PDA; *microconidia* abundant, straight to reniform, 0(–2)-septate, arising from aerial mono- and polyphialides; *sporodochia* rare, with monophialides give

rise to thick-walled, unequal dorsiventrally curved, 3–5-septate *macroconidia* with a short, curved, pointed apical cell and poorly to well-developed, foot-shaped basal cell; *chlamydospores* abundant, formed rapidly in aerial mycelium, submerged hyphae and on agar surface, verruculose and pale brown, in chains or clusters (Marasas *et al.* 1998, Leslie & Summerell 2006).

Notes: *Fusarium chlamydosporum* (FCSC) is common in soils and grains from arid and semi-arid regions (Burgess & Summerell 1992, Kanaan & Bahkali 1993, Sangalang *et al*. 1995a), and from plant material displaying disease symptoms that include crown rot (Du *et al*. 2017), blight (Satou *et al*. 2001), damping-off (Engelbrecht *et al*. 1983, Lazreg *et al.* 2013) and stem canker (Fugro 1999). It has also been implicated in human and animal fusarioses (O'Donnell *et al*. 2009). Records prior to Lombard *et al.* (2019) need to be interpreted with care, as this was shown to be a species complex O'Donnell *et al*. (2009, 2018). Subsequent to these studies, five of these taxa were named, with several additional species in the FCSC still awaiting formal description. Furthermore, *F. chlamydosporum* var. *fuscum* was raised to species level, as *F. coffeatum,* in the *F. incarnatum-equiseti* species complex (FIESC) (Lombard *et al.* 2019).

Fusarium humicola L. Lombard & Crous, *Fungal Syst. Evol*. **4**: 191. 2019. MB 831561.

Holotypus: CBS H-24016.

Ex-type culture: ATCC 24372 = CBS 124.73 = IMI 128101 = NRRL 25535.

Type locality: **Pakistan**.

Type substrate: Soil.

Description and illustrations: See Lombard *et al.* (2019).

Diagnostic features: *Colonies* fulvous to ochreous in the centre becoming vinaceous to livid red towards the margin, reverse dark vinaceous to vinaceous on PDA; aerial mono- to polyphialides giving rise to *microconidia* in false heads, ellipsoidal to obovoid, 0–3-septate; *sporodochia* pale luteous to pale salmon, with monophialides give rise to falcate, mostly straight with dorsiventrally curved apical and basal cells 3–5-septate *macroconidia* with a curved, blunt to papillate apical cell and well-developed, foot-shaped basal cell; *chlamydospores* not observed (Lombard *et al.* 2019).

Note: *Fusarium humicola* is closely related to *F. nelsonii*, which has smaller, more strongly curved sporodochial conidia, and abundant chlamydospores.

Fusarium microconidium L. Lombard & Crous, *Fungal Syst. Evol*. **4**: 192. 2019. MB 831562.

Holotypus: CBS H-24017.

Ex-type culture: CBS 119843 = KSU 11396 = MRC 8391.

Type locality: Unknown.

Type substrate: Unknown.

Description and illustrations: See Lombard *et al*. (2019).

Diagnostic features: *Colonies* rose to rosy vinaceous to pale luteous on surface, with abundant aerial mycelium, and livid red to dark vinaceous in reverse on PDA; aerial mono- or polyphialides giving rise to *microconidia*, fusoid to ellipsoidal to obovoid, 0–1-septate; *sporodochia* and *chlamydospores* not observed (Lombard *et al*. 2019).

Notes: *Fusarium microconidium* is distinguished from other species in the FCSC based on the production of predominantly aseptate microconidia and lack of sporodochia and chlamydospores.

Fusarium nelsonii Marasas & Logrieco, *Mycologia* **90**: 508. 1998. MB 443596.

Holotypus: BPI 802927; *isotypi* DAOM 225260 and PREM 55396.

Ex-type culture: ATCC 201410 = CBS 119876 = FRC R-8670 = ITEM 1229 = MRC 4570 = NRRL 28505 = NRRL 53945.

Type locality: **South Africa**, Western Cape Province, Malmesbury.

Type substrate: Plant debris in wheat field soil.

Descriptions and illustrations: See Marasas *et al.* (1998) and Leslie & Summerell (2006).

Diagnostic features: *Colonies* with white floccose mycelium and red pigmentation on PDA, having optimal growth at 30 °C; aerial polyphialides giving rise to *mesoconidia*, fusoid to lanceolate, straight to curved, (0–)3-septate; *sporodochia* cream coloured, with monophialides giving rise to straight or falcate, 3(–5)-septate *macroconidia* with a curved, blunt apical cell (beak-like) and poorly-developed, foot-shaped basal cell; *chlamydospores* abundant and rapidly formed in aerial and submerged hyphae, intercalary or terminal, single, in pairs, chains or clumps (Marasas *et al.* 1998, Leslie & Summerell 2006).

Notes: *Fusarium nelsonii* was described from South Africa, where it was isolated from *Triticum* soil, plant debris, *Medicago* roots, *Sorghum* malt and *Zea mays* kernels (Marasas *et al.* 1998). It has been reported from *Triticum* in Iran (Chehri *et al.* 2010), *Sorghum* in India (Lincy *et al.* 2011), fruit blight of *Cucumis sativus var*. *sativus* and stalk rot of *Zea mays* in China (Ahmad *et al.* 2020, Zhang *et al*. 2021).

Fusarium nelsonii produces macro- and mesoconidia (aerial mycelium), which distinguishes it from *F. musarum* (macroconidia absent), and has shorter meso- and macroconidia than *F. camptoceras*.

Fusarium peruvianum L. Lombard & Crous, *Fungal Syst. Evol*. **4**: 194. 2019. MB 831564.

Holotypus: CBS H-24019.

Ex-type culture: CBS 511.75.

Type locality: **Peru**.

Type substrate: Seedlings of *Gossypium* sp.

Description and illustrations: See Lombard *et al*. (2019).

Diagnostic features: *Colonies* fulvous to ochreous in the centre becoming coral to vinaceous towards the margin, with abundant aerial mycelium, and livid red to dark vinaceous in reverse on PDA; aerial phialides mostly polyphialidic, giving rise to micro- and macroconidia; *microconidia* ellipsoid to obovoid, 0–3(–4)-septate, *macroconidia* fusoid to falcate, straight or gently dorsiventrally curved, with a blunt apical cell and indistinct papillate to poorly-developed, foot-shaped basal cell; *chlamydospores* abundant, intercalary or terminal, single or in pairs; *sporodochia* not observed (Lombard *et al*. 2019).

Note: *Fusarium peruvianum* can be distinguished from other species in the FCSC by having falcate aerial macroconidia and 4-septate obovoid microconidia.

Fusarium spinosum L. Lombard *et al*., *Fungal Syst. Evol*. **4**: 195. 2019. MB 831565.

Holotypus: CBS H-24020.

Ex-type culture: CBS 122438.

Type locality: **Brazil**.

Type substrate: *Galia melon* imported into the Netherlands.

Description and illustrations: See Lombard *et al*. (2019).

Diagnostic features: *Colonies* rose to rosy vinaceous to pale luteous in the centre, with abundant aerial mycelium, reverse fulvous to ochreous with rosy vinaceous flames on PDA; aerial mono- to polyphialides giving rise to micro- and macroconidia in false heads; *microconidia* fusoid to ellipsoidal to obovoid, straight to curved, 0–3-septate; *macroconidia* falcate, slightly dorsiventrally curved, 3-septate, apex blunt, with an indistinct papillate to poorly-developed foot-shaped basal cell; *chlamydospores* abundant, intercalary or terminal, single or in chains; *sporodochia* not observed (Marasas *et al.* 1998, Leslie & Summerell 2006).

Note: *Fusarium spinosum* is distinguished from other species in the FCSC by only forming 3-septate, falcate macroconidia.

Fusarium sporodochiale L. Lombard & Crous, *Fungal Syst. Evol*. **4**: 196. 2019. MB 831566.

Holotypus: CBS H-12681.

Ex-type culture: ATCC 14167 = CBS 220.61 = MUCL 8047 = NRRL 20842.

Type locality: **South Africa**, Gauteng Province, Johannesburg.

Type substrate: Soil.

Description and illustrations: See Lombard *et al*. (2019).

Diagnostic features: *Colonies* rose to rosy vinaceous to sulphur yellow, with abundant aerial mycelium, reverse livid red to dark vinaceous on PDA; aerial phialides mostly polyphialidic, giving rise to *microconidia* in false heads, fusoid to ellipsoidal to obovoid, (0–)1-septate; *sporodochia* pale luteous to pale orange, with monophialides giving rise to falcate, slightly to strongly dorsiventrally curved *macroconidia*, tapering towards both ends, with an elongated, strongly curved apical cell and a blunt and distinct foot-shaped basal cell, (1–)5–6(–10)-septate; *chlamydospores* not observed (Lombard *et al*. 2019).

Notes: *Fusarium sporodochiale* is unique within the FCSC, producing up to 10-septate sporodochial macroconidia. Additionally, the apical cell of macroconidia is more elongated and hooked than those of other species in this complex.

Fusarium citricola species complex (FCCSC)

Fusarium aconidiale L. Lombard & Crous, *Persoonia* **46**: 523. 2021. MB 839622.

Holotypus: CBS H-24769.

Ex-type culture: CBS 147772 = CPC 37959 = UBOCC-A-109005.

Type locality: **France**.

Type substrate: *Triticum aestivum*.

Description and illustrations: See Crous *et al.* (2021a).

Diagnostic features: *Colonies* white to rosy buff, flat, woolly to cottony with radial patches of white aerial mycelium, reverse white to pale rosy buff on PDA; aerial phialides monophialidic, but *microconidia* not observed; *sporodochia* crystalline to pale cream, with monophialides giving rise to falcate, straight to moderately curved *macroconidia*, tapering towards the basal part, apical cell more or less equally sized than the adjacent cell, curved to hooked; basal cell well-developed, foot-shaped, rarely papillate, 3(–5)-septate; *chlamydospores* not observed (Crous *et al.* 2021a).

Notes: *Fusarium aconidiale* is similar to *F. juglandicola* but does not produce red pigment under continuous white light nor any chlamydospores or aerial microconidia, distinguishing it from other members of the FCCSC. Furthermore, *F. aconidiale* produces predominantly 3-septate sporodochial conidia and much less frequently 4- and 5-septate sporodochial conidia compared to *F. juglandicola*. (Crous *et al.* 2021a).

Fusarium celtidicola Q.J. Shang *et al.*, *Phytotaxa* **361**: 255. 2018. MB 553845. Figs 11, 12.

Holotypus: MFLU 15-3646; *isotypus* HKAS 95020.

Ex-type culture: KUMCC 16-0019 = MFLUCC 16-0526; ex-isotype culture KUMCC 16-0019 = MFLUCC 16-0526.

Type locality: **Italy**, Forlì-Cesena Province, Forlì, Viale dell'Appennino.

Type substrate: Dead branch of *Celtis australis*.

Description and illustrations: See Shang *et al.* (2018).

