# Known from trees and the tropics: new insights into the *Fusarium lateritium* species complex

M.M. Costa<sup>1\*</sup>, M. Sandoval-Denis<sup>1</sup>, G.M. Moreira<sup>2</sup>, H. Kandemir<sup>1</sup>, A. Kermode<sup>3</sup>, A.G. Buddie<sup>3</sup>, M.J. Ryan<sup>3</sup>, Y. Becker<sup>4</sup>, A. Yurkov<sup>5</sup>, W. Maier<sup>4</sup>, J.Z. Groenewald<sup>1</sup>, L.H. Pfenning<sup>2</sup>, P.W. Crous<sup>1,6,7\*</sup>

<sup>1</sup>Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; <sup>2</sup>Department of Plant Pathology, Universidade Federal de Lavras, 37200-900, Lavras MG, Brazil; <sup>3</sup>CAB International (CABI), Bakeham Lane, TW20 9TY Egham, Surrey, United Kingdom; <sup>4</sup>Institute for Epidemiology and Pathogen Diagnostics, Julius Kühn Institute (JKI), Federal Research Centre for Cultivated Plants, Messeweg 11-12, 38104 Braunschweig, Germany; <sup>5</sup>Department of Bioresources for Bioeconomy and Health Research, Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Inhoffenstraße 7B, 38124 Braunschweig, Germany; <sup>6</sup>Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; <sup>7</sup>Microbiology, Department of Biology, Utrecht University, Padualaan 8, Utrecht, 3584 CH, The Netherlands

\*Corresponding authors: M.M. Costa, m.costa@wi.knaw.nl; P.W. Crous, p.crous@wi.knaw.nl

**Abstract:** The *Fusarium lateritium* species complex (FLSC) currently comprises 11 phylogenetic species, including accepted names such as *F. lateritium*, *F. sarcochroum*, and *F. stilboides*, which have mostly been reported in association with citrus and coffee. Many varieties were documented by Wollenweber & Reinking (1935), which is indicative of a wider diversity of species within this group. The lack of type material in some cases, especially for the older names, means that definition by molecular phylogeny is very difficult. In the present study, we examined 179 strains related to *F. lateritium* from different countries and substrates. Historic reference material, including representative strains from the Wollenweber & Reinking (1935) varieties were included in this study, DNA sequences were generated for comparison, and the morphology correlated with original descriptions to enable the correct application of older names. Strains were characterized by multi-gene phylogenetic analyses based on fragments of the β-tubulin (*tub2*), calmodulin (*CaM*), RNA polymerase II second largest subunit (*rpb2*), and translation elongation factor 1-alpha (*tef1*) genes, evaluation of morphological characters and host-substrate preferences. The biological species concept was tested by crossings *in vitro*. Strains previously identified as *F. lateritium*, *F. stilboides*, or one of their varieties based on morphology, were found to belong to 16 species in the FLSC, but also to species from six other species complexes (SC), including the *F. citricola* SC, *F. heterosporum* SC, *F. incarnatum-equiseti* SC, *F. redolens* SC, *F. sambucinum* SC, and the *F. tricinctum* SC. Eleven new phylogenetic and two biological species are described in the FLSC, and emended descriptions are provided for four previously described species. An epitype is designated for *F. lateritium*, and *F. lateritium*, a former variety within the FLSC, is lecto- and epitypified, and elevated to species level with a replacement name.

Key words: Biological species concept, fungal taxonomy, multigene phylogeny, new taxa.

Taxonomic novelties: New species: F. aurantii M.M. Costa, Sand.-Den. & Crous, F. chlamydocopiosum M.M. Costa, Sand.-Den. & Crous, F. citri-sinensis L. Zhao & J.X. Deng, F. coffeibaccae M.M. Costa, L.H. Pfenning, Sand.-Den. & Crous, F. crocatum M.M. Costa, Sand.-Den. & Crous, F. malawiense M.M. Costa, Sand.-Den. & Crous, F. microcyclum M.M. Costa, Sand.-Den. & Crous, F. oliniae M.M. Costa, Sand.-Den. & Crous; F. rufum M.M. Costa, Sand.-Den. & Crous, F. stramineum M.M. Costa, Sand.-Den. & Crous, F. velutinum M.M. Costa, Sand.-Den. & Crous, F. veruculosum M.M. Costa, Sand.-Den. & Crous; Replacement name: F. hanswilhelmii M.M. Costa, Sand.-Den. & Crous; Epitype (basionym): F. lateritium var. longum Wollenw.; Lectotype (basionym): F. lateritium var. longum Wollenw.

**Citation:** Costa MM, Sandoval-Denis M, Moreira GM, Kandemir H, Kermode A, Buddie AG, Ryan MJ, Becker Y, Yurkov A, Maier W, Groenewald JZ, Pfenning LH, Crous PW (2024). Known from trees and the tropics: new insights into the *Fusarium lateritium* species complex. *Studies in Mycology* **109**: 403–450. doi: 10.3114/sim.2024.109.06

Received: 12 June 2024; Accepted: 25 August 2024; Effectively published online: 26 September 2024 Corresponding editor: R.A. Samson

## INTRODUCTION

The genus *Fusarium* is considered one of the most significant fungal genera, comprising over 330 species (www.fusarium.org). Many species are plant pathogens, human and animal opportunistic pathogens, or produce mycotoxins harmful to human and animals, impacting food security and safety (Wu 2007, Dean *et al.* 2012, Proctor *et al.* 2013, Crous *et al.* 2021). *Fusarium lateritium* holds a historically significant position within the genus *Fusarium*. Nees first introduced the name in 1817 from a collection of *Fagus* twigs. A hundred years later, in 1917, Wollenweber established the Section *Lateritium* to accommodate species characterized by pale- to rose-coloured cultures with blue erumpent sclerotia, producing intercalary but no terminal chlamydospores. Members of the Section were also

defined by the shape of their macroconidia, being relatively straight but with a curved, often beaked apical cell and a pedicellate footcell. The second species added to the Section was *F. uncinatum* (Wollenweber 1917), later reduced to a variety of *F. lateritium* (Wollenweber 1930). This variety was later synonymized under *F. udum* (Padwick 1940). However, phylogenetic analyses revealed that *F. udum* is a member of the *F. fujikuroi* species complex (FFSC) (Pfenning *et al.* 2019, Yilmaz *et al.* 2021).

Well-established species within Section Lateritium include F. lateritium, F. stilboides, and F. sarcochroum. Within F. lateritium, initially five varieties had been defined, namely F. lateritium var. mori, F. lateritium var. minus, F. lateritium var. uncinatum, F. lateritium var. majus, and F. lateritium var. longum (Wollenweber 1931, Wollenweber & Reinking 1935). Some modifications have been

© 2024 Westerdijk Fungal Biodiversity Institute. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/bync-nd/4.0/).

proposed for this system, expanding or reducing the number of taxa and varieties (Snyder & Hansen 1945, Raillo 1950, Bilaĭ 1955). The use of *forma specialis* (*f. sp.*) as informal subspecific rank was also introduced in *F. lateritium*, but the names *F. lateritium f. sp. cajani* and *F. lateritium f. sp. crotalariae* (Gordon 1952) actually represent *F. udum* (Pfenning *et al.* 2019, Yilmaz *et al.* 2021). Additional *ff. spp.* were proposed by Booth (1971), including *f. sp. pini, f. sp. mori,* and *f. sp. cerealis*. More recently, some of those *ff. spp.* have been reclassified into other *Fusarium* species complexes, such as the *F. fujikuroi* SC (FFSC) and *F. oxysporum* SC (FOSC) (Lombard *et al.* 2019, Pfenning *et al.* 2019, Yilmaz *et al.* 2021).

Names for the sexual morphs of species and forms of Section *Lateritium* are mentioned as *Gibberella baccata* (*F. lateritium*) and *G. pseudopulicaris* (*F. sarcochroum*), with the varieties *Gibberella baccata* var. *evonymi* (asexual morph *F. lateritium* var. *fructigenum*), *G. baccata* var. *moricola* (asex. *F. lateritium* var. *mori*) and *G. baccata* var. *major* (asex. *F. lateritium* var. *mori*) and *G. baccata* var. *major* (asex. *F. lateritium* var. *mori*) and *G. baccata* var. *major* (asex. *F. lateritium* var. *majus*) (Wollenweber 1931, Wollenweber & Reinking 1935). A sexual morph of *F. stilboides* was mentioned by Wollenweber & Reinking (1935), but only named later as *G. stilboides* (Booth 1971). However, the real relationship between these asexual and sexual morphs must still be confirmed and validated.

The FLSC was first introduced in 2013 in a phylogenetic study that included the species F. lateritium, F. stilboides, and F. sarcochroum (O'Donnell et al. 2013). Currently, 11 phylogenetic species constitute the F. lateritium species complex (FLSC), including, besides the older names, recently introduced species, as F. camelliae, F. cartwrightiae, F. cassiae, F. endophyticum, F. fujianense, F. magnoliae-champaca, F. massalimae, and F. ramsdenii (Cavalcanti et al. 2020, Perera et al. 2020, Crous et al. 2022, Hyde et al. 2023, Suwannarach et al. 2023, Tan & Shivas 2023, He et al. 2024). Phylogenetically, the FLSC resolves as a sister clade to the F. buharicum and F. torreyae species complexes (Crous et al. 2021, Geiser et al. 2021). The FLSC comprises fungi commonly found associated with arboreal plants such as Araucaria cunninghamii, Cassia fistula, Citrus spp., and Coffea spp., but also on Camellia leaves (Geiser et al. 2005, Cavalcanti et al. 2020, Perera et al. 2020, Crous et al. 2022, Hyde et al. 2023). Limited information is available about the production of secondary metabolites, including mycotoxins, by species from the FLSC. Genome sequences are available for representative strains of F. sarcochroum, and preliminary investigations have shown the presence of gene clusters that are probably related to the production of sphinganine-analog metabolites (SAMs) (Kim et al. 2020).

Phylogenetic investigations have already provided evidence that numerous undescribed phylogenetic species exist within the FLSC (Geiser *et al.* 2005, Wang *et al.* 2022). The high number of varieties or *ff. spp.* reported in literature as well as the long list of supposed synonyms (Wollenweber 1931, Wollenweber & Reinking 1935, Gerlach & Nirenberg 1982), are indicative of a broader species diversity within this group. Recently, Crous *et al.* (2021) designated a lectotype for *F. lateritium*, but the designation of an epitype is still pending.

Over the last hundred years, many strains related to *F. lateritium* and the varieties reported by Wollenweber (1931) and Wollenweber & Reinking (1935) have been deposited in the culture collections of the Westerdijk Fungal Biodiversity Institute (WI), Utrecht, The Netherlands; CAB International (CABI), (IMI), UK; the Julius Kühn Institute (JKI), previously Biologische Bundesanstalt für Land- und Forstwirtschaft (BBA) Braunschweig, Germany; and Coleção Micológica de Lavras (CML), Lavras MG, Brazil. The

present study aims to stabilize the taxonomy and nomenclature of *F. lateritium* and related species. Available strains from these culture collections were characterized by multi-gene phylogenetic analyses using nucleotide sequences of the partial  $\beta$ -tubulin (*tub2*), calmodulin (*CaM*), RNA polymerase II second largest subunit (*rpb2*), and translation elongation factor 1-alpha (*tef1*) genes, as well as evaluation of morphological characters, host-substrate preferences, and geographic distribution. The application of the biological species concept was studied through laboratory crossings, and identifying their mating-type allele composition. Old names are revisited, and their taxonomy is reconsidered based on a re-examination of the original material, as far as possible. We also designate an epitype for *F. lateritium* and introduce Latin binomials for 11 phylogenetic species.

## MATERIAL AND METHODS

## **Fungal isolates**

In this study, we analyzed 179 *Fusarium* strains, most of them previously identified as *F. lateritium*, *F. stilboides*, or one of their varieties. These strains were obtained from the culture collections of the CAB International (CABI) (IMI, UK), the US Agricultural Research Service (NRRL, USA), the Westerdijk Fungal Biodiversity Institute (WI) (CBS, The Netherlands), the Julius Kühn Institute (JKI), former Biologische Bundesanstalt für Land- und Forstwirtschaft (BBA, Germany), the Coleção Micológica de Lavras (CML, Brazil), and the personal collection of P.W. Crous (CPC) housed at the WI (Tables 1, S1).

## DNA extraction, PCR and sequencing

Total genomic DNA was obtained from isolates cultured on malt extract agar (MEA; Crous et al. 2019) and incubated at room temperature for 7 d. Portions of mycelia were removed carefully from the surface of the colony, and DNA was extracted using the Wizard® Genomic DNA Kit (Promega Corporation, Madison, WI, USA), according to the manufacturer's instructions. Fragments of the β-tubulin (tub2), calmodulin (CaM), RNA polymerase II second largest subunit (rpb2), and translation elongation factor 1-alpha (tef1) genes were amplified using the primer pairs T1/TUB4Rd for tub2 (O'Donnell & Cigelnik 1997, Woudenberg et al. 2009), CAL228F/ CAL2RD for CaM (Carbone & Kohn 1999, Groenewald et al. 2013), RPB2-5F2/fRPB2-7cR and fRPB2-7cF/RPB2-11aR for rpb2 (Liu et al. 1999, Sung et al. 2007), and EF-1/EF-2 for tef1 (O'Donnell et al. 1998, 2008), following the cycle conditions described by O'Donnell & Cigelnik (1997), and O'Donnell et al. (2007, 2008). Sequencing of PCR products was done using the same primers. Consensus sequences of each strain were assembled using Geneious Prime v. 2023.2.1 (Biomatters Inc., New Zealand).

## Phylogenetic analyses

Sequence alignments for each gene region were obtained using MAFFT v. 7 (Li *et al.* 2015, Katoh *et al.* 2019), with default settings on the European Bioinformatics Institute (EMBL-EBI) web server (http://www.ebi.ac.uk/Tools/msa/mafft/). Alignments were manually edited using MEGA v. 7 (Kumar *et al.* 2016), when necessary. DNA sequences from selected *Fusarium* species were downloaded from NCBI GenBank and added to the alignments (Tables 1, S2).

Table 1. Fusarium cultures an	d DNA accesion numbers included i	n this study.								
		Deposited in the			Mating		GenBar	ık accession r	number <sup>3</sup>	
pecies name	Strain code <sup>1</sup>	culture collection as	Host/substrate	Country	type <sup>2</sup>	tef1	tub2	rpb2-part 1	rpb2-part 2	CaM
: aurantii sp. nov.	BBA 65609 <sup>T</sup> = CBS 152039 = CPC 44982 = DSM 115149	F. lateritium var. longum	Citrus aurantium	Cuba	MAT-1	PQ000452	PQ000532	PQ000617	PQ000695	PQ000774
	FRC L-200	Ι	Soil	Philippines		AY707168	AY707150	Ι	I	Ι
	IMI 310541 = CPC 44539	F. udum	Cajanus cajan, phyllosphere	India	MAT-1	PQ000453	PQ000533	PQ000618	PQ000696	PQ000775
	IMI 338937 = CPC 42982	F. stilboides	Vigna angularis, seed	India	MAT-1	PQ000454	PQ000534	PQ000619	PQ000697	PQ000776
F. camelliae	GUCC 21010 <sup>T</sup>	Ι	Camellia sp.	China	I	OP757314	Ι	OP800100	Ι	Ι
	GUCC 21011	Ι	Camellia sp.	China	I	OP800102	Ι	OP820349	Ι	Ι
F. cartwrightiae	BRIP 74113d <sup>T</sup> = CBS 150776	I	Ziziphus mauritiana, stem canker	Australia	Ι	OR335749	PQ000582	OR335732	I	PQ000824
F. cassiae	BBA 65092 = CPC 47105 = DSM 115143	F. lateritium var. longum	Ceiba insignis	Cuba	I	PQ000502	PQ000583	PQ000666	PQ000744	PQ000825
	BBA 72582 = CPC 47273 = DSM 116938	F. graminearum	Oroxylum sp.	Thailand	MAT-2	PQ000503	PQ000584	PQ000667	PQ000745	PQ000826
	BBA 72583 = CPC 47274 = DSM 116939	F. graminearum	Oroxylum sp.	Thailand	MAT-2	PQ000504	PQ000585	PQ000668	PQ000746	PQ000827
	BBA 72584 = CPC 47275 = DSM 116940	F. graminearum	Oroxylum sp.	Thailand	MAT-2	PQ000505	PQ000586	PQ000669	PQ000747	PQ000828
	LC13727 = F092	Ι	Coffea sp.	China	I	MW594307	MW533911	MW474540	MW474540	I
	MFLUCC 18-0573 <sup>T</sup>	Ι	Cassia fistula, pods	Thailand		MT212205	I	MT212197	I	Ι
F. chlamydocopiosum sp. nov.	CBS 152063 <sup>T</sup> = CPC 37116	Ι	Citrus sinensis	South Africa	MAT-2	PQ000506	PQ000587	PQ000670	PQ000748	PQ000829
	CBS 152064 = CPC 37118	Ι	Citrus sinensis	South Africa	MAT-2	PQ000507	PQ000588	PQ000671	PQ000749	PQ000830
	CBS 152065 = CPC 37119		Citrus sinensis	South Africa	MAT-2	PQ000508	PQ000589	PQ000672	PQ000750	PQ000831
F. citri-sinensis	BBA 67503 <sup>T</sup> = CBS 152066 = CPC 44985 = DSM 115153	F. lateritium var. longum	Albizia julibrissin	USA	MAT-2	PQ000509	PQ000590	PQ000673	PQ000751	PQ000832
	YZU 191316	Ι	Citrus sinensis, rotted fruit	China		MW855826	Ι	MW855854	Ι	Ι
	YZU 181391	Ι	Citrus sinensis, rotted fruit	China		MW855825	Ι	Ι	Ι	Ι
F. coffeibaccae sp. nov.	BBA 62428 = CPC 46655 = DSM 115998	F. stilboides	Coffea sp.	Kenya	l	PQ000455	PQ000535	PQ000620	PQ000698	PQ000777
	BBA 62429 = CPC 46656 = DSM 115999	F. stilboides	Coffea arabica	Ethiopia	MAT-2	PQ000456	PQ000536	PQ000621	PQ000699	PQ000778
	BBA 62430 = CPC 46657 = DSM 116000	F. stilboides	Coffea arabica	Ethiopia	MAT-2	PQ000457	PQ000537	PQ000622	PQ000700	PQ000779
	CBS 178.31 = NRRL 20838	F. lateritium var. longum	Coffea sp.	East Africa	Ι	PQ000458	PQ000538	PQ000623	PQ000701	PQ000780



Table 1. (Continued).										
		Deposited in the			Mating		GenBa	nk accession r	number <sup>3</sup>	
Species name	Strain code <sup>1</sup>	culture collection as	Host/substrate	Country	type <sup>2</sup>	tef1	tub2	rpb2-part 1	rpb2-part 2	CaM
	CBS 101890	Ι	Coffea sp., fruit	Brazil	MAT-1	PQ000459	PQ000539	PQ000624	PQ000702	PQ000781
	CBS 101891	Ι	Coffea sp., fruit	Brazil	MAT-1	PQ000460	PQ000540	PQ000625	PQ000703	PQ000782
	CBS 101892	Ι	Coffea sp., fruit	Brazil	MAT-2	PQ000461	PQ000541	PQ000626	PQ000704	PQ000783
	CBS 119871 = BBA 62458 = DSM 62458 = MRC 1845	F. lateritium	Coffea arabica	Ethiopia	MAT-2	PQ000462	PQ000542	PQ000627	PQ000705	PQ000784
	CBS 119872 = MRC 2465	F. lateritium	Unknown	Unknown	I	PQ000463	PQ000543	PQ000628	PQ000706	PQ000785
	CML 90 <sup>T</sup> = CBS 152040 = CPC 46658	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000464	PQ000544	PQ000629	PQ000707	PQ000786
	CML 178 = CPC 46661	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000465	PQ000545	PQ000630	PQ000708	PQ000787
	CML 2400 = CBS 152041 = CPC 46659	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000466	PQ000546	PQ000631	PQ000709	PQ000788
	CML 4403 = CBS 152042 = CPC 46662	F. stilboides	Coffea arabica, fruit	Brazil	I	PQ000467	PQ000547	PQ000632	PQ000710	PQ000789
	CML 4404 = CBS 152043 = CPC 46663	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000468	PQ000548	PQ000633	PQ000711	PQ000790
	CML 4405 = CBS 152044 = CPC 46664	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000469	PQ000549	PQ000634	PQ000712	PQ000791
	CML 4407 = CBS 152045 = CPC 46666	F. stilboides	Coffea arabica, fruit	Brazil	MAT-2	PQ000470	PQ000550	PQ000635	PQ000713	PQ000792
	CML 4408 = CBS 152269 = CPC 46667	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000471	PQ000551	PQ000636	PQ000714	PQ000793
	CML 4409 = CBS 152046 = CPC 46668	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000472	PQ000552	PQ000637	PQ000715	PQ000794
	CML 4410 = CBS 152047 = CPC 46669	F. stilboides	Coffea arabica, fruit	Brazil	I	PQ000473	PQ000553	PQ000638	PQ000716	PQ000795
	CML 4411 = CBS 152048 = CPC 46670	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000474	PQ000554	PQ000639	PQ000717	PQ000796
	CML 4414 = CBS 152049 = CPC 46671	F. stilboides	Coffea arabica, fruit	Brazil	MAT-2	PQ000475	PQ000555	PQ000640	PQ000718	PQ000797
	CML 4415 = CBS 152050 = CPC 46672	F. stilboides	Coffea arabica, fruit	Brazil	MAT-1	PQ000476	PQ000556	PQ000641	PQ000719	PQ000798
	CML 4423 = CBS 152051 = CPC 46677	F. stilboides	Coffea arabica, fruit	Brazil	MAT-2	PQ000477	PQ000557	PQ000642	PQ000720	PQ000799
	CML 4424 = CBS 152052 = CPC 46678	F. stilboides	Coffea arabica, fruit	Brazil	MAT-2	PQ000478	PQ000558	PQ000643	PQ000721	PQ000800

COSTA ET AL.

