



Mycosphere Notes 102–168: Saprotrophic fungi on *Vitis* in China, Italy, Russia and Thailand

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Abstract

This is the third paper in the series, *Mycosphe notes*, wherein we provide notes on various fungal taxa. In this set of notes, we deal with species found on the grape genus, *Vitis*, one of the most important economically important crops, grown worldwide. We provide notes on 67 taxa, including two new species, *Alternaria italica* and *Alfaria vitis*, an asexual morph for *Alfaria cyperi-esculenti* and 41 new host records or distribution records. The taxonomic placement of most taxa discussed in this study is based on a modern taxonomic framework based on analysis of multi-gene sequence data.

Key words – 2 new species – *Alfaria vitis* – *Alternaria italica* – Grapevine – Molecular phylogeny – New host records – Saprotrophs

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Introduction

This paper is a continuation of the series, *Mycosphere notes*, which provides notes on new species and new records of fungal taxa (Thambugala et al. 2017, Boonmee et al. 2017). In this paper we provide notes, illustrations, descriptions and phylogenies of 67 fresh collections of saprotrophs and pathogens from the grape genus, *Vitis*. Grapes are an economically important crop belonging to the family *Vitaceae* and commonly known as grapevine (Fig. 1). Grapes are used both for direct consumption and for the production of wine. This genus comprises 79 accepted species of perennial woody and herbaceous vines. Species of *Vitis* are dioecious and highly heterozygous as a result of enforced outcrossing (Walker 2015). Most *Vitis* species are found in the temperate regions of the Northern Hemisphere in North America and Asia, with a few species in the tropics. *Vitis* species are wind pollinated. *Vitis* can be distinguished from other genera of *Vitaceae* by having petals which remain joined at the tip and detach from the base to fall together as a calyptras (Stace 2010). *Vitis* is often divided into two sections based on the number of chromosomes; *Vitis* and *Muscadina* (Walker 2015). All species within the *Vitis* section are interfertile and have 38 chromosomes, while species within the *Muscadine* section have 40 chromosomes (Bennet & Leitch 2012). There are thousands of cultivars of *V. vinifera* L., a species that is grown around the globe. This species is highly important in production of wine, raisins, as well as table grapes.

There have been a few thorough studies of major pathogens on grapes using both morphology and phylogeny (Úrbez-torrez et al. 2012, 2013, Dissanayake et al. 2015, Jayawardena et al. 2015, 2016, Chethana et al. 2017). Even though a number of sexual and asexual fungal taxa have been reported on *Vitis* species, updated information of the taxa present in this genus is lacking. Only some have good illustrations and gene sequence data.

In this study, we collected fungi on *Vitis* species in China, Italy, Thailand and Russia. Comprehensive descriptions with detailed illustrations of these fresh collections, together with multi-gene phylogenetic analyses, were used to establish their taxonomic placements. We treat 67 taxa belonging to *Amorosiaceae*, *Botryosphaeriaceae*, *Chaetomiaceae*, *Chaetosphaeriaceae*, *Cladosporiaceae*, *Diaporthaceae*, *Didymellaceae*, *Didymosphaeriaceae*, *Diatrypaeae*, *Glomerellaceae*, *Hypocreaceae*, *Lophiostomataceae*, *Massariaceae*, *Mucoraceae*,

Mycosphaerellaceae, Nectriaceae, Peniophoraceae, Pleosporaceae, Pythiaceae, Rhizopodaceae, Saccotheciaceae, Schizoparmaceae, Sclerotiniaceae, Sporocadaceae, Stachybotriaceae, Teichosporaceae and *Trichocomaceae*.



Fig. 1 – a-c Habitats d-e Inflorescences f Immature fruits g-h Mature fruits.

Material & Methods

Collection and Isolation

Fungal species associated with *Vitis vinifera*. were collected from China (Beijing, Sichuan and Yunnan Provinces), Italy (Province of Forli-Cesena), Russia (Rostov Region) and Thailand (Chiang Saen). Specimens were incubated in a moist chamber for 3–7 days at 25° C, to induce sporulation. Fungi were isolated by a modified single spore isolation method (Manamgoda et al.

2012, Chomnunti et al. 2014). Growth rate, colony characteristics and sexual/asexual morph morphology were determined from cultures grown on potato dextrose agar (PDA) at 25–28° C, under 12 h light/12 h dark. Fungal mycelia and spores were examined by differential interference contrast (DIC) and photographed with an axio Imager Z2 photographic microscope (Carl Zeiss Microscopy, Germany). Forty conidial measurements were taken for each isolate. All microscopic measurements were recorded with ZeM PRo 2012 software. Representative specimens are deposited in the herbarium of Mae Fah Luang University, Chiang Rai, Thailand (MFLU) and in Kunming, China (KIB). Representative cultures are deposited at Mae Fah Luang Culture Collection (MFLUCC), Beijing Academy of Agriculture and Forestry Sciences, China (JZB) and Kunming Culture Collection (KUMCC). Faces of fungi numbers and Index Fungorum numbers were obtained as outlined in Jayasiri et al. (2015) and Index Fungorum (2018).

DNA extraction, PCR amplification and sequencing

DNA extraction followed the method of Thambugala et al. (2015). The PCR amplifications were performed in a total volume of 25 µl of PCR mixture containing TaKaRa Ex-Taq DNA polymerase 0.3 µl, 12.5 µl of 2×PCR buffer, 2.5 µl of dNTPs, 1 µl of genomic DNA, 1 µl of each primer and 12.2 µl of ddH₂O. The ACT, CAL, CHS, TEF1, GAPDH, ITS, LSU, SSU, RPB2 and TUB2 gene regions were amplified for relevant strains following the conditions stipulated in Table 1. The PCR products were verified by staining with ethidium bromide after separation on 1.2% agarose electrophoresis gels and purified according to the manufacturer's instructions of a Qiagen purification kit (Qiagen, Hilden, Germany). DNA sequencing was done by Sunbiotech Company, Beijing, China. The DNA sequences generated in this study are deposited in GenBank.

Phylogenetic analysis

Based on blast searches in GenBank, using LSU or ITS sequence data, specific genera were identified. Additional sequences were downloaded from GenBank, based on blast searches and recent publications. Separate phylogenetic analyses were carried out to determine the placement of each fungal taxon based on selected ACT, CAL, CHS, TEF1, GAPDH, ITS, LSU, SSU, RPB2 and TUB2 sequence data. DNASTar V.5.1 and SeqMan V.5.0 were used to obtain consensus sequences from sequences generated from forward and reverse primers. Sequences were aligned with Clustal X v.1.81 (Thompson et al. 1997). The sequences were further aligned using default settings of MAFFT v.7 (Katoh & Toh 2008, <http://mafft.cbrc.jp/alignment/server/>) and manually adjusted using BioEdit V.7.0.9.0 (Hall 1999) where necessary.

Maximum parsimony analysis (MP) was performed using PAUP v. 4.0b10 (Swofford 2002) to obtain the most parsimonious trees. Gaps were treated as missing data and ambiguously aligned regions were excluded. Trees were inferred using the heuristic search option with Tree Bisection Reconnection (TBR) branch swapping and 1000 random sequence additions. Maxtrees were set up to 5,000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Descriptive tree statistics for parsimony (tree length [TL], consistency index [CI], retention index [RI], rescaled consistency index [RC], and homoplasy index [HI]) were calculated for trees generated under different optimality criteria. The robustness of the most parsimonious trees was evaluated by 1000 bootstrap replications resulting from maximum parsimony analysis (Hillis & Bull 1993). Kishino-Hasegawa tests (KHT) (Kishino & Hasegawa 1989) were performed in order to determine whether trees were significantly different. Bayesian inference (BI) was used in addition to construct the phylogenies using Mr. Bayes v.3.1.2 (Ronquist & Huelsenbeck 2003). MrModeltest v. 2.3 (Nylander 2004) was used to carry out statistical selection of best-fit model of nucleotide substitution. Six simultaneous Markov chains were run for 1000000 generations and trees were sampled every 100th generation. The 2000 trees representing the burn-in phase of the analyses were discarded and the remaining 8000 trees used for calculating posterior probabilities (PP) in the majority rule consensus tree.

Maximum likelihood analysis was performed in raxmlGUIv.0.9b2 (Silvestro & Michalak 2010). The RAXML analyses were run with a rapid bootstrap analysis using a random starting tree

and 1000 ML bootstrap replicates. The search strategy was set to rapid bootstrapping with one thousand non parametric bootstrapping iterations using the general time reversible model (GTR) with a discrete gamma distribution. The best scoring tree was selected.

Trees were rooted with given outgroups in each analysis. The best scoring trees were selected and visualized in Treeview (Page 1996). MP/ML bootstrap supports (BS) (greater than or equal to 70 %) and Bayesian posterior probability (greater than or equal to 0.90) are shown below or above each branch. All the sequences newly generated in this study listed in Table 2. The resulting phylogenetic trees are presented under each relevant description. Alignments are deposited in TreeBASE under S21936.

Results

Taxonomy

In this study 67 fungal taxa were studied in 42 genera and 27 families. Species descriptions, phylogenetic results and notes are presented under the relevant family and genus.

Ascomycota

The treatment of classes, orders, families and genera of Ascomycota by Wijayawardene et al. (2018) is followed here.

Dothideomycetes

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, in Schoch, Shoemaker, Seifert, Hambleton, Spatafora & Crous, *Mycologia* 98(6): 1050 (2007) [2006]

Botryosphaeriaceae Theiss. & Syd., *Annls mycol.* 16(1/2): 16 (1918)

This family is one of the largest in the class Dothideomycetes. Members of this family are plant pathogens, endophytes or saprotrophs (Liu et al. 2013, Hyde et al. 2013). They have a wide distribution and have been recorded from grapevine as pathogens as well as endophytes and saprotrophs (Philips et al. 2013, Jayawardena et al. 2018).