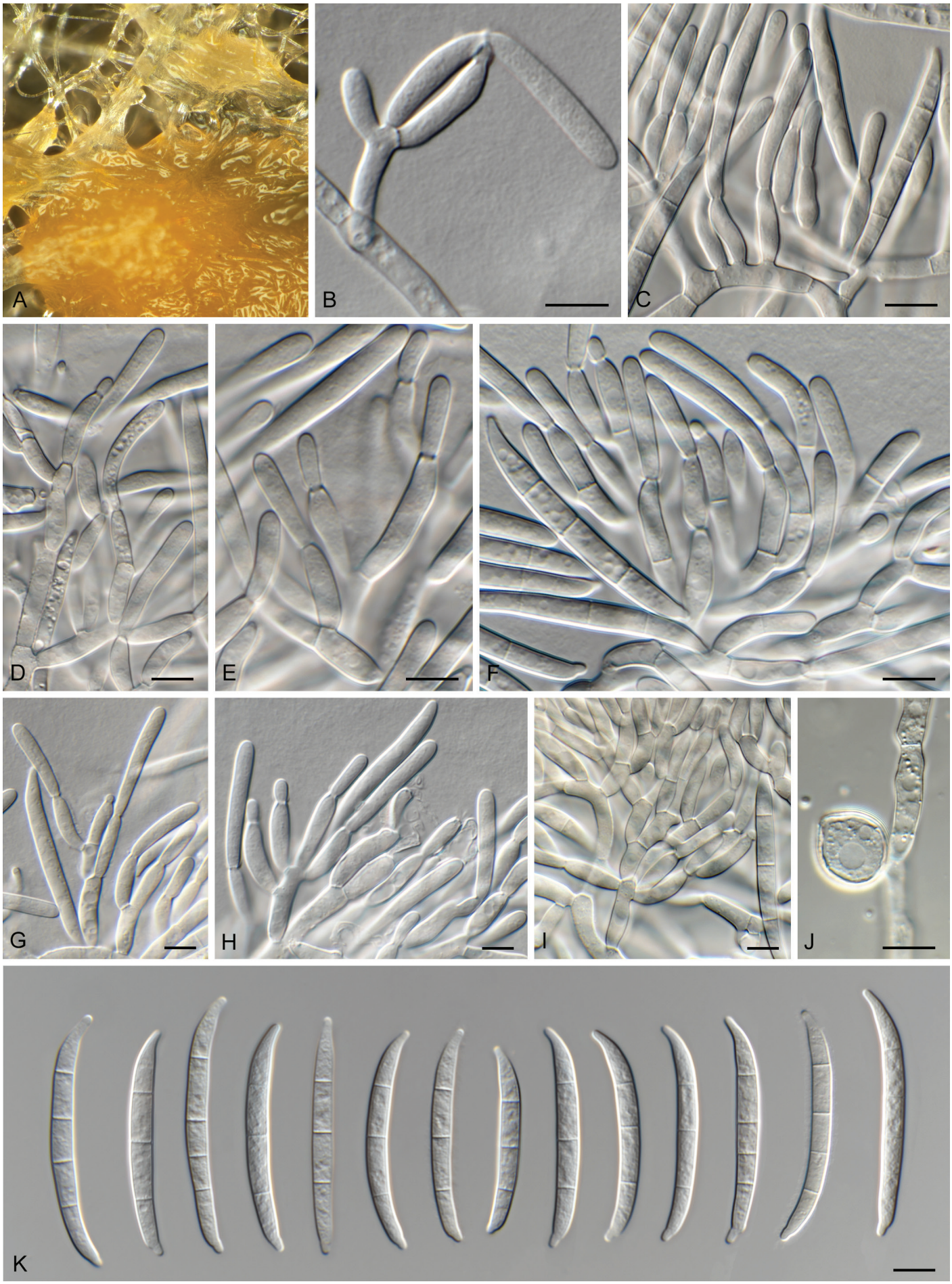

Fig. 11. *Fusarium celtidicola* (MFLUCC 16-0526). **A.** Sporodochium on CLA. **B.** Aerial conidiophore. **C–I.** Sporodochial conidiophores with monophialides. **J.** Chlamydospore. **K.** Macroconidia. Scale bars = 10 µm.

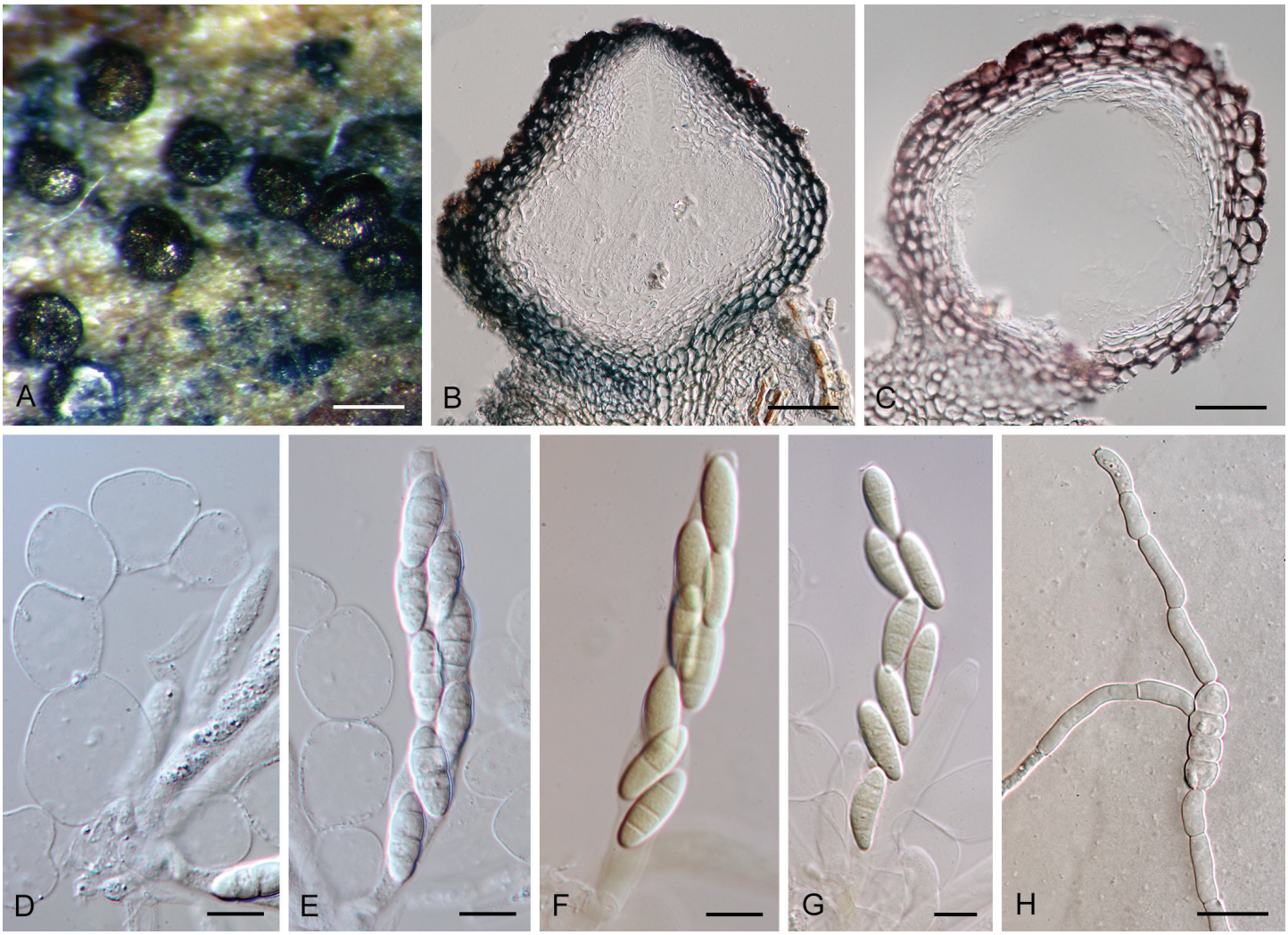

Fig. 12. *Fusarium celtidicola* (MFLUCC 16-0526). **A.** Perithecial ascomata on host surface. **B, C.** Vertical section through perithecia. **D–G.** Hamathecial catenophyses, and asci. **H.** Germinating ascospore. (F, G in Melzer's reagent). Scale bars: A = 100 µm, B, C = 30 µm, D–H = 10 µm (Photos from Shang *et al.* 2018).

Diagnostic features: *Colonies* on the surface white, reddish at the centre, and reddish white in reverse on PDA; aerial monophialides giving rise to micro- and macroconidia; *microconidia* oblong to naviculate, straight or curved, 1–3-septate; *macroconidia* naviculate to falcate, 3–5-septate with a curved, blunt apical cell and poorly-developed, foot-shaped basal cell; *chlamydospores* intercalary in aerial hyphae, in pairs or chains (Shang *et al.* 2018).

Notes: *Fusarium celtidicola* is distinct from other members of the FCCSC in that it produces chlamydospores, and has a sexual morph with blue-black to dark purple perithecia, and ellipsoid to obovoid to fusoid, 0–3-septate, smooth-walled ascospores (Shang *et al.* 2018).

Fusarium citricola Guarnaccia *et al.*, *Persoonia* **40**: 12. 2017 (2018). MB 820246.

Holotypus: CBS H-23020 (dried SNA/CL culture).

Ex-type culture: CBS 142421 = CPC 27805.

Type locality: **Italy**, Cosenza, Rocca Imperiale.

Type substrate: Crown of *Citrus reticulata* 'Caffin'.

Description and illustrations: See Sandoval-Denis *et al.* (2018a).

Diagnostic features: *Colonies* pale luteous to pale yellow on surface (orange to red when incubated in light), reverse pale luteous to straw (diffusible pigment absent in the dark, an orange to red pigment sometimes present when incubated in the light) on PDA; aerial monophialides giving rise to *microconidia*, ellipsoidal to falcate, 0–3-septate; *sporodochia* bright orange, with monophialides giving rise to falcate, dorsiventrally curved *macroconidia* with almost parallel sides, tapering slightly towards both ends, with a blunt to papillate, curved apical cell and poorly to well-developed, foot-shaped basal cell, (1–)2–4(–6)-septate; *chlamydospores* absent (Sandoval-Denis *et al.* 2018a).

Notes: *Fusarium citricola* was shown to be the cause of cankers on diverse *Citrus* spp. in Apulia and Calabria in southern Italy. *Fusarium citricola* resembles *F. salinense*, but can be distinguished in having slightly smaller sporodochial conidia, often with a gentle and symmetrical dorsiventral curvature, and 0–3-septate microconidia (*vs* the often asymmetrically curved macroconidia and 0–1(–2)-septate microconidia in *F. salinense*) (Sandoval-Denis *et al.* 2018a).

Fusarium juglandicola L. Lombard & Crous, Persoonia **46**: 521. 2021. MB 839621.

Holotypus: CBS H-24770.

Ex-type culture: CBS 147773 = CPC 37962 = UBOCC-A-119001.

Type locality: **France**, Rhone-Alps region.

Type substrate: Bud of *Juglans regia*.

Description and illustrations: See Crous *et al.* (2021a).

Diagnostic features: *Colonies* white to pale luteous on surface and reverse on PDA; aerial monophialides giving rise to macroconidia; *microconidia* absent; *sporodochia* with monophialides giving rise to falcate, moderately dorsiventrally curved *macroconidia* with almost parallel sides, tapering towards both ends, with a blunt to slightly hooked, somewhat curved apical cell and papillate to well-developed, foot-shaped basal cell, (1–)3–4(–5)-septate; *chlamydospores* absent (Crous *et al.* 2021a).

