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Fungi of quarantine concern for China I: *Dothideomycetes*

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Key words

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new taxa
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plant pathogens
typification

Abstract The current list of Chinese quarantine pests includes 130 fungal species. However, recent changes in the taxonomy of fungi following the one fungus = one name initiative and the implementation of DNA phylogeny in taxonomic revisions, resulted in many changes of these species names, necessitating an update of the current list. In addition, many quarantine fungi lack modern morphological descriptions and authentic DNA sequences, posing significant challenges for the development of diagnostic protocols. The aim of the present study was to review the taxonomy and names of the 33 Chinese quarantine fungi in *Dothideomycetes*, and provide reliable DNA barcodes to facilitate rapid identification. Of these, 23 names were updated according to the single name nomenclature system, including one new combination, namely *Cophinforma tumefaciens* comb. nov. (syn. *Sphaeropsis tumefaciens*). On the basis of phylogenetic analyses and morphological comparisons, a new genus *Xenosphaeropsis* is introduced to accommodate the monotypic species *Xenosphaeropsis pyriputrescens* comb. nov. (syn. *Sphaeropsis pyriputrescens*), the causal agent of a post-harvest disease of pears. Furthermore, four lectotypes (*Ascochyta petroselini*, *Mycosphaerella ligulicola*, *Physalospora laricina*, *Sphaeria lingam*), three epitypes (*Ascochyta petroselini*, *Phoma lycopersici*, *Sphaeria lingam*), and two neotypes (*Ascochyta pinodella*, *Deuterophoma tracheiphila*) are designated to stabilise the use of these names. A further four reference strains are introduced for *Cophinforma tumefaciens*, *Helminthosporium solani*, *Mycocentrospora acerina*, and *Septoria linicola*. In addition, to assist future studies on these important pathogens, we sequenced and assembled whole genomes for 17 species, including *Alternaria triticina*, *Boeremia foveata*, *B. lycopersici*, *Cladosporium cucumerinum*, *Didymella glomerata*, *Didymella pinodella*, *Diplodia mutila*, *Helminthosporium solani*, *Mycocentrospora acerina*, *Neofusicoccum laricinum*, *Parastagonospora pseudonodorum*, *Plenodomus libanotidis*, *Plenodomus lingam*, *Plenodomus tracheiphilus*, *Septoria petroselini*, *Stagonosporopsis chrysanthemi*, and *Xenosphaeropsis pyriputrescens*.

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INTRODUCTION

Trade in agricultural produce and living plant materials is increasing, resulting in serious global risks of invasive alien pests and pathogens. A recent study showed that the annual rate of new records of alien species has increased globally during the past 200 years, without any sign of saturation (Seebens et al. 2017). Introduction of alien pests and pathogens into certain areas may break down the classical biogeographic boundaries, and have a far-reaching impact on native biota, ecosystem functioning, human health and economy (Hulme 2009, Pyšek & Richardson 2010, Simberloff et al. 2013, Capinha et al. 2015). One of the most notorious alien microbes is *Phytophthora infestans*, initially migrating from central Mexico to North America or Europe and then spreading worldwide. It subsequently caused the 1840s European, the 1845 Irish, and the 1846 highland potato famines (Goss et al. 2014). In contrast, the earliest record of serious losses caused by potato blight in China was in 1940, leading to more than 90 % of the yield losses in the Chongqing area (Xiang 1957), followed by the first nationwide outbreak of the disease in the 1950s (Guo et al. 2010). *Verticillium dahliae*, another serious quarantine fungus, was introduced to China from the United States in 1935 and caused severe and continuous outbreaks of verticillium wilt of cotton (Zhu et al. 2017). Currently, the annual economic loss caused by verticillium wilt of cotton is about 250–310 million US dollars in China (Wang et al. 2016). In addition to cotton, *Verticillium dahliae* also infects over 600 other plant species including many economically important agricultural crops (Fradin & Thomma 2006, Klosterman et al. 2009, Inderbitzin & Subbarao 2014). Therefore, preventing the global spread of alien pests and pathogens is an increasingly important concern for most countries, including China.

Dothideomycetes species are very invasive and therefore of concern to Chinese agriculture and forestry. For example, *Plenodomus lindquistii* (syn. *Leptosphaeria lindquistii*) was introduced to China via sunflower seeds in 2005, and caused severe damage to sunflower production in the Xinjiang Uygur Autonomous Region, with the incidence of severely diseased fields up to 100 %, and a mortality rate of approximately 50 % (Chen et al. 2008). Another important pathogen is *Plenodomus lingam* (syn. *Leptosphaeria maculans*), the causal agent of blackleg of *Brassica* crops, which often leads to serious losses

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in Australia, Europe and North America (Fitt et al. 2006). Although it is currently absent in China, strict quarantine measures remain in place to ensure that *P. lingam* is not introduced by accident, since many Chinese cultivars are highly susceptible to this pathogen.

In order to reduce phytosanitary risks due to growing international trade, various laws and regulations are being employed. The Chinese quarantine pest list currently includes 446 pest and quarantine organisms, covering bacteria, insects, molluscs, fungi, nematodes, viruses, virus-like organisms, and weeds (http://dzs.customs.gov.cn/dzs/2746776/3699554/index.html; accessed 15 May 2021). Among them, 130 are fungal species, and some are also listed as quarantine organisms in other countries, e.g., *Apiosporina morbosa*, *Atropellis pinicola* (current name: *Godronia zelleri*), *Gymnosporangium clavipes*, *Mycosphaerella gibsonii* (current name: *Pseudocercospora pinidensiflorae*) and *Ophiostoma wageneri* (current name: *Grosmannia wageneri*) (EPPO A1 list).

However, a major problem in identifying these quarantine fungi is the fact that many lack modern morphological descriptions and DNA sequence data. Type specimens of many species, especially those published in the 1800s, are either lost or failed to provide sufficient and useful morphological and molecular data. This is a problem not only faced by quarantine personnel, but also a problem for the whole mycological community. According to our preliminary findings, type specimens or type-derived molecular data of 17 *Dothideomycetes* species on the Chinese quarantine list are missing, which include *Apiosporina morbosa*, *Didymella ligulicola*, *Didymella lycopersici*, *Helminthosporium solani*, *Leptosphaeria libanotis*, *Leptosphaeria maculans*, *Microcyclus ulei*, *Mycocentrospora acerina*, *Mycosphaerella gibsonii*, *Mycosphaerella linicola*, *Periconia circinata*, *Phoma pinodella*, *Phoma tracheiphila*, *Septoria petroselini*, *Sphaeropsis tumefaciens*, *Stagonospora avenae* f.sp. *tritici*, and *Stagonospora sacchari*. The lack of reference data represents a major hurdle to phytosanitary workers, taxonomists, and plant pathologists alike. Besides, recent advances in the taxonomy of fungi have resulted in many name changes, and many species have been reclassified, leading to an urgent demand for a revision of the Chinese quarantine list (Duan et al. 2015).

The objectives of this study were therefore to:

1. characterise phytopathogenic *Dothideomycetes* species of Chinese quarantine significance via the examination of the type or voucher specimens and cultures;
2. generate informative reference DNA barcodes to distinguish quarantine fungi from their closest relatives;
3. provide core references of these quarantine species, including disease symptoms, morphological characteristics, habitats, geographic distributions, DNA barcodes, and whole genome sequences.

MATERIALS AND METHODS

Isolates and specimens

Fungal isolates were obtained from the following biological resource centres: Westerdijk Fungal Biodiversity Institute, the Netherlands (CBS), American Type Culture Collection, USA (ATCC), Microorganisms section of the NIAS (National Institute of Agrobiological Sciences) Genebank, Japan (MAFF), CABI Bioscience, Egham, UK (IMI), and BCCM/MUCL Collection, Université Catholique de Louvain, Belgium (MUCL). Ex-type cultures, as well as other vouchers used for morphological and phylogenetic analyses are presented in Table S1. Loan requests of type specimens were sent to the following 31 fungaria, viz. B, BPI, BR, CAN, CBS, DAOM, E, FI, FLAS, GH, HBG, HUH, IMI, JSTOR, K, LI, MICH, MT, NY, PAV, PC, PDD, PH, PRM, RM, RP, S, STR, TRT, W, and WSU.

Morphology

Morphological descriptions were made from isolates cultivated on potato dextrose agar (PDA; Difco), malt extract agar (MEA),

Table 1 Primers used in this study, with sequences and references.

Locus[a]	Primer	Primer sequences 5' to 3'	Annealing temperature	Orientation	References
small subunit ribosomal DNA (SSU)	NS1	GTAGTCATATGCTTGTCTC	52	Forward	Gargas & DePriest (1996)
	NS4	CTTCCGTCAATTCCTTTAAG	52	Reverse	White et al. (1990)
large subunit ribosomal DNA (LSU)	LR0R	ACCCGCTGAACTTAAGC	52	Forward	Rehner & Samuels (1994)
	LR5	ATCCTGAGGGAAACTTC	52	Reverse	Rehner & Samuels (1994)
Internal transcribed spacer (ITS)	ITS1	TCCGTAGGTGAACCTGCGG	52	Forward	White et al. (1990)
	ITS4	TCCTCCGCTTATTGATATGC	52	Reverse	White et al. (1990)
beta-tubulin (*tub2*)	T1	AACATGCGTGAGATTGTAAGT	55	Forward	O'Donnell & Cigelnik (1997)
	Bt2a	GGTAACCAAATCGGTGCTGCTTTC	55	Forward	Glass & Donaldson (1995)
	tub2fd	GTBCACCTYCARACCGGYCARTG	55	Forward	Woudenberg et al. (2009)
	tub1fd	CANMATGMGKGARATCGTRGT	55	Forward	Groenewald et al. (2013)
	T22	TCTGGATGTTGTTGGGAATCC	55	Reverse	O'Donnell & Cigelnik (1997)
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC	55	Reverse	Glass & Donaldson (1995)
	tub4rd	CCRGAYTGRCCRAARACRAAGTTGTC	55	Reverse	Woudenberg et al. (2009)
translation elongation factor 1-alpha (*tef 1-α*)	EF 1-728F	CATCGAGAAGTTCGAGAAGG	55	Forward	Carbone & Kohn (1999)
	EF2	GGARGTACCAGTSATCATGTT	55	Reverse	O'Donnell et al. (1998)
actin (*act*)	ACT512F	ATGTGCAAGGCCGGTTTCGC	52	Forward	Carbone & Kohn (1999)
	ACT783R	TACGAGTCCTTCTGGCCCAT	52	Reverse	Carbone & Kohn (1999)
glyceraldehyde-3-phosphate dehydrogenase (*gapdh*)	gpd1	CAACGGCTTCGGTCGCATTG	55	Forward	Berbee et al. (1999)
	gpd2	GCCAAGCAGTTGGTTGTGC	55	Reverse	Berbee et al. (1999)
RNA polymerase II second largest subunit (*rpb2*)	fRPB2-5F	GAYGAYMGWGATCAYTTYGG	56–59	Forward	Liu et al. (1999)
	fRPB2-5F2	GGGGWGAYCAGAAGAAGGC	56–59	Forward	Sung et al. (2007)
	fRPB2-7cR	CCCATRGCTTGYTTRCCCAT	56–59	Reverse	Liu et al. (1999)
guanine nucleotide-binding protein subunit beta (*ms204*)	MS204F.cerato	AAGGGCACCCTCGAGGGCCAC	55	Forward	Fourie et al. (2015)
	MS204R.cerato	GATGGTRACGGTGTTGATGTA	55	Reverse	Fourie et al. (2015)
Plasma membrane ATPase (*atpase*)	ATPDF1	ATCGTCTCCATGACCGAGTTCG	56	Forward	Lawrence et al. (2013)
	ATPDR1	TCCGATGGAGTTCATGATAGCC	56	Reverse	Lawrence et al. (2013)

[a] Beta-tubulin was amplified using primer pairs of T1/T22, T1/Bt2b, tub2fd/tub4rd, T1/tub4rd, or Bt2a/Bt2b to successfully obtain PCR amplification products.

oatmeal agar (OA) (Crous et al. 2019) and synthetic nutrient-poor agar (SNA, Nirenberg 1976) amended with autoclaved stems of *Anthriscus sylvestris* or pine needles placed onto the agar surface. Cultures were incubated at 20 °C in a 12 h day/night regime. Colony diameters were measured after 7 d, and colony morphologies determined after 7–14 d of incubation. Colony colours on the surface and reverse of inoculated Petri dishes were assessed according to the colour charts of Rayner (1970). Morphological observations of reproductive structures were determined using a Nikon AZ100 dissecting microscope and a Nikon Eclipse 80i compound microscope with differential interference contrast (DIC) illumination, both equipped with a Nikon DS-Ri2 high-definition colour digital camera. Slide preparations were made with lactic acid, and at least 30 measurements per structure were determined. For the fungarium specimens studied, sporocarps were rehydrated in 10 % lactic acid for examination. To study the pseudothecial/pycnidial wall, sections of pseudothecia/pycnidia were made by a Leica CM1950 freezing microtome. Observations of specimens were conducted using the same methods as described for cultures above.

Molecular analyses

Total genomic DNA of living cultures was extracted from fungal mycelia using the CTAB method (Liu et al. 2016), and primer sets used for nucleotide PCR amplification and sequencing listed in Table 1. PCR amplifications were performed in a total volume of 25 µL containing 2.5 µL 10× EasyTaq Buffer (TransGen Biotech, Beijing, China), 50 µM dNTPs, 0.1 µM of each primer, 0.75 U Taq DNA polymerase and 1–10 ng genomic DNA. PCR amplification conditions were set as follows: an initial denaturation temperature of 95 °C for 5 min, followed by 35 cycles at the denaturation temperature of 95 °C for 45 s, primer annealing at the temperature stipulated in Table 1, primer extension at 72 °C for 1 min and a final extension step at 72 °C for 10 min. Purification and sequencing of PCR amplifications were carried out by the Omegagenetics Company, Beijing, China. MEGA v. 7.0.26 was used to obtain consensus sequences from DNA sequences generated from forward and reverse primers.

Reference sequences for each genus were listed in Table S1. Sequence alignment was performed with MAFFT v. 7, and manually improved with MEGA v. 7.0.26. Bayesian infer-

Table 2 The 33 *Dothideomycetes* species listed as the Chinese quarantine organisms and their current names.

Chinese quarantine list (CQL)			Current Latin name	Recommend update of the CQL
No.	Chinese name	Latin name		
159	小麦叶疫病菌	*Alternaria triticina* Prasada et Prabhu	*Alternaria triticina* Prasada & Prabhu	
161	李黑节病菌	*Apiosporina morbosa* (Schweinitz) von Arx	*Apiosporina morbosa* (Schwein.) Arx	
164	落叶松枯梢病菌	*Botryosphaeria laricina* (K.Sawada) Y. Zhong	*Neofusicoccum laricinum* (Sawada) Y. Hattori & C. Nakash.	√
165	苹果壳色单隔孢溃疡病菌	*Botryosphaeria stevensii* Shoemaker	*Diplodia mutila* (Fr.: Fr.) Fr.	√
173	黄瓜黑星病菌	*Cladosporium cucumerinum* Ellis & Arthur	*Cladosporium cucumerinum* Ellis & Arthur	
188	菊花花枯病菌	*Didymella ligulicola* (K.F.Baker, Dimock & L.H.Davis) von Arx	*Stagonosporopsis chrysanthemi* (F. Stevens) Crous, Vaghefi & P.W.J. Taylor	√
189	番茄亚隔孢壳茎腐病菌	*Didymella lycopersici* Klebahn	*Boeremia lycopersici* (Cooke) Aveskamp, Gruyter & Verkley	√
207	马铃薯银屑病菌	*Helminthosporium solani* Durieu et Mont.	*Helminthosporium solani* Durieu & Mont.	
210	胡萝卜褐腐病菌	*Leptosphaeria libanotis* (Fuckel) Sacc.	*Plenodomus libanotidis* (Fuckel) Gruyter, Aveskamp & Verkley	√
211	十字花科蔬菜黑胫病菌	*Leptosphaeria maculans* (Desm.) Ces. & De Not.	*Plenodomus lingam* (Tode) Höhn.	√
216	橡胶南美叶疫病菌	*Microcyclus ulei* (P.Henn.) von Arx	*Pseudocercospora ulei* (Henn.) B.T. Hora & Mizubuti	√
221	香菜腐烂病菌	*Mycocentrospora acerina* (Hartig) Deighton	*Mycocentrospora acerina* (R. Hartig) Deighton	
222	松针褐斑病菌	*Mycosphaerella dearnessii* M.E.Barr	*Lecanosticta acicola* (Thüm.) Syd.	√
223	香蕉黑条叶斑病菌	*Mycosphaerella fijiensis* Morelet	*Pseudocercospora fijiensis* (M. Morelet) Deighton	√
224	松针褐枯病菌	*Mycosphaerella gibsonii* H.C. Evans	*Pseudocercospora pini-densiflorae* (Hori & Nambu) Deighton	√
225	亚麻褐斑病菌	*Mycosphaerella linicola* Naumov	*Septoria linicola* (Speg.) Garass.	√
226	香蕉黄条叶斑病菌	*Mycosphaerella musicola* J.L. Mulder	*Pseudocercospora musae* (Zimm.) Deighton	√
227	松针红斑病菌	*Mycosphaerella pini* E. Rostrup	*Dothistroma septosporum* (Dorog.) M. Morelet	√
233	高粱根腐病菌	*Periconia circinata* (M. Mangin) Sacc.	*Periconia circinata* (L. Mangin) Sacc.	
238	柑橘斑点病菌	*Phaeoramularia angolensis* (T. Carvalho & O. Mendes) P.M. Kirk	*Pseudocercospora angolensis* (T. Carvalho & O. Mendes) Crous & U. Braun	√
241	马铃薯坏疽病菌	*Phoma exigua* Desmazières f. sp. *foveata* (Foister) Boerema	*Boeremia foveata* (Foister) Aveskamp, Gruyter & Verkley	√
243	葡萄茎枯病菌	*Phoma glomerata* (Corda) Wollenweber & Hochapfel	*Didymella glomerata* (Corda) Qian Chen & L. Cai	√
244	豌豆脚腐病菌	*Phoma pinodella* (L.K. Jones) Morgan-Jones & K.B. Burch	*Didymella pinodella* (L.K. Jones) Qian Chen & L. Cai	√
245	柠檬干枯病菌	*Phoma tracheiphila* (Petri) L.A. Kantsch. & Gikaschvili	*Plenodomus tracheiphilus* (Petri) Gruyter, Aveskamp & Verkley	√
261	小麦基腐病菌	*Pseudocercosporella herpotrichoides* (Fron) Deighton	*Oculimacula yallundae* (Wallwork & Spooner) Crous & W. Gams	√
265	洋葱粉色根腐病菌	*Pyrenochaeta terrestris* (Hansen) Gorenz, Walker & Larson	*Setophoma terrestris* (H.N. Hansen) Gruyter, Aveskamp & Verkley	√
267	甜菜叶斑病菌	*Ramularia beticola* Fautr. & Lambotte	*Ramularia beticola* Fautrey & Lambotte	
271	欧芹壳针孢叶斑病菌	*Septoria petroselini* (Lib.) Desm.	*Septoria petroselini* (Lib.) Desm.	
272	苹果球壳孢腐烂病菌	*Sphaeropsis pyriputrescens* Xiao & J. D. Rogers	*Xenosphaeropsis pyriputrescens* (C.L. Xiao & J.D. Rogers) F. Liu, Crous & L. Cai	√
273	柑橘枝瘤病菌	*Sphaeropsis tumefaciens* Hedges	*Cophinforma tumefaciens* (Hedges) F. Liu, Crous & L. Cai	√
274	麦类壳多胞斑点病菌	*Stagonospora avenae* Bissett f. sp. *triticea* T. Johnson	*Parastagonospora pseudonodorum* B.A. McDonald, P.C. Brunner, Croll, D. Pereira & Crous	√
275	甘蔗壳多胞叶枯病菌	*Stagonospora sacchari* Lo & Ling	*Stagonospora sacchari* T.T. Lo & L. Ling	
282	苹果黑星病菌	*Venturia inaequalis* (Cooke) Winter	*Venturia inaequalis* (Cooke) G. Winter	

ence (BI) and Maximum likelihood (ML) methods were implemented. Bayesian analyses were performed using MrBayes v. 3.2.2 (Ronquist et al. 2012) as outlined by Liu et al. (2014). Maximum likelihood analyses were performed using RAxML v. 7.0.3 (Stamatakis 2006) with 1000 replicates under the GTR-GAMMA model.

Taxonomy

Each of the 33 *Dothideomycetes* species was treated along with their respective disease symptoms, morphological characteristics, habitat, geographic distribution, and nucleotide sequence dataset (including whole genome sequences for some species). The fungal names (in Latin and Chinese) on the list of Chinese quarantine pests, and their current names are summarised in Table 2.

Alternaria triticina Prasada & Prabhu, Indian Phytopathol. 15: 292. 1962 — Fig. 1, 2

Typus. India, Delhi, on leaves, leaf sheaths and glumes of *Triticum aestivum*, *E.G. Simmons*, Mar. 1960, holotype BPI 802696, culture ex-holotype ITCC 1186; isotype CBS H-6701, culture ex-isotype CBS 763.84 = ATCC 36205 = MUCL 44210 = IMI 289962 = E.G.S. 17-061 = CGMCC 3.9868.

Symptoms — The lesions caused by *Alternaria triticina* on leaves are initially small, oval, discoloured and scattered. As the lesions enlarge, they become dark brown to grey and irregular in shape, reaching 1 cm diam or more. Some lesions are surrounded by a bright yellow marginal zone (Singh 2017). As the disease progresses, several lesions coalesce to form large blotches, resulting in the death of the entire leaf. In some cases, once lesions appear, the leaf starts prematurely drying up from the tip. In severe cases, similar symptoms are produced on the leaf sheath and stem, as well as the awns and glumes if spikes are infected at the pre-anthesis stage (Chalkley 2015).

Hyphae initially hyaline, later olivaceous buff to honey, branched, septate, 2–7 µm broad. *Primary conidiophores* simple, branched or unbranched, septate, straight or geniculate, pale brown with a relatively paler colour at the tip, variable in length, 15–30 × 3–6 µm, bearing one or several apical or lateral conidiogenous loci. *Conidia* solitary or in chains of 2–4, ovoid, obovoid, obclavate, or long-ellipsoid, not constricted or slightly constricted at some septa, smooth or verrucose, pale brown, with 1–7 transverse and 0–5 longitudinal septa, varying in size, 15–53 × 5–12 µm (av. ± S.D. = 25.8 ± 8.8 × 7.8 ± 1.5 µm). Conidial body sometimes gradually tapering into a beak, 2–43 × 3–7 µm, and multi-locus apical or lateral *secondary conidiophores* can be formed, concolourous with the main conidial body, geniculate.

Culture characteristics — Colonies on MEA 7.5–8 cm diam in 10 d, flat or effuse, entire; aerial mycelia fluffy to cottony, deep olive grey; reverse greenish olivaceous. Colonies on PDA up to 9 cm diam, flat or effuse, entire, aerial mycelia fluffy to cottony, olivaceous buff; reverse olivaceous. Colonies on OA 7.5–8 cm diam in 10 d, flat or effuse, entire, grey olivaceous to dark grey olivaceous.

Habitat — *Avena sativa* (oats), *Hordeum vulgare*, *Secale cereale* (rye), *Sesamum indicum*, × *Triticosecale* (Triticale), *Triticum aestivum* and other *Triticum* spp.

Geographic distribution — Africa: Egypt (Beshir 1994), Nigeria (Wiese 1987). – America: Argentina (Perelló & Sisterna 2006), Mexico (Waller 1981). – Asia: Bangladesh (Rashid et al. 1985, Ahmed et al. 1994), China (Shang et al. 2000, Zhang 2000, Yang & Ma 2001, Guo 2005), India (Prasada & Prabhu 1962), Iran (Simmons 2007), Iraq (Khudhair et al. 2014), Israel

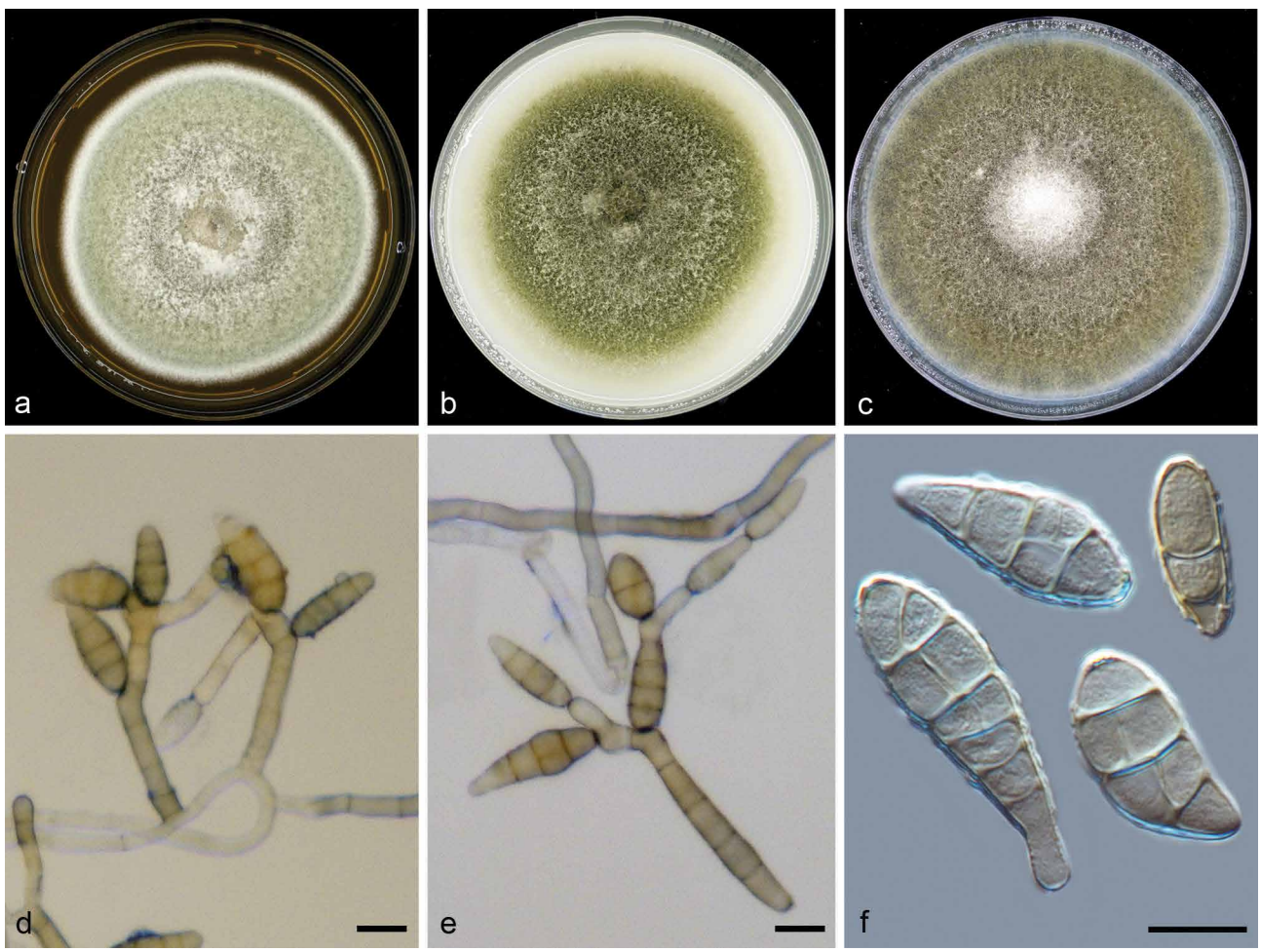

Fig. 1 *Alternaria triticina* (ex-isotype CBS 763.84). a–c. Colonies in 10 d (20 °C, a. on MEA; b. on OA; c. on PDA); d–e. conidiophores and conidia; f. conidia. — Scale bars: d–f = 10 µm.

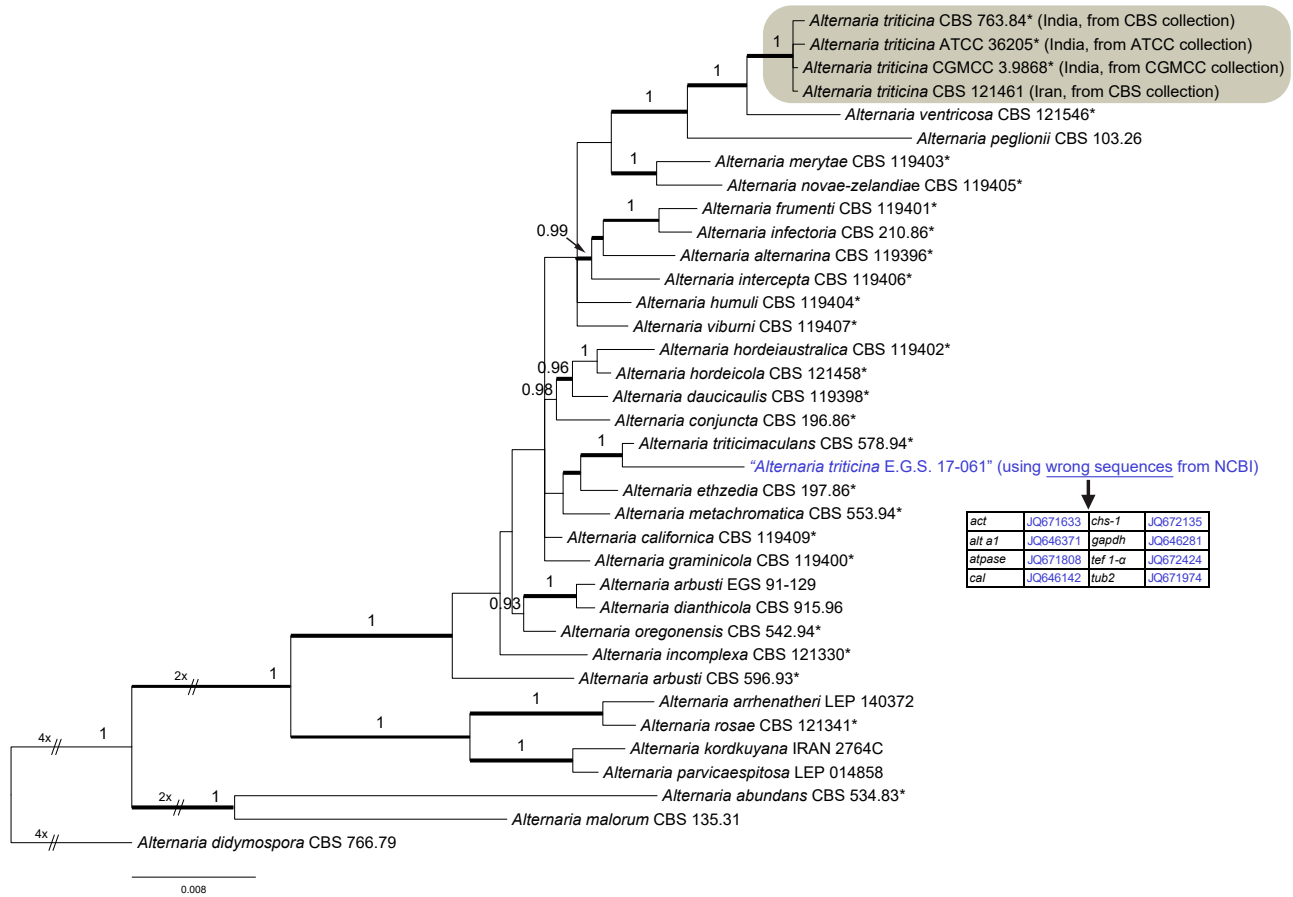

Fig. 2 Phylogenetic tree of *Alternaria* sect. *Infectoriae* and related species calculated with Bayesian analysis on a three-locus combined dataset (*atpase*, *gapdh*, ITS). Thickened branches indicate branches present in the Bayesian tree with > 0.90 posterior probabilities. The RAxML bootstrap support values (> 50 %) are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

(IMI Herbarium), Lebanon (Logrieco et al. 1990), Pakistan (IMI Herbarium), Turkey (Ozcelik & Ozcelik 1997), Yemen (IMI Herbarium). – Europe: France (Logrieco et al. 1990), Greece (Logrieco et al. 1990), Italy (Logrieco et al. 1990), Macedonia (Logrieco et al. 1990), Portugal (Logrieco et al. 1990), Russian Federation (Gor'kovenko 2001).

NCBI Genome ID: JAGKPX000000000 (CBS 763.84, this study).

Notes — *Alternaria triticina* causes leaf blight of wheat, and can lead to significant yield losses on the Indian subcontinent (Prasada & Prabhu 1962). As a seed-borne pathogen of wheat and durum, *A. triticina* might be introduced along with wheat seed, agricultural machinery, and bulk feed grains, or even in the inadvertent entry (intentional or unintentional with travellers' goods). Thus, the entry potential of *A. triticina* is high and is cause for significant attention at the ports of entry.

Although several studies have reported the occurrence of *A. triticina* from many regions (see the geographic distribution listed above), the records are in need of accurate reassessment using molecular data. According to the revised taxonomic system of *Alternaria*, *A. triticina* belongs to sect. *Infectoriae* (Lawrence et al. 2013). However, we noticed that sequences of the ex-type cultures (ATCC 36205, CGMCC 3.9868, IMI 289962, E.G.S. 17-061, MUCL 44210, ITCC F 1186) generated from different publications are inconsistent. For example, the ITS sequence of MUCL 44210/IMI 289962/E.G.S. 17-061 (AY714476) (Mercado et al. 2006) differs from AY762948 (E.G.S. 17-061) (Xue & Zhang 2007) in nine nucleotides; *gapdh* sequence of CBS 763.84 (FJ214846) (Andersen et al. 2009) differs from JQ646281 (E.G.S. 17-061) (Lawrence et al. 2013) in 22 nucleotides. In general, currently deposited sequences in GenBank are unreliable in many cases, and mistakes might exist in previous publications. To resolve this problem, we re-sequenced ex-type strains of *A. triticina* obtained from three culture collections in the present study, i.e., CBS 763.84, CGMCC 3.9868, and ATCC 36205. As expected, sequences of the three strains are consistent and the phylogenetic analysis showed that *A. triticina* is closely related with *A. ventricosa* (Fig. 2). The sequences of E.G.S. 17-061 generated in Lawrence et al. (2013) is incorrect, as the strain formed a well-supported clade with *A. triticimaculans* CBS 578.94 (Fig. 2).

Apiosporina morbosa (Schwein.) Arx, Acta Bot. Neerl. 3: 86. 1954 — Fig. 3

Basionym. *Sphaeria morbosa* Schwein., Schriften Berlin. Ges. Naturf. Freunde 1: 40. 1822.

Synonyms. *Cucurbitaria morbosa* (Schwein.) Ellis, N. Amer. Fungi, Ser. 1: 691. 1881.

Plowrightia morbosa (Schwein.) Sacc., Syll. Fung. 2: 638. 1883.

Otthia morbosa (Schwein.) Ellis & Everh., N. Amer. Pyrenomyc.: 251. 1892.

Dibotryon morbosum (Schwein.) Theiss. & Syd., Ann. Mycol. 13: 663. 1915.

Typus. USA, Pennsylvania, Bethlehem, on *Prunus* sp., *L.D. von Schweinitz*, syntypes PH-01048831, 01048832, 01048838, 01048839, 01048840.

Symptoms — *Apiosporina morbosa* causes rough greenish brown to black galls (black knots) on twigs and branches, that are spindle-shaped. The knot is usually confined to one side of a branch; externally it is composed of fungal pseudoparenchyma, but internally it consists of both fungus and host cells (Zhang et al. 2005).

Ascomata densely gregarious, subglobose, triangular or oblong, often flattened on the top, black, 160–230 × 170–250 µm

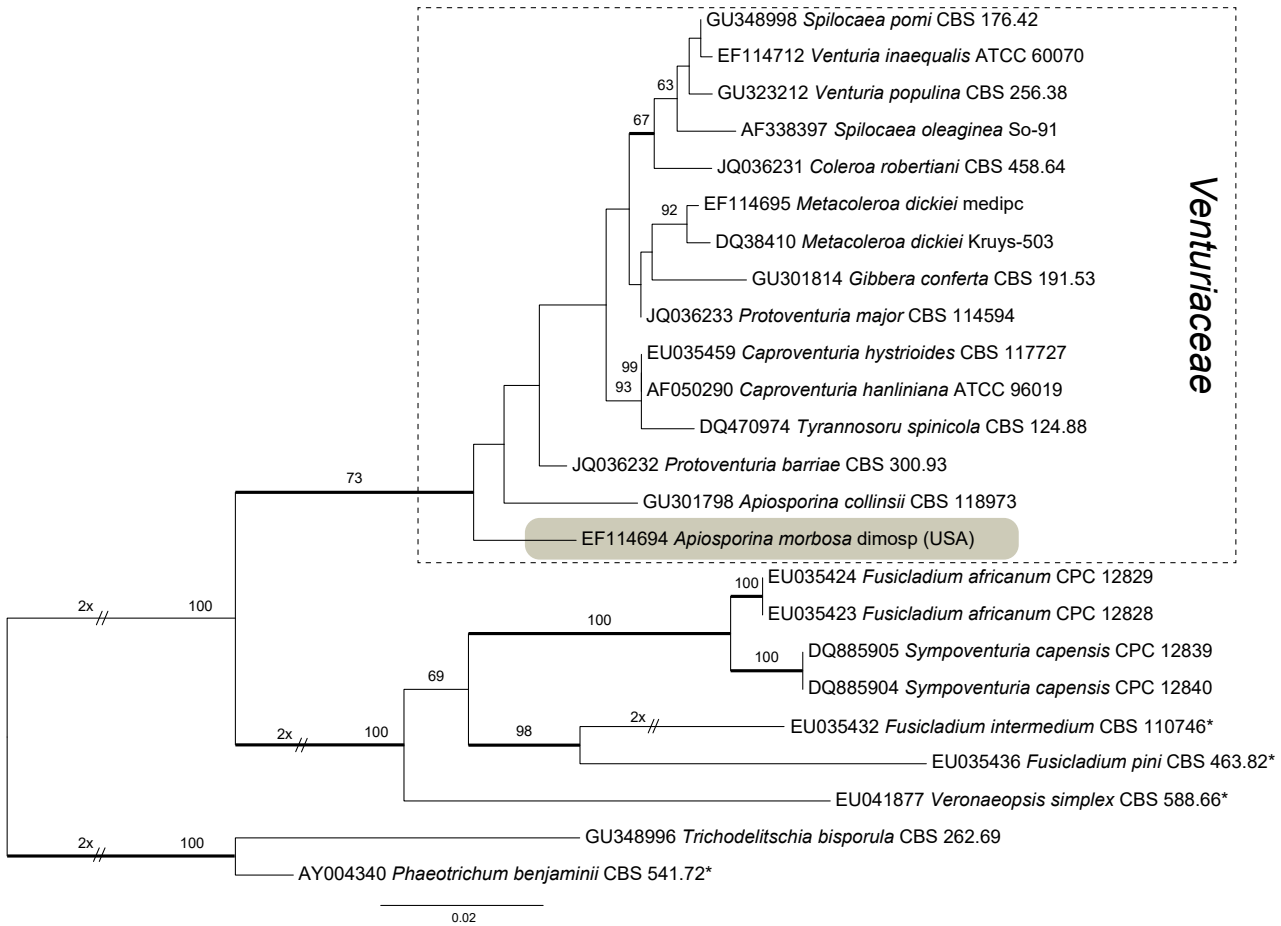

Fig. 3 Phylogenetic tree of *Apiosporina morbosa* and related species calculated with RAxML on LSU sequences. Thickened branches indicate branches present posterior probabilities (> 0.90) in the Bayesian tree. The bootstrap support values > 50 % are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

diam. *Peridium* 30–45 µm wide, wall composed of one layer, heavily pigmented, thick-walled *textura angularis*, cells 3–7 µm diam. *Pseudoparaphyses* dense, septate, branched, 1.5–3 µm wide. *Asci* subcylindrical or broadly clavate, 8-spored, bitunicate, 68–90 × 12.5–15 µm (av. = 73 × 13 µm). *Ascospores* biseriate, clavate, tapered towards the base, apex obtusely rounded, one septate near the lower end, barely constricted at the septum, hyaline to pale brown, smooth-walled, 15–19 × 5–7.5 µm (av. = 17.4 × 6.8 µm) (adapted from Zhang et al. 2011). *Conidiophores* in loose to dense fascicles, erect, flexuous, or geniculate, unbranched or branched at the base, septate, pale olivaceous to pale brown, paler towards the apex, smooth, thick-walled, somewhat swollen at the base, 20–95 × 3–7 µm. *Conidiogenous cells* integrated, terminal or intercalary, with several conidiogenous loci, proliferation sympodial, loci denticulate, 1–1.5 µm wide. *Conidia* solitary or rarely in short chains, often laterally fused in pairs, ovoid, obovoid, ellipsoid or irregular, 0–1-septate, pale olivaceous, smooth, thick-walled, 4–19 × 3–6 µm, hilum 1–1.5 µm wide (adapted from Schubert et al. 2003).

For symptom and microstructure illustrations see Corlett (1976) and Zhang et al. (2011).

Habitat — *Prunus* spp.

Geographic distribution — America: Canada, Mexico, USA (EPPO A1 list, https://www.eppo.int/ACTIVITIES/plant_quarantine/A1_list).

Notes — *Apiosporina morbosa* causes black knot disease of wild and cultivated *Prunus* species, and commonly occurs throughout Canada and the USA (Corlett 1976). Losses caused by *A. morbosa* have been estimated to be 10 % on plums and 1 % on cherries (Cramer 1967). Many countries in America, Asia, and Europe have listed *Apiosporina morbosa* as a quarantine pest (EPPO 2019a).

Unfortunately, all ITS reference sequences of *Apiosporina morbosa* deposited in GenBank (AF493983, AY166451, AY842353, AY165751, AF493984, AF493982, MK575461) are incorrect and showed highest similarities with *Cladosporium* spp. (*Cladosporiales*) (Abdollahzadeh et al. 2020) or *Fuscostagonospora* and *Periconia* (*Pleosporales*), including the sequence of ATCC 15085 which was mistakenly regarded as ex-type of *A. morbosa* in previous studies (Fernando et al. 2005, Zhang et al. 2005). We suspected that the strains used in Fernando et al. (2005) and Zhang et al. (2005) were *Cladosporium* spp. rather than *A. morbosa*, because *Cladosporium* spp. (*C. lycoperdinum* and *C. xylophilum*) had been isolated from galls of *A. morbosa* on *Prunus* spp. from Canada (Bensch et al. 2012).

Presently the only reliable sequences of *A. morbosa* are EF114718 (SSU) and EF114694 (LSU) (Winton et al. 2007), and the LSU phylogram indicates that *A. morbosa* belongs to *Venturiaceae*, *Venturiales* (Shen et al. 2020; Fig. 3).

Boeremia foveata (Foister) Aveskamp et al., Stud. Mycol. 65: 40. 2010 — Fig. 4, 5

Basionym. *Phoma foveata* Foister, Trans. Bot. Soc. Edinburgh 33: 66. 1940.

Typus. UK, from a tuber of *Solanum tuberosum*, *C.E. Foister*, Mar. 1937, culture ex-isotype CBS 200.37.

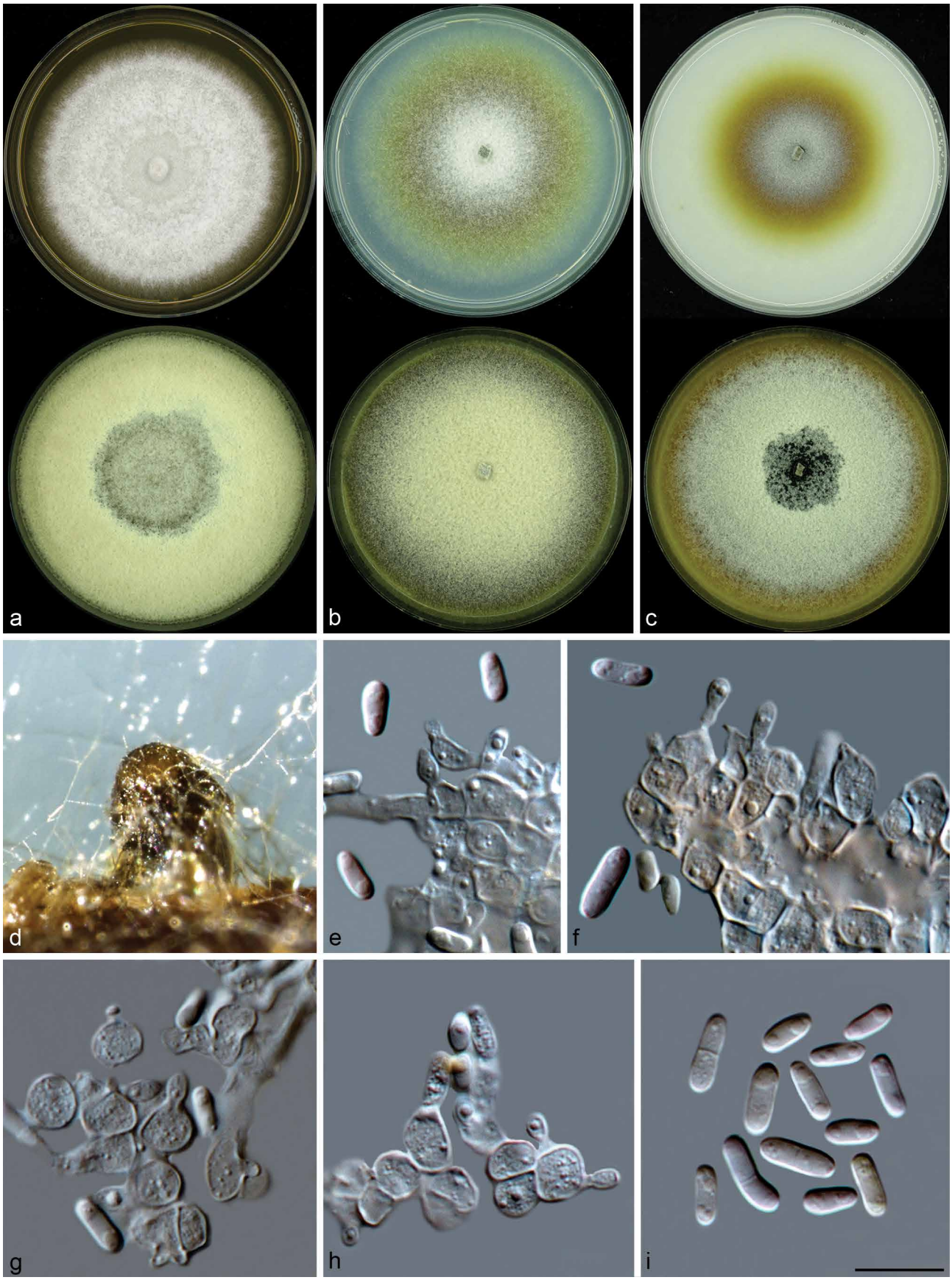

Fig. 4 *Boeremia foveata* (a–c. CBS 200.37, d–i. CBS 109176). a–c. Colonies on MEA, PDA, and OA in one wk (upper row) and two wk (below) (20 °C); d. pycnidia; e–h. conidiogenous cells and conidia; i. conidia. — Scale bar: i = 10 µm, applies to e–i.