		t2 CaM	2 PQ000801	23 PQ000802	24 PQ000803	25 PQ000804	16 PQ000805	27 PQ000806	28 PQ000807	9 PQ000808	0 PQ000809	11 PQ000810	2 PQ000811	Ι	I	I	I	I	I	Ι	Ι	I	
	number	rpb2-pari	PQ00072	PQ00073	PQ00073	PQ00073	Ι	I	I	I	Ι	I	I	I	I								
	k accession	rpb2-part 1	PQ000644	PQ000645	PQ000646	PQ000647	PQ000648	PQ000649	PQ000650	PQ000651	PQ000652	PQ000653	PQ000654	Ι	Ι	Ι	Ι	I	I	Ι	Ι	Ι	
1	GenBan	tub2	PQ000559	PQ000560	PQ000561	PQ000562	PQ000563	PQ000564	PQ000565	PQ000566	PQ000567	PQ000568	PQ000569	AY707137	AY707140	AY707141	AY707142	AY707143	AY 707145	AY 707146	AY 707151	AY707152	
		tef1	PQ000479	PQ000480	PQ000481	PQ000482	PQ000483	PQ000484	PQ000485	PQ000486	PQ000487	PQ000488	PQ000489	AY 707155	AY 707158	AY 707159	AY707160	AY707161	AY707163	AY707164	AY707169	AY707170	
	Mating	type <sup>2</sup>	MAT-1	MAT-1	MAT-1	MAT-1	MAT-2	I	I	MAT-1	MAT-1	MAT-1	MAT-1		I	I		I	Ι		I	I	
		Country	Brazil	Zimbabwe	New Guinea	New Guinea	New Guinea	New Caledonia	Guinea	Zimbabwe	Brazil	Brazil											
		Host/substrate	Coffea arabica, fruit	Citrus aurantifolia, fruit	Coffea arabica	Coffea arabica	Coffea arabica, fruit	Coffea sp., fruit	Coffea sp., fruit	Coffea sp., fruit	Coffea sp., fruit	<i>Coffea canephora</i> , vascular bundle	Coffea sp.	Coffea sp., fruit	Coffea sp.								
	Deposited in the	culture collection as	F. stilboides	Ι	Ι	Ι	Ι	I	I	Ι	Ι	I											
		Strain code <sup>1</sup>	CML 4427 = CBS 152053 = CPC 46679	CML 4428 = CBS 152054 = CPC 46680	CML 4430 = CBS 152055 = CPC 46681	CML 4431 = CBS 152056 = CPC 46682	CML 4432 = CBS 152057 = CPC 46683	CML 4435 = CBS 152058 = CPC 46685	CML 4436 = CBS 152059 = CPC 46686	CML 4437 = CBS 152274 = CPC 46687	CML 4438 = CBS 152060 = CPC 46688	CML 4440 = CBS 152061 = CPC 46690	CML 4443 = CBS 152062 = CPC 46691	FRC L-69	FRC L-83	FRC L-84	FRC L-86	FRC L-87	FRC L-101 = BBA 62455	FRC L-107 = MRC 1926	FRC L-375	FRC L-376	
Table 1. (Continued).		Species name																					

WESTERDIJK FUNGALBIO DIVERSITY INSTITUTE

Deposited in the     Mating       Strain code <sup>1</sup> Deposited in the       MI 194631 = CPC 42976     F. stilboides       Confree     Confree arabica	/substrate Country type <sup>2</sup> tef	Country Mating Country type <sup>2</sup> teft Papua New MAT-2 PQ	Mating type <sup>2</sup> tef <sup>1</sup> MAT-2 PQ	PQ	000490	GenBar tub2 PQ000570	ık accession n <i>rpb</i> 2-part 1 PQ000655	umber <sup>3</sup> <i>rpb2</i> -part 2 PQ000733	<i>CaM</i> PQ000812
IMI 194631 = CPC 42976 F. stilboides Coffea arabica Papua New M. Guinea IMI 275737 = CPC 44569 F. decemcellulare Coffea arabica. bark Malawi —	ia arabica Papua New M. Guinea a arabica: bark Malawi —	Papua New <i>M.</i> Guinea Malawi —	Ϋ́ Ι	AT-2	PQ000490 PQ000491	PQ000570 PQ000571	PQ000655 PQ000656	PQ00073( PQ000734	~ -·
IMI 312020 = CPC 42980 F. stilboides Coffea sp. Papua New Guinea	a sp. Papua New Guinea	Papua New Guinea		MAT-1	PQ000492	PQ000572	PQ000657	PQ000735	Q
IMI 328353 = CPC 42981 <i>F. stilboides</i> Coffea arabica, leaf surface Papua New Guinea	<i>ia arabica</i> , leaf surface Papua New Guinea	Papua New Guinea		MAT-2	PQ000493	PQ000573	PQ000658	PQ000736	PQ000
IMI 343160 = CPC 42983 F. stilboides Coffea arabica Kenya	a arabica Kenya	Kenya		MAT-1	PQ000494	PQ000574	PQ000659	PQ000737	PQ000
IMI 343468 = CPC 42984 F. stilboides Coffea arabica Ethiopia A	a <i>arabica</i> Ethiopia M	Ethiopia A	$\sim$	AAT-2	PQ000495	PQ000575	PQ000660	PQ000738	PQ0008
IMI 375911 = CPC 42985 F. stilboides Coffea arabica, stem Ethiopia A	<i>a arabica</i> , stem Ethiopia A	Ethiopia A	$\sim$	AAT-2	PQ000496	PQ000576	PQ000661	PQ000739	PQ0008
IMI 389578 = CPC 46697 F. stilboides Coffea arabica, stem Ethiopia N	a <i>arabica</i> , stem Ethiopia /	Ethiopia A	<	AAT-1	PQ000497	PQ000577	PQ000662	PQ000740	PQ0008
IMI 389580 = CPC 46699 F. stilboides Coffea arabica, stem Ethiopia I	a arabica, stem Ethiopia	Ethiopia		MAT-2	PQ000498	PQ000578	PQ000663	PQ000741	PQ0008
IMI 392282 = CPC 42972 F. lateritium Coffea sp., fruit Guinea	a sp., fruit Guinea	Guinea		MAT-1	PQ000499	PQ000579	PQ000664	PQ000742	PQ00082
IMI 393591 = CPC 44771 Fusarium sp. Coffea arabica Unknown	a arabica Unknown	Unknown		MAT-1	PQ000500	PQ000580	PQ000665	PQ000743	PQ00082
LC13732 = F085 Coffea sp. China	a sp. China	China		Ι	MW594312	MW533916	MW474545	Ι	Ι
LC13733 = F088 Coffea sp. China	ea sp. China	China		I	MW594313	MW533917	MW474546	Ι	Ι
NRRL 20429 = ATCC 15662 = F. stilboides Coffea sp., bark Nyasaland CBS 151960 = GORDON 4843	a sp., bark Nyasaland	Nyasaland		I	PQ000501	PQ000581	JX171582	JX171582	PQ00082
BBA 65674 = CPC 44983 = <i>F. lateritium</i> var. <i>longum Herbaceous vine</i> Venezuela DSM 115150	aceous vine Venezuela	Venezuela		MAT-2	PQ000510	I	PQ000674	PQ000752	PQ00083
BBA 65926 <sup>T</sup> = CBS 152067 = <i>F. lateritium</i> var. <i>longum</i> Grass CPC 44984 = DSM 115152	Venezuela	Venezuela		MAT-1	PQ000511	PQ000591	PQ000675	PQ000753	PQ0008
CBS 130184 = BBA 65687 = <i>F. lateritium</i> var. <i>longum Bambusa vulgaris</i> Venezuela DSM 115151 = NRRL 25197	busa vulgaris Venezuela	Venezuela		MAT-2	PQ000512	PQ000592	PQ000676	PQ000754	PQ0008;
CBS 319.73 = ATCC 24391 = <i>F. stilboides</i> Citrus aurantium Honduras CPC 42975 = FRC L-403 = IMI 155795 = NRRL 25482	s aurantium Honduras	Honduras		MAT-2	PQ000513	PQ000593	PQ000677	PQ000755	PQ0008;
CML 4473 = CBS 152068 = <i>Fusarium</i> sp. Coffea canephora, stem Brazil CPC 46692	<i>ia canephora</i> , stem Brazil	Brazil		MAT-2	PQ000514	PQ000594	PQ000678	PQ000756	PQ0008;
FRC L-82 — Citrus sp., twig New Caledonia	s sp., twig Caledonia	New Caledonia		I	AY707157	AY707139	Ι	Ι	I
FRC L-120 — Coffea sp. Unknown	ła sp. Unknown	Unknown		Ι	AY707167	AY707149	I	Ι	Ι
IMI 373356 = CPC 46708 F. stilboides Coffea arabica Jamaica	a arabica Jamaica	Jamaica		MAT-2	PQ000515	PQ000595	PQ000679	PQ000757	PQ00083

COSTA ET AL.

lable 1. (Continuea).										
		Deposited in the			Mating		GenBan	ık accession r	number <sup>3</sup>	
Species name	Strain code <sup>1</sup>	culture collection as	Host/substrate	Country	type <sup>2</sup>	tef1	tub2	rpb2-part 1	rpb2-part 2	CaM
	SDBR-CMU465 <sup>T</sup>	Ι	Camellia sinensis var. assamica, leaf	Thailand	I	OQ686616	I	OQ686618	I	I
	SDBR-CMU466	I	Camellia sinensis var. assamica, leaf	Thailand	I	OQ686617	I	OQ686619	I	I
F. fujianense	CFCC 57576 <sup>T</sup> = LC14	I	Cunninghamia lanceolata, leaf spots	China	I	ON734389	ON734409	ON734369	I	I
	LC14-1	I	Cunninghamia lanceolata, leaf spots	China	I	ON734390	ON734410	ON734370	I	Ι
	LC14-2	I	Cunninghamia lanceolata, leaf spots	China	I	ON734391	ON734411	ON734371	I	Ι
F. hanswilhelmii nom. nov.	CBS 633.76 <sup>ET</sup> = BBA 63665 = DSM 115136 = NRRL 25484	F. lateritium var. longum	Citrus sinensis, fruit	New Zealand	I	PQ000516	PQ000596	PQ000680	PQ000758	PQ000839
F. lateritium	CBS 127477 = HMAS 86477	Ι	Twig	China	MAT-2	PQ000517	PQ000597	PQ000681	PQ000759	PQ000840
	NRRL 13622 <sup>ET</sup> = ATCC 60188 = CBS 151946 = FRC L-55 = NRRLA-26433	F. lateritium	<i>Ulmus</i> sp.	NSA	I	PQ000518	PQ000598	JX171571	JX171571	PQ000841
F. magnoliae-champaca	MFLUCC 18-0580 <sup>T</sup>	I	Magnolia champaca, fruit	Thailand	I	Ι	Ι	MT212198	Ι	Ι
F. malawiense sp. nov.	CBS 737.74 <sup>T</sup> = ATCC 24375 = CPC 42954 = IMI 158154 = NRRL 20533	F. lateritium	Citrus sp.	Malawi	MAT-2	PQ000519	PQ000599	PQ000682	PQ000760	PQ000842
F. massalimae	FCCUFG 05	Ι	Handroanthus chrysotrichus, leaf	Brazil	MAT-2	MN939764	MN939760	MN939768	I	I
	URM 8239 <sup>T</sup>	Ι	Handroanthus chrysotrichus, leaf	Brazil	MAT-2	MN939763	MN939759	MN939767	I	I
F. microcyclum sp. nov.	IMI 128389 <sup>T</sup> = ATCC 24396 = CBS 137.73 = CPC 46696	F. stilboides	Coffea excelsa	Canada	MAT-2	PQ000520	PQ000600	PQ000683	PQ000761	PQ000843
	IMI 392677 = ATCC 36325 = CPC 44278 = DSM 62456 = FUS005	I	Coffea excelsa	French Equatorial Africa		PQ000521	PQ000601	PQ000684	PQ000762	PQ000844
F. oliniae sp. nov.	CBS 152069 = CPC 38826 <sup>T</sup>	Ι	Olinia sp.	South Africa	MAT-2	PQ000522	PQ000602	PQ000685	PQ000763	PQ000845
F. ramsdenii	BRIP 62306a <sup>T</sup> = CBS 150771	Ι	Araucaria cunninghamii, stem canker	Australia	I	OL332732	OL332734	OL332733	PQ000764	PQ000846
F. rufum sp. nov.	IMI 294142 = CPC 42977	F. stilboides	Citrus medica var. acida	India	MAT-2	PQ000523	PQ000603	PQ000686	PQ000765	PQ000847
	IMI 300505 <sup>T</sup> = CPC 43032	F. graminearum	Parkia sp.	India	I	PQ000524	PQ000604	PQ000687	PQ000766	PQ000848
F. sarcochroum	CBS 745.79 <sup>NT</sup> = BBA 63714 = NRRL 20472	F. sarcochroum	Viscum album	Switzerland	I	MW834278	PQ000605	JX171586	JX171586	PQ000849

WESTERDIJK FUNGALBIO DIVERSITY INSTITUTE

Table 1. (Continued).										
		Deposited in the			Mating		GenBai	nk accession r	number <sup>3</sup>	
Species name	Strain code <sup>1</sup>	culture collection as	Host/substrate	Country	type <sup>2</sup>	tef1	tub2	<i>rpb2</i> -part 1	rpb2-part 2	CaM
	CBS 152070 = CPC 26369	Ι	Citrus limon, twig	Italy	MAT-1	LT746207	PQ000606	LT746320	LT746320	PQ000850
	CBS 152071 = CPC 26370	Ι	Citrus limon, twig	Italy	MAT-1	LT746208	PQ000607	LT746321	LT746321	PQ000851
	CBS 152072 = CPC 26851	Ι	Citrus reticulata	Greece	I	LT746209	PQ000608	LT746322	LT746322	PQ000852
	CBS 152073 = CPC 27921	Ι	Citrus sinensis	Italy	MAT-1	LT746210	PQ000609	LT746323	LT746323	PQ000853
	CBS 152075 = CPC 28116	Ι	Citrus reticulata, twig	Spain	I	LT746212	PQ000610	LT746325	LT746325	PQ000854
F. stilboides	BBA 65608 = CPC 44981 = DSM 115148	F. lateritium var. longum	Unknown	Cuba	MAT-2	PQ000525	PQ000611	PQ000688	PQ000767	PQ000855
	CBS 746.79 <sup>ET</sup> = BBA 63887 = NRRL 25485	F. stilboides	Citrus sp.	Cook Islands	Ι	MW928843	PQ000612	MW928832	MW928832	PQ000856
	CBS 115043 = HKUCC 6063	F. stilboides	<i>Brucea javanic</i> a, stem	China		PQ000526	PQ000613	PQ000689	PQ000768	PQ000857
	FRC L-81	I	Citrus sp., twig	New Caledonia	I	AY707156	AY707138	I	I	I
	LC13728 = CQ1109	Ι	Forsythia sp.	China	I	MW594308	MW533912	MW474541	I	I
	LC13729 = CQ993	I	Hedera nepalensis var. sinensis	China	I	MW594309	MW533913	MW474542	I	I
	LC13730 = F004	Ι	Acer palmatum	Japan	I	MW594310	MW533914	MW474543	Ι	Ι
	LC13731 = M0759	Ι	Schima noronhae	China	I	MW594311	MW533915	MW474544	Ι	I
F. stramineum sp. nov.	BBA 65675 <sup>T</sup> = CBS 152076 = CPC 47569 = DSM 116943	F. lateritium var. longum	Woody twig	Venezuela	MAT-2	PQ000527	PQ000614	PQ000690	PQ000769	PQ000858
F. velutinum sp. nov.	CBS 256.93 = INIFAT C91/223- 6F = NRRL 25490	I	Macadamia ternifolia, leaf	Cuba	MAT-2	PQ000528	PQ000615	PQ000691	PQ000770	PQ000859
	IMI 353670 <sup>T</sup> = CPC 44738	<i>Fusarium</i> sp.	Macadamia ternifolia, leaf	Cuba	MAT-2	PQ000529	PQ000616	PQ000692	PQ000771	PQ000860
F. verruculosum sp. nov.	BBA 68498 = CPC 46464 = DSM 116556	F. brachygibbosum	Soil	Spain	I	PQ000530	I	PQ000693	PQ000772	PQ000861
	BBA 68499 <sup>T</sup> = CBS 152077 = CPC 44987 = DSM 115156	F. lateritium var. lateritium	Triticum aestivum	Austria	MAT-2	PQ000531	I	PQ000694	PQ000773	PQ000862
Fusarium sp.	FRC L-110	I	Coffea sp., twig	Papua New Guinea	I	AY707165	AY707147	I	I	I
Fusarium sp.	FRC L-112	I	Coffea sp., twig	Papua New Guinea	I	AY707166	AY707148	I	I	I
Outgroup										
F. sublunatum	CBS 189.34 <sup>ET</sup> = BBA 62431 = DSM 62431 = IMB 5238 = NRRL 13384 = NRRL 20840	I	Soil of banana plantation	Costa Rica		OM160871	KM232076	JX171565	JX171565	KM231389

### COSTA ET AL.



noused at the Institute for Epidemiology and Pathogen Diagnostics, Braunschweig, Germany; BRIP: Queensland Plant Pathology Herbarium, Brisbane, Queensland, Australia; CBS: Centraalbureau voor Schimmelcultures collection of Lei Cai, State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; MFLUCC: Mae Fah Luang University herbarium, Chiang Rai, Thailand; MRC: Microbial Culture Sustainable Development of Biological Resources, Faculty of Science, Chiang Mai University (SDBR-CMU), Chiang Mai Province, Thailand; URM: University Recife Mycology (later IMUR - Instituto de Micologia da Universidade ATCC: American Type Culture Collection, Manassas, VA, USA; BBA: Collection of the Julius Kühn Institute – Federal Research Centre for Cultivated Plants (former Biologische Bundesanstalt für Land- und Forstwirtschaft) Collection of G.J. Samuels, USDA-ARS, USA; GUCC: Culture Collection of the Department of Plant Pathology, College of Agriculture, Guizhou University, Guiyang, Guizhou, China; HKUCC: The University of Hong Kong international Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, United Kingdom; INIFAT: Institute for Fundamental Research on Tropical Agriculture "Alexander Humboldt", Ciudad de La Habana, Cuba; LC: Personal collection housed at Westerdijk Fungal Biodiverity Institute (WI), Ufrecht, The Netherlands; CML: Coleção Micológica de Lavras, Universidade Federal de Lavras, Minas Gerais, Brazil; CPC: Personal collection of P.W. Crous, at Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; DSM: Deutsche Sammlung von Mikrorrganismen und Zellkulturen GmbH, Braunschweig, Germany; F: University of Sydney, New South Wales. Australia; FCCUFG: Fungal Culture Collection of the Universidade Federal de Goiás, Universidade Federal de Goiás, Goiánia, Goiás, Brazil; FRC: Fusarium Research Center, Pennsylvannia State University, PA, USA; GJS. Culture Collection, Hong Kong, China; HMAS: Herbarium Mycologicum Academiae Sinicae, Institute of Microbiology, Chinese Academy of Sciences, Bejing, China; IMB: Institut für Mykologie, BBA, Berlin-Dahlem, Germany; IMI: Collection, South African Medical Research Council, Tygerberg, South Africa; NRRL: Agricultural Research Service Culture Collection, National Center for Agricultural Utilization Research, USDA, Peoria, IL, USA; SDBR-CM: the Recife [Institute of Mycology of the University of Recife]. Universidade Federal de Pernambuco, Recife, Brazil, YZU: Herbanium of Yangtze University (YZU), Jingzhou, Hubei, China. ET: Ex-epitype, NT: Ex-neotype, T: Ex-type.

MAT-1: indicates strains are mating type MAT-2: indicates strains are mating type MAT-2. Data are not shown for strains that failed to produce a diagnostic band in the PCR assay or showed ambiguous results.

CaM: Calmodulin; rpb2: RNA polymerase II largest subunit; tef1: Translation elongation factor 1-alpha; tub2: Beta-tubulin. Sequences generated in this study are shown in bold

Phylogenetic analyses were performed using Maximum Likelihood (ML) and Bayesian inference (BI), by employing various software tools: RAxML-HPC2 on XSEDE v. 8.2.12 (Stamatakis 2014) was utilized for ML analyses on the CIPRES Science Gateway portal v. 3.3 (Miller et al. 2012), employing the default GTR substitution model and 1 000 rapid bootstrap replications for branch support estimations. The ML analyses were also conducted with IQ-TREE v. 2.1.2 (Nguyen et al. 2015, Minh et al. 2020), incorporating ultrafast bootstrapping (UFBoot2; Hoang et al. 2018). The bestfitting nucleotide substitution model for each gene partition was determined using ModelFinder (Kalyaanamoorthy et al. 2017, Minh et al. 2020) within IQ-TREE. Bayesian Inference (BI) analyses were executed with MrBayes v. 3.2.7 (Ronquist et al. 2012), employing two independent runs for 5 000 000 generations each, from which trees were sampled every 500 generations, and the initial 25 % of trees were discarded as burn-in. This resulted in 7 500 sampled trees based on which a 50 % majority rule consensus tree and the posterior probabilites were computed. MrModelTest v. 2.2 (Nylander 2004) was used to determine the best nucleotide substitution model for each locus for the Bayesian analyses. The resulting trees were visualized using FigTree v. 1.4.2 (http://tree.bio.ed.ac.uk/software/figtree).

A ML phylogenetic analysis (RAxML) based on 287 tef1 sequences was generated to infer the phylogenetic position of 179 strains obtained from BBA, CBS, CML, IMI, and NRRL culture collections. The analysis also included sequences from strains of several Fusarium species complexes, and Rectifusarium ventricosum (CBS 748.79) as outgroup taxon (Fig. S1. Table S1). The best-fitting model of evolution selected was GTR+G+I, and the tef1 dataset consisted of 772 characters including gaps. Among these, 275 were conserved, 461 were variable, 383 were phylogenetically informative. After the first general tef1 identification, individual and concatenated alignments for four gene regions (tef1, tub2, rpb2, CaM) were generated for strains belonging to the FLSC, with sequences from F. sublunatum (CBS 189.34 = NRRL 13384) as the outgroup taxon (Fig. 1). Maximumlikelihood (RAxML, IQ-TREE) and BI analyses were used to generate the phylogenetic trees for the concatenated alignment of four gene regions, and ML analyses (RAxML) were generated for the individual gene regions (rpb2, tub2, and CaM) and the concatenated alignment (tef1+tub2). The multilocus dataset (tef1+tub2+rpb2+CaM) consisted of 3 381 characters (tef1: 745, rpb2: 1 463, tub2: 608, and CaM: 565), including alignment gaps. Of these, 2 314 were conserved (*tef1*: 460, *rpb2*: 1 091, *tub2*: 407, CaM: 356), 1 071 were variable (tef1: 285, rpb2: 376, tub2: 201, CaM: 209), and 835 were phylogenetically informative (tef1: 218, rpb2: 322, tub2: 139, CaM: 156). The multilocus dataset (tef1+tub2) consisted of 1 356 characters (tef1: 749, and tub2: 607). Of these, 869 were conserved (tef1: 466, tub2: 403), 482 were variable (tef1: 280, tub2: 202), and 357 were phylogenetically informative (tef1: 215, tub2: 142). The best-fit models of evolution selected according to the rModelTest criterion were GTR+G for tef1 and tub2, SYM+I+G for rpb2, and SYM+G for CaM. The BI lasted for 1 145 000 generations, and the posterior probabilities (PP) were calculated from a total of 1 720 trees after the first 25 % of trees were discarded as the burn-in. The topologies observed for both the ML and BI analyses were congruent. The individual and *tef1+tub2* trees are shown in the Supplementary Figs S1–S5. Sequences generated in this study were deposited in GenBank (Table 1), the alignments in figshare (doi: 10.6084/ m9.figshare.26808253), and taxonomic novelties in MycoBank (www.MycoBank.org; Crous et al. 2004).