Botryosphaeria Ces. & De Not., *Comm. Soc. crittog. Ital.* 1(fasc. 4): 211 (1863)

Species of this genus are well-known pathogens on *Vitis vinifera* causing die back (Úrbez-Torres 2011). Currently this genus comprises ten species (Dissanayake et al. 2016). We show the placement of our strains in *Botryosphaeria* where they cluster with *B. dothidea* (Fig. 2).

Botryosphaeria dothidea (Moug.) Ces. & De Not., *Comm. Soc. crittog. Ital.* 1(fasc. 4): 212 (1863)

Facesoffungi number: FoF03512

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** *Ascomata* 200–350 µm diam., 175–280 µm high, erumpent, aggregated or solitary, globose with a central ostiole. *Peridium* comprising 5–10 layers of *textura angularis*, outer region of dark brown cells, inner region of 2–4 layers of hyaline cells lining the locule. *Hamathecium* comprising 2–4 µm wide cells. *Pseudoparaphyses* filiform, septate, constricted at the septa, rarely branched. *Asci* 60–120×15–21 µm (\bar{x} =95×18 µm, n=30), 8-spored, bitunicate, fissitunicate, cylindrical, forming between pseudoparaphyses, pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 20–24×6–8 µm (\bar{x} =23×6 µm, n=30), fusoid to ovoid, sometimes with tapered ends and appearing spindle-shaped, biseriate in the ascus. **Asexual morph:** *Conidiomata* stromatic, 250–450 µm (\bar{x} =320 µm, n=20). *Paraphyses* hyaline, septate, up to 100 µm long, tapering to acutely rounded apices. *Conidiophores* hyaline, cylindrical, smooth. *Conidiogenous cells* hyaline, sub-cylindrical, 4–16×2–5 µm (\bar{x} =8 µm, n=20). *Conidia* 15–26×5–9 µm (\bar{x} =18 µm, n=40), hyaline, unicellular, narrowly fusiform, with a sub-truncate to bluntly rounded base, forming a septum before germination, smooth-walled with a granular content.

Culture characteristics — Colonies olivaceous, becoming grey, reverse black. Mycelial mat moderately dense, margin smooth. Colony on PDA reaching 50 mm diam. after 4 d at 28 °C.

Material examined — ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead aerial branch of *Vitis vinifera*, 21 February 2015, Erio Camporesi IT 2385 (MFLU 15-3509), culture MFLUCC 17-0961; CHINA, Beijing, on dead branch of *V. vinifera*, 3 June 2015, Ruvishika S. Jayawardena, culture JZB310176.

Notes — *Botryosphaeria dothidea* has been isolated from almost all grape growing regions in the world (Phillips et al. 2013, Dissanayake et al. 2016). According to the combined phylogenetic analysis of ITS and EF gene regions, the isolates obtained from *Vitis vinifera* clustered with *Botryosphaeria dothidea* with a high bootstrap support (Fig. 2).

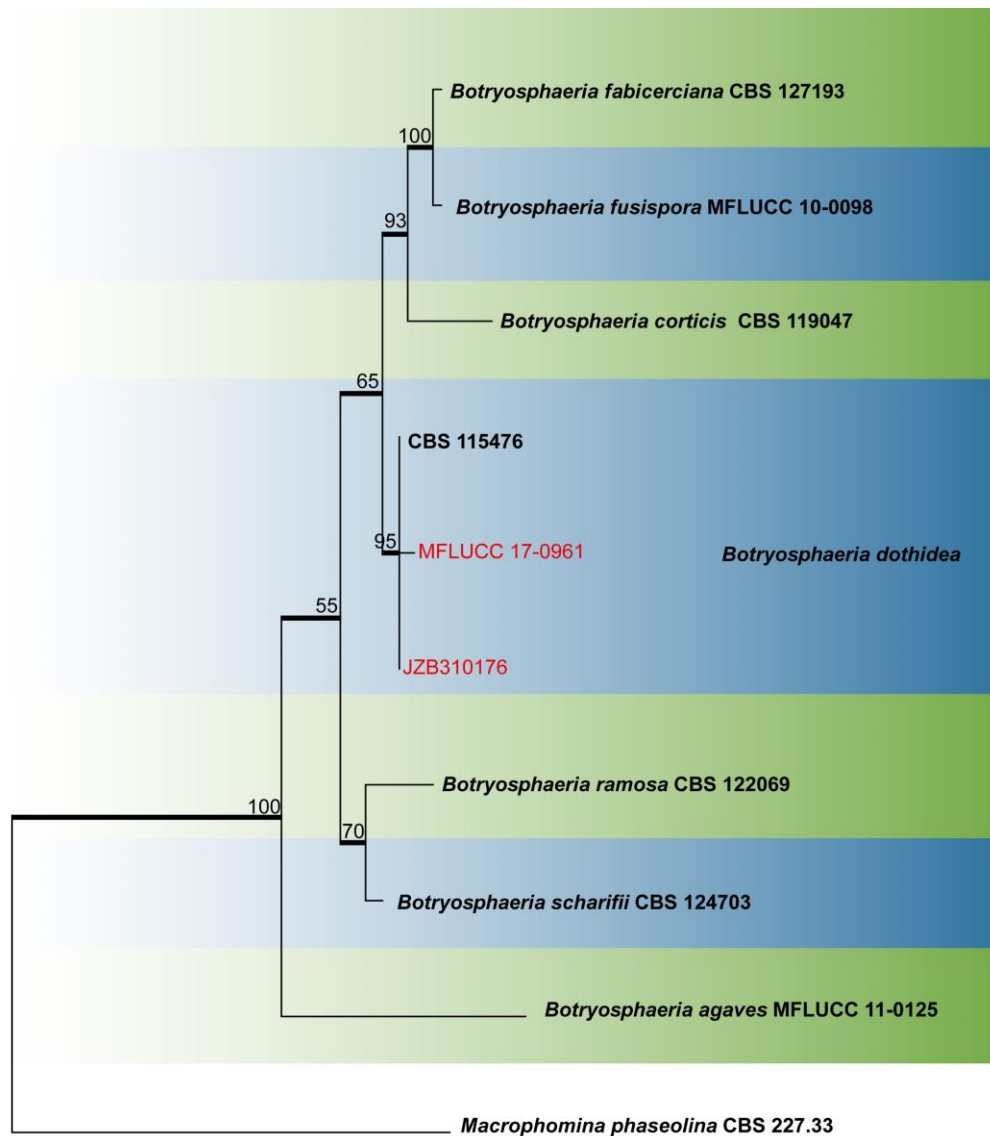


Fig. 2 – RAxML¹ phylogram obtained from the combined ITS and TEF1 sequence data of *Botryosphaeria* species. Ex-type strains are in bold. The strains isolated in this study are shown in red. RAxML bootstrap support (BS) values $\geq 50\%$ are shown at the nodes and branches with Bayesian posterior probability scores ≥ 0.90 given in bold. The tree is rooted with *Macrophomina phaseolina* (CBS 227.33).