Symptoms — The first visible signs of gangrene on potato tubers are small and dark. Depressed patches enlarge slowly and may coalesce. Some patches do not develop further but shrivel up and are easily removed, leaving a clean dry cavity. Larger lesions, which may almost entirely cover the tuber, have an irregular outline and are occasionally wrinkled. Even if an external lesion is small, the internal rot can be more or less extensive; cavities often develop, lined with grey or dark brown to purple mycelia, in which conidiomatal pycnidia may be found (Smith et al. 1992).

Conidiomata pycnidial, only produced on pine needles on SNA in this study, usually solitary, globose to sub-globose, brown, semi-immersed. *Ostiole* single, slightly papillate. *Pycnidial wall* pseudoparenchymatous, composed of isodiametric cells, 4–5 layers, 21–30 µm thick. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform or subglobose, 4–7 × 3–6 µm. *Conidia* cylindrical or subcylindrical, some oblong, incidentally slightly curved, few reniform, hyaline, aseptate, rarely 1-septate, 4.5–8.5 × 2–3 µm (av. ± S.D. = 6.5 ± 0.9 × 2.5 ± 0.2), with or without minute guttules.

Culture characteristics — Colonies on PDA 75–77 mm diam after 7 d, margin regular. Immersed mycelia olivaceous buff to grey olivaceous. Aerial mycelia floccose, white. Reverse olivaceous buff to grey olivaceous. Colonies on OA 63–65 mm diam after 7 d, margin regular. Immersed mycelia olivaceous buff. Aerial mycelia white or smoke grey. Reverse olivaceous buff to grey olivaceous. Colonies on MEA 76 mm diam after 7 d, margin regular. Aerial mycelia floccose, white. Reverse pure yellow to buff.

Additional materials examined. Bulgaria, from a tuber of *Solanum tuberosum*, *H. de Gruyter*, deposited in CBS culture collection Jan. 2001, culture CBS 109176 = CECT 2828 = PD 94/1394. – Ireland, from a tuber of *Solanum tuberosum*, deposited by *C. Logan*, unknown collection date, culture ATCC 24771. – Netherlands, tuber of *Solanum tuberosum* with gangrene lesions, *C. Logan*, 1979, culture CBS 341.67 = CECT 20055 = IMI 331912 = CECT 20798 (strongly pathogenic).

Habitat — *Solanum tuberosum*, occasionally isolated from other plants (e.g., *Beta vulgaris*, *Hordeum vulgare*, *Pisum sativum*).

Geographic distribution — (EPPO global database https://gd.eppo.int/taxon/PHOMEF/distribution, Farr & Rossman 2021): Africa: Egypt, Sierra Leone, South Africa. – America: Chile, Colombia, Peru, USA. – Asia: China (restricted in Gansu Province), India, Libya, Yemen. – Europe: Austria, Belgium, Bulgaria, Croatia, Cyprus, Czech Republic, Denmark, Finland,

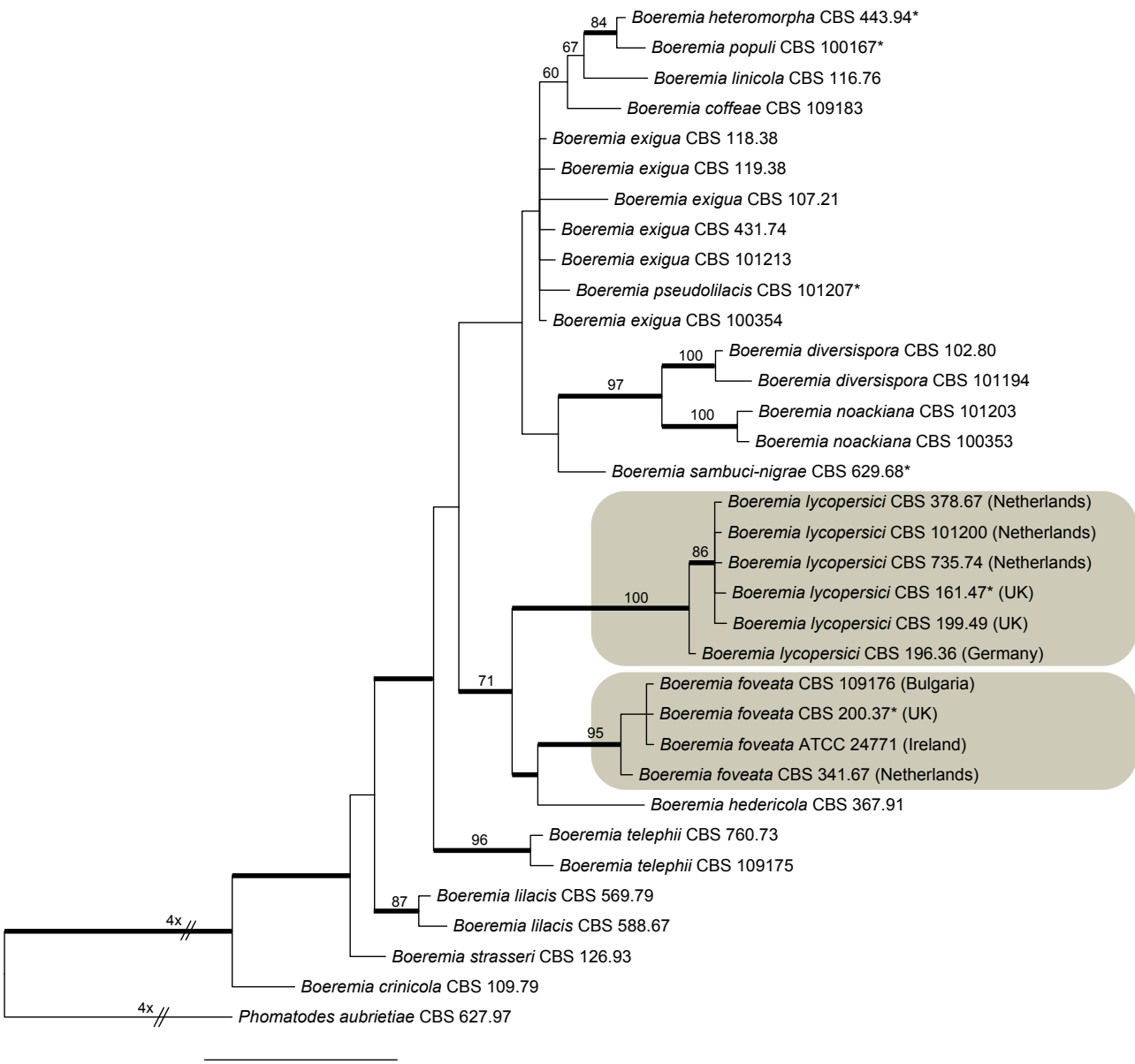

Fig. 5 Phylogenetic tree of *Boeremia* calculated with Bayesian analysis on a three-gene combined dataset (ITS, *rpb2*, *tub2*) showing affinities of *B. foveata* and *B. lycopersici* with members of *Boeremia* species. Thickened branches indicate branches present in the Bayesian tree with > 0.90 posterior probabilities. The RAxML bootstrap support values (> 50 %) are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

France, Germany, Greece, Ireland, Latvia, Lithuania, Netherlands, Norway, Poland, Romania, Serbia, Slovakia, Sweden, Switzerland, UK. – Oceania: Australia, New Zealand.

NCBI Genome ID: JAFISF000000000 (CBS 200.37, this study).

Notes — *Boeremia foveata* (Aveskamp et al. 2010) was listed in the Chinese quarantine pest directory as *Phoma exigua* f.sp. *foveata*. This fungus mainly infects *Solanum tuberosum*, and was occasionally isolated from *Beta vulgaris*, *Hordeum vulgare*, and *Pisum sativum* (Data sheet of EPPO list A2). Four isolates (CBS 109176, CBS 200.37, CBS 341.67, and ATCC 24771) from *Solanum tuberosum* from Europe formed a distinct clade (95/1.00), representing *B. foveata* (Fig. 5). Loci sequenced from these four strains are identical, while the independent branch of CBS 341.67 is due to the missing *rpb2* sequence in the analysed sequence dataset. Since the ex-isotype strain CBS 200.37 remained sterile, we illustrated this species using a phylogenetically conspecific strain CBS 109176 (Aveskamp et al. 2010; Fig. 5 in the present study).

Phoma foveata was once reported to cause potato gangrene in Gansu Province in China (Yang et al. 2012). However, we were unable to accurately identify it solely based on the public ITS sequence (JQ804843), since the latter is identical to not only the sequences of *B. foveata*, but also to *B. exigua*, *B. heteromorpha*, *B. populi*, *B. pseudolilacis*, and *B. telephii*. Morphologically, the Gansu isolate produces somewhat longer conidia than *B. foveata* (5.8–11.5 × 2–4 µm vs 4.5–8.5 × 2–3 µm). Therefore, the identification of pathogen on potato in Gansu Province needs further confirmation, and its distribution in China remains unconfirmed.

Boeremia lycopersici (Cooke) Aveskamp et al., Stud. Mycol. 65: 40. 2010 — Fig. 5, 6

Basionym. *Phoma lycopersici* Cooke, Grevillea 13: 94. 1885.
Synonyms. *Didymella lycopersici* Kleb., Z. Pflanzenkrankh. 31: 9. 1921.
Didymella lycopersici Hollós, Ann. Mus. Nat. Hung. 5: 461. 1907.
Sphaeronaema lycopersici Plowr., Gard. Chron. 16: 260. 1881.
Ascochyta lycopersici (Plowr.) Brunaud, Bull. Soc. Bot. France 34: 430. 1887.
Phoma lycopersici (Plowr.) Jacz., Nouv. Mem. Soc. Imp. Naturalistes Moscou 15: 350. 1898 (Nom. illegit.).

Typus. UK, Wales, Montgomeryshire, forden, on stem of *Solanum lycopersicum*, unknown collection date, *J.E. Vize* (ex herb. M.C. Cooke, Fungi britannici exs.), holotype K(M) 197430; from *S. lycopersicum*, unknown collection date, isolated by *E. Sheard*, epitype designated here CBS H-24764, MBT 10001719, culture ex-epitype CBS 161.47.

Symptoms — Lesions caused by *Boeremia lycopersici* are initially dark brown and sunken, which eventually may girdle the stem just above soil level.

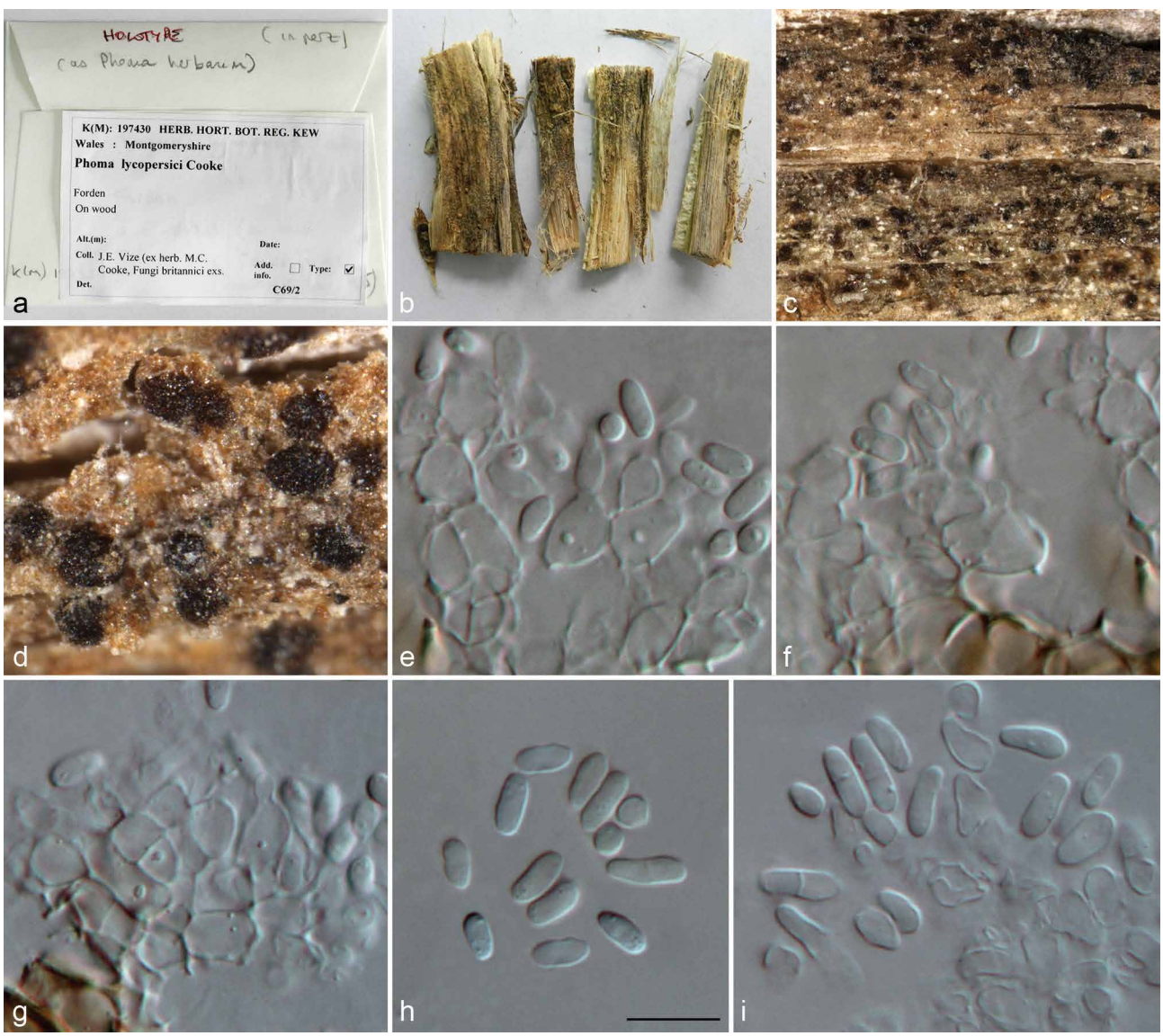

Fig. 6 *Boeremia lycopersici* (holotype K(M)197430). a. Type collection packet; b. type specimen; c–d. pycnidia on wood; e–g. conidiogenous cells; h–i. conidia. — Scale bar: h = 10 µm, applies to e–i.

Later, secondary cankers may develop higher up the stem. Numerous conidiomata and conidia form on the soft and outer diseased tissues in damp conditions (Holliday & Punithalingam 1970).

Ascomata perithecial, punctiform, black, densely gregarious, at first covered by the cuticle, ultimately more or less exposed. *Ascospores* lanceolate, binucleate, 12 × 4 µm (adapted from Cooke 1885). *Conidiomata* pycnidial, solitary or confluent, globose or subglobose. *Conidiogenous cells* phialidic, hyaline, simple, smooth, ampulliform, 4.5–8 × 3–5.5(–11) µm. *Conidia* aseptate, rarely 1-septate, hyaline, subglobose, ellipsoidal or cylindrical, 4–7.5 × 2–3.5 µm (av. ± S.D. = 6 ± 0.6 × 2.8 ± 0.2 µm).

Additional materials examined. Germany, Berlin, from fruit of *S. lycopersicum*, Nov. 1936, *H.W. Wollenweber*, CBS 196.36 = ATCC 11847 = MUCL 9560. – Netherlands, Heerde, from fruit of *S. lycopersicum*, Aug. 1967, *G.H. Boerema*, culture CBS 378.67 = PD 76/276; Wageningen, from *S. lycopersicum*, unknown collection date, *M.A. Dorenbosch*, culture CBS 101200 = PD 72/863; from *S. lycopersicum*, *G.J. Bollen*, unknown collection date, culture CBS 735.74. – UK, unknown substrate and collection date, isolated by *P.H. Williams*, culture CBS 199.49.

Habitat — *Solanum lycopersicum.*

Unverified habitat — (Farr & Rossman 2021): *Capsicum* sp., *Citrullus vulgaris*, *Cucumis* sp., *Cucurbita maxima*, *Solanum melongena*, *S. tuberosum*, *Telfairia pedata.*

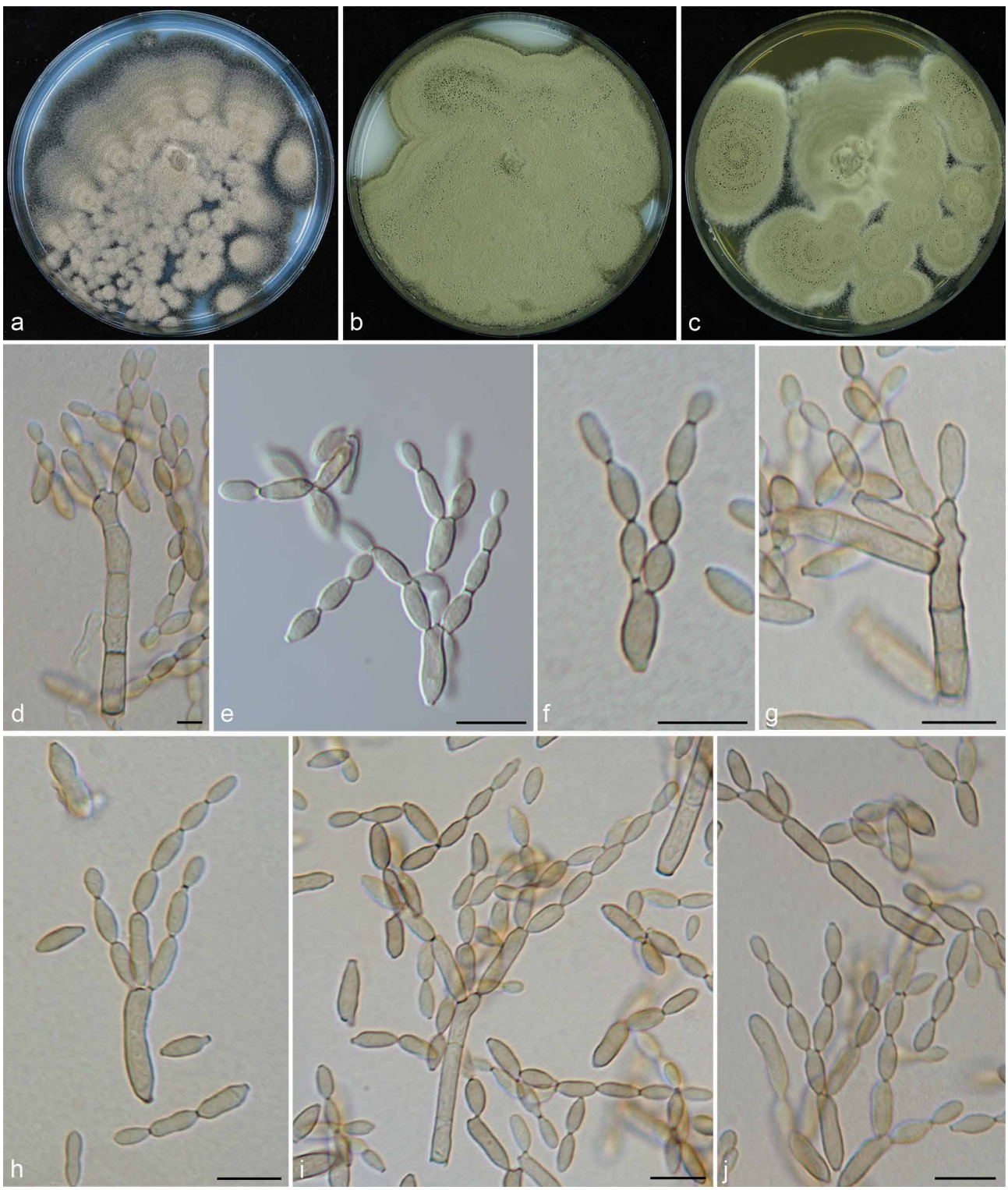

Fig. 7 *Cladosporium cucumerinum* (ex-epitype CBS 171.52). a–c. Colonies in two wk (20 °C, a. on PDA; b. on OA; c. on MEA); d–j. conidiophores and conidial chains. — Scale bars: d–j = 10 µm.

Geographic distribution — (Farr & Rossman 2021): Africa: Côte d'Ivoire, Nigeria, South Africa, Togo. – America: Brazil, Canada, Trinidad and Tobago, USA. – Asia: Brunei Darussalam, India, Japan, Malaysia. – Europe: Germany, Greece, Italy, Netherlands, Poland, Sweden, UK. – Oceania: New Zealand, Papua New Guinea, Tonga.

NCBI Genome ID: JAGKPY000000000 (CBS 378.67, this study).

Notes — *Boeremia lycopersici* was listed in the Chinese quarantine pest directory as *Didymella lycopersici*, and its asexual morph was described under the name *Phoma lycopersici*. Although both morphs have been morphologically described several times (e.g., Cooke 1885, Brooks & Searle 1921, Klebahn 1921, Holliday & Punithalingam 1970, Morgan-Jones & Burch 1988), the type specimens of both have never been clearly designated in previous publications (Cooke 1885, Klebahn 1921). Requests for type material of both morphs were sent to 11 fungaria (B, BPI, CBS, E, HBG, HUH, IMI, K, PAV, PC, PDD), and we eventually received the type of *P. lycopersici* from K (No. 197430) and compiled a description and illustration (Fig. 6). Unfortunately, the type of *D. lycopersici* was destroyed during World War II (B, curator pers. comm.).

Phoma lycopersici was transferred to *Boeremia* as *B. lycopersici* to comply with single name nomenclature (Aveskamp et al. 2010). In order to stabilise the application of this name, we located suitable strains for the designation of an epitype. *Phoma lycopersici* and *D. lycopersici* were originally reported from *Solanum lycopersicum* from the UK and Germany, respectively (Cooke 1885, Klebahn 1921). Two strains (CBS 161.47 and CBS 199.49) from tomato from the UK, one (CBS 196.36) from Germany and three (CBS 101200, CBS 735.74, CBS 378.67) from the Netherlands were obtained in this study, and they formed a distinct clade with high bootstrap value and posterior probability (100/1.00), representing *B. lycopersici* (Fig. 5). Sequences of strain CBS 196.36 differed from the other five strains only in one base pair in ITS and one in *tub2*. Unfortunately, all strains of *B. lycopersici* examined in this study remained sterile.

Cladosporium cucumerinum Ellis & Arthur, Bull. Indiana Agric. Stat. 19: 9. 1889 — Fig. 7, 8

Synonyms. *Scolicotrichum melophthorum* Prill. & Delacr., Bull. Soc. Mycol. France 7: 219. 1891.
Cladosporium cucumeris A.B. Frank, Z. Pflanzenkrankh. 3: 31. 1893.
Cladosporium scabies Cooke, Gard. Chron. 34: 100. 1903.

Typus. Netherlands, from fruits of *Cucumis sativus*, isolated by *N. Hubbeling*, epitype CBS H-20429, culture ex-epitype CBS 171.52 = MUCL 10092. – USA, New York, Geneva, on fruits of *Cucumis sativus* (*Cucurbitaceae*), *J.C. Arthur*, holotype NY.

Symptoms — Leaf spots are slightly water-soaked or pale green, usually numerous and appearing on and between veins. Elongate spots may develop on stems and petioles. Spots gradually turn grey or white and become roughly circular to angular, often with yellow margins. Lesions on fruit are

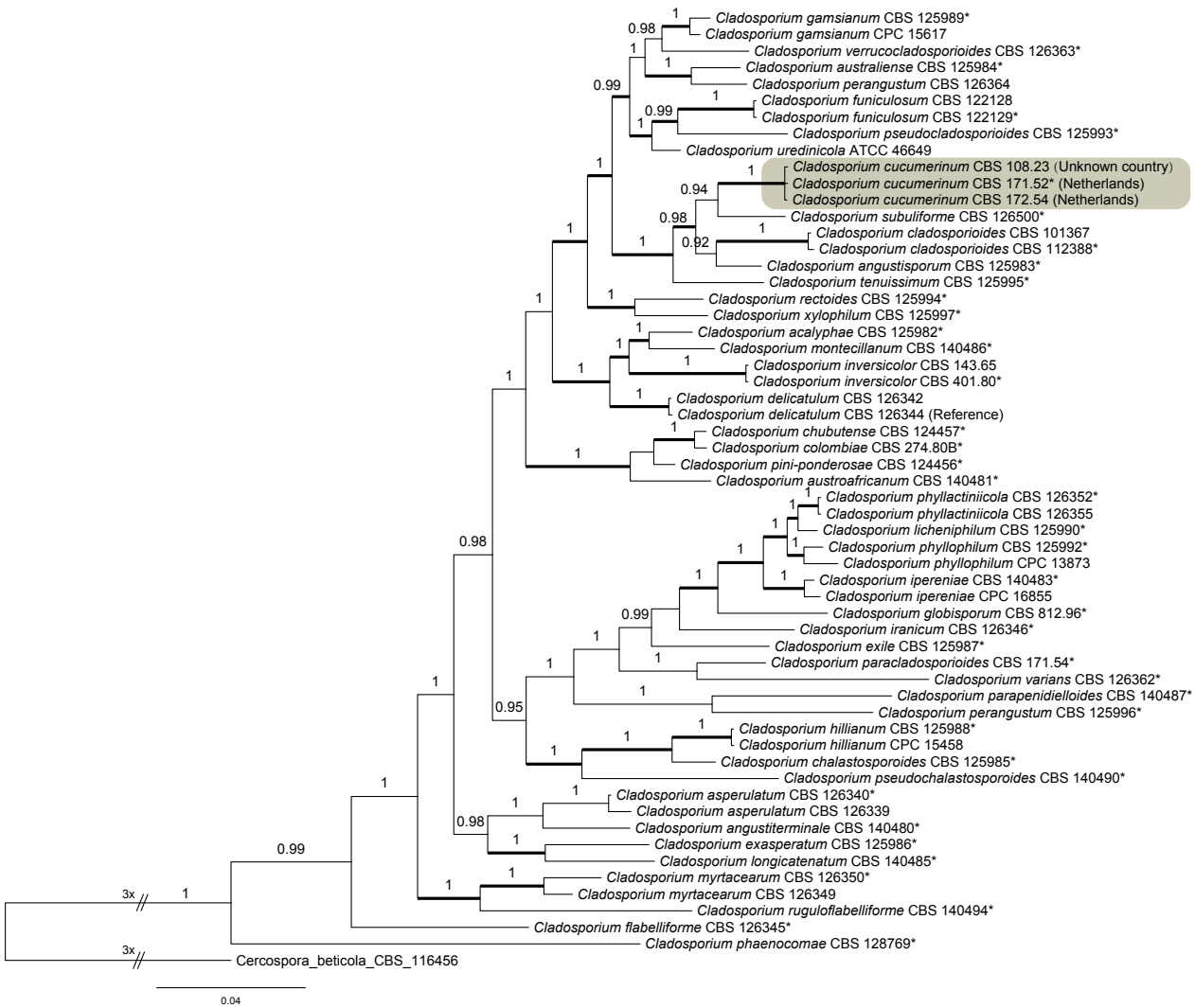

Fig. 8 Phylogenetic tree of *Cladosporium cladosporioides* complex calculated with Bayesian analysis on *act*, ITS, and *tef 1-α* sequences showing affinities of *C. cucumerinum* with allied species. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

water-soaked at first, small, up to 1 cm long and 0.5 cm deep, then becoming darker with age and may create a cavity, and a gummy brown substance is exuded in drops from the infected area (Dixon 1981).

Mycelia immersed or superficial in culture, hyphae branched, septate, subhyaline, pale brown or pale olivaceous brown. *Conidiophores* pale brown to medium brown, smooth, solitary, macro- and micronematous, branched or unbranched, septate, straight to slightly flexuous, sometimes geniculate with lateral conidiogenous loci. *Conidiogenous cells* cylindrical or oblong, straight, rarely slightly curved, sometimes geniculate, 2–5 loci, 1.5–3 µm diam. *Ramoconidia* occasionally formed, cylindrical or oblong, smooth, 9–43 × 2.5–4 µm, 0–2-septate, not constricted at the septum. *Conidia* catenate, in branched chains, straight, pale brown to medium brown, smooth, terminal conidia tear-shaped, obovoid to ellipsoid-ovoid, aseptate, 4–6.5 × 2–3.5 µm (av. ± SD = 5.4 ± 0.7 × 2.4 ± 0.3), hila 0.5–1 µm diam,

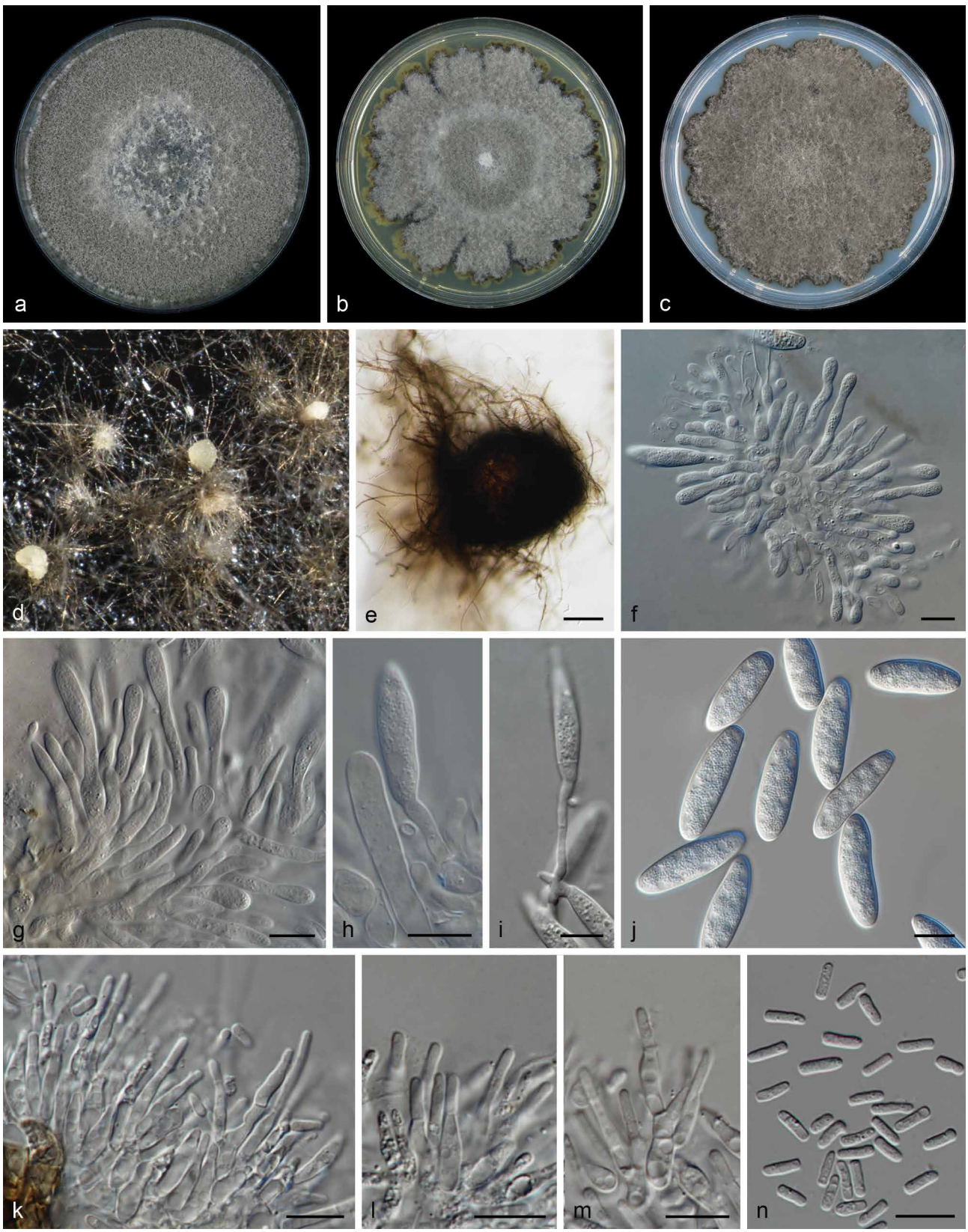

Fig. 9 *Cophinforma tumefaciens* (CBS 124934). a–c. Colonies in two wk (20 °C, a. on OA; b. on MEA; c. on PDA); d–e. conidiomata; f–i. conidiophores and conidia; j. conidia; k–m. spermatophores; n. spermatia. — Scale bars: e–n = 10 µm.

intercalary conidia ellipsoid or fusiform, sometimes subcylindrical, aseptate, 6–10 × 2.5–4.5 µm (av. ± SD = 7.4 ± 0.8 × 3.4 ± 0.3); secondary ramoconidia cylindrical to cylindrical-oblong, 0–1-septate, 7–40 × 2.5–5.5 µm, hila 1.5–2.5 µm diam, sometimes thickened (adapted from Bensch et al. 2010).

Culture characteristics — Colonies on PDA flat with undulate edge, smoke grey with pale mouse grey concentric round rings, the margin olivaceous black, reverse olivaceous black. Colonies on OA flat with entire edge, greenish glaucous, reverse olivaceous black. Colonies on MEA flat with undulate edge, greenish glaucous with concentric round rings, reverse olivaceous black.

Habitat — On leaves, stems, and fruits of *Cucurbitaceae*, especially *Cucumis sativus*, *C. melo*, and *Cucurbita pepo*. Other host genera include *Citrullus*, *Lagenaria*, *Luffa*, *Momordica*, and *Sechium*.

Geographic distribution — Cosmopolitan. The reports of *Cladosporium cucumerinum* in China (Tai 1979, Zhang 2003, Zhuang 2005) are in need of confirmation using molecular analyses.

NCBI Genome ID: JAFISC000000000 (CBS 171.52, this study).

Notes — *Cladosporium cucumerinum* belongs to the *Cladosporium cladosporioides* complex (Bensch et al. 2010, 2012) and clusters as a sister clade to *C. subuliforme* (Fig. 8). However, we noticed that there is a probable sequence error in the GenBank sequence (ITS, HM148072) from the ex-epitype strain CBS 171.52 (at position 146–170 and 512), and the newly generated sequence (confirmed twice) is deposited in GenBank as MW810260 in this study.

Although it has been reported as pathogenic to various plants other than *Cucumis sativus*, either in *Cucurbitaceae* or other hosts (e.g., *Canavalia ensiformis*, *Capsicum annuum*, *Helianthus annuus*, *Solanum melongena*, *S. tuberosum*) (Hasija 1967, Roberts et al. 1986, Kwon et al. 1999, 2000), molecular examinations are necessary to confirm their identities (Bensch et al. 2010). For detailed information of *C. cucumerinum* see Bensch et al. (2010, 2012).

Cophinforma tumefaciens (Hedges) F. Liu, Crous & L. Cai, *comb. nov.* — MycoBank MB 840270; Fig. 9, 10

Basionym. *Sphaeropsis tumefaciens* Hedges, Phytopathology 1: 64. 1911.

Synonyms. *Fusicoccum atrovirens* Mehl & Slippers, Mycologia 103: 543. 2011.

Cophinforma atrovirens (Mehl & Slippers) A. Alves & A.J.L. Phillips, Stud. Mycol. 76: 80. 2013.

Cophinforma eucalypti Doilom et al., Fungal Diversity 57: 174. 2012.

Typus. Jamaica, Browns town, St. Anns, on *Citrus* × *sinensis*, *J.G. Hall*, 2 Jan. 1909?, syntype? BPI 366136.

Symptoms — The fungus can infect either old or young trees, but usually grows on fairly old limbs. It causes knots on lime trees, which appear similar to the symptoms caused by scale insects. The knots are usually approximately round but they may be somewhat elongated (Hedges 1911).

Conidiomata pycnidial, superficial or semi-immersed, 135–400 µm diam, solitary or confluent, dark brown to black, complex, effuse, (sub-)globose, densely covered with dark brown hyphae; wall composed of three layers, outer layer of wall *textura angularis*, thick-walled dark to light brown, middle layer cells thin-walled, light brown, inner layer of cells thin-walled,

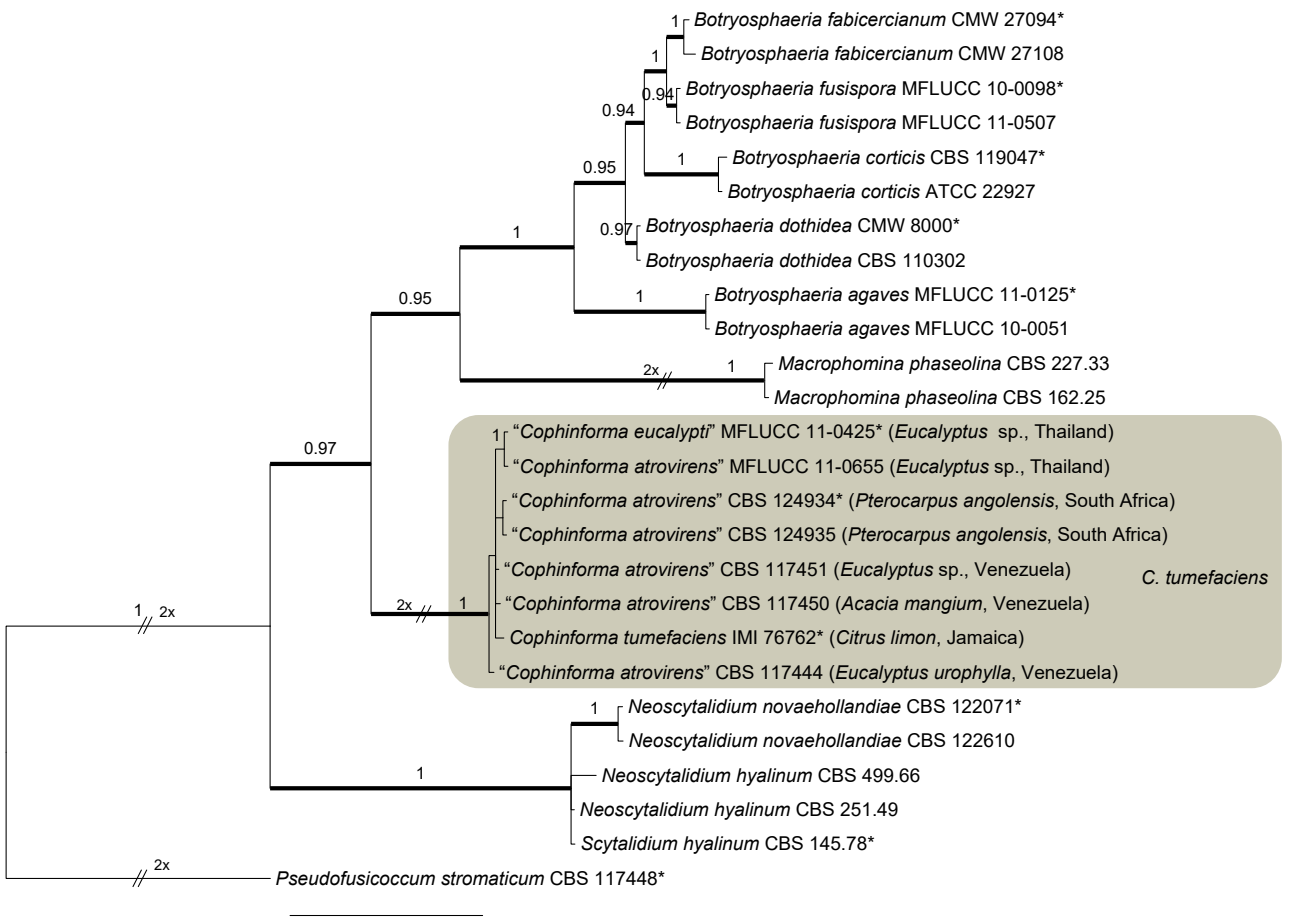

Fig. 10 Phylogenetic tree calculated with Bayesian analysis on ITS, *tef 1-α*, and *tub2* sequences showing affinities of *Cophinforma tumefaciens* with other species in *Botryosphaeriaceae*. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

hyaline. *Conidiophores* hyaline, branched, or reduced to conidiogenous cells. *Conidiogenous cells* hyaline, holoblastic, smooth, discrete, cylindrical, 11–20(–24) × 2.5–4 µm (av. = 15.6 × 3.4 µm). *Conidia* hyaline, thin-walled, aseptate, granular, ellipsoid to obovoid, 18–31.5 × 7.5–10 µm (av. = 26.5 × 8.6 µm). *Spermatophores* hyaline, smooth, branched, or reduced to solitary spermatogenous cells, occurring intermingled among conidiophores in the same conidioma. *Spermatogenous cells* ampulliform or subcylindrical, 8–21 × 2.5–4.5 µm. *Spermatia* hyaline, smooth, cylindrical, straight or slightly curved, apex obtuse, base truncate, 3.5–7.5 × 1.5–2.5 µm.

Culture characteristics — Colonies on OA reaching 85 mm diam after 14 d at 25 °C, margin regular, aerial mycelium floccose, mouse grey; reverse dark mouse grey. Colonies on MEA reaching 85 mm diam after 14 d, with lobate margin, covered by woolly aerial mycelium, mouse grey, with pale olivaceous margin; reverse umber. Colonies on PDA reaching 80 mm diam after 7 d, with lobate margin, covered by felty aerial mycelium, olivaceous grey; reverse olivaceous black at centre, grey olivaceous at periphery.

Additional materials examined. Jamaica, Browns town, St. Anns, on *C. limon*, 24 Apr. 1959, unknown *collector*, representative strain of *Sphaeropsis tumefaciens* IMI 76762. – South Africa, Mpumalanga Province, Mawewe Nature Reserve, from an asymptomatic branch of *Pterocarpus angolensis*, Dec. 2005, *J.W.M. Mehl* & *J. Roux*, ex-holotype of *Cophinforma atrovirens* CBS 124934.

Habitat (Farr & Rossman 2021) — *Bauhinia* spp., *Callistemon* spp., *Carissa* sp., *Cinnamomum camphora*, *Citrofortunella mitis*, *Citrus* spp., *Eucalyptus cinerea*, *Eucalyptus urophylla*, *Eucalyptus* sp., *Eugenia* sp., *Hypericum edisonianum*, *Ilex* spp., *Jatropha* sp., *Lagerstroemia indica*, *Mangifera indica*, *Morus alba*, *Myrica cerifera*, *Nerium oleander*, *Persea americana*, *Pittosporum tobira*, *Poncirus trifoliate*, *Portlandia grandiflora*, *Pyracantha coccinea*, *Schinus terebinthifolius*, *Vigna angularis*, *Wisteria sinensis*.

Geographic distribution (Farr & Rossman 2021) — Africa: Cameroon. – America: Cuba, Jamaica, USA, Venezuela, West Indies. – Asia: India, Japan, Pakistan. – Europe: Austria, Greece.

Notes — This fungus was listed in the Chinese quarantine pest directory as *Sphaeropsis tumefaciens*. It was first described from branches of *Citrus hystrix* as the causing agent of lime and orange knot (Hedges 1911). However, the holotype specimen was not designated in Hedges (1911) and could not

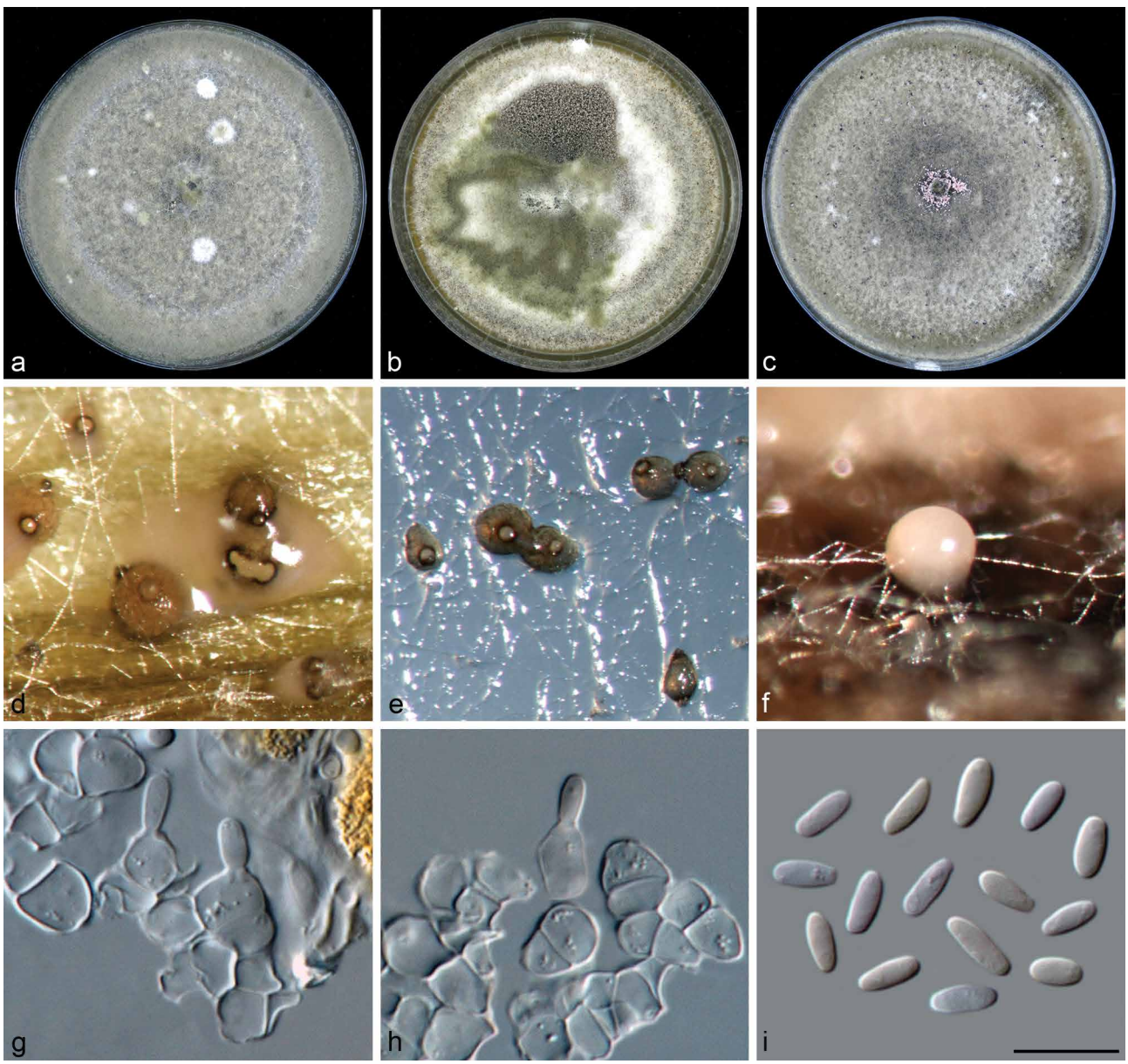

Fig. 11 *Didymella glomerata* (ex-epitype CBS 528.66). a–c. Colonies in 14 d (20 °C, a. on PDA; b. on MEA; c. on OA); d–e. pycnidia; f. conidial matrix; g–h. conidiogenous cells and conidia; i. conidia. — Scale bar: i = 10 µm, applies to g–i.

be traced in the US fungaria where *S. tumefaciens* may have been deposited, e.g., BPI, HUH, NY, WSU.