Notes: *Fusarium juglandicola* was isolated from walnut, *Juniperus* sp., and eggs from an unknown species in southeast France. *Fusarium juglandicola* is unique within the FCCSC by lacking microconidia and red pigments, even when incubated under continuous white light (Crous *et al.* 2021a).

Fusarium salinense Sand.-Den. *et al*., *Persoonia* **40**: 15. 2017 (2018). MB 820245.

Holotypus: CBS H-23019 (dried SNA/CL culture).

Ex-type culture: CBS 142420 = CPC 26973.

Type locality: **Italy**, Sicily, Messina, Leni.

Type substrate: Twigs of *Citrus sinensis*.

Description and illustrations: See Sandoval-Denis *et al.* (2018a).

Diagnostic features: *Colony* surface pale luteous to sulphur yellow with white to pale luteous margins, reverse pale luteous to orange toward the centre of the colony. Yellow diffusible pigment sometimes present, while red colonies and diffusible pigments occur when incubated in light on PDA, having optimal growth at 25 °C; aerial monophialides giving rise to *microconidia*, ovoid, ellipsoid to falcate, 0–1(–2)-septate; *sporodochia* flesh, salmon to orange coloured, with monophialides give rise to falcate, (2–)3–4(–5)-septate, slender *macroconidia*, with a gentle curvature and nearly parallel dorsiventral lines or an unequal curvature, slightly more pronounced in the upper part of the spore, tapering slightly towards the basal end, with a papillate and curved apical cell and a poorly-developed, foot-shaped basal cell; *chlamydospores* absent, but rounded, thin-walled hyphal swellings sometimes present in old cultures. (Sandoval-Denis *et al.* 2018a).

Notes: *Fusarium salinense* is known from Sicily (Italy), and Salina (Aeolian Island), and is associated with canker symptoms on three different *Citrus* species. It produces sparingly branched conidiophores in the aerial mycelium, especially in young cultures, but its growth soon becomes pionnotal. *Fusarium salinense* can be distinguished from *F. citricola* by producing shorter sporodochial phialides and slightly longer and robust macroconidia, often with an unequal dorsiventral curvature (Sandoval-Denis *et al.* 2018a).

Fusarium concolor species complex (FCOSC)

Fusarium bambusarum M.M. Wang & L. Cai, *Persoonia* **48**: 25. 2022. MB 346784.

Typus: HMAS 351575 (dried SNA/CL culture).

Type locality: **China**, Jiangxi Province.

Type substrate: From bamboo.

Descriptions and illustrations: See Wang *et al*. (2022).

Diagnostic features: *Colonies* white on PDA, with dense aerial mycelium; aerial monophialides giving rise to *microconidia* in false heads, ovoid to fusoid-ellipsoid, aseptate; *sporodochia* orange grey on carnation leaf agar, with monophialides give rise to falcate *macroconidia*, slightly bent with parallel sides, with a papillate to hooked, curved apical cell, and well-developed, foot-shaped basal cell, 3–6-septate; *chlamydospores* terminal, globose, becoming rough and thick-walled (Wang *et al.* 2022).

Notes: *Fusarium bambusarum* is distinguished from other taxa in the FCOSC based on its 3–6-septate macroconidia, and having monophalidic aerial phialides (Wang *et al.* 2022). Presently this taxon is only known from bamboo collected in Jiangxi Province, China.

Fusarium anguioides Sherb., *Mem. Cornell Univ. Agric. Exp. Sta*. **6**: 169. 1915. MB 159197.
Synonym: *Fusarium avenaceum* var. *anguioides* (Sherb.) Bilaĭ, *Mikrobiologicheskij Zhurnal* (Kiev) **49**: 6. 1987. MB 346784.

Typus: ?CUP-007479, BPI 72044 neotype (not Code compliant).

Type locality: **USA**, New York, Castile.

Type substrate: *Solanum tuberosum*.

Descriptions and illustrations: See Sherbakoff (1915), Gerlach & Nirenberg (1982) and Nelson *et al*. (1995).

Diagnostic features: *Colonies* cream, pink, rose to carmine or yellowish to ochre, becoming yellowish brown or red-brown to brown with age on PDA, having optimal growth at 25 °C; aerial mono- to polyphialides giving rise to *microconidia*, ovoid to fusoid, 0–3-septate; *sporodochia* orange to cinnamon or brick coloured, with monophialides give rise to falcate, *macroconidia*, slightly bent to anguiform, slender, tapering toward both ends, with an elongated, elegantly curved apical cell and well-developed, foot-shaped basal cell, (3–)5–7-septate; *chlamydospores* absent, but hyphal swellings do occur (Gerlach & Nirenberg 1982).

Notes: Sherbakoff (1915) provided an illustration with the original protologue of *F. anguioides* and placed material in CUP,

as CUP-007479. The neotype (BPI 72044) designated by Nelson *et al*. (1995) originated from China and was isolated from soil in a bamboo grove, and is thus unsuitable. An isolate from the original locality (USA) and host (*Solanum tuberosum*) needs to be selected.

Fusarium austroafricanum A. Jacobs *et al.*, *Mycologia* **110**: 1197. 2018. MB 823959. Fig. 13.

Holotypus: PREM 62137 (dried culture); *paratypi* PREM 62138 and PREM 62139 (dried cultures).

Ex-holotype culture: NRRL 66741 = PPRI 10408 = PPRI 23548; ex-paratype cultures: CBS 120990 = DAOM 192987 = FRC M-2406 = NRRL 53441 = PPRI 23546 and NRRL 66742 = PPRI 10412.

Type locality: **South Africa**, Eastern Cape Province, Humansdorp.

Type substrate: Endophyte of *Pennisetum clandestinum*.

Description and illustrations: See Jacobs-Venter *et al*. (2018).

Diagnostic features: *Colony* surface white to reddish white, reverse pale orange on PDA, having optimal growth at 30 °C; aerial mono- to polyphialides giving rise to *microconidia*, oval to obovoid, aseptate; *sporodochia* with monophialides give rise to falcate, (3–)5(–8)-septate *macroconidia* with a blunt apical cell and poorly-developed, foot-shaped basal cell; *chlamydospores* singly or in intercalary or terminal clusters (Jacobs-Venter *et al*. 2018).

Notes: *Fusarium austroafricanum* is similar morphologically to *F. concolor* and *F. babinda*, but forms white to reddish white colonies on PDA, whereas those of *F. concolor* are white to pale orange, and those of *F. babinda* are pale orange to violet. Morphologically, *F. austroafricanum* differs from *F. concolor* and *F. babinda* in the shape of the apical cell on the macroconidia, *i.e*. blunt (*F. austroafricanum*), papillate (*F. concolor*) or slightly curved to hooked (*F. babinda*) (Reinking 1934, Marasas *et al.* 1986, Jacobs-Venter *et al*. 2018).

Fusarium concolor Reinking, *Zentralbl. Bakteriol.,* Abt. 2, **89**: 512. 1934. MB 261626.
Synonym: *Fusarium polyphialidicum* Marasas *et al.*, *Mycologia* **78**: 678. 1986. MB 102972.

Holotypus: IMI 112502.

Ex-type culture: BBA 2607 = BBA 63601 = CBS 183.34 = DAOM 225131 = DSM 62179 = IMB 10330 = IMI 112502 = NRRL 13994.

Type locality: **Uruguay**, Montevideo.

Type substrate: *Hordeum vulgare*.

Descriptions and illustrations: See Gerlach & Nirenberg (1982) and Marasas *et al.* (1986).

Diagnostic features: *Colonies* whitish, reverse white to yellow on PDA, having optimal growth at 25 °C; aerial mono- to polyphialides giving rise to *microconidia* in false heads, obovoid, fusoid to subclavate, (0–)1(–2-)septate; *sporodochia* white to pale orange, with mono- to polyphialides give rise to straight or falcate, 3–5(–9)-septate *macroconidia* with a long and tapered to curved apical cell and well-developed, foot-shaped basal cell; *chlamydospores* abundant, intercalary and terminal in hyphae and conidia, single, in pairs, chains or clusters (Gerlach & Nirenberg 1982, Marasas *et al.* 1986).

Notes: Balmas *et al*. (2010) and Jacobs-Venter *et al*. (2018) considered that *F. polyphialidicum* was a synonym of *F. concolor*, which was originally described based on a single isolate from diseased barley in Uruguay (Reinking 1934). *Fusarium concolor* has a wide distribution and host range, occurring in Africa (South Africa, Zimbabwe), Australasia (Australia), Europe (Italy, Spain), South America (Uruguay), and North America (USA, Hawaii), and has also been associated with human infections (Jacobs-Venter *et al*. 2018).

Taxonomic novelties

Novel species are described in *Fusicolla* and *Neocosmospora*. Additionally, arguments for recognising distinct genera in the terminal fusarioid clade of the *Nectriaceae* were presented by Crous *et al*. (2021b) and Hill *et al*. (2022). In this regard, several species recently assigned to *Fusarium s. str*., are herewith allocated to *Neocosmospora*.

Fusicolla elongata Decock, Crous & Sand.-Den., ***sp. nov.*** MycoBank MB 843499. Fig. 14.

Etymology: From Latin *elongare*, meaning elongated, in reference to its long conidia.

Description: *Conidiophores* prostrate, emerging from vegetative hyphae, intermixed and confluent, commonly as single phialides borne laterally on hyphae or reduced to phialidic pegs; rarely and mostly on the colony periphery, conidiophores erect, simple or branched once or twice laterally and irregularly, terminating in a single conidiogenous cell. *Conidiogenous cells* monophialidic, subcylindrical, (3–)8–31.5(–40) × (1.5–)2–4(–4.5) µm, smooth- and thin-walled, with or without noticeable periclinal thickening, and a minute, non-flared apical collarette. *Macroconidia* slender to somewhat elongate, almost straight to gently curved, apical cell barely curved with a rounded apex, basal cell obtuse, non-foot-shaped, (3–)4–5-septate, predominantly 5-septate, hyaline, smooth- and thin-walled; 3-septate conidia: 66.5–82 × 2.5–3 µm (av. 73.6 × 2.8 µm); 4-septate, (64–)74.5–92.5(–97) × (2.5–)3–4 µm (av. 83.5 × 3.2 µm); 5-septate, (81.5–)85–96(–100.5) × 2.5–4 µm (av. 90.5 × 3.3 µm). *Microconidia*, *chlamydospores* and *sexual morph* not observed.

Culture characteristics: Colonies at 25 °C after 7 d: On PDA reaching 17–22 mm diam, orange to apricot at centre, white to pale salmon at periphery, flat, slightly folded to cerebriform at centre, membranous to slimy, lacking aerial mycelium, margin entire; reverse white to pale salmon, without diffusible pigments. On SNA reaching 15–22 mm diam, buff to pale salmon, flat, membranous to slimy at centre, aerial mycelium lacking or scattered in irregular, short patches; reverse white to pale saffron without diffusible pigments. On OA reaching 22–28 mm diam, pale luteous, pale amber to ochraceous, flat, membranous, with abundant and confluent sporulation forming slimy masses and concentric rings, lacking aerial mycelium, margin entire to filamentous; reverse pale luteous without diffusible pigments.