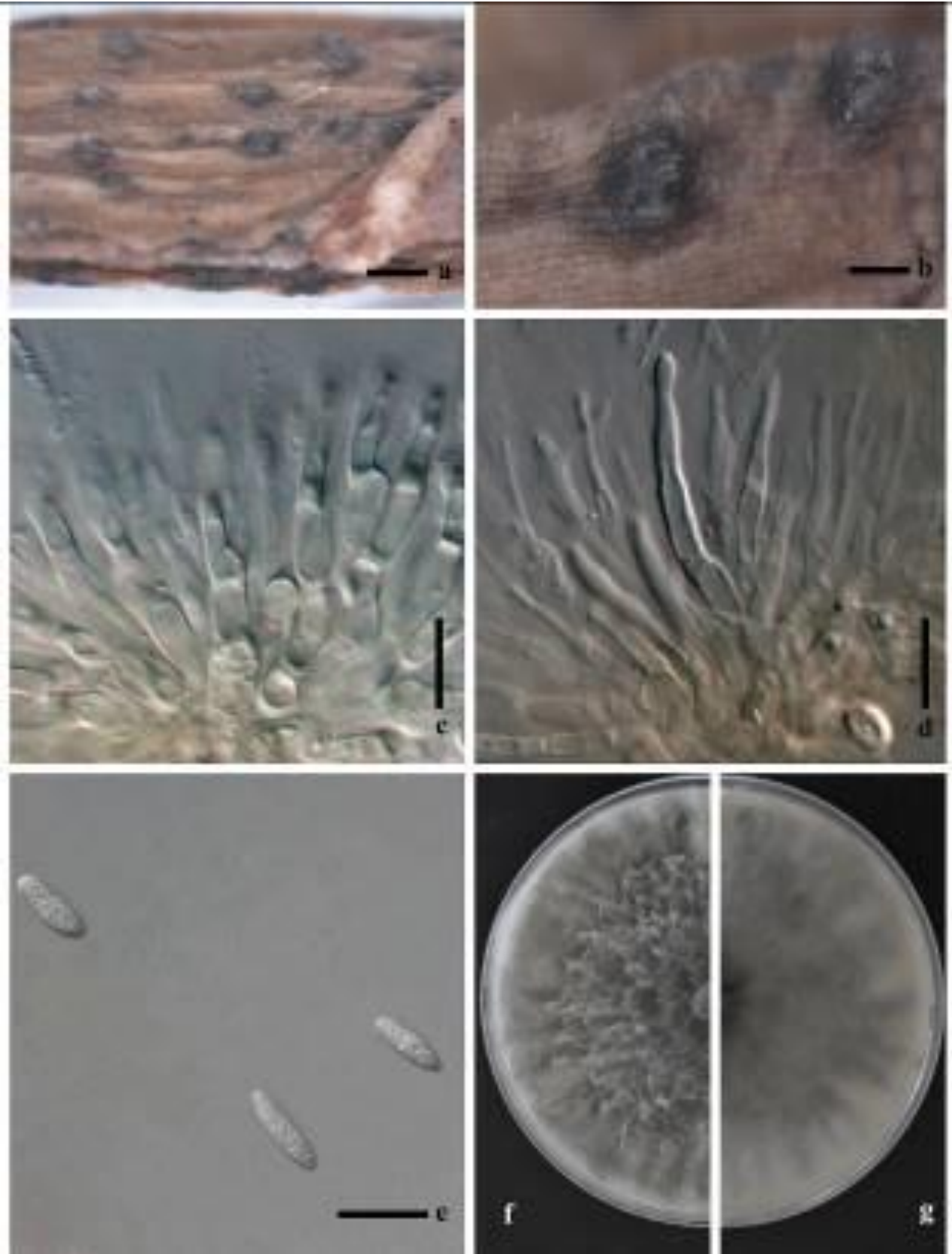


Fig. 3 – Asexual morph of *Botryosphaeria dothidea*. a, b. Appearance of conidiomata on host. c, d. Conidiophores. e. Conidia. f. Upper view of 7 day old culture. g. Reverse view of 7 day old culture. Scale bars: a, b=0.2 mm, c, d, e=20 μ m.

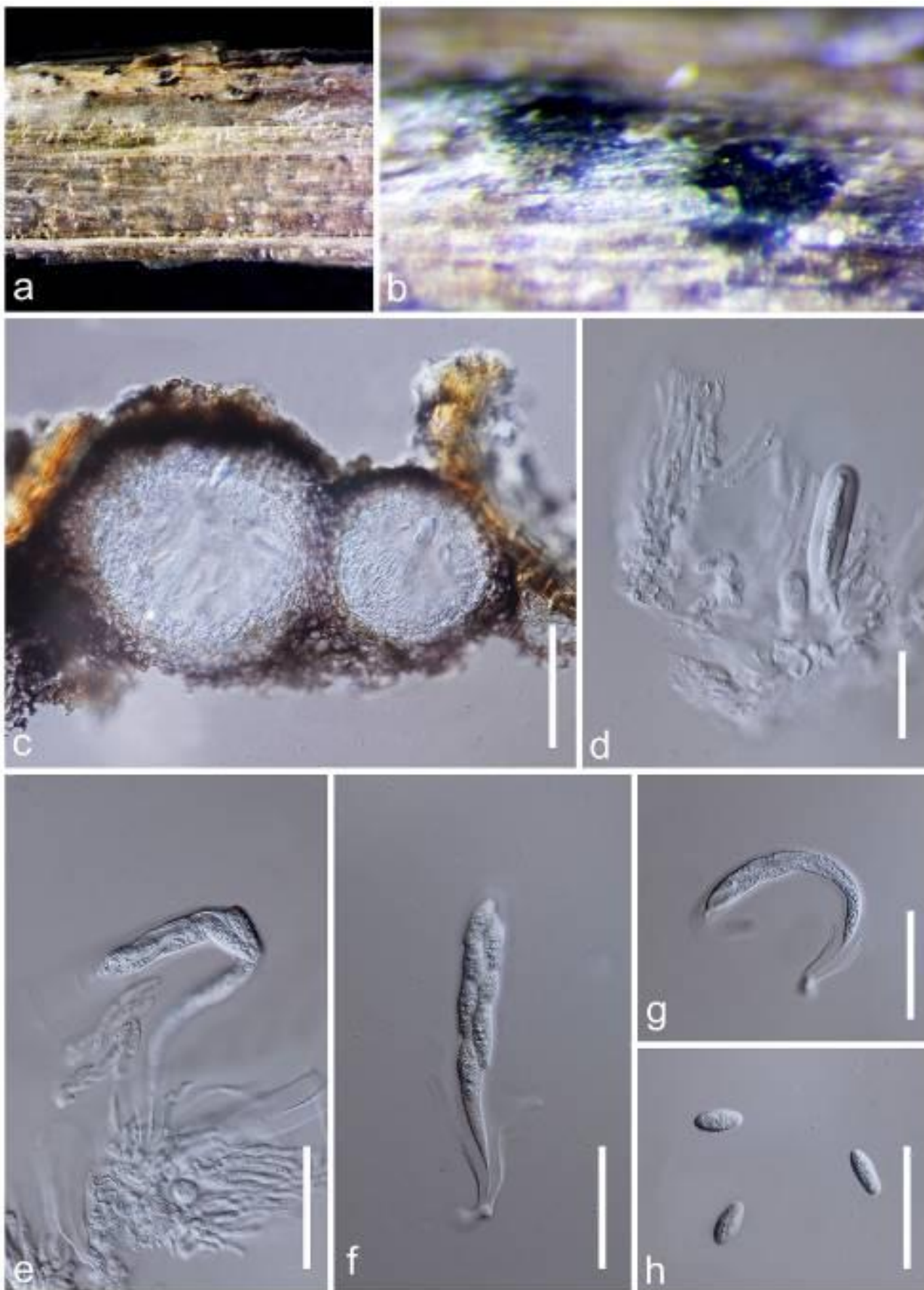


Fig. 4 – Sexual morph of *Botryosphaeria dothidea*. a, b. Appearance of ascomata immersed on host surface. c. Section through ascomata (immersed in host fungi). d, g. Immature asci. e, f. Mature bitunicate asci. h. Ascospores. Scale bars: c=100 μ m, d–h=50 μ m.

Diplodia Fr., in Montagne, *Annls Sci. Nat., Bot., sér. 2* 1: 302 (1834)

Species of this genus are pathogens or saprotrophs, mainly on woody hosts with a worldwide distribution (Philips et al. 2013). Currently, only 17 species have molecular data, therefore recollection, epitypification and molecular analysis is needed for this genus (Philips et al. 2013). Our strains clustered together with the type strain of *D. seriata* (Fig. 5).

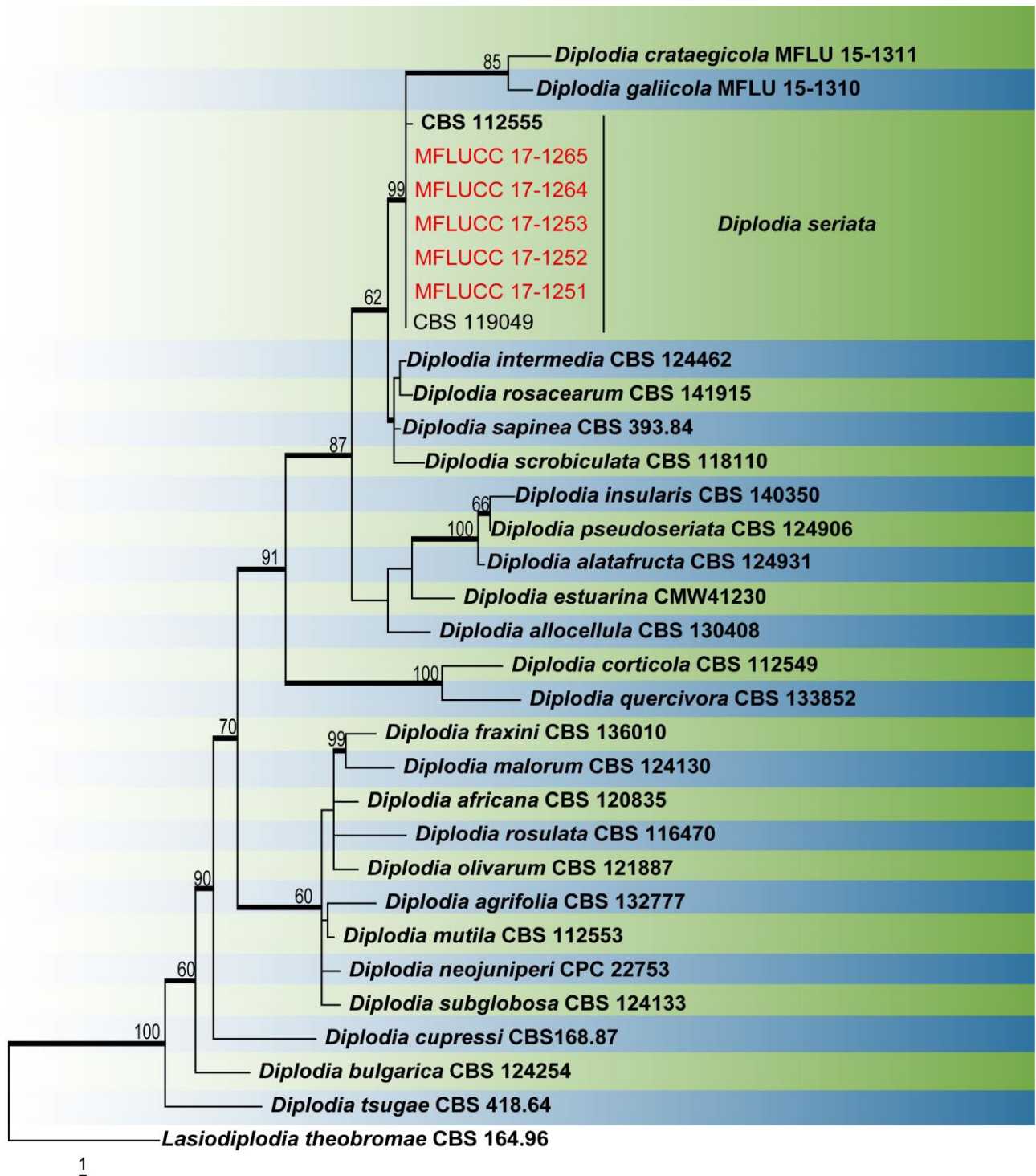


Fig. 5 – RAxML phylogram obtained from the combined ITS and TEF1 sequence data of *Diplodia* species. Ex-type strains are in bold. Strains isolated in this study are in red. RAxML bootstrap support (BS) values $\geq 50\%$ are shown at the nodes and branches with Bayesian posterior probability scores ≥ 0.90 given in bold. The tree is rooted with *Lasiodiplodia theobromae* CBS 164.96.