Morphologically, the macroconidia and spermatia/microconidia of this species (Hedges 1911, Marlatt & Ridings 1974) fit the generic circumscriptions of *Botryosphaeria*, *Cophinforma*, or *Neofusicoccum*, rather than *Sphaeropsis*. Meanwhile, strain IMI 76762 isolated from *Citrus limon* from the originally reported location of *Sphaeropsis tumefaciens* (Jamaica), considered here as a representative of *S. tumefaciens*, clustered within *Cophinforma* (Fig. 10). *Sphaeropsis tumefaciens* is thus combined into *Cophinforma* as *C. tumefaciens. Cophinforma atrovirens and C. eucalypti* are phylogenetically identical to *C. tumefaciens* (Fig. 10), with the older name *C. tumefaciens* having priority.

Didymella glomerata (Corda) Qian Chen & L. Cai, Stud. Mycol. 82: 176. 2015 — Fig. 11, 12

Basionym. *Coniothyrium glomeratum* Corda, Icon. Fungorum (Prague) 4: 39. 1840.

Synonyms. *Phoma glomerata* (Corda) Wollenw. & Hochapfel, Z. Parasitenk. 3 (5): 592. 1936.

Peyronellaea glomerata (Corda) Goid. ex Togliani, Ann. Sperim. Agrar. III 6: 93. 1952.

Typus. Netherlands, on *Chrysanthemum* sp., deposited in CBS Sept. 1963, unknown *collector*, ex-epitype culture CBS 528.66 = PD 63/590.

Symptoms — *Didymella glomerata* causes a blight of vine flowers and grapes. It is a secondary invader causing rot of tomato, potato tubers and citrus. It can also cause leaf and fruit spot of apple and damping off of conifers (Morgan-Jones 1967).

Conidiomata pycnidial, solitary or aggregated, globose or subglobose, 100–300 µm diam, glabrous, superficial or semi-immersed, papillate, with 1(–3) ostioles. *Pycnidial wall* pseudoparenchymatous, composed of more or less isodiametric cells, 4–7 layers, outer layers pigmented. *Conidial matrix* rosy buff to salmon, cream. *Conidiogenous cells* phialidic, hyaline, smooth, mostly ampulliform, sometimes subglobose, 3.5–9 × 4–8 µm. *Conidia* oblong to cylindrical, sometimes ovoid or obovate, smooth- and thin-walled, aseptate and hyaline, 4.5–6.5 × 2–3 µm (av. ± S.D. = 5.7 ± 0.4 × 2.3 ± 0.2 µm), partially guttulate. *Chlamydospores* dark brown to black, variable in shape and

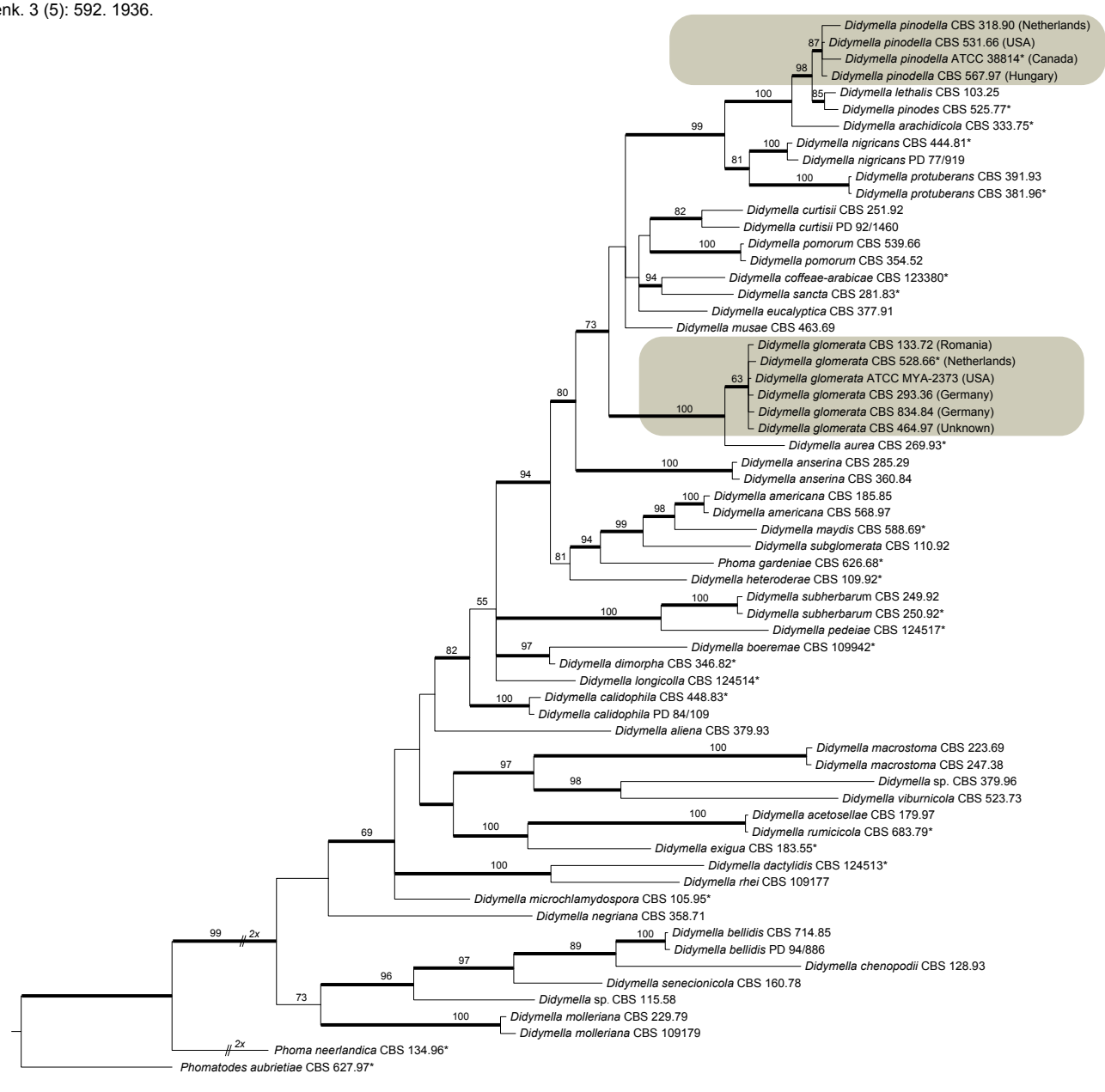

Fig. 12 Phylogenetic tree of *Didymella* calculated with Bayesian analysis on a four-gene combined dataset (LSU, ITS, *rpb2*, and *tub2*) showing affinities of *D. glomerata* and *D. pinodella* with members of *Didymella* species. Thickened branches indicate branches present in the Bayesian tree with > 0.90 posterior probabilities. The RAxML bootstrap support values (> 50 %) are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

dimensions, multicellular-dictyosporous or occasionally solitary-terminal, usually in branched or unbranched chains of 2–20 or more elements, smooth at first, later roughened, 18–80 × 12–35 µm (adapted from Boerema et al. 2004).

Culture characteristics — Colonies on OA, 70 mm diam after 7 d, smoke grey to grey olivaceous, covered by fluffy, white to grey aerial mycelia, black pycnidia and rosy vinaceous conidial masses visible; reverse pale mouse grey. Colonies on MEA 73 mm diam after 7 d, covered by floccose, white and greenish olivaceous aerial mycelia, black pycnidia and rosy vinaceous conidial masses visible; reverse olivaceous black, pale luteous near the margin. Colonies on PDA, 76–78 mm diam after 7 d, densely covered by floccose, white and grey aerial mycelia, smoke grey; reverse glaucous grey to grey olivaceous.

Additional materials examined. Germany, Berlin-Zehlendorf, Domäne Düppel, on *Solanum tuberosum*, unknown collection date, *H.W. Wollenweber*, culture CBS 293.36 = MUCL 9882; Monheim, on leaf of *Hordeum sativum*, 3 May 1984, *M. Hossfeld*, CBS H-16335, culture CBS 834.84. – Romania, Bucuresti, from fresco in church, Nov. 1971, *I. Ionita*, CBS H-16340, culture CBS 133.72. – Unknown country, collected from bathroom, unknown collection date, *O.C.G. Adan*, culture CBS 464.97. – USA, New Jersey, South River, on leaves of *Platanus occidentalis*, deposited at ATCC by *J.F. White*, culture ATCC MYA-2373.

Habitat — Various host plants, soil, animal, human, fresco in a church and inorganic material.

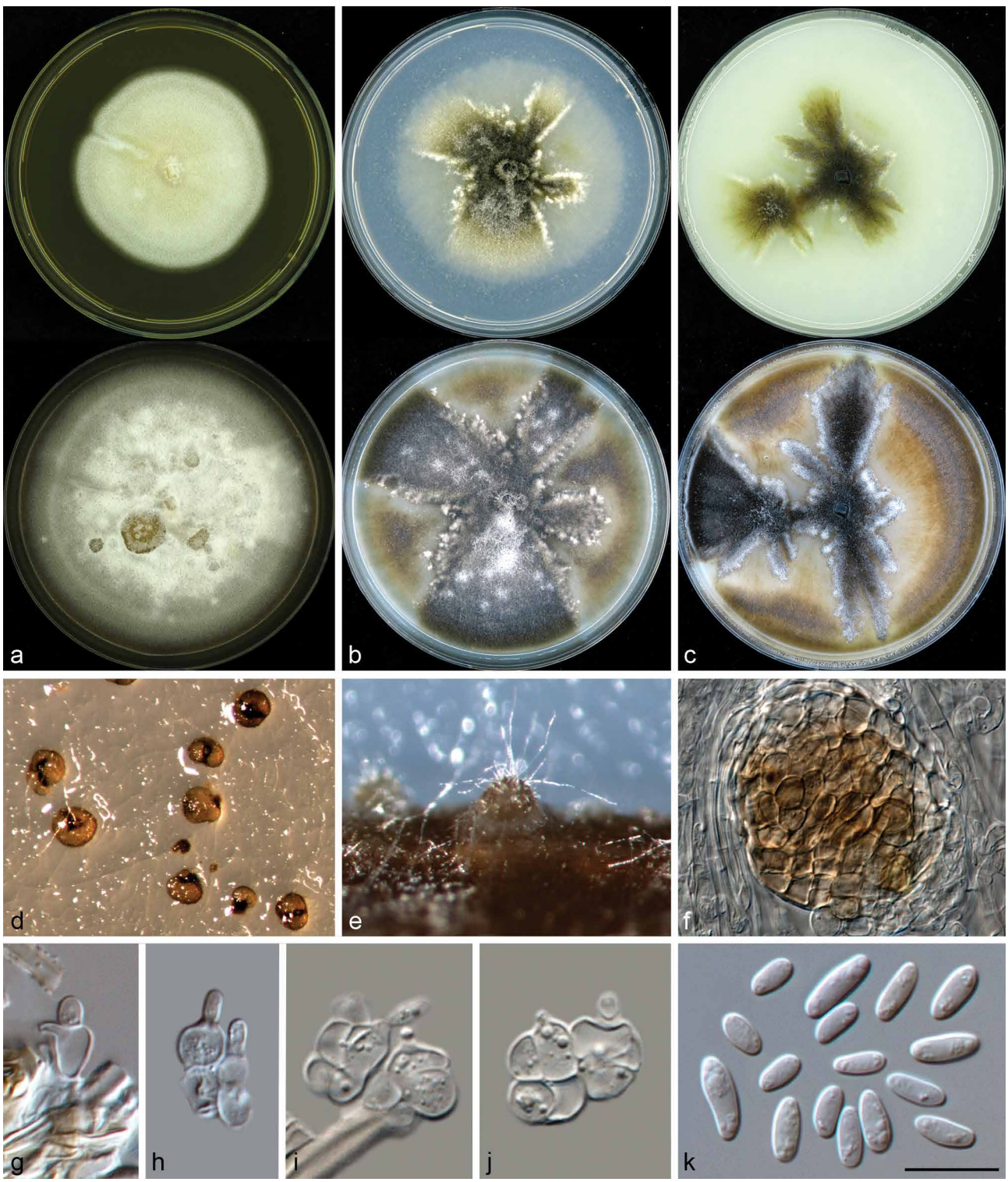

Fig. 13 *Didymella pinodella* (a–h, k. CBS 531.66, i–j. CBS 318.90). a–c. Colonies in 7 d (up) and two wk (below) (20 °C, a. on MEA; b. on PDA; c. on OA); d–f. pycnidia; g–j. conidiogenous cells; k. conidia. — Scale bar: k = 10 µm, applies to g–k.

Geographic distribution — America: USA (Duan et al. 2020). – Asia: China (Chen et al. 2017, Huang et al. 2018, Pan et al. 2018), Iran (Soleimani et al. 2018), Japan (CBS culture collection, Duan et al. 2020). – Europe: Germany, Italy, Netherlands, Spain, Switzerland, Romania, Russia, Uruguay (CBS culture collection, Casieri et al. 2009, Gonzalez & Tello 2011, Duan et al. 2020). – Oceania: Australia (Zhang et al. 2020).

NCBI Genome ID: JAFJTP000000000 (CBS 528.66, this study).

Notes — *Didymella glomerata* (Chen et al. 2015) was listed in the Chinese quarantine pest directory as *Phoma glomerata*. This fungus is widely distributed and ubiquitous, and has been recovered from various host plants, soil, a fresco in a church and inorganic materials (Punithalingam 1979, De Hoog et al. 2000). *Didymella glomerata* can be clearly differentiated from relatives via molecular data (Fig. 12), especially based on *tub2* and *rpb2*.

Didymella pinodella (L.K. Jones) Qian Chen & L. Cai, Stud. Mycol. 82: 178. 2015 — Fig. 13

Basionym. *Ascochyta pinodella* L.K. Jones, Bull. New York State Agric. Exp. Sta. 547: 10. 1927.

Synonyms. *Phoma medicaginis* var. *pinodella* (L.K. Jones) Boerema apud Boerema et al., Netherlands J. Pl. Pathol. 71: 88. 1965.

Phoma pinodella (L.K. Jones) Morgan-Jones & K.B. Burch, Mycotaxon 29: 485. 1987.

Peyronellaea pinodella (L.K. Jones) Aveskamp et al., Stud. Mycol. 65: 33. 2010.

Typus. Canada, from *Pisum sativum*, unknown collection date, deposited by *V.R. Wallen*, neotype designated here HMAS 350266, MBT 10001721, culture ex-neotype ATCC 38814.

Symptoms — *Didymella pinodella* causes black stem lesions and leaf spots on peas and clover which can lead to serious crop losses. Lesions seldom extend below ground level.

Conidiomata pycnidial, abundant in the pigmented flabellate region on PDA and OA, solitary or aggregated, globose, subglobose or irregular, pale brown to dark brown, 90–350 µm diam, glabrous, semi-immersed or immersed, papillate with one ostiole, dark brown to black at the ostiole margin. *Conidial matrix* whitish to vinaceous buff. *Conidiogenous cells* hyaline, smooth, ampulliform, doliiform, or lageniform, 3–6.5 × 3–6 µm. *Conidia* subcylindrical to cylindrical, ellipsoidal, guttulate, aseptate, 5–8.5 × 1.5–3 µm (av. ± S.D. = 6.4 ± 0.7 × 2.2 ± 0.3). *Chlamydospores* seldom observed, intercalary, solitary, pale brown, subglobose, 6–8 µm diam.

Culture characteristics — Colonies on OA 50–65 mm diam after 7 d, regular, greenish olivaceous, yellowish olivaceous or olivaceous, margin pale, distinctly radially filamentous, aerial mycelia practically absent; radially filamentous regions greenish black after 2 wk, margin greyish sepia or isabelline. Colonies on PDA similar, but 66–69 mm diam after 7 d. Colonies on MEA slowly growing, 55–68 mm diam after 7 d, margin regular, white to pale yellow, aerial mycelia sparse at first and then cottony after about 2 wk.

Additional materials examined. Hungary, from *Glycine max*, unknown collection date, *G. Kövics*, culture CBS 567.97 = PD 97/2160. – Netherlands, from a stem of *Pisum sativum*, deposited in CBS July 1990 by *M.E. Noordeloos*, culture CBS 318.90 = PD 81/729. – USA, Minnesota, from *Trifolium pratense*, deposited in CBS in Sept. 1966, isolated by Univ. of Minnesota, No. 0-RC-1, culture CBS 531.66.

Habitat — *Glycine max*, *Pisum sativum*, *Trifolium pratense*.

Unverified habitat — *Beta vulgaris*, *Casuarina*, *Coffea arabica*, *Gossypium*, *Lens culinaris* subsp. *culinaris*, *Medicago sativa*, *Oryza*, *Petroselinum crispum*, *Pisum sativum*, *Trifolium hybridum*, *T. incarnatum*, *T. repens*, *Trigonella foenum-graecum*, *Vicia faba*, *Vigna radiata*, *V. unguiculata*.

Geographic distribution — America: Canada, USA. – Asia: Japan (Chen et al. 2017). – Europe: Hungary, Netherlands, Poland.

NCBI Genome ID: JAGKQD000000000 (ATCC 38814, this study).

Notes — *Didymella pinodella* (Chen et al. 2015) was listed in the Chinese quarantine pest directory as *Phoma pinodella*. This fungus was first reported from *Pisum sativum* in the USA and Canada without designation of a type (Jones 1927). Inquiries were sent to 13 fungaria (viz. DAOM, CAN, MT, TRT, BPI, CBS, FLAS, GH, IMI, JSTOR, MICH, NY, and HUH) where type materials might have been preserved, but all were unsuccessful. We assumed that the type had been lost or destroyed. An ideal strain ATCC 38814 isolated from *Pisum sativum* from Canada was therefore designated as the ex-neotype of *Didymella pinodella* in this study, and it clustered together with the other three American and European strains on a strongly supported phylogenetic clade (Fig. 12). The neotpye designation helps to stabilise the application of the name.

Diplodia mutila (Fr.: Fr.) Fr., Summa Veg. Scand. 2: 417. 1849 — Fig. 14, 15

Basionym. *Sphaeria mutila* Fr.: Fr., Syst. Mycol. 2: 424. 1823.

Synonyms. *Physalospora mutila* (Fr.: Fr.) N.E. Stevens, Mycologia 28: 333. 1936.

Botryosphaeria stevensii Shoemaker, Canad. J. Bot. 42: 1299. 1964.

Typus. England, Cornwall, Saltash, on bark of *Malus* sp., 22 Aug. 1935, *N.E. Stevens*, lectotype of *Physalospora mutila*, BPI 599153. – France, Ardenne, Sedan, on bark of *Populus nigra*, date unknown, *Montagne*, isotype of *Diplodia mutila*, K99664. – Portugal, Beira Litoral, Aveiro, on *P. alba*, 2012, *A. Alves*, epitype of *D. mutila* LISE 96136, culture ex-epitype CBS 136014.

Symptoms — *Diplodia mutila* causes cankers on twigs, branch crotches, and tree trunks. Cankers are elliptical, flattened, and often resinous. Branch cankers are normally difficult to detect unless the outer bark is removed. Some cankers quickly girdle small branches, causing rapid death of foliage beyond the canker margin. Coalescing cankers occasionally girdle main stems, causing death of the top 1–2 m of the crowns (Tisserat et al. 1988).

Ascomata solitary or clustered, immersed, globose, unilocular, up to 300 mm diam, dark brown to black, outer layers of wall *textura angularis*, thick, dark brown, inner layers thin-walled, hyaline, *textura angularis*. *Ostiole* central, circular, papillate, periphysate. *Pseudoparaphyses* hyaline, branched, septate, 2–3 mm wide. *Asci* clavate, stipitate, bitunicate, 8-spored, 100–160 × 14–22 mm (including stipe). *Ascospores* biseriate, fusiform to oval, both ends obtuse, thin-walled, smooth, aseptate, hyaline, rarely becoming pale brown and 1–2-septate with age, 25–36 × 9.5–13.5 µm (av. ± S.D. = 31.5 ± 2.3 × 11.4 ± 0.9 µm), L/W ratio = 2.8 ± 0.3 (adapted from Alves et al. 2014). *Conidiomata* solitary or aggregated, immersed, dark brown, more or less globose, up to 600 µm diam, wall composed of three layers, outer layer dark brown, thick-walled *textura angularis*, middle layer dark brown, thin-walled, inner layer thin-walled, hyaline. *Ostiole* central, circular, papillate. *Conidiophores* usually reduced to conidiogenous cells, 0–1-septate. *Conidiogenous cells* holoblastic, discrete, cylindrical, ovoid to obpyriform, straight or occasionally geniculate, hyaline, smooth, 9–21.5 × 2.5–4(–5.5) µm. *Conidia* hyaline, aseptate, sometimes becoming pale brown and 1-septate with age, smooth, thick-walled, oblong to ovoid, straight, both ends broadly rounded, 22–28 × 10–15.5 µm (av. ± S.D. = 25.7 ± 1.9 × 12.3 ± 1.2 µm).

Culture characteristics — Strain CBS 112553 is fast growing on PDA, OA, and MEA, reaching 90 mm diam in 7 d. Colonies on PDA olivaceous black, aerial mycelia cottony, glaucous, reverse olivaceous to black. Colonies on OA greenish glaucous to

greyish yellow-green, aerial mycelia cottony, reverse olivaceous grey to iron grey. Colonies on MEA greenish glaucous, aerial mycelia cottony, forming lots of pellets of mycelium, reverse vinaceous grey to olivaceous.

Additional materials examined. Portugal, Alentejo, Montemor-o-Novo, on *Vitis vinifera*, 1996, *A.J.L. Phillips*, CBS H-20187, living culture CBS 112553. – USA, California, on *Phoenix dactylifera*, July 1930, *L.L. Huillier*, living culture CBS 230.30.

Habitat — *Chamaecyparis lawsoniana*, *Fraxinus* spp., *Malus* spp., *Populus* spp., *Taxus baccata*, *Vitis vinifera*.

Geographic distribution — Africa: South Africa (Damm et al. 2007). – America: Canada (Ginns 1986), Cuba (Urtiaga 1986), USA (Lynch et al. 2013). – Europe: England, France, Greece (Pantidou 1973), Hungary (Van Niekerk et al. 2006), Italy, Netherlands (Phillips et al. 2005), Portugal, Spain (Alves et al. 2006), Sweden (Bakys et al. 2009). – Oceania: Australia (Taylor et al. 2005), New Zealand (Baskarathevan et al. 2008).

NCBI Genome ID: JAFISB000000000 (CBS 112553, this study).

Notes — *Diplodia mutila* was listed in the Chinese quarantine pest directory as *Botryosphaeria stevensii*. The relationship between *D. mutila* and its synonyms (*B. stevensii*, *Physalospora mutila*, *Sphaeria mutila*) has been elucidated by Alves et al. (2014), and an epitype was designated to stabilise the application of this name. In the phylogenetic analysis, strains of *D. mutila* from multiple countries clustered as a sister clade to *D. subglobosa* (Fig. 15). For more details of *Diplodia mutila* see Alves et al. (2004, 2014).

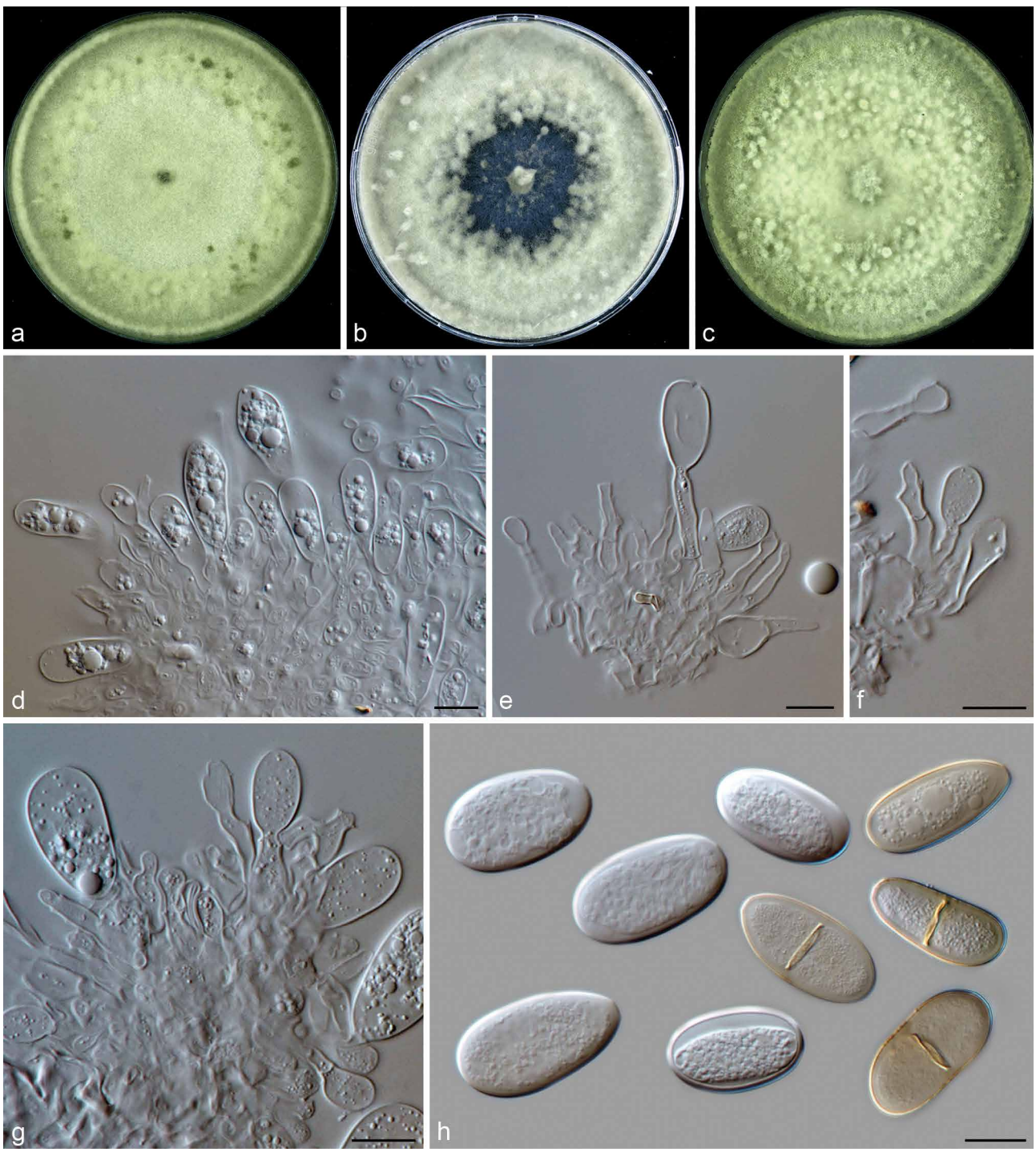

Fig. 14 *Diplodia mutila* (CBS 112553). a–c. Colonies in two wk (20 °C, a. on OA; b. on PDA; c. on MEA); d–g. conidiophores and conidia; h. conidia. — Scale bars: d–h = 10 µm.

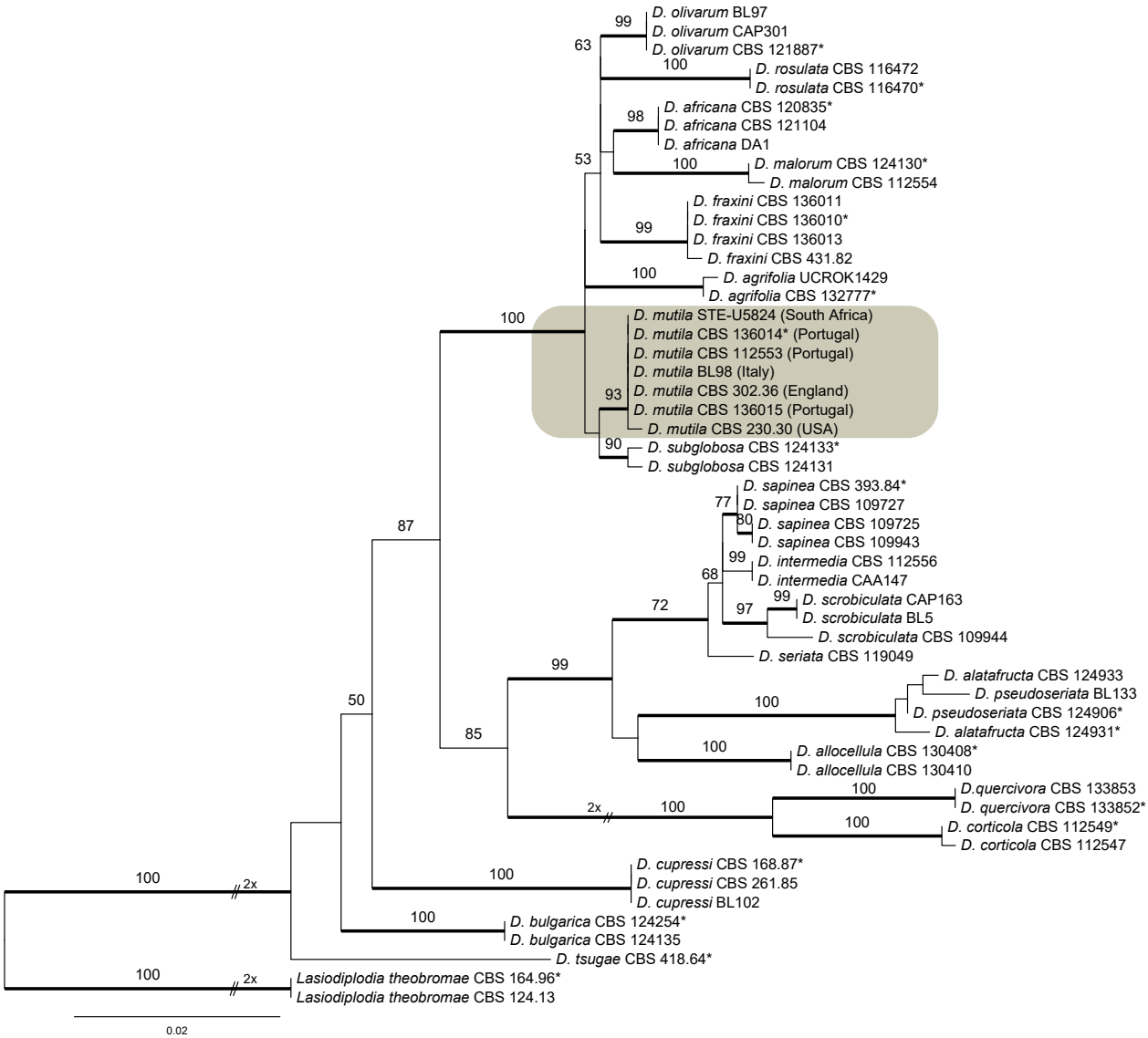

Fig. 15 Phylogenetic tree of *Diplodia* calculated with RAxML on ITS and *tef 1-α* sequences showing affinities of *D. mutila* with allied species. Thickened branches indicate branches present posterior probabilities (> 0.90) in the Bayesian tree. The bootstrap support values > 50 % are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Dothistroma septosporum (Dorog.) M. Morelet (as '*septospora*'), Bull. Soc. Sci. nat. Archéol. Toulon Var 177: 9. 1968 — Fig. 16, 17

Basionym. Cytosporina septospora Dorog., Bull. Trimestriel Soc. Mycol. France 27: 106. 1911.

Synonyms. *Septoriella septospora* (Dorog.) Sacc., Syll. Fung. 25: 480. 1931.

Septoria septospora (Dorog.) Arx, Proc. Kon. Ned. Akad. Wetensch. C 86: 33. 1983.

Actinothyrium marginatum Sacc., Nuovo Giorn. Bot. Ital. 27: 83. 1920.

Dothistroma pini var. *lineare* Thyr & C.G. Shaw, Mycologia 56: 107. 1964.

Dothistroma septosporum (as '*septospora*') var. *lineare* (Thyr & C.G. Shaw) B. Sutton, The Coelomycetes (Kew): 173. 1980.

Dothistroma pini var. *keniense* M.H. Ivory (as '*keniensis*'), Trans. Brit. Mycol. Soc. 50: 294. 1967.

Dothistroma septosporum var. *keniense* (M.H. Ivory) B. Sutton, The Coelomycetes (Kew): 174. 1980.

Mycosphaerella pini Rostr., Dansk Bot. Ark. 17: 312. 1957.

Eruptio pini (Rostr.) M.E. Barr, Mycotaxon 60: 438. 1996.

Scirrhia pini A. Funk & A.K. Parker, Canad. J. Bot. 44: 1171. 1966.

Mycosphaerella pini (A. Funk & A.K. Parker) Arx, Proc. Kon. Ned. Akad. Wetensch. C 86: 33. 1983 (nom. illegit., Art. 53).

Typus. Russia, St. Petersburg, Park Sosnovka, from planted but native *Pinus sylvestris*, 14 Nov. 2013, *R. Drenkhan* & *D. L. Musolin*, neotype CBS H-22299, ex-neotype culture CMW 44656 = CBS 140339 = TAAM 168554A.

Symptoms — *Dothistroma septosporum* causes Dothistroma needle blight, also known as red band needle blight. Initial symptoms appear as water-soaked lesions on the infected needles, then black conidiomata develop at the infection sites, surrounded by a red band. Infected needles become necrotic and defoliate 2–3 wk after the first appearance of symptoms, leading to growth retardation and tree death in severe cases (Gibson et al. 1964, Barnes et al. 2004). For illustrations of Dothistroma needle blight symptoms see Barnes et al. (2004, 2016).

Ascomata aggregated in red bands on diseased pine needles, black, subepidermal, erumpent, globose to pear-shaped, ostiolate, uniloculate to multiloculate, up to 1000 µm wide. *Pseudoparenchyma* dark-brown, thick-walled. *Trichogynes* brown, septate, 36–100 × 4–5 µm. *Ascogonia* brown, coiled or flexuous, approximately 20 µm long and up to 6 µm wide. *Spermatogenous cells* in columnar chains in locules. *Spermatia* embedded in mucous, rod-shaped, hyaline, 1.5–2.5 × 0.5–1 µm. *Asci* cylindrical, bitunicate, 8-spored, hyaline, 35–55 × 6–9 µm. *Ascospores* elliptical, 1-septate, hyaline, typically 4-guttulate, smooth, 10–15 × 3–4 µm (adapted from European and Mediterranean Plant Protection Organization 2015). *Conidiomata* solitary or confluent, (sub-)immersed, becoming erumpent, at maturity acervular, dark brown to black, up to 780 µm in length, lined internally with pseudoparenchymatous cells giving rise to conidiophores. *Conidial masses* white to cream. *Conidio-*

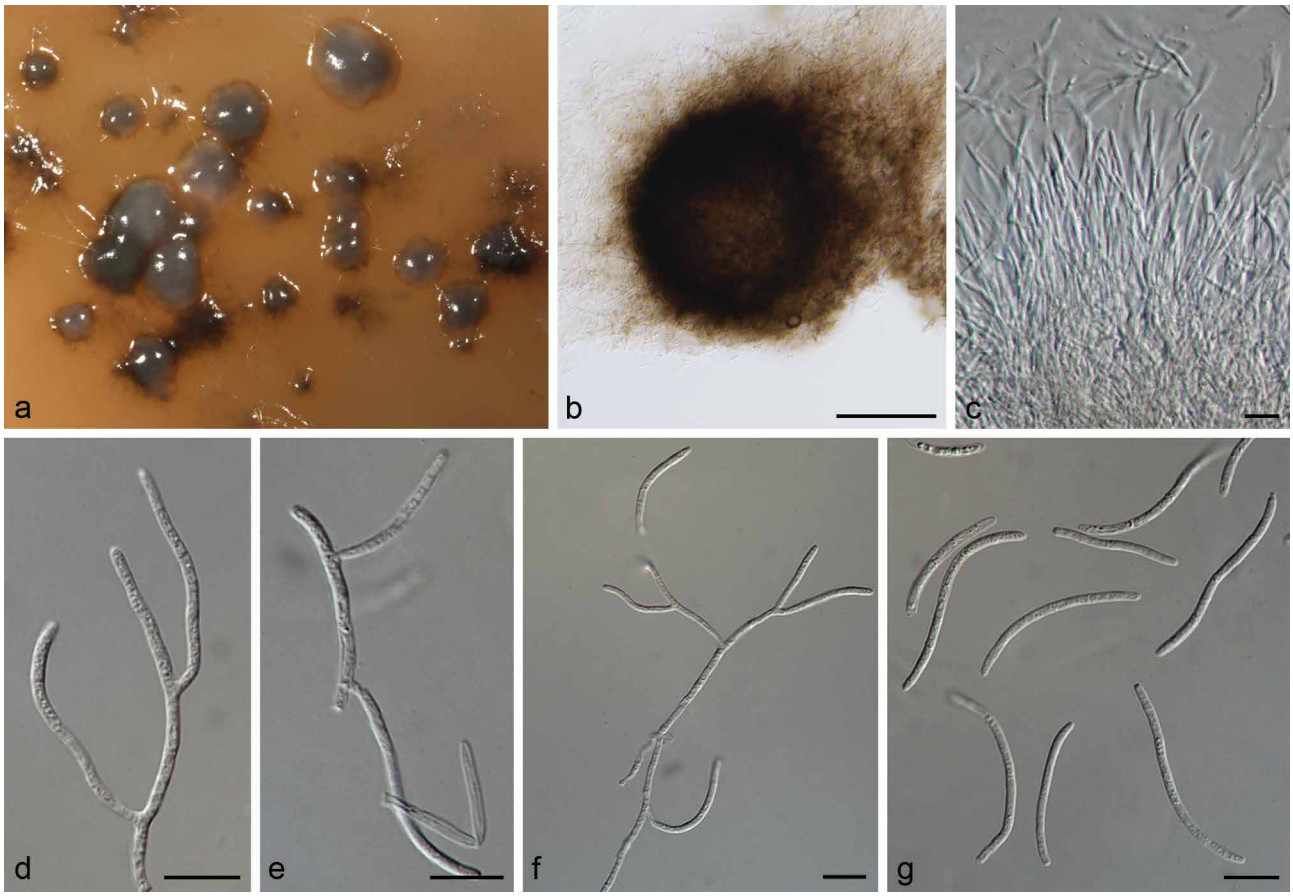

Fig. 16 *Dothistroma septosporum* (ex-neotype CBS 140339). a. Colony on OA (20 °C); b. conidioma; c–f. conidiophores, conidiogenous cells and conidia; g. conidia. — Scale bars: b–g = 10 µm.

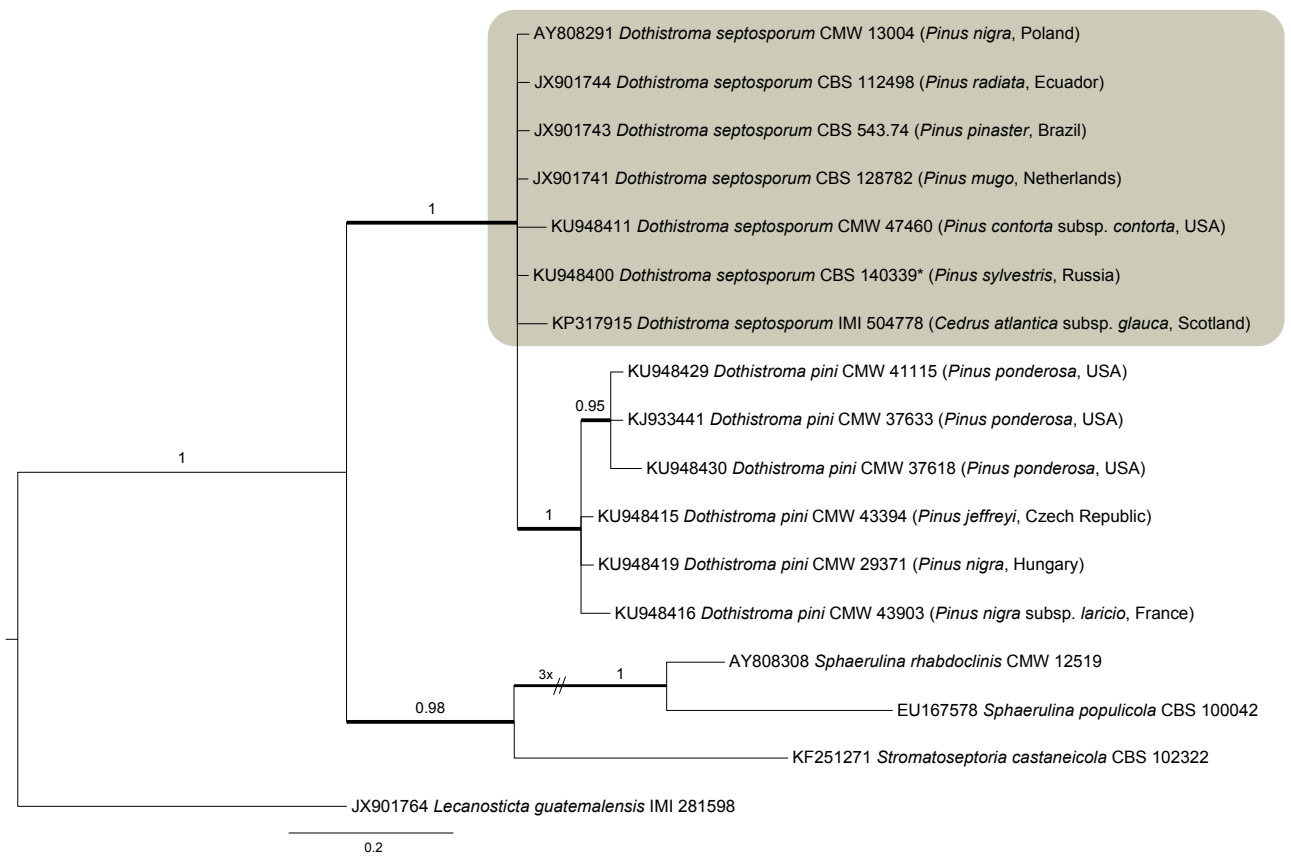

Fig. 17 Phylogenetic tree representing *Dothistroma septosporum* and *D. pini* generated from the ITS region using Bayesian analysis. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes.

phores hyaline, smooth, densely aggregated, subcylindrical to irregular, 0–4-septate, branched or simple, 11–34 × 1–2.5 µm. *Conidiogenous cells* integrated, hyaline, smooth, subcylindrical, 5.5–21 × 1.5–2.5 µm. *Conidia* thin-walled, hyaline, smooth, subcylindrical, filiform, obtuse at the apices, truncate to obconically subtruncate at the bases, 0–3-septate, 14–40 × 1.5–2.5 µm (av. = 31.5 × 2 µm).

Habitat — *Abies balsamea*, *Cedrus atlantica* subsp. *glauca*, *Picea* spp., *Pinus* spp., *Larix decidua*, *Pseudotsuga menziesii*.

Geographic distribution (Drenkhan et al. 2016, Farr & Rossman 2021) — Africa: Kenya, South Africa, Zambia. – America: Brazil, Canada, Chile, Colombia, Ecuador, Guatemala, USA. – Asia: Bhutan, Japan. – Europe: Austria, Belarus, Belgium, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Latvia, Lithuania, Montenegro, Netherlands, Norway, Poland, Portugal, Romania, Russia, Scotland, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Turkey, Ukraine, UK. – Oceania: Australia, New Zealand, Papua New Guinea.

NCBI Genome ID: NBZR00000000 (CBS 140339 = CMW 44656).

Notes — *Dothistroma septosporum* (Barnes et al. 2016) was listed in the Chinese quarantine pest directory as *Mycosphaerella pini*. Presently there are only two species recognised in the genus *Dothistroma*, *D. pini* and *D. septosporum*, and both cause Dothistroma needle blight (DNB) of pine. The disease is also commonly known as 'red-band disease', 'red spot' or 'red-band needle blight'. DNB occurs on about 95 *Pinus* species or their subspecies in almost all areas where susceptible pines are found.

Although *D. pini* and *D. septosporum* are morphologically similar to each other, they can be effectively distinguished through molecular data (Fig. 17). Accurate and rapid differentiation on these two important pathogens can also be made using mating type specific primer sets, DpiniMat1f (AGTAAGCGACGCGCTCCCATG) and DpiniMat2f (GTAAGTGATCGTTGAACATGC), and DseptoMat1f (CGCAGTAAGTGATGCCCTGAC) and DseptoMat2f (GTGAGTGAA- CGCCGCACATGG) (Groenewald et al. 2007).