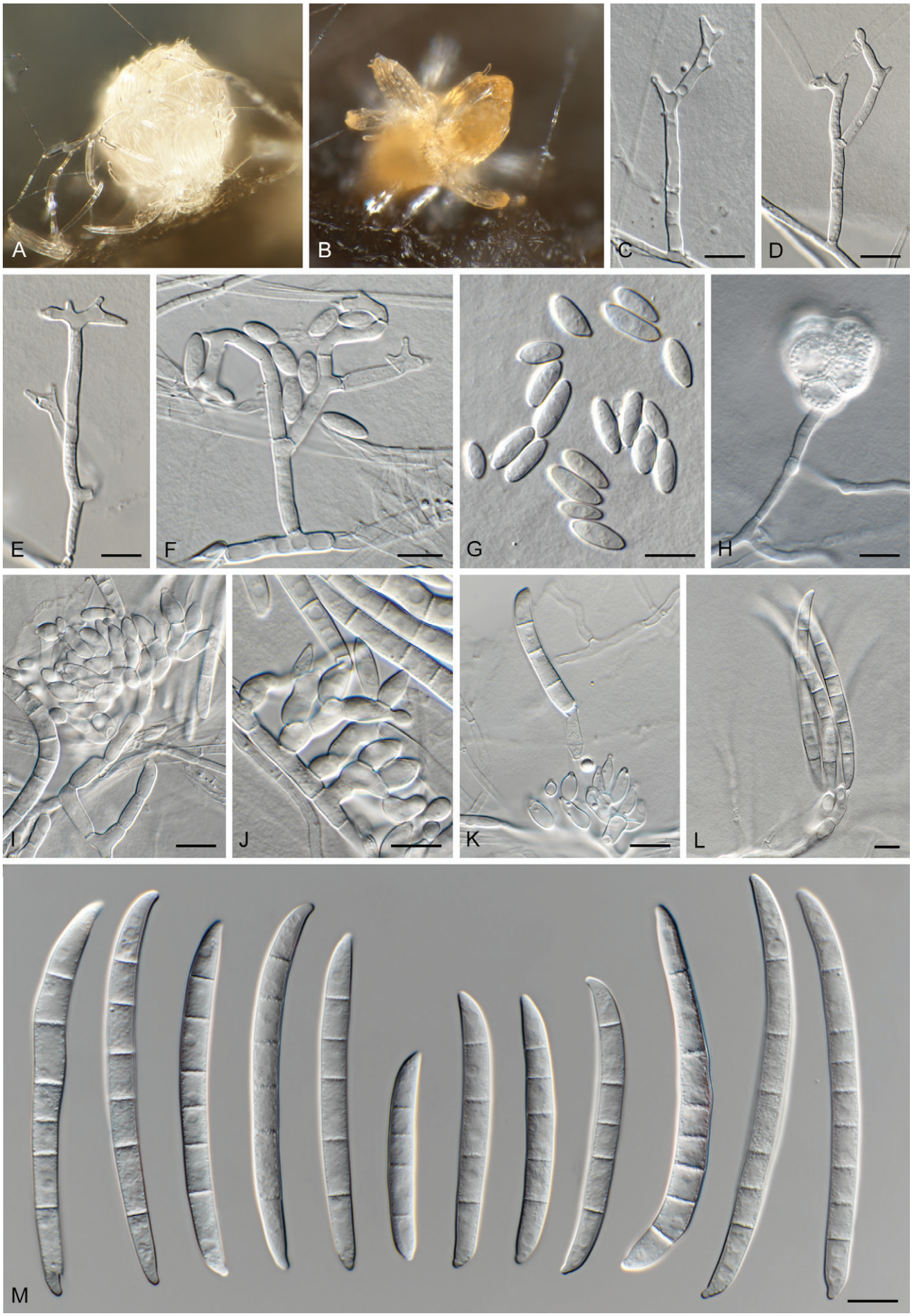

Fig. 13. *Fusarium austroafricanum* (CBS 120990). **A, B.** Sporodochia on CLA. **C–F.** Aerial conidiophores with polyphialides giving rise to microconidia. **G.** Microconidia. **H.** Chlamydospore. **I–L.** Sporodochial conidiophores giving rise to macroconidia. **M.** Macroconidia. Scale bars = 10 µm.

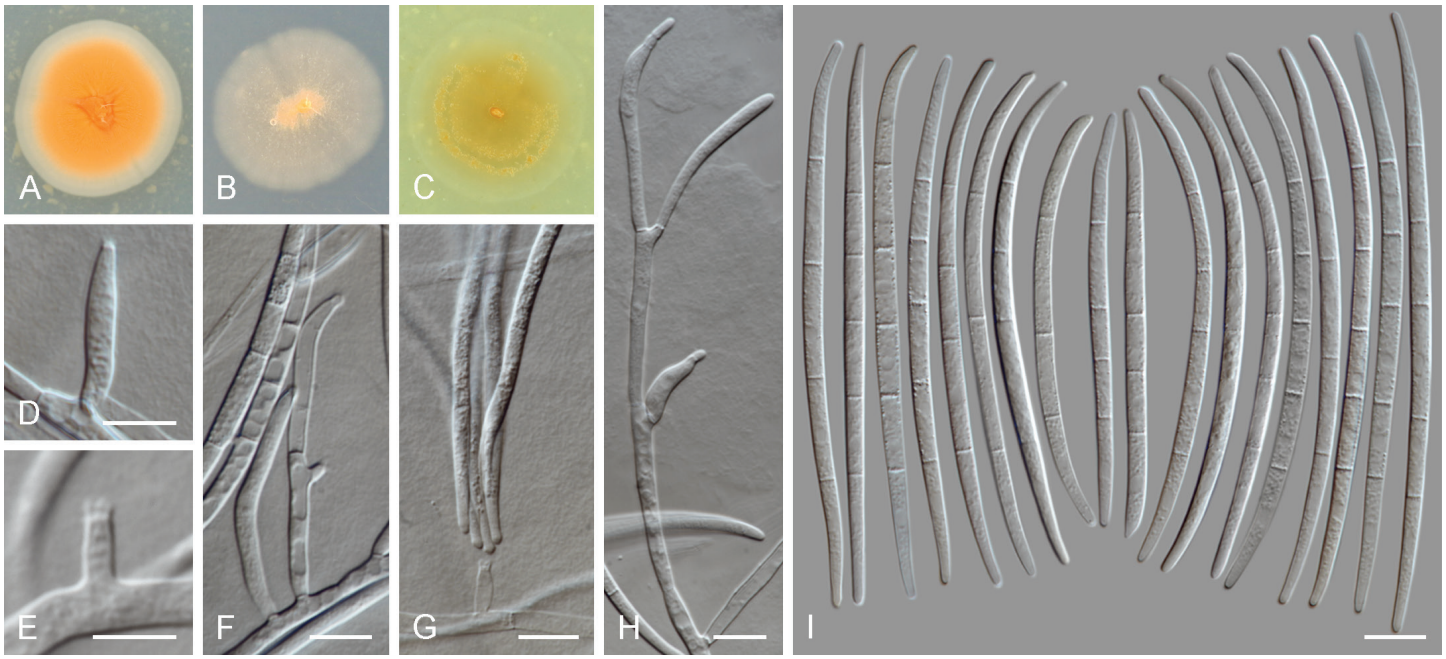

Fig. 14. *Fusicolla elongata* (MUCL 58143 ex-type). **A–C.** Colony surface on PDA, SNA and OA, respectively. **D–H.** Conidiophores and conidiogenous cells. **I.** Conidia. Scale bars: E = 5 µm; all others = 10 µm.

Typus: **Zimbabwe**, Matabeleland North, Victoria Falls area, from soil, Apr. 1996, *C. Decock*, isol. number 51V (**holotype** CBS H-24945, culture ex-type MUCL 58143 = CBS 148934).

Additional material examined: **Zimbabwe**, Matabeleland North, Victoria Falls area, from soil, Apr. 1996, *C. Decock*, isol. number 52V, culture MUCL 58144 = CBS 148935.

Notes: *Fusicolla elongata* produces characteristic long 3–5-septate conidia. Other *Fusicolla* species producing conidia with similar septation include *Fu. acetilerea*, *Fu. violacea*. However, *Fu. elongata* forms exceptionally long conidia which distinguishes this species from every other known species in the genus. *Fusicolla elongata* can be further distinguished from *Fu. acetilerea* by the lack of chlamydospores in the former species. Additionally, while both *Fu. acetilerea* and *Fu. violacea* have brownish to dark red-brown colony pigmentation, colonies of *Fu. elongata* are consistently orange to salmon coloured (Gerlach & Nirenberg 1982).

Fusicolla gigas Chang Liu, Z.Q. Zeng & W.Y. Zhuang, ***sp. nov.*** MycoBank MB 844496.

Etymology: Name refers to the large-sized macroconidia produced by this species.

Holotypus: CGMCC 3.20680 (permanently preserved in a metabolically inactive state).

Ex-type culture: CGMCC 3.20680.

Type locality: **China**, Chongqing City, Wushan County, Hongchiba National Forest Park.

Type substrate: Isolated from soil.

Description and illustration: Liu *et al*. (*Phytotaxa* **536**: 167. 2022).

Diagnostic features: *Colonies* orange to pale yellow with orange margin and slimy appearance on PDA; aerial monophialides giving rise to micro- and macroconidia; *microconidia* aseptate, slightly to markedly curved; *macroconidia* falcate to long-fusiform, (1–)3(–4)-septate, with a hooked apical cell and foot-shaped basal cell; *chlamydospores* and *sexual morph* not observed (Liu *et al*. 2022).

Fusicolla guangxiensis Z.Q. Zeng, C. Liu & W.Y. Zhuang, ***sp. nov.*** MycoBank MB 844497.

Etymology: Name refers to the type locality of the type specimen.

Holotypus: CGMCC 3.20679 (permanently preserved in a metabolically inactive state).

Ex-type culture: CGMCC 3.20679.

Type locality: **China**, Guangxi autonomous region, Fangchenggang City, Shangsi County, Shiwandashan National Forest Park.

Type substrate: Isolated from an unidentified rotten twig.

Description and illustration: Liu *et al*. (*Phytotaxa* **536**: 169. 2022).

Diagnostic features: *Colonies* orange with pale luteous margin and slimy appearance on PDA; aerial monophialides giving rise to macroconidia; *macroconidia* falcate to long-fusiform, (0–)1(–3)-septate, with an acute to hooked apical cell and an acute, non-pedicellate basal cell; *microconidia*, *chlamydospores* and *sexual morph* not observed (Liu *et al*. 2022).

Notes: *Fusicolla gigas* and *Fu. guangxiensis* were invalidly published because the protologue did not explicitly mention the

holotypes were preserved in a metabolically inactive state [Art. 40.8 (Shenzhen)]. Both species are validated here.

Longinectria O. Savary, M. Coton, E. Coton & J-L. Jany, ***gen. nov.*** MycoBank MB 844395.

Etymology: From the Latin *longus* = long, "Longi-" refers to the phialides length observed for the *Longinectria* species and "*-nectria*" refers to the *Nectriaceae* family.