## Mating type identification and induction of the sexual morph

Mating-type idiomorphs (MAT-1 and MAT-2) were determined according to protocols described previously (Kerényi et al. 2004, Costa et al. 2022). Different strains representing opposite mating types within each species were paired in crosses by the spermatization method, ensuring that each strain acted as a female parent in combination with all strains of the opposite mating type as male parents (Klittich & Leslie 1988, Leslie & Summerell 2006). Strains that failed to produce a positive diagnostic band in the PCR assay or showed ambiguous results were intercrossed in all possible combinations with all other strains belonging to the same species to verify the possibility of fertile crossings. Each cross was performed in duplicates. Following the crossings, plates were incubated at 22 °C under a 12/12 h near-ultraviolet light (nuv)/dark cycle. Over a period of at least five wk, the formations of perithecia and ascospore exudation were monitored twice per week. Ascospore cirri were extracted from three perithecia from every fertile cross, suspended in sterile water, and dispersed onto the surface of 2 % water agar (WA) within Petri dishes. The plates were then incubated overnight at room temperature, after which they were checked for ascospore germination (Leslie & Summerell 2006, Lima et al. 2012).

## Morphology and physiological characterization

Strains were cultivated for 3-14 d at 24 °C in darkness on potato dextrose agar (PDA; Crous et al. 2019) and oatmeal agar (OA; Crous et al. 2019) to evaluate colony characteristics such as growth rates and production of odours (Leslie & Summerell 2006, Sandoval-Denis et al. 2019). Growth rates were documented after 3 d of incubation by assessing radial colonial expansion in two intersecting directions. Colony colours were determined after 14 d of incubation following the colour charts of Rayner (1970). Micromorphological characters were studied from colonies grown on carnation leaf-piece agar (CLA; Nirenberg 1976, Crous et al. 2019) for 3-14 d at 22 °C under a 12/12 h near-ultraviolet light/ dark cycle. Microconidial and macroconidial shape, arrangement of conidiogenous cells and presence or absence of chlamydospores were evaluated. Perithecia, asci and ascospores were characterized from crosses produced on carrot agar (CA) (Klittich & Leslie 1988). Perithecia were treated with 3 % KOH (aq) and 100 % lactic acid, to observe possible colour reaction (Samuels et al. 2001, Zeller et al. 2003). Micromorphological characteristics were examined and photo-documented using water as mounting medium. All measurements and images were taken using a Zeiss Axio Imager microscope, equipped with Differential Interference Contrast optics, and a Nikon DS-Ri camera using the NIS-Elements BR imaging software (Nikon, Tokyo, Japan). Measurements were taken for at least 50 fungal structures, and maximum - minimum values with averages were determined. Photographic plates were prepared using PhotoShop CSS.

## RESULTS

## Phylogeny

412

identified as F. lateritium, F. stilboides, or one of their varieties based on morphology, actually belong to the FLSC (Fig. S1). Ninety-nine strains grouped with reference material in six different SC, namely the F. citricola SC (FCCSC; n = 69), F. heterosporum SC (FHSC; n = 4), F. incarnatum-equiseti SC (FIESC; n = 1), F. redolens SC (FRSC; n = 1), F. sambucinum SC (FSAMSC; n = 2), and the F. tricinctum SC (FTSC; n = 22). In FCCSC, strains clustered with three known species, namely F. aconidiale, F. citricola, and F. salinense. Forty-three strains grouped in an unresolved clade that contains the type strains of F. juglandicola and F. celtidicola. Additionally, 18 strains formed two distinct clades, probably representing two new phylogenetic species. In the FTSC, strains clustered with F. paeoniae and within three clades not currently assigned to any known species. One putative new species could be identified, respectively, in the FHSC and FIESC, and two in the FSAMSC. One strain clustered with reference sequences of F. redolens in the FRSC.

The multilocus and individual gene region analyses (Figs 1, S1– S5) revealed that the strains from the FLSC belonged to *F. cassiae* (n = 4), *F. citri-sinensis* (n = 1), *F. endophyticum* (n = 3), *F. lateritium* (n = 2), and *F. stilboides* (n = 2). Three strains (CBS 319.73, CML 4473, IMI 373356) identified as *F. endophyticum* grouped in a highly supported clade (RAxML-BS = 100 % / IQ-TREE-BS = 100 % / PP = 1) that contains sequences of reference strains of this species, but also from *F. cartwrightiae* (Fig. 1). Depending on the specific gene region, strains within this clade moved to different positions (Figs S1, S3). Here we propose to maintain the name *F. endophyticum*, until more information will become available. Genealogical concordance analyses based on a four gene multilocus data set supported the occurrence of 11 novel phylogenetic lineages (Figs 1, 2, S1–S5), which are formally introduced in this study as new species and described below.

The topologies that were observed in the individual and combined phylogeny analyses of the four gene regions exhibit varying degrees of resolution, with the positioning of certain species potentially varying depending on the marker employed (Figs S1–S3). The *tef1*, *tub2*, and *rpb2* gene regions provided the best resolution for discriminating the species in the FLSC when analyzed individually and in combination, while *CaM* appeared to be the least informative gene region (Figs S1–S3). For example, it displayed the lowest resolution in differentiating species within the clade containing *F. aurantii*, *F. cassiae*, *F. citri-sinensis*, *F. endophyticum*, and *F. stilboides*. The loci *tub2* and *CaM* are not well represented in the dataset, with some of the ex-type strains missing data (Table 1).

## Mating type and laboratory crosses

Mating type idiomorphs (*MAT-1/MAT-2*) were identified for those strains that showed positive results in the PCR amplifications. Only one mating type idiomorph was detected in each strain across the species (Table 1). Fertile crossings were obtained for two species, *F. coffeibaccae* and *F. crocatum*. Among the 47 strains of *F. coffeibaccae*, 24 carried the *MAT-1* allele and 14 carried the *MAT-2* allele. Among the three strains of *F. crocatum*, one carried the *MAT-1* allele and two carried the *MAT-2* allele (Table 1). Among strains of *F. coffeibaccae*, 23 fertile crossings were obtained, that produced fertile perithecia within 4–5 wk after the crossing. Two strains from Brazil, CML 4411 (*MAT-1*) and CBS 101892 (*MAT-2*), were the most fertile as female parents and produced fertile perithecia when crossed with multiple strains of the opposite mating type. They were therefore selected as female-fertile testers



Fig. 1. Phylogenetic tree inferred from a Maximum Likelihood (RAxML) analysis based on concatenated *tef1*, *tub2*, *rpb2*, and *CaM* sequences of species from the FLSC. Ex-type, ex-epitype, and ex-neotype strains are indicated with T, ET, and NT respectively. Numbers at branches indicate support values (RAxML-BS / IQ-TREE-BS / BI-PP) above 70 % / 70 % / 0.7. The tree was rooted to *Fusarium sublunatum* (CBS 189.34 = NRRL 13384). Scale bar represents expected number of changes per site.



0.03

Table 2. Fertile cross combination	ations of Fus	arium coffeibaccae an	d Fusarium crocatum strain	S.	
♀ ( <b>MAT-1)</b> ª	×	് ( <i>MAT-2</i> )⁵	♀ ( <i>MAT-2</i> )°	×	് ( <i>MAT-1</i> )്
Fusarium coffeibaccae					
CML 2400	×	CBS 119871	CBS 101892	×	CBS 101891
CML 4408	×	CBS 101892*		×	CML 2400*
	×	CBS 119871		×	CML 4408
CML 4411	×	CBS 101892*		×	CML 4411*
	×	CML 4414*		×	CML 4415*
	×	CML 4424*		×	CML 4427*
CML 4427	×	CBS 101892*		×	CML 4428
	×	CBS 119871		×	CML 4430
CML 4430	×	CBS 101892		×	CML 4431
	×	CML 4424*	CBS 119871	×	CML 2400
CML 4440	×	CML 4414	CML 4414	×	CML 4415*
			CML 4432	×	CML 4411
Fusarium crocatum					
BBA 65926	x	BBA 65674*	CBS 130184	×	BBA 65926*

<sup>a</sup>♀ (MAT-1) indicates strains of mating type MAT-1 that were fertile as female parents.

<sup>b</sup>♂ (MAT-2) indicates strains of mating type MAT-2 that were fertile as male parents.

° $\bigcirc$  (*MAT-2*) indicates strains of mating type *MAT-2* that were fertile as female parents.

d∂ (MAT-1) indicates strains of mating type MAT-1 that were fertile as male parents.

\*Indicates crosses where a high number of perithecia were produced, with more than 300 mature perithecia per Petri dish.

(Table 2). Two fertile crosses were obtained between *F. crocatum* strains, that produced a larger number of fertile perithecia within three wk after the crossing (Table 2). The strains BBA 65926 and CBS 130184 acted as female parents in the fertile crossings. Ascospores germinated after 16 h of incubation on 2 % WA. Strains of *F. coffeibaccae* and *F. crocatum* did not intercross.

#### Taxonomy

In this section we designate an epitype for *F. lateritium* and provide an emended description for this species. A lectotype and epitype is designated for *F. lateritium* var. *longum*, here elevated to species level with a replacement name, *F. hanswilhelmii*. Latin binomials are provided for 11 novel species resolved in this study, namely *F. aurantii* sp. nov., *F. chlamydocopiosum* sp. nov., *F. coffeibaccae* sp. nov., *F. crocatum* sp. nov., *F. malawiense* sp. nov., *F. microcyclum* sp. nov., *F. oliniae* sp. nov., *F. rufum* sp. nov., *F. stramineum* sp. nov., *F. velutinum* sp. nov. and *F. verruculosum* sp. nov. In addition, *F. citri-sinensis* is validated, and emended descriptions are provided for *F. cassiae*, *F. citri-sinensis*, *F. endophyticum*, and *F. stilboides*.

*Fusarium aurantii* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854629. Fig. 2.

*Etymology: "aurantii"* in reference to the host species from which it was isolated, *Citrus aurantium.* 

*Typus*: **Cuba**, Santiago de las Vegas, from *Citrus aurantium*, unknown date and collector (**holotype** CBS H-25436 designated here, culture ex-type BBA 65609 = CBS 152039 = CPC 44982 = DSM 115149).

Aerial conidiophores borne laterally on hyphae, up to 200  $\mu m$  tall, erect and simple, straight or flexuous, reduced to single

monophialides or branched laterally, smooth- and thin-walled; aerial conidiogenous cells monophialidic, ampulliform, subulate, cylindrical to subcylindrical, (4.9-)11.5-21.0(-34.8) × 2.3-4.7 µm (av. 15.6 × 3.5  $\mu$ m), smooth- and thin-walled. Aerial conidia of two types: microconidia ellipsoidal, obovoid to fusiform 0-1-septate, hyaline, smooth- and thin-walled; 0-septate conidia: 8.5-11.7 × 3.4-4.2 µm (av. 10.0 × 3.5 µm); 1-septate conidia: 13.6-17.6 × 3.7-4.4 μm (av. 15.5 × 4.0 μm); macroconidia moderately to distinctly dorsiventrally curved, generally more curved than macroconidia from sporodochial, apical cell often equal in length to adjacent cell, basal cell papillate to poorly to well-developed, foot-shaped, 0-5-septate, hyaline, smooth- and thin-walled; 0-septate conidia: 11.5 × 3.2 µm; 1-septate conidia: 13.6-15.0(-16.6) × 3.6-4.6 µm (av. 14.3 × 4.1 μm); 2-septate conidia: 18.5–21.5 × 4.3–5.1 μm (av. 20.2 × 4.5 μm); 3-septate conidia: (20.9–)25.0–44.5(–48.3) × 3.4–5.6 µm (av. 35 × 4.5 µm); 4-septate conidia: (42.8–)47.5–48.3 × 4.6–4.9 µm (av. 47.9 × 4.8 µm); 5-septate conidia: 44.5 × 5.1 µm. Sporodochia luteous to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subcylindrical to subulate, 15.4-21.2(-29.0)  $\times$  3.0–4.3 µm (av. 18.3  $\times$  3.8 µm), smooth- and thin-walled. Sporodochial conidia slightly curved, gradually tapering toward both ends, with a blunt and pointed apical cell, basal cell poorly to well developed, foot-shaped, 3-5-septate, hyaline, smooth- and thick-walled; 3-septate conidia: (31.0-)33.7-53.3 × 3.8-5.3 µm (av. 45.2 × 4.7 μm); 4-septate conidia: 45.8–59.2(–66.5) × 4.2–5.7 μm (av. 52.0 × 4.8 µm); 5-septate conidia: 50.3–67.3 × 4.2–6.0 µm (av. 57.0 × 4.8 µm). Chlamydospores not observed. Projections on the hyphae resembling chlamydospores may occur.

*Culture characteristics*: Colonies on PDA growing in the dark reaching 26–32 mm diam in 3 d at 24 °C; peach to flesh aerial mycelium more concentrated in the centre of the colony, and



**Fig. 2.** *Fusarium aurantii sp. nov.* (ex-type culture BBA 65609). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C–F.** Sporodochia formed on the surface of carnation leaves and agar surface. **G, H, J–L, N, O**. Aerial conidiophores, conidiogenous cells and conidia. **I**. Projections on the hyphae. **M.** Aerial conidia. **P.** Sporodochial conidiophores and conidiogenous cells. **Q.** Sporodochial conidia. Scale bars: C, D = 200 µm; E, F = 100 µm; G = 50 µm; H, J–L, P = 20 µm; I, M, N, Q = 10 µm; O = 5 µm.



#### COSTA ET AL.

abundant production of sporodochia. Surface changing the colour towards the margin, from apricot, peach, rosy vinaceous and pale luteous, with aerial mycelium growing in a radiate and concentric arrangement; margin entire. Odour absent. Reverse sienna to saffron. On OA growing in the dark reaching 26–30 mm diam in 3 d at 24 °C; surface apricot in the center, peach to pale luteous towards the margin, with white cottony aerial mycelium, and sometimes mycelia growing in a radiate arrangement; margin entire. Odour absent. Reverse saffron.

Additional materials examined: India, from Cajanus cajan, unknown date, R.S. Mehrotra, culture IMI 310541 = CPC 44539; from Vigna angularis, unknown date, K.M. Ahmed & N.C. Joshi, culture IMI 338937 = CPC 42982.

*Notes: Fusarium aurantii* is introduced here as a distinct species within the FLSC. Identification of *F. aurantii* can be achieved through both multi- (*tef1+tub2+rpb2+CaM*) and single gene phylogenetic analyses. This species is phylogenetically closely related to *F. cassiae* and *F. stilboides*. No *tub2* and *CaM* sequences for *F. cassiae* were available for comparison. Morphologically, *F. aurantii* can be distinguished from *F. stilboides* and *F. cassiae* by the absence of chlamydospores, a characteristic observed in the latter two species. *Fusarium aurantii* rarely produces microconidia on aerial mycelium, frequently observed in *F. stilboides* but absent in *F. cassiae*. Macroconidia produced on aerial mycelium in *F. aurantii* are more curved compared to the other two species.

*Fusarium cassiae* R.H. Perera *et al.*, Mycosphere 11: 2138. 2020. Fig. 3.

Additional description and illustrations: See Perera et al. (2020).

Emended description: Aerial conidiophores borne on substrate mycelium or laterally on hyphae, up to 152 µm tall, erect and simple, mostly reduced to single monophialides, and sometimes branched laterally, smooth- and thin-walled; aerial conidiogenous cells monoand polyphialidic, subulate to subcylindrical, 15.0-40.7(-48.9) × 2.4-4.4(-5.0) µm (av. 27.0 × 3.3 µm), smooth- and thin-walled. Aerial conidia curved to straight, basal cell obtuse to papillate, and foot-shaped, 2-5-septate, hyaline, smooth- and thin-walled; 2-septate conidia: 27.0-29.8 × 3.4-4.4 µm; 3-septate conidia: 27.2-49.8(-55.0) × 4.0-5.3 µm (av. 41.0 × 4.7 µm); 4-septate conidia: 52.0 × 5.8 µm; 5-septate conidia: 70.0 × 4.6 µm. Sporodochia pale rosy. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical, 4.0-16.3  $\times$  2.6–3.7(–5.5) µm (av. 8.3  $\times$  3.3 µm), smooth- and thin-walled. Sporodochial conidia moderately dorsiventrally curved to nearly straight, tapering toward both ends, apicall cell blunt to conical, basal cell poorly to well-developed, foot-shaped, 4-8-septate, hyaline, smooth- and thick-walled; 4-septate conidia: 55.5 × 5.4 μm; 5-septate conidia: 55.2–70.4(–77.5) × 4.8–6.5 μm (av. 63.4 × 5.6 µm); 6-septate conidia: 63.9–77.3 × 4.0–6.2 µm (av. 71.4 × 5.2  $\mu$ m); 7-septate conidia: 70.6–76.4 × 4.9–6.0  $\mu$ m (av. 73.6 × 5.5  $\mu$ m); 8-septate conidia: 76.0 × 6.6 µm. Chlamydospores subglobose to globose, smooth- and thick-walled, 5.0-8.2 µm diam, usually in pairs, in chains, terminal or intercalary in hyphae.

*Culture characteristics*: *Colonies* on PDA and OA growing in the dark reaching 27–30 mm diam in 3 d at 24 °C; On PDA surface dirty white and salmon, with concentric rings of aerial mycelium; margin entire. Odour absent. Reverse dirty white to straw. On OA surface

dirty white to pale straw, with scarce aerial mycelium; margin entire. Odour absent. Reverse dirty white to straw.

*Material examined*: **Cuba**, Havana, from *Ceiba insignis*, before 29 Aug. 1988, *R.F. Castañeda-Ruiz*, culture BBA 65092 = CPC 47105 = DSM 115143.

*Notes: Fusarium cassiae* is phylogenetically closely related to *F. aurantii*, *F. citri-sinensis* and *F. stilboides*. This species was described based on the sexual morph from perithecia on decaying pods of *Cassia fistula* in Thailand. Here we provide the morphological characters for the asexual morph of *F. cassiae*, using as reference material the strain BBA 65092, isolated from *Ceiba insignis* in Cuba.

*Fusarium chlamydocopiosum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854635. Fig. 4.

Etymology: In reference to its abundant chlamydospore production.

*Typus*: **South Africa**, soil under *Citrus sinensis*, 2018, *V. Guarnaccia* (**holotype** CBS H-25375 designated here, culture ex-type CBS 152063 = CPC 37116).

Aerial conidiophores borne laterally on hyphae, up to 99 µm tall, erect and simple, straight or flexuous, most of the time reduced to single monophialides, sometimes branched laterally and verticillately, smooth- and thin-walled; aerial conidiogenous cells monophialidic, short ampulliform, subulate, cylindrical to subcylindrical, (4.7-)12.0-25.9(-33.0) × 2.0-5.3 µm (av. 17.6 × 3.8 µm), smooth- and thin-walled, often proliferating percurrently, with a conspicuous collarette. Aerial conidia fusiform, straight to falcate, robust, apical cell blunt, hooked or inconspicuous, basal cell barely to distinctly notched and straight, (1-)3-5-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 12.4-18.4 × 3.5-4.5 µm (av. 15.0 × 3.9 µm); 3-septate conidia: (20.0-)23.0-34.3(-42.0) × 4.7-5.2(-6.2) µm (av. 30.5 × 4.9 µm); 4-septate conidia: 41.0-45.2 × 5.0-5.9(-6.5) µm (av. 43.0 × 5.3 µm); 5-septate conidia: 43.7-44.3 × 5.5-6.0 µm. Sporodochia pale yellow to orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells mono- and polyphialidic, ampulliform, subulate, cylindrical to subcylindrical, (11.0-)16.0-18.7(-29.0) × 3.0-5.7 µm (av. 17.6 × 4.7 µm), smooth- and thin-walled. Sporodochial conidia, falcate, slightly curved, robust, apical cell often shorter than the adjacent cell with curved apex, basal cell papillate to distinctly notched, 3-6-septate, hyaline, smooth- and thick-walled; 3-septate conidia: (30.3–)41.7–45.5(–48.2) × 5.5–7.0(–8.5) μm (av. 44.0 × 6.3 μm); 4-septate conidia: 43.3-53.8 × 5.5-8.3 µm (av. 48.5 × 6.6 µm); 5-septate conidia: (45.7–)49.5–57.6 × 6.0–7.5 µm (av. 53.5 × 6.8 μm); 6-septate conidia: 52.0 × 6.0 μm. Chlamydospores abundantly formed in mycelium, agar surface, and sporodochia, subglobose to globose, smooth to verruculose and thick-walled, 5.0–10.9(–12.0) µm diam, terminal or intercalary in hyphae or conidia, solitary, in chains or in clusters. Sterile, coiled, sometimes branched hyphal projections abundantly formed laterally from the substrate and aerial mycelium.

*Culture characteristics*: Colonies on PDA growing in the dark reaching 17–23 mm diam in 3 d at 24 °C; surface white to straw, flat, with scarce aerial mycelium, becoming less dense at the margins; margin irregular to rhizoid. Odour absent. Reverse saffron to pale luteous. On OA growing in the dark reaching 18–25 mm diam in 3 d



**Fig. 3.** *Fusarium cassiae* (BBA 65092). **A**, **B**. Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C**, **D**. Sporodochia formed on the surface of carnation leaves. **E–N**. Aerial conidiophores, conidiogenous cells and conidia. **O–Q**. Chlamydospores. **R**. Aerial conidia. **S–U**. Sporodochial conidiophores, conidiogenous cells and conidia. Scale bars: C, D = 100 µm; E, H–V = 10 µm; F, G = 20 µm.