Helminthosporium solani Durieu & Mont., Expl. Sci. Algérie 1: 356. 1848 — Fig. 18, 19

Synonyms. *Brachysporium solani* (Durieu & Mont.) Sacc., Syll. Fung. 4: 428. 1886.

Dematium atrovirens Harz, Bull. Soc. Imp. Naturalistes Moscou 44: 129. 1871.

Spondylocladium atrovirens (Harz) Harz ex Sacc., Syll. Fung. 4: 483. 1886.

Helminthosporium atrovirens (Harz) E.W. Mason & S. Hughes, Canad. J. Bot. 31: 631. 1953.

Cladosporium abietinum Zukal, Verh. Zool.-Bot. Ges. Wien 37: 44. 1887.

Symptoms — *Helminthosporium solani* causes silver scurf on the tuber surface of potatoes. In severe cases, lesions may cover the entire tuber surface and cause an increase in the rate of dehydration resulting in loss of turgidity.

Mycelia immersed or superficial in culture, hyphae hyaline to dark brown, smooth or verrucose, 1.5–5.5(–8.5) µm wide, sometimes constricted at the septum. *Conidiomata* superficial, stromatic, brown, globose, solitary or gregarious, covered with floccose aerial mycelia. *Conidiophores* solitary or fasciculate, erect, straight or flexuous, pale brown to dark brown, smooth or sometimes verrucose, septate, with small pores at the apex and laterally beneath the upper septa, 120–600 µm long, 4.5–6.5 µm wide, tapering to 1.5–3 µm near the apex. *Conidia* straight, obclavate, smooth, subhyaline to brown, 4–7-pseudosepta te, 21.5–45 × 6.5–10 µm (av. ± S.D. = 33.9 ± 6.56 × 8.1 ± 0.72 µm), tapering to 1.5–5 µm wide at the apex, with a 1.5–3.5 µm wide (av. ± S.D. = 2.4 ± 0.6) blackish brown to black scar at the base.

Culture characteristics — Colonies on PDA attaining 30–31 mm diam after 14 d, greenish grey, aerial mycelia white, reverse olivaceous grey to iron grey. Colonies on MEA reaching 19–20 mm diam after 14 d, pale olivaceous grey to leaden grey, margin white, undulate, reverse mouse grey to dark mouse grey. Colonies on OA attaining 25 mm diam after 14 d, greenish black, aerial mycelia sparse and white, margin white, lobate, reverse iron grey.

Material examined. Netherlands, Haren, from *Solanum tuberosum*, unknown collection date, isolated by *H. Reinartz*, representative strain CBS 640.85.

Habitat — *Solanum tuberosum.*

Geographic distribution — Africa: Libya (El-Buni & Rattan 1981), Morocco (El Immane-Collet et al. 1995), South Africa (Denner et al. 1997). – America: Argentina (CMI 1978), Bolivia (CMI 1978), Brazil (Mendes et al. 1998), Canada (CMI 1978), Chile (CMI 1978), Colombia (CMI 1978), Cuba (Delgado-Rodriguez et al. 2002), Mexico (CMI 1978), Peru (CMI 1978), West Indies (Minter et al. 2001), USA (CMI 1978), Venezuela (CMI 1978). – Asia: China (only reported from Hebei Province and Hong Kong; Lu et al. 2000, Tian et al. 2007), India (CMI 1978), Iran (CMI 1978), Israel (CMI 1978), Japan (CMI 1978), Korea (Cho & Shin 2004), Myanmar (CMI 1978), Singapore (Chua & Chuo 1980), Turkey (CMI 1978). – Europe: Austria (CMI 1978), Belarus (Ivanyuk & Zezyulina 1991), Bulgaria (Dimitrov 1982), Denmark (CMI 1978), France (CMI 1978), Germany (CMI 1978), Greece (Pantidou 1973), Hungary (CMI 1978), Ireland (CMI 1978), Italy (CMI 1978), Netherlands (CMI 1978), Norway (CMI 1978), Poland (Mulenko et al. 2008), Romania (CMI 1978), Sweden (Bang 1976), Switzerland, UK (CMI 1978). – Oceania: Australia (Cunnington 2003), New Zealand (CMI 1978), Papua New Guinea (Shaw 1984).

NCBI Genome ID: JAFISD000000000 (CBS 640.85, this study).

Notes — *Helminthosporium solani* causes silver scurf disease of potato tubers worldwide, especially in the USA and Europe, and survives on infected seed tubers and on plant debris in infested soil.

Helminthosporium solani was first reported from potato in Durieu, Canada (De Bory & De Durieu 1846–1869) but without designation of a type specimen. The BLASTn search of NCBI GenBank using the ITS sequence of CBS 640.85 showed 100 % identity to the sequences (GenBank KC106739, AF073904) of *H. solani* isolated from Canada and USA, North Dakota (Olivier & Loria 1998, Al-Mughrabi et al. 2013), and the *tub2* sequence of CBS 640.85 showed 99 % similarity to the sequences (GenBank Y10670, AF461130, AF461127) of *H. solani* isolates from Northern Ireland, Belfast and USA, California (McKay & Cooke 1997, Cunha & Rizzo 2003). Phylogenetic analysis using ITS sequences of *Helminthosporium* retrieved from GenBank also demonstrated the identity of CBS 640.85 with several strains associated with potato from many countries (Fig. 19), i.e., Canada, Netherlands, North Ireland, UK, and the USA. We therefore considered the culture CBS 640.85 as a representative strain of *Helminthosporium solani*.

Lecanosticta acicola (Thüm.) Syd., Ann. Mycol. 22: 400. 1924 — Fig. 20, 21

Basionym. *Cryptosporium acicola* Thüm., Regensburg 61: 178. 1878.

Synonyms. *Septoria acicola* (Thüm.) Sacc., Syll. Fung. 3: 507. 1884.

Dothistroma acicola (Thüm.) Schischkina & Tsanava, Novosti Sist. Nizsh. Rast.: 277. 1967.

Fig. 18 *Helminthosporium solani* (CBS 640.85). a–c. Colonies (20 °C, a. on OA; b. on MEA; c. on PDA); d. conidiomata; e–i. conidiogenous cells and conidia; j. tip of straight conidiogenous cell; k. base of straight conidiogenous cell; l. conidia. — Scale bars: e–l = 10 µm.

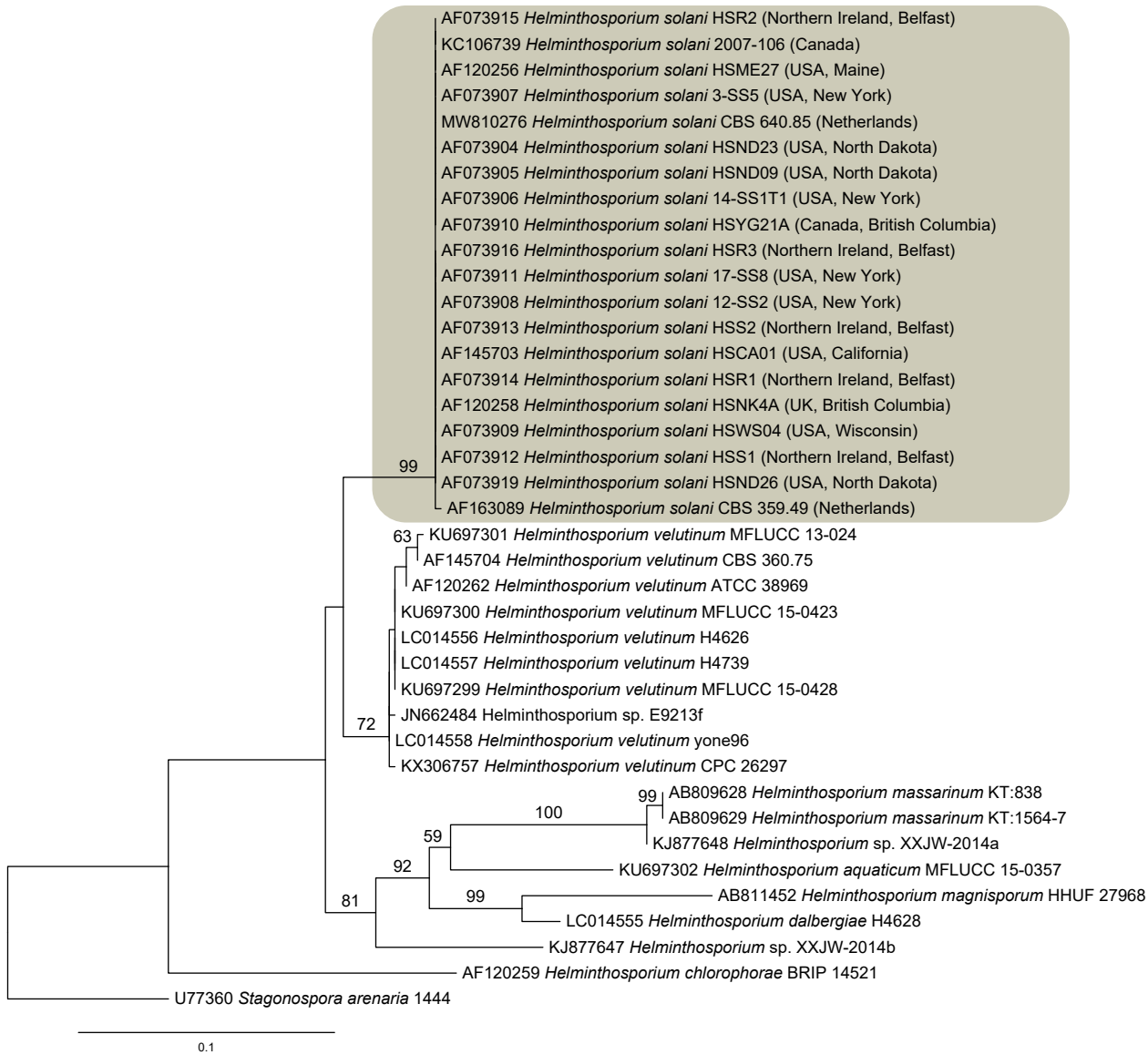

Fig. 19 Maximum likelihood tree of ITS sequences from 38 isolates of *Helminthosporium* and an outgroup *Stagonospora arenaria* retrieved from GenBank. The tree was constructed using RAxML. Bootstrap support values (1 000 replicates) above 50 % are shown at the nodes. Colour box highlights *Helminthosporium solani*.

Lecanosticta pini Syd., Ann. Mycol. 20: 211. 1922.
Oligostroma acicola Dearn., Mycologia 18: 251. 1926.
Scirrhia acicola (Dearn.) Sigg., Phytopathology 29: 1076. 1939.
Systremma acicola (Dearn.) F.A. Wolf & Barbour, Phytopathology 31: 70. 1941.
Dothidea acicola (Dearn.) M. Morelet, Ann. Soc. Sci. Nat. Archéol. Toulon Var 177: 9. 1968.
Mycosphaerella dearnessii M.E. Barr, Contr. Univ. Michigan Herb. 9: 587. 1972.

Typus. USA, New Hampshire, Blackwater, on needles of *Pinus strobus*, 15 June 2011, *B. Ostrofsky*, epitype CBS H-21113, culture ex-epitype CBS 133791 = WPF13.12.

Symptoms — Disease symptoms caused by *Lecanosticta acicola* can vary depending on the host species of *Pinus* affected. Typically, small yellow, sometimes light grey green or reddish brown, irregular spots with defined margins appear on the infected pine needles, which become brown over time. The spots may be surrounded by a yellow halo. These characteristic brown spots develop to form narrow brown bands that result in needle death from the tips down to the point of infection. Needles are prematurely shed, leaving bare branches with tufts of new needles at the branch tips. Infection is usually most severe in the lower parts of the canopy and then progresses upwards into the trees (Van der Nest et al. 2019a).

Conidiomata acervular, erumpent, brown, up to 520 µm diam, conidial masses dull green, confluent. *Conidiophores* aggregated, mostly branched, 1–3-septate, hyaline at beginning, dark brown with age, smooth or verruculose, 22–61 × 2.5–5 µm. *Conidiogenous cells* terminal, subcylindrical, rarely ampulliform, hyaline, smooth or verruculose, sometimes proliferating 2–3 times percurrently near the apex, 6–21 × 2.5–4 µm. *Conidia* straight or curved, subcylindrical with obtusely rounded but tapering apex, base truncate, greyish yellow-green to olivaceous buff with olivaceous edge, guttulate, verruculose, 0–3-septate, 26–55 × 3–5 µm.

Culture characteristics — Colonies on OA reaching 14 mm diam after 2 wk at 25 °C, erumpent, spreading, with medium aerial mycelia, with smooth, lobate margin, pale olivaceous grey with diffuse umber pigment. Colonies on MEA reaching 20 mm diam, erumpent, spreading, with medium aerial mycelia, with smooth, lobate margin, surface olivaceous green with white margin, reverse olivaceous grey. Colonies on PDA reaching 17 mm diam, erumpent, spreading, with sparse aerial mycelia, with smooth, entire margin, olivaceous green with diffuse pale umber pigment in agar, reverse olivaceous.

Habitat — Reported from 53 *Pinus* species and hybrids, and once from *Picea glauca* (Van der Nest et al. 2019a).

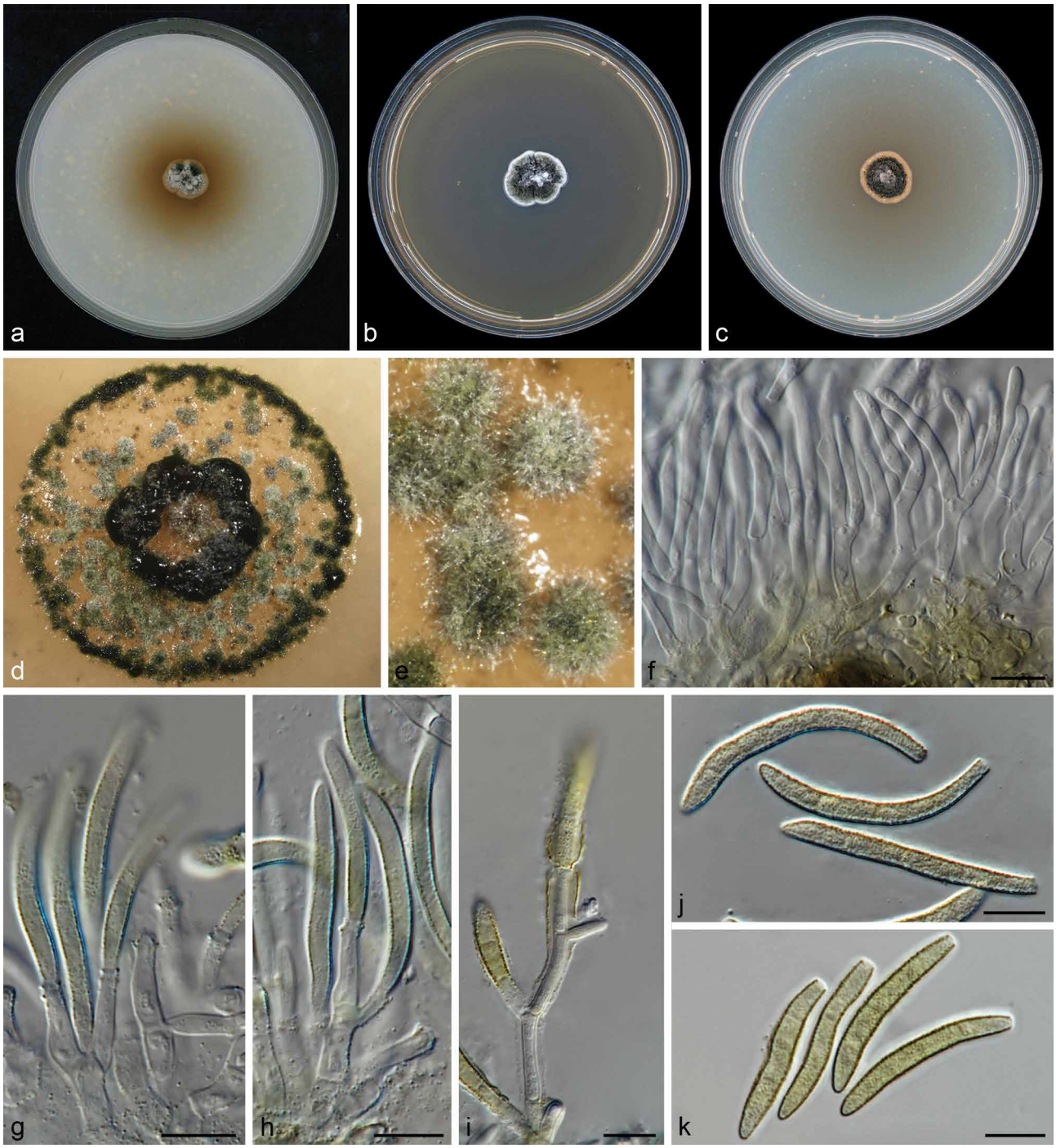

Fig. 20 *Lecanosticta acicola* (ex-epitype CBS 133791). a–c. Colonies (20 °C, a. on OA; b. on MEA; c. on PDA); d–e. conidiomata; f–i. conidiophores, conidiogeous cells and conidia; j–k. conidia. — Scale bars: f–k = 10 µm.

Geographic distribution — America (Janoušek et al. 2016): Canada, Colombia, Guatemala, Mexico, USA. – Asia: China (once reported in Anhui, Fujian, Guangdong, Guangxi, Jiangsu, Jiangxi and Zhejiang; Li et al. 1986, Huang et al. 1995), Japan (Janoušek et al. 2016), South Korea (Janoušek et al. 2016). – Europe: Austria (Janoušek et al. 2016), Croatia (Janoušek et al. 2016), Czech Republic (Janoušek et al. 2016), Estonia (Janoušek et al. 2016), France (Janoušek et al. 2016), Germany (Janoušek et al. 2016), Ireland (Mullett et al. 2018), Italy (Janoušek et al. 2016), Latvia (Mullett et al. 2018), Lithuania (Janoušek et al. 2016), Portugal (Mullett et al. 2018), Romania (EPPO 2019b), Russia (Mullett et al. 2018), Slovenia (Janoušek et al. 2016), Spain (Janoušek et al. 2016), Sweden, Switzerland (Janoušek et al. 2016).

NCBI Genome ID: GCA_000504345.2 (culture B3_MdHEF).

Notes — This fungus was listed in the Chinese quarantine pest directory as *Mycosphaerella dearnessii*, but its current name is *Lecanosticta acicola* since *Mycosphaerella* s.str. is only linked to *Ramularia* (Verkley et al. 2004, Crous et al. 2009, Videira et al. 2016). *Lecanosticta acicola* causes brown spot needle blight on pines, and is widely distributed. The impact of brown-spot disease on long leaf pine could result in reduction of total annual growth by more than 453 000 m^3 of timber (http://www.cabi.org/isc/datasheet/49057). Due to severity of the disease, *L. acicola* has been afforded an A1 quarantine status in Africa (Morocco), America (Argentina, Brazil, Chile, Uruguay), Asia (Bahrain, Kazakhstan), Europe (Russia, Turkey, Ukraine), and A2 quarantine status in Jordan and Europe (https://gd.eppo.int/taxon/SCIRAC/categorization).

The symptoms of brown spot needle blight (BSNB) caused by *L. acicola* can be easily confused with those of Dothistroma

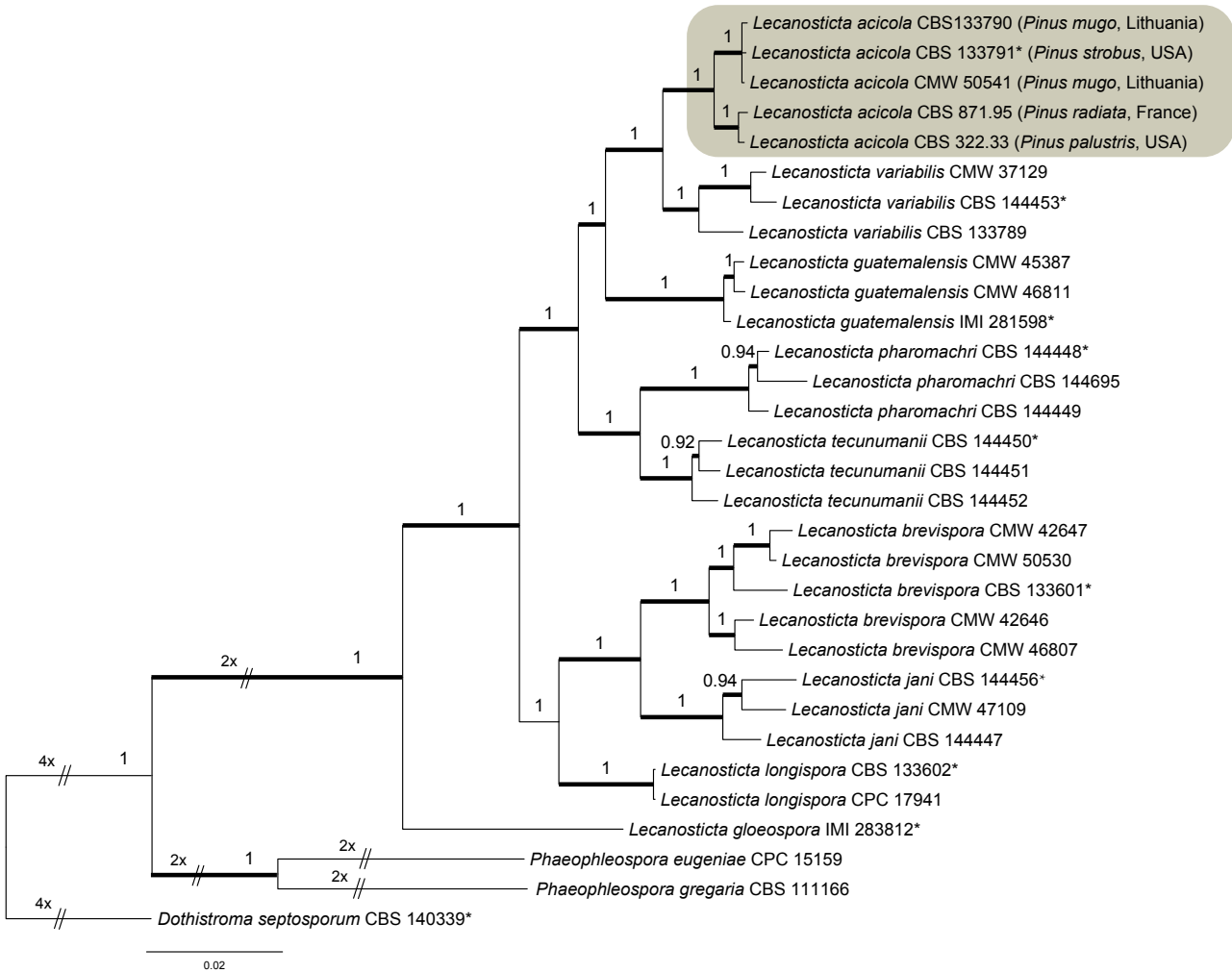

Fig. 21 Phylogenetic tree of *Lecanosticta* calculated with Bayesian analysis on ITS, *ms204*, *rpb2*, *tef 1-α*, and *tub2* sequences showing affinities of *L. acicola* with allied species associated with pines. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

needle blight (DNB), which is caused by *Dothistroma septosporum* and *D. pini* (Barnes et al. 2004, 2016). In addition to *L. acicola*, eight closely related species in *Lecanosticta* (Fig. 21) can also infect pines and cause disease symptoms (Van der Nest et al. 2019b). Therefore, to make accurate identification and give proper quarantine measures on symptomatic tissues, molecular diagnostics are important. Except the multiple-locus phylogeny employed in this study, a rapid method based on real-time PCR assay has been designed based on targeted gene translation elongation by Ioos et al. (2010), with the forward/reverse primers LAtef-F1: 5'-CCTCCTTCATCTTCCCCTTC-3' and LAtef-R1: 5'-TGTGGGAGATAGCGTTGTCA-3', and the hydrolysis probe LAtef-P1: 5'-Cy5-CAAGCACTCTTGGAACACACCGC-BHQ3-3'.

Lecanosticta was thought to have a Central American centre of origin (Evans 1984). However, a recent investigation of *Lecanosticta* on pine did not find any *L. acicula* in this region (Van der Nest et al. 2019b). According to a recent publication, *L. acicula* is confirmed to be present in Mexico and the USA, and is thus hypothesised to be a Northern Hemisphere taxon (Van der Nest et al. 2019b). Although *L. acicula* was once reported from southeast of China (Li et al. 1986, 1987, Huang et al. 1995, Chen 2002), the identifications were questionable because the phenetic tree constructed using the RAPD genetic distance matrix in Huang et al. (1995) revealed that those Chinese isolates formed a distinct clade from the U.S. isolates, which may represent a cryptic species of *Lecanosticta*. Therefore, Chinese isolates are in need of further collection and accurate identification using DNA barcodes to confirm its presence in China.

Mycocentrospora acerina (R. Hartig) Deighton, Taxon 21: 716. 1972 — Fig. 22

Basionym. *Cercospora acerina* R. Hartig, Untersuch. Forstbot. Inst. München 1: 58. 1880.

Synonyms. *Sporidesmium acerinum* (R. Hartig) A.B. Frank, Krankh. Pfl. 2: 318. 1896.

Centrospora acerina (R. Hartig) G. Arnaud, Bull. Soc. Pathol. Vég. Fr. 5: 59. 1918.

Ansatospora acerina (R. Hartig) H.N. Hansen & Tompkins, Pathopathology 35: 220. 1945.

Centrospora acerina (R. Hartig) A.G. Newhall, Phytopathology 36: 894. 1946.

Centrospora acerina (R. Hartig) Vienn.-Bourg., Rev. Mycol., N.S. 10: 130. 1946.

Cercospora ailanthi P. Syd., Hedwigia 38: 140. 1899.

Cercosporella callosa Allesch., Fungi Bavaria Exsic.: no. 697. 1900.

Cercosporella ulmicola Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 111: 1046. 1902.

Cercosporella anemonis Baudyš, Lotos 62: 60. 1916.

Cercospora macrospora Osterw., Mitth. Thurgauischen Naturf. Ges. 25: 73. 1924.

Cercospora cari Westerd. & Luijk, Meded. Phytopathol. Lab. "Willie Commelin Scholten" 8: 54. 1924.

Cercospora praelonga R. Sprague, Mycologia 29: 431. 1937.

Cercospora ohlsenii Neerg., Zentralbl. Bakteriol., 2. Abt., 104: 411. 1942.

Anguillospora flagellifera Ingold, Trans. Brit. Mycol. Soc. 32: 345. 1949.

Spermospora impatientis Mel'nik, Mikol. Fitopatol. 1: 255. 1967.

Typus. Neotype B, Thümen Herb. Mycol. Oecon. no. 743. *Lectotype* Plate (Taf.) IV, f. 1–9 (Hartig, Untersuch. Forstbot. Inst. München 1. 1880).

Symptoms — *Mycocentrospora acerina* causes leaf spot of pansy, storage rot of celery, root rot, canker and black crown rot of parsnip, and liquorice root of carrots (Sutton & Gibson 1977). Initially the infected spots are pale greenish, yellowish ochraceous, later becoming brown or blackish brown, finally appearing as various symptoms, sometimes with greyish white centre and indefinite, dark and narrow margin, sometimes with a broad diffuse yellowish halo, and sometimes zonate with papery and dry centre and forming shot-holes (Braun 1995).

Primary mycelium internal, hyphae hyaline or subhyaline, septate, branched, 1.5–5 µm wide, stromata absent, sometimes forming small, loose aggregations of swollen hyphae, up to 15 µm wide; *secondary mycelium* absent to well-developed, external, superficial, repent. *Conidiophores* solitary or in loose fascicles, occasionally branched, erect, subcylindrical or ampulliform, geniculate-sinuous, hyaline, smooth, 10–65 × 4–10 µm. *Conidiogenous cells* monoblastic or polyblastic, sympodial, conidial scars conspicuous, terminal and lateral or at the end of short protuberances, 3–6 µm wide. *Conidia* solitary, smooth, broadly obclavate-acicular, 50–290 × 4–16.5 µm, 1–24-septate, sometimes constricted at the septum, hyaline, occasionally pale dull olivaceous, central cells of the conidia sometimes becoming yellowish to pale brown and thick-walled, apex tapering towards a long and narrow rostrum, subacute, sometimes with a narrow and lateral basal appendage, aseptate or septate, 8–150 × 2–3 µm (adapted from Braun 1995).
For illustrations see De Hoog et al. (2000).

Additional materials examined. Netherlands, Baarn, Hooge Vuursche, from *Viola tricolor*, unknown collection date, *Hogenberg*, representative strain CBS 105.43 = DSM 1202. – UK, University of East Anglia, from *Daucus carota*, 18 Aug. 1969, unknown *collector*, culture IMI 142050.

Habitat (Braun 1995, Farr & Rossman 2021) — *Acer campestre*, *A. opulus*, *A. platanoides*, *A. pseudoplatanus*, *A. tataricum*, *Adenostyles alliariae*, *Ailanthus altissima*, *A. glandulosa*, *Anemone nemorosa*, *Apium graveolens*, *Aquilegia* sp., *Arum maculatum*, *Asarum heterotropoides*, *Asclepias tuberosa*, *Beta vulgaris*, *Brassica oleracea*, *Callistephus sinensis*, *Campanula medium*, *Carum carvi*, *Centaurea cyanus*, *Chrysanthemum maximum*, *Coriandrum* sp., *Daucus carota*, *Delphinium* × *cultorum*, *Fragaria* × *ananassa*, *Godetia grandiflora*, *Heterodera glycines*, *Impatiens parviflora*, *Lactuca* sp., *Linaria genistifolia*, *Liquidambar styraciflua*, *Lobelia hybrida*, *Lycopersicon esculentum*, *Malcolmia maritima*, *Odontonema strictum*, *Omphalodes linifolia*, *Osmorrhiza chilensis*, *Paeonia lactiflora*, *Panax notoginseng*, *Pastinaca sativa*, *Penstemon barbatus*, *Petroselinum crispum*, *Petunia hybrida*, *Picea sitchensis*, *Pisum sativum*, *Potamogeton nodosus*, *Potentilla palustris*, *Primula* sp., *Ranunculus asiaticus*, *Scabiosa atropurpurea*, *Spiraea media*, *Stellaria holostea*, *Ulmus campestris*, *U. scabra*, *Verbena hybrida*, *Viola cornuta*, *V. odorata*, *V. reichenbachiana*, *V. sylvestris*, *V. tricolor*.

Geographical distribution – America: Canada (Cheeseman et al. 1985), Chile (Gilchrist et al. 2015), USA (French 1989), West Indies (Minter et al. 2001). – Asia: China (restricted in Yunnan and Northeast China, Zhuang 2005), Japan (Kobayashi 2007), Uzbekistan (Braun 1995). – Europe: Czechoslovakia (Sutton & Gibson 1977), Denmark (Richardson 1990), France (Fabre 1998), Germany (Sutton & Gibson 1977), Netherlands (Kastelein et al. 2007), Poland (Mulenko et al. 2008), UK (Dennis 1986), Ukraine (Dudka et al. 2004). – Oceania: Australia (Cunnington 2003), New Zealand (Gadgil 2005).

NCBI Genome ID: JAGKQC000000000 (CBS 105.43, this study).

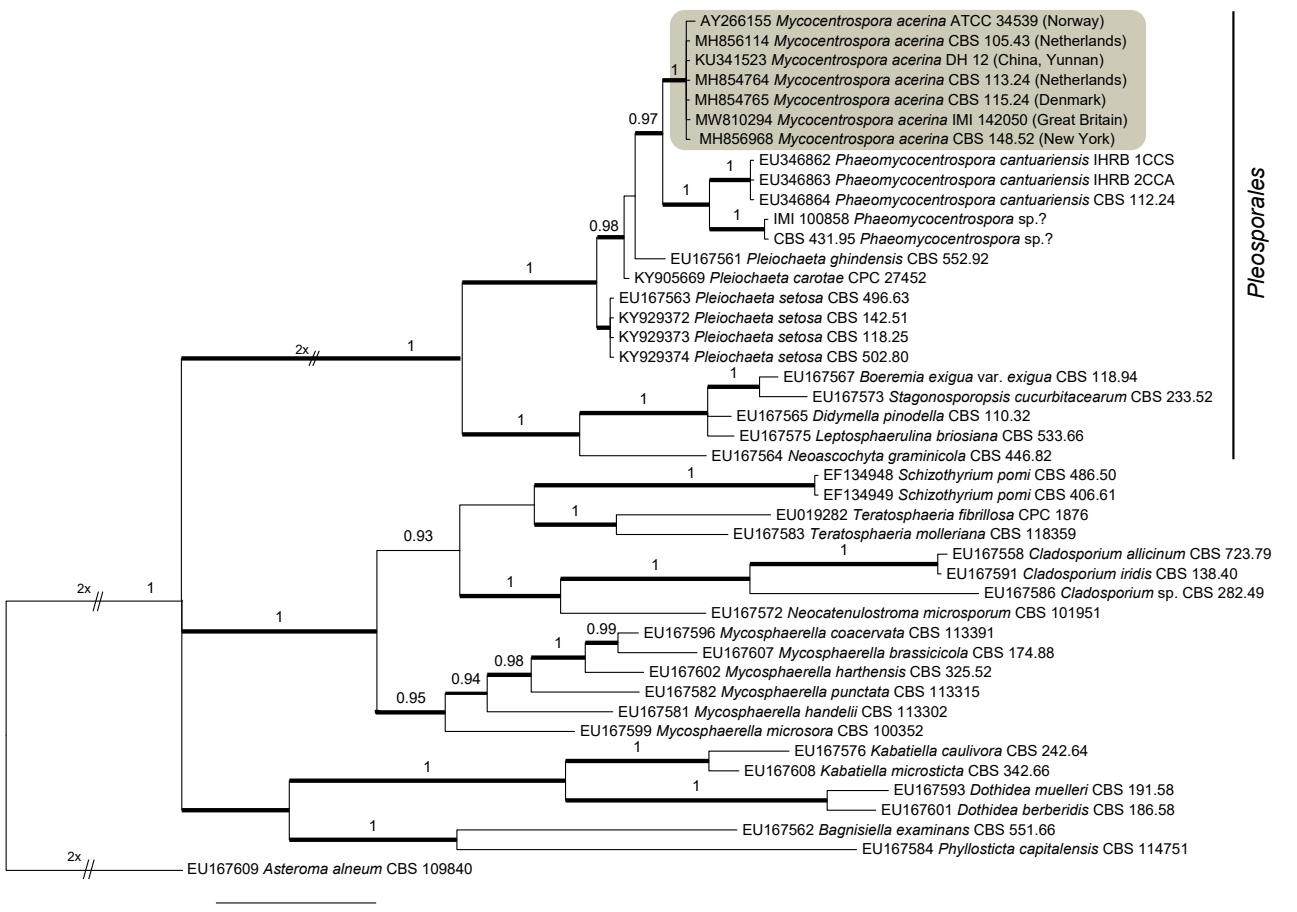

Fig. 22 Phylogenetic tree of *Mycocentrospora acerina* and related species calculated with MrBayes on ITS sequences. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes.

Notes — *Mycocentrospora acerina* causes severe damages on various plants, e.g., pansy, celery, carrot, and parsnip (Sutton & Gibson 1977, Braun 1995). Except its parasitic nature, *M. acerina* is also saprophytic in soil, submerged leaves in streams and dead plants (Braun 1995), and is cosmopolitan in distribution (Sutton & Gibson 1977). The type of *M. acerina* is inexistent (confirmed by the curator of K). The ITS sequences of the two examined strains (IMI 142050 and CBS 105.43) are identical to most *M. acerina* sequences deposited in GenBank, except that of ATCC 34539 (showing 3 bp differences), and their identical phylogenetic status are supported in Fig. 22. Unfortunately, both strains were sterile in culture media in this study, which makes the neotypification of this fungus inappropriate. Further collections and typification of *M. acerina* is urgently needed to fix the application of the name.

Neofusicoccum laricinum (Sawada) Y. Hattori & C. Nakash., Mycoscience 62: 252. 2021 — Fig. 23

Basionym. Physalospora laricina Sawada, Bull. Gov. Forest Exp. Sta. 46: 126. 1950.

Synonyms. Guignardia laricina (Sawada) W. Yamam. & Kaz. Itô, Sci. Rep. Hyogo Univ. Agric. 5: 9. 1961.

Botryosphaeria laricina (Sawada) Y.Z. Shang, Acta Microbiol. Sin. 6: 249. 1987.

Typus. Japan, Ibaraki, Mito, on *Larix decidua*, 14 June 1973, *H. Kondo*, epitype FPH-4038, culture ex-epitype FFPRI 411215 = MUCC 2662. Lectotype *of Physalospora laricina* designated here, MBT 10001722, *K. Sawada*, Bulletin of the Government Forest Experimental Station Meguro 46: pl. II, f. 16, 1950.

Symptoms — The disease caused by *Neofusicoccum laricinum* is conspicuous as a discolouration, wilting and death of the succulent current season's growth. Old twigs remain unaffected. Early attack, between June and September causes hanging of the top of shoots, accompanied by a yellowing and browning of leaves which may fall. Late infections, occurring in September to early October, do not show the characteristic hanging, owing to the lignified nature of the twigs. On needles, symptoms appear as brown spots with chlorotic haloes, which subsequently coalesce (EPPO 2014).

Ascomata pseudothecial, single or in groups, black, globose to subglobose, ostiolate and erumpent, 300–400 × 265–440 µm. *Paraphyses* abundant, hyaline, straight or branched. *Asci* clavate, hyaline, round at the apex, stipitate at the base, 102–140 × 22–45 µm. *Ascospores* aseptate, oblong, hyaline, smooth, and round at the apex, 24–41 × 8–17 µm. *Conidiomata* pycnidial, similar to ascomata in general shape and superficial appearance, but thinner walled, 123–325 × 176–265 µm. *Conidia* oblong, straight or somewhat curved, hyaline, 22–37 × 6–10 µm (adapted from Ito 1963, EPPO 2014).
For illustration of *Neofusicoccum laricinum*, see Ito (1963).

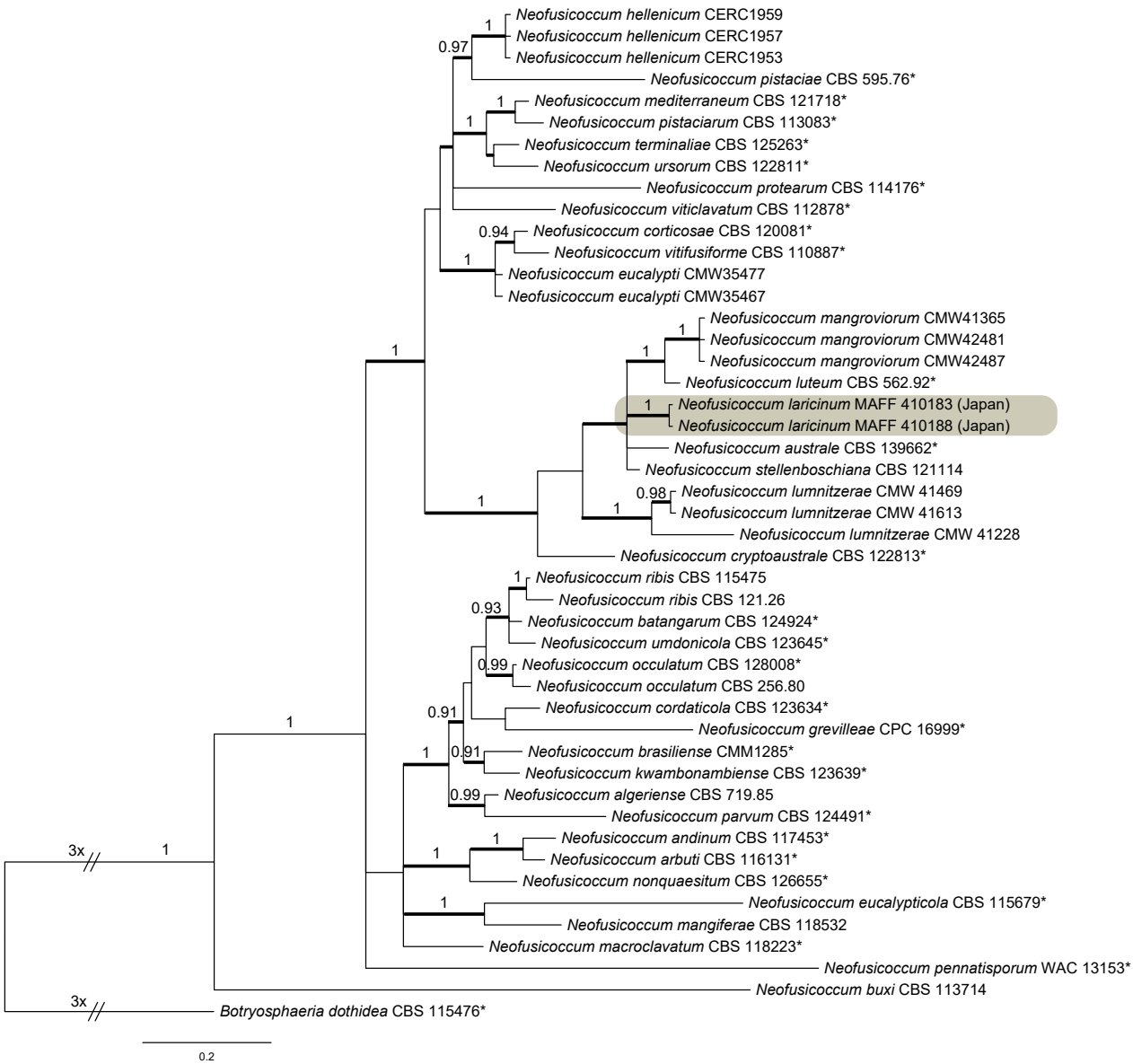

Fig. 23 Phylogenetic tree of *Neofusicoccum* calculated with Bayesian analysis on a four-gene combined dataset (ITS, rpb2, *tef 1-α*, *tub2*) showing affinities of *N. laricinum* with members of *Neofucicoccum* species. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Additional materials examined. Japan, Hokkaido, on *Larix leptolepis*, July 1971, isolated by *T. Yokota*, deposited in MAFF culture collection by *S. Kaneko*, representative strain MAFF 410183 = GC-74; ibid., living culture MAFF 410188.

Habitat — *Larix* spp., *Pseudotsuga menziesii* (incidental host).

Geographic distribution — Asia: China (Kobayashi & Zhao 1989), Japan (Anonymous 1964, Kobayashi 1976), Korea (Cho & Shin 2004).

NCBI Genome ID: JAGKQB000000000 (MAFF 410183, this study).

Notes — *Neofusicoccum laricinum* was listed in the Chinese quarantine pest directory as *Botryosphaeria laricina* (Shang 1987). The pathogen causes a shoot blight disease of *Larix* spp. and is also regulated in Council Directive 2000/29/EC (Annex IAI) as a harmful organism, whose introduction into the EU is prohibited. Another host of *B. laricina* is *Pseudotsuga menziesii*. Other various conifers have also been reported as susceptible following artificial inoculation (EFSA Panel on Plant Health 2018).

Botryosphaeria laricina was first described as *Physalospora laricina*, the causal agent of shoot blight of Japanese larch (*Larix leptolepis*) (Sawada 1950). It was subsequently allocated to the genus *Guignaridia* as *G. laricina* (Yamamoto 1961). Shang (1987) proposed a new combination for *G. laricina* in *Botryosphaeria* as *B. laricina*, based on the developmental type of locule (*Pleospora*).

Holotype requests of *Physalospora laricina* were sent to TAI, where Sawada usually preserved specimens, and several other Japanese fungaria (e.g., NMNH, TI, and TNS), but all without success. A recent proposed epitype in Hattori et al. (2021) is, however, not published Code compliant (International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code), Art. 9.9).

Of the 284 *Botryosphaeria* names listed in Index Fungorum and 298 in MycoBank (retrieved on 2 April 2021), only eight species are currently retained in *Botryosphaeria* (Zhang et al. 2021). Most of these names have been transferred to *Neofusicoccum* and other related genera (Dayarathne et al. 2016). In this study, sequences of a representative strain MAFF 410183 resided within the genus *Neofusicoccum* and are closely related to *N. australe* and *N. stellenboschiana* (Fig. 23).

Guignardia cryptomeriae, frequently found on larch shoots with blight or die-back, is morphologically similar but phylogenetically distinct from *N. laricinum* (Motohashi et al. 2009). For more details about their biology, and intraspecific diversity, refer to the EFSA Panel on Plant Health (PLH) (2018).

Oculimacula yallundae (Wallwork & Spooner) Crous & W. Gams, Eur. J. Plant Pathol. 109: 846. 2003 — Fig. 24

Basionym. *Tapesia yallundae* Wallwork & Spooner, Trans. Brit. Mycol. Soc. 71: 703. 1988.

Synonyms. *Cercosporella herpotrichoides* Fron, Ann. Sci. Agron. Franç. Étrangère, Sér. 4, 1: 11. 1912.

Helgardia herpotrichoides (Fron) Crous & W. Gams, Eur. J. Plant Pathol. 109: 846. 2003.

Pseudocercosporella herpotrichoides (Fron) Deighton, Mycol. Pap. 133: 46. 1973.

Ramulispora herpotrichoides (Fron) Arx, Proc. Kon. Ned. Akad. Wetensch. C 86: 36. 1983.

Typus. Australia, Yallunda Flat, on wheat stubble, 18 Nov. 1986, *H. Wallwork* & *B. Spooner*, holotype K(M) 233697. – South Africa, Western Cape Province, Moorreesburg, on wheat stubble, 1991, *F. Bester*, epitype CBS H-23003, culture ex-epitype of *Helgardia herpotrichoides* CBS 110665 (LSU, ITS, *tef 1-α*, and *tub2* sequences GenBank MW715035, MG934456, MG934498, and MZ073922).