Diplodia seriata De Not., Micr. Ital., Dec. 4: no. 6 (1842)

Facesoffungi number: FoF03596

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed (see Philips et al. 2013 for description). **Asexual morph:** *Conidiomata* stromatic, separate or aggregated and confluent, immersed in the host, partially emergent at maturity, dark brown to black, ostiolate, apapillate, thick-walled, outer layers composed of dark brown *textura angularis*, inner layers of thin-walled hyaline. *Conidiogenous cells* 3–6×7–12 µm, hyaline, thin-walled, smooth, cylindrical, swollen at the base, discrete, producing a single conidium at the tip, indeterminate, proliferating internally giving rise to periclinal thickenings or proliferating percurrently forming 2–3 annellations. *Conidia* 22–28×11–15 µm (\bar{x} =25×12 µm, n=20), initially hyaline, becoming dark brown, moderately thick-walled, wall externally smooth, roughened on the inner surface, aseptate, ovoid, widest in the middle, apex obtuse, base truncate or rounded.

Culture characteristics — Colonies on PDA pale mouse grey to mouse grey, reverse dark mouse grey to fuscous black with sinuate edge, attaining 80 mm diam. in 7 days. Mycelium dark, septate, appressed to the medium surface.

Material examined — ITALY, Province of Forlì-Cesena, Trivella di Predappio, on dead and aerial branch of *Vitis vinifera*, 9 December 2015, Erio Camporesi IT 136 (MFLU 15-1081); culture, MFLUCC 17-1190, 17-1191; ITALY, Province of Forlì-Cesena, Trivella di Predappio, on dead and aerial branch of *Vitis vinifera*, 9 December 2015, Erio Camporesi IT 2726 (MFLU 16-0648); culture, MFLUCC 17-1251, 17-1252, 17-1253; ITALY, Province of Forlì-Cesena, Trivella di Predappio, on dead and aerial branch of *Vitis vinifera*, 9 December 2015, Erio Camporesi IT 2809 (MFLU 16-0514); culture, MFLUCC 17-1264, 17-1265.

Notes — Species of *Diplodia* are well-known to be associated with Botryosphaeria die back of grapevine worldwide. *Diplodia seriata* has been recorded as a saprobe or a weak secondary pathogen of grapevine (Úrbez-Torres et al. 2008). This species has also been recorded as a pathogen causing brown streaking of the wood and canker as well die back and “black dead arm” (Auger et al. 2004).

Dothiorella Sacc., Michelia 2(no. 6): 5 (1880)

Dothiorella was introduced by Saccardo (1880). Species of this genus are widely distributed on many host plants worldwide (Dissanayake et al. 2016). We provide an updated tree for *Dothiorella* (Fig. 7), where our strains cluster with *Dothiorella iberica* and *D. sarmentorum*.

Dothiorella iberica A.J.L. Phillips, J. Luque & A. Alves, Mycologia 97(2): 524 (2005)

Facesoffungi number: FoF 03513

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* up to 250 µm high, 400 µm diam., pycnidial, stromatic, solitary, globose, thick-walled, composed of dark brown thick-walled *textura angularis*, becoming thin-walled and hyaline towards the inner region. *Conidiophores* absent. *Conidiogenous cells* 8–15×3–5 µm, lining the pycnidial cavity, holoblastic, hyaline, subcylindrical. *Conidia* 19–24×9–10 µm (\bar{x} =22×9 µm, n=30), initially hyaline, becoming dark brown and one-euseptate, often while still attached to the conidiogenous cell, ovoid with a broadly rounded apex and truncate base, brown walled, 1-septate, slightly constricted at the septum.

Culture characteristics — *Colonies* initially white to olivaceous buff, becoming greenish olivaceous from the middle of colonies within 7 days, iron-grey (surface) and black (reverse) with age, with suppressed, moderately fluffy mycelium, covering 90 mm diam Petri dishes after 4 days in the dark.

Material examined — ITALY, Province of Forlì-Cesena, Tessello - Cesena, on dead and aerial branch of *Vitis vinifera*, 5 March 2015, Erio Camporesi IT 2404 (MFLU 15-3513), culture, MFLUCC 17-0964.

Notes — *Dothiorella iberica* has been widely isolated from *Vitis vinifera* world-wide and is a causal agent of Botryosphaeria die back (Phillips et al. 2013). This study provides the first report of *D. iberica* as a saprotroph on *Vitis vinifera* from Italy.

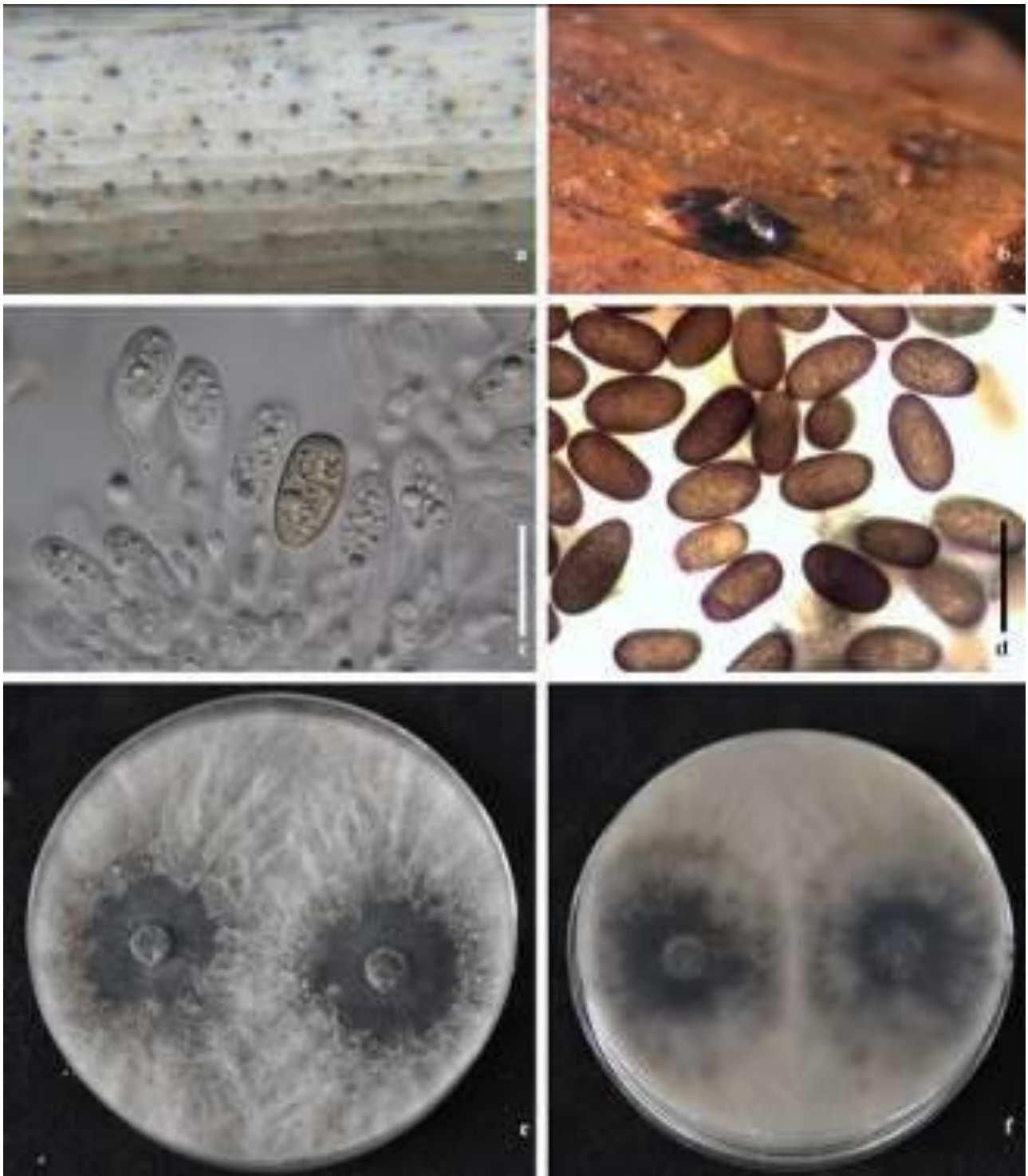


Fig. 6 – *Diplodia seriata*. a, b. Conidiomata on host tissue. c. Conidiogenous cells with developing conidia. d. Mature conidia. e. Upper view of 7 day old culture. f. Reverse view of 7 day old culture. Scale bars: c, d=20 μ m.

Dothiorella sarmentorum (Fr.) A.J.L. Phillips, A. Alves & J. Luque, Mycologia 97(2): 522 (2005)
Facesoffungi number: FoF00171

Saprotrophic on dead and aerial branches and leaves of *Vitis vinifera*. **Sexual morph:** Not observed (see Phillips et al. 2013 for a description). **Asexual morph:** *Conidiomata* 300–440 μ m

high×215–290 µm diam. (\bar{x} =376×250 µm, n=5), stromatic, solitary or scattered in small groups, immersed, uniloculate, individual or aggregated, black, globose to subglobose, ostiolate. *Conidiomatal wall* comprising several layers; outer layers composed of thick-walled, dark brown, somewhat flattened cells of *textura angularis* and inner layers of larger, thin-walled, lightly pigmented or hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–15×3–5 µm (\bar{x} =10×3 µm, n=15), lining the conidiomatal cavity, holoblastic, hyaline, subcylindrical, proliferating at the same level giving rise to periclinal thickenings. *Conidia* 18–23×8–10 µm (\bar{x} =20×9 µm, n=30), ovoid, with a broadly rounded apex and truncate base, initially hyaline to lightly pigmented and aseptate, becoming dark brown and 1-septate, slightly constricted at the septum, smooth-walled.