**Fig. 4.** *Fusarium chlamydocopiosum sp. nov.* (ex-type culture CBS 152063). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves (C), and agar surface (D). **E–M.** Aerial conidiophores, conidiogenous cells and conidia. **N, O.** Sterile hyphal projections. **P.** Aerial conidia. **Q–T.** Chlamydospores. **U, V.** Sporodochial conidiophores, conidiogenous cells and conidia. **W.** Sporodochial conidia. Scale bars: C = 100 µm; D = 20 µm; E, F–M, P, S, U–W = 10 µm; N, O, Q, R, T = 5 µm.

at 24 °C; Surface saffron to cinnamon, with scarce aerial mycelium; margin irregular. Odour absent. Reverse saffron to cinnamon.

Additional materials examined: **South Africa**, soil under Citrus sinensis, 2018, V. Guarnaccia, cultures CPC 37118, and CPC 37119.

Notes: Fusarium chlamydocopiosum is described here from strains obtained from soil under citrus in South Africa. It displays a unique and distinct morphology compared to other species in the FLSC. Morphological features of F. chlamydocopiosum include the abundant production of subglobose to globose chlamydospores, smooth to verruculose, formed in mycelium, agar surface, and sporodochia. Additionally, it produces sterile and coiled hyphal projections. The production of sterile, coiled hyphae has been observed and reported in other Fusarium species, such as F. pseudocircinatum, F. sterilihyphosum (Leslie & Summerell 2006), and F. convolutans (Sandoval-Denis et al. 2018), which belong to the F. fujikuroi and F. buharicum species complexes, respectively. However, within the FLSC, F. chlamydocopiosum is the only species characterized to date as exhibiting this particular feature, enabling its differentiation from other species within the FLSC. Fusarium chlamydocopiosum can also be easily distinguished from other FLSC species by the production of relatively simple conidiophores and shorter phialides, a characteristic also observed in in the new species F. microcyclum. Additionally, it exhibits slower growth rates on PDA and OA, providing a distinguishing criterion from most species in the FLSC.

*Fusarium citri-sinensis* L. Zhao & J.X. Deng, *sp. nov.* MycoBank MB 854636. Fig. 5.

Synonym: Fusarium citri-sinensis Lin Zhao & J.X. Deng, Phytotaxa 555: 263. 2022. Nom. inval. Art. 40.8.

*Etymology*: In reference to the host on which it was first collected, *Citrus sinensis.* 

*Typus*: **USA**, Alabama, from *Albizia julibrissin*, 1992, *G.J. Samuels* (**holotype** CBS H-25377 designated here, culture ex-type BBA 67503 = CBS 152066 = CPC 44985 = DSM 115153).

Additional description and illustrations: See Zhao et al. (2022).

Sporodochia pale to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells mono- and polyphialidic, ampulliform, subulate to subcylindrical, 14.0-22.7(-25.7) × 3.5-4.6 μm (av. 19.1 × 3.9 μm), smooth- and thin-walled. Sporodochial conidia moderately dorsiventrally curved to nearly straight, tapering toward both ends, apical cell curved to blunt, basal cell papillate, non-foot-shaped and sometimes poorly to well-developed, footshaped, 3-9(-13)-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 39.7–52.5 × 4.0–4.9 µm (av. 46.2 × 4.4 µm); 4-septate conidia: 48.2–55.1 × 4.6–5.4 μm (av. 52.4 × 5.1 μm); 5-septate conidia: 48.7-60.7 × 4.5-5.8 µm (av. 55.6 × 5.2 µm); 6-septate conidia: 53.1-54.6 × 5.8-6.0 µm; 7-septate conidia: 81.5 × 7.2 μm; 8-septate conidia: 73.9 × 6.4 μm; 9-septate conidia: 82.3-84.7 × 6.8-7.4 µm (av. 83.5 × 7.1 µm); 13-septate conidia: 99.5 × 7.7 µm.

*Notes: Fusarium citri-sinensis* was invalidly published as a distinct phylogenetic species in the FLSC associated to fruit of *Citrus sinensis*, in China (Zhao *et al.* 2022). The species was invalidated since the protologue failed to specify the preservation of the listed



culture in a metabolically inactive state (Art. 40.8, Shenzhen Code). Here, we validate the name using the strain BBA 67503 isolated from *Albizia julibrissin*, which also suggests that *F. citri-sinensis* has a wider host range than originally assumed (Zhao *et al.* 2022). Because the name is already established in literature, we choose to retain it by validating the species. A morphological description is also included to account for previously undocumented features, *i.e.*, sporodochial conidia with up to 13 septa and > 99 µm long. Additionally, colonies of *F. citri-sinensis* on PDA were originally reported to exhibit a pale pink colour with a pinkish white reverse and pale pink pigment. However, for BBA 67503, the colony colour was flesh, peach, and coral, with a salmon to saffron colouration at the margin, and it produced a red pigment clearly observed on the reverse side.

*Fusarium coffeibaccae* M.M. Costa, L.H. Pfenning, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854633. Figs 6, 7.

Etymology: From the Latin meaning "of Coffea-berries".

*Typus*: **Brazil**, Lavras, Minas Gerais, from fruit of *Coffea arabica*, Jan. 1999, *L.H. Pfenning* (**holotype** CBS H-25440 designated here, culture extype CML 90 = CBS 152040 = CPC 46658).

Sporulation abundant from conidiophores on aerial mycelium floccose and powdery. Aerial conidiophores abundant, up to 380 µm tall, erect on substrate mycelium, commonly borne from mycelial tufts, densely aggregated and branched, smooth- and thinwalled, straight or flexuous, sometimes reduced to a single phialide borne laterally on aerial hyphae, rarely sparingly branched, bearing terminal, single mono- or polyphialides; aerial conidiogenous cells mono- and polyphialidic, subulate, subcylindrical to cylindrical,  $7.5-57.9 \times 1.8-3.9(-4.5) \mu m$  (av.  $17.4 \times 3.0 \mu m$ ), smooth- and thinwalled. Aerial conidia of two types: microconidia straight to slightly curved, sometimes with a flattened base, oval, allantoid, obovoid, fusiform to subcylindrical, 0-1(-3)-septate, hyaline, smooth- and thin-walled, 0-septate conidia: 5.2-12.4(-14.2) × (2.8-)3.5-4.0(-4.6) µm (av. 8.3 × 3.6 µm); 1-septate conidia: (9.6-)10.6-17.0(-20.3) × 3.5-5.1 µm (av. 13.8 × 4.0 µm); 2-septate conidia: 17.9–19.9 × 4.5–5.0 μm (av. 18.2 × 4.8 μm); 3-septate conidia: 18.9–21.9 × 4.6–5.4(–6.0) μm (av. 20.6 × 5.3 μm); mesoconidia fusiform to falcate, almost straight to moderately dorsiventrally curved, tapering toward the apical and basal part, widest at the basal portion with a small flattened base, apical cell generally slender than the basal cell, 2-5-septate, hyaline, smooth- and thin-walled; 2-septate conidia: 23.0–25.7  $\times$  4.0–4.5  $\mu m$  (av. 24.4 × 4.3 μm); 3-septate conidia: 26.5–36.0(–43.7) × 4.0–5.0(–6.3) μm (av. 29.0 × 4.7 µm); 4-septate conidia: 33.5–36.5(–41.5) × 5.0–6.0 μm (av. 35.4 × 5.7 μm); 5-septate conidia: (37.6-)40.2-42.2(-56.0) × 5.2–5.8 µm (av. 41.2 × 5.5 µm). Sporodochia pale rosy to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous *cells* monophialidic, subulate, subcylindrical to cylindrical, (19.5–)  $21.6-32.6(-35.4) \times (2.8-)3.5-3.8(-4.0) \ \mu m$  (av.  $25.6 \times 3.6 \ \mu m$ ), smooth- and thin-walled. Sporodochial conidia barely dorsiventrally curved, almost straight in its ventral portion, tapering and becoming more pronouncedly curved towards the basal and apical levels, apical cell curved, basal cell non-foot-shaped and sometimes poorly developed, foot-shaped, (1–)3–5-septate, hyaline, smoothand thick-walled; 1-septate (12.3–)15.0–23.2(–29.0) × 3.0–5.0 µm (av. 19.0 × 4.0 μm); 3-septate conidia: (24.3–)37.0–51.4(–54.1) × 4.0-5.3 µm (av. 44.1 × 5.0 µm); 4-septate conidia: (46.2-)50.0-



**Fig. 5.** *Fusarium citri-sinensis* (ex-type culture BBA 67503). **A**, **B**. Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C–E**. Sporodochia formed on the surface of carnation leaves and agar surface. **F–J**, **M–Q**. Aerial conidiophores, conidiogenous cells and conidia. **K**, **L**. Chlamydospores. **R**. Aerial conidia. **S–U**. Sporodochial conidiophores, conidiogenous cells and conidia. **V**. Sporodochial conidia. Scale bars: C, D = 100 μm; E, F, U = 20 μm; G, H, K, L, O–T, V = 10 μm; I, J, M, N = 5 μm.



**Fig. 6.** *Fusarium coffeibaccae sp. nov.* (ex-type culture CML 90). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–Q.** Aerial conidiophores, conidiogenous cells and conidia. **R.** Aerial conidia, including mesoconidia. **S, T.** Chlamydospores. **U, V.** Sporodochial conidiophores, conidiogenous cells and conidia. **W.** Sporodochial conidia. Scale bars: C, E = 100 µm; D = 200 µm; F–T, W = 10 µm; U = 20 µm; V = 50 µm.





**Fig. 7.** Sexual morph of *Fusarium coffeibaccae sp. nov.* (CML 4411 × CML 101892). **A–D.** Perithecia. **C, D**. Perithecia oozing ascospores. **E, F.** Section through perithecium. **G–K.** Asci and ascospores. **L, M**. Ascospores. **M**. Germinating ascospore. Scale bars: A–D = 100 μm; E–G = 50 μm; H–M = 10 μm.

58.5(-64.0) × 4.0–5.3 µm (av. 54.0 × 4.5 µm); 5-septate conidia: (53.0–)55.1–70.0(-85.0) × 4.0–6.2 µm (av. 65.0 × 5.1 µm). *Chlamydospores* subglobose to globose, smooth- and thick-walled, 3.9–6.2(-8.5) µm diam, intercalary in hyphae, solitary or in chains.

Sexual morph produced in culture on carrot agar. Perithecia produced within 3–5 wk after crossing, solitary to aggregate in groups of up to 20 perithecia, and seated on a minute stromatic base, broadly pyriform to obpyriform and warty, blue black, 150–325 × 100–300 µm (av. 250 × 200 µm); perithecial wall 12.1–40.2 µm (av. 22.6 µm) µm thick, consisting of two regions; outer region 10–30 µm, cells angular to elliptic,  $3.5-19.1 \times 1.8-8.7$  µm (av.  $8.5 \times 5.1$  µm), cell walls 0.9-3.6 µm (av. 2.0 µm) thick; inner region 2.4-12.7 µm, cells angular to elliptic,  $5.5-13.5 \times 1.6-4.3$  µm (av.  $7.6 \times 3.1$  µm), cell walls 0.5-1.9 µm (av. 0.9 µm) thick. Asci 8-spored, clavate,  $65.9-115.8 \times 6.0-14.0$  µm (av.  $99.1 \times 11.5$  µm). Ascospores fusiform to obovoid, smooth-walled, pale goldenbrown at maturity, 1–3 septate:  $15.4-20.9(-22.0) \times 4-6$  µm (av.  $19.5 \times 5.0$  µm), 2-septate:  $20.3-25.6 \times 5.3-6.9$  µm (av.  $22.4 \times 6.0$  µm), 3-septate:  $22.3-30.1 \times 6.0-9.0$  µm (av.  $24.0 \times 7.5$  µm).

*Culture characteristics*: Colonies on PDA growing in the dark reaching 30–32 mm diam in 3 d at 24 °C; producing a red pigment, surface straw, pale luteous, sienna, saffron, orange to red, flat, commonly with white aerial mycelium arranged in circadian rings; margin entire. Odour absent. Reverse pale straw to red. On OA growing in the dark reaching 30–31 mm diam in 3 d at 24 °C; saffron to apricot, darker in the centre with white aerial mycelium arranged in circadian rings; margin entire. Odour absent. Reverse pale straw to red. On OA growing in the dark reaching 30–31 mm diam in 3 d at 24 °C; saffron to apricot, darker in the centre with white aerial mycelium arranged in circadian rings; margin entire. Odour absent. Reverse red in the centre to pale straw at the margin.

Additional materials examined: **Brazil**, Araguari, Minas Gerais, from fruit of *Coffea arabica*, 2018, *M.M. Costa*, cultures CML 4403 = CPC 46662, CML 4404 = CPC 46663, and CML 4405 = 46664; Lavras, Minas Gerais, from fruit of *C. arabica*, 2018, *M.M. Costa*, cultures CML 4408 = CPC 46667, CML 4428 = CPC 46680, CML 4435 = CPC 46685; and CML 4437 = CPC 46687; Nepomuceno, Minas Gerais, from fruit of *C. arabica*, 2018, *M.M. Costa*, cultures CML 4409 = CPC 46668, and CML 4411 = CPC 46670; Patrocínio, Minas Gerais, from fruit of *C. arabica*, 2018, *M.M. Costa*, cultures CML 4424 = CPC 46678; from fruit of *Citrus aurantifolia*, 2018, *M.M. Costa*, culture CML 4438 = CPC 46688; Boa Esperança, Minas Gerais, from fruit of *Hylocereus* sp., 2019, *M.M. Costa*, culture CML 4415 = CPC 46672.

Cultures examined: Culture with perithecia from fertile crosses of CML 2400 × CBS 119871; CML 4408 × CBS 101892 and CBS 119871; CML 4411 × CBS 101892, CML 4414 and CML 4424; CML 4427 × CBS 101892, and CBS 119871; CML 4430 × CBS 101892 and CML 4424; CML 4440 × CML 4414.

*Notes: Fusarium coffeibaccae* represents the most common and diverse species in the FLSC. It is a widespread species reported in various countries, including Brazil, and African countries. Strains belonging to this species have been isolated from diverse hosts and substrates. It causes bark diseases and fruit rots, particularly affecting *Coffea arabica, Coffea canephora* and citrus in New Guinea, eastern Africa (Geiser *et al.* 2005), and Brazil, but also dragon fruit (*Hylocereus* sp.) in Brazil. The most closely related species to *F. coffeibaccae* are *F. oliniae* and *F. rufum* (Fig. 1). Morphologically, *F. coffeibaccae* differentiates itself from other phylogenetic species of the FLSC by producing aerial conidia from well-developed, predominantly polyblastic conidiogenous cells and mycelial tufts on aerial mycelium (Fig. 6). The production



of mesoconidia from polyblastic conidiogenous cells is not a common characteristic observed in species of the genus Fusarium but has been documented for some species, as F. ophioides, F. camptoceras, F. chlamydosporum (Jacobs et al. 2010, Yilmaz et al. 2021, Pascoe 1990). The macroconidia produced on sporodochia by F. coffeibaccae are also narrower compared to other species in the FLSC. Colonies of F. coffeibaccae strains produce a red pigment on PDA with circadian rings of white aerial mycelium. The production of circadian rings of white aerial mycelium appears to be a common characteristic observed in strains belonging to FLSC species, such as F. aurantii and F. rufum. However, the production of a red pigment on PDA seems to be restricted to the species F. coffeibaccae, F. aurantii, F. rufum, F. oliniae and F. citri-sinensis. Fusarium coffeibaccae also represents a biological species in the FLSC, as fertile crosses were obtained between strains from Brazil and Ethiopia. Lawrence et al. (1985a) also obtained fertile crosses between strains morphologically identified as F. lateritium, but which represent F. coffeibaccae. Ascospores produced by F. coffeibaccae are larger in size and more septated compared to those produced by F. cassiae and F. magnoliae-champaca (Perera et al. 2020). Perithecia, asci, and ascospores of F. coffeibaccae are larger in size compared to those described for F. lateritium and F. stilboides (Booth 1971).

*Fusarium crocatum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854638. Figs 8, 9.

*Etymology: "crocatum*" referring to the saffron-sulphur yellow surface colour of MEA colonies.

*Typus*: **Venezuela**, from grass, 1991, *G.J. Samuels* (**holotype** CBS H-25437 designated here, culture ex-type BBA 65926 = CBS 152067 = CPC 44984 = DSM 115152).

Aerial conidiophores borne laterally on hyphae, erect and simple, up to 203 µm tall, straight or flexuous, most of the time reduced to single phialides, sometimes branched laterally, smooth- and thin-walled; aerial conidiogenous cells mono- and polyphialidic, subulate, cylindrical to subcylindrical (4.6-)10.5-50.0(-62.0) × (2.0-)2.5-5.0(-6.4) µm (av. 25.5 × 4.0 µm), smooth- and thinwalled, with a visible collarette, often proliferating percurrently. Aerial conidia of two types: microconidia fusiform and clavate, often with a flattened base, 0-1(-3)-septate, hyaline, smooth- and thin-walled; 0-septate conidia: 11.0-12.0 × 3.5-4.7 µm (av. 11.7 × 4.0 µm); 1-septate conidia: 11.6–18.7(–19.5) × 3.5–5.5 µm (av. 14.7 × 4.4 µm); 3-septate conidia: 25.5–30.0 × 5.0–6.0 µm (av.  $27.4 \times 5.6 \ \mu\text{m}$ ; macroconidia falcate, straight to slightly curved, apical cell curved, basal cell papillate to poorly developed, footshaped, clustering in false heads at tip of mono- or polyphialides, 1-3-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 19.0-24.0(-25.9) × 4.3-5.6 µm (av. 22.5 × 4.8 µm); 2-septate conidia: (23.0–)25.5–26.0(–34.8) × 4.6–5.8 µm (av. 25.7 × 5.2 µm); 3-septate conidia: (20.0-)25.8-48.0(-59.5) × 3.6-6.0(-6.5) µm (av. 34.5 × 5.0 µm). Sporodochia cream to pale rosy. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subulate to subcylindrical, 16.2-25.0 × 3.4-6.0 µm (av. 20.6 × 4.8 µm), smooth- and thin-walled. Sporodochial conidia, moderately dorsiventrally curved to nearly straight, tapering gently toward both ends, apical cell curved, blunt to hooked, basal cell poorly to welldeveloped, foot-shaped, 3-5(-7)-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 33.9-48.2 × 3.5-6.0 µm (av. 40.8 ×



**Fig. 8.** *Fusarium crocatum sp. nov.* (ex-type culture BBA 65926). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–N.** Aerial conidiophores, conidiogenous cells and conidia. **P, Q.** Sporodochial conidia. Scale bars: C, D = 200 µm; E = 50 µm; F = 20 µm; G–R = 10 µm.



Fig. 9. Sexual morph of *Fusarium crocatum sp. nov.* (BBA 65926 × BBA 65674). A–C. Perithecia. C. Perithecia oozing ascospores. D–G. Section through perithecium. H–K. Asci and ascospores. L, M. Ascospores. Scale bars: C, D = 200 µm; E = 50 µm; F, H, I = 20 µm; G, J, M = 10 µm; K, L = 5 µm.

5.1 µm); 4-septate conidia:  $40.0-59.0 \times 4.8-6.7$  µm (av.  $50.4 \times 5.6$  µm); 5-septate conidia:  $49.3-69.7(-73.3) \times 4.9-7.0$  µm (av.  $61.0 \times 6.0$  µm); 6-septate conidia:  $68.0-92.4 \times 5.5-6.5$  µm; 7-septate conidia:  $75.7-80.3 \times 5.5-6.8$  µm. *Chlamydospores* not observed.

Sexual morph produced in culture on carrot agar. Perithecia produced within 3–4 wk after fertilization, solitary to aggregated in groups up to 13 perithecia and seated on a minute stromatic base, broadly pyriform to obpyriform and warty, blue black, and shiny in some crosses,  $100-250 \times 100-200 \,\mu\text{m}$  (av.  $150 \times 140 \,\mu\text{m}$ ); perithecial wall 13.5–45.1  $\mu\text{m}$  (av. 25.6  $\mu\text{m}$ )  $\mu\text{m}$  thick, consisting of two regions: outer region 11.3–35.2  $\mu\text{m}$ , cells angular to elliptic, 6.5–21.4 × 1.5–8.8  $\mu\text{m}$  (av. 10.5 × 6.2  $\mu\text{m}$ ), cell walls 0.7–3.1  $\mu\text{m}$  (av. 1.9  $\mu\text{m}$ )  $\mu\text{m}$  thick; inner region 5.3–20.8  $\mu\text{m}$ , cells angular to elliptic, 7.2–13.8 × 1.7–4.8  $\mu\text{m}$  (av. 8.6–3.5  $\mu\text{m}$ ), cell walls 0.5–1.9  $\mu\text{m}$  (av. 1.0  $\mu\text{m}$ )  $\mu\text{m}$  thick. Asci 8-spored, clavate, 40.0–70.0 × 7.0–11.0  $\mu\text{m}$  (av. 50.5 × 10.5  $\mu\text{m}$ ). Ascospores ellipsoidal to

obovoid, pale golden brown, smooth-walled to finely ornamented, 0–1-septate, mostly 1-septate, 0-septate:  $12.5 \times 4.0 \ \mu m$ , 1-septate:  $(12.5-)15.0-17.5(-21.0) \times 4.0-6.0 \ \mu m$ .

*Culture characteristics: Colonies* on PDA and OA growing in the dark reaching 33–36 mm diam in 3 d at 24 °C; On PDA white to dirty white, sometimes with white aerial mycelium in a radiate arrangement; margin entire. Reverse dirty white. Odour absent. On OA surface white to dirty white, sometimes with white aerial mycelium in a radiate arrangement; margin entire. Reverse dirty white. Odour absent. Odour absent.

Additional materials examined: **Venezuela**, from Bambusa vulgaris, 1991, G.J. Samuels, dep. J. Swezey, culture CBS 130184 = BBA 65687 = DSM 115151 = NRRL 25197; from herbaceous vine, 1991, G.J. Samuels, culture BBA 65674 = CPC 44983 = DSM 115150.

*Cultures examined*: Culture with perithecia from fertile crosses of BBA 65926 × BBA 65674, and CBS 130184 × BBA 65926.