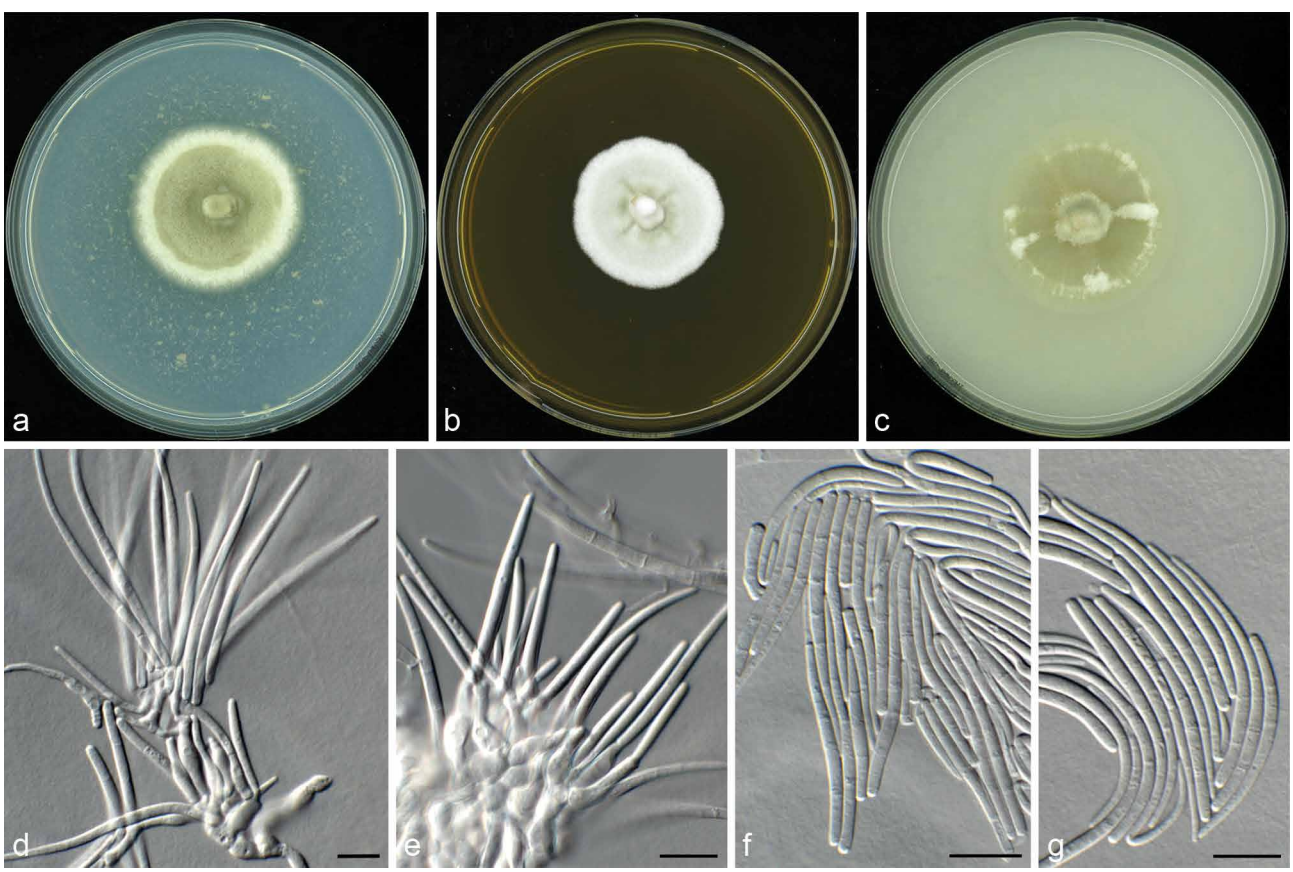

Fig. 24 *Oculimacula yallundae* (a–c. CBS 110665, d–g. CPC 34945). a–c. Colonies (20 °C, a. on PDA; b. on MEA; c. on OA); d–g. conidiophores and conidia (from Crous et al. (2021a) with permission). — Scale bars: d–g = 10 µm.

Symptoms — *Oculimacula yallundae* causes eyespot disease on various gramineous plants, including wheat, barley, oats, etc. The disease is also known as 'foot rot', 'foot-rot of cereals', 'stem break of cereals', and 'eyespot of cereals'. The eye-shaped elliptical lesions are straw yellow, often with black pupil-like dots in the centre, and are bordered by greenish brown to dark brown rings (Prescott et al. 1986).

Apothecia gregarious, sessile, 0.5–1.5 mm diam, developing on a mat of pale brown subicular hyphae, outline circular or lobate. *Paraphyses* filiform, hyaline, septate, similar in length to asci, 2–2.5 µm diam. *Asci* cylindrical to clavate, tapered towards the apex, narrowed to a short stalk, 37–60 × 4–6 µm, 8-spored. *Ascospores* hyaline, cylindrical to fusiform, rounded at the ends, straight or rarely slightly curved, aseptate or rarely 1-septate, 7–11 × 1.5–2 µm (adapted from Wallwork & Spooner 1988). *Conidiophores* sympodial, hyaline, subcylindrical to geniculate-sinuous, branched, 0–3-septate. *Conidiogenous cells* integrated, proliferating at apex, subcylindrical to obclavate, or obpyriform, straight or slightly curved, 9–23 × 2.5–5 µm, conidiogenous loci inconspicuous, truncate, unthickened, c. 1 µm diam. *Conidia* hyaline, smooth, arranged in slimy packets, filiform, straight or curved, acicular at apex, truncate at the base, 3–7-septate, 21–58 × 1.5–2 µm.

Culture characteristics — Colonies on PDA attaining 38–39 mm diam after 14 d, entire, pale grey, margin white, reverse white to pale yellow. Colonies on MEA reaching 33–34 mm diam after 14 d, entire to erose or dentate, white to greenish glaucous, reverse buff to honey. Colonies on OA attaining 42–43 mm diam after 14 d, entire, white, aerial mycelia sparse and fluffy, reverse pale buff.

Additional material examined. UK, on *Triticum aestivum*, unknown collection date, unknown *collector*, culture CPC 34945.

Habitat — *Avena sativa*, *Hordeum vulgare*, *Secale cereal*, and *Triticum aestivum*. Also occurs on many wild and cultivated grasses, including *Aegilops*, *Agropogon*, *Agrostis*, *Alopecurus*, *Bromus*, *Dactylis*, *Festuca*, *Koeleria*, *Lolium*, and *Poa*.

Geographic distribution — (EPPO 2019b): Africa: Morocco, South Africa, Tunisia. – America: Canada, USA. – Europe: widespread in Europe. – Oceania: Australia, New Zealand.

Notes — *Oculimacula yallundae* (Crous et al. 2013, 2021a) was listed in the Chinese quarantine pest directory as *Pseudocercosporella herpotrichoides* and therefore assumed to be a member of *Dothideomycetes*. However, the phylogeny of this pathogen has since been resolved as belonging to *Ploettnerulaceae* (*Helotiales*).

The pathogen can survive long periods in infected crop debris in soil and can infect susceptible crops planted at intervals of several years. Severe cases of the eyespot disease can reduce yield by up to 50 % (Fitt et al. 1988). In addition to *O. yallundae*, *O. acuformis* is also associated with eyespot disease of cereals in temperate regions, and their phylogenetic relationship was inferred in Marin-Felix et al. (2019b) and Crous et al. (2021a).

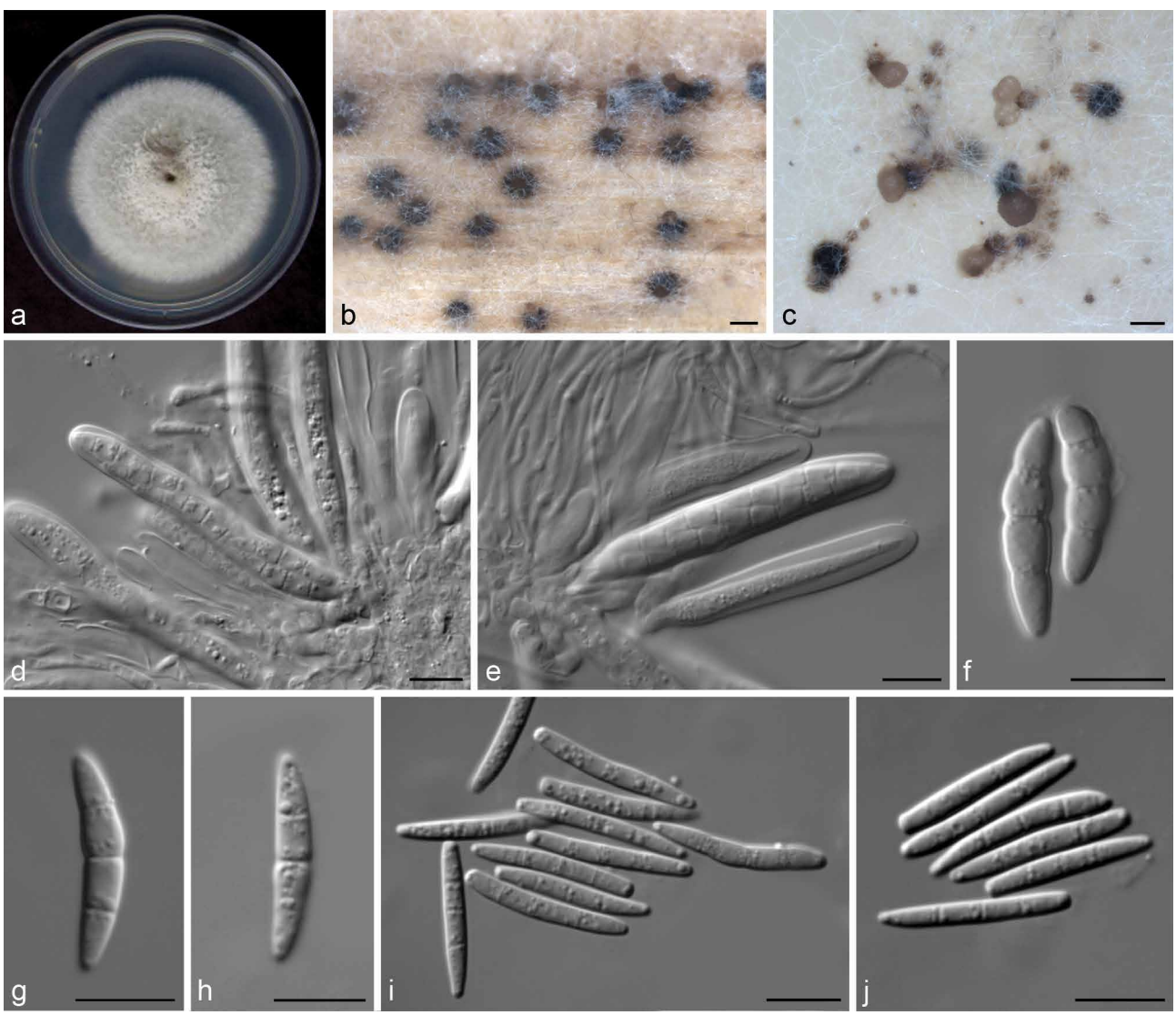

Fig. 25 *Parastagonospora pseudonodorum* (15225-17). a. Colony on PDA (20 °C); b. perithecia on leaf; c. pycnidia on water agar (WA); d–e. asci and paraphyses; f–h. ascospores; i–j. conidia. — Scale bars: b–c = 0.2 mm, d–j = 10 µm (kindly provided by J.P. Yi).

Parastagonospora pseudonodorum B.A. McDonald et al., Persoonia 46: 124. 2021 — Fig. 25, 26

Synonyms. *Leptosphaeria avenaria* f.sp. *triticea* T. Johnson, Canad. J. Res., Sect. C, Bot. Sci. 25: 262. 1947.

Phaeosphaeria avenaria f.sp. *tritici* (T. Johnson) Shoemaker & C.E. Babc. (as '*triticae*'), Canad. J. Bot. 67: 1522. 1989.

Septoria avenae f.sp. *tritici* T. Johnson (as '*triticea*'), Canad. J. Res., Sect. C, Bot. Sci. 25: 262. 1947.

Stagonospora avenae f.sp. *tritici* (T. Johnson) Bissett (as '*triticae*'), Fungi Canadenses 239: 1. 1982.

Typus. Canada, Winnipeg, Manitoba, on leaves and sheaths of *Triticum durum*, 7 Sept. 1944, *T. Johnson*, holotype of *Leptosphaeria avenaria* f.sp. *triticea*, DAOM 19545 (ITS sequence GenBank MZ049615); on *T. durum*, variety Gaza, Aug. 1944, *T. Johnson*, holotype of *Septoria avenae* f.sp. *triticea*, DAOM 19546. – Iran, Golestan Province, on infected *T. aestivum*, 2010, *M. Razavi*, holotype of *Parastagonospora pseudonodorum*, CBS H-24384, culture ex-type CBS 146867 = CPC 36208 = Pat-1 IR_5.2B.

Symptoms — Leaf spots oval, frequently coalescing, straw or buff coloured, central portion bearing pycnidial conidiomata, often grey to black (Johnson 1947).

Ascomata perithecial, subepidermal, erumpent with age, brown to black, globose or subglobose, scattered or gregarious, 170–290 µm diam. *Paraphyses* filamentous, septate, hyaline. *Asci* cylindrical to clavate, straight or slightly curved, hyaline, 49–68 × 7–10 µm, 8-spored. *Ascospores* fusoid, straight or curved, biseriately arranged (2–)3(–4)-septate, constricted at the septum, hyaline, 16–24 × 3.5–6 µm. *Conidiomata pycnidial*, scattered or gregarious, spherical or ellipsoid, 60–220 µm diam, wall composed of 3–4 layers of brown cells, ostiole circular or oval, 10–15 µm diam. *Conidia* cylindrical, straight or slightly curved, slightly tapered towards the apex, hyaline, smooth, obtuse at the apex, obtuse to truncate at the base, 3–4-septate, not constricted at the septum, 19–33 × 2.5–4.5 µm.

Additional materials examined. Canada, on *Hordeum vulgare*, intercepted by Zhoushan Customs, P.R. China, 2018, isolated by *L.F. Ye*, living cultures 18332-5 (ITS, *tef 1-α*, and *tub2* sequences GenBank MZ049616, MZ073994, and MZ073989), 2289-3 = PA1 (ITS and *tub2* sequences GenBank MZ049619 and MZ073992), 2289-5 = PA2 (ITS and *tub2* sequences GenBank MZ049620 and MZ073993). – France, on *Hordeum vulgare*, intercepted by Zhoushan Customs, P.R. China, 2015, isolated by *L.F. Ye*, living culture 15225-17 (ITS and *tub2* sequences GenBank MZ049618 and MZ073991).

Habitat — *Agrostis capillaris*, *Anthoxanthum odoratum*, *Arrhenatherum elatius*, *Avena* spp., *Bromus carinatus*, *Festuca obtusa*, *Glyceria canadensis*, *G. striata*, *Hordeum vulgare*,

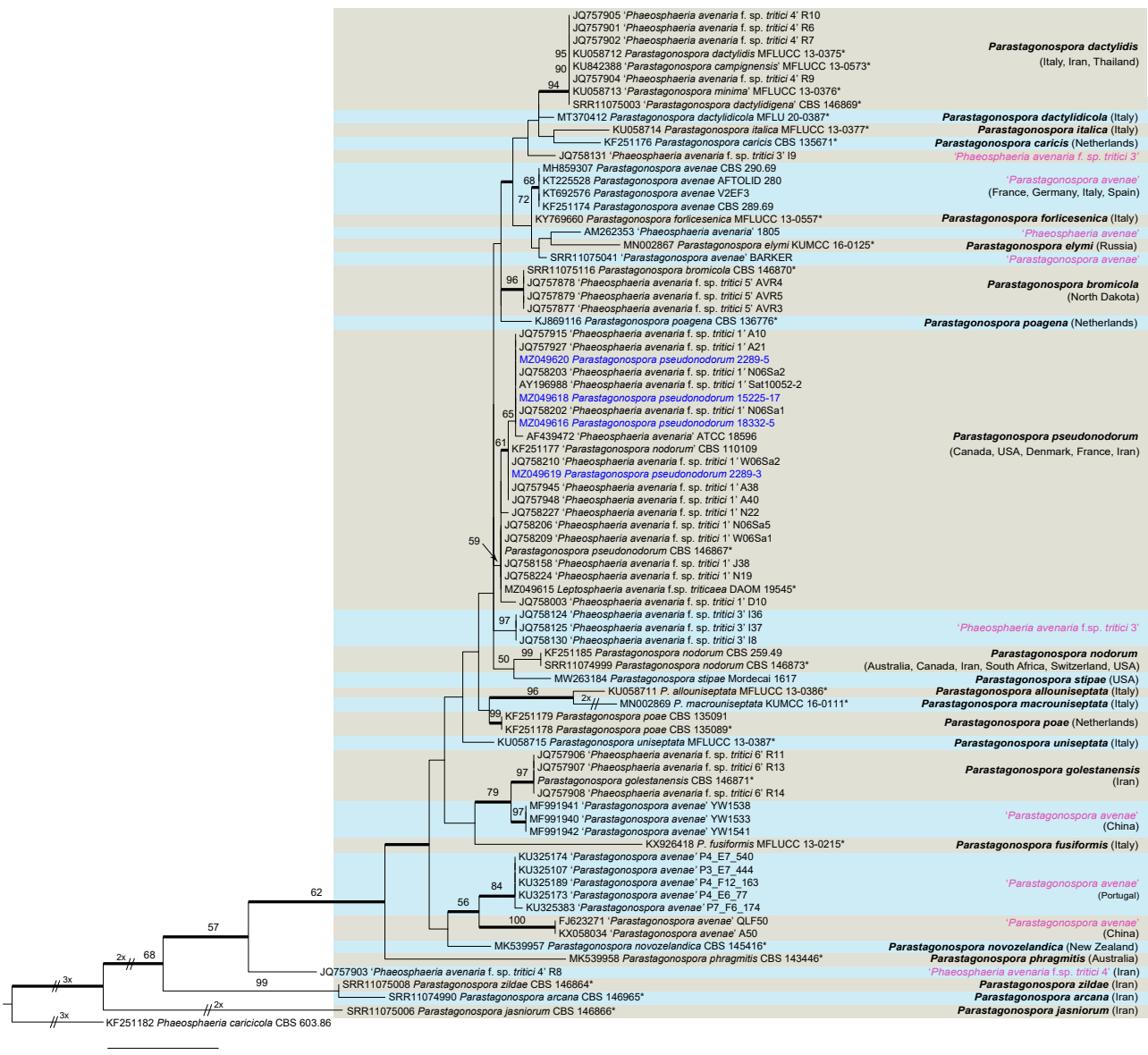

Fig. 26 Phylogenetic tree of *Parastagonospora pseudonodorum* and its closely relatives calculated with RAxML on ITS sequences. Thickened branches indicate branches present in the Bayesian tree with > 0.90 posterior probabilities. The bootstrap support values > 50 % are displayed at the nodes. The blue numbered strains were isolated from wheat intercepted by the Customs District P.R. China, and the Latin names in pink colour represent species with undetermined taxonomic status. Asterisks (*) indicate ex-type cultures.

Hystrix patula, *Lolium perenne*, *Secale cereal*, *Sphenopholis nitida*, *Triticum aestivum*, *T. durum*, *T. vulgare*.

Geographic distribution — Africa: South Africa (McDonald et al. 2012). – America: Canada (Hilton 2000, McDonald et al. 2012), USA (Da Luz & Bergstrom 1986, McDonald et al. 2012). – Asia: Iran (McDonald et al. 2012, Croll et al. 2021). – Europe: Germany (Quaedvlieg et al. 2013, Vu et al. 2019), Denmark, France, Netherlands, Poland (Mulenko et al. 2008). – Oceania: Australia (McDonald et al. 2012).

NCBI Genome ID: JAFJTR000000000 (18332-5, this study).

Notes — *Parastagonospora pseudonodorum* was listed in the Chinese quarantine pest directory as *Stagonospora avenae* f.sp. *triticea*. It was originally described as *Leptosphaeria avenae* f.sp. *triticea* and then placed in *Phaeosphaeria* by Shoemaker & Babcock (1989) as *Ph. avenaria* f.sp. *tritici.* The species was once split into six genetic groups (i.e., *Pat* 1–6) through restriction fragment length polymorphisms (RFLPs) (Ueng & Chen 1994), ITS sequences (Ueng et al. 1998) and multi-locus (ITS, *tubA*, β-xylosidase) DNA sequence analyses (McDonald et al. 2012), among which *Pat* 1 is the dominant wheat-infecting pathogen within this group of fungi. Subsequently, a new genus *Parastagonospora* was introduced to accommodate several serious cereal pathogens that were formerly accommodated in either *Septoria*/*Stagonospora*, or *Leptosphaeria*/*Phaeosphaeria* on the basis of a morphological and phylogenetic study (Quaedvlieg et al. 2013). *Parastagonospora pseudonodorum* was subsequently introduced corresponding to *Pat* 1 (Croll et al. 2021), *Pa. dactylidis* corresponding to *Pat* 4 (Li et al. 2015), *Pa. bromicola* corresponding to *Pat* 5 (Croll et al. 2021), and *Pa. golestanensis* corresponding to *Pat* 6 (Croll et al. 2021). Based on the ITS phylogenetic analysis in this study (Fig. 26), the holotype of *L. avenaria* f.sp. *triticea* DAOM 19545 was revealed residing within the clade of *Pa. pseudonodorum*. *Leptosphaeria avenaria* f.sp. *triticea* is thus synonymised here under *Pa. pseudonodorum*, as formae speciales do not have priority over species (Turland et al. 2018: Note 4 under Article 4).

Based on current knowledge, only two unnamed species of *Parastagonospora* have been reported from China (Fig. 26), and other wheat infecting species should therefore be treated as potentially serious quarantine pathogens.

Fig. 27 *Periconia circinata* (CBS 414.50). a–c. Colonies (20 °C, a. on OA; b. on MEA; c. on PDA); d–j. conidiophores and conida; k. conidia; l. conidia and chlamydospores. — Scale bars: d–k = 10 µm, l = 20 µm.

Furthermore, ITS sequences of the four *Dactylis* associated species *Pa. campignensis*, *Pa. dactylidigena*, *Pa. dactylidis*, and *Pa. minima* are identical (Fig. 26), and a synonymy is therefore proposed, with *Pa. dactylidis* having priority.

Parastagonospora dactylidis W.J. Li et al., Mycosphere 6: 691. 2015

Synonyms. Parastagonospora campignensis Tibpromma et al. (as '*cumpignensis*'), Fungal Diversity 78: 48. 2016.

Parastagonospora minima W.J. Li et al., Mycosphere 6: 691. 2015.

Parastagonospora dactylidigena B.A. McDonald et al., Persoonia 46: 122. 2021.

Periconia circinata (L. Mangin) Sacc., Syll. Fung. 18: 569. 1905 — Fig. 27, 28

Basionym. *Aspergillus circinatus* L. Mangin, Bull. Soc. Mycol. France: 223. 1899.

Symptoms — *Periconia circinata* causes root rot, stunted seedlings and leaf curl of sorghum. Crowns of diseased plants when split show a dark red discolouration. Plants may die as seedlings with the roots completely rotted (Mangin 1899).

Mycelia hyaline to pale brown, smooth or verruculose, 2–5 µm wide, darker and more coarsely warted at the point of origin of the conidiophores. *Conidiophores* solitary or aggregated, grey to dark brown, septate, branched, up to 680 µm long, 2.5–9 µm wide at the base, 2.5–7 µm wide immediately below the head; a few short branches with smooth or sometimes warted walls formed below the apex of the conidiophores, on which globose and pale brown cells are borne, 4.5–8.8 µm diam. *Conidia* solitary, sometimes in short chains, globose, rarely obclavate, formed on hyphae or macronematous conidiophores, brown to dark brown, echinulate, 11–29 µm diam.

Culture characteristics — Colonies on OA reaching 85 mm diam after 14 d at 25 °C, margin regular, aerial mycelia flat, buff to pale luteous; reverse pale luteous. Colonies on MEA reaching 85 mm diam after 14 d, margin regular, covered by felty aerial mycelia, buff at centre, rosy buff at periphery; reverse umber. Colonies on PDA reaching 80 mm diam after 7 d, margin regular, covered by felty aerial mycelia, vinaceous buff at centre, buff at periphery; reverse buff to honey.

Materials examined. UK, Rothamsted, from soil, 24 Feb. 1937?, isolated by *M.D. Glynne*, living culture CBS 263.37 = IMI 7301. – Unknown location, on cereals, unknown collection date, isolated and deposited by *R.W. Leukel*, living culture CBS 414.50 = ATCC 9354 = QM 352.

Habitat — *Agropyron cristatum*, *A. inerme*, *A. intermedium*, *A. michnoi*, *A. semicostatum*, *A. trachycaulum*, *Agrostis* sp., *Andropogon hallii*, *A. scoparius*, *Arthraxon hispidus* var. *cryptatherus*, *A. hispidus*, *Avena fatua*, *A. nuda*, *A. sativa*, *Bromus inermis*, *Calamovilfa longifolia*, *Dactylis glomerata*, *Elymus dahuricus*, *E. junceus*, *E. salsuginosus*, *Eragrostis cilianensis*, *Eucalyptus viminalis*, *Festuca elatior*, *F. octoflora*, *Glycine max*, *Hordeum brevisubulatum*, *H. vulgare*, *Hyparrhenia confinis*, *Koeleria cristata*, *Medicago sativa*, *Panicum miliaceum*, *Phleum pratense*, *Poa juncifolia*, *Setaria italica*, *S. viridis*, *Sorghastrum nutans*, *Sorghum bicolor*, *S. caffrorum*, *S. halepense*, *S. vulgare*, *S. vulgare* var. *sudanense*, *Triticum aestivum*, *T. dicoccum*, *T. durum*, *Zea mays* (Farr & Rossman 2021).

Geographic distribution — Africa: South Africa (Crous et al. 2000), Tanzania (Lenne 1990). – America: Argentina (Carmaran & Novas 2003), Mexico (Ramakrishnan 1971), USA (Ramakrishnan 1971). – Oceania: Australia (Shivas 1989).

Notes — *Periconia circinata* was initially described as *Aspergillus circinatus* c. 120 years ago, without the designation of a type specimen, but a line drawing based on type material was provided (Mangin 1899).

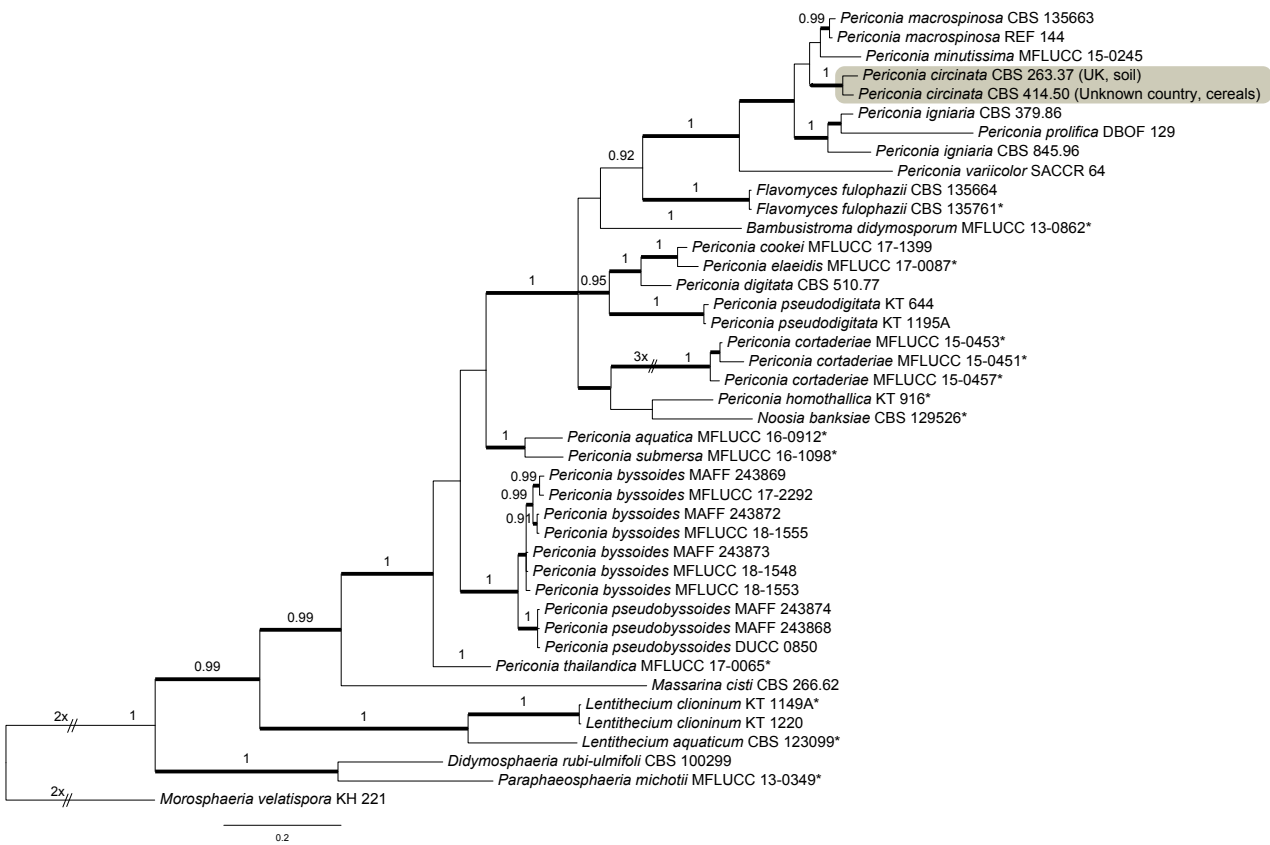

Fig. 28 Phylogenetic tree of *Periconia circinata* and its closely relatives calculated with Bayesian analysis on LSU and ITS sequences. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Fig. 29 *Plenodomus libanotidis* (a–i. type of *Pleospora libanotidis* G00266366, j–o. type? of *Leptosphaeria libanotis* PH1060163). a, j. Type collection packets; b, k. ascomata on host substrate; c–e, m. section of ascomata; f, l, n. asci and pseudoparaphyses; g–i. ascospores; o. pseudoparaphyses. — Scale bars: c–e = 20 µm, f–i, l–o = 10 µm.

Up to now, only four sequences of *Periconia circinata* have been deposited in the GenBank database, which were generated from CBS 263.37 and CBS 414.50. Phylogenetically, these two strains clustered together in the LSU and ITS tree (Fig. 28). However, neither of the two strains is ideal for the designation of an epitype, since CBS 414.50 is avirulent and CBS 263.37 is sterile. Further collections and study of *Periconia circinata* is therefore needed.

Plenodomus libanotidis (Fuckel) Gruyter et al., Stud. Mycol. 75: 22. 2013 — Fig. 29, 30, 31

Basionym. *Pleospora libanotidis* Fuckel, Jahrb. Nassauischen Vereins Naturk. 27–28: 24. 1873 (as '*libanotis*').

Synonyms. *Leptosphaeria libanotis* (Fuckel) Niessl, Verh. Naturf. Vereins Brünn 14: 165. 1876 (as '*libanotidis*').

Leptosphaeria libanotidis (Fuckel) Sacc., Syll. Fung. 2: 16. 1883 (as '*libanotis*').

Phoma sanguinolenta Rostr., Z. Pflanzenkrankh. 4: 195. 1894 (not *Phoma sanguinolenta* Grove, J. Bot., Lond. 23: 162. 1885) (Nom. illegit.).

Phoma rostrupii Sacc., Syll. Fung. 11: 490. 1895.

Typus. Switzerland, Jura, E6°46'12" N46°56'20", on stems of *Libanotis montana*, in spring (unknown collection date), *Morthier*, holotype of *Pleospora libanotis* G00266366.

Symptoms — *Plenodomus libanotidis* causes brown rot of *Apiaceae*, especially on carrots. It causes dark brown spots on the stalk, spadix, flowers, stems and tap root of carrot. Later, the spots on above-ground parts of the plant turn violet and exude a sticky substance. Infected tissues dry and break easily, and the leaves eventually die. Sunken greyish spots on damaged tap roots are more visible during the storage period, under which the tissue disintegrates, dries and develops cracks (Baramidze et al. 2015).

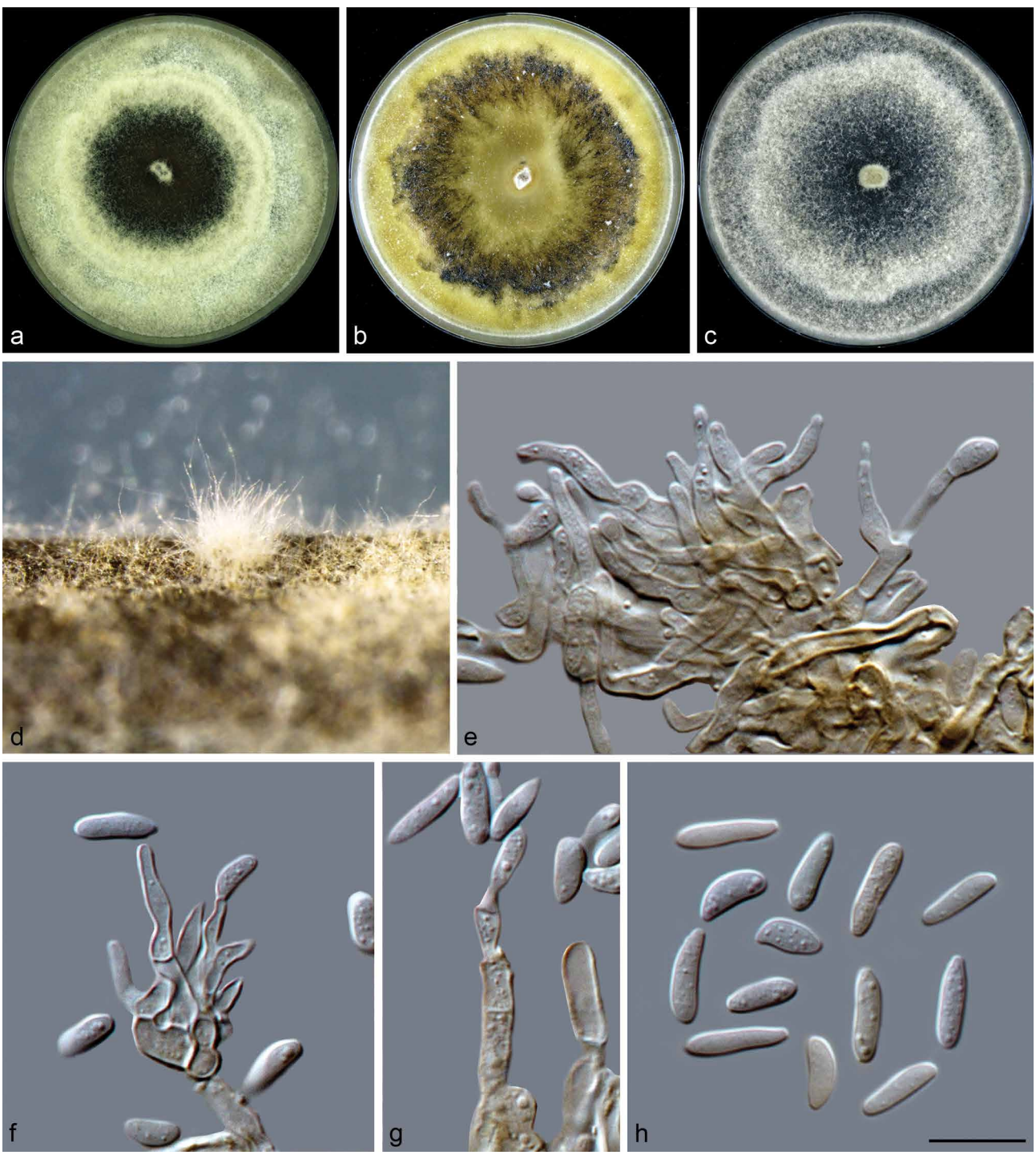

Fig. 30 *Plenodomus libanotidis* (CBS 113795). a–c. Colonies in 14 d (20 °C, a. on MEA; b. on OA; c. on PDA); d. pycnidia; e–g. conidiogenous cells and conidia; h. conidia. — Scale bar: h = 10 µm, applies to e–h.

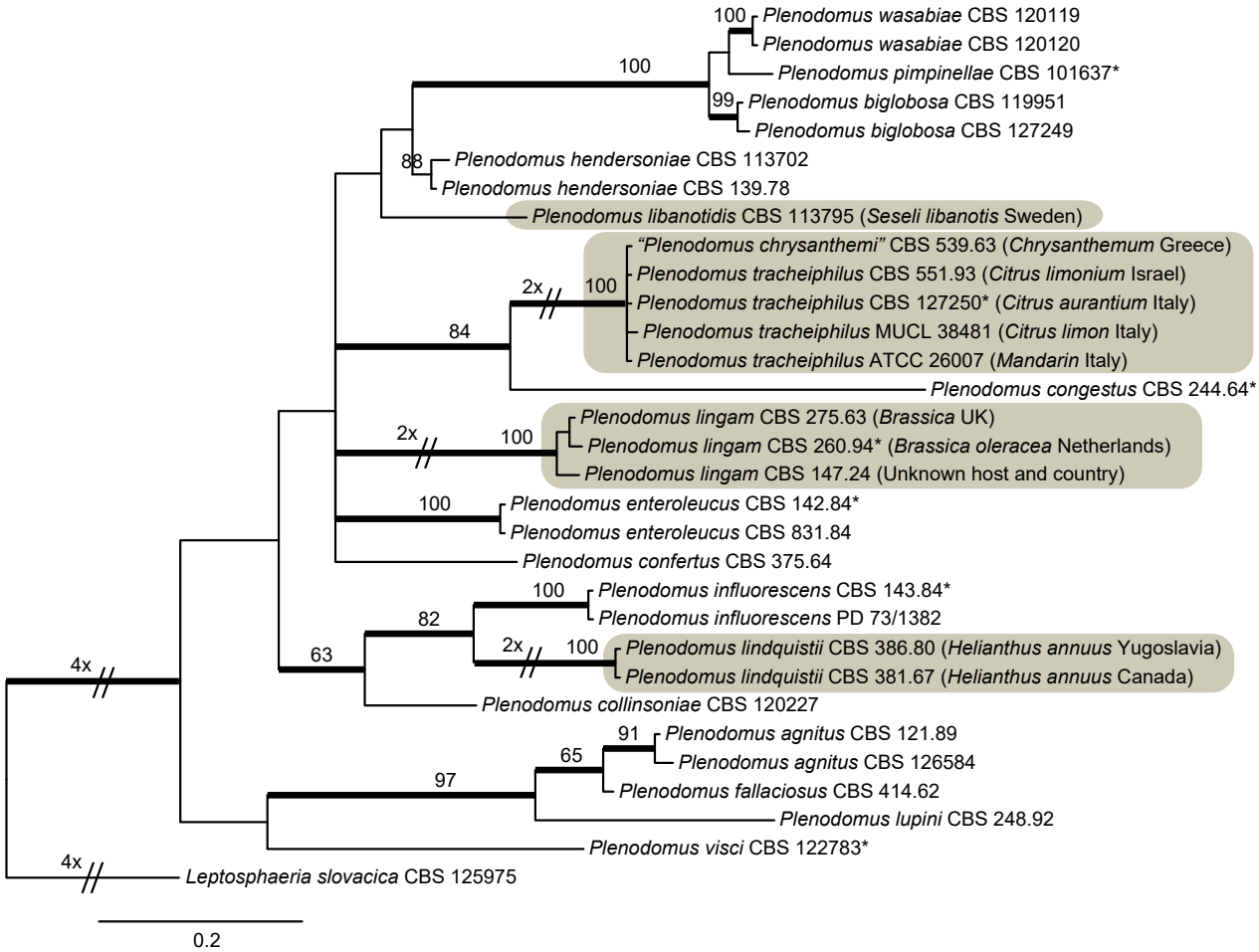

Fig. 31 Phylogenetic tree of *Plenodomus* calculated with Bayesian analysis on a combined dataset of LSU and ITS showing affinities of *P. lingam* and *P. tracheiphilus* with members of *Plenodomus* species. Thickened branches indicate branches present in the Bayesian tree with > 0.90 posterior probabilities. The RAxML bootstrap support values (> 50 %) are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Ascomata not observed in culture in this study. *In vivo*: *Ascomata* pseudothecial, mostly 360–415 µm diam, globose or conical globose with flattened base. *Asci* 100–125 × 8–11 µm, cylindrical, 8-spored, uniseriate. *Ascospores* mostly 18–20 × 5.5–7 µm, fusiform to ellipsoidal, hyaline to pale brown, smooth, 3-septate, constricted at septa, second cell from the apex enlarged. *Conidiomatal* pycnidia only formed on *Anthriscus sylvestris* stem on SNA in this study, globose to subglobose, solitary, covered by white and fluffy aerial mycelia, with or without ostiole, thin-walled; conidial exudate not observed. *Conidiogenous cells* hyaline or pale brown, smooth, ampulliform, subcylindrical, 3.5–12.5 × 1.5–3 µm. *Conidia* 5.5–11 × 2–3 µm (av. = 8.5 × 2.7 µm), L/W ratio = 3.1, hyaline, cylindrical, ellipsoidal or reniform, multiple guttules. *Chlamydospores* absent.

Culture characteristics — Colonies fast growing, reaching 85 mm diam after 7 d on PDA, aerial mycelia velvety-cottony, slate blue in the centre and white in the periphery, often with a white zone, reverse grey to fuscous black. Colonies on MEA attaining 80–84 mm diam after 7 d, aerial mycelia white to light yellow, velvety-cottony, dark mouse grey in the centre of the colony and white to light greenish glaucous in the periphery, reverse livid vinaceous in the centre and citrine to brown vinaceous in the periphery. Colonies on OA attaining 67–68 mm diam after 7 d, aerial mycelia sparse and white, smoke grey in the forward, often with a grey olivaceous zone, reverse greenish grey.

Additional materials examined. Germany, unknown host plant, May 1875, *J. Kunze*, type? of *Leptosphaeria libanotis* PH00041016 (PH#1060163). – Sweden, Uppland, Gröna strand, on *Seseli libanotis* (*Apiaceae*), 19 May 1987, *K. & L. Holm*, living culture CBS 113795 = UPSC 2219.

Habitat — Various species in *Apiaceae*.

Geographical distribution — Africa: South Africa (Gorter 1977). – Europe: Germany, Russia (Richardson 1990), Sweden, Switzerland.

NCBI Genome ID: JAGKQA000000000 (CBS 113795, this study).

Notes — *Plenodomus libanotidis* (De Gruyter et al. 2013) was listed in the Chinese quarantine pest directory as *Leptosphaeria libanotis*. This fungus was known as a serious pathogen of carrots in northern Europe. However, the ex-type living cultures of both *Plenodomus libanotidis* and its asexual morph *Phoma rostrupii* were not noted in the original publications. Therefore, morphological characters based on the type specimen of *Pleospora libanotidis* (basionym) was illustrated in this study (Fig. 29).

Published molecular data of *P. libanotidis* has thus far been restricted to the reference strain CBS 113795 (De Gruyter et al. 2013), and it is clearly distinct from other relatives (Fig. 31). However, we found that CBS 113795 is morphologically different from the representative strains SHD 2009 and SHD 2163 used in Boerema et al. (2004) in conidial size (5.5–11 × 2–3 µm, av. 8.5 × 2.7 µm vs 5–6.5 × 1.5–2.5 µm). Besides, SHD 2009 and SHD 2163 produced dumb-bell-shaped conidia (Boerema et al. 2004), which were absent in CBS 113795. Considering the taxonomic ambiguity and severity it caused on plants, epitypification of *P. libanotidis* using a suitable strain is urgently required.

Plenodomus lingam (Tode) Höhn., Sitzungsber. Kaiserl. Akad. Wiss., Math.-Naturwiss. Cl., Abt. I 120: 463. 1911 — Fig. 31, 32, 33

Basionym. *Sphaeria lingam* Tode, Fungi Mecklenb. Sel. 2: 51. 1791.

Synonyms. *Phoma lingam* (Tode) Desm., Ann. Sci. Nat., Bot. Ser. 3, 11: 281. 1849.

Sphaeria maculans Desm., Ann. Sci. Nat., Bot. Ser. 3, 6: 77. 1846 (nom. illeg.)

Leptosphaeria maculans Ces. & De Not., Comment. Soc. Crittog. Ital. Milan 1: 235. 1863.

Plenodomus rabenhorstii Preuss, Linnaea 24: 145. 1851.

Sphaeria napi Fuckel, Fungi Rhenani Exsicc. 895. 1864.

Leptosphaeria napi (Fuckel) Sacc., Syll. Fung. 2: 45. 1883.

Pleospora napi (Fuckel) Fuckel, Jahrb. Nassauischen Vereins Naturk. 23–24: 136. 1870.

Sphaeria (*Caulicolae*) *virginica* Cooke & Ellis, Grevillea 8: 16. Sept. 1879.

Leptosphaeria virginica (Cooke & Ellis) Sacc., Syll. Fung. 2: 35. 1883.

Typus. Lectotype of *Sphaeria lingam* designated here (MBT 10001928): t. XVI, f. 126, in Tode HI. 1791. Fungi mecklenburgenses selecti. Netherlands, near Goes, from *Brassica oleracea*, 1978, *M.M.J. Dorenbosch*, epitype designated here CBS H-24655, MBT 10001723, culture ex-epitype CBS 260.94 = PD 78/989 = CCM F-700.

Symptoms — *Plenodomus lingam* causes canker, dry rot and blackleg on *Brassica* spp. Initially, pale lesions appear on the seedling stem, cotyledons and first true leaves, which then become greyish with the development of conidiomata. Lesions on the leaves and other above-ground parts of older plants often have purplish margins. The stem, root and bulb are attacked causing necrotic, girdling cankers and transverse splits; severe infection of stems or roots leads to wilt or the whole plant toppling over (Punithalingam & Holliday 1972).

Conidiomata pycnidial, not produced on PDA, MEA and OA, but formed on *Anthriscus* stem or underneath CMA and SNA media, isabelline on SNA and olivaceous to black on CMA, solitary or aggregated, generally subglobose or flask-shaped with broad base, with narrow ostioles, outer layers pigmented; conidial exudate not observed. *Conidiogenous cells* hyaline, smooth, doliiform, ampulliform or bullet-shaped, 3–5.5 × 4–5 µm. *Conidia* most straight, cylindrical, sometimes reniform, ellipsoidal, or broadly ellipsoidal, hyaline, guttulate, aseptate, 3–5 × 1.5–2 µm (av. ± S.D. = 4.2 ± 0.27 × 1.8 ± 0.11 µm).