Ascomatal morph unknown. *Conidiophores* with variable-length phialides, sometimes extremely long (*e.g.* 153–237 µm), lateral, sometimes verticillate, hyaline. *Macroconidia* straight to slightly curved, apical cell morphology blunt to papillate and a basal cell often notched, 0–3-septate, hyaline. *Microconidia* ovoid, ellipsoid to allantoid, 0–1 septate, hyaline. *Chlamydospores* absent to abundant, globose, single, in pairs or chains, intercalary or terminal (from Savary *et al*. 2021).

Type species: *Longinectria lagenoides* O. Savary, M. Coton, E. Coton & J-L. Jany

Notes: The genus *Longinectria*, together with its two known species, *L. lagenoides* and *L. verticilliformis*, were invalidly published as two numbers were cited as holotypes for each species [Art. 40.7, 40.8 (Shenzhen)] (Savary *et al*. 2021). The names were subsequently published in *Index Fungorum*, but as the type species of the genus was not indicated, the genus was still not validly published [Art. 40.1 (Shenzhen)], and the species also rendered invalid [Art. 35.1 (Shenzhen)]. The genus and species are thus validated here.

Longinectria lagenoides O. Savary, M. Coton, E. Coton & J-L. Jany, ***sp. nov.*** MycoBank MB 844396.

Holotypus: UBOCC-A-120039 (permanently preserved in a metabolically inactive state).

Ex-type culture: UBOCC-A-120039 = CBS 147588.

Type locality: **France**.

Type substrate: Isolated from Swiss cheese.

Description and illustration: Savary *et al*. (*Mycosphere* **12**: 1089. 2021) .

Etymology: From Latin *lagoena* = bottle, refers to the observed phialide shape.

Diagnostic features: *Colonies* brown with folded surface and brown pigmentation and powdery aerial mycelium (sporulation) on PDA, growing between 5 and 25 °C, having optimal growth at 20 °C; aerial monophialides giving rise to micro- and macroconidia; monophialides extremely long or reduced to conidiogenous pegs on hyphae; *microconidia* 0–1-septate, ovoid to allantoid; *macroconidia* straight, 0–3-septate, apical cell blunt to papillate, and poorly-developed, foot-shaped basal cell; *chlamydospores* globose, typically intercalary, or terminal, two or more. No known mycotoxins already described to be produced by *Fusarium*, *Penicillium*, *Aspergillus* or *Alternaria* spp. were detected (Savary *et al*. 2021).

Longinectria verticilliformis O. Savary, M. Coton, E. Coton & J-L. Jany, ***sp. nov.*** MycoBank MB 844397.

Etymology: Name refers to the subverticillate arrangement of phialides.

Holotypus: UBOCC-A-120043 (permanently preserved in a metabolically inactive state).

Ex-type culture: UBOCC-A-120043 = CBS 147589.

Type locality: **France**.

Type substrate: Isolated from an Italian cheese (Alpeggio).

Description and illustration: Savary *et al*. (*Mycosphere* **12**: 1091. 2021).

Diagnostic features: *Colonies* white to white grey with powdery to cottony aerial mycelium on PDA, growing between 5 and 25 °C, with optimal growth at 20 °C; aerial monophialides giving rise to micro- and macroconidia; *microconidia* 0–1-septate, straight or curved, reniform; *macroconidia* straight, ellipsoidal, 1–3-septate, with a blunt to papillate apical cell and foot-shaped basal cell; *chlamydospores* not observed. No known mycotoxins already described to be produced by *Fusarium*, *Penicillium*, *Aspergillus* or *Alternaria* spp. were detected (Savary *et al*. 2021).

Neocosmospora akasia (Lynn & I. Barnes) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843501.
Basionym: *Fusarium akasia* Lynn & I. Barnes, *Mycologia* **113**: 544. 2021. MB 834436.

Holotypus: PREM 62607; *paratypi* PREM 62608 and PREM 62609.

Ex-type culture: CBS 146880 = CMW 54735 = PPRI 27978; ex-paratype cultures CBS 146881 = CMW 54741 = PPRI 27979 and CBS 147161 = CMW 54752 = PPRI 27980.

Type locality: **Indonesia**, Riau, Pelalawan.

Type substrate: From head (including mycangium) of *Euwallacea perbrevis* (TSHBa) in stems of *Acacia crassicarpa.*

Description and illustrations: Lynn *et al.* (2021).

Diagnostic features: *Colony* surface white, buff to saffron or fulvous in dark, buff to honey darkening to red, blood red in ambient daylight, reverse yellowish white to buff ,darkening to isabelline or cinnamon in the dark, saffron to orange, darkening to rust and blood red after 1 mo in ambient daylight on PDA, having optimal growth at 30 °C; aerial monophialides giving rise to *microconidia* in false heads, ovoid to obovoid, slightly curved, 0–1(–2)-septate; *sporodochia* buff to pale orange, with monophialides give rise to slightly curved, clavate, with ridged appearance, (0–)1–4(–5)-septate *macroconidia* with a blunt apical cell and obtuse to poorly-developed, foot-shaped basal cell; *chlamydospores* sparse, in hyphae and conidia, single or in pairs (Lynn *et al.* 2021).

Notes: *Neocosmospora akasia* is associated with the ambrosia beetles, *Euwallacea perbrevis* and *E. similis* in plantations of

Acacia crassicarpa in Indonesia. It is characterized by clavate conidia which are slightly constricted at the septa, giving it a ridged appearance, and having arched, thick aerial conidiophores that taper slightly at the base (Lynn *et al.* 2021).

Neocosmospora awan (Lynn & I. Barnes) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843502.
Basionym: *Fusarium awan* Lynn & I. Barnes, *Mycologia* **113**: 544. 2021. MB 834437.

Holotypus: PREM 62602; *paratypi* PREM 62594 and PREM 62604.

Ex-type culture: CBS 146882 = CMW 54719 = PPRI 27973; ex-paratype cultures CBS 146883 = CMW 53705 = PPRI 27957 and CBS 146884 = CMW 54722 = PPRI 27975.

Type locality: **Indonesia**, Riau, Pelalawan.

Type substrate: From head (including mycangium) of *Euwallacea similis* in stems of *Acacia crassicarpa.*

Description and illustrations: Lynn *et al.* (2021).

Diagnostic features: *Colony* surface colour white in the dark, white darkening to honey after 1 mo in ambient daylight, in reverse yellowish white to buff in the dark, buff darkening to ochreous after 1 mo in ambient daylight on PDA, having optimal growth at 30 °C; aerial monophialides giving rise to *microconidia* in false heads, ovoid, 0–1(–2)-septate, and flute-shaped, 1–3-septate *macroconidia*; sporodochia luteous to ochreous, with monophialides giving rise to curved, cylindrical or slightly clavate or flute-shaped, (0–)2–3(–4)-septate macroconidia with a narrowly papillate to blunt apical cell and obtuse to poorly-developed, foot-shaped basal cell; *chlamydospores* abundant, intercalary and terminal in hyphae and conidia, single, in pairs or chains (Lynn *et al.* 2021).

Notes: *Neocosmospora awan* is associated with ambrosia beetles, *Euwallacea perbrevis* and *E. similis*, in plantations of *Acacia crassicarpa* in Indonesia. It is characterised by having abundant chlamydospores that form in hyphae and mature conidia, having multiseptate aerial macroconidia that are elongated-ovoid in shape, and very narrow sporodochial macroconidia. Furthermore, phylogenetically it groups separate from the Ambrosia Clade within *Neocosmospora*.

Neocosmospora brevis Sand.-Den. & Crous, *Persoonia* **43**: 119. 2019. MB 831176.
Synonym: *Fusarium breve* (Sand.-Den. & Crous) O'Donnell *et al.*, *Index Fungorum* **440**: 1. 2020. MB 557673.
New synonym: *Fusarium rosicola* Lin Huang *et al.*, *Pl. Pathol.* **70**: 2065. 2021. MB 839201.

Holotypus: CBS H-23975.

Ex-type culture: CBS 144387 = MUCL 16108.

Type locality: **Belgium**, Heverlee.

Type substrate: Soil-water polluted with diethylene glycerol and ethylene glycerol.

Description and illustrations: Sandoval-Denis *et al.* (2019), He *et al.* (2021).

Diagnostic features: *Colony* surface orange to saffron or pale yellow, reverse orange, luteous to amber to pale yellow on PDA, having optimal growth at 25 °C; aerial monophialides giving rise to *microconidia* in false heads, oval, ellipsoidal to subclavate, straight or slightly curved, 0–1(–2)-septate; *sporodochia* with monophialides give rise to falcate, slightly dorsiventrally curved, 3–5-septate *macroconidia*, apical cell blunt and rounded, basal cell without a well-developed foot-shaped basal cell; *chlamydospores* abundant, globose to subglobose, terminal or intercalary on hyphae or conidia, solitary or in chains (Sandoval-Denis *et al.* 2019).

Notes: *Fusarium rosicola* was described as a pathogen of Chinese rose (*Rosa chinensis*) (He *et al*. 2021). Apparent morphological and physiological differences with its closest relative, *N. brevis*, in their phylogenetic analysis were not supported in our analysis (Fig. 3). We attribute these differences to intraspecific variability in *N. brevis*.

Neocosmospora drepaniformis (T. Aoki *et al.*) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843503.
Basionym: *Fusarium drepaniforme* T. Aoki *et al.*, *Mycologia* **113**: 1098. 2021. MB 558018.

Holotypus: BPI 923530 (dried culture), *isotypus* IMI 351954.

Ex-type culture: NRRL 62941 (= KOD 147) = MAFF 247230.

Type locality: **Singapore**.

Type substrate: Unknown woody host.

Description and illustrations: Aoki *et al.* (2021).

Diagnostic features: *Colony* surface white, yellowish white to pale yellow, becoming pale orange, light orange to greyish orange with age, reverse yellowish white or pale yellow to greyish yellow on PDA, having optimal growth at 25 °C; aerial monophialides giving rise to *microconidia* in false heads, ellipsoidal, oblong-ellipsoidal, fusoid-ellipsoidal to clavate, straight or sometimes curved and reniform or crescent-shaped, some obovate to comma-shaped, 0–1(–3)-septate; *sporodochia* sparse, with monophialides give rise to clavate and straight (in the dark), to falcate (under nuv-light), (0–)3–7-septate *macroconidia*, with a papillate apical cell and poorly to well-developed, foot-shaped basal cell; *chlamydospores* intercalary and terminal in hyphae and conidia, single, in chains or small clusters (Aoki *et al*. 2021).

Notes: *Neocosmospora drepaniformis* was originally deposited as "*F. bugnicourtii*" (on *Camellia sinensis*: West Bengal) based on IMI 351954. It is characterised by forming multiseptate curved conidia, especially under nuv-light. Some conidia become swollen in the apical part, appearing wedge-shaped (Aoki *et al*. 2021).

Neocosmospora duplosperma (T. Aoki *et al.*) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843504.
Basionym: *Fusarium duplospermum* T. Aoki *et al.*, *Mycologia* **113**: 1091. 2021. MB 558017.

Holotypus: BPI 923529 (dried culture).

Ex-type culture: NRRL 62583 = MAFF 247220.

Type locality: **USA**, Florida, Miami-Dade County, Homestead.

Type substrate: From the oral mycangium of *Euwallacea perbrevis* trapped in a *Persea americana* grove.