Culture characteristics — Colonies on PDA at 25° C attaining 80 mm diam in 5 days, circular, flat, moderately dense, surface initially white, becoming greenish olivaceous to greyish within 7 days, smooth surface with entire to slightly undulate edge.

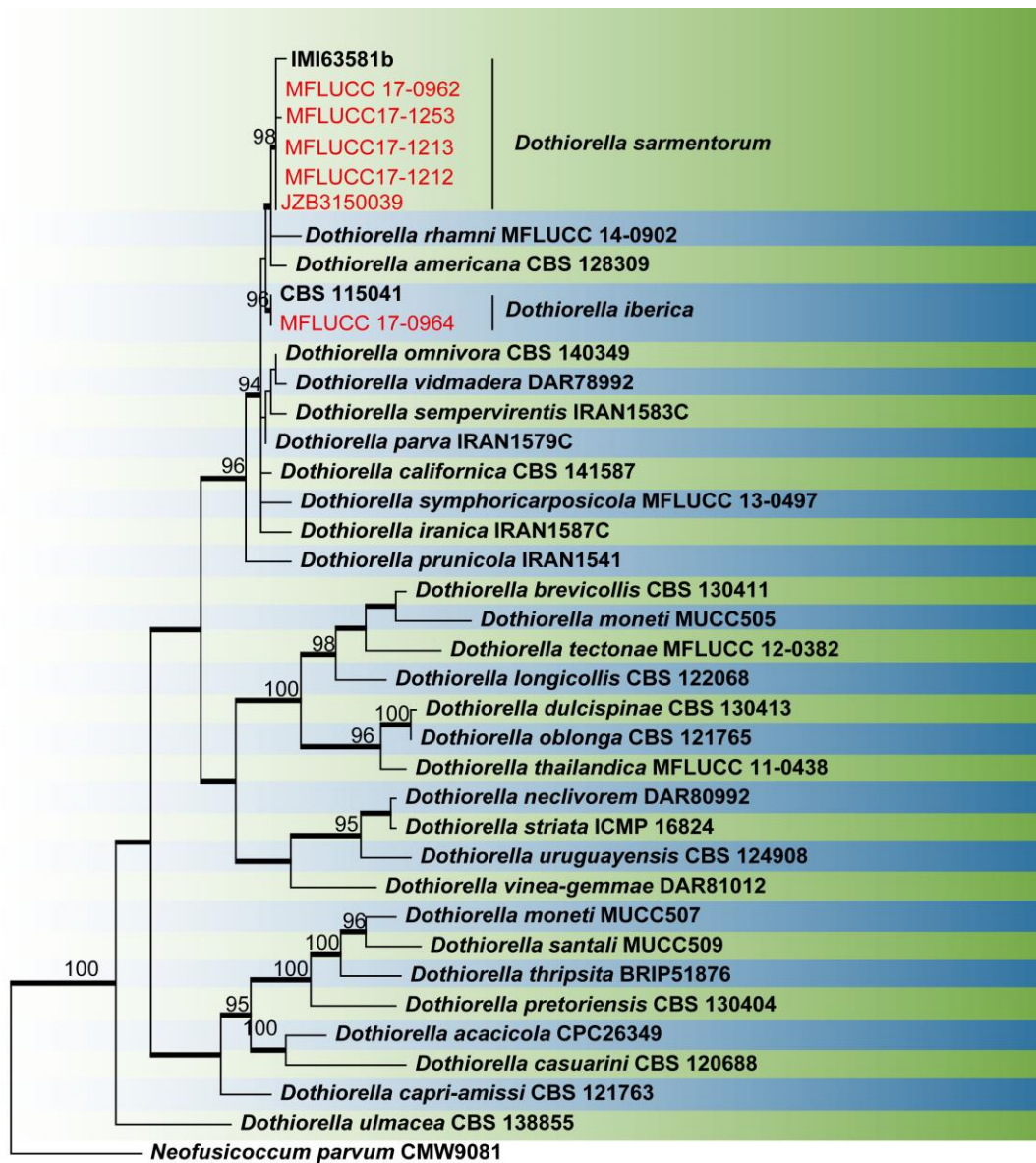


Fig. 7 – RAxML phylogram obtained from the combined ITS and TEF1 sequence data of *Diplodia* species. The ex-type strains are in bold. The strains isolated in this study are shown in red. RAxML bootstrap support (BS) values $\geq 50\%$ are shown at the nodes and branches with Bayesian posterior probability scores ≥ 0.90 are given in bold. The tree is rooted with *Neofusicoccum parvum* CMW 9081.

Material examined — ITALY, Province of Forlì-Cesena, near Pieve di Rivoschio, on dead and aerial branch of *Vitis vinifera*, 2 February 2015, Erio Camporesi IT 2363 (MFLU 15-1082); culture, MFLUCC 17-1212, 17-1213, 17-1253; ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 21 February 2015, Erio Camporesi IT 2386 (MFLU 15-3510); culture, MFLUCC 17-0962; CHINA, Beijing, on dead attached leaf of *Vitis vinifera*, 3 June 2015, Ruvishika S. Jayawardena, culture JZB3150039.

Notes — According to the combined phylogenetic analysis of ITS and TEF gene regions, the isolates obtained from *V. vinifera* in this study are recognized as *D. sarmentorum*. *Dothiorella sarmentorum* has a world-wide distribution (Dissanayake et al. 2016) and reported to be a major pathogen in grapevine trunk diseases (Pitt et al. 2013).

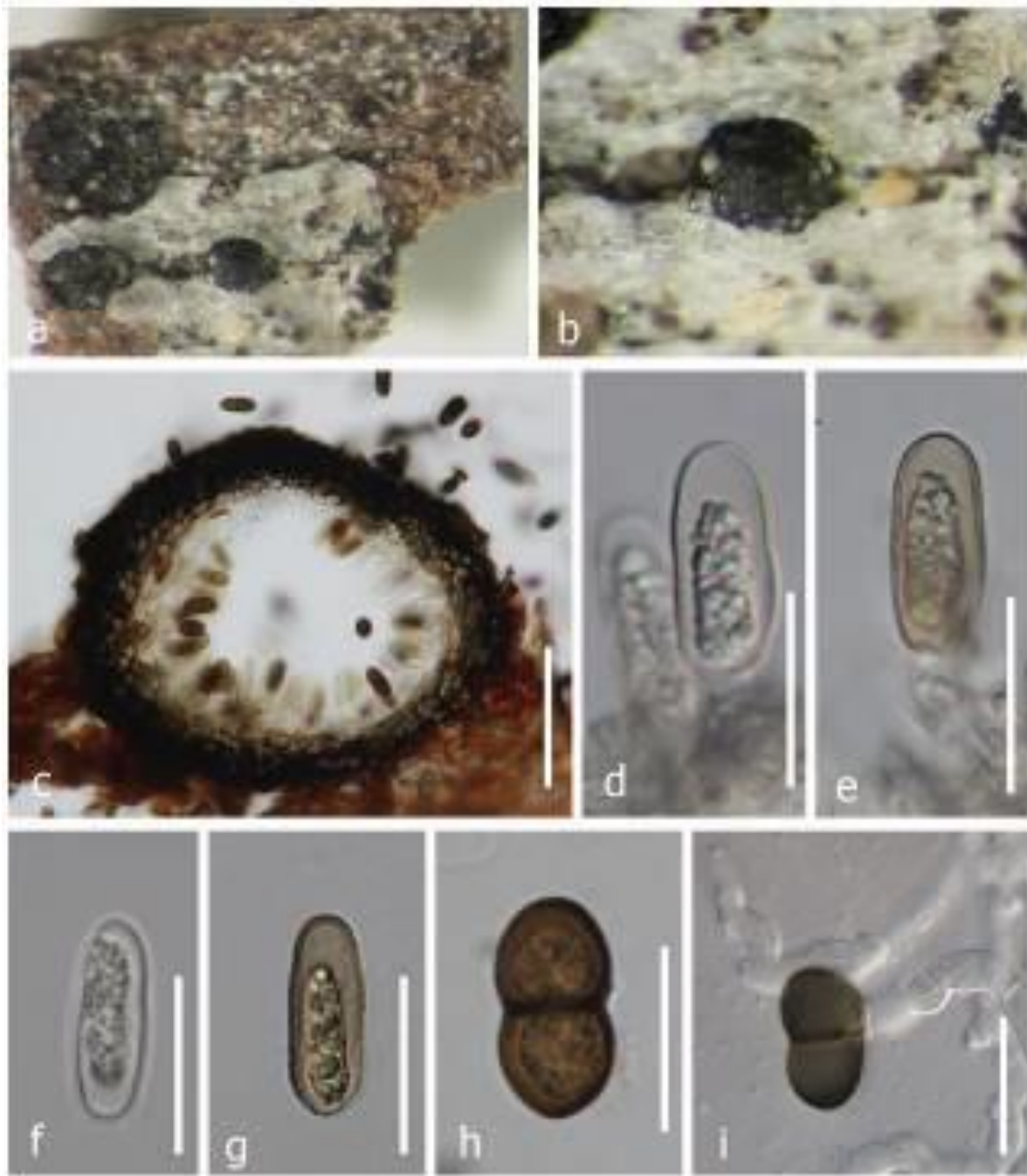


Fig. 8 – *Dothiorella iberica*. a, b. Conidiomata immersed on host surface. c. Longitudinal section of a conidioma. d, e. Conidiogenous cells with developing conidia. f. Immature conidium. g, h. Mature conidia. i. Germinating conidium. Scale bars: c=100 μ m, d–i=20 μ m.