#### COSTA ET AL.

Notes: Fusarium crocatum shares similar morphology to F. aurantii and F. velutinum, but it can be distinguished from F. aurantii, which does not produce polyphialides on aerial mycelium. Additionally, the production of microconidia in aerial mycelium is not commonly observed in strains belonging to F. aurantii but is frequently observed in strains of F. crocatum. Fusarium crocatum can be distinguished from F. velutinum by the production of chlamydospores, which are lacking in F. crocatum. Moreover, colonies of F. crocatum on PDA exhibit a white to dirty white colour in contrast to the apricot, peach, rosy vinaceous and pale luteous colours of F. aurantii, and greyish rose, livid red to livid vinaceous of F. velutinum. Fusarium crocatum also represents a biological species within the FLSC. Fertile crosses were successfully achieved when the strains CBS 130184 isolated from B. vulgaris, BBA 65926 isolated from grass, and BBA 65674 isolated from herbaceous vines were crossed with each other. Additionally, strains BBA 65926 and CBS 130184 were identified as female-fertile. Ascospores produced by F. crocatum are similar in shape to those produced by F. cassiae and F. magnoliae-champaca (Perera et al. 2020), and less septate from those described for F. lateritium and F. stilboides (Booth 1971).

*Fusarium endophyticum* N. Suwannarach *et al.*, Phytotaxa 606: 47. 2023. Fig. 10.

Additional description and illustrations: See Suwannarach et al. (2023).

Emended description: Aerial conidiophores borne on substrate mycelium or laterally on hyphae, up to 150 µm tall, erect and simple, mostly reduced to single monophialides, and sometimes branched laterally, straight or flexuous, smooth- and thin-walled; aerial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical (5.4–)10.2–22.8(–27.8)  $\times$  3.4–5.5  $\mu m$  (av. 16.1  $\times$ 4.2 µm), smooth- and thin-walled; Aerial conidia curved to straight, basal cell obtuse to papillate, and foot-shaped, 1-5-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 22.2-27.0 × 3.5-5.4 μm (av. 24.6 × 5.0 μm); 2-septate conidia: 24.6–28.2 × 5.0–5.9 μm (av. 26.4 × 5.6 μm); 3-septate conidia: 32.0–33.0 × 4.2–5.2 μm; 4-septate conidia: 47.6 × 5.7 µm; 5-septate conidia: 38.2-54.0(-62.7) × 4.2–5.2 µm (av. 46.0 × 4.8 µm). Sporodochia pale to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical, 15.3-25.4(-28.9) × 3.5–4.7  $\mu$ m (av. 20.8 × 4.1  $\mu$ m), smooth- and thin-walled. Sporodochial conidia moderately dorsiventrally curved, tapering toward both ends, apical cell blunt to conical, basal cell papillate and poorly to well-developed, foot-shaped, 3-6-septate, hyaline, smoothand thick-walled; 3-septate conidia: 65.4 × 5.6 µm; 4-septate conidia: 42.2–61.7 × 5.3–5.5 µm; 5-septate conidia: (43.3–)51.0–76.5(–81.0) × 4.5–5.9(–6.6) µm (av. 63.8 × 5.3 µm); 6-septate conidia: (64.6–) 68.9-79.3(-83.2) × 3.9-5.5(-6.6) μm. Chlamydospores formed in the aerial mycelium and sporodochia, subglobose to globose, smooth- and thick-walled, 6.2-8.2 µm diam, solitary, in chains, in clusters in hyphae or conidia, and terminal in hyphae.

*Culture characteristics: Colonies* on PDA and OA growing in the dark reaching 26–30 mm diam in 3 d at 24 °C; On PDA surface white, pale luteous, with concentric rings of aerial mycelium; margin entire. Reverse white to pale straw. Odour absent. On OA surface dirty white to pale straw, with scarce aerial mycelium; margin entire. Odour absent. Reverse dirty white to straw.

*Materials examined*: **Brazil**, Jaguaré, Espírito Santo, from stem of *Coffea canephora*, 2023, *E.A. Pozza*, culture CML 4473. **Honduras**, Belize, from *Citrus aurantium*, unknown date, and *collector*, isol. *H.J. Fagan*, dep. C. Booth, culture CBS 319.73 = ATCC 24391 = FRC L-403 = IMI 155795 = NRRL 25482 = CPC 42975.

Notes: Fusarium endophyticum was recently described as a new species within the FLSC by Suwannarach *et al.* (2023). Originally isolated from the leaves of *Camellia sinensis* var. *assamica* in Thailand, and our study reports the presence of this species associated with coffee plants in Brazil, *Citrus aurantium* in Honduras, and berries in Jamaica. In the original description, *F. endophyticum* was noted to produce macroconidia only on aerial mycelium, with no production of sporodochia. However, in our study, strains identified as *F. endophyticum* produced macroconidia on both aerial mycelium and sporodochia. Conidia produced on aerial mycelium were up to 62.7 µm in length with five septa, whereas in the original description, they were up to 74.2 µm with three septa.

Fusarium cartwrightiae, recently described as a new phylogenetic species in the FLSC (Tan & Shivas 2023), was isolated from stem cankers of Ziziphus mauritiana in Australia, and it is closely related to F. endophyticum. In the original description of F. cartwrightiae, sequences of the type of F. endophyticum were not included in the phylogenetic analyses, and there is no morphological description for comparison purposes. The tef1 sequences of F. endophyticum (SDBR-CMU465) and F. cartwrightiae (BRIP 74113d = CBS 150776) differ by 9 bp positions. Sequences of tub2 and CaM from F. endophyticum are not available for comparison to determine the true phylogenetic relationship between these two species. The strain CML 4473 clusters with F. endophyticum (SDBR-CMU465) and F. cartwrightiae (BRIP 74113d = CBS 150776) strains in tef1 phylogenetic tree (Fig. S1). The tef1 sequence of CML 4473 differs by 9 positions from F. endophyticum (SDBR-CMU465) and by 5 positions from F. cartwrightiae (BRIP 74113d = CBS 150776). The rpb2 sequence (part A) of CML 4473 differs by 5 bp from F. endophyticum (SDBR-CMU465) and by 3 bp from F. cartwrightiae (BRIP 74113d = CBS 150776). The sequence of CML 4473 differs by 9 bp from F. cartwrightiae (BRIP 74113d = CBS 150776) for tub2, and by 4 bp in CaM. Based on these findings, we named this strain as F. endophyticum.

*Fusarium hanswilhelmii* M.M. Costa, Sand.-Den. & Crous, *nom. nov.* MycoBank MB 854711. Figs 11, 12.

Replaced synonym: Fusarium lateritium var. longum Wollenw., Z. Parasitenk. 3: 385. 1931. [MB#269057], non F. longum (Wallr.) Sacc., Syll. Fung. 4: 719. 1886 [MB#229791]

For synonyms see Crous *et al.* (2021), Index Fungorum and MycoBank.

*Etymology: "hanswilhelmii*" honouring Hans Wilhelm Wollenweber who described the variety.

*Typus*: **Honduras**, living leaf of *Citrus* sp. infested with scale insects, Jan. 1925, O.A. *Reinking* (**lectotype** of *Fusarium lateritium* var. *longum*, MBT 10021273, illustration f. 964 in Wollenweber HW (1930), Fusaria Autographice Delineata 3, designated here). **New Zealand**, Auckland, from fruit of *Citrus sinensis*, 17 Sep. 1976, coll. *J. Chignell*, isol. and dep. *W. Gerlach* (**epitype** of *Fusarium lateritium* var. *longum* CBS H-626 designated here MBT 10021274; culture ex-epitype CBS 633.76 = BBA 63665 = DSM 115136 = NRRL 25484).

Additional descriptions and illustrations: See Wollenweber (1931), Wollenweber & Reinking (1935), and Gerlach & Nirenberg (1982).



**Fig. 10.** *Fusarium endophyticum* (CBS 319.73). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–M.** Aerial conidiophores, conidiogenous cells and conidia. **N.** Aerial conidia. **O, P.** Chlamydospores. **Q–S.** Sporodochial conidiophores, conidiophores, conidiogenous cells and conidia. **Scale** bars: C, D = 100  $\mu$ m; E, F = 50  $\mu$ m; G, I–K, M–T = 10  $\mu$ m; H = 20  $\mu$ m; L = 5  $\mu$ m.



**Fig. 11.** *Fusarium hanswilhelmii nom. nov.* (ex-epitype culture CBS 633.76). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–O.** Aerial conidiophores, conidiogenous cells and conidia. **P, Q.** Chlamydospores. **R.** Aerial conidia. **S, T.** Sporodochial conidiophores, conidiogenous cells and conidia. **U.** Sporodochial conidia. Scale bars: C, D = 100 µm; E–H, L–P, S, T = 20 µm; I–K, Q, R, U = 10 µm.



Fig. 12. Fusarium hanswilhelmii nom. nov. Lectotype of F. lateritium var. longum as illustrated in protologue by Wollenweber (1930).

Emended description: Aerial conidiophores borne on substrate mycelium or laterally on hyphae, up to 207 µm tall, erect and simple, straight or flexuous, smooth- and thin-walled, mostly branched laterally, usually aggregated and sometimes reduced to single monophialides; conidiogenous cells monophialidic, subulate to subcylindrical, (15.0-)17.3-33.8(-36.0) × (2.0-)2.8-3.5(-4.0) µm (av. 27.4 × 3.3 µm), smooth- and thin-walled, often proliferating percurrently, with a very distinct collarette, swellings at the base of the conidiophore may occur, occasionally with an extremely inflated rhomboid terminal cell. Aerial conidia slightly curved, gradually tapering toward both ends, with a slightly hooked and pointed apical cell and a barely evident basal cell papillate to no foot-shaped, 1-6-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 34.0-40.0 × 3.0-4.5 µm (av. 37.5 × 3.5 µm); 2-septate conidia: 33.0-42.0 × 4.0-4.5 µm (av. 39.5 × 4.3 µm); 3-septate conidia: (23.5–)38.0–40.0 × 3.0–5.0 µm (av. 38.8 × 3.9); 4-septate conidia: (39.5-)45.0-57.5(-63.6) × 3.0-5.5(-6.0) µm (av. 48.3 × 4.1 µm); 5-septate conidia: (44.7–)60.0–66.5(–70.0) × 3.8-5.0 µm (av. 63.1 × 4.5 µm); 6-septate conidia: 77.0-77.5 × 4.8-5.5 µm. Sporodochia pale rosy, orange and sometimes pale yellow. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subulate, subcylindrical to cylindrical, (12.5-) 6.0-27.9(-32.3) × 3.0-4.5(-5.5) μm (av. 20.5 × 3.7 μm), smoothand thin-walled. Sporodochial conidia slightly curved to straight, gradually tapering toward both ends, with a slightly hooked and pointed apical cell, basal cell poorly to well-developed, foot-shaped, (3–)5–7(–10)-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 49.0-51.0 × 4.5-5.5 µm; 5-septate conidia: 57.4-66.7 × 5.0-6.0 µm; 6-septate conidia: (75.4-)80.0-93.4(-106.4) × 4.6-6.3 μm (av. 91.9 × 5.8 μm); 7-septate conidia: 86.0 × 97.3(-108.5) μm; 8-septate conidia: 104.3-114.0 × 5.5-6.0 μm (av. 109.2 × 5.7 µm); 9-septate conidia: 116.0–116.5 × 5.0–5.5 µm; 10-septate conidia: 105.0–105.5 × 5.5–6.5 µm. Chlamydospores subglobose to globose, smooth- and thick-walled, (5.5–)6.0–9.0(–10) µm diam, intercalary in hyphae or in chains.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 24–27 mm diam in 3 d at 24 °C; On PDA surface white to pale straw, abundant production of aerial mycelium; margin entire. Reverse white to pale straw. Odour absent. On OA surface dirty white to pale straw, with scarce aerial mycelium; margin entire. Reverse dirty white to straw. Odour absent.

*Notes*: The new name *Fusarium hanswilhelmii* is introduced here for the variety *Fusarium lateritium* var. *longum*. This variety was initially described by Wollenweber and typified using the strain 1839b, illustrated in Fus. autogr. delin. no. 964 in 1930. It was isolated from a citrus leaf infested with scale insects in Honduras, collected by Reinking in 1925. *Fusarium lateritium* var. *longum* was accepted as a distinct variety due to the longer and more septate conidia (Wollenweber 1931). This classification was also agreed upon by Wollenweber & Reinking (1935), Doidge (1938), and Gerlach & Nirenberg (1982).

Because the original type specimen is no longer available, a neotype was designated for *Fusarium lateritium* var. *longum* based on strain CBS 633.76 = BBA 63665 = DSM 115136 = NRRL 25484, and a specimen was deposited in the CBS herbarium under CBS H-626. However, according to Art. 9.13 (Shenzhen Code) a neotype designation is superseded if any of the original materials are found to exist. An illustration referenced in the protologue of *F. lateritium* var. *longum*, Wollenweber (1930), is designated here as the lectotype (Fig. 12). Therefore, CBS 633.76 = BBA 63665 = DSM 115136 = NRRL 25484, isolated from a citrus fruit in New Zealand and considered as a representative strain of *F. lateritium* var. *longum* by Gerlach & Nirenberg (1982) is chosen as epitype.

![](_page_26_Picture_8.jpeg)

Presently, this species has been isolated only from citrus. Other strains previously designated as Fusarium lateritium var. longum belong to other species within the FLSC, including F. coffeibaccae and F. crocatum (Tables 1, S1). Phylogenetically, F. hanswilhelmii is closely related to F. malawiense and F. massalimae (Fig. 1). Furthermore, F. hanswilhelmii differs from F. massalimae and from F. malawiense in tef1 sequences (33 bp and 23 bp differences, respectively). Fusarium hanswilhelmii differs from F. massalimae in 4 bp differences for rpb2 sequences (part A only), and 12 bp differences comparing to F. malawiense (part A and B). No CaM sequence is available for F. massalimae strains for comparison. The *tub2* sequence of the type strain of *F. massalimae* (URM 8239) were generated using a different set of primers from those used in our study. Its tub2 sequence (272 bp) is shorter than those of F. hanswilhelmii (546 bp) and F. malawiense (592 bp) and only partially overlaps by 227 and 272 alignment positions, respectively. For the overlapping part, F. massalimae differs by one position from F. hanswilhelmii (CBS 633.76) and by two positions from F. malawiense (CBS 737.74). Lastly, since the epithet longum is already in use for a different taxon (F. longum (Wallr.) Sacc.), therefore a new name, F. hanswilhelmii, is introduced.

*Fusarium lateritium* Nees, Syst. Pilze: 31. 1817. Figs 13, 14. *Synonyms: Selenosporium lateritium* (Nees) Desm., Fl. Cryptog. Flandres 2: 99. 1867.

Fusarium microsporum Schltdl., Fl. Berol. 2: 139. 1824.

Fusarium fructigenum Fr., Syst. Mycol. 3: 471. 1832.

*Fusarium lateritium* var. *fructigenum* (Fr.) Wollenw., Fusaria Autogr. Delin. 3: 959. 1930.

Sphaeria baccata Wallroth, Fl. Crypt. Germ. 2: 838. 1833.

*Gibberella baccata* (Wallr.) Fuckel, Jahrb. Nassauischen Vereins Naturk. 23–24: 167. 1870.

*Gibberella pulicaris* subsp. *baccata* (Wallr.) Sacc., Michelia 1(3): 317. 1878.

Gibberella baccata (Wallr.) Sacc., Syll. Fung. 2: 553. 1883.

Selenosporium urticarum Corda (as 'urticearum'), Icon. Fung. 2: 7. 1838.

Fusarium urticarum (Corda) Sacc., Syll. Fung. 4: 698. 1886.

*Gloeosporium berkeleyi* Mont., Ann. Sci. Nat., Bot. 12: 296. 1849. *Fusarium berkeleyi* (Mont.) Berk. & Broome, N. Amer. Fung.: 108. 1875.

Botryosphaeria moricola Ces. & De Not., Hedwigia 4: 27. 1865.

Gibberella moricola (Ces. & De Not.) Sacc., Syll. Fung. 2: 553. 1883.

*Gibbera euonymi* Fuckel, Jahrb. Nassauischen Vereins Naturk. 23–24: 167. 1870.

Gibberella euonymi (Fuckel) Sacc., Michelia 1: 318. 1878.

Hendersonia euonymi (Fuckel) Sacc., Syll. Fung. 2: 556. 1883.

For additional synonyms see Crous *et al.* (2021), Index Fungorum and MycoBank.

*Typus*: **Germany**, *Fagus*, 1817, G.C.D. Nees von Esenbeck [**lectotype** of *F. lateritium*, G.C.D. Nees von Esenbeck, in System der Pilze und Schwaemme: 31, tab. 2, fig. 26, designated by Crous *et al.* (2021, MBT 10000710)]. **USA**, Louisiana, Pineville, Elm tree with canker and branch dieback, before 1 Jul. 1973, collector unknown, dep. P.E. Nelson (**epitype** of *F. lateritium*, CBS-H-25441 designated here, MBT 10021275, culture ex-epitype NRRL 13622 = NRRL A-26433 = ATCC 60188 = CBS 151946 = FRC L-55).

Additional descriptions and illustrations: See Wollenweber (1931), Wollenweber & Reinking (1935), Raillo (1950), Bilaĭ (1955), and Gerlach & Nirenberg (1982).

Aerial conidiophores at first arising as single lateral phialides on aerial mycelium, up to 162 µm tall, sometimes reduced to a single phialide borne laterally on aerial hyphae, smooth- and thin-walled; conidiogenous cells monophialidic, often percurrently proliferating, but polyphialides occasionally observed, subulate to subcylindrical, 10.2–29.3(–38.7) × (2.3–)3.0–4.0 µm (av. 22.2 × 3.5 µm), smoothand thin-walled. Aerial conidia of two types: macroconidia straight to slightly curved, basal cell papillate to poorly developed, footshaped, 1-5-septate, hyaline, smooth- and thin-walled; 1-septate conidia: (16.5–)21.7–22.7 × 3.2–3.6(–5.0) µm (av. 22.2 × 3.4 µm); 2-septate conidia: 21.5–23.5 × 4.0–4.9 µm (av. 22.4 × 4.6 µm); 3-septate conidia: (22.3–)27.5–48.5 × 3.7–5.5 µm (av. 38.8 × 4.7 μm); 4-septate conidia: 44.3 × 4.7 μm; 5-septate conidia: 48.0 × 5.3 µm; microconidia are rarely observed, fusiform to obovoid, straight to slightly curved, often with a flattened base, 0-2-septate, hyaline, smooth- and thin-walled; 0-septate conidia: (9.8-)13.6-15.3 × 3.8-4.2 μm (av. 14.5 × 4.0 μm); 1-septate conidia: (10.9–)13.9–19.9 × (3.0–)4.0–5.2 μm (av. 17.6 × 4.5 μm); 2-septate conidia: 22.6 × 5.0 µm. Sporodochia pale to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subulate to subcylindrical, (9.0–)12.0–16.5(–21.0) × 3.0–4.5(–5.5) µm (av. 14.2 × 3.9 µm), smooth- and thin-walled. Sporodochial conidia straight to falcate, apical cell often equal to adjacent cell, curved to hooked, basal cell poorly to well-developed, foot-shaped, 3-6(-9)-septate, hyaline, smooth- and thick-walled; 3-septate conidia: (36.9-)42.9-44.0(-50.0) × 5.0-5.5 µm (av. 43.5 × 5.3 µm); 4-septate conidia: 51.4 × 4.8 µm; 5-septate conidia: (48.8–)61.4–76.4 × 4.6–6.5 µm (av. 68.4 × 5.6 µm); 6-septate conidia: (70.0–)75.3–78.9(–82.0) × 5.0-6.5 µm (av. 76.0 × 5.8 µm); 7-septate conidia: 83.0-83.4 × 6.2-6.5 µm; 8-septate conidia: 80.9 × 6.4 µm; Chlamydospores globose to subglobose, smooth- and thick-walled, 6.6-9.8(-12.0) µm diam, intercalary in hyphae, solitary or in chains, intercalary in hyphae.

*Culture characteristics: Colonies* on PDA and OA growing in the dark reaching 26–28 mm diam in 3 d at 24 °C. On PDA surface reaching from salmon, saffron to rosy buff; margin entire. Odour absent. Reverse white, pale straw to salmon. On OA surface dirty white to pale straw, with scarce aerial mycelium; margin entire. Reverse dirty white, pale tuteous to straw. Odour absent.

Additional materials examined: China, Henan, from twig, unknown date, coll. W.Y. Zhuang & Y. Nong, isol. Y. Nong, culture CBS 127477 = HMAS 86477.

Notes: Fusarium lateritium was originally described by Nees in 1817, isolated from a twig of Fagus. Later, it was placed within the Section Lateritium by Wollenweber (1917), along with other Fusarium species and numerous varieties and forms based on similarity of the micro- and macroconidial morphology and dimensions (Wollenweber 1931, Wollenweber & Reinking 1935, Booth 1971, Gerlach & Nirenberg 1982). Since no type material of F. lateritium could be located, and in order to fix the use of the name, a lectotype was designated by Crous et al. (2021) from the original description of the species, which is reproduced here (Fig. 14). Furthermore, an epitype is chosen for F. lateritium, based on the strain NRRL 13622 = NRRL A-26433 = ATCC 60188 = CBS 151946 = FRC L-55. This strain presents morphological features similar to those reported for F. lateritium by Gerlach & Nirenberg (1982), Wollenweber (1931), and Wollenweber & Reinking (1935). However, the macroconidia produced in sporodochia are larger and more septate than those reported by Booth (1971) and Gerlach & Nirenberg (1982).

![](_page_28_Picture_1.jpeg)

**Fig. 13.** *Fusarium lateritium* (NRRL 13622). **A**, **B**. Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C–E**. Sporodochia formed on the surface of carnation leaves and agar surface. **F–N**, **Q**. Aerial conidiophores, conidiogenous cells and conidia. **O**. Chlamydospores. **P**. Aerial conidia. **R–U**. Sporodochial conidiophores, conidiogenous cells and conidia. **V**. Sporodochial conidia. Scale bars:  $C = 200 \mu m$ ;  $D = 100 \mu m$ ;  $E = 40 \mu m$ ;  $F, G = 50 \mu m$ ;  $H = 30 \mu m$ ; I, K, M–P, R, U, V = 10  $\mu m$ ; J = 5  $\mu m$ ; L = 2  $\mu m$ ; Q, S, T = 20  $\mu m$ .

![](_page_28_Picture_3.jpeg)

![](_page_29_Picture_1.jpeg)

Fig. 14. Lectotype of Fusarium lateritium as illustrate and described in Nees (1817). A. On a twig of beech in natural size. B. Detached, enlarged. +. Vertical section mounted on water.