Culture characteristics — Colonies on PDA attaining 72–74 mm diam after 7 d, flat or effuse, margin entire, usually with copious aerial mycelia, white, but smoke grey in the centre, cottony, fluffy. Colonies on MEA reaching 29–30 mm diam after 7 d, flat or effuse, margin undulate, aerial mycelia white and fluffy. Colonies on OA attaining 68 mm diam after 7 d, flat or effuse, margin entire, with copious aerial mycelia, white, light smoke grey in the centre, cottony.

Additional materials examined. UK, from *Brassica* sp., 1963, *B.C. Sutton*, culture CBS 275.63 = MUCL 9901= UPSC 1025. – Unknown country, unknown substrate, Mar. 1924, *A. Weber*, living culture CBS 147.24.

Habitat — *Brassica* spp., *Raphanus raphanistrum*.

Unverified habitat — (Farr & Rossman 2021): *Alliaria officinalis*, *A. petiolata*, *Arabis glabra*, *Argemone mexicana*, *Astragalus adsurgens*, *Avena sativa*, *Beta vulgaris*, *Capsella bursa-pastoris*, *Cardamine bellidifolia*, *Cardaria draba*, *Cheiranthus cheiri*, *Clematis vitalba*, *Echinops* sp., *Eucalyptus globulus*, *Gentiana cruciata*, *Hibiscus rosa-sinensis*, *Iberis umbellata*, *Ledum palustre*, *Lepidium virginicum*, *Lobularia maritima*, *Lolium perenne*, *Lupinus albicaulis* var. *albicaulis*, *Lupinus* sp., *Matthiola incana*, *M. tristis*, *Populus* × *canadensis*, *Raphanus raphanistrum*, *R. sativus*, *R. sativus* var. *longipinnatus*, *R. sativus* var. *sativus*, *Rorippa curvisiliqua*, *Scirpus lacustris*, *Secale cereale*, *Sinapis alba*, *Sisymbrium altissimum*, *Thlaspi arvense*.

Geographic distribution — Africa: Ethiopia (IMI herbarium), Kenya (Piening et al. 1975), Mozambique (de Carvalho & Mendes 1958), Nigeria (Alasoadura 1970), South Africa (Crous et al. 2000), Zambia (IMI herbarium), Zimbabwe (Whiteside 1966). – America: Argentina (Garbagnoli & Irigoyen 1999), Brazil (Punithalingham & Holliday 1972), Canada (Pedras 2001), Costa Rica (Punithalingham & Holliday 1972), El Salvador (Punithalingham & Holliday 1972), Guadeloupe (Pauvert 1971), Mexico (Moreno-Rico et al. 2002), Panama (Toler et al. 1959), USA (Hershman & Perkins 1995, Pongam et al. 1999, EPPO

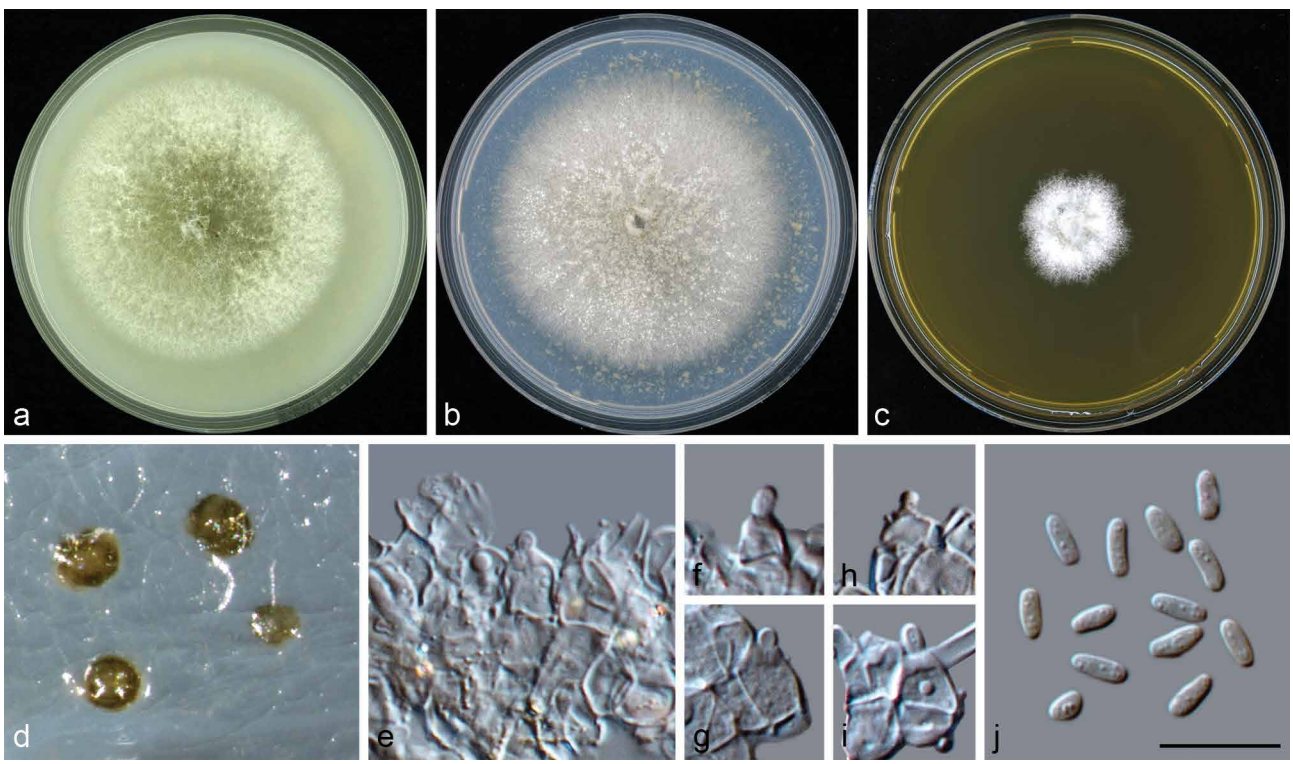

Fig. 32 *Plenodomus lingam* (ex-epitype CBS 260.94). a–c. Colonies in 10 d (20 °C, a. on OA; b. on PDA; c. on MEA); d. pycnidia on SNA; e–i. conidiogenous cells and conidia; j. conidia. — Scale bar: j = 10 µm, applies to e–j.

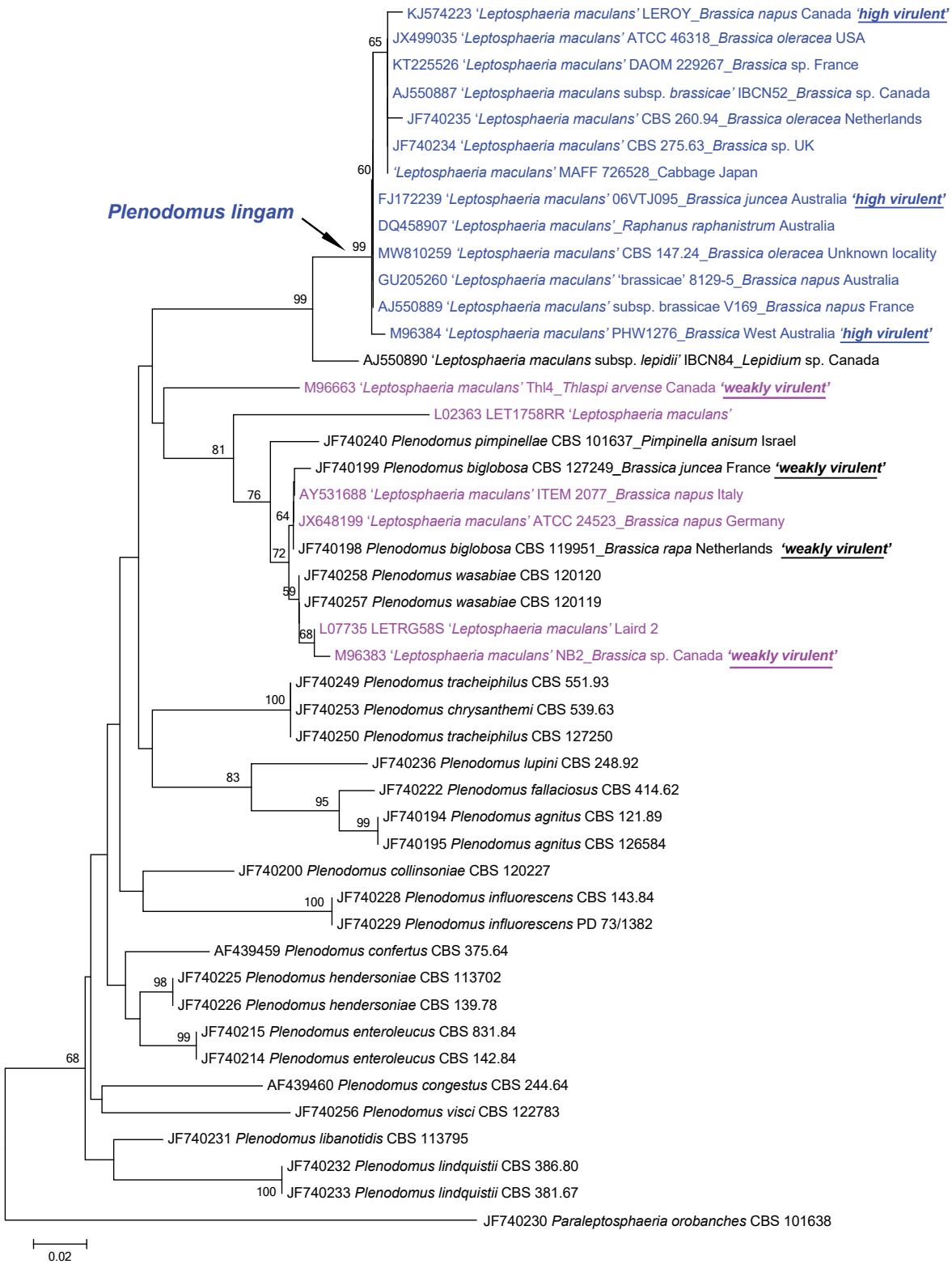

Fig. 33 Neighbour-joining tree of ITS sequences from 49 isolates of *Plenodomus* and an outgroup *Paraleptosphaeria orobanches* retrieved from GenBank. The tree was constructed using MEGA v. 7.0.21 software. The Kimura-2-parameter method was used. Bootstrap support values (1 000 replicates) above 50 % are shown at the nodes. Strains in blue colour indicate isolates from *Brassica* spp. that belong to *P. lingam*, and strains in purple colour indicate isolates from *Brassica* spp. that exclude from *P. lingam*; GenBank accessions are followed by taxonomic name as originally identified, strain number, host and country of origin.

2019b). – Asia: India (Rani et al. 1978), Iran (Scharif & Ershad 1966), Israel (Reichert 1939), Japan (Kubota & Abiko 1998), Korea (Anonymous 1972), Malaysia (Williams & Liu 1976), Pakistan (Ahmad 1978), Philippines (Teodoro 1937), Thailand (Chandrasrikul 1962). – Europe: widespread (EPPO 2019b). – Oceania: Australia (Marcroft et al. 2004), New Caledonia (Anonymous 1962), New Zealand (IMI herbarium), Papua New Guinea (IMI herbarium).

NCBI Genome ID: JAGKPZ000000000 (CBS 260.94, this study).

Notes — *Plenodomus lingam* was listed in the Chinese quarantine pest directory as *Leptosphaeria maculans*. Its connection with the asexual morph was established by Müller & Tomaševič (1957) and Boerema & Van Kesteren (1964), and *P. lingam* was designated as the current name for this fungus (De Gruyter et al. 2013, Ariyawansa et al. 2015).

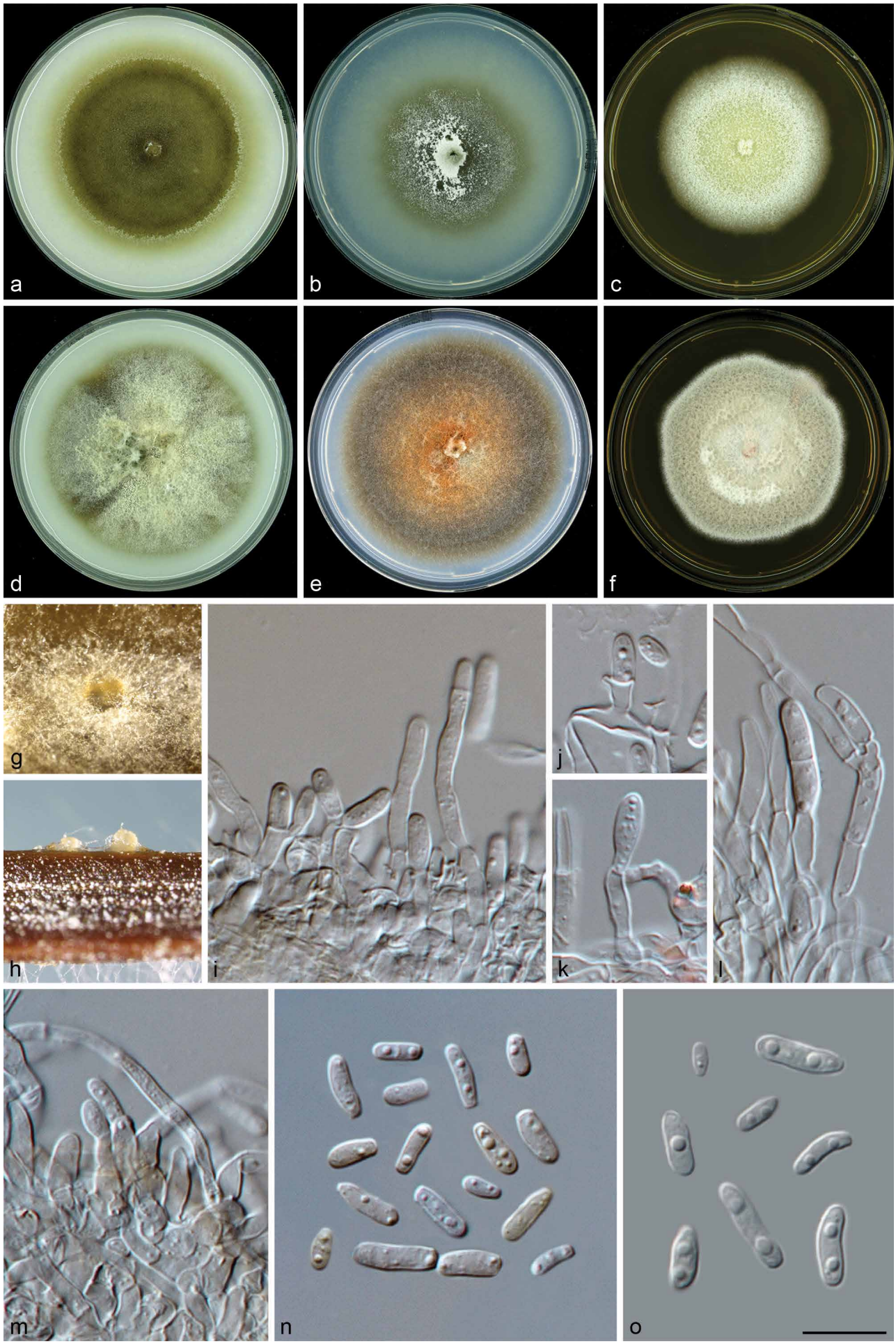

Fig. 34 *Plenodomus tracheiphilus* (a–c, h, o. ex-neotype CBS 127250, d–n. CBS 551.93). a–f. Colonies in 2 wk (20 °C, a, d. on OA; b, e. on PDA; c, f. on MEA); g–h. pycnidia; i–m. conidiogenous cells and conidia; n–o. conidia. — Scale bar: o = 10 µm, applies to i–o.

Plenodomus lingam mainly causes serious stem base canker (blackleg) on cultivated *Brassica* spp. (*Brassicaceae*) in Australia, Europe, and North America (West et al. 2001, Fitt et al. 2006), and has not been reported from China. In this study, three isolates representing *P. lingam* (CBS 275.63 (UK), CBS 260.94 (The Netherlands), and CBS 147.24 (unknown country)) formed a well-supported distinct clade (100/1.00) (Fig. 31). *Plenodomus lingam* was also recorded on other cultivated and wild *Cruciferae*. However, identification of these isolates remains to be confirmed based on the current classification of *Plenodomus*.

Furthermore, we noticed that many ITS sequences of *P. lingam* and its relatives, associated with *Brassica* spp., had been deposited in GenBank. A further phylogenetic analysis based on more ITS sequences was therefore performed. The ITS tree (Fig. 33) showed that highly aggressive isolates from *Brassica* spp. (e.g., LEROY, PHW1276) from many countries (e.g., Australia, Canada, France, Japan, Netherlands, UK, and USA), formerly identified as *Leptosphaeria maculans* (sexual morph of *P. lingam*), clustered together in a distinct clade with high bootstrap support (99 %), representing *P. lingam*. The weakly aggressive isolates formed a sister clade with *P. lingam*, which, however, showed a closer relationship to other species, i.e., *P. pimpinellae*, *P. biglobosa*, and *P. wasabiae*. Our results are consistent with previous studies that, weakly aggressive (or non-aggressive) isolates and highly aggressive isolates (producing toxic secondary metabolites Tox$^+$) from *Brassica* spp. segregate into two different species, namely *P. biglobosus* and *P. lingam* (Morales et al. 1993, Shoemaker & Brun 2001, Mendes-Pereira et al. 2003, Boerema et al. 2004, De Gruyter et al. 2013).

The basionym *Sphaeria lingam* was introduced without the designation of a type specimen (Tode 1791), and the description and illustration of which was very brief. The type materials of Tode including the original material of *Sphaeria lingam* were unfortunately destroyed. Therefore, we designated the illustration by Tode here as lectotype and CBS H-24655 (made from the Netherlands culture CBS 260.94) as epitype. Unfortunately, the sexual morph of CBS 260.94 was not observed in this study.

Plenodomus tracheiphilus (Petri) Gruyter et al., Stud. Mycol. 75: 22. 2012 — Fig. 31, 34

Basionym. *Deuterophoma tracheiphila* Petri, Boll. Staz. Patol. Veg. Roma 9: 396. 1929.

Synonyms. *Bakerophoma tracheiphila* (Petri) Cif., Ist. Bot. Reale Univ. Reale Lab. Crittog. Pavia Atti Ser. V, 5: 307. 1946.

Phoma tracheiphila (Petri) L.A. Kantsch. & Gikaschvili, Trudy Inst. Zasch. Rast. Tiflis 5: 20. 1948.

Cephalosporium chrysanthemi Zachos et al., Ann. Inst. Phytopath. Benaki, N.S. 3: 55. 1960.

Plenodomus chrysanthemi (Zachos et al.) Gruyter et al., Stud. Mycol. 75: 21. 2012. (Nom. inval.)

Phialophora chrysanthemi (Zachos et al.) W. Gams, Cephalosporium-artige Schimmelpilze (Stuttgart): 207. 1971.

Phoma vasinfecta Boerema, Gruyter & Kesteren, Persoonia 15: 484. 1994.

Typus. Italy, Sicily, Palermo, on *Citrus aurantium*, 1993, unknown *collector*, neotype designated here CBS H-24656, MBT 10001724, culture ex-neotype CBS 127250 = FC 40 = PD 09/04597141.

Symptoms — *Plenodomus tracheiphilus* causes red strands in stem xylem as well as veinal chlorosis, wilt and shedding of leaves, dieback of twigs and branches. Cuts into the wood (before wilt and death of the bark) reveal the characteristic orange-yellow to reddish discolouration of the vascular tissue (Chalkley 2021).

Conidiomata pycnidial, sparsely produced, pale yellow, surrounded by aerial mycelia, thin-walled and open irregularly at maturity. *Conidiogenous cells* monophialidic, integrated, hyaline, cylindrical or flask-shaped, determinate with well-defined collarettes. *Conidia* variable in shape and size, hyaline, cylindrical, ellipsoidal, reniform, clavate, straight or curved, aseptate, occasionally 1-septate, usually with 2 or more guttules, 2.5–11.5 × 1–3 µm (av. ± S.D. = 6.8 ± 2.13 × 2.3 ± 0.44 µm).

Culture characteristics — On OA the colonies reaching 25–35 mm diam after 7 d, flat with little aerial mycelia; pigmentation of mycelial mat and medium variable, depending on strain and ranging from pale pink or bright orange to dark olive brown. On application of NaOH the reddish pigments turn blue (the presence of helminthosporin and cynodontin have been demonstrated). Colonies on PDA 35–36 mm diam after 7 d, orange to olivaceous or olivaceous grey, reverse fawn or livid vinaceous to dark vinaceous. Colonies on MEA 28–30 mm diam after 7 d, glaucous grey or pale olivaceous grey, reverse bust, margin pure yellow.

Additional materials examined. Greece, from *Chrysanthemum* sp., Apr. 1963, *D.G. Zachos*, holotype CBS H-7576, ex-holotype culture of *Cephalosporium chrysanthemi* CBS 539.63. – Israel, on *Citrus limon*, deposited at CBS by *J. de Gruyter* in Oct. 1993, culture CBS 551.93 = PD 81/782. – Italy, Sicily, Palermo, Bagheria, on *Citrus limon*, 1983, probably *Faretra*, culture Pt 52 = MUCL 38481 (sterile); on *Citrus* sp. twigs, probably 1971, deposited at ATCC by *S. Grasso*, culture ATCC 26007.

Habitat — Common on *Citrus limon* and other *Citrus* spp., occasionally on *Chrysanthemum* sp.

Geographic distribution — (EPPO 2019b, Farr & Rossman 2021): Africa: Algeria, Egypt, Libya, Tunisia. – Asia: Iraq, Israel, Lebanon, Russia, Syria, Yemen. – Europe: Albania, Cyprus, France, Georgia, Greece, Italy, Russia, Turkey.

NCBI Genome ID: JAFISG000000000 (MUCL 38481, this study).

Notes — *Plenodomus tracheiphilus* (De Gruyter et al. 2013) was listed in the Chinese quarantine pest directory as *Phoma tracheiphila*. It causes vascular diseases (maldel secco) and serious damage to host plants, particularly on *Citrus* and related genera. Almost all *Citrus* species are susceptible to *P. tracheiphilus* (Perrotta & Graniti 1988). Major characteristics of this disease include leaf chlorosis around veins (Perrotta & Graniti 1988), typical salmon-pink to orange-red discoloration of the xylem (Migheli et al. 2009), and an ashy colour of the dead twigs (Perrotta & Graniti 1988).

Plenodomus tracheiphilus was originally described as *Deuterophoma tracheiphila* (Petri 1929) from *Citrus limon* from Italy. However, the type of this fungus is either lost or destroyed, as the request of type specimen from several fungaria (BPI, E, FI, K, LI) where it might have been deposited, proved unsuccessful. In this study, four strains of *P. tracheiphilus* from *Citrus* spp. from Italy and Israel, as well as the ex-holotype (CBS 539.63) of *Cephalosporium chrysanthemi*, formed a distinct clade with high supported value (Fig. 31). Although the strain MUCL 38481 was isolated from exactly the same host as the holotype of *Plenodomus tracheiphilus*, it is sterile in this study and thus improper for the designation of a type. A neotype of this fungus from *Citrus aurantium* from Italy (CBS H-24656) was therefore designated herein.

Pseudocercospora angolensis (T. Carvalho & O. Mendes) Crous & U. Braun, Sydowia 55: 301. 2003 — Fig. 35, 36

Basionym. *Cercospora angolensis* T. Carvalho & O. Mendes, Bolm Soc. Broteriana, Coimbra, sér. 2, 27: 201. 1953.

Synonyms. *Phaeoramularia angolensis* (T. Carvalho & O. Mendes) P.M. Kirk, Mycopathologia 94: 177. 1986.

Pseudophaeoramularia angolensis (T. Carvalho & O. Mendes) U. Braun, Cryptog. Mycol. 20: 171. 1999.

Typus. Angola, Mozambique Province, on leaves of *Citrus* × *aurantium* (= × *sinensis*), Dec. 1951, *T. Carvalho* & *O. Mendes*, holotype IMI 56597, culture ex-holotype CBS 149.53 = ATCC 11669, isosyntypes BPI 442837, BPI 432660, and BPI 442839.

Symptoms — *Pseudocercospora angolensis* causes spots and lesions on the leaves and fruits of *Citrus* species, hybrids and varieties. Leaf symptoms initially appear as greenish yellow patches and then become amphigenous with age, mainly hypophyllous, pale brown to brown, blackish brown when sporulation is dense, surrounded by a dark brown margin and a yellow halo, the centre often becoming detached resulting in a shot-hole spot. The lesions on young fruit tumour-like and surrounded by yellow halos, while on mature fruit are normally flat, but sometimes with a slightly sunken brown centre and raised surrounding ring, giving the fruit a blistered appearance. The lesions of infected stems are dark brown and usually occur as an extension of the lesions on the petioles, which may coalesce resulting in stem dieback or formation of corky internodal regions (Seif & Hillocks 1993).

Conidiophores solitary, fasciculate or forming loose synnemata, 12–45 µm wide, unbranched, 1–3-septate, smooth, pale brown to brown, (60–)120–240 × 4.5–7 µm, usually arising from a dark stroma 30–60 µm diam. *Conidia* solitary or catenulate, pale brown, smooth, cylindrical to obclavate, straight or slightly flexuous to more or less curved, apex rounded, base truncate, hila and scars inconspicuous or minutely thickened, 1–6-septate, 24–79 × 4–6.5 µm (adapted from Kirk 1986, and Pretorius et al. 2003).

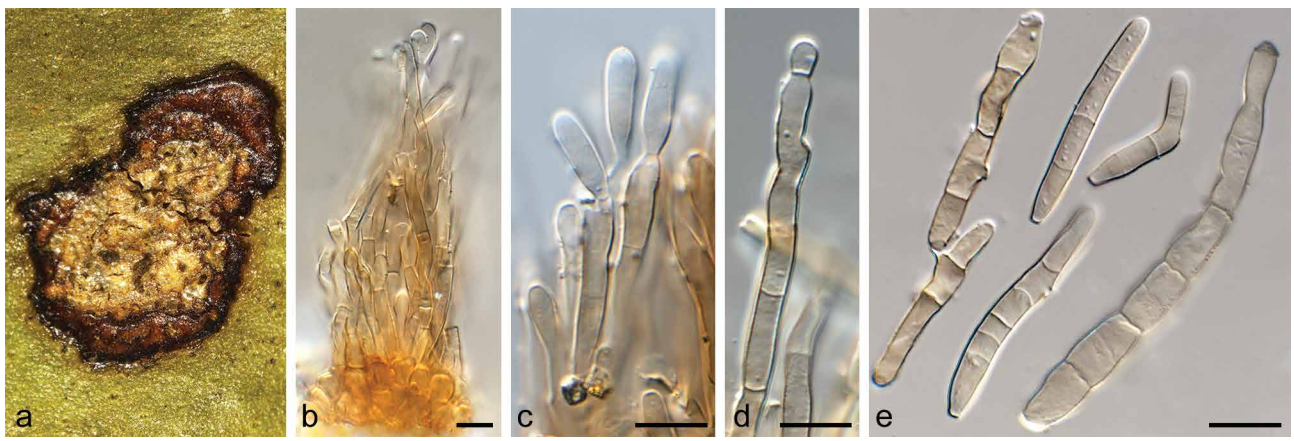

Fig. 35 *Pseudocercospora angolensis* (CBS H-20851). a. Disease symptom on leaf; b–d. conidiophores, conidiogenous cells and conidia; e. conidia. — Scale bars: b–e = 10 µm.

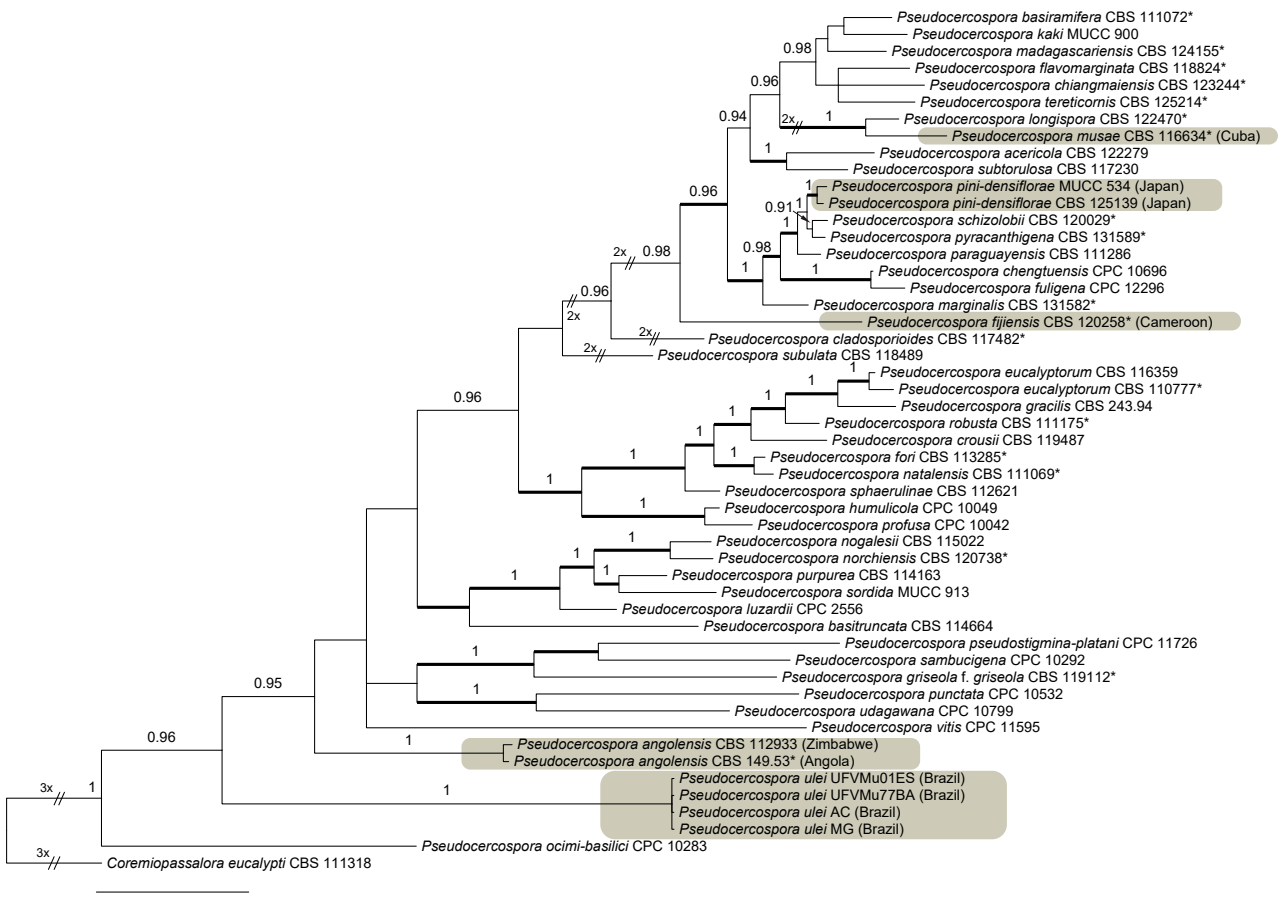

Fig. 36 Phylogenetic tree of *Pseudocercospora* calculated with Bayesian analysis on *act*, ITS, and *tef 1-α* sequences showing affinities of the five quarantine fungi (*P. angolensis*, *P. fijiensis*, *P. musae*, *P. pini-densiflorae*, and *P. ulei*) with their allied species. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Additional material examined. Zimbabwe, Bindura, on leaves of *Citrus* sp., Sept. 2000, *M.C. Pretorius*, CBS H-20851, culture CBS 112933 (superfluously designated as epitype in Crous et al. (2013)).

Habitat — *Citrus* spp.

Geographic distribution — (Pretorius et al. 2003, EPPO 2019b): Africa: Angola, Burundi, Cameroon, Central African Republic, Comoros, Congo, Cote d'Ivoire, Ethiopia, Gabon, Gambia, Ghana, Guinea, Ivory Coast, Kenya, Mozambique, Nigeria, Rwanda, Sierra Leone, Tanzania, Togo, Uganda, West Africa, Zaire, Zambia, Zimbabwe. – Asia: Yemen.

Notes — *Pseudocercospora angolensis* (Pretorius et al. 2003, Quaedvlieg et al. 2012, Crous et al. 2013) was listed in the Chinese quarantine pest directory as *Phaeoramularia angolensis*. It is also of quarantine significance to the EU.

Pseudocercospora angolensis causes leaf and fruit spots on *Citrus* and is currently endemic to Africa and Yemen, where it occurs on all major *Citrus* species and varieties. Phylogenetically, *P. angolensis* differed easily from other species (Fig. 36). Because of the slow growth of *P. angolensis* on culture media, rapid and specific detection is significant to prevent biological invasion to the new areas. A real-time quantitative PCR assay for *P. angolensis* based on the *tef 1-α* gene was developed for quick identification (Ahmed et al. 2019), with the forward/reverse primers P.ango-F (CCACACATTCCTCTGCTCCT) and P.ango-R (AGGCATCGTATCAGCAAGCT), and the probe P.ango-P (CY5-TGAGCATCGACAACAACACGCT-BHQ2). The amplicon length using above PCR assay is 77 bp.

Pseudocercospora fijiensis (M. Morelet) Deighton, Mycol. Pap. 140: 144. 1976 — Fig. 36, 37

Basionym. Cercospora fijiensis M. Morelet, Ann. Soc. Sci. Nat. Archéol. Toulon Var 21: 105. 1969.

Synonyms. *Paracercospora fijiensis* (M. Morelet) Deighton, Mycol. Pap. 144: 51. 1979.

Cercospora fijiensis var. *difformis* J.L. Mulder & R.H. Stover, Trans. Brit. Mycol. Soc. 67: 82. 1976.

Paracercospora fijiensis var. *difformis* (J.L. Mulder & R.H. Stover) Deighton, Mycol. Pap. 144: 52. 1979.

Mycosphaerella fijiensis M. Morelet, Ann. Soc. Sci. Nat. Archéol. Toulon Var 21: 105. 1969.

Mycosphaerella fijiensis var. *difformis* J.L. Mulder & R.H. Stover, Trans. Brit. Mycol. Soc. 67: 82. 1976.

Typus. Cameroon, on *Musa* sp., unknown collection date, *J. Carlier*, epitype CBS H-20037, culture ex-epitype CBS 120258 = CIRAD 86. – USA, Hawaii, on leaves of *Musa* sp., 12 Dec. 1968, *D.S. Meredith* & *J.S. Lawrence*, holotype IMI 136696; on *Musa* sp., 9 Dec. 1968, *D.S. Meredith*, isotype BPI 608017.

Symptoms — Symptoms are first visible as faint, minute, reddish brown specks on the lower surface of the leaf, which then become elongate and slightly wider and form a narrow, reddish brown streak, with the long axis parallel to leaf veins, 20 × 2 mm. Streaks frequently overlap, and the entire leaf can blacken if streaks are numerous. If less densely congregated, streaks broaden and become fusiform or elliptical spots. Water-soaked borders appear around spots and surrounding leaf tissue yellows slightly. The centres of spots become slightly depressed and dry out, becoming light grey or buff. Each spot has a well-defined, narrow dark brown or black border and surrounding tissue is often yellow. Whole sections of leaves can become necrotic as spots coalesce (Meredith & Lawrence 1969). For symptom illustration see Crous et al. (2013).

Ascomata perithecial, globose, with protruding ostioles, 50–85 µm diam. *Asci* bitunicate, obclavate, 8-spored, paraphyses absent. *Ascospores* biseriate, fusiform to clavate, hyaline, 1-septate, slightly constricted at the septum, 11.5–16 × 2.5–5 µm (adapted from Meredith & Lawrence 1969). *Conidiophores* pale to medium olivaceous-brown, becoming slightly paler towards the tip, straight or bent, often with geniculations and sometimes with a basal swelling, branched, 0–5-septate, 16.5–62.5 × 4–7 µm. *Conidiogenous cells* up to 25 µm long, 2–4 µm wide at the apex, with 1–3 minutely thickened scars. *Conidia* subhyaline, pale-green or olivaceous, straight or curved, obclavate to cylindro-obclavate, obtuse at the apex, truncate or rounded at the base with a slightly thickened and darkened hilum, 1–10-septate, 10–120 × 2.5–5 µm (adapted from Crous & Mourichon 2002).

Culture characteristics — Colonies growing very slowly on cultural media. On OA 14–16 mm diam after 14 d, flat with undulate edge, smoke grey to grey olivaceous, aerial mycelia sparse, white. Colonies on PDA 10–11 mm diam after 14 d, flat with undulate edge, aerial mycelia dense and white in the colony centre, but sparse in the edge, margin smoke grey to grey olivaceous. Colonies on MEA 10–14 mm diam after 14 d, flat with undulate edge, white or glaucous grey.

Additional material examined. Mexico, on *Musa* sp., 2008, *M. Yarez-Morales*, living culture CPC 16301.

Habitat — Mainly on *Musa* sp., occasionally on *Heliconia psittacorum*.

Geographic distribution — (EPPO 2014): Widely distributed in many countries of Africa, America, Asia (once reported from Guangdong (Mourichon & Fullerton 1990), Hainan (Stover & Simmonds 1987), and Yunnan (Jones & Mourichon 1993) in China), and Oceania.

NCBI Genome ID: GCA_000340215.1 (Ohm et al. 2012).

Notes — *Pseudocercospora fijiensis* (Verkley et al. 2004, Arzanlou et al. 2008, Crous et al. 2009) was listed in the Chinese quarantine pest directory as *Mycosphaerella fijiensis*. It causes black Sigatoka disease (or black leaf streak) on mainly cultivated banana and the wild banana species *Musa acuminata* (subsp. *banksia* and subsp. *zebrina*), which leads to a

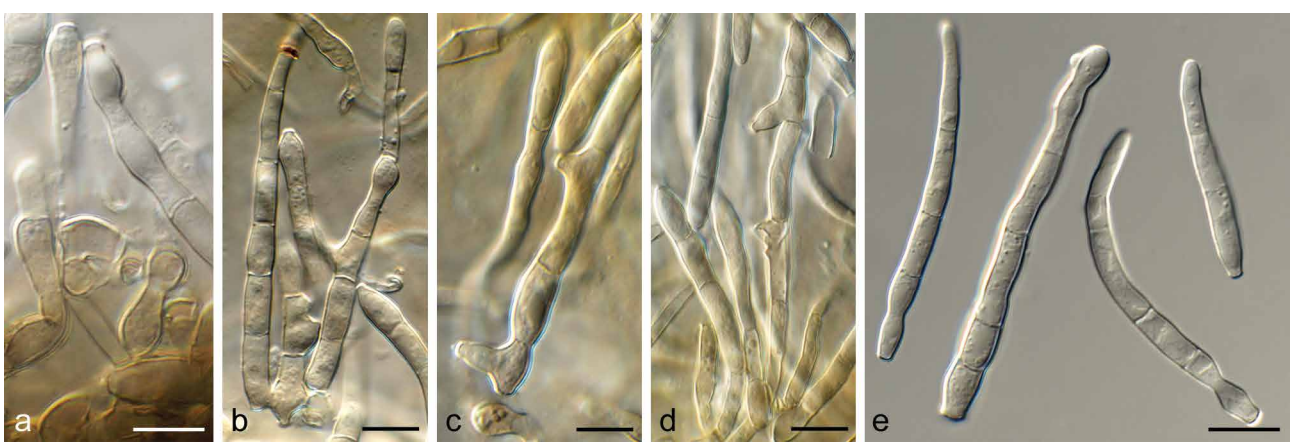

Fig. 37 *Pseudocercospora fijiensis* (CPC 16301). a–d. Conidiophores, conidiogenous cells and conidia; e. conidia. — Scale bar: a–e = 10 µm.

decrease in production by 22–69 % in various countries, e.g., Central America, Costa Rica, Panama (Woods 1980, Stover 1983, Romero 1986, Jaramillo 1987, Bureau 1990). Both fruits and leaves of banana should arouse high quarantine attention during transportation.

Presently, at least seven species of *Pseudocercospora* are correlated with foliar diseases of banana, i.e., *P. assamensis*, *P. eumusae*, *P. fijiensis*, *P. indonesiana*, *P. longispora*, *P. musae*, and *P. pseudomusae*, as well as some *Mycosphaerella*-related species (Arzanlou et al. 2008, Crous et al. 2021b). Although these species can be more or less distinguishable based on morphological and cultural characteristics, the species boundaries are rather ambiguous, making explicit identification possible only by the combination of morphology with DNA sequence data (Fig. 36).

Pseudocercospora musae (Zimm.) Deighton, Mycol. Pap. 140: 148. 1976 — Fig. 36, 38

Basionym. *Cercospora musae* Zimm., Centralbl. Bakteriol. Parasitenk. 8: 219. 1902.

Synonyms. *Cercospora musae* Massee, Bull. Misc. Inform. Kew 28: 159. 1914.

Mycosphaerella musicola R. Leach ex J.L. Mulder, Trans. Brit. Mycol. Soc. 67: 77. 1976.

Mycosphaerella musicola R. Leach, Trop. Agric. (Trinidad) 18: 92. 1941. (nom. nud.).

Typus. Cuba, on leaves of *Musa* sp., unknown collection date, *J. Carlier*, epitype CBS H-20038, culture ex-epitype IMI 123823 = CBS 116634. – Jamaica, on leaves of *Musa sapientum*, Jan. 1959, *R. Leach*, holotype IMI 75804a.

Symptoms — Initial symptoms caused by *P. musae* appear in the form of slight discolouration or narrow specks between the leaf's secondary veins. Over time, these specks develop into streaks running parallel to the leaf veins. The streaks elongate and expand laterally to become elliptical in shape and turn to brown or rusty red. The depressed grey centre is surrounded by a yellow halo. As the disease progresses, the lesions coalesce and kill a large area of the leaf. For symptom illustration see Gomes et al. (2013).

Ascomata perithecial dark brown or black, 47–72 µm diam. *Asci* oblong to clavate, 29–36 × 8–11 µm. *Ascospores* hyaline, ellipsoid, obtuse, 1-septate, slightly constricted at the septum, 14.5–18 × 3–4 µm (adapted from Mulder & Stover 1976). *Stroma* dark brown to black, 15–35 µm diam, erumpent. *Conidiophores* in dense fascicles, pale to very pale olivaceous brown, straight or slightly curved, rarely branched, 0–1-septate, tapered towards apex, mostly ampulliform, 5–25 × 2–6 µm. *Conidia* pale to olivaceous, cylindrical to obclavate-cylindrical, straight or curved, apex round or obtuse, basal hilum unthickened, 1–5 (or more)-septate, 10–50(–110) × 2–6 µm (adapted from Mulder & Holliday 1974).

Additional material examined. South Africa, on leaves of *Musa* sp., 24 Jan. 2000, *A. Viljoen*, living culture CMW 6365.

Habitat — *Musae* spp.

Geographic distribution — (EPPO 2019b): Africa: Angola, Cameroon, Cape Verde, Congo, Cote d'Ivoire, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Madagascar, Malawi, Mauritius, Mozambique, Nigeria, Sao Tome & Principe, Sierra Leone, Somalia, South Africa, Tanzania, Togo, Uganda, Zambia. – America: Antigua and Barbuda, Argentina, Bahamas, Barbados, Belize, Bolivia, Brazil, Cayman Islands, Colombia, Costa Rica, Cuba, Dominica, Dominican Republic, Ecuador, El Salvador, French Guiana, Grenada, Guadeloupe, Guatemala, Guyana, Haiti, Honduras, Jamaica, Martinique, Mexico, Montserrat, Nicaragua, Panama, Peru, Puerto Rico, Saint Lucia, St Kitts-Nevis, St Vincent and the Grenadines, Suriname, Trinidad and Tobago, USA, Venezuela. – Asia: Bhutan, Brunei Darussalam, Cambodia, China (once reported from Fujian, Guangdong, Guangxi, Yunnan (Zhou & Xie 1992), Hong Kong (IMI herbarium record)), India, Indonesia, Lao, Malaysia, Nepal, Philippines, Sri Lanka, Thailand, Vietnam, Yemen. – Oceania: American Samoa, Australia, Cook Islands, Fiji, French Polynesia, Guam, Kiribati, Micronesia, New Caledonia, Niue, Norfolk Island, Palau, Papua New Guinea, Samoa, Solomon Islands, Tonga, Tuvalu, Vanuatu, Wallis and Futuna Islands.

Genome GenBank ID: LFZO00000000.1 (culture CBS 116634).

Notes — *Pseudocercospora musae* was listed in the Chinese quarantine pest directory as *Mycosphaerella musicola*. This fungus causes yellow Sigatoka (Gomes et al. 2013), one of the two major leaf spot diseases on banana. The other important leaf spot disease is the black leaf streak, caused by *P. fijiensis*. Identification of the two phytopathogenic species is often difficult due to the limited and overlapping morphological characteristics, and thus phylogenetic analysis (Fig. 36) and real-time quantitative PCR (primers MMBF-CACACATCAAGAGCAGCACAG & MMBRtaq-TGGCACTTGGCGGAAGTTTG, probe FMEP-CACGTCTGATCTCCAGCTCGAGCGCATG) are more applicable to make explicit species delimitation (Arzanlou et al. 2007).

Pseudocercospora pini-densiflorae (Hori & Nambu) Deighton, Trans. Brit. Mycol. Soc. 88: 390. 1987 — Fig. 36

Basionym. *Cercospora pini-densiflorae* Hori & Nambu, J. Pl. Protect., Tokyo 4: 353. 1917.

Synonyms. *Cercoseptoria pini-densiflorae* (Hori & Nambu) Deighton, Mycol. Pap. 140: 167. 1976.

Mycosphaerella gibsonii H.C. Evans, Mycol. Pap. 153: 61. 1984.

Typus. Japan, Kagoshima, Magome, on needles of *Pinus densiflora*, 1 Oct. 1915, unknown *collector*, identified by *Hara*, neotype NIAES C-511.

Symptoms — Lesions are initially pale-green, then yellowish brown to grey, appearing towards the distal part of the needles, especially on seedlings 1–2-yr-old. The lesions coalesce with time, resulting in complete needle necrosis and subsequent needle cast. Numerous sporocarps appear as sooty spots on the lesions (EPPO 2019a).