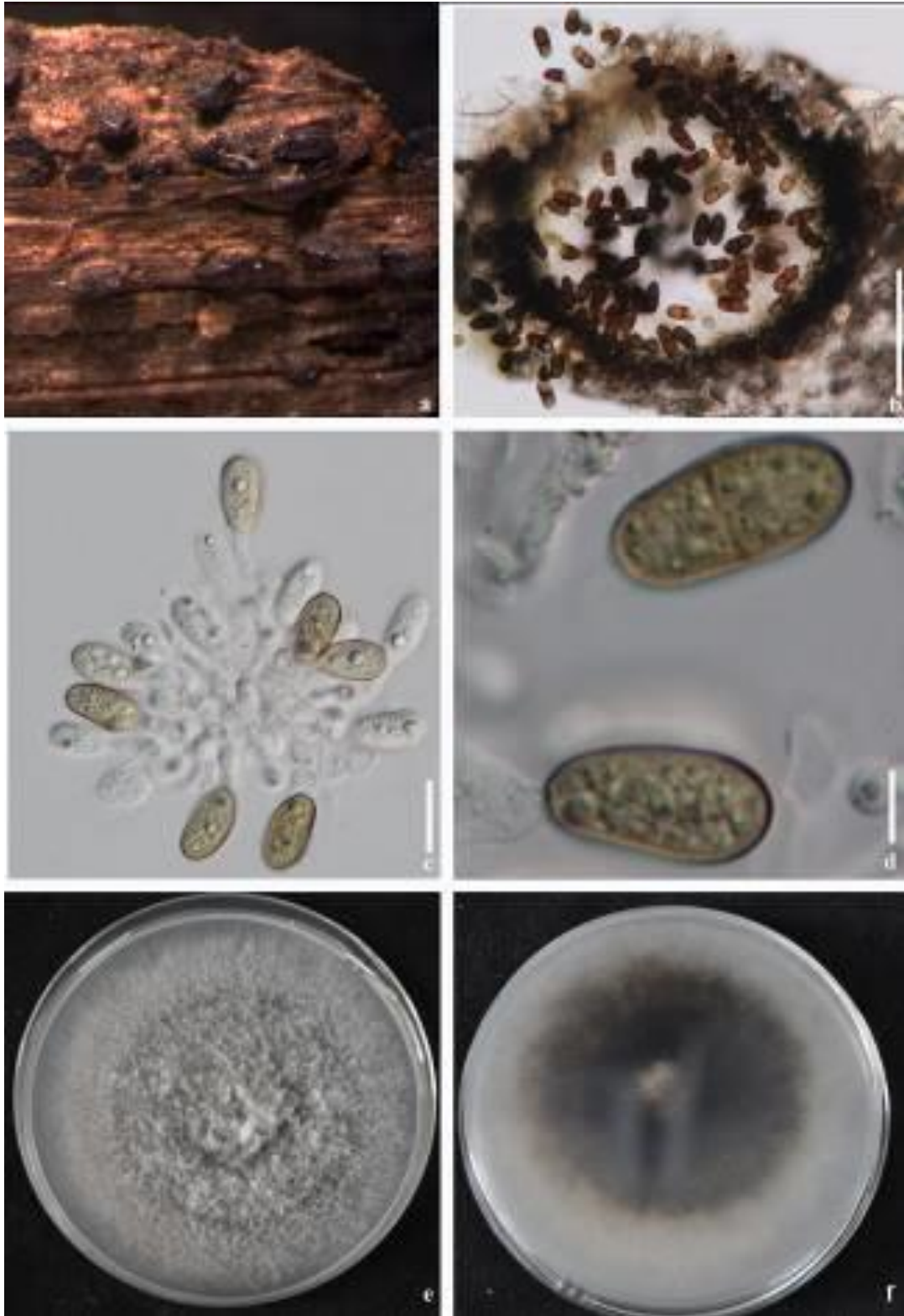


Fig. 9 – *Dothiorella sarmentorum*. a. Conidiomata immersed on host surface. b. Section of a conidioma. c. Conidiogenous cells with developing conidia. d. Mature conidia. Scale bars: b=100 μ m, c–d=20 μ m.

Neofusicoccum Crous, Slippers & A.J.L. Phillips, Stud. Mycol. 55: 247 (2006)

Neofusicoccum is morphologically similar to *Botryosphaeria*. Therefore, morphological characters cannot be used to distinguish these two genera (Phillips et al. 2013). In an updated tree for *Neofusicoccum*, our strains cluster with *Neofusicoccum italicum* and *N. parvum* (Fig. 10).

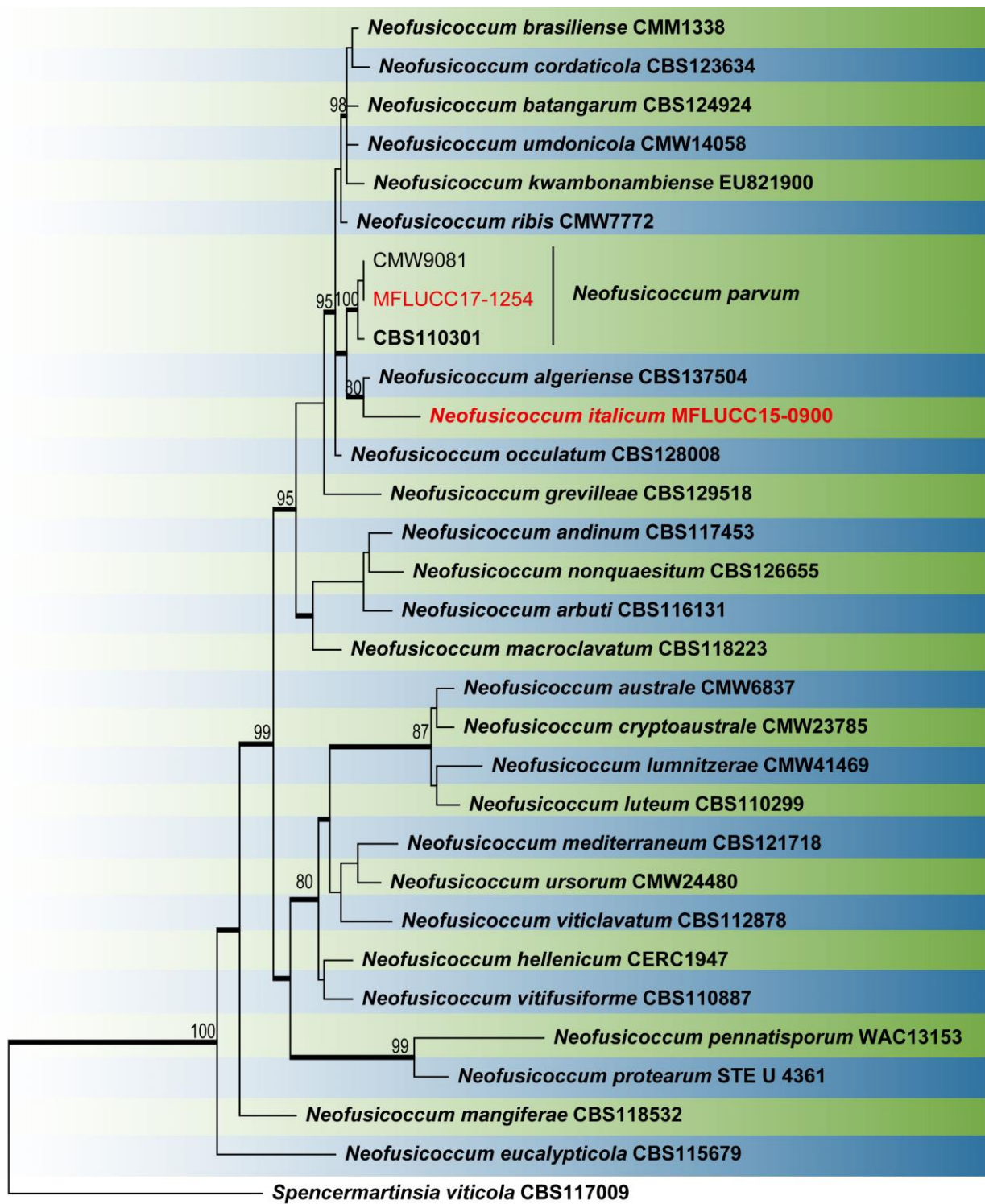


Fig. 10 – RAxML phylogram obtained from the combined ITS and TEF1 sequence data of *Neofusicoccum* species. The ex-type strains are in bold. The strains isolated in this study are shown in red. RAxML bootstrap support (BS) values $\geq 50\%$ are shown at the nodes and branches with Bayesian posterior probability scores ≥ 0.90 are given in bold. The tree is rooted with *Spencermartinsia viticola* CBS 117009.

Neofusicoccum italicum Dissan. & K.D. Hyde, in Marin-Felix et al., Stud. Mycol. 86: 170 (2017)
Facesoffungi number: FoF03820
 See Marin-Felix et al. (2017) for the description of this species.

Material examined — ITALY, Province of Forlì-Cesena, Farazzano - Forlì, on dead land branch of *Vitis vinifera*, 10 November 2016, Erio Camporesi IT 117 (MFLU 16-2872); culture, MFLUCC 15-0900.

Notes — This species have been recorded only on *Vitis vinifera* from Italy and is a saprotroph (Marin-Felix et al. 2017).