This difference may be attributed to different culture cultivation conditions used for the description. The strain NRRL 13622 = NRRL A-26433 = ATCC 60188 = CBS 151946 = FRC L-55 also clusters in a phylogenetic clade that has consistently been associated with the species *F. lateritium* in phylogenetic studies involving the FLSC (Geiser *et al.* 2005, O'Donnell *et al.* 2013, Crous *et al.* 2021, Geiser *et al.* 2021). *Fusarium lateritium* clusters alongside representative strains of the species *F. stilboides* and *F. sarcochroum*. Thus, we maintain the contemporary interpretation of this species.

*Fusarium malawiense* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854712. Fig. 15.

*Etymology*: In reference to the country where it was collected, Malawi.

*Typus*: **Malawi**, from *Citrus* sp., unknown date and *collector*, isol. Armiger (**holotype** CBS H-25374 designated here, culture ex-type CBS 737.74 = ATCC 24375 = IMI 158154 = NRRL 20533 = CPC 42954).

Aerial conidiophores borne on substrate mycelium or laterally on hyphae, up to 207 µm tall, erect and simple, straight or flexuous, mostly branched laterally, smooth- and thin-walled; aerial conidiogenous cells mostly monophialidic, but polyphialides occasionally observed, subcylindrical to subulate, (12.0-)17.0-33.5(-39.0) × (2.0-)2.3-4.5 µm (av. 25.7 × 3.5 µm), smooth- and thin-walled, often proliferating percurrently, with a very distinct collarette, swellings at the base of the conidiophore may occur. Aerial conidia slightly curved to falcate, sometimes straight cylindrical, gradually tapering toward both ends, with a slightly hooked and pointed apical cell and a barely evident basal cell, 1-7-septate, hyaline, smooth- and thin-walled; 1-septate conidia: (16.5–)17.0–17.5 × 4.0–4.5 µm (av. 17.2 × 4.3 µm); 2-septate conidia: 33.4-35.0 × 4.0-6.0 µm (av. 34.0 × 4.8 µm); 3-septate conidia: (34.5-)38.4-66.0(-76.3) × 4.0-5.3(-6.0 µm) (av. 49.8 × 4.8 µm); 4-septate conidia: 45.4-56.6 × 4.4-5.3 µm (av. 50.3 × 4.8 μm); 5-septate conidia: (64.6–)69.0–77.6(–86.0) × 4.5–5.7 μm (av. 74.8 × 5.2 µm); 6-septate conidia: (70.0–)71.0–87.0(–90.0) × 5.0-6.4 µm (av. 78.4 × 5.8 µm); 7-septate conidia: 96.0-97.5 × 5.5-5.9 µm (av. 96.8 × 5.7 µm). Sporodochia pale yellow to dark orange. Sporodochial conidiophores densely aggregated, irregularly and verticillate branched; *sporodochial conidiogenous cells* monophialidic, subcylindrical to subulate, (11.0–)17.2–22.5 × 3.8–5.0(–5.5) µm (av. 18.4 × 4.2 µm), smooth- and thin-walled. *Sporodochial conidia* slightly curved to straight, gradually tapering toward both ends, with a slightly hooked and pointed apical cell, basal cell poorly to well-developed, foot-shaped, 4–7-septate, hyaline, smooth- and thick-walled; 4-septate conidia: 67.0–67.5 × 5.0–5.5 µm; 5-septate conidia: 75.5–80.0 × 5.5–6.7 µm (av. 77.4 × 5.7 µm); 6-septate conidia: 71.7–90.7 × 4.5–6.6 µm (av. 79.6 × 5.7 µm); 7-septate conidia: 81.0–87.6(–94.7) × 5.0–6.5 µm (av. 83.1 × 5.7 µm). *Chlamydospores* subglobose to globose, smooth- to finely verruculose, thick-walled, 4.8–9.7(–10.2) µm diam, solitary or intercalary in hyphae or in chains.

*Culture characteristics*: Colonies on PDA growing in the dark reaching 30–33 mm diam in 3 d at 24 °C; surface buff to cream, with irregularly distributed white aerial mycelium, more concentrated in the centre of the colony, agar pigmentation ranges from salmon, buff to rosy buff; margin entire. Reverse pale straw in the centre, rosy vinaceous on the margins; margin entire to filiform. Odour absent. On OA growing in the dark reaching 23–25 mm diam in 3 d at 24 °C; surface dirty white to buff, production of aerial mycelium more concentrated towards the margins; margin entire. Odour absent. Reverse dirty white to buff.

Notes: Fusarium malawiense is introduced as a new species of the FLSC based on a strain obtained from citrus in Malawi, exhibiting symptoms of bark disease. This species is phylogenetically close related to *F. hanswilhelmii* and *F. massalimae*. It differs morphologically due to the production of polyphialides, which are absent in *F. hanswilhelmii* strains. *Fusarium malawiense* can be distinguished from *F. massalimae* by the slow growth rate, and orange colour produced by *F. massalimae* strains on PDA (Cavalcanti *et al.* 2020). Furthermore, *F. malawiense* shows clear differences from *F. hanswilhelmii* in *tef1* sequences (23 bp differences) and *rpb2* sequences (12 bp differences). *Fusarium malawiense* also differs from *F. massalimae* in *tef1* sequences (28 bp differences). For more information, see notes under *Fusarium hanswilhelmii*.

![](_page_30_Picture_1.jpeg)

Fig. 15. *Fusarium malawiense sp. nov.* (ex-type culture CBS 737.74). A, B. Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. C, D. Sporodochia formed on the surface of carnation leaves. E–J. Aerial conidiophores, conidiogenous cells and conidia. K–M. Chlamydospores. N, O. Aerial conidia. P. Sporodochial conidiophores, conidiogenous cells and conidia. Q. Sporodochial conidia. Scale bars: C, D = 100  $\mu$ m; E–G = 20  $\mu$ m; H, I, K, N–Q = 10  $\mu$ m; J, L, M = 5  $\mu$ m.

![](_page_30_Picture_3.jpeg)

*Fusarium microcyclum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854713. Fig. 16.

*Etymology: "microcyclum*" in reference to the microcyclic conidiation.

*Typus*: **Canada**, Manitoba, Winnipeg, from *Coffea excelsa*, before 1971, dep. *W.L. Gordon* (**holotype** CBS H-25397 designated here, culture extype IMI 128389 = CPC 46696 = CBS 137.73 = ATCC 24396).

Aerial conidiophores borne laterally on hyphae, up to 81 µm tall, erect and simple and straight, most of the time reduced to single phialides, smooth- and thin-walled; conidiogenous cells monophialidic, and less common polyphialidic, cylindrical to subcylindrical, 2.0-6.6(-10.6) × 1.6-4.3 µm (av. 4.6 × 2.7 µm), smooth- and thin-walled. Aerial conidia clustering in false heads at tip of short phialides, or direct from other conidia, straight to curved, apical cell curved to blunt, basal cell papillate to poorlydeveloped, foot-shaped, (0-)1-3-septate, hyaline, smooth- and thin-walled; 0-septate conidia: 12.8–17.8  $\times$  2.6–4.4  $\mu m$  (av. 15.0  $\times$ 3.5 µm); 1-septate conidia: 19.4–27.4 × 2.6–4.3 µm (av. 20.7 × 3.4 μm); 2-septate conidia: 27.8–31.2 × 3.9–4.9 μm (av. 29.0 × 4.5 μm); 3-septate conidia: 28.4-42.7 × 3.5-4.8(-5.4) µm (av. 36.4 × 4.1 µm). Sporodochia pale rosy to orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subcylindrical to subulate, (4.8–)7.5–21.5 × 2.5–4.5 µm (av. 13.8 × 3.8 µm), smoothand thin-walled. Sporodochial conidia moderately dorsiventrally curved to nearly straight, tapering toward both ends, apical cell curved to hooked, basal cell papillate or poorly to well-developed, foot-shaped, and mostly slightly extended, (1–)3–7-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 51.0-55.8 × 4.3-4.5 µm (av. 53.4 × 4.4 µm); 4-septate conidia: 56.9-65.8(-70.3) × 4.4-5.0 µm (av. 62.3 × 4.7 µm); 5-septate conidia: (60.0–)62.2–87.0 × 3.9–5.5 µm (av. 72.2 × 4.5 µm); 6-septate conidia: (67.5–)82.9–97.4 × 4.6–5.4 µm (av. 88.0 × 5.1 µm). Chlamydospores not observed.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 16–20 mm diam in 3 d at 24 °C. On PDA surface white, rosy white to buff, flat and irregular in shape, velvety to felty, with short, and more concentrated aerial mycelium in the centre; margin highly irregular. Odour absent. Reverse white to dirty white. On OA dirty white to rosy buff; margin entire. Odour absent. Reverse dirty white to rosy buff.

Additional material examined: French Equatorial Africa, from Coffea excelsa, unknown date, *J. Kranz*, culture IMI 392677 = CPC 44278 = ATCC 36325 = FUS005 = DSM 62456.

*Notes: Fusarium microcyclum* is distinct from other species in the FLSC. The primary morphological characteristic of *F. microcyclum* is the production of aerial conidiophores reduced to conidiogenous pegs on hyphae. The macroconidia produced in sporodochia are among the largest within the complex, reaching up to 97.4 µm in length. Another characteristic of the species is the microcyclic conidiation, the direct production of conidia on other macroconidia. *Fusarium microcyclum* also exhibits a slow growth rate on PDA and OA at 24 °C compared to other species in the FLSC. Based on the strain history, both IMI strains included here likely represent the same strain, with the additional strain being deposited at IMI by ATCC, while the ex-type strain was deposited at IMI by W.L. Gordon from Canada. Based on the molecular analyses, we can confirm that these two strains are indeed the same.

*Fusarium oliniae* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854714. Fig. 17.

*Etymology*: "oliniae" referring to the host genus from which it was isolated.

*Typus*: **South Africa**, Mpumalanga Province, Mbombela, from *Olinia* sp., Nov. 2019, *P.W. Crous* (**holotype** CBS H-25372 designated here, culture ex-type CBS 152069 = CPC 38826).

Sporulation abundant from conidiophores on aerial mycelium floccose and powdery. Aerial conidiophores abundant, borne on substrate or laterally on aerial hyphae, up to 183 µm tall, densely aggregated and branched, straight or flexuous, smoothand thin-walled sometimes reduced to a single phialide; Aerial conidiogenous cells monophialidic, subulate, subcylindrical to cylindrical, 11.3-51.9 × 3.3-4.3 µm (av. 31.6 × 3.8 µm), smoothand thin-walled. Aerial conidia curved, apical cell curved, pointed and blunt, basal cell obtuse, papillate, non-foot-shaped and sometimes poorly-developed, foot-shaped, 1-4-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 19.9-24.4(-30.1) × 3.9-5.3 µm (av. 21.8 × 4.6 µm); 2-septate conidia: 25.2 × 4.7 µm; 3-septate conidia: 33.1-54.0(-58.9) × 4.1-5.7 µm (av. 46.6 × 5.0 μm); 4-septate conidia: 54.6 × 4.8 μm. Sporodochia pale rosy to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical, 20.6-26.5(-32.0) × 3.0-3.9 µm (av. 24.3 × 3.5 µm), smooth- and thinwalled. Sporodochial conidia, slightly curved, gradually tapering toward both ends, with a slightly hooked and pointed apical cell; basal cell poorly to well-developed, foot-shaped, 3-6(-10)-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 71.1 × 5.9 μm; 5-septate conidia: 67.0–83.1 × 4.7–6.9 μm (av. 75.0 × 5.6 μm); 6-septate conidia: 82.5 × 5.5 µm; 10-septate conidia: 111.2 × 8.2 µm. Chlamydospores not observed.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 34–37 mm diam in 3 d at 24 °C. On PDA surface rosy vinaceous, sienna to red; margin entire. Odour absent. Reverse pale straw to red. On OA surface dirty white to pale straw, with scarce aerial mycelium; margin entire. Odour absent. Reverse dirty white to pale straw.

*Notes: Fusarium oliniae* is a phylogenetic sister species to *F. coffeibaccae*. The species clade is well-supported in the phylogenetic analyses (IQ-TREE-BS = 100 %; RAxML-BS= 100 %; BI-PP = 1). *Fusarium oliniae* differentiates itself from *F. coffeibaccae* by lacking chlamydospores and the production of macroconidia on aerial mycelium and sporodochia that are more curved than those produced by *F. coffeibaccae*.

*Fusarium rufum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854715. Fig. 18.

*Etymology*: "*rufum*" named after the red pigment produced on PDA.

*Typus*: **India**, from *Parkia*, unknown date, *S.R. Singh* (**holotype** CBS H-25396 designated here, culture ex-type IMI 300505 = CPC 43032).

Aerial conidiophores borne laterally on hyphae, up to 280 µm tall, erect and simple, straight or flexuous, most of the time reduced to single phialides, sometimes branched laterally, smooth- and thin-walled; *aerial conidiogenous cells* mono- and polyphialidic,

![](_page_32_Picture_1.jpeg)

**Fig. 16.** *Fusarium microcyclum sp. nov.* (ex-type culture IMI 128389). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C–E.** Sporodochia formed on the surface of carnation leaves and agar surface. **F–P.** Aerial conidiophores, conidiogenous cells and conidia. **Q.** Aerial conidia. **R–T.** Aerial conidiophores, conidiogenous cells and conidia. **U, V.** Sporodochial conidiophores and conidiogenous cells. **W.** Sporodochial conidia. Scale bars: C–E = 50 µm; F, O–T, W = 10 µm; G–N = 5 µm; U, V = 20 µm.

![](_page_33_Picture_1.jpeg)

**Fig. 17.** *Fusarium oliniae sp. nov.* (ex-type culture CBS 152069). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–J.** Aerial conidiophores, conidiogenous cells and conidia. **K.** Aerial conidia. **L, M.** Sporodochial conidia. Scale bars: C, D = 200 µm, E = 100 µm; F, H–K, N = 10 µm; G = 5 µm; L, M = 20 µm.

![](_page_34_Picture_1.jpeg)

**Fig. 18**. *Fusarium rufum sp. nov.* (ex-type culture IMI 300505). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–M.** Aerial conidiophores, conidiogenous cells and conidia. **N.** Aerial conidia. **O–Q.** Sporodochial conidiophores and conidiogenous cells. **R.** Sporodochial conidia. Scale bars: C, D = 200 µm; E–N, R = 10 µm; O–Q = 20 µm.

ampulliform, subulate to subcylindrical (4.0-)8.7-15.4(-28.4) × 2.0-3.8 µm (av. 12.2 × 2.8 µm), smooth- and thin-walled. Aerial conidia clustering in false heads at tip of mono- or polyphialides, 1-3(-4)-septate, hyaline, smooth- and thin-walled, straight to curved, basal cell papillate to poorly-developed, foot-shaped; 1-septate conidia: 14.7-24.6(-28.9) × 3.5-4.3 µm (av. 19.4 × 3.9 μm); 2-septate conidia: 23.3-25.7(-27.5) × 4.2-5.4 μm (av. 23.9 × 4.8 µm); 3-septate conidia: (23.7–)27.2–42.9(–52.6) × 4.3–5.6(– 6.0) μm (av. 33.8 × 4.8 μm); 4-septate conidia: 45.4 × 4.7 μm. Sporodochia pale rosy to orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subcylindrical to subulate, (9.6–)14.3–19.5 × 3.0–4.0 µm (av. 16.8 × 3.5 µm), smooth- and thin-walled. Sporodochial conidia falcate, narrowing gently toward base, apical cell curved to blunt, basal cell distinctly notched, poorly to well-developed, foot-shaped, 3-5(-10)-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 29.0-46.8 × 4.5-5.8 µm (av. 37.6 × 5.0 µm); 4-septate conidia: 43.0-57.2 × 4.7-6.3 μm (av. 51.3 × 5.3 μm); 5-septate conidia: 48.0-74.8(-77.5) × 4.5–6.8 μm (av. 59.7 × 5.5 μm); 6-septate conidia: 68.5 × 6.2 μm; 7-septate conidia 58.5–75.9 × 4.9–7.0 μm (av. 70 × 5.6 μm); 8-septate conidia: 90.3 × 4.5 µm; 10-septate conidia: 83.2 × 5.9 µm. Chlamydospores not observed.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 27–30 mm diam in 3 d at 24 °C. On PDA surface straw, peach in the centre, sienna, saffron, orange to red towards the margin, flat, with white aerial mycelium arranged in rings, producing a red pigment; margin entire. Odour absent. Reverse pale straw to red. On OA surface pale luteous to luteous, commonly with aerial mycelium arranged in circadian rings; margin entire. Odour absent. Reverse pale luteous and luteous.

Additional material examined: India, Citrus medica var. acida fruit, unknown date, *N.I. Singh*, culture IMI 294142 = CPC 42977.

*Notes: Fusarium rufum* is a distinct phylogenetic species in the FLSC, closely related to *F. coffeibaccae* and *F. oliniae*. It can be morphologically distinguished from *F. oliniae* by the production of a red pigment on PDA with concentric rings of white aerial mycelium. This characteristic is also observed in *F. coffeibaccae*. However, *F. coffeibaccae* produces mesoconidia on aerial mycelium, lacking in *F. rufum*. Additionally, sporodochial conidia produced by *F. rufum* are more curved and have more evident basal cell compared to strains of *F. coffeibaccae*.

*Fusarium sarcochroum* (Desm.) Sacc., Michelia 1: 534. 1879. Fig. 19.

Basionym: Selenosporium sarcochroum Desm., Ann. Sci. Nat., Bot., sér. 3, 14: 112. 1850.

Synonyms: Fusarium diplosporum Cooke & Ellis, Grevillea 7: 38. 1878.

*Fusarium desciscens* Oudem., Ned. Kruidk. Arch., sér. 2, 5: 515. 1889.

*Fusarium robiniae* Pass., Atti Reale Accad. Lincei, Rendiconti Cl. Sci. Fis., sér. 4, 7: 51. 1891.

*Fusarium sarcochroum* var. *robiniae* (Pass.) Wollenw., Z. Parasitenk. (Berlin) 3: 388. 1931.

*Fusarium sarcochroum f. polygalae-myrtifoliae* Henn., Verh. Bot. Vereins Prov. Brandenburg 40: 174. 1898 [1899].

*Fusarium sarcochroum* var. *casei* Loubière, Rech. Mucédinées: 53. 1924.

*Gibberella pseudopulicaris* Wollenw., Z. Parasitenk. (Berlin) 3: 387. 1931.

*Typus*: **Switzerland**, *Viscum album*, isol. 1977, isol. W. Gerlach [**neotype** of *Selenosporium sarcochroum* CBS 745.79 preserved as metabolically inactive culture, designated by Crous *et al.* (2021; MBT 10000741), culture ex-neotype BBA 63714 = CBS 745.79 = NRRL 20472].

*Descriptions and illustrations*: See Wollenweber (1931), Wollenweber & Reinking (1935), Raillo (1950), Bilaĭ (1955), Gerlach & Nirenberg (1982).

*Notes: Fusarium sarcochroum* was first described as *Selenosporium* sarcochroum, and later transferred to the genus *Fusarium* by Saccardo in 1879. It was later accepted as a distinct species by Wollenweber (1916, 1935, 1931). Since the original type material for *F. sarcochroum* could not be found, the strain BBA 63714 = CBS 745.79 = NRRL 20472, which was isolated from *Viscum album*, and considered as a representative strain of *F. sarcochroum*, was designated as neotype by Crous *et al.* (2021). The morphological characters for this strain are shown in Fig. 19.

*Fusarium stilboides* Wollenw., Fusaria Autogr. Delin. 2: 615. 1924. Figs 20, 21.

Synonyms: Fusarium lateritium var. stilboides (Wollenw.) Bilaĭ, Fusarii (Biologija i sistematika): 266. 1955. Nom. inval., Art. 41.5. Fusarium lateritium var. stilboides (Wollenw.) Bilaĭ, Mikrobiol.

Zhurn. 49: 6. 1987.

*Fusarium stilboides* var. *minus* (Wollenw.) Wollenw., Z. Parasitenk. (Berlin) 3: 333. 1931.

*Fusarium stilboides* 'f. 1' Raillo, Fungi of the Genus Fusarium: 271. 1950.

*Gibberella stilboides* W.L. Gordon ex C. Booth, The Genus Fusarium: 119. 1971.

*Typus*: **Cook Islands**, *Citrus* sp., isol. Sep. 1978, isol. G.F. Laundon [**epitype** of *F. stilboides* CBS 746.79 preserved as metabolically inactive culture, designated by Crous *et al.* (2021; MBT 10000748), culture ex-epitype BBA 63887 = CBS 746.79 = ICMP10624 = NRRL 25485]. **Philippines**, Los Baños, living twigs of *Citrus* sp., invaded by coccids, 1917, *O.A. Reinking* [**lectotype** of *Fusarium stilboides*, an illustration of the fungus from living twig of *Citrus* sp., invaded by coccids, 1917, *O.A. Reinking*, in Fusaria Autographice Delineata 2: 615, designated by Crous *et al.* (2021; MBT 10000747)].

Additional descriptions and illustrations: See Wollenweber (1924, 1930), Wollenweber & Reinking (1935), Doidge (1938), Raillo (1950), Booth (1971), Gerlach & Nirenberg (1982).

*Emended description: Aerial conidiophores* abundant on floccose and powdery aerial mycelium, up to 126 µm tall, erect on substrate mycelium, at first arising as single lateral phialides in the aerial mycelium, branching later, irregularly and verticillately, and sometimes reduced to a single phialide, smooth- and thin-walled; *Aerial conidiogenous cells* mono- and polyphialidic, subulate to subcylindrical, (10.6–)13.0–35.0(–38.5) × (2.5–)3.0–5.2 µm (av. 22.0 × 3.8 µm), smooth- and thin-walled. *Aerial conidia* of two types clustering in false heads at tip of mono- or polyphialides: *microconidia* fusiform to oval, 0–3-septate, hyaline, smooth- and thin-walled; 0-septate conidia: 11.0 × 5.5 µm; 1-septate conidia: 10.5–19.0(–22.9) × 3.8–5.8(–6.3) µm (av. 14.2 × 4.7 µm); 2-septate conidia: 19.2 × 5.4 µm; 3-septate conidia: 25.3–27.2 × 4.0–4.3 µm; *macroconidia* falcate, basal cell papillate to poorly-developed,

![](_page_36_Picture_1.jpeg)

Fig. 19. Fusarium sarcochroum (CBS 745.79). A, B. Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. C–E. Sporodochia formed on the surface of carnation leaves and agar surface. F–L. Aerial conidiophores, conidiogenous cells and conidia. M–P. Chlamydospores. Q. Aerial conidia. R, S. Sporodochial conidiophores, conidiogenous cells and conidia. T. Sporodochial conidia. Scale bars: C, D = 100  $\mu$ m; E–G, R, S = 20  $\mu$ m; H, J–Q, T = 10  $\mu$ m; I = 5  $\mu$ m.