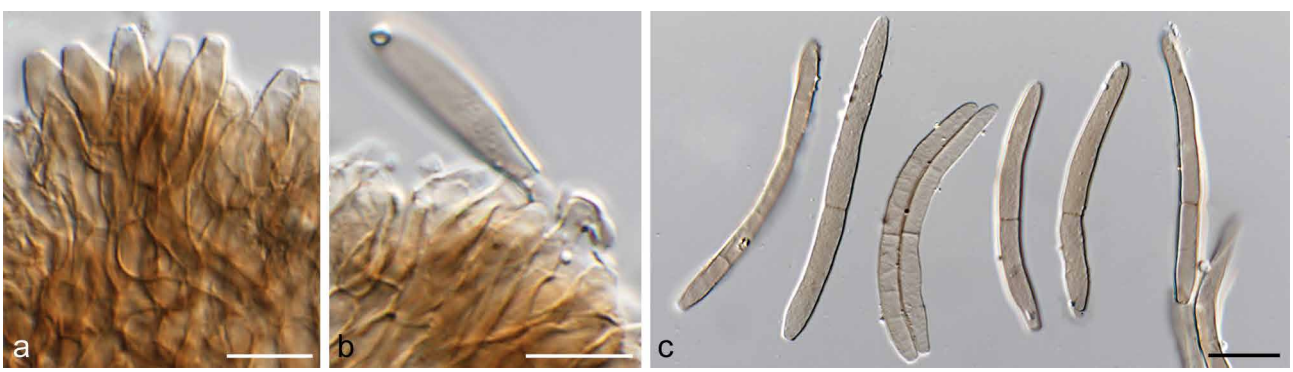

Fig. 38 *Pseudocercospora musae* (CMW 6365). a–b. Conidiophores and conidiogenous cells; c. conidia. — Scale bars: a–c = 10 µm.

Ascostromata variable, dark brown to black, discrete, subepidermal, unilocular, globose, 50–120 µm diam, or multiloculate, 150–800(–1400) µm long, 70–125(–160) µm wide and 90–150 µm deep, occasionally laterally united in bands. *Stromata* pseudoparenchymatous, cells 3–8(–12) µm diam, thickened-walled. *Locules* globose to flask-shaped, (45–)50–75(–95) × 55–75 µm, ostiolate, periphysate, often with an apical stromatic shield, 70–90 µm diam, in longitudinal series. *Asci* bitunicate, clavate to cylindrical, 8-spored, 33–38 × 5.5–7 µm, with a thickened bluntly rounded apex, rarely saccate, 32–36 × 6–8 µm. *Ascospores* hyaline, ellipsoid to cuneate, guttulate, 1-septate, 7.5–12.5 × 1.5–3 µm (adapted from Evans 1984). *Stromata* substomatal, subglobose, 20–150 µm diam, brown to dark brown, composed of thick-walled, swollen hyphal cells, 2–6 µm diam. *Conidiophores* abundant, in fascicles, straight, subcylindrical or narrowed towards the tip to geniculate-sinuous, unbranched, subhyaline to uniformly olivaceous or olivaceous-brown, 0–3-septate, thin-walled, smooth, 5–50 × 2.5–4 µm. *Conidiogenous cells* terminal, with fine, not very conspicuous annellations, 5–25 µm long. *Conidia* solitary, obclavate or obclavate-cylindrical, straight to somewhat curved, subhyaline to pale olivaceous, thin-walled, smooth, 1–10-septate, 10–80 × 2–5 µm, apex obtuse to subacute, base obconically truncate, 1.5–2.5 µm wide, hila unthickened, not darkened (adapted from Braun et al. 2013).
For illustrations see Braun et al. (2013).

Culture characteristics — Colonies growing very slowly on cultural media. On OA 23–25 mm diam after 14 d, flat with entire edge, white to pale grey, smoke grey in the edge. Colonies on PDA 22–25 mm diam after 14 d, flat with entire edge, white to creamy. Colonies on MEA 18–19 mm diam after 14 d, flat with undulate edge, white.

Additional materials examined. Japan, Kumamoto, on *P. thunbergii*, 24 Apr. 1964, *Y. Tokushige*, living culture MUCC 534; Shimane, on *P. thunbergii*, unknown collection date, unknown *collector*, deposited by *S. Sung-Oui*, representative living culture CBS 125139 = ATCC 24602.

Habitat — *Pinus* spp.

Geographic distribution — (EPPO 2019b): Africa: Kenya, Madagascar, Malawi, South Africa, Swaziland, Tanzania, Zambia, Zimbabwe. – America: Brazil, Chile, Costa Rica, Honduras, Jamaica, Netherlands Antilles, Nicaragua. – Asia: Bangladesh, China (Anhui, Fujian, Guangdong, Guangxi, Hunan, Jiangsu, Jiangxi, Hong Kong, Taiwan), India, Japan, Korea, Peninsular Malaysia, Nepal, Philippines, Sri Lanka, Thailand, Vietnam. – Oceania: Papua New Guinea.

Genome GenBank ID: AWYD00000000.2 (culture CBS 125139).

Notes — *Pseudocercospora pini-densiflorae* (Quaedvlieg et al. 2012) was listed in the Chinese quarantine pest directory as *Mycosphaerella gibsoni*. It causes brown needle blight of pine, which gives rise to slow growth of seedlings and in some cases causes mortality of up to 85 % (Ivory 1987). Pine needle blight is a major obstacle in the production of pine seedlings (especially *Pinus pinaster*, *Pi. thunbergii*, and *Pi. densiflora*) in Japan.

A specimen of *P. pini-densiflorae* was recently designated as neotype (Braun et al. 2013), but not yet sequenced. In this study, we provided the nucleotide sequences of representative strains (CBS 125139 and MUCC 534) to facilitate the identification of *P. pini-densiflorae* (Fig. 36).

Pseudocercospora ulei (Henn.) B.T. Hora & Mizubuti, PLoS One 9: 6. 2014 — Fig. 36

Basionym. *Aposphaeria ulei* Henn., Notizbl. Königl. Bot. Gart. Berlin 4: 135. 1904.

Synonyms. *Microcyclus ulei* (Henn.) Arx, Beitr. Kryptogamenfl. Schweiz 11(2): 323. 1962.

Melanopsammopsis ulei (Henn.) Stahel, Bull. Dep. Landb. Suriname 34: 1–111. 1917.

Dothidella ulei Henn., Hedwigia 43: 254. 1904.

Fusicladium macrosporum Kuyper, Recueil Trav. Bot. Néerl. 8: 374. 1911.

Fusicladium heveae K. Schub. & U. Braun, CBS Diversity Ser. 1: 481. 2003.

Typus. Brazil, Amazonas, Juruá, on *Heveae* sp., 1900, *E. Ule*, syntype of *Dothidella ulei* F57179; Rio Juruá, on *H. brasiliensis*, Aug. 1900, *E. Ule*, syntype of *Dothidella ulei* F57180. – Peru, Cerro de Escaler, on *Hevea* sp., Nov. 1902, *E. Ule*, syntype of *Aposphaeria ulei* BPI 360549; Rio Huallaga, Cerro de Cumbasso, on *H.* sp., Nov. 1902, *E. Ule*, isotype of *Aposphaeria ulei* F22176; Rio Amazonas, on *H. brasiliensis*, July 1902, *E. Ule*, syntype of *Dothidella ulei* F57178.

Symptoms — *Pseudocercospora ulei* causes lesions on stems, petioles, inflorescences, fruits and leaves of *Hevea* spp. Sexual morph lesions initially punctiform, becoming circular to subcircular, necrotic, pale brown centrally, surrounded with a ring of prominent black stromata, growing with age and leading to loss of subcircular fragments (shot-holes) and foliage distortions or even leaf drop. As for asexual morph lesions, leaf spots are variable in shape, subcircular to elongated along leaf veins to angular or irregular, 1–7 × 1–2.5 mm, greyish brown to black, scattered, sometimes somewhat raised, coalescing with age and leading to premature leaf drop (Da Hora Júnior et al. 2014).

Ascomata pseudothecial, epiphyllous, spherical, 128–165 × 90–192 µm, walls *textura angularis*, brown, smooth, 42–57.5 µm thick. *Dehiscence* ostiolate, 2–10 µm diam. *Asci* bitunicate, clavate, 8-spored, 66.5–90 × 13–16.5 µm. *Ascospores* ellipsoidal, hyaline, smooth, 1-septate, constricted at septum, 15–20 × 4–5 µm. *Conidiophores* amphigenous, usually reduced to conidiogenous cells, sparse or subfasciculate, cylindrical, straight or slightly flexuous to geniculate towards apices, unbranched, 0–1-septate, pale brown, smooth, 31–56 × 4–6 µm. *Conidiogenous cells* integrated, cylindrical to subcylindrical, proliferating sympodially with 1–3 loci, 2 µm diam. *Conidia* solitary, obclavate, straight, curved or sigmoid, 0–1-septate, slightly constricted at the septum, subhyaline to pale brown, smooth to somewhat roughened, 27–62 × 6–11 µm, apex rounded, base attenuated to a truncate hilum, hilum 2 µm wide. *Spermogonia* globose, 112–138 × 87–150 µm, walls *textura angularis*, 4–8-layer, pale to dark brown, 37.5–92.5 µm. *Spermatiophores* phialidic, lageniform, integrated, 10–16 × 1–2 µm, hyaline, smooth. *Spermatia* dumb-bell-shaped, 7–4 × 1 µm, aseptate, hyaline, smooth (adapted from Da Hora Júnior et al. 2014).
For illustrations see Da Hora Júnior et al. (2014).

Habitat — Restricted to *Hevea* spp.

Geographical distribution — (Da Hora Júnior et al. 2014, EPPO 2019b, Farr & Rossman 2021): Africa: Cameroon, Gabon, Nigeria, West Africa. – America: Belize, Bolivia, Brazil, Colombia, Costa Rica, Ecuador, El Salvador, French Guiana, Guatemala, Guyana, Haiti, Honduras, Mexico, Nicaragua, Panama, Peru, Suriname, Trinidad & Tobago, Venezuela.

Notes — *Pseudocercospora ulei* (Da Hora Júnior et al. 2014) was listed in the Chinese quarantine pest directory as *Microcyclus ulei*. South American leaf blight (SALB) of rubber trees caused by *P. ulei* is recognised as the most serious threat to the natural rubber industry worldwide (Holliday 1970, Lieberei 2007, Van Beilen & Poirier 2007). Because of the potential serious economic consequences, strict quarantine measures have been made to prevent SALB from establishing in the rubber tree production areas in West Africa and Southeast Asia

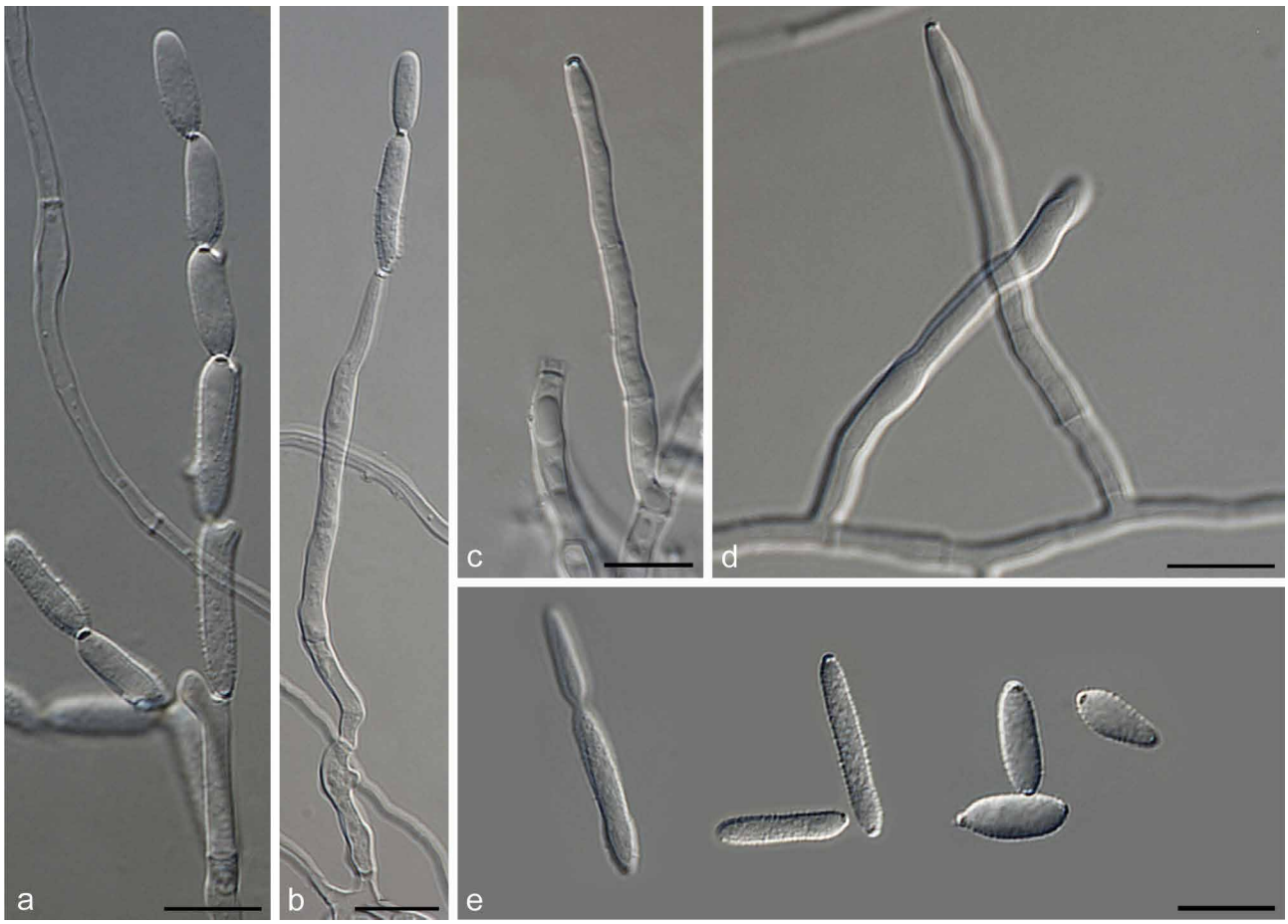

Fig. 39 *Ramularia beticola* (ex-epitype CBS 141109). a–d. Conidiophores and conidia; e. conidia (from Videira et al. (2016) with permission). — Scale bars: a–e = 10 µm.

(Gasparotto et al. 1997, Lieberei 2007). Four representative strains of *P. ulei* formed a distinct clade at basal (*act*, ITS, *tef 1-α*) in the phylogenetic tree (Fig. 36).

Ramularia beticola Fautrey & Lambotte, Revue Mycol. (Toulouse) 19: 54. 1897 — Fig. 39, 40

Synonym. *Ramularia betae* Rostr., Bot. Tidsskr. 22: 272. 1899.

Typus. France, Dumont, on *Beta vulgaris*, 1896, *Fautrey* (Roum., Fungi Sel. Exs. 7261; lectotype, designated in Braun (1998), PC); Fresney-l'Évêque, on leaf spot of *Beta vulgaris*, 2011, *A. Champeil*, epitype CBS H-22519, ex-epitype culture CBS 141109 = CPC 30066.

Symptoms — *Ramularia beticola* causes pale brown leaf spots on beet, which are amphigenous, circular, elliptical to somewhat angular-irregular, 1–10 mm diam; affected leaves turn yellow, become necrotic and die (Videira et al. 2016).

Conidiophores hyaline, thin-walled, smooth, erect, straight or flexuous, unbranched, 1–4-septate, 19.5–83 × 2–3 µm, sometimes reduced to conidiogenous cells. *Conidiogenous cells* forming on mycelium or terminal on conidiophores, cylindrical, tapering toward the apex, 7–30 × 2–3 µm, with 1–4 apical conidiogenous loci, thickened and refractive. *Conidia* hyaline, thin-walled, smooth to slightly verruculose, catenate, with thickened and refractive hila. *Ramoconidia* subcylindrical to clavate, 8–22 × 3–4 µm, 0–1-septate. *Intercalary conidia* cylindrical to subcylindrical, straight, rarely slightly curved, 0–1-septate, 8.5–20 × 2.5–4 µm. *Terminal conidia* subcylindrical to obovoid, aseptate, 3.5–11 × 2–5 µm (adapted from Videira et al. 2016).

Habitat — *Beta trigyna*, *B. vulgaris*.

Geographic distribution — America: Brazil (Mendes et al. 1998), Canada (Ginns 1986, Braun 1998), USA (Braun 1998). – Asia: China (only reported in Yunnan, Shaanxi and Taiwan (Braun 1998, Gui et al. 2003)), Kazakhstan (Braun 1998), Russia (Braun 1998). – Europe (Braun 1998, Harveson et al. 2009): Austria, Belgium, Bulgaria, Caucasus, Czech Republic, Denmark, France, Germany, Hungary, Ireland, Latvia, Lithuania, Poland, Portugal, Romania, Sweden, UK, Ukraine. – Oceania: Australia.

Notes — Based on current knowledge, *R. beticola* is host-specific on beet, and phylogenetically clearly distinct from other species of *Ramularia* (Fig. 40). It was reported from *Beta vulgaris* var. *cicla* in Yunnan and Shaanxi in China, but without morphological description and molecular data, and the cited specimens (HFNWAU 8212, 0281, and 0366) listed in Gui et al. (2003) were unavailable for study. Further research is therefore needed to confirm the presence of *R. beticola* in China.

Septoria linicola (Speg.) Garass., Revista Fac. Agron. Univ. Nac. La Plata ser. 2, 22: 104. 1938 — Fig. 41

Basionym. *Phlyctema linicola* Speg., Anales Mus. Nac. Hist. Nat. Buenos Aires, Ser. 3 13: 389. 1911.

Synonyms. *Mycosphaerella linicola* Naumov, Mater. Mikol. Fitopatol. Rossii 5: 2. 1926.

Sphaerella linicola (Naumov) Wollenw., Rev. Bot. Inst. Miguel Lillo 2: 483. 1938.

Typus. Russia, Leningrad Province, Djetskoje District, Sjelo, on *Linum usitatissimum*, Sept. 1925, *Naoumov*, isotype BPI 608709.

Symptoms — *Septoria linicola* causes pasmo disease of flax. The lesions on stems first develop as small elongated spots which then enlarge and coalesce, extending around the stem as well as longitudinally. A striking

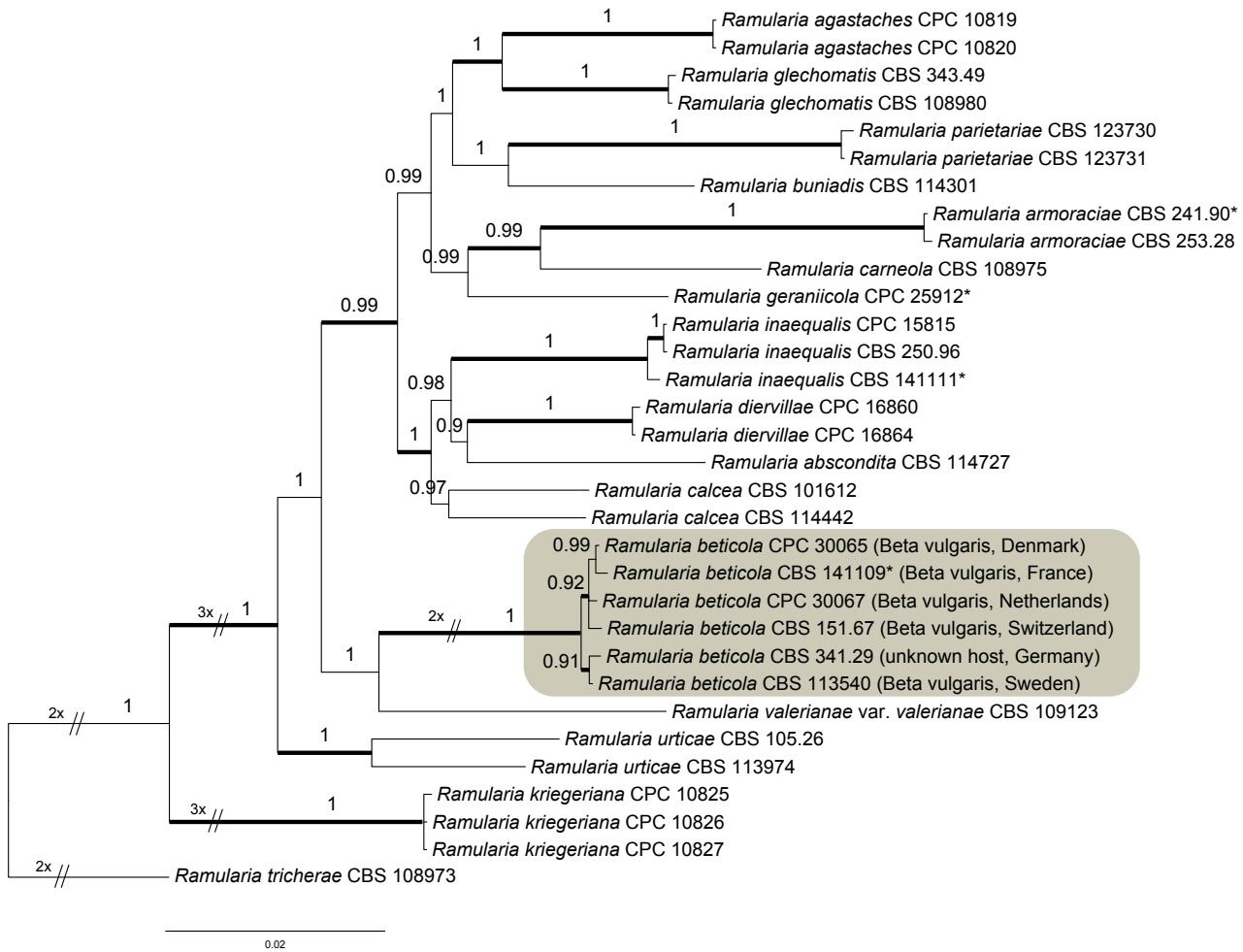

Fig. 40 Phylogenetic tree of *Ramularia beticola* and its closely relatives calculated with Bayesian analysis on *act*, *gapdh*, ITS, *rpb2*, and *tef 1-α* sequences. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Fig. 41 *Septoria linicola* (CBS 316.37). a–c. Colonies in two wk (20 °C, a. on PDA; b. on OA; c. on MEA); d. pycnidium; e–g. conidiophores and conidia; h. conidia. — Scale bars: e–h = 10 µm.

characteristic of the disease is the alternate brown and green banding of the stem which occurs until infection becomes severe and the lesions coalesce. In areas where the disease is severe, the stems turn brown as the plants become defoliated. It also infects the pedicels to cause serious yield loss (De Tempe 1963, Bedlan 1984).

Ascomata pseudothecial, immersed, scattered, globose to subglobose, 75–120 µm wide, ostiolate, wall composed of 3–5 layers, up to 13 µm thick, outer cells thick-walled and dark brown, inner cells hyaline and thin-walled. *Asci* fasciculate, bitunicate, thick-walled, 8-spored, 30–50 × 8–9 µm. *Ascospores* hyaline, 1-septate, constricted at the septum, 13–17 × 2.5–4 µm (adapted from Sivanesan & Holliday 1981). *Conidiomata* pycnidial, immersed, up to 120 µm broad, ostiolate, globose to subglobose, thin-walled, exuding hyaline conidial masses. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, subcylindrical to obpyriform, or inconspicuously protruding from the pycnidial wall cell. *Conidia* hyaline, smooth, thin-walled, subcylindrical to cylindrical, straight or irregularly curved, slightly tapering towards the apex, base long obconically truncate, 0–3-septate, (12–)20.5–34.5(–43.5) × 2–3.5 µm (av. ± S.D. = 26.3 ± 3.9 × 2.6 ± 0.3).

Culture characteristics — Colony on PDA flat with entire edge, glaucous grey to smoke grey from centre to edge, 41–43 mm diam, aerial mycelia floccose, white to pale grey. Colony on OA flat with entire edge, greenish olivaceous to olivaceous, 38–40 mm diam, aerial mycelia sparse. Colony on MEA generally flat

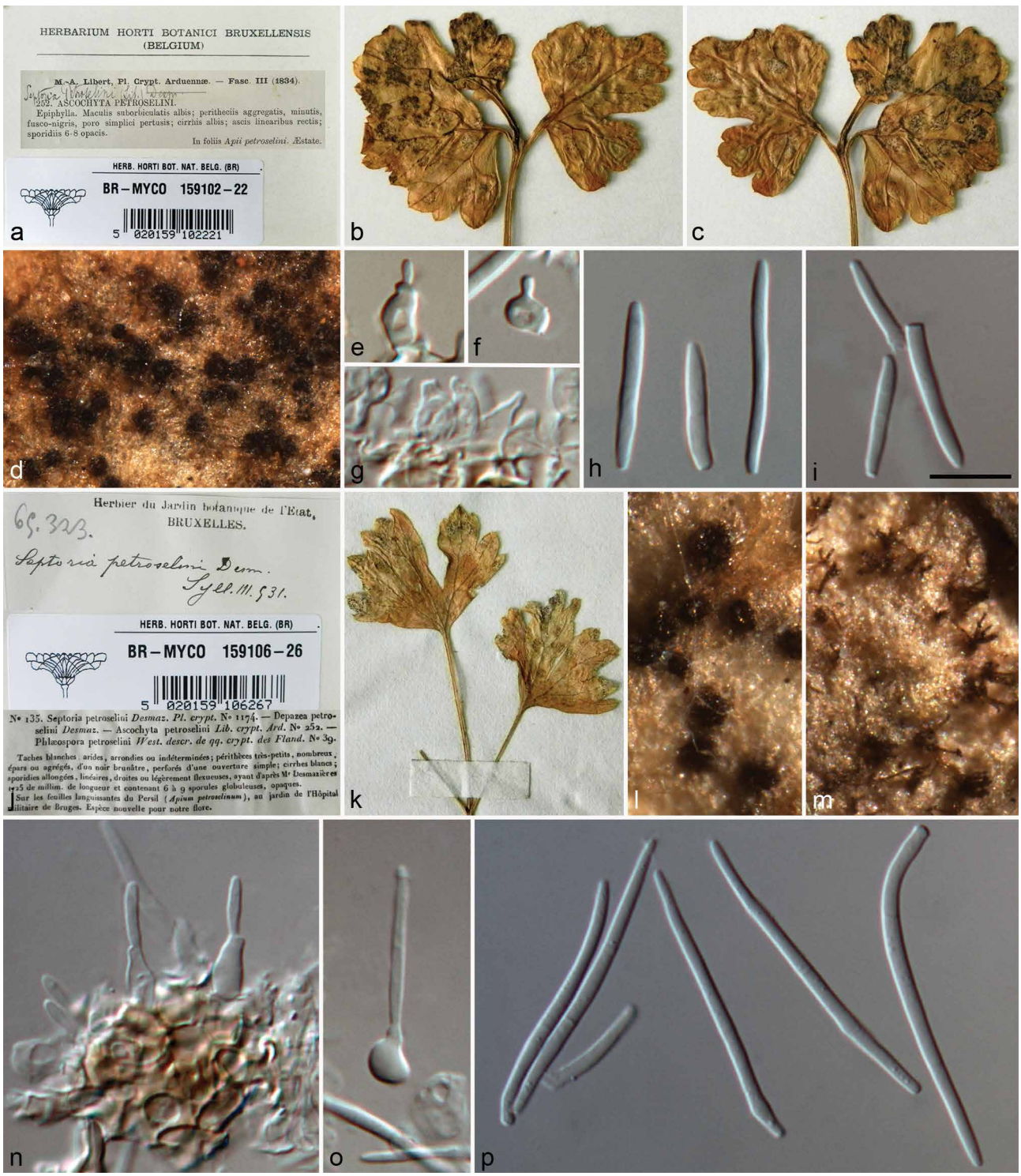

Fig. 42 *Septoria petroselini* (a–i. lectotype of *Ascochyta petroselini*, BR5020159102221, j–p. BR5020159106267). a, j. Collection packets; b–c, k. symptoms on hosts; d, l–m. pycnidia on the leave surface; e–g, n–o. conidiogenous cells and conidia; h–i, p. conidia. — Scale bar: i = 10 µm, applies to e–i, n–p.

with undulate edge, rugged near the centre, with radiating lines, white to olivaceous buff from centre to the edge, 33–37 mm diam, aerial mycelia sparse.

Additional material examined. Argentina, on *L. usitatissimum*, July 1937, deposited by *H.W. Wollenweber*, representative strain CBS 316.37.

Habitat — *Linum austriacum*, *L. bienne*, *L. catharticum*, *L. marginale*, *L. monogynum*, *L. perenne*, *L. usitatissimum*, and other *Linum* spp.

Geographic distribution — (EPPO 2019b, Farr & Rossman 2021): Africa: Ethiopia, Kenya, Tanzania, Tunisia. – America: Argentina, Brazil, Canada, Mexico, Peru, Uruguay, USA. – Asia: Kazakhstan. – Europe: Belarus, Belgium, Bulgaria, Croatia, France, Greece, Hungary, Italy, Lithuania, Netherlands, Poland, Romania, Russia, Serbia, Slovenia, Sweden, Turkey, Ukraine, UK. – Oceania: Australia, New Zealand.

Notes — *Septoria linicola* (Verkley et al. 2013) was listed in the Chinese quarantine pest directory as *Mycosphaerella linicola*. It is the causal agent of pasmo disease on *L. usitatissimum* and other *Linum* spp., which can reduce oil content by 9 % and total seed and fibre yield by 40–70 % (Plonka & Anselme 1956, Frederiksen & Culbertson 1962) and diminish the quality of both oil and fibre. The ex-type strain of *S. linicola* was not designated in the original publication and unfortunately, no suitable strain from the original reported location in Russia was found for epitypification in this study.

Septoria petroselini (Lib.) Desm., Mem. Soc. Roy. Sci. Lille 1843: 97. 1843 — Fig. 42, 43, 44

Basionym. *Ascochyta petroselini* Lib., Pl. Crypt. Arduenna 3: 252. 1834.
Synonym. *Phloeospora petroselini* (Lib.) Westend., Bull. Acad. Roy. Sci. Bruxelles 12: 252. 1845.

Typus. Belgium, on leaves of *Petroselinum crispum* (syn. *P. sativum*, *Apium Petroselinum*), prior to 1834, *M.A. Libert* (lectotype of *Ascochyta petroselini* designated here BR5020159102221, MBT 10001725). – Netherlands, Laren, on living leaves of *P. crispum*, June 1944, *S.D. de Wit*, epitype designated here CBS H-18128, MBT 10001726, culture ex-epitype CBS 182.44 = IMI 100279.

Symptoms — Leaf spots indefinite, without a distinct border, pale brown, visible on both sides in green parts of leaves or barely discoloured petioles (Verkley et al. 2013).

In vivo — *Conidiomata* pycnidial, numerous, epiphyllous, semi-immersed, dark brown to black, 70–200 µm diam, ostiolate, wall composed of 1–4 layers, pale brown to brown, angular or circular. *Conidiogenous cells* hyaline, discrete, holoblastic, ampulliform, 6–10 × 3–6 µm. *Conidia* hyaline, filiform, straight or flexuous, tapering towards to the obtuse apex, relatively truncate at the base, 0–7-septate, 17.5–42 × 1–2.5 µm.

In vitro — *Conidiomata* pycnidial, numerous, semi-immersed or immersed, fuscous black to black, mostly 80–200 mm diam, extruding vinaceous buff or isabelline conidial masses. *Conidiomatal wall* composed of 1–2 layers of brown-walled and angular cells, lined by a layer of hyaline cells. *Conidiogenous cells* hyaline, discrete, holoblastic, ampulliform, 6–10 × 3–6 mm. *Conidia* hyaline, filiform, straight or flexuous, attenuated gradually to the rounded apex and to the truncate base,

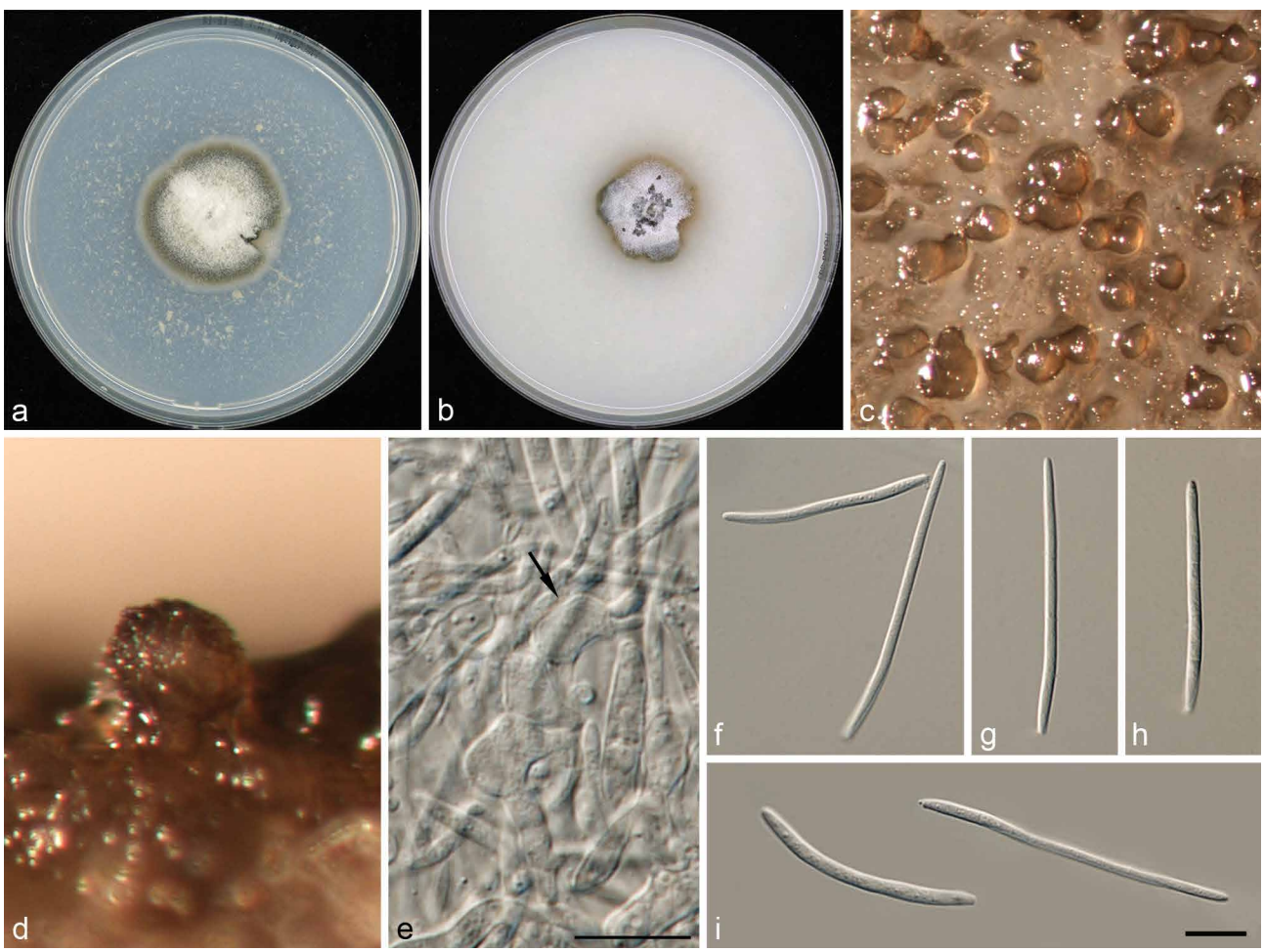

Fig. 43 *Septoria petroselini* (a–d, f–i. ex-epitype CBS 182.44, e. CBS H-21166). a–b. Colonies in two wk (20 °C, a. on PDA; b. on OA); c–d. pycnidia; e. conidiogenous cells; f–i. conidia. — Scale bars: e, i = 10 µm, i applies to f–i.

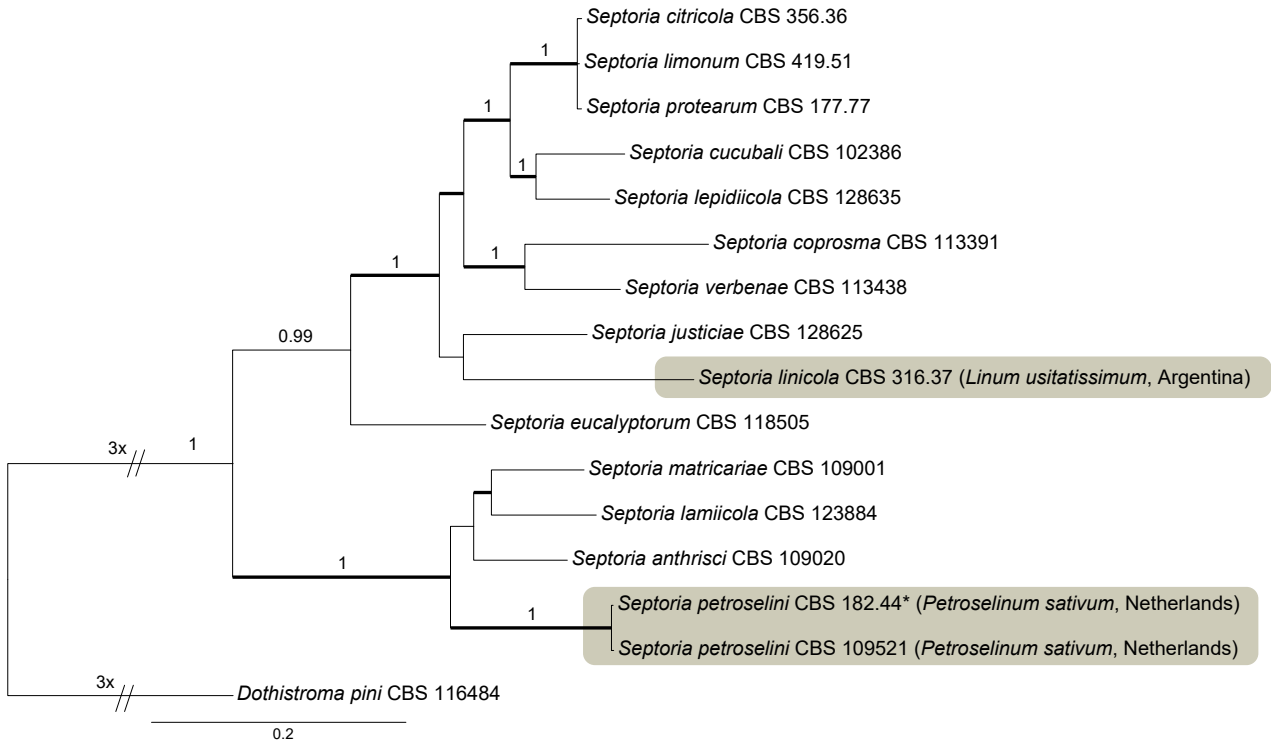

Fig. 44 Phylogenetic tree of *Septoria linicola*, *S. petroselini* and their most closely relatives calculated with Bayesian analysis on ITS, *rpb2*, *tef 1-α*, and *tub2* sequences. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

0–7-septate, 29–54(–67) × (0.5–)1–2.5 µm (av. ± mean = 41.3 ± 5.5 × 1.6 ± 0.4).

Culture characteristics — *Colonies* on PDA 35 mm diam in 14 d, flat with entire edge, pale mouse grey covered by white aerial mycelia in the centre, with white margin, reverse mouse grey. *Colonies* on OA 25 mm in 14 d, flat with undulate edge, smoke grey or grey olivaceous covered by white aerial mycelia, reverse mouse grey.

Additional materials examined. Belgium, unknown substrate, unknown collection date, *G.D. Westendorp*, BR5020159105253; Brugge, Au jardin de l'Höpital militaire, on leaves of *P. crispum*, 1829, *G.D. Westendorp* & *A.C.F. Wallays*, BR5020159106267. – Netherlands, Utrecht, Baarn, garden Eemnesserweg 90, on living leaves of *P. crispum*, 29 Mar. 2001, *H.A. van der Aa*, CBS H-21166, living culture CBS 109521.

Habitat — *Anethum graveolens*, *Apium graveolens*, *Carum carvi*, *C. petroselinum*, *Conioselinum scopulorum*, *Coriandrum sativum*, *Petroselinum crispum*, *P. hortense*, *P. sativum*, and other *Petroselinum* spp.

Geographic distribution — (Farr & Rossman 2021): Africa: Kenya, Libya, Mauritius, South Africa, Tanzania, Zimbabwe. – America: Brazil, Bolivia, Canada, Chile, Dominican Republic, USA, Venezuela. – Asia: India, Korea, Malaysia. – Europe: Belgium, Bulgaria, Canary Islands, Denmark, Finland, France, Germany, Greece, Italy, Netherlands, Poland, Romania, Scotland, Spain, Turkey, UK, Ukraine. – Oceania: Australia, New Caledonia, New Zealand.

NCBI Genome ID: JAFJTQ000000000 (CBS 182.44, this study).

Notes — *Septoria petroselini* was originally reported from Gallia (the region of Western Europe occupied by present-day France, Belgium, Germany and other neighbouring countries), America and Australia on *Petroselinum crispum* (syn. *P. sativum*) according to Saccardo (1884). However, a search for the type specimen in the fungaria of CBS, HBG, HUH, K, NYBG, PC, and RM of these countries proved unsuccessful. Three specimens of *S. petroselini* from BR (BR5020159102221, BR5020159105253, BR5020159106267), collected by M.A. Libert (authority of the basionym name *Ascochyta petroselini*) and G.-D. Westendorp (authority of the synonym *Phleospora petroselini*) from Belgium, were examined in this study. The conidial size of these specimens (17.5–42 × 1–2.5 µm) agreed with those given for *S. petroselini* by most authors (26–45(–52) × (1–)1.5–2 µm cf. Priest 2006; 16–46 × 1–2 mm cf. Jørstad 1965; 29–80 × 1.9–2.5 µm cf. Verkley et al. 2013). One of the specimens collected by M.A. Libert (BR5020159102221) was designated as lectotype, and one specimen collected in the Netherlands was designated as epitype. Phylogenetically, *S. petroselini* is close to *S. anthrisci* (Fig. 44), from which it can be distinguished by *act*, *tef 1-α*, and *rpb2* sequences.

Setophoma terrestris (H.N. Hansen) Gruyter et al., Mycologia 102: 1077. 2010 — Fig. 45

Basionym. *Phoma terrestris* H.N. Hansen, Phytopathology 19: 699. 1929.
Synonym. *Pyrenochaeta terrestris* (H.N. Hansen) Gorenz et al., Phytopathology 38: 838. 1948.

Typus. North America, on root of *Allium sativum*, Dec. 1929, *H.N. Hansen*, lectotype CBS H-20311, culture ex-lectotype CBS 335.29.

Symptoms — *Setophoma terrestris* causes pink rot of onion. Infected roots first turn light pink, then darken to red and purple, shrivel, turn black, and die. The pinkish red discolouration may extend up into the scales of the bulb, and the plants become stunted if infection continues. The infection is usually confined to roots and outer scales of the bulb, and seldom results in plant death.

Conidiomata pycnidial, solitary or gregarious, immersed, globose, brown to black, up to 400 µm diam, ostiolate, sometimes slightly beaked, setae 60–180 µm long, septate, walls composed of several layers, lining the entire pycnidial cavity, outer cells pigmented and thick-walled, inner cells thin-walled and pseudoparenchymatic. *Conidiogenous cells* phialidic, hyaline, simple, obpyriform. *Conidia* hyaline, aseptate, ovoid to allantoid, biguttulate, rounded in the ends, 4–7 × 1.5–2 µm (adapted from Punithalingam & Holliday 1973).
For illustrations see Punithalingam & Holliday (1973).

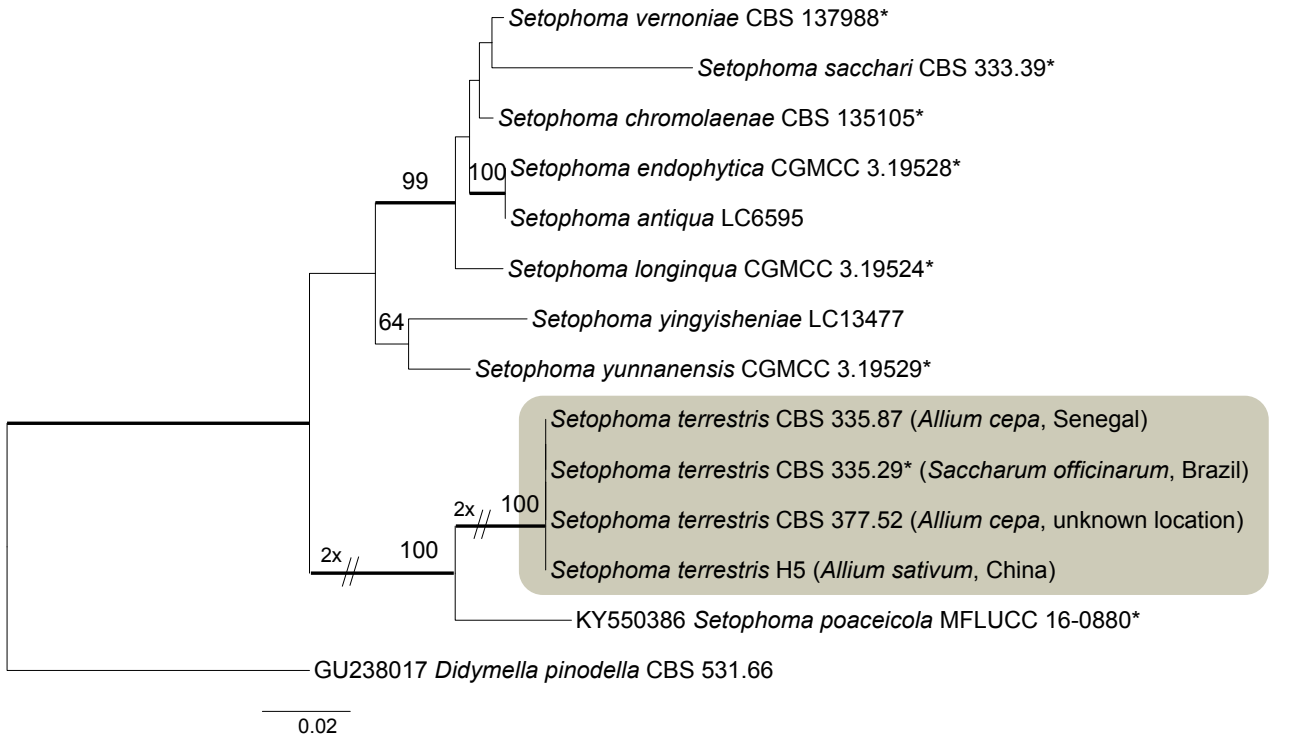

Fig. 45 Phylogenetic tree of *Setophoma terrestris* and its closely relatives calculated with RAxML on LSU and ITS sequences. Thickened branches indicate branches present posterior probabilities (> 0.90) in the Bayesian tree. The bootstrap support values > 50% are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

Habitat — *Allium cepa*, *A. chinense*, *A. sativum*, *A. porrum*, *Allium* spp., *Avena sativa*, *Brassica* sp., *Calathea crocata*, *Cucurbita maxima*, *C. moschata*, *Medicago sativa*, *Oryza sativa*, *Phaseolus limensis*, *P. lunatus*, *Pisum sativum*, *Saccharum officinarum*, *Solanum carolinense*, *S. lycopersicum*, *Triticum aestivum*, *Vigna sinensis*, *Zea mays.*

Geographic distribution — Africa: Senegal (De Gruyter et al. 2010), Venezuela (Boerema et al. 2004). – America: Brazil (Boerema et al. 2004), Canada (Yang et al. 2017), USA (De Gruyter et al. 2010, Rivedal et al. 2018). – Asia: China (confined to Jinxiang, Shandong Province and Feng County, Jiangsu Province; Zhang et al. 2019), Japan (Ikeda et al. 2012), Vietnam (Luong et al. 2008). – Europe: Netherlands (De Gruyter et al. 2002). – Oceania: Australia (Boerema et al. 2004).