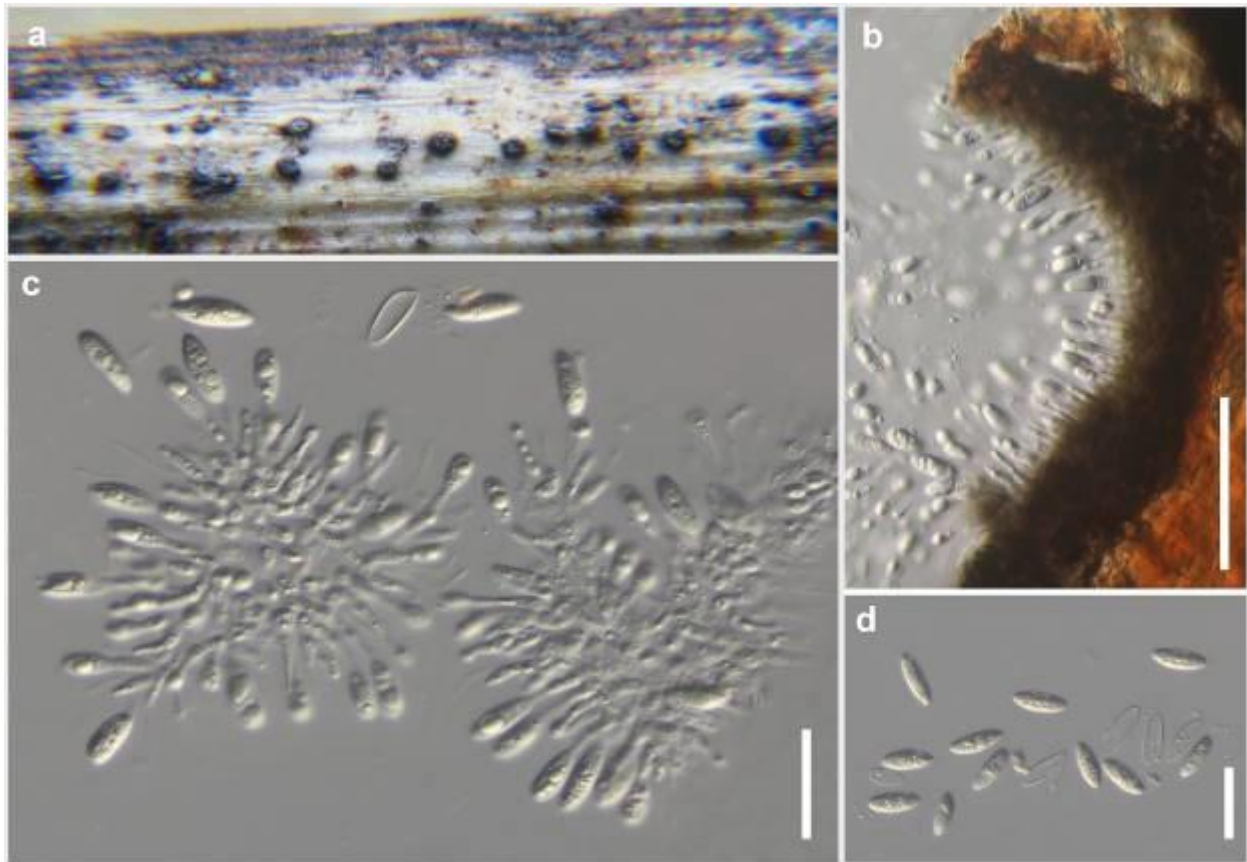


Fig. 11 – *Neofusicoccum italicum* a. Conidiomata on host substrate. b. Cross section of conidioma. c. Immature and mature conidia attached to conidiogenous cells. d. Mature conidia. Scale bars: b=100 μ m, c–d=20 μ m.

Neofusicoccum parvum (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips, in Crous, Slippers, Wingfield, Rheeder, Marasas, Phillips, Alves, Burgess, Barber & Groenewald, Stud. Mycol. 55: 248 (2006)

Facesoffungi number: FoF02411

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed (see Phillips et al. 2013 for a description). **Asexual morph:** *Conidiomata* 210–290 μ m diam., globose and apapillate to pyriform with a short, acute papilla, entire locule lined with conidiogenous cells. *Conidiogenous cells* 7–25 \times 2–4 μ m (\bar{x} =15 \times 3 μ m, n=20), holoblastic, hyaline, subcylindrical, proliferating percurrently to form 1–2 annellations, or proliferating at the same level to form periclinal thickenings. *Conidia* 12–23 \times 4–6 μ m (\bar{x} =15 \times 3 μ m, n=30), ellipsoidal with apex round and base flat, unicellular, hyaline, old conidia becoming 1–2-septate, hyaline, or light brown with the middle cell darker than the end cells.

Cultural characteristics — Colonies on PDA reaching 80 mm diam. in 5 days at 25° C. Mycelium white, flat and dense, becoming light iron-grey after 14 days, with entire margin with slightly undulate edge.

Material examined — ITALY, Province of Forlì-Cesena, Trivella di Predappio, on dead and aerial branch of *Vitis vinifera*, 9 December 2015, Erio Camporesi IT 2726 (MFLU 16-0648); culture, MFLUCC 17-1254.

Notes — *Neofusicoccum parvum* has a wide host range and a wide distribution. This species is an important pathogen of grapevine causing Botryosphaeria die back in many grape growing regions in the world (Philips et al. 2013).

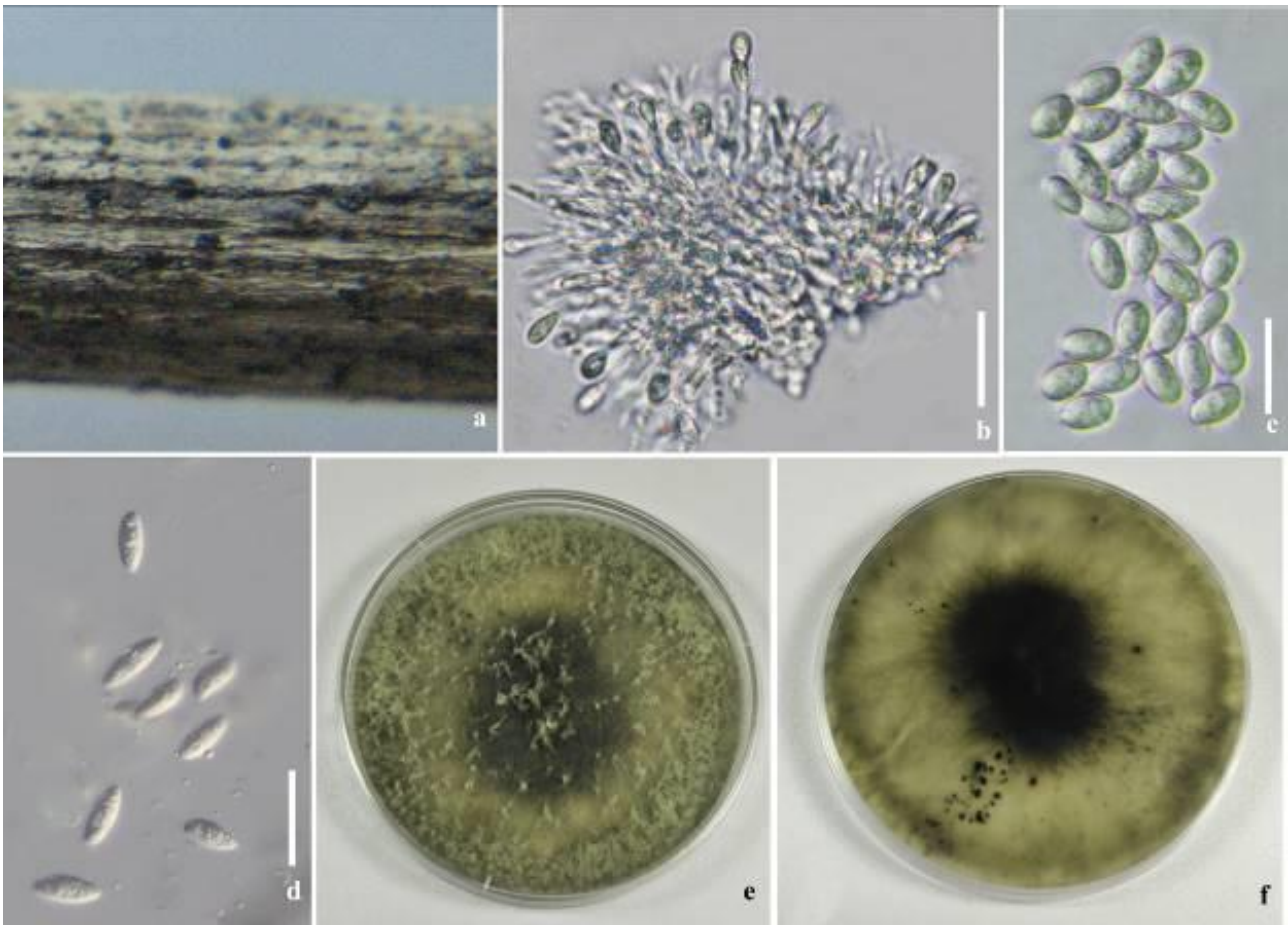


Fig. 12 – *Neofusicoccum parvum*. a. Conidiomata on host. b. Conidiogenous cells. c-d. Conidia. e. Surface view of the colony. f. Reverse view of the colony. Scale bars: b–d=10 µm.

Capnodiales Woron., Annls mycol. 23(1/2): 177 (1925)

Cladosporiaceae Nann., Repert. mic. uomo: 404 (1934)

This family is homotypic with the genus *Cladosporium*, including holomorphs with asexual hyphomycetous and their sexual “*dauidiella*” states (Hyde et al. 2013).