![](_page_37_Picture_1.jpeg)

**Fig. 20.** *Fusarium stilboides* (CBS 746.79). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–H, J–M, Q–S**. Aerial conidiophores, conidiogenous cells and conidia. **I, N.** Aerial conidia. **O, P.** Chlamydospores. **T, U.** Sporodochial conidiophores, conidiogenous cells and conidia. Scale bars: C–E = 100 µm; F–J, L–P, T–V = 10 µm; K = 5 µm; Q–S = 20 µm.

![](_page_38_Figure_1.jpeg)

Fig. 21. Lectotype of Fusarium stilboides as illustrated in protologue by Wollenweber (1924).

foot-shaped, 1-6-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 15.7–19.2 × 4.5–5.5 μm (av. 17.5 × 5.2 μm); 2-septate conidia: 18.9-23.2(-35.5) × 4.5-5.8 µm (av. 21.5 × 5.0 μm); 3-septate conidia: (20.3–)26.0–51.5 × 4.3–6.0 μm (av. 38.0 × 5.1 µm); 4-septate conidia: (40.2–)45.0–65.6 × 4.5–5.6 µm (av. 55.8 × 5.1 μm); 5-septate conidia: 43.5–66.0(–77.5) × 4.5–6.0 μm (av. 58.5 × 5.1 μm); 6-septate conidia: 32.9-57.3 × 4.2-4.8 μm (av. 45.0 × 4.5 µm). Sporodochia bright orange or sometimes pale yellow. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical, 7.6-14.9(-17.6) × 3.0–4.7 µm (av. 10.5 × 3.9 µm), smooth- and thin-walled, conidiogenous loci lacking periclinal thickening or collarettes. Sporodochial conidia slightly curved, gradually tapering toward both ends, with a blunt and pointed apical cell, basal cell poorly to well-developed, foot-shaped, 3-5-septate, hyaline, smooth- and thick-walled; 3-septate conidia: 40.3–52.6 × 4.3–5.5 µm (av. 46.0 × 4.8 µm); 4-septate conidia: 48.0–52.6 × 5.0–6.5 µm (av. 50.5 × 5.8 μm); 5-septate conidia: 62.0 × 4.4 μm. Chlamydospores globose to subglobose, smooth- and thick-walled, 7.9-11.2 µm diam, intercalary in hyphae or conidia, in pairs or chains.

*Culture characteristics*: *Colonies* on PDA and OA growing in the dark reaching 20–32 mm diam in 3 d at 24 °C; surface white, pale luteous, flesh to salmon; margin entire. Odour absent. Reverse white, dirty white to pale straw.

Additional materials examined: China, Hong Kong, Lamma Island, from stem of *Brucea javanica*, 3 Mar. 2000, *K.D. Hyde*, culture CBS 115043 = HKUCC 6063. Cuba, Havana, unknown host, before 1991, *R.F. Castañeda-Ruiz*, culture BBA 65608 = CPC 44981 = DSM 115148.

![](_page_38_Picture_6.jpeg)

Notes: Fusarium stilboides was introduced with its synonyms, variety minus and majus. This species was considered synonymous with F. lateritium by several authors (Snyder & Hansen 1945, Bilaĭ 1955, Nelson et al. 1983). In 1982, Gerlach & Nirenberg regarded F. stilboides var. stilboides and F. lateritium var. stilboides as synonyms. Fusarium stilboides is a well-defined species in the FLSC. Since no type material could be located, a lectotype was designated by Crous et al. (2021) using a drawing from the original description of the species, which is reproduced here (Fig. 21). The species was also epitypified based on the strain BBA 63887 = CBS 746.79 = NRRL 25485 obtained from citrus fruit in Cook Islands. Here, we provide an emended morphological description for F. stilboides based on the strain CBS 746.79. When compared to the lectotype of F. stilboides, the conidia of strain CBS 746.79 match the shape presented in the lectotype. However, macroconidia with up to 16 septa, as shown in the lectotype drawing, were not observed for CBS 746.79 in our study.

*Fusarium stramineum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854716. Fig. 22.

*Etymology: "stramineum*" referring to the straw-coloured colonies on MEA.

*Typus*: **Venezuela**, from woody twig, unknown host, before 1991, *G.J. Samuels* (**holotype** CBS H-25438 designated here, culture ex-type BBA 65675 = CBS 152076 = CPC 47569 = DSM 116943).

Aerial conidiophores densely aggregated and branched, up 106 µm tall, smooth- and thin-walled, straight or flexuous, sometimes reduced to a single phialide borne laterally on aerial hyphae,

![](_page_39_Picture_1.jpeg)

**Fig. 22.** *Fusarium stramineum sp. nov.* (ex-type culture BBA 65675). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C, D.** Sporodochia formed on the surface of carnation leaves. **E–I, K, L.** Aerial conidiophores, conidiogenous cells and conidia. **J.** Aerial conidia. **M, N.** Sporodochial conidia. **C.** De 100 μm; E–L, N, O = 10 μm; M = 20 μm.

bearing terminal, single phialides, smooth- and thin-walled. Aerial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical, 11.3–51.9 × 3.3–4.3 µm (av. 31.6 × 3.8 µm), smooth- and thin-walled. Aerial conidia curved to straight, basal cell non-foot-shaped and sometimes poorly developed, foot-shaped, 1-4-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 23.2 × 5.6 µm; 3-septate conidia: 37.6–53.0 × 5.2–6.0 µm (av. 46.3 × 5.7 µm); 4-septate conidia: 53.0–53.5 × 5.6 µm. Sporodochia pale to bright orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, ampulliform, subulate to subcylindrical, 10.3- $40.4 \times 3.5$ – $4.7 \mu m$  (av. 25.6 × 3.9  $\mu m$ ), smooth- and thin-walled. Sporodochial conidia, moderately dorsiventrally curved, apicall cell curved to blunt, basal cell poorly to well-developed, foot-shaped, 1-4-septate, hyaline, smooth- and thick-walled; 1-septate conidia: 31.7 × 5.4 µm; 3-septate conidia: 45.1–49.9(–53.3) × 5.3–6.4 µm (av. 48.3 × 5.8 μm); 4-septate conidia: 51.6–67.4 × 5.5–6.5 μm (av. 60.7 × 6.0 µm); Chlamydospores not observed.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 15–20 mm diam in 3 d at 24 °C; On PDA surface white, flesh to peach, pale luteous, with concentric rings of white aerial mycelium; margin entire to irregular. Reverse white to pale straw. Odour absent. On OA surface, apricot, cinnamon and sienna; margin irregular, filiform. Reverse sienna. Odour absent.

*Notes*: The main morphological character of *F. stramineum* is the slow growth rate on both OA and PDA at 24 °C. This characteristic is only comparable to *F. microcyclum*, however the two species are not phylogenetically closely related. Additionally, colonies of *F. stramineum* on OA exhibit a combination of apricot, cinnamon, and sienna colouration, which is not observed in any other species within the FLSC.

*Fusarium velutinum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854717. Fig. 23.

*Etymology*: "velutinum" referring to the velvety appearance of the colonies on PDA.

*Typus*: **Cuba**, from leaf of *Macadamia ternifolia*, before 1992, *J. Guarro* (**holotype** CBS H-25395 designated here, culture ex-type IMI 353670 = CPC 44738).

Aerial conidiophores borne laterally on hyphae, up to 290 µm tall, erect and simple, straight or flexuous, most of the time reduced to single phialides, sometimes branched laterally, smooth- and thin-walled; aerial conidiogenous cells mono- and polyphialidic, cylindrical to subcylindrical, 13.0-31.3(-39.9) × 2.5-4.5 µm (av.  $21.1 \times 3.7 \mu m$ ), smooth- and thin-walled, with a visible collarette. Aerial conidia of two types, clustering in false heads at tip of monoor polyphialides. Microconidia fusiform, 1-septate, hyaline, smoothand thin-walled,  $15.5-20.8 \times 3.7-4.3 \ \mu m$  (av.  $18.1 \times 4.0 \ \mu m$ ). Macroconidia falcate, straight to slightly curved, apical cell curved, basal cell non-foot-shaped and sometimes poorly developed, footshaped, obtuse, and papillate, 1-4-septate, hyaline, smooth- and thin-walled; 1-septate conidia: 15.0-28.5(-32.8) × 3.8-5.0 µm (av. 22.0 × 4.3 μm); 2-septate conidia: 27.7-34.7 × 4.3-5.3 μm (av. 30.2 × 4.8 µm); 3-septate conidia: (22.5-)24.0-42.3(-47.3) × 4.3-6.0 µm (av. 33.4 × 5.0 µm); 4-septate conidia: 41.9-47.0 × 5.4-5.5 µm. Sporodochia pale rosy to orange. Sporodochial conidiophores densely aggregated, irregularly and verticillately

![](_page_40_Picture_7.jpeg)

branched; *sporodochial conidiogenous cells* monophialidic, subcylindrical to subulate,  $(9.0-)11.0-17.3(-19.0) \times 3.0-5.0 \mu m$  (av. 14.5 × 4.0 µm), smooth- and thin-walled. *Sporodochial conidia*, moderately dorsiventrally curved to nearly straight, tapering toward both ends, apicall cell blunt to conical, basal cell papillate and poorly to well-developed, foot-shaped, (1-)3-5-septate, hyaline, smooth- and thick-walled; 1-septate conidia:  $19.4 \times 3.9 \mu m$ ; 3-septate conidia:  $25.0-59.1(-63.8) \times 3.9-5.9 \mu m$  (av.  $40.3 \times 4.8 \mu m$ ); 4-septate conidia:  $41.8-60.2 \times 4.3-5.9 \mu m$  (av.  $53.8 \times 5.4 \mu m$ ); 5-septate conidia:  $48.3-62.9 \times 4.8-6.3 \mu m$  (av.  $53.8 \times 5.4 \mu m$ ). *Chlamydospores* globose to subglobose, smooth- and thick-walled,  $8.5-9.0 \mu m$  diam, terminal or intercalary in hyphae, solitary or in chains.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 25–27 mm diam in 3 d at 24 °C; On PDA surface greyish rose, livid red to livid vinaceous with concentric rings of white aerial mycelium; margin entire. Odour absent. Reverse straw to greyish rose. On OA surface pale luteous, sulphur yellow and ochreous; margin entire to irregular. Odour absent. Reverse ochreous.

Additional material examined: **Cuba**, Santiago de las Vegas, from leave of *Macadamia ternifolia*, 4 Dec. 1991, *R.F. Castañeda*, culture CBS 256.93 = NRRL 25490 = INIFAT C91/223-6F.

Notes: Fusarium velutinum is phylogenetically closely related to F. lateritium, F. ramsdenii, F. camelliae, and F. magnoliae-champaca. It can be distinguished from F. lateritium and F. ramsdenii based on phylogenetic analyses for all individual gene regions (tef1, tub2, rpb2, CaM). Fusarium velutinum can be distinguished from F. camelliae based on tef1 and rpb2 phylogenies (Figs S1, S4). The species clade is well-supported in both BI and ML analyses (IQ-TREE-BS = 100 %; RAxML-BS = 100 %). No tub2 and CaM sequences of F. camelliae, and no tef, tub2, and CaM sequences of F. magnoliae-champaca were available on GenBank for comparison. Morphologically, F. velutinum frequently produces polyphialides on aerial mycelium and rarely produces microconidia, a characteristic commonly observed in some species of the FLSC, such as F. lateritium. Additionally, colonies of F. velutinum on PDA exhibit a greyish rose, livid red to livid vinaceous appearance, contrasting with the salmon to rosy buff colouration of F. lateritium, and the orange colour of F. camelliae.

*Fusarium verruculosum* M.M. Costa, Sand.-Den. & Crous, *sp. nov.* MycoBank MB 854718. Fig. 24.

*Etymology: "verruculosum*" named after the surface ornamentation of the chlamydospores.

*Typus*: **Austria**, from *Triticum aestivum*, 1993, unknown *collector* (**holotype** CBS H-25376 designated here, culture ex-type BBA 68499 = CBS 152077 = CPC 44987 = DSM 115156).

Aerial conidiophores borne laterally on hyphae, up to 80 µm tall, erect and simple, mostly straight, less often flexuous, usually reduced to single monophialides, and sometimes branched laterally, smooth- and thin-walled; *aerial conidiogenous cells* monophialidic, subulate, cylindrical to subcylindrical, swelling in the apical part can sometimes occur,  $(12.0-)14.0-19.5(-25.0) \times 2.4-4.9$  µm (av. 16.2 × 3.6 µm), smooth- and thin-walled, with a visible collarette. *Aerial conidia* navicular, fusiform to falcate, straight or curved, apical cell curved to hooked, base commonly flattened to barely notched, and

![](_page_41_Figure_1.jpeg)

Fig. 23. Fusarium velutinum sp. nov. (ex-type culture IMI 353670). A, B. Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. C, D. Sporodochia formed on the surface of carnation leaves. E–I, L–P. Aerial conidiophores, conidiogenous cells and conidia. J. Chlamydospores. K. Aerial conidia. Q. Sporodochial conidiophores, conidiogenous cells and conidia. R. Sporodochial conidia. Scale bars: C, D = 100  $\mu$ m; E–I, K, L, N–P, R = 10  $\mu$ m; J = 4; M = 5  $\mu$ m; Q = 20  $\mu$ m.

![](_page_42_Picture_1.jpeg)

**Fig. 24.** *Fusarium verruculosum sp. nov.* (ex-type culture BBA 68499). **A, B.** Colonies on PDA and OA, respectively, after 14 d at 24 °C in the dark. **C–E.** Sporodochia formed on the surface of carnation leaves and agar surface. **F–N.** Aerial conidiophores, conidiogenous cells and conidia. **O–S.** Chlamydospores. **T.** Aerial conidia. **U–W.** Sporodochial conidiophores, conidiogenous cells and conidia. **X.** Sporodochial conidia. Scale bars: C, D = 100  $\mu$ m; E = 50; F–H, U, V = 20  $\mu$ m; I–T, W, X = 10  $\mu$ m.

![](_page_42_Picture_3.jpeg)

papillate, 1-3-septate, hyaline, smooth- and thin-walled; 1-septate conidia: (15.5–)20.0–25.4(–45.4) × 3.0–3.6(–5.0) µm (av. 22.7 × 3.1 μm); 3-septate conidia: 28.8–39.4 × 4.5–5.5 μm (av. 33.9 × 4.9) μm. Sporodochia bright cream to pale rosy. Sporodochial conidiophores densely aggregated, irregularly and verticillately branched; sporodochial conidiogenous cells monophialidic, subcylindrical to subulate, 11.8-18.9(-23.8) × 3.2-4.4 µm (av. 15.8 × 3.9 µm), smooth- and thin-walled. Sporodochial conidia falcate, apical cell commonly smaller then adjacent cell, blunt to somewhat conical with curved and rounded apex, basal cell papillate, indistinctly to moderately notched and poorly to well developed, foot-shaped, (1-)3-4(-5)-septate, hyaline, smooth- and thick-walled; 1-septate conidia: 49.3 × 5.7 µm; 3-septate conidia: (28.0–)37.3–48.8(–50.7) × 4.8-5.8 µm (av. 42.6 × 5.3 µm); 4-septate conidia: 41.5-51.0 × 4.8–5.9 µm (av. 46.6 × 5.4 µm); 5-septate conidia: 54.3 × 5.2 µm. Chlamydospores abundantly formed in the aerial mycelium, agar surface, and sporodochia, coarsely roughened, smooth to verruculose- and thick-walled, 5.0-15.0 µm diam, solitary, in chains or in clusters.

*Culture characteristics*: Colonies on PDA and OA growing in the dark reaching 29–32 mm diam in 3 d at 24 °C. On PDA surface white, straw and flesh, flat, with concentric and radial rings of aerial mycelium; margin entire. Reverse white, rosy buff, and straw. Odour absent. On OA surface straw and cinnamon; margin entire. Reverse saffron and straw, arranged in concentric rings. Odour absent.

Additional material examined: **Spain**, from soil, before 1994, unknown *collector*, culture BBA 68498 = CPC 46464 = DSM 116556.

Notes: Fusarium verruculosum is introduced here as a distinct species within the FLSC, based on two strains respectively obtained from Triticum aestivum in Austria and soil in Spain. The two strains representing F. verruculosum form a strongly supported, genealogically exclusive lineage in the phylogeny inferred from all four gene regions (Fig. 1). Morphologically, F. verruculosum is characterized by the production of verruculose chlamydospores formed in the aerial mycelium, agar surface, and sporodochia, while not producing microconidia. This combination of characteristics has not been observed in other species within the FLSC. Macroconidia produced in sporodochia are shorter than those produced by other species in the complex, with the exception of those produced by F. chlamydocopiosum strains. In comparison to F. chlamydocopiosum, F. verruculosum produces less septate and more curved sporodochial conidia, mostly 3-septate in the latter species versus mostly 5-septate in F. chlamydocopiosum.

## DISCUSSION

This study presents the first extensive multilocus molecular phylogeny of the FLSC. Here, we investigated a representative set of *Fusarium* strains from different culture collections, labelled with names of the FLSC, using phylogenetic analyses, morphological characters and experimental crossings of strains to test the biological species concept. Multilocus phylogenetic analyses supported the identification of five already known species in the FLSC among the strains used in the current study, as well as the discovery of 11 novel species. Individual analyses of partial sequences of the four gene regions (*tef1, tub2, rpb2, CaM*) included in this study

revealed that the *tef1*, *tub2*, and *rpb2* gene regions provided the best resolution to discriminate species within the FLSC.

## Taxonomy

The taxonomic status of *Fusarium lateritium* has historically remained unresolved due to the absence of a designated nomenclatural type. Addressing this challenge, Crous *et al.* (2021) designated a lectotype from the original species description, providing a definitive reference. In this study, we designated an epitype for *F. lateritium*, based on morphological features following Wollenweber (1931), Wollenweber & Reinking (1935), Booth (1971), and Gerlach & Nirenberg (1982), as well as based on previous phylogenetic studies involving the FLSC (Geiser *et al.* 2005, O'Donnell *et al.* 2013, Crous *et al.* 2021, Geiser *et al.* 2021). As a result, assigning an epitype for *F. lateritium* has crucial importance for the taxonomic classification system within this complex.

Historically, the identification of F. lateritium strains and related species has mostly been based on the morphological species concept developed by Wollenweber (1917). During our research, we analyzed numerous strains previously identified as F. lateritium, *F. stilboides*, or one of their varieties, including varieties *lateritium*, buxi, longum, and majus. However, based on phylogenetic analyses, we have shown that these strains belong not only to species in the FLSC but also to several other species and newly described taxa in other Fusarium species complexes, including FCCSC, FHSC, FIESC, FTSC, and FSAMSC. Surprisingly, the majority of the strains represent species in FTSC and FCCSC. The FTSC is a well-known species complex that includes pathogens of wheat, barley, and oats (Xue et al. 2019, Cowger et al. 2020, Pereira et al. 2021), which may produce mycotoxins such as beauvericin, enniatins, and moniliformin (Logrieco et al. 2002, Laraba et al. 2022). The FCCSC is currently composed of five formally described species (Sandoval-Denis et al. 2018, Crous et al. 2021). Except for one isolate, BBA 67503, which belongs to F. citri-sinensis within the FLSC, most of the strains, that were identified as the variety majus, belong to these non-lateritium complexes, including the isolate BBA 62246, treated by Gerlach & Nirenberg (1982) as a representative strain of the respective variety. This result indicates that many of the isolates treated in the literature as being F. lateritium based on morphology only may belong to other Fusarium species.

A replacement name is proposed here, *F. hanswilhelmii*, which corresponds to *F. lateritium* var. *longum*, one of the *F. lateritium* varieties described by Wollenweber (1931). The type specimen from the original description of Wollenweber (1930) was not available. Therefore, the original illustration referenced in the protologue is designated as the lectotype. Subsequently, the strain CBS 633.76, isolated from a citrus fruit in the Cook Islands, and recognized as a representative strain of *Fusarium lateritium* var. *longum* by Gerlach & Nirenberg (1982), was designated as an epitype. Moreover, *Fusarium citri-sinensis*, reported from *Citrus sinensis* fruit in China (Zhao *et al.* 2022), has been validated in this study. This validation is warranted due to the absence of a statement in the protologue indicating that the culture is maintained in a metabolically inactive state.

An emended description is presented herein for *F. endophyticum*, *F. cassiae*, and *F. stilboides*. *Fusarium endophyticum*, recently identified as a novel species, was isolated from leaves of *Camellia sinensis* var. *assamica* in Thailand (Suwannarach *et al.* 2023). In our study, representative strains of this species, obtained from *Citrus aurantium* in Honduras, exhibit the production of macroconidia in sporodochia, a trait not included in the original description. *Fusarium cassiae* was initially characterized based on its sexual morph found on decaying pods of *Cassia fistula* in Thailand (Perera *et al.* 2020), and herein, we provide insights into the morphology of the asexual morph of this species. Additionally, *F. stilboides*, a well-defined species within the FLSC (Wollenweber & Reinking 1935), is shown to produce polyphialides, a feature not previously documented in its original description.

## Morphology

One of the main morphological characters for F. lateritium and related species, as treated by Wollenweber (1917) when he established the Section Lateritium, was the relatively straight shape of the macroconidia and the production of chlamydospores. The majority of the newly described species in this study exhibit these characteristics regarding the shape of their macroconidia, although it is slightly less pronounced in F. chlamydocopiosum and F. verruculosum. Among the 11 newly described species in this study, chlamydospore production was not observed in six species, namely F. aurantii, F. crocatum, F. microcyclum, F. oliniae, F. rufum, and F. stramineum. Another characteristic of the FLSC is the limited production or complete absence of microconidia in several of the described species: F. chlamydocopiosum, F. cassiae, F. hanswilhelmii, F. malawiense, F. microcyclum, F. oliniae, F. rufum, F. stramineum, and F. verruculosum. This trait has been previously noted in species within the Section Lateritium, including F. lateritium (Gerlach & Nirenberg 1982), and in recently described species such as F. endophyticum (Suwannarach et al. 2023), F. massalimae (Cavalcanti et al. 2020), and F. citri-sinensis (Zhao et al. 2022).