Description and illustrations: Aoki *et al*. (2021).

Diagnostic features: *Colony* surface white, yellowish white, pale yellow, light yellow to greyish yellow, becoming pale orange to greyish orange, or reddish white to pale red, reddish grey to greyish red with age in the dark, reverse pigment absent or yellowish white, pale yellow to light yellow, some greyish orange, brownish orange to yellowish brown or brown, sometimes with yellowish pigments in the agar on PDA, having optimal growth at 25 °C; aerial monophialides giving rise to *microconidia* in false heads, ellipsoid, oblong-ellipsoid, fusoid-ellipsoid to short-clavate, straight or sometimes curved, reniform or crescent-shaped, some obovate to comma-shaped, 0–1-septate; *sporodochia* with monophialides give rise to two distinct conidial types, i) short-clavate to obovate or naviculate, straight or curved, with obtuse apex and truncate base, 0–1(–2)-septate, and ii) straight or curved, wedge-shaped, (1–)3–5(–7)-septate, swollen in the apical region, with a tapering apical cell, base with a poorly to well-developed, foot-shaped basal cell; *chlamydospores* delayed, intercalary and terminal in hyphae and conidia, single or in chains (Aoki *et al*. 2021).

Notes: *Neocosmospora duplosperma* can be distinguished by forming two morphologically distinct types of multiseptate conidia, namely (i) long, slender, and falcate, or (ii) relatively short, apically swollen, curved and wedge-shaped ("dolphin-like"). Furthermore, *N. duplosperma* is characterised by forming brownish orange colonies on PDA, which differs other species in the *Neocosmospora* Ambrosia Clade, which typically produce whitish, yellowish, or greyish coloured colonies on PDA (Aoki *et al*. 2021).

Neocosmospora geoasparagicola Sand.-Den., Crous, de Boer, Katschnig & W. Jonkers, ***sp. nov.*** MycoBank MB 843505. Fig. 15.

Etymology: Named after the substrate from which all the original specimens were collected: soil from *Asparagus officinalis* fields.

Conidiophores erect or prostrate, borne on the agar substrate and aerial mycelium, 45–190 µm tall, simple or branched laterally and sympodially, bearing terminal single phialides; aerial conidiogenous cells monophialidic, subulate to subcylindrical, smooth- and thin-walled, 21–61 × 2.5–5 µm, with short and flared apical collarettes, periclinal thickening inconspicuous or absent, rarely proliferating laterally and apically. *Aerial conidia* falcate, smooth- and thick-walled, gently dorsiventrally curved, robust, with a blunt, slightly curved apical cell, basal cell obtuse to poorly-developed, foot-shaped, undistinguishable in shape from sporodochial conidia, 3–4(–5)-septate, predominantly 3-septate, 3-septate conidia: (37–)39–50(–56.5) × (4–)5–6.5 µm (av. 44 × 5.3 µm); 4-septate conidia: (49–)51–63(–67.5) × 5.5–7 µm (av. 56.5 × 6 µm); 5-septate conidia: 54.5 × 5.5 µm (only one element observed); overall: (37–)39–54(–67.5) × 4.5–6.5 µm (av. 46.6 × 5.4 µm), borne at the tip of monophialides and accumulating forming elongated false-heads. *Sporodochia* pale luteous to pale orange, formed on aerial and substrate mycelium, and on the surface of carnation leaves. *Sporodochial conidiophores* simple or laterally and irregularly branched bearing terminal monophialides or groups of 2–4 monophialides; *sporodochial conidiogenous cells* monophialidic, doliiform, subulate to subcylindrical, (13–)14.5–22(–31) × 3.5–6 µm, smooth and thin-walled, with a vasiform apical collarette and inconspicuous to absent periclinal thickening. *Sporodochial conidia* falcate, gently dorsiventrally curved, robust, with a blunt, slightly curved apical cell, basal cell obtuse to poorly-developed, foot-shaped, 3–5-septate, predominantly 4-septate, hyaline, smooth- and thick-walled; 3-septate conidia: (43.5–)47–55(–60) × 5–7 µm (av. 51 × 6 µm); 4-septate conidia: (46–)52–60(–63) × 5–7 µm (av. 56.1 × 6 µm); 5-septate conidia: (52.5–)55–64(–68) × 5–7 µm (av. 59.2 × 6.1 µm); overall: (43.5–)52–61(–68) × 5–7 µm (av. 56.6 × 6 µm). *Chlamydospores* and *sexual form* not observed.

Culture characteristics: Colonies at 25 °C after 7 d: On PDA reaching 38–43 mm diam, white to pale buff, pale vinaceous buff at periphery, flat, dusty to felty with or without cottony patches or concentric rings of short aerial mycelium, membranous at periphery, margin entire to slightly filamentous; reverse white to pale buff, ochreous to umber at centre, without diffusible pigments. On SNA reaching 36–42 mm diam, white to pale buff, flat, membranous to dusty at centre, aerial mycelium scarce; reverse white, without diffusible pigments. On OA reaching 40–48 mm diam, white to pale buff, flat, felty, with concentric rings of short, white aerial mycelium, margin entire to slightly lobate; reverse pale buff without diffusible pigments.

Typus: **Netherlands**, Limburg, Kessel, from field soil cultured with *Asparagus officinalis* '*Guelph Millennium*' field, 19 Nov. 2020, *M. Sandoval-Denis & L. Lombard* (holotype CBS H-24947, culture ex-type CBS 148937 = CPC 40592).

Additional material examined: **Netherlands**, Limburg, Kessel, from field soil cultured with *Asparagus officinalis* field, 2019, *W. de Boer* (cultures CBS 148936 = CPC 39928, 39931, 39932); from field soil cultured with *Asparagus officinalis* '*Cygnus*' field, 13 Nov. 2020, *M. Sandoval-Denis & L. Lombard* (culture CPC 40579); from field soil cultured with *A. officinalis* '*Grolim*' field. 13 Nov. 2020, *M. Sandoval-Denis & L. Lombard* (culture CPC 40571); from field soil cultured with *A. officinalis* '*Schneekopf*' field, 13 Nov. 2020, *M. Sandoval-Denis & L. Lombard* (culture CPC 40628).

Notes: *Neocosmospora geoasparagicola* was isolated from soil from several *Asparagus officinalis* experimental fields (Bejo Zaden, Kessel, Limburg, Netherlands) where diverse *Asparagus* varieties have been cultivated. *Neocosmospora geoasparagicola* nested within Clade 2 of *Neocosmospora*, which contains mostly species from Asia and the Americas, including *N. phaseoli*, an important root pathogen of *Fabaceae* (O'Donnell 2000, Nalim *et al*. 2011, Sandoval-Denis *et al*. 2019). Subsequent pathogenicity testing, however, showed that *N. geoasparagicola* is not a pathogen of *A. officinalis* (data not shown).

Species in *Neocosmospora* Clade 2 are characterised by forming often large multiseptate macroconidia from aerial and sporodochial phialides, while generally lacking microconidia. While consistent with general morphological features of taxa in Clade 2, *N. geoasparagicola* clustered basally, and

Fig. 15. *Neocosmospora geoasparagicola* (CBS 148937 ex-type). **A–D.** Sporodochia formed on the surface of carnation leaves. **E–H.** Aerial conidiophores and conidiogenous cells. **I–K.** Sporodochial conidiophores and conidiogenous cells. **L.** Conidia. Scale bars: B–D = 20 µm; J = 5 µm; all others = 10 µm.

clearly separated phylogenetically and biogeographically from the remaining species in this group. Morphologically, *N. geoasparagicola* is most similar to *N. cryptoseptata* and *N. nirenbergiana*. *Neocosmospora geoasparagicola* can be differentiated from *N. cryptoseptata* by it slightly longer conidia and sporodochial phialides. There is considerable morphological overlap between *N. geoasparagicola* and *N. nirenbergiana*. However, sporodochial conidia of *N. geoasparagicola,* which are indistinguishable from aerial macroconidia, are shorter and tend to present longer apical cells than those of *N. nirenbergiana*. By contrast, aerial conidia of *N. nirenbergiana* are considerably different from its sporodochial counterparts, being shorter and somewhat pointy. Additionally, *N. geoasparagicola* lacks reddish pigments, a feature commonly observed in *N. nirenbergiana*.

Neocosmospora mekan (Lynn & I. Barnes) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843506.
Basionym: *Fusarium mekan* Lynn & I. Barnes, *Mycologia* **113**: 547. 2021. MB 834438.

Holotypus: PREM 62600; *isotypi* PREM 62601 and PREM 62602.

Ex-type culture: CBS 146885 = CMW 54714 = PPRI 27971; ex-paratype cultures CBS 146886 = CMW 53696 = PPRI 27956 and CBS 146887 = CMW 54717 = PPRI 27972.

Type locality: **Indonesia**, Riau, Pelalawan.

Type substrate: From head (including mycangium) of *Euwallacea similis* in stems of *Acacia crassicarpa.*

Description and illustrations: Lynn *et al.* (2021).

Diagnostic features: *Colony* surface white, greyish flax blue to greyish violet in the dark, white to pale mouse grey darkening to purple slate and rust after 1 mo in ambient daylight, reverse yellowish white to fawn in the dark, bay darkening to chestnut and blood red after 1 mo in ambient daylight on PDA, having optimal growth at 30 °C; aerial monophialides giving rise to *microconidia* in false heads, ovoid to obovoid, rarely pyriform, 0–1(–2)-septate, aerial macroconidia long ovoid, apex blunt, basal cell obtuse, 0–3(–4)-septate; *sporodochia* luteous to ochreous, with monophialides give rise to straight or slightly curved, sub-fusoid, widest in apical third, wedge-shaped, 0–5(–6)-septate *macroconidia* with a blunt apical cell and obtuse to poorly-developed, foot-shaped basal cell; *chlamydospores* abundant, intercalary and terminal in hyphae and conidia, single, in pairs or chains, rarely in clusters (Lynn *et al.* 2021).

Notes: *Neocosmospora mekan* is associated with *Euwallacea perbrevis* and *E. similis* beetles in plantations of *Acacia crassicarpa* in Indonesia. It is distinguished by its multiseptate (evenly spaced), slightly curved, elongate, subfusoid to wedge-shaped macroconidia, and chlamydospores that tend to form at both the apex and base of mature macroconidia (Lynn *et al.* 2021).

Neocosmospora papillata (T. Aoki *et al.*) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843507.
Basionym: *Fusarium papillatum* T. Aoki *et al.*, *Mycologia* **113**: 1097. 2021. MB 558019.

Holotypus: BPI 923531 (dried culture).

Ex-type culture: NRRL 62943 (= KOD 796) = MAFF 247228.

Type locality: **Sri Lanka**, Central Province, Kandy.

Type substrate: From the mycangium of a living female *Euwallacea perbrevis* beetle from a gallery in a branch of infested *Camellia sinensis* bush.

Description and illustrations: Aoki *et al*. (2021).