Notes — *Setophoma terrestris* (De Gruyter et al. 2010) was listed in the Chinese quarantine pest directory as *Pyrenochaeta terrestris*. This fungus was recently reported for one case on *Allium sativum* in Shandong and Jiangsu Province in China based on morphology and LSU sequence analysis (Zhang et al. 2019), and this identification is supported in this study (Fig. 45). For more information about the genus *Setophoma* see Liu et al. (2019) and Marin-Felix et al. (2019a).

Stagonospora sacchari T.T. Lo & L. Ling, J. Sugarcane Res. Taiwan 4: 333. 1950

Symptoms — Leaf spots initially small (0.5–3 × 0.3–1 mm), red or brown, with a chlorotic halo. They elongate along the vascular bundles, forming spindle-shaped streaks which coalesce to form large spots (5–17 × 0.3–1 cm), with straw-coloured centres and reddish margins. On older leaves the spots do not usually elongate into streaks (Sivanesan 1983, Plant Knowledge Bank http://www.plantwise.org/knowledgebank/datasheet.aspx?dsid=51372).

Conidiomata pycnidial, immersed, scattered, globose to subglobose, dark brown, 150–250 µm diam, ostiolate, pseudoparenchymatous wall up to 17 µm thick. *Conidiogenous cells* discrete, hyaline, doliiform or ampulliform, formed from the inner cells of the pycnidial wall, 2–3.5 × 3 µm, sometimes annellidic with one percurrent proliferation. *Conidia* hyaline, fusoid to ellipsoidal, tapering toward the apex and rounded to truncate at the base, straight to slightly curved, 3–(4–5)-septate, constricted at the septum, 36–51.5 × 8–10.5 µm (adapted from Sivanesan 1983). For illustrations see Sivanesan (1983).

Habitat — *Saccharum officinarum*, *S. spontaneum*, *Miscanthus japonicus* and *M. sinensis*. Inoculations proved successful on *S. barberi* and *S. sinense*.

Geographic distribution — (EPPO 2019b): Africa: South Africa. – America: Argentina, Panama. – Asia: China (Taiwan), India, Japan, Philippines, Thailand, Vietnam.

Notes — This fungus is listed in the Chinese quarantine pest directory as *Stagonospora sacchari*. However, according to the morphological structures shown in Sivanesan (1983), it appears to be incorrectly identified and should be transferred to *Parastagonospora* or a related genus. Since the type specimen was not found in various fungaria including NMNH, TAI, TAIF, and TNS, fresh collections from the original location, Taiwan, are needed to resolve the taxonomic uncertainty of this fungus.

Stagonosporopsis chrysanthemi (F. Stevens) Crous et al., Australas. Pl. Pathol. 41: 681. 2012 — Fig. 46, 47

Basionym. *Ascochyta chrysanthemi* F. Stevens, Bot. Gaz. 44: 246. 1907.
Synonyms. *Mycosphaerella ligulicola* K.F. Baker et al., Phytopathology 39: 799. 1949.
Didymella ligulicola (K.F. Baker et al.) Arx, Beitr. Kryptogamenfl. Schweiz 11: 364. 1962.
Didymella ligulicola (K.F. Baker et al.) Arx var. *ligulicola*, Stud. Mycol. 32: 9. 1990.
Stagonosporopsis ligulicola (K.F. Baker et al.) Aveskamp et al. var. *ligulicola*, Stud. Mycol. 65: 46. 2010.
Phoma ligulicola Boerema var. *ligulicola*, Stud. Mycol. 32: 9. 1990.

Typus. USA, North Carolina, West Raleigh, on *Chrysanthemum indicum*, Dec. 1906, *F.L. Stevens*, syntypes of *Ascochyta chrysanthemi* BPI 371303 and BPI 371302, lectotype of *A. chrysanthemi* C0004169F; on *Chrysanthemum* × *morifolium*, June 1948, deposited by *L.H. Davis*, epitype of

A. chrysanthemi ATCC 10748 (preserved in a metabolically inactive state); North Carolina, Pittsboro, on *Chrysanthemum* × *morifolium*, 8 June 1948, *K.F. Baker*, lectotype of *Mycosphaerella ligulicola* designed here, BPI 608685, MBT 10001727.

Symptoms — *Stagonosporopsis chrysanthemi* causes irregular blotches on plant leaves, 2–3 cm diam, brown to black, which rapidly coalesce under favourable conditions. When affecting flowers, spots initially develop on one side of the blossom, appearing reddish on light-coloured cultivars and brownish on darker ones. Infection subsequently spreads rapidly and complete rotting of the flower head may occur, which eventually droops and wilts. The lesions are also found girdling the stem and often localised at the base or nodes of adult plants. Stem lesions are always associated with abnormal appearance in the corresponding shoots (EPPO 2014).

Ascomata perithecial, erumpent, globose or subglobose, ostiolate, 96–224 µm diam, with a black membranous wall. *Asci* fasciculate, cylindrical, tapering gradually near apex, short stipitate, 8-spored, uniseriate or irregularly biseriate, 45–90 × 7–12 µm. *Ascospores* hyaline, ellipsoid to fusoid, 1-septate, constricted at the septum, guttulate, the upper cell abruptly swollen just above the septum, the lower cell narrower and acute, 12–16 × 4–7 µm (adapted from Baker et al. 1949, De Gruyter et al. 2002). *Conidiomata* pycnidial, abundant, scattered to confluent, globose to subglobose, honey to olivaceous, ostiolate, extruding buff conidial masses, walls composed of 2–7 layers of vinaceous, hazel or umber, thin-walled cells. *Conidiogenous cells* globose, subglobose to ampulliform, 6.5–10 × 3–8 µm (av. ± S.D. = 7.7 ± 1.1 × 6.9 ± 1.5 µm). *Conidia* hyaline, ovoid, ellipsoidal, oblong to cylindrical, straight or slightly curved, usually with 2 or more guttules, mostly aseptate, 4.5–9.5 × 2–4.5 µm (av. ± S.D. = 6.3 ± 1.2 × 2.9 ± 0.4 µm), sometimes 1-septate, with or without constriction at the septum, 8.5–14.5 × 3–5(–7) µm (av. ± S.D. = 11.5 ± 1.9 × 3.7 ± 0.5 µm).

Culture characteristics — Colony on MEA 68 mm after 7 d, flat with entire edge, aerial mycelia sparse, white, becoming dark brick to olivaceous grey with time, sometimes with a salmon

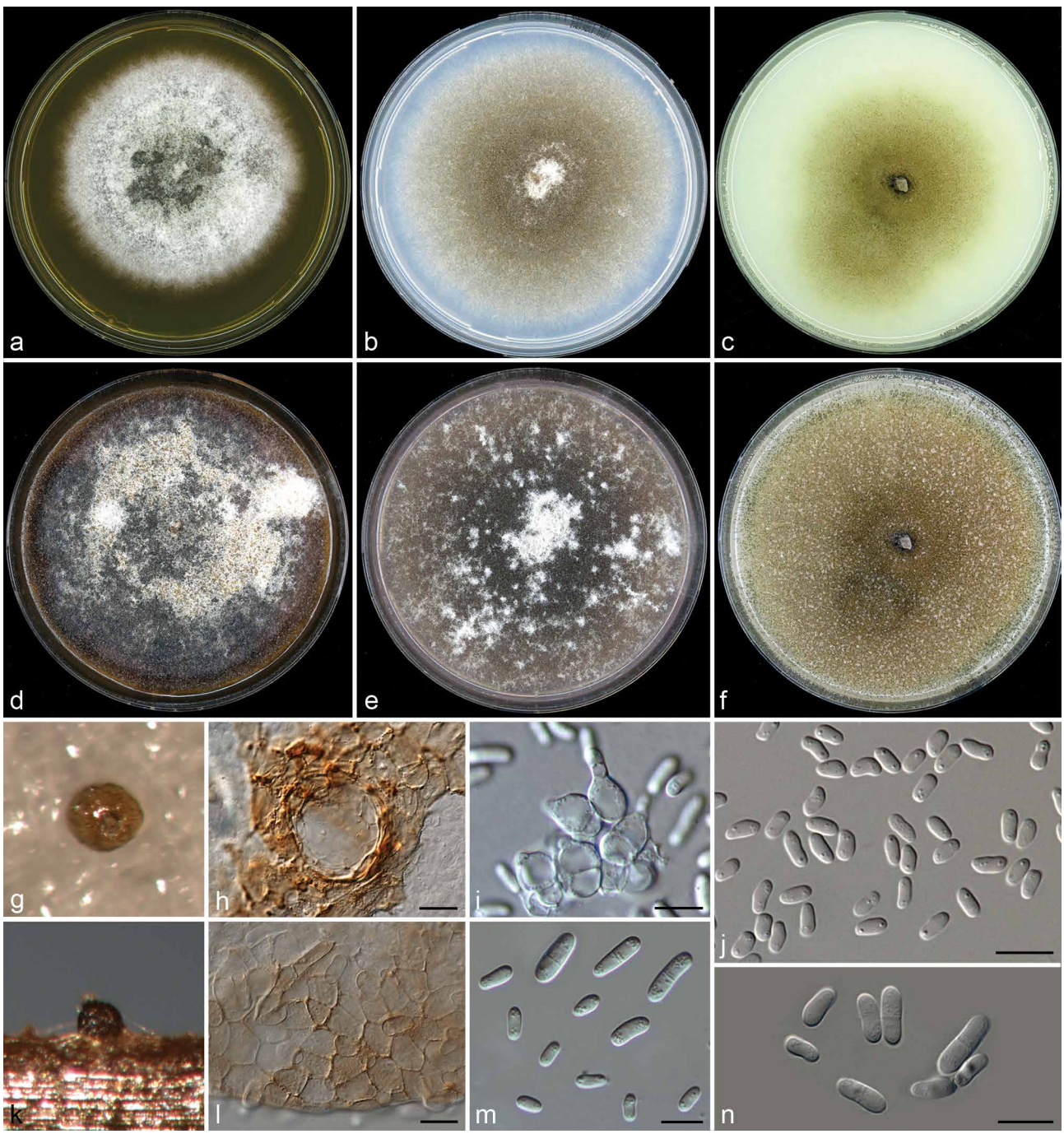

Fig. 46 *Stagonosporopsis chrysanthemi* (a–g, j–k. CBS 500.63; h–i. CBS 124241). a–c. Colonies in one wk; d–f. colonies in two wk (20 °C, a, d. on MEA; b, e. on PDA; c, f. on OA); g, k. pycnidia; h, l. pycnidial wall; i. conidiogenous cells and conidia; j, m–n. 0–1-septate conidia. — Scale bars: h–j, l–n = 10 µm.

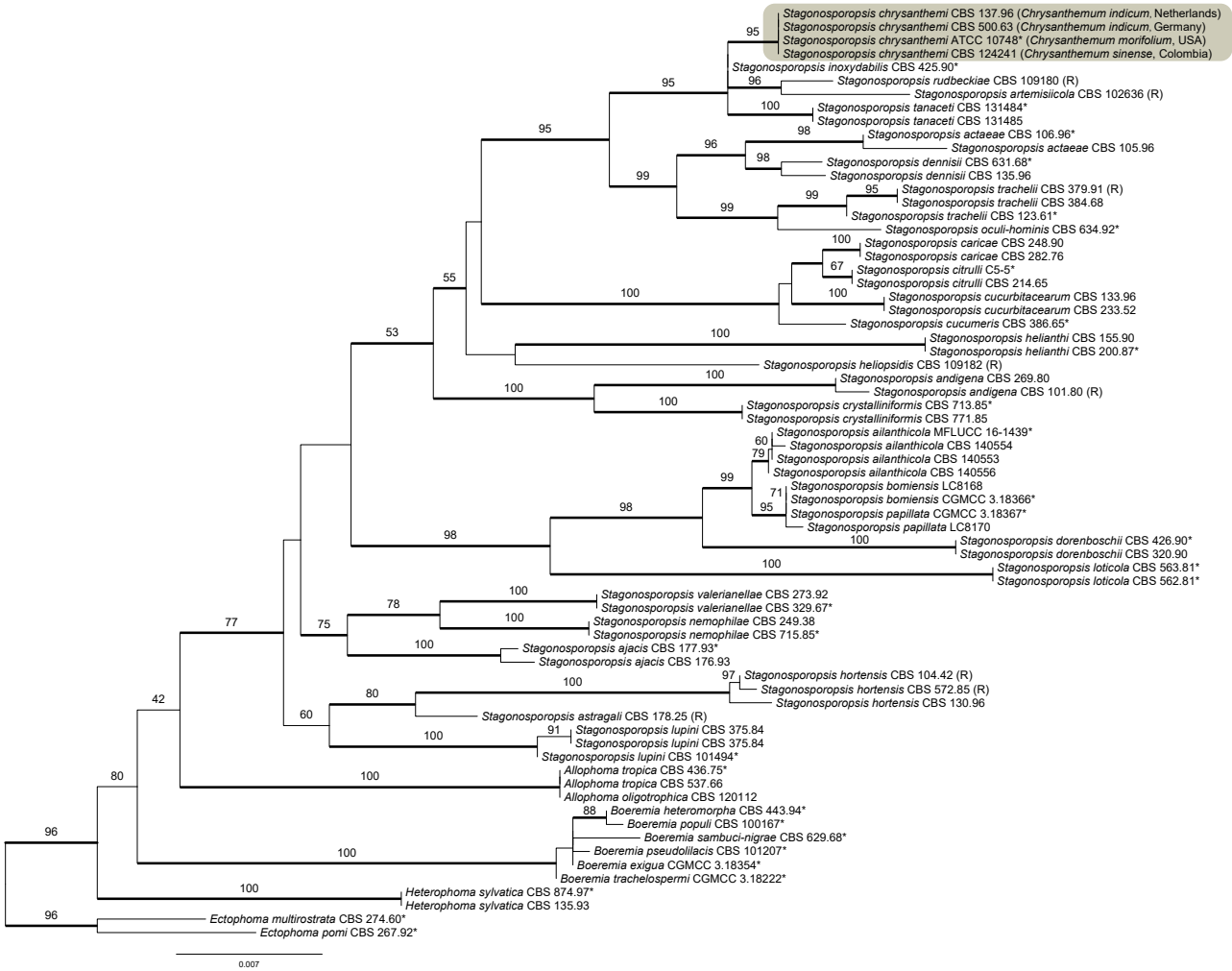

Fig. 47 Phylogenetic tree of *Stagonosporopsis* and related taxa calculated with RAxML on LSU, ITS, and *tub2* sequences showing affinities of *S. chrysanthemi* with allied species. Thickened branches indicate branches present posterior probabilities (> 0.90) in the Bayesian tree. The bootstrap support values > 50% are displayed at the nodes. Asterisks (*) indicate ex-type cultures.

shade due to conidial masses. Colony on PDA 80 mm after 7 d, flat with entire edge, aerial mycelia seldom, isabelline to smoke grey from centre to the edge, becoming pale olivaceous to olivaceous black with time. Colony on OA 70 mm after 7 d, flat with entire edge, aerial mycelia absent, olivaceous buff to greenish olivaceous, often in a zonate pattern.

Additional materials examined. Colombia, on necrotic tissue of *C. sinense*, unknown collection date, *W. Veenbaas*, living culture CBS 124241 = PD 89/1016-4. – Germany, Berlin, on *Chrysanthemum morifolium*, 1963, *R. Schneider*, CBS H-11952, living culture CBS 500.63 = MUCL 8090. – Netherlands, on *C. morifolium*, unknown collection date, unknown *collector*, living culture CBS 137.96 = CBS 109178 = PD 84/75.

Habitat — *Chrysanthemum cinerariifolium*, *C. indicum*, *Chrysanthemum* × *morifolium*, *C. sinense*.

Geographic distribution — (EPPO 2019b, Farr & Rossman 2021): Africa: Kenya, Malawi, South Africa, Tanzania, Tunisia, Zimbabwe. – America: Canada, Mexico, USA. – Asia: Armenia, Israel, Japan. – Europe: Belgium, France, Germany, Ireland, Israel, Italy, Lithuania, Luxembourg, Moldova, Netherlands, Norway, Poland, Romania, Serbia, Slovakia, Sweden, UK. – Oceania: Australia, New Zealand, Papua New Guinea.

NCBI Genome ID: JAFISE000000000 (CBS 500.63, this study).

Notes — *Stagonosporopsis chrysanthemi* (Vaghefi et al. 2012) was listed in the Chinese quarantine pest directory as *Didymella ligulicola*. It causes ray blight (or flower blight) of chrysanthemum (*Asteraceae*), occurring almost everywhere the host is cultivated, and is also listed on the A2 list by the European and Mediterranean Plant Protection Organization (EPPO 2019c). Except *S. chrysanthemi*, other species in this genus also have quarantine importance. For instance, *S. inoxydabilis* and *S. tanaceti*, associated with ray blight of *Asteraceae*, are important quarantine pathogens in many parts of the world (Vaghefi et al. 2016); *S. andigena* has been listed in Annex IAI by European Union (EU) and in A1 list by EPPO (EPPO 2019b). These species of quarantine significance could be easily distinguished from each other based on multi-locus phylogenetic analysis (Fig. 47).

Ascochyta chrysanthemi (the basionym of *Stagonosporopsis chrysanthemi*) was originally described on *Chrysanthemum indicum* from North Carolina (USA) but without designation of a type specimen (Stevens 1907). Considering that the two specimens BPI 371302 and BPI 371303 were labelled as type and collected by Stevens in 1906 according to the USDA database (Farr & Rossman 2021), they represent syntypes of *A. chrysanthemi*.

The link of the asexual (*Ascochyta chrysanthemi*) and sexual morph (*Mycosphaerella ligulicola*) of this fungus was confirmed by Baker et al. (1949). Although the type of *M. ligulicola* was not designated in Baker et al. (1949), their originally studied specimens had been deposited in several fungaria (BPI, K, NY, herbaria of Harvard University, University of California, and University of Georgia) and the cultures in the CBS and ATCC culture collections. We therefore selected BPI 608685 as

lectotype of *M. ligulicola* in this study. A multi-locus phylogram showed that ex-epitype of *A. chrysanthemi* ATCC 10748 clustered together with three *Chrysanthemum* related strains from Europe and Colombia (Fig. 47), implying the host specificity of this fungus on *Chrysanthemum*. For more historical and taxonomic details of this fungus, please refer to De Gruyter et al. (2002) and Vaghefi et al. (2012, 2016).

Venturia inaequalis (Cooke) G. Winter, Mycoth. Univ. Cent. 3: no. 261. 1875 — Fig. 48, 49

Basionym. *Sphaerella inaequalis* Cooke, J. Bot. 4: 248. 1866.

Synonyms. *Didymosphaeria inaequalis* (Cooke) Niessl, Fungi Eur. Exsicc. no. 2663. 1881.

Endostigme inaequalis (Cooke) Syd., Ann. Mycol. 21: 171. 1923.

Spilosticta inaequalis (Cooke) Petr., Ann. Mycol. 38: 193. 1940.

Fusicladium pomi (Fr.) Lind, Danish fungi as represented in the herbarium of E. Rostrup 521. 1913.

For additional synonyms see Shen et al. (2020).

Typus. Czech Republic, Brünn, falling leaves of *Sorbus torminalis* (*Rosaceae*), June of unknown year, *Niessl*, isotypes of *Sphaerella inaequalis* NY 00914442, NY 00914443, NY 00914444. – Sweden, on *Malus domestica* (*Rosaceae*), unknown collection date, unknown *collector*, ex-epitype CBS 120627. – UK, Surrey, Shere, on *S. aria* (*Rosaceae*), Apr. 1866, *M.C. Cooke*, lectotype of *Sphaerella inaequalis* K(M) 237177, isolectotypes of *Sphaerella inaequalis* BPI 798917, BPI 739265, K(M) Nos. 237173, 237174, 237175, 237176, 237178; London, on *M. pumila*?, 1865, *M.C. Cooke*, IMI 161335 (slide, probably made from type specimen).

Symptoms — *Venturia inaequalis* causes scab on leaves, petioles, blossoms, sepals, fruit, and pedicels of apple, and less frequently on young shoots and bud scales. Infections on leaves first appear as a light shade of green, and soon become velvety brown to olive green due to the abundant production of conidiophores and conidia, with indistinct margins. Later, some lesions appear metallic black and the margins become distinct, but they may be obscured if several lesions coalesce. On fruit, infection causes an uneven surface and small lesions in the early stage, then cracks appear in the skin and flesh, or the fruit may become deformed (MacHardy 1996).

Ascomata pseudothecial, scattered, globose to subglobose, dark brown to black, 120–225 µm diam, immersed, erumpent with age, with or without setae. *Setae* dark brown, 28–65 × 5–7 µm. *Peridium* 11–28 µm wide, wall composed of 3–4 layers. *Pseudoparaphyses* hyaline, septate, 2–4 µm wide. *Asci* 8-spored, bitunicate, cylindrical, 56–79 × 11–15 µm (av. = 63.4 × 12.3 µm). *Ascospores* cylindrical to clavate, olivaceous brown, smooth, uniseriate, 1-septate, with septum at the upper third, usually constricted at the septum, the upper cell tapers toward the apex, the lower cell usually with a broadly rounded end,

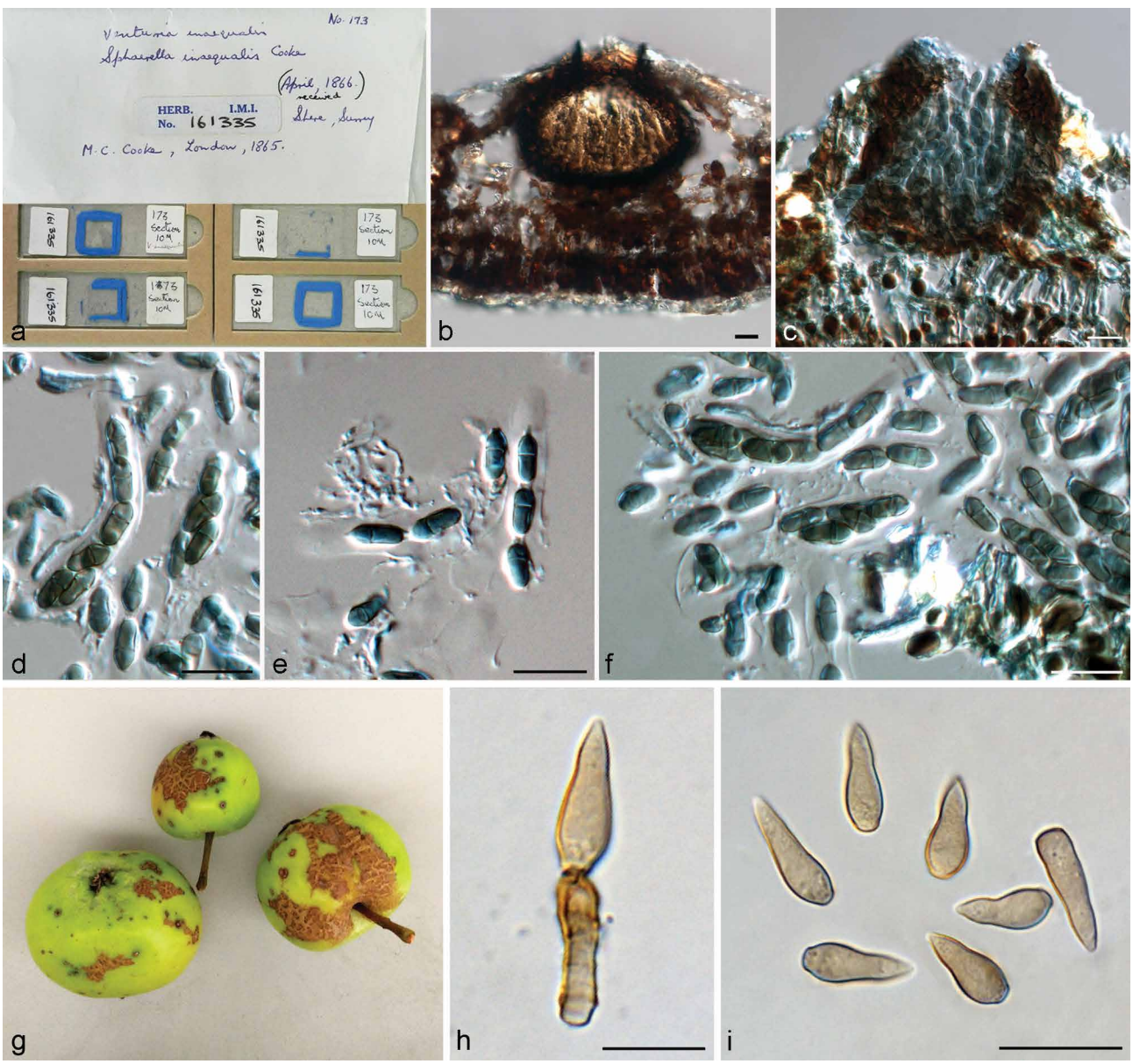

Fig. 48 *Venturia inaequalis* (a–f. IMI 161335, g. HMAS 291533, h–i. NY 00914443). a. Specimen collection packet; b–c. section of ascomata; d–f. asci and ascospores; g. symptom on apple fruit; h. conidiogenous cell and conidium; i. conidia. — Scale bars: b–f, i = 20 µm, h = 10 µm (h–i. kindly provided by Y. Zhang).

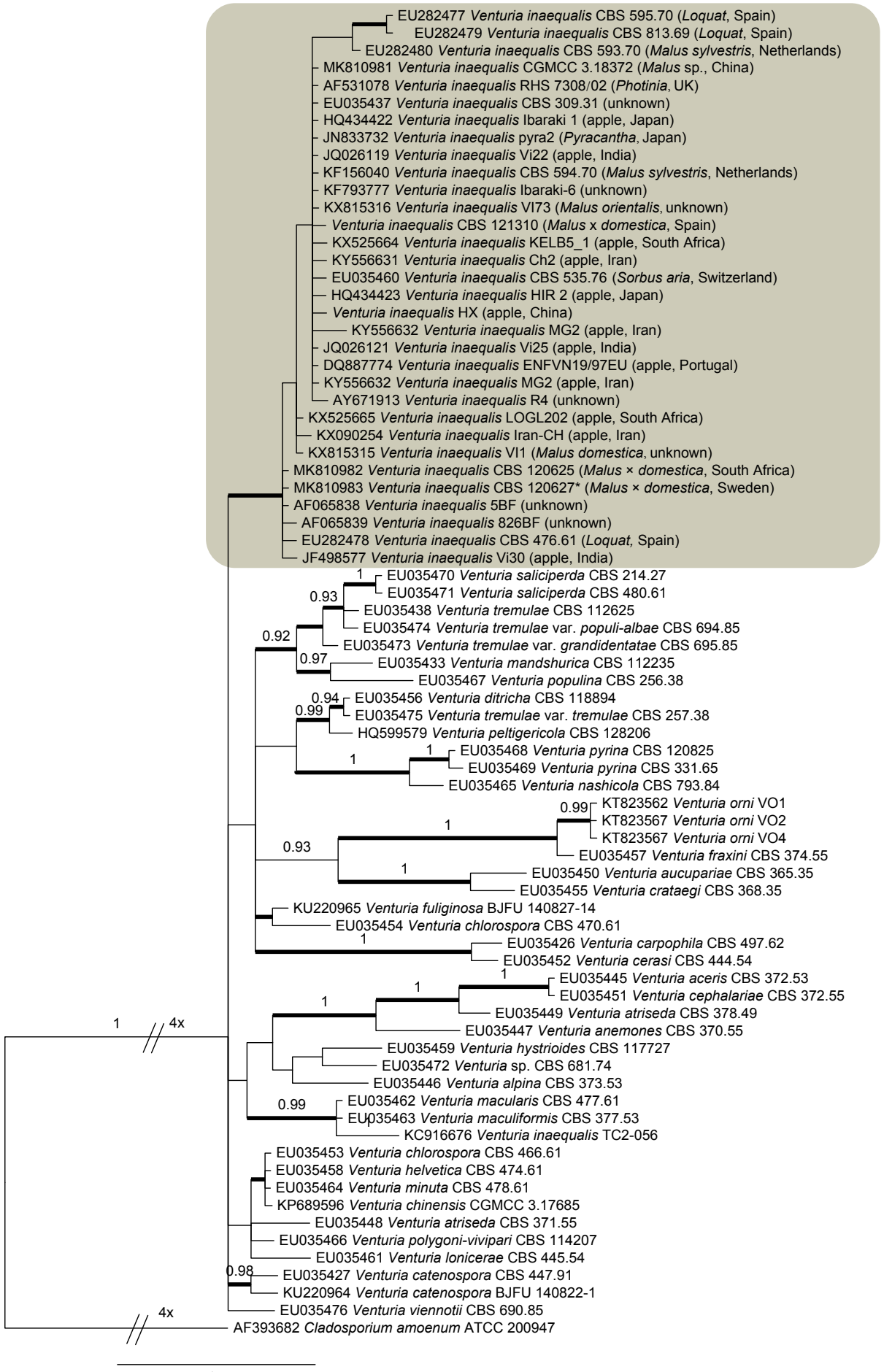

Fig. 49 Phylogenetic tree of *Venturia* calculated with Bayesian analysis on ITS sequences showing affinities of *V. inaequalis* with allied species. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisk (*) indicate ex-type culture.

11.5–15 × 4.5–6 µm (av. ± S.D. = 13.1 ± 0.8 × 5.3 ± 0.4 µm). *Stromata* variable in size, pale olivaceous to brown, composed of thin-walled parenchyma cells, angular or circular, 4–7 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* solitary or sparsely gregarious, arising from stromata or hyphae, straight or flexuous, proliferating, unbranched, pale to medium brown, smooth to verruculose, 0–1-septate, wall thickened, 16–35 × 5–6 µm, base usually swollen. *Conidia* obpyriform or obclavate, pale brown to brown, 18–29 × 6–8 µm, 0–1-septate, tapering towards the apex, obtuse, base truncate, 4–5 µm wide (adapted from Shen et al. 2020).

Additional materials examined. China, Xinjiang, on fruit of *Malus pumila*, 2016, *X.L. Zhang*, specimen HMAS 291533 = HX. – Netherlands, on fruit of *M. sylvestris* cv. Yellow Transparent, unknown collection date, isolated and deposited by *A. Kaars Sijpesteijn*, CBS 593.70. – Spain, on *Malus* × *domestica*, unknown collection date, deposited by *B. Le Cam*, living culture CBS 121310 = SP05GO37. – Switzerland, on leaf of *Sorbus aria*, unknown collection date, isolated by *F. Stadelmann* in Aug. 1972, living culture CBS 535.76.

Habitat — Principally on apple (*Malus pumila*), and other species of *Malus*. Also recorded on *Cotoneaster integerrima*, *Crataegus oxyacantha*, *Loquat*, *Photinia*, *Pyracantha*, *Pyrus* spp., *Sarcocephalus esculentus*, *Sorbus* spp., *Viburnum* sp.

Geographic distribution — (Farr & Rossman 2021; Fig. 49): Africa: Ethiopia, Kenya, Libya, South Africa, Zimbabwe. – America: Brazil, Canada, Mexico, USA. – Asia: China (restricted in Xinjiang; Zhuang 2005), India, Iran, Japan, Korea, Pakistan, Uzbekistan. – Europe: Belgium, Bulgaria, Chile, Czech Republic, Denmark, Finland, France, Germany, Greece, Italy, Netherlands, Poland, Portugal, Romania, Scotland, Spain, Sweden,

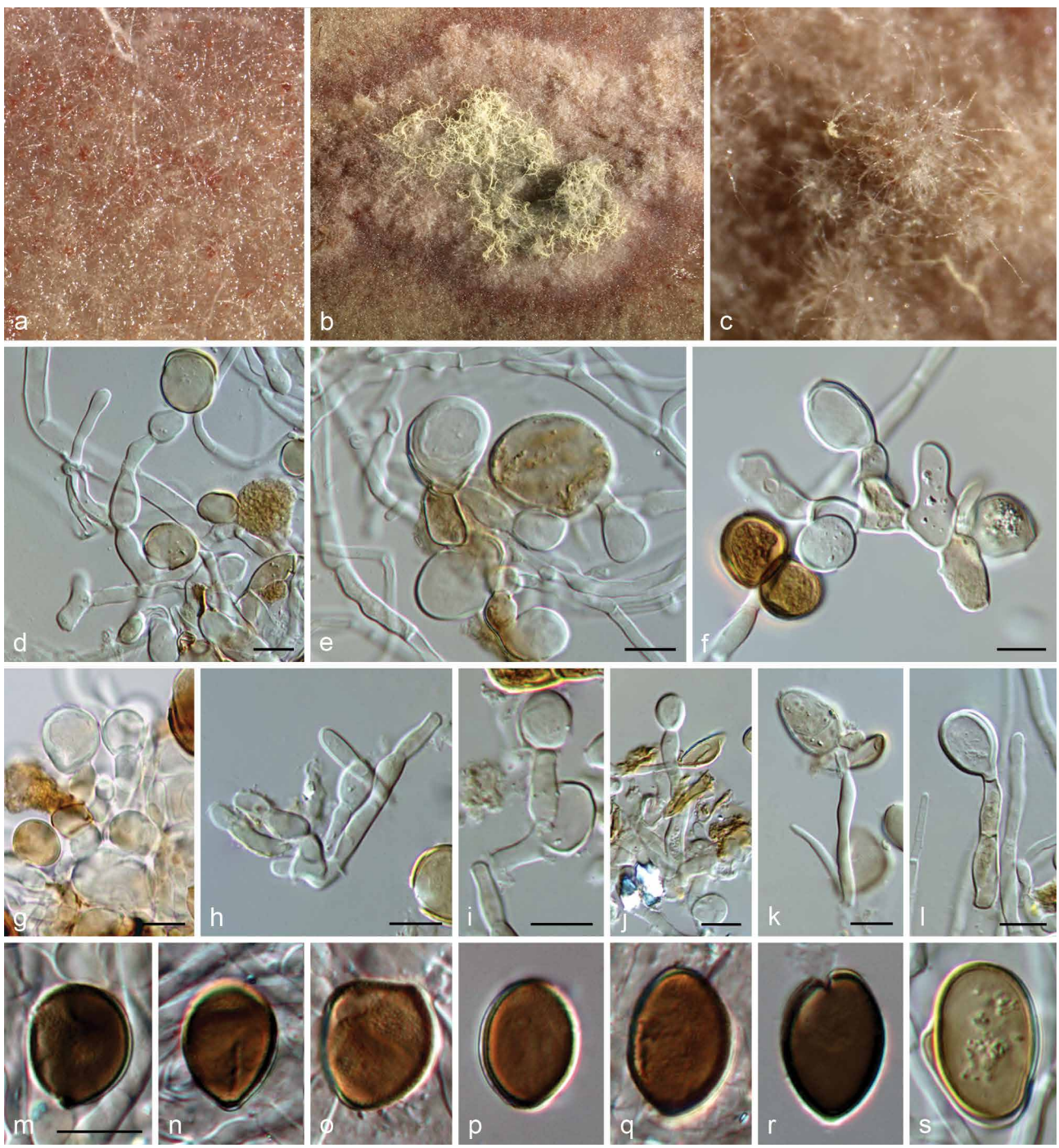

Fig. 50 *Xenosphaeropsis pyriputrescens* (CBS 115176). a. Colony on PDA (20 °C); b. green aerial mycelia producing on the surface of medium with time; c. pycnidia covered with white aerial mycelia; d–l. conidiogenous cells bearing immature conidia; m–s. mature conidia. — Scale bars: d–m = 10 µm, m applies to n–s.

Switzerland, Turkey, Ukraine, UK. – Oceania: Australia, New Zealand.

Notes — *Venturia inaequalis* was originally reported from ash, hawthorn, pear, apple and *Pyrus aria* (Cooke 1866). Many *Rosaceae* associated strains of *V. inaequalis* from multiple countries, including the ex-epitype recently designated by Shen et al. (2020), clustered together in the ITS tree (Fig. 49), indicating that *V. inaequalis* is monophyletic, polyphagous and widespread.

Xenosphaeropsis F. Liu, Crous & L. Cai, *gen. nov.* — MycoBank MB 840272

Etymology. Xeno = ξένος in Greek, alien, distinct; sphaeropsis = sphaeropsis-like conidia.

Conidiomata pycnidial on agar surface or immersed, subglobose or more or less flattened at the apex, solitary or aggregate in small numbers, thick-walled. *Ostioles* poroid, inconspicuous. *Conidiogenous cells* subglobose, lining wall of pycnidium, possibly proliferating percurrently. *Conidia* brown, smooth-walled, aseptate, variable in shape, clavate to subglobose or irregular, flattened at bottom.

Type species. *Xenosphaeropsis pyriputrescens* (C.L. Xiao & J.D. Rogers) F. Liu, Crous & L. Cai

Xenosphaeropsis pyriputrescens (C.L. Xiao & J.D. Rogers) F. Liu, Crous & L. Cai, *comb. nov.* — MycoBank MB 840273 — Fig. 50, 51

Basionym. *Sphaeropsis pyriputrescens* C.L. Xiao & J.D. Rogers, Pl. Dis. 88: 116. 2004.

Typus. USA, Washington State, Wenatchee, Chelan County, on fruit of d'Anjou pear (*Pyrus communis*), 19 Mar. 2002, *C.L. Xiao*, holotype of *Sphaeropsis pyriputrescens* WSP 70466, isotype WSP 70467.

Symptoms — *Xenosphaeropsis pyriputrescens* causes stem-end rot, calyx-end rot and wound-associated rot on fruit. The decayed tissue is initially firm or spongy, brown. Subsequently, as the disease advances, the decayed areas remain brown or turn dark brown to dark due to the black pycnidia produced by the fungus. Decay in the fruit flesh originates from infection of the stem or calyx and then develops along the vascular tissue, brown (Xiao & Rogers 2004).

Conidiomata pycnidial, sub-immersed or immersed, subglobose, separate to aggregate in small numbers, off-white to salmon, covered by white aerial mycelia. *Conidiophores* hyaline, rarely pale brown, constricted at the septum, often reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical to cylindrical, obclavate, 7.5–25(–37) × 3–7 µm, lining wall of pycnidium, hyaline, rarely pale brown. *Conidia* hyaline when immature, becoming brown with time, aseptate, clavate, ovoid, subglobose,

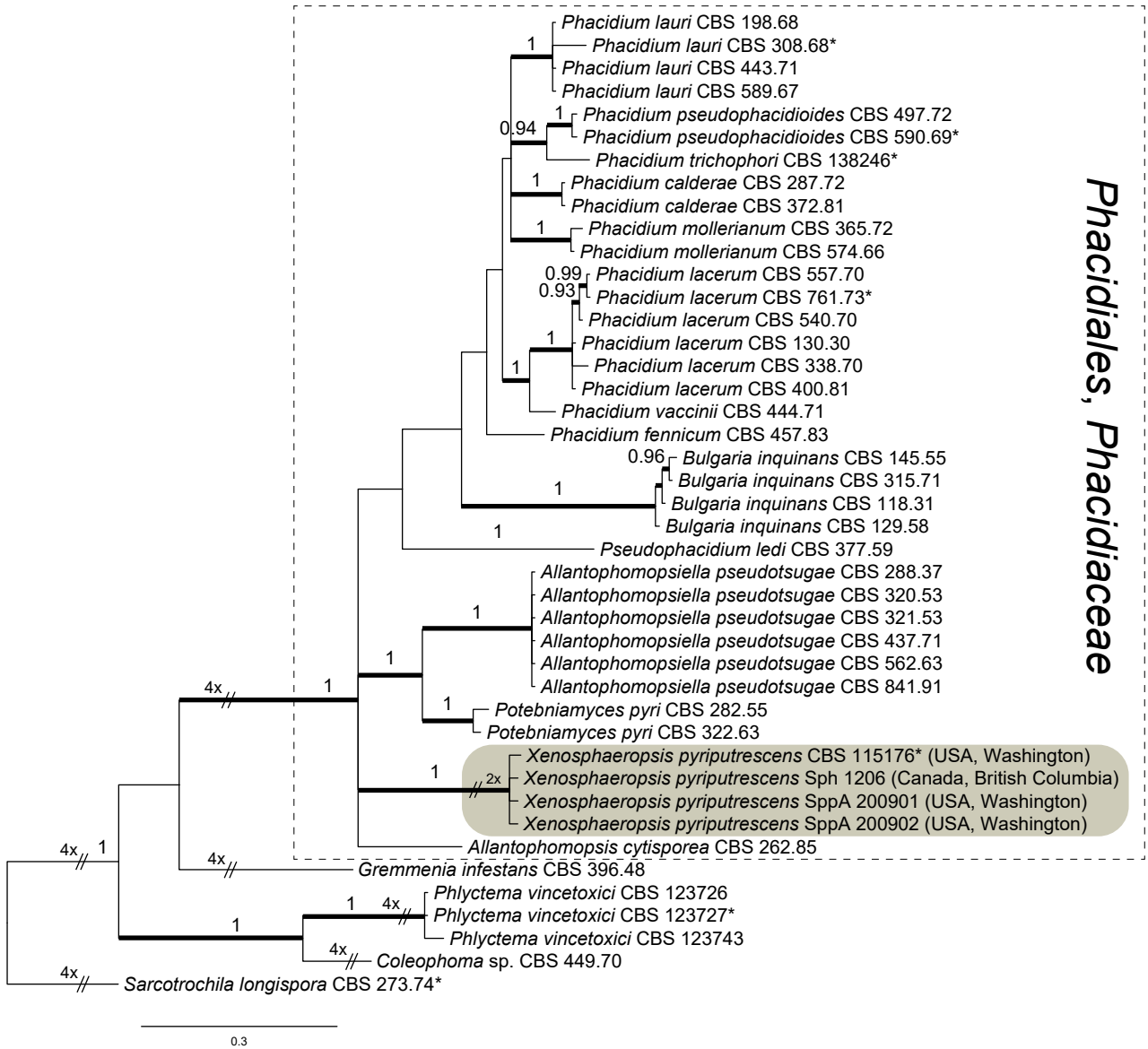

Fig. 51 Phylogenetic tree of *Xenosphaeropsis pyriputrescens* calculated with Bayesian analysis on LSU, ITS, and *rpb2* sequences showing affinities of *X. pyriputrescens* with allied species. Thickened branches indicate branches present bootstrap support values (> 50 %) in the RAxML tree. The posterior probabilities > 0.90 are displayed at the nodes. Asterisk (*) indicate ex-type culture.

or occasionally ellipsoidal, smooth, 10–19.5 × 7.5–13.5 µm (av. ± S.D. = 14.6 ± 2.4 × 10.9 ± 1.8 µm).

Additional material examined. USA, Washington State, Peshastin, Chelan County, dried culture isolated from a decayed fruit of d'Anjou pear (*P. communis*) collected from a commercial fruit packinghouse, 12 Dec. 2001, *C.L. Xiao*, WSP 70468, living culture CBS 115176 = ATCC MYA-2947.

Habitat — *Malus domestica*, *M. sylvestris*, *Pyrus communis*.

Geographic distribution — America: Canada, USA.

NCBI Genome ID: JAGKQE000000000 (CBS 115176, this study).

Notes — Although the holotype (WSP 70466) and isotype (WSP 70467) of *Sphaeropsis pyriputrescens* were designated in Xiao & Rogers (2004), their corresponding cultures and sequences were not mentioned, and could not be located. Therefore, the living culture ATCC MYA-2947 listed as representative in Xiao & Rogers (2004) was examined and sequenced in this study.

Sphaeropsis was clarified as the asexual morph of *Phaeobotryosphaeria*, taxonomically belonging to *Botryosphaeriaceae* (*Botryosphaeriales*) (Phillips et al. 2008, Zhang et al. 2021). However, multi-locus (LSU, ITS, *rpb2*) phylogenetic analysis allocated the ex-paratype of *S. pyriputrescens* (CBS 115176) in the clade of *Phacidiaceae* (*Phacidiales*) (Fig. 51). It clustered together with three reference strains from pear and apple, and showed certain morphological differences and phylogenetic distance from other genera in *Phacidiaceae*. A novel monotypic genus, *Xenosphaeropsis*, was therefore introduced to accommodate this species. *Xenosphaeropsis pyriputrescens* is currently limited on *Pyrus communis* in Washington and British Columbia (Xiao & Rogers 2004, Sholberg et al. 2009) and on *Malus* sp. in Washington and New York (Xiao & Rogers 2004, Xiao & Boal 2005, Kim & Xiao 2008, Kim et al. 2013, 2014, Xiao et al. 2014).

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Supplementary material

Table S1 Details of isolates included in the phylogenetic analyses.