In a phylogenetic study involving strains from the FLSC, Geiser *et al.* (2005) identified four distinct clades (Clades I, IIA, IIB, and III). Strains within Clades I, IIA, and IIB were noted to exhibit a red pigment on PDA (Geiser *et al.* 2005). These characteristics were also observed in our examination of strains belonging to *F. aurantii*, *F. citri-sinensis*, *F. coffeibaccae*, *F. oliniae*, and *F. rufum*. In our phylogenetic trees, *F. coffeibaccae*, *F. rufum*, and *F. oliniae* cluster within a clade corresponding to Clade I as delineated by Geiser *et al.* (2005). On the other hand, *F. citri-sinensis* and *F. aurantii* form a clade that includes representative strains from *F. lateritium* clades IIA and IIB *sensu* Geiser *et al.* (2005), along with other closely related phylogenetic species such as *F. cassiae*, and *F. endophyticum*, which do not exhibit the characteristic red pigment on PDA.

## Host-substrate association and geographic distribution

Recent species descriptions in the FLSC, along with the novel taxa outlined in this study, have confirmed the wide geographic distribution of the species, spanning a broad range of ecological interactions from pathogenic to latent and endophytic associations. However, in general, our data did not allow definitive assignment of most of the new species to specific hosts or locations, mainly due to the limited number of strains representing them. So far, *F. coffeibaccae* appears to be the most prevalent and diverse species of the FLSC described in our study. Strains belonging to this species have been isolated from various hosts and substrates, causing bark diseases or fruit rots in coffee, citrus, *Hylocereus* sp. (dragon fruit) in Brazil, New Guinea, and eastern Africa (Geiser *et al.* 2005). This species seems to have a particular affinity with coffee plants,

![](_page_44_Picture_6.jpeg)

as most F. coffeibaccae strains from our study were isolated from berries and bark of coffee plants. In extensive fungal isolations from coffee berries in many regions of Brazil, F. coffeibaccae was among the most frequently isolated fungi (unpubl. data). The other newly described species were isolated from at least 20 different hosts or substrates. Fusarium aurantii is the second most diverse species and was isolated from Citrus aurantium in Cuba, Cajanus cajan and Vigna angularis in India, and soil in Philippines. Most of the novel Fusarium species described in this study were associated with asymptomatic plant tissue, and pathogenicity studies are still pending for many of the species within the FLSC. Fusarium lateritium, F. stilboides, and F. sarcochroum are mainly known to be associated with woody plants such as coffee and citrus (Wollenweber 1931, Wollenweber & Reinking 1935, Booth 1971, Gerlach & Nirenberg 1982, Sandoval-Denis et al. 2018). However, future research should focus on further elucidating the true lifestyle of these species, as well as their pathogenicity to coffee, citrus, and other plants, as some of the previous conclusions were based solely on morphological identification of strains.

## **Biological species concept**

Sexual morphs could be induced for F. coffeibaccae and F. crocatum in this study. For coffeibaccae, fertile crosses were obtained among strains from Brazil. Similarly, for F. crocatum, fertile crosses were successfully achieved by crossing strains of opposite mating types from different hosts. All of the strains belonging to F. coffeibaccae and F. crocatum presented only one mating type in the PCR assay, indicating heterothallism of the strains. To date, few studies have been conducted for mating type identification and/or induction of the sexual morph in vitro for species within the FLSC (Afanide et al. 1976, Lawrence et al. 1985a, Cavalcanti et al. 2020). Lawrence et al. (1985a) conducted experiments in which the sexual morph was obtained when strains, morphologically identified as F. lateritium, were crossed among themselves, and these strains were also identified as heterothallic. Some of those strains were included in our phylogenetic analyses and represent, in fact, two different phylogenetic species, F. lateritium (strains L-55 = NRRL 13622) and the new species described here, F. coffeibaccae (strains L-83, L-86, L-87, and L-107). For F. massalimae, it was shown that the two analyzed isolates carry only the MAT1-2 allele, suggesting that it is a heterothallic species (Cavalcanti et al. 2020).

The occurrence of the sexual morph of *F. lateritium* is reported in various substrates, often associated with disease symptoms (Wollenweber & Reinking 1935, Booth 1971, Geiser et al. 2005). Two Fusarium strains (L-110 and L-112) reported by Geiser et al. (2005) were obtained from perithecia on coffee twigs in Papua New Guinea, and indeed represent an undescribed species in the FLSC (Fig. S2). However, many of the studies reporting the sexual morph of F. lateritium in nature identified isolates based solely on morphological characters. Nevertheless, the majority of the strains named as F. lateritium were proven in this study to belong to other phylogenetic species in the FLSC or in other species complexes. In the FLSC, the sexual morph has been reported for F. lateritium (G. baccata) (Booth 1971, Afanide et al. 1976, Lawrence et al. 1985a, 1985b), F. stilboides (G. stilboides) (Booth 1971), F. sarcochroum (G. pseudopulicaris) (Wollenweber 1931), F. magnoliae-champaca, F. cassiae (Perera et al. 2020), and for F. coffeibaccae and F. crocatum in this study. Further research is required to investigate the taxonomic and morphological relationships for the first three biological species. Additionally, there may be several other biological species in the FLSC that still require characterization.

A more detailed investigation is necessary to provide answers about the true organization of the mating type genes in strains belonging to species of the FLSC and the potential occurrence of homothallism, as mentioned by Booth (1971).

## ACKNOWLEDGEMENTS

We are thankful to Edson Luis Rezende from the Department of Plant Pathology, Universidade Federal de Lavras, Lavras MG, Brazil, Kristin Müller and Katrin Balke from the Institute for Epidemiology and Pathogen Diagnostics, Julius Kühn Institute, Germany, and Marjan Vermaas from the Westerdijk Fungal Biodiversity Institute, The Netherlands, for technical assistance. We are grateful to Konstanze Bensch for suggestions on nomenclatural issues. The Odo van Vloten Foundation is acknowledged for financial support to M.M. Costa. We are very grateful to the reviewers whose suggestions helped improve this manuscript.

## DECLARATION ON CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

## REFERENCES

- Afanide B, Mabadeje SA, Naqvi SHZ (1976). *Gibberella baccata*, the perfect state of *Fusarium lateritium* in Nigeria. *Mycologia* **68**: 1108–1111.
- Bilaĭ VI (1955). *Fusarii (Biologija i sistematika)*. Isdatelstvo Akademii Nauk Ukraniskoi SSE, Kiev, Ukraine (in Russian).
- Booth C (1971). *The genus Fusarium*. Commonwealth Mycological Institute, Kew, Surrey, England, UK.
- Carbone I, Kohn LM. (1999). A method for designing primer sets for speciation studies in filamentous ascomycetes. *Mycologia* **91**: 553–556.
- Cavalcanti AD, Santos ACS, Ferro LO, et al. (2020). Fusarium massalimae sp. nov. (F. lateritium species complex) occurs endophytically in leaves of Handroanthus chrysotrichus. Mycological Progress 19: 1133–1142.
- Costa MM, Saleh AA, Melo MP, et al. (2022). Fusarium mirum sp. nov., intertwining Fusarium madaense and Fusarium andiyazi, pathogens of tropical grasses. Fungal Biology **126**: 250–266.
- Cowger C, Ward TJ, Nilsson K, et al. (2020). Regional and field-specific differences in *Fusarium* species and mycotoxins associated with blighted North Carolina wheat. *International Journal of Food Microbiology* 323: 108594.
- Crous PW, Gams W, Stalpers JA, *et al.* (2004). MycoBank: an online initiative to launch mycology into the 21<sup>st</sup> century. *Studies in Mycology* **50**: 19–22.
- Crous PW, Boers J, Holdom D, et al. (2022). Fungal Planet description sheets: 1383–1435. Persoonia 48: 261–371.
- Crous PW, Lombard L, Sandoval-Denis M, et al. (2021). Fusarium: more than a node or a foot cell. Studies in Mycology **98**: 100116.
- Crous PW, Verkley GJM, Groenewald JZ, et al. (2019). Fungal Biodiversity. Westerdijk Laboratory Manual Series 1. Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands.
- Dean R, Van Kan JAL, Pretorius ZA, *et al.* (2012). The top 10 fungal pathogens in molecular plant pathology. *Molecular Plant Pathology* **13**: 414–430.

Doidge EM (1938). Some South African fusaria. Bothalia 3: 331-483.

- Geiser DM, Al-Hatmi A, Aoki T, *et al.* (2021). Phylogenomic analysis of a 55.1 kb 19-gene dataset resolves a monophyletic *Fusarium* that includes the *Fusarium solani* species complex. *Phytopathology* **111**: 1064–1079.
- Geiser DM, Lewis Ivey ML, Hakiza G, et al. (2005). Gibberella xylarioides (anamorph: Fusarium xylarioides), a causative agent of coffee wilt disease in Africa, is a previously unrecognized member of the *G.* fujikuroi species complex. Mycologia **97**: 191–201.

- 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.
- Gordon WL (1952). The occurrence of *Fusarium* species in Canada. II. Prevalence and taxonomy of *Fusarium* species in cereal seeds. *Canadian Journal of Botany* **30**: 209–251.
- Groenewald JZ, Nakashima C, Nishikawa J, *et al.* (2013). Species concepts in *Cercospora*: spotting the weeds among the roses. *Studies in Mycology* **75**: 115–170.
- He J, Li DW, Cui WL, *et al.* (2024). Morphological and phylogenetic analyses reveal three new species of *Fusarium* (*Hypocreales, Nectriaceae*) associated with leaf blight on *Cunninghamia lanceolata* in China. *MycoKeys* **101**: 45–80.
- Hoang DT, Chernomor O, von Haeseler A, et al. (2018). UFBoot2: improving the ultrafast bootstrap spproximation. *Molecular Biology* and Evolution **35**: 518–522.
- Hyde KD, Norphanphoun C, Ma J, *et al.* (2023). Mycosphere notes 387–412 novel species of fungal taxa from around the world. *Mycosphere* **14**: 663–744.
- Jacobs A (2010). *Taxonomy of species within Gibberella fujikuroi complex*. Ph.D. dissertation. University of Pretoria, Pretoria, South Africa.
- Kalyaanamoorthy S, Minh BQ, Wong TKF, et al. (2017). ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14: 587–589.
- Katoh K, Rozewicki J, Yamada KD (2019). MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* **20**: 1160–1166.
- Kerényi Z, Moretti A, Waalwijk C, et al. (2004). Mating type sequences in asexually reproducing *Fusarium* species. Applied and Environmental Microbiology 70: 4419–4423.
- Kim HS, Lohmar JM, Busman M, et al. (2020). Identification and distribution of gene clusters required for synthesis of sphingolipid metabolism inhibitors in diverse species of the filamentous fungus *Fusarium*. BMC Genomics 21: 510.
- Klittich C, Leslie JF (1988). Nitrate reduction mutants of *Fusarium* moniliforme. Genetics **118**: 417–423.
- Kumar S, Stecher G, Tamura K (2016). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology* and Evolution 33: 1870–1874.
- Laraba I, Busman M, Geiser DM, *et al.* (2022). Phylogenetic diversity and mycotoxin potential of emergent phytopathogens within the *Fusarium tricinctum* species complex. *Phytopathology* **112**: 1284–1298.
- Lawrence EB, Nelson PE, Toussoun TA (1985a). Inheritance of compatibility and sex in *Gibberella baccata*. *Phytopathology* **75**: 322–324.
- Lawrence EB, Nelson PE, Toussoun TA (1985b). Genetics of certain morphological characteristics in *Gibberella baccata*. *Phytopathology* 75: 741–747.
- Leslie JF, Summerell BA (2006). *The Fusarium laboratory manual*. Blackwell Publishing Professional, USA.
- Li W, Cowley A, Uludag M, *et al.* (2015). The EMBL-EBI bioinformatics web and programmatic tools framework. *Nucleic Acids Research* **43**: W580–W584.
- Lima CS, Pfenning LH, Costa SS, *et al.* (2012). *Fusarium tupiense sp. nov.*, a member of the *Gibberella fujikuroi* complex that causes mango malformation in Brazil. *Mycologia* **104**: 1408–1419.
- Liu YJ, Whelen S, Hall BD (1999). Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution* **16**: 1799–1808.
- Logrieco A, Rizzo A, Ferracane R, Ritieni A (2002). Occurrence of beauvericin and enniatins in wheat affected by *Fusarium avenaceum* head blight. *Applied and Environmental Microbiology* **68**: 82–85.
- Lombard L, Sandoval-Denis M, Lamprecht SC, et al. (2019). Epitypification of Fusarium oxysporum – clearing the taxonomic chaos. Persoonia 43: 1–47.
- Minh BQ, Schmidt HA, Chernomor O, *et al.* (2020). IQ-TREE 2: new models and efficient methods for phylogenetic inference in in the genomic era. *Molecular Biology and Evolution* **37**: 1530–1534.
- Miller MA, Pfeiffer W, Schwartz T (2012). The CIPRES science gateway: enabling high-impact science for phylogenetics researchers with

limited resources. In: Proceedings of the 1<sup>st</sup> conference of the extreme science and engineering discovery environment: Bridging from the extreme to the campus and beyond. Association for Computing Machinery, USA: 1–8.

- Nees von Esenbeck CG (1817). Das System der Pilze und Schwaemme: Ein Versuch. In der Stahelschen Buchhandlung, Würzburg, Germany.
- Nelson PE, Toussoun TA, Marasas WFO (1983). *Fusarium species: An illustrated manual for identification*. Pennsylvania State University Press, USA.
- 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.
- Nirenberg HI (1976). Untersuchungen über die morphologische und biologische Differenzierung in der Fusarium-Sektion Liseola. Mitteilungen aus der Biologischen Bundesanstalt für Land- und Forstwirtschaft Berlin-Dahlem 169: 1–117.
- Nylander JAA (2004). *MrModeltest v2*. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Sweden.
- O'Donnell K, Cigelnik E (1997). Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. *Molecular Phylogenetics and Evolution* 7: 103–116.
- O'Donnell K, Cigelnik E, Nirenberg HI (1998). Molecular systematics and phylogeography of the *Gibberella fujikuroi* species complex. *Mycologia* **90**: 465–493.
- O'Donnell K, Rooney AP, Proctor RH, *et al.* (2013). Phylogenetic analyses of *RPB1* and *RPB2* support a middle Cretaceous origin for a clade comprising all agriculturally and medically important fusaria. *Fungal Genetics and Biology* **52**: 20–31.
- O'Donnell K, Sarver BAJ, Brandt M, et al. (2007). Phylogenetic diversity and microsphere array-based genotyping of human pathogenic Fusaria, including isolates from the multistate contact lens-associated U.S. keratitis outbreaks of 2005 and 2006. *Journal of Clinical Microbiology* 45: 2235–2248.
- O'Donnell K, Sutton DA, Fothergill A, *et al.* (2008). Molecular phylogenetic diversity, multilocus haplotype nomenclature, and *in vitro* antifungal resistance within the *Fusarium solani* species complex. *Journal of Clinical Microbiology* **46**: 2477–2490.
- Padwick GW (1940). The genus Fusarium. V. Fusarium udum Butler, F. vasinfectum Atk. and F. lateritium Nees var. uncinatum Wr. The Indian Journal of Agricultural Sciences 10: 869–878.
- Pascoe IG (1990). Fusarium morphology I. Identification and characterization of a third conidial type, the mesoconidium. Mycotaxon 37: 121–160.
- Pereira CB, Ward TJ, Del Ponte EM, *et al.* (2021). Five-year survey uncovers extensive diversity and temporal fluctuations among fusarium head blight pathogens of wheat and barley in Brazil. *Plant Pathology* **70**: 426–435.
- Perera RH, Hyde KD, Maharachchikumbura SSN, *et al.* (2020). Fungi on wild seeds and fruits. *Mycosphere* **11**: 2108–2480.
- Pfenning LH, de Melo MP, Costa MM, et al. (2019). Fusarium udum revisited: a common, but poorly understood member of the Fusarium fujikuroi species complex. Mycological Progress **18**: 107–117.
- Proctor RH, Van Hove F, Susca A, *et al.* (2013). Birth, death and horizontal transfer of the fumonisin biosynthetic gene cluster during the evolutionary diversification of *Fusarium*. *Molecular Microbiology* **90**: 290–306.
- Raillo A (1950). *Fungi of the genus Fusarium*. State Publishing House of Agricultural Literature, Moscow, USSR.
- Rayner RW (1970). A mycological colour chart. CMI and British Mycological Society. Kew, Surrey, England, UK.
- Ronquist F, Teslenko M, Van der Mark P, *et al.* (2012). MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* **61**: 539–542.
- Saccardo PA (1879). Fungi Gallici lecti a cl. viris P. Brunaud, C.C. Gillet et Abb. Letendre. *Michelia* 1: 500–538.
- Samuels GJ, Nirenberg HI, Seifert KA (2001). Perithecial species of Fusarium. In: Fusarium: Paul E. Nelson Memorial Symposium (Summerell BA, Leslie JF, Backhouse D, Bryden WL, Burgess LW, eds). APS Press, USA: 1–14.

![](_page_46_Picture_23.jpeg)

- Sandoval-Denis M, Guarnaccia V, Polizzi G, et al. (2018). 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.
- Snyder WC, Hansen HN (1945). The species concept in *Fusarium* with reference to *Discolour* and other sections. *American Journal of Botany* **32**: 657–666.
- Stamatakis A (2014). RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenetics. *Bioinformatics* **30**: 1312–1313.
- Sung GH, Sung JM, Hywel-Jones NL, et al. (2007). A multi-gene phylogeny of Clavicipitaceae (Ascomycota, Fungi): identification of localized incongruence using a combinational bootstrap approach. Molecular Phylogenetics and Evolution 44: 1204–1223.
- Suwannarach N, Khuna S, Kumla J, et al. (2023). Fusarium endophyticum sp. nov. (Nectriaceae, Hypocreales), a new endophytic fungus from northern Thailand. Phytotaxa 606: 43–53.
- Tan YP, Shivas RG (2023). Nomenclatural novelties. *Index of Australian Fungi* **10**:1–17.
- 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 (1924). Pyrenomyceten-Studien. I. Angewandte Botanik 6: 300–313.
- Wollenweber HW (1916–1935). *Fusaria autographice delineata*. Selbstverlag, Berlin, Germany.
- Wollenweber HW (1917). Fusaria Autographice Delineata. Annales Mycologici 15: 1–56.
- Wollenweber HW (1930). *Fusaria Autographice Delineata* **3**: 660–1100. Berlin, Germany.
- Wollenweber HW (1931). Fusarium Monographie. Fungi parasitici et saprophytici. Zeitschrift für Parasitenkunde 3: 260–516.
- Wollenweber HW, Reinking OA (1935). *Die Fusarien*. Verlagsbuchandlung Paul Parey, Berlin, Germany.
- Woudenberg JHC, Aveskamp MM, De Gruyter J, et al. (2009). Multiple Didymella teleomorphs are linked to the Phoma clematidina morphotype. Persoonia 22: 56–62.
- Wu F (2007). Measuring the economic impacts of *Fusarium* toxins in animal feeds. *Animal Feed Science and Technology* 137: 363–374.
- Xue AG, Chen Y, Seifert K, et al. (2019). Prevalence of Fusarium species causing head blight of spring wheat, barley and oat in Ontario during 2001-2017. Canadian Journal of Plant Pathology 41: 392–402.
- Yilmaz N, Sandoval-Denis M, Lombard L, et al. (2021). Redefining species limits in the Fusarium fujikuroi species complex. Persoonia 46: 129– 162.
- Zeller KA, Summerell BA, Bullock S, *et al.* (2003). *Gibberella konza* (*Fusarium konzum*) *sp. nov.* from prairie grasses, a new species in the *Gibberella fujikuroi* species complex. *Mycologia* **95**: 943–954
- Zhao L, Wei X, Huang CX, et al. (2022). Fusarium citri-sinensis sp. nov. (Ascomycota: Nectriaceae) isolated from fruit of Citrus sinensis in China. Phytotaxa 555: 259–266.

#### Supplementary Material: https://studiesinmycology.org/

**Fig. S1.** Phylogenetic tree inferred from a Maximum Likelihood (RAxML) analysis based on *tef1* sequences of species from FLSC and other complexes of *Fusarium*. Strains deposited in the culture collection as *F. lateritium* are indicated in dark blue font, whereas strains deposited as *F. lateritium* var. *lateritium* are in red font, strains deposited as *F. lateritium* var. *majus* are in green, as *F. lateritium* var. *buxi* in orange, as *F. lateritium* var. *mori* in pink, and as *F. stilboides* in light green. Ex-type, ex-epitype, ex-isotype, and ex-neotype strains are indicated with T, ET, IT, and NT respectively. Numbers at branches indicate bootstrap support values RAxML-BS above 50 %. The tree was rooted to *Rectifusarium ventricosum* (CBS 748.79). Scale bar represents expected number of changes per site. **Fig. S2.** Phylogenetic tree inferred from a Maximum Likelihood (RAxML) analysis based on concatenated *tef1* and *tub2* sequences of species from FLSC. Ex-type, ex-epitype, and ex-neotype strains are indicated with T, ET, and NT respectively. Numbers at branches at branches per site.

support values RAxML-BS above 50 %. The tree was rooted to *Fusarium sublunatum* (CBS 189.34 = NRRL 13384). Scale bar represents expected number of changes per site.

**Fig. S3.** Phylogenetic tree inferred from a Maximum Likelihood (RAxML) analysis based on *tub2* sequences of species from FLSC. Ex-type, ex-epitype, and ex-neotype strains are indicated with T, ET, and NT respectively. Numbers at branches indicate bootstrap support values RAxML-BS above 50 %. The tree was rooted to *Fusarium sublunatum* (CBS 189.34 = NRRL 13384). Scale bar represents expected number of changes per site.

**Fig. S4.** Phylogenetic tree inferred from a Maximum Likelihood (RAxML) analysis based on *rpb2* sequences of species from FLSC. Ex-type, ex-epitype, and ex-neotype strains are indicated with T, ET, and NT respectively. Numbers at branches indicate bootstrap support values RAxML-BS above 50 %. The tree was rooted to *Fusarium sublunatum* (CBS 189.34 = NRRL 13384). Scale bar represents expected number of changes per site.

**Fig. S5.** Phylogenetic tree inferred from a Maximum Likelihood (RAxML) analysis based on concatenated *CaM* sequences of species from FLSC. Ex-type, ex-epitype, and ex-neotype strains are indicated with T, ET, and NT respectively. Numbers at branches indicate bootstrap support values RAxML-BS above 50 %. The tree was rooted to *Fusarium sublunatum* (CBS 189.34 = NRRL 13384). Scale bar represents expected number of changes per site.

 Table S1. Fusarium strains used in this study.

Table S2. Details of *Fusarium* sequences included in the phylogenetic analyses.