Diagnostic features: *Colony* surface white, yellow white to pale yellow, orange white initially, becoming partly pale orange to greyish orange in the dark, reverse pale yellow to light yellow, or greyish yellow on PDA, having optimal growth at 25 °C; aerial monophialides giving rise to *microconidia* in false heads, oblong-ellipsoid, fusoid-ellipsoid to clavate, straight or crescent- or comma-shaped, also sometimes forming swollen clavate to falcate, straight or curved conidia, 0–1(–3)-septate; *sporodochia* with monophialides give rise clavate to falcate, often gently curved, sometimes crescent-shaped (0–)3–7(–8)-septate *macroconidia*, often swollen in their upper parts with a papillate apical cell (protrude ventrally), with poorly to well-developed, foot-shaped basal cell; *chlamydospores* intercalary and terminal in hyphae and conidia, single or in chains (Aoki *et al*. 2021).

Notes: *Neocosmospora papillata* frequently forms multiseptate clavate conidia with papillate apical cells that protrude ventrally, especially under nuv-light, which distinguishes it from other species in the *Neocosmospora* Ambrosia Clade. Morphologically it resembles *N. drepaniformis*, but is distinct in that macroconidia often possess a papillum protruding ventrally from the apical cells, and their ultimate and penultimate apical cells are often swollen so that they are widest in the terminal half. Macroconidia of *N. drepaniformis*, however, are often widest at the second to fourth cells from the apex (Aoki *et al*. 2021).

Neocosmospora variasi (Lynn & I. Barnes) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843508.
Basionym: *Fusarium variasi* Lynn & I. Barnes, *Mycologia* **113**: 549. 2021. MB 834439.

Holotypus: PREM 62595; *paratypi* PREM 62596 and PREM 62597.

Ex-type culture: CBS 146888 = CMW 53734 = PPRI 27958; ex-paratype cultures CBS 146889 = CMW 53735 = PPRI 27959 and CBS 146890 = CMW 54696 = PPRI 27968.

Type locality: **Indonesia**, Riau, Pelalawan.

Type substrate: From *Euwallacea perbrevis* in stems of *Acacia crassicarpa.*

Description and illustrations: Lynn *et al.* (2021).

Diagnostic features: *Colony* surface white or livid purple to fawn in the dark, with white to livid purple to bay segments, darkening to dark brick or violate slate or black after 1 mo in ambient daylight, reverse yellowish white to fawn in the dark, with white with rust to umber segments, occasionally entirely darkening to umber or black after 1 mo in ambient daylight on PDA, having optimal growth at 30 °C; aerial monophialides giving rise to *microconidia* in false heads, ovoid to obovoid, or short-clavate, curved,

0–1(–2)-septate; *sporodochia* luteous to ochreous or dull green to dark violet, with monophialides that give rise to falcate to clavate, 3–6(–7)-septate *macroconidia* with a papillate apical cell and poorly to well-developed, foot-shaped basal cell; *chlamydospores* abundant, intercalary and terminal in hyphae and conidia, single, in pairs, chains or often in clusters (Lynn *et al.* 2021).

Notes: *Neocosmospora variasi* is associated with the ambrosia beetle, *Euwallacea perbrevis*, in plantations of *Acacia crassicarpa* in Indonesia. It is characterised by having aerial micro- and macroconidia, which vary in size and shape. Furthermore, it produces abundant chlamydospores in clusters, which is unusual for species in the Ambrosia Clade of *Neocosmospora*. Lynn *et al.* (2021) were also of the opinion that as presently defined, *N. variasi* might represent two cryptic taxa.

Neocosmospora warna (Lynn & I. Barnes) Crous & Sand.-Den., ***comb. nov.*** MycoBank MB 843509.
Basionym: *Fusarium warna* Lynn & I. Barnes, *Mycologia* **113**: 551. 2021. MB 834440.

Holotypus: PREM 62603; *paratypi* PREM 62605 and PREM 62606.

Ex-type culture: CBS 146891 = CMW 54720 = PPRI 27974; ex-paratype cultures CBS 146892 = CMW 54724 = PPRI 27976 and CBS 146893 = CMW 54726 = PPRI 27977.

Type locality: **Indonesia**, Riau, Pelalawan.

Type substrate: From head (including mycangium) of *Euwallacea perbrevis* in stems of *Acacia crassicarpa.*

Description and illustrations: Lynn *et al.* (2021).

Diagnostic features: *Colony* surface white to livid purple to vinaceous purple, with white segments, to fawn at margins in the dark, lavender to violet or livid violet with white segments, darkening to livid vinaceous or dark vinaceous to dark purple with sepia margins after 1 mo in ambient daylight, reverse yellowish white to fawn in the dark, pale vinaceous grey white with rust to umber, darkening to dark brick after 1 mo in ambient daylight on PDA, having optimal growth at 25 °C; aerial monophialides giving rise to *microconidia* in false heads, obovoid to ovoid to short-clavate, rarely curved, 0–3(–4-) septate; sporodochia luteous to ochreous, or dull green to sepia, with monophialides giving rise to short-clavate, wedge-shaped (widest at apical septum), 1–4(–6)-septate *macroconidia* with a papillate apical cell and obtuse basal cell; *chlamydospores* sparse, intercalary and terminal in hyphae and conidia, single, in pairs, often clusters (Lynn *et al.* 2021).

Notes: *Neocosmospora warna* is associated with *Euwallacea perbrevis* beetles in plantations of *Acacia crassicarpa* in Indonesia. It is characterised by multi-septate, thick, short-clavate, wedge-shaped (widest at apical septum), papillate sporodochial conidia that taper toward the obtuse basal cell, and small chlamydospores (Lynn *et al.* 2021).

Genome announcements

Other than providing illustrations, diagnoses and multilocus phylogenies of fusarioid taxa, a further aim of the FUSA series is to also provide access to genome data of newly sequenced species, the first of which are published here.

The assemblies of *Fusarium secorum* (CBS 175.32), *Microcera coccophila* (CBS 310.34), *Rectifusarium robinianum* (CBS 430.91), *Rugonectria rugulosa* (CBS 126565), and *Thelonectria blattea* (CBS 952.68) are announced here. They were obtained from high coverage Illumina data (168–283×). Quality assessment done with BUSCO against 758 genes from the library for *Fungi* showed a high completeness (> 98 %) and a low duplication level (< 1 %) for the analysed genomes. The genome sizes varied from 34.7 Mbp to 50.5 Mbp. Assemblies of *R. rugulosa, M. coccophila, R. robinianum*, and *T. blattea* showed similar number of scaffolds while in the *F. secorum* genome their amount was significantly increased due to a high number (> 10 k) of scaffolds with sizes smaller than < 1 kbp. The total number of annotated gene models varied from 24 411 in *M. coccophila* to 46 001 in *F. secorum*. All assemblies were deposited in GenBank, detailed statistics and BioProject numbers are shown in Table 3.

Conflict of interest: The authors declare that there is no conflict of interest.

REFERENCES

Adamčík S, Cai L, Chakraborty D, *et al.* (2015). Fungal Biodiversity Profiles 1–10. *Cryptogamie, Mycologie* **36**: 121–166.

Ahmad A, Akram W, Shahzadi I, *et al*. (2020). First report of *Fusarium nelsonii* causing early-stage fruit blight of cucumber in Guangzhou, China. *Plant Disease* **104**: 1542.

Aoki T, Liyanage PNH, Konkol JL, *et al.* (2021). Three novel Ambrosia *Fusarium* Clade species producing multiseptate "dolphin-shaped" conidia, and an augmented description of *Fusarium kuroshium*. *Mycologia* **113**: 1089–1109.

Aoki T, O'Donnell K, Geiser D (2014). Systematics of key phytopathogenic *Fusarium* species: current status and future challenges. *Journal of General Plant Pathology* **80**: 189–201.

Balmas V, Migheli Q, Scherm B, *et al*. (2010). Multilocus phylogenetics show high levels of endemic fusaria inhabiting Sardinian soils (*Tyrrhenian Islands*). *Mycologia* **102**: 803–812.

Benyon FHL, Burgess LW, Sharp PJ (2000). Molecular genetic investigations and reclassification of *Fusarium* species in sections *Fusarium* and *Roseum*. *Mycological Research* **104**: 1164–1174.

Bolger AM, Lohse M, Usadel B (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* **30**: 2114–2120.

Booth C (1971). The genus *Fusarium*. Commonwealth Mycological Institute, Kew, Surrey, England.

Bushnell B (2021). BBMap short read aligner. http://sourceforge.net/projects/bbmap/

Burgess LW, Liddell CM, Summerell BA (1994). *Laboratory manual for* Fusarium *research*, 3rd edn. University of Sydney, Sydney.

Burgess LW, Summerell BA (1992). Mycogeography of *Fusarium*: survey of *Fusarium* species in subtropical and semi-arid grassland soils from Queensland, Australia. *Mycological Research* **96**: 780–784.

Cantarel BL, Korf I, Robb SM, *et al.* (2008). MAKER: an easy-to-use annotation pipeline designed for emerging model organism genomes. *Genome Research* **18**: 188–196.

Chehri K, Salleh B, Yli-Mattila T, *et al*. (2010). Occurrence, pathogenicity and distribution of *Fusarium* spp. in stored wheat seeds Kermanshah Province, Iran. *Pakistan Journal of Biological Sciences* **13**: 1178–1186.

Crous PW, Cowan DA, Maggs-Kölling G, *et al.* (2021a). Fungal Planet description sheets: 1182–1283. *Persoonia* **46**: 313–528.

Crous PW, Gams W, Stalpers JA, *et al.* (2004). MycoBank: an online initiative to launch mycology into the 21st century. *Studies in Mycology* **50**: 19–22.

Crous PW, Groenewald JZ, Shivas RG, *et al*. (2011). Fungal Planet description sheets: 69–91. *Persoonia* **26**: 108–156.

Crous PW, Lombard L, Sandoval-Denis M, *et al.* (2021b). *Fusarium*: more than a node or a foot-shaped basal cell. *Studies in Mycology* **98**: 100116.

Crous PW, Giraldo A, Hawksworth D, *et al.* (2014). The Genera of Fungi: fixing the application of type species of generic names. *IMA Fungus* **5**: 141–160.

Crous PW, Schumacher RK, Wingfield MJ, *et al.* (2015). Fungal Systematics and Evolution: FUSE 1. *Sydowia* **67**: 81–118.

Crous PW, Schumacher RK, Wingfield MJ, *et al*. (2018). New and interesting fungi. 1. *Fungal Systematics and Evolution* **1**: 169–215.

Du YX, Chen FR, Shi NN, *et al*. (2017). First report of *Fusarium chlamydosporum* causing banana crown rot in Fujian Province, China. *Plant Disease* **101**: 1048.

Engelbrecht MC, Smit WA, Knox-Davies PS (1983). Damping-off of rooibos tea, *Aspalathus linearis*. *Phytophylactica* **15**: 121–124.

Fugro PA (1999). A new disease of okra (*Abelmoschus esculentus* L.) in India. *Journal of Mycology and Plant Pathology* **29**: 264.

Gerlach W, Nirenberg H (1982). The genus *Fusarium* – a pictorial atlas. *Mitteilungen aus der Biologischen Bundesanstalt für Land- und Forstwirtschaft Berlin-Dahlem* **209**: 1–406.

Gerlach W, Scharif G (1970). Erreger einer Fusskrankheit an *Hibiscus cannabinus* in Iran – *Fusarium bucharicum* Jaczewski. *Phytopathologische Zeit*schrift **68**: 323–333.

He J, Li DW, Zhang Y, *et al*. (2021). *Fusarium rosicola sp. nov*. causing vascular wilt on *Rosa chinensis. Plant Pathology* **70**: 2062–2073.