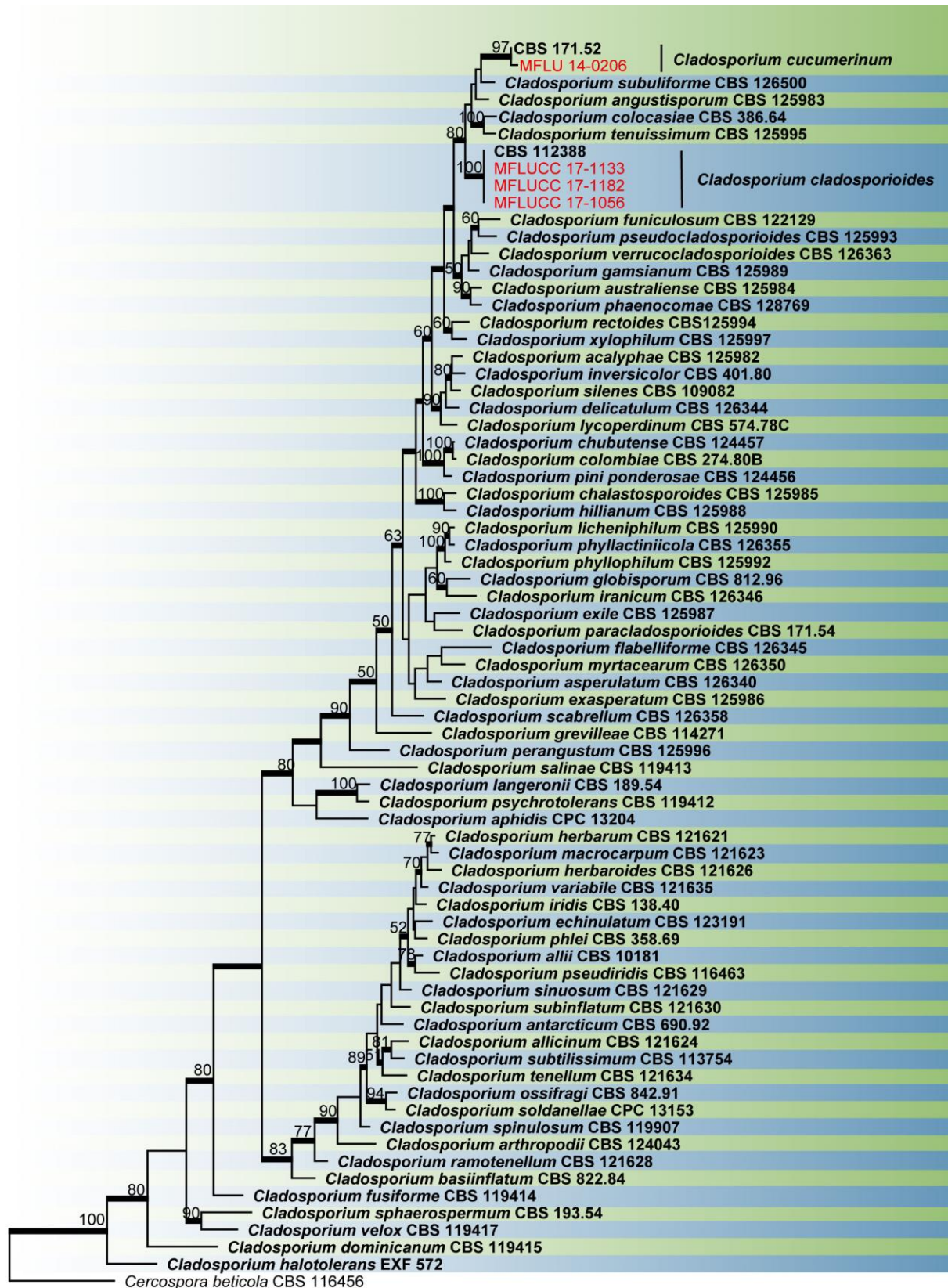
Cladosporium Link, Mag. Gesell. naturf. Freunde, Berlin 7: 37 (1816) [1815]

Cladosporium is one of the largest genera of dematiaceous hyphomycetes (Bensch et al. 2015). Members of this genus are characterized by a unique coronate structure of the conidiogenous loci and conidial hila, consisting of a central convex dome surrounded by a raised periclinal rim (Bensch et al. 2015). Species are saprotrophs, endophytes, animal, human and plant pathogens, worldwide (Seifert et al. 2011). Our strains cluster with *Cladosporium cucumerinum* and *C. cladosporioides* (Fig. 13).

Cladosporium cladosporioides (Fresen.) G.A. de Vries, Contrib. Knowledge of the Genus *Cladosporium* Link ex Fries: 57 (1952)

Faces of fungi number: FoF 03131

Saprotrophic on dead and aerial branches and roots of *Vitis vinifera*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiophores* solitary, macronematous, arising terminally from ascending hyphae, cylindrical-oblong, 40–300×3–6 µm. *Conidiogenous cells* integrated, usually terminal, cylindrical-oblong, 40 µm long, with up to four loci crowded at the apex. *Ramoconidia*



10

Fig. 13 – One of the ten most parsimonious trees obtained from a heuristic search of combined ITS, LSU and ACT sequence data of taxa from the *Cladosporium*. Parsimony bootstrap support values $\geq 75\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. The ex-type strains are in bold. The strains isolated in this study are shown in red. The tree is rooted with *Cercospora beticola* CBS 116456.

seceding at one of the upper, somewhat darkened septa, straight to slightly curved, cylindrical-oblong, 15–50×3–5 µm, with up to three septa, pale olivaceous-brown, concolorous with tips of conidiophores, smooth, base 2.5–4 µm wide, unthickened or slightly thickened, sometimes slightly refractive. *Conidia* numerous, catenate in long branched chains, small terminal conidia subglobose, obovoid or ovoid, aseptate, intercalary conidia limoniform, ellipsoid, 5–12×2–3 µm (\bar{x} =7×3, n=40).

Culture characteristics — Colonies on PDA reach 3–5 cm diam., after 5 days at 25 °C grey-olivaceous to dull green, margin regular, black, reverse black, with white feather margin.

Material examined — ITALY, Province of Forlì-Cesena, near Meldola, on dead and aerial branch of *Vitis vinifera*, 28 January 2016, Erio Camporesi IT 2809, (MFLU 16–0514), culture: MFLUCC 17–1056; CHINA, Beijing, on dead shoot of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika S. Jayawardena, culture MFLUCC 17-1113; CHINA, Yunnan, on dead root of *V. vinifera* cv. CarbanateGernischet, 11 June 2015, X.H. Li, culture: MFLUCC 17-1182.

Notes — *Cladosporium cladosporioides* is known as a saprotroph as well as a secondary invader on grapevine (Bensch et al. 2010). This species has been isolated as a pathogen causing fruit rots, as an endophyte and a saprotroph of *Vitis* sp.

Cladosporium cucumerinum Ellis & Arthur, Bull. Indiana Agric. Stat. 19: 9 (1889)

Faces of fungi number: FoF03823

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, partly immersed on the substrate, composed of septate, branched, smooth, thin-walled, subhyaline to light brown hyphae. *Conidiophores* 150–256×8–11 µm diam (\bar{x} =189×10 µm, n=100), macronematous, subhyaline to light brown, thin-walled, smooth, 0–1-septate, unbranched, straight or flexuous, cylindrical. *Conidiogenous cells* 10–16×6–7 µm (\bar{x} =11×6 µm, n=100), holoblastic, monoblastic, integrated, terminal, determinate, cylindrical to subulate, hyaline to subhyaline, rough. *Conidia* 28–52×4–6 µm (\bar{x} =45×5 µm, n=100), acrogenous, enteroblastic, phialidic, hyaline to subhyaline, 0–1-septate, subglobose, clavate, rough, thin-walled.

Material examined — ITALY, Province of Forlì-Cesena, Farazzano, on dead and aerial branch of *Vitis vinifera*, 30 January 2014, Erio Camporesi, IT 1690 (MFLU 14–0206).

Notes — *Cladosporium cucumerinum* is a well known pathogen causing scab disease of cucumber (Ogorek et al. 2012). This study provides the first record of this species as a saprotroph on *Vitis vinifera*.

Mycosphaerellaceae Lindau, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 421 (1897)

This family is recognized by having characteristic pseudothecial ascomata that are superficial or immersed (Hyde et al. 2013). Several studies have shown that *Mycosphaerellaceae* is polyphyletic (Videira et al. 2017). Videira et al. (2017) resolved the phylogenetic relationships among the genera currently recognized within this family based on morphology and multigene phylogeny.

Pseudocercospora Speg., Anal. Mus. nac. B. Aires, Ser. 3 13: 437 (1911)

This is the second largest cercosporoid genus. Many species are plant pathogens, while some are endophytes or saprotrophs (de Breejen et al. 2006). *Pseudocercospora* is a large cosmopolitan genus that is commonly associated with leaf spots and blights on a wide range of plant hosts. Species occur in a wide range of climates (Videira et al. 2017). Phylogenetic placement of this genus is well-established within the family *Mycosphaerellaceae* (Crous et al. 2013, Videira et al. 2017). Strains isolated in this study clustered with the reference specimen of *P. vitis* with high bootstrap support (Fig. 16).



Fig. 14 – *Cladosporium cladosporioides*. a. Fruiting bodies on host tissue. b. Conidiomata. c-e. Macro- and micronematous conidiophores and conidia chains. f. Secondary ramoconidia. g. Conidia. h. Upper view of colony. i. Reverse view of colony. Scale bars: b–c, e–f=50 μm , d–g=10 μm .