Hill R, Buggs RJA, Vu DT, *et al.* (2022). Lifestyle transitions in fusarioid fungi are frequent and lack clear genomic signatures. *Molecular Biology and Evolution* **39**: msac085.

Jacobs-Venter A, Laraba I, Geiser DM, *et al*. (2018). Molecular systematics of two sister clades, the *Fusarium concolor* and *F. babinda* species complexes, and the discovery of a novel microcycle macroconidium–producing species from South Africa. *Mycologia* **110**: 1189–1204.

Kanaan YM, Bahkali AH (1993). Frequency and cellulolytic activity of seed-borne *Fusarium* species isolated from Sausi Arabian cereal cultivars. *Zeitschrift für Pflanzenkrankheiten und Pflanzenschutz* **100**: 291–298.

Kasson MT, O'Donnell K, Rooney AP, *et al.* (2013). An inordinate fondness for *Fusarium*: Phylogenetic diversity of fusaria cultivated by ambrosia beetles in the genus *Euwallacea* on avocado and other plant hosts. *Fungal Genetics and Biology* **56**: 147–157.

Kirk PM, Stalpers JA, Braun U, *et al.* (2013). A without-prejudice list of generic names of fungi for protection under the International Code of Nomenclature for algae, fungi and plants. *IMA Fungus* **4**: 381–443.

Kruse J, Doehlemann G, Kemen E, *et al.* (2017). Asexual and sexual morphs of *Moesziomyces* revisited. *IMA Fungus* **8**: 117–129.

Laraba I, Keddad A, Boureghda, *et al*. (2017). *Fusarium algeriense sp. nov*., a novel toxigenic crown rot pathogen of durum wheat from Algeria is nested in the *Fusarium burgessii* species complex. *Mycologia* **109**: 935–950.

Laurence MH, Summerell BA, Burgess LW, *et al*. (2011). *Fusarium burgessii sp. nov*. representing a novel lineage in the genus *Fusarium*. *Fungal Diversity* **49**: 101–112.

Laurence MH, Walsh JL, Shuttleworth LA, *et al*. (2016). Six novel species of *Fusarium* from natural ecosystems in Australia. *Fungal Diversity* **77**: 349–366.

Lazreg F, Belabid L, Sanchez J, *et al.* (2013). First report of *Fusarium chlamydosporum* causing damping-off disease on Aleppo pine in Algeria. *Plant Disease* **97**: 1506.

Leslie JF, Summerell BA (2006). *The Fusarium laboratory manual*. Blackwell Publishing Professional, USA.

Leslie JF, Summerell BA (2011). In search of new *Fusarium* species. *Plant Breeding and Seed Science* **63**: 94–101.

Lincy SV, Chandrashekar A, Narayan MS, *et al.* (2011). Natural occurrence of trichothecene-producing Fusaria isolated from India with particular reference to sorghum. *World Journal of Microbiology and Biotechnology* **27**: 981–989.

Liu JK, Hyde KD, Jones EBG, *et al.* (2015). Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* **72**: 1–197.

Liu C, Zhuang WY, Yu ZH, *et al.* (2022). Two new species of *Fusicolla* (*Hypocreales*) from China. *Phytotaxa* **536**: 165–174.

Lombard L, van der Merwe NA, Groenewald JZ, *et al.* (2015). Generic concepts in *Nectriaceae*. *Studies in Mycology* **80**: 189–245.

Lombard L, Van Doorn R, Crous PW (2019). Neotypification of *Fusarium chlamydosporum* - a reappraisal of a clinically important species complex. *Fungal Systematics and Evolution* **4**: 183–200.

Lynn KMT, Wingfield MJ, Durán A, *et al.* (2021). Novel *Fusarium* mutualists of two *Euwallacea* species infesting *Acacia crassicarpa* in Indonesia. *Mycologia* **113**: 536–558.

Manni M, Berkeley MR, Seppey M, *et al.* (2021). BUSCO Update: Novel and streamlined workflows along with broader and deeper phylogenetic coverage for scoring of eukaryotic, prokaryotic, and viral genomes. *Molecular Biology and Evolution* **38**: 4647–465.

Marasas WFO, Nelson PE, Toussoun TA, *et al.* (1986). *Fusarium polyphialidicum*, a new species from South Africa. *Mycologia* **78**: 678–682.

Marasas WFO, Rheeder JP, Logrieco A, *et al*. (1998). *Fusarium nelsonii* and *F. musarum*: two new species in section *Arthrosporiella* related to *F. camptoceras*. *Mycologia* **90**: 505–513.

Marin-Felix Y, Groenewald JZ, Cai L, *et al.* (2017). Genera of phytopathogenic fungi: GOPHY 1. *Studies in Mycology* **86**: 99–216.

Maryani N, Sandoval-Denis M, Lombard L, *et al.* (2019). New endemic *Fusarium* species hitch-hiking with pathogenic *Fusarium* strains causing Panama disease in small-holder banana plots in Indonesia. *Persoonia* **43**: 48–69.

Minh Q, Schmidt HA, Chernomor O, *et al.* (2020). IQ-TREE2: new models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution* **37**: 1530–1534.

Mishra B, Gupta DK, Pfenninger M, *et al.* (2018). A reference genome of the European beech (*Fagus sylvatica L.*). *GigaScience* **7**: giy063.

Mohamed Nor NMI, Salleh B, Leslie JF (2019). *Fusarium* species from Sorghum in Thailand. *The Plant Pathology Journal* **35**: 301–312.

Nalim FA, Samuels GJ, Wijesundera RL, *et al*. (2011). New species from the *Fusarium solani* species complex derived from perithecia and soil in the Old World tropics. *Mycologia* **103**: 1302–1330.

Nelson PE, Dignani MC, Anaissie EJ (1994). Taxonomy, biology, and clinical aspects of *Fusarium* species. *Clinical Microbiology Reviews* **7**: 479–504.

Nelson PE, Toussoun TA, Burgess LW (1987). Characterization of *Fusarium beomiforme sp. nov. Mycologia* **79**: 884–889.

Nelson PE, Toussoun TA, Marasas WFO (1995). Neotypification and emended description of *Fusarium anguioides. Mycologia* **87**: 543–546.

Nguyen LT, Schmidt HA, von Haeseler A, *et al*. (2015). IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood

phylogenies. *Molecular Biology and Evolution* **32**: 268–274.
O'Donnell K (2000). Molecular phylogeny of the *Nectria haematococca-Fusarium solani* species complex. *Mycologia* **92**: 919–938.
O'Donnell K, Gräfenhan T, Laraba I, *et al*. (2022). *Fusarium abutilonis* and *F. guadeloupense*, two novel species in the *Fusarium buharicum* clade supported by multilocus molecular phylogenetic analyses. *Mycologia* DOI: 10.1080/00275514.2022.2071563.
O'Donnell K, Gueidan C, Sink S, *et al.* (2009). A two-locus DNA sequence database for typing plant and human pathogens within the *Fusarium oxysporum* species complex. *Fungal Genetics and Biology* **46**: 936–948.
O'Donnell K, McCormick SP, Busman M, *et al*. (2018). Marasas *et al*. 1984 "Toxigenic *Fusarium* species: Identity and mycotoxicology" revisited. *Mycologia* **110**: 1058–1080.
Özer G, Imren M, Paulitz TC, *et al.* (2020). First report of crown rot caused by *Fusarium algeriense* on wheat in Azerbaijan. *Plant Disease* **104**: 582–582.
Raillo AI (1950). *Griby roda* Fusarium. State publishing house of agricultural literature, Moscow.
Reinking OA (1934). Interesting new *Fusaria*. *Zentralblatt für Bakteriologie und Parasitenkunde, Abteilung 2.* **89**: 509–514.
Ronquist F, Huelsenbeck JP (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**: 1572–1574.
Sandoval-Denis M, Guarnaccia V, Polizzi G, *et al*. (2018a). Symptomatic *Citrus* trees reveal a new pathogenic lineage in *Fusarium* and two new *Neocosmospora* species. *Persoonia* **40**: 1–25.
Sandoval-Denis M, Lombard L, Crous PW (2019). Back to the roots: a reappraisal of *Neocosmospora*. *Persoonia* **43**: 90–185.
Sandoval-Denis M, Swart WJ, Crous PW (2018b). New *Fusarium* species from the Kruger National Park, South Africa. *MycoKeys* **34**: 63–92.
Sangalang AE, Burgess LW, Backhouse D, *et al*. (1995a). Mycogeography of *Fusarium* species in soils from tropical, arid and mediterranean regions of Australia. *Mycological Research* **99**: 523–528.
Sangalang AE, Summerell BA, Burgess LW, *et al*. (1995b). Taxonomy of *Fusarium*: characterization of *Fusarium avenaceum* subsp. *aywerte* and *Fusarium avenaceum* subsp. *nurragi*. *Mycological Research* **99**: 287–290.
Satou M, Ichinoe M, Fukumoto F, *et al*. (2001). Fusarium blight of kangaroo paw (*Anigozanthos* spp.) caused by *Fusarium chlamydosporum* and *Fusarium semitectum*. *Journal of Phytopathology* **149**: 203–206.
Savary O, Coton M, Frisvad JC, *et al*. (2021). Unexpected *Nectriaceae* species diversity in cheese, description of *Bisifusarium allantoides sp. nov*., *Bisifusarium penicilloides sp. nov*., *Longinectria gen. nov. lagenoides sp. nov.* and *Longinectria verticilliforme sp. nov*. *Mycosphere* **12**: 1077–1100.
Shang QJ, Phookamsak R, Camporesi E, *et al*. (2018). The holomorph of *Fusarium celtidicola sp. nov*. from *Celtis australis*. *Phytotaxa* **361**: 251–265.
Sherbakoff CD (1915). Fusaria of potatoes. *Memoirs of the Cornell University Agricultural Experimental Station* **6**: 87–270.
Summerell BA, Salleh B, Leslie JF (2003). A utilitarian approach to *Fusarium* identification. *Plant Disease* **87**: 117–128.
Thambugala KM, Wanasinghe DN, Phillips AJL, *et al*. (2017). Mycosphere notes 1–50: Grass (*Poaceae*) inhabiting *Dothideomycetes*. *Mycosphere* **8**: 697–796.
van Diepeningen A, Al-Hatmi A, Brankovics B, *et al*. (2014). Taxonomy and clinical spectra of *Fusarium* species: Where do we stand in 2014? *Current Clinical Microbiology Reports* **1**: 10–18.
Wang MM, Crous PW, Sandoval-Denis M, *et al.* (2022). *Fusarium* and allied genera from China: species diversity and distribution. *Persoonia* **48**: 1– 53.
Wollenweber HW, Reinking OA (1935). *Die Fusarien*. Verlagsbuchandlung Paul Parey, Berlin, Germany.
Xia JW, Sandoval_Denis M, Crous PW, *et al*. (2019). Numbers to names – restyling the *Fusarium incarnatum-equiseti* species complex. *Persoonia* **43**: 186–221.
Zerbino DR, Birney E (2008). Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Research* **18**: 821–829.
Zhang X, Guo C, Wang C, *et al*. (2021). First report of maize stalk rot caused by *Fusarium nelsonii* in China. *Plant Disease* **105**: 4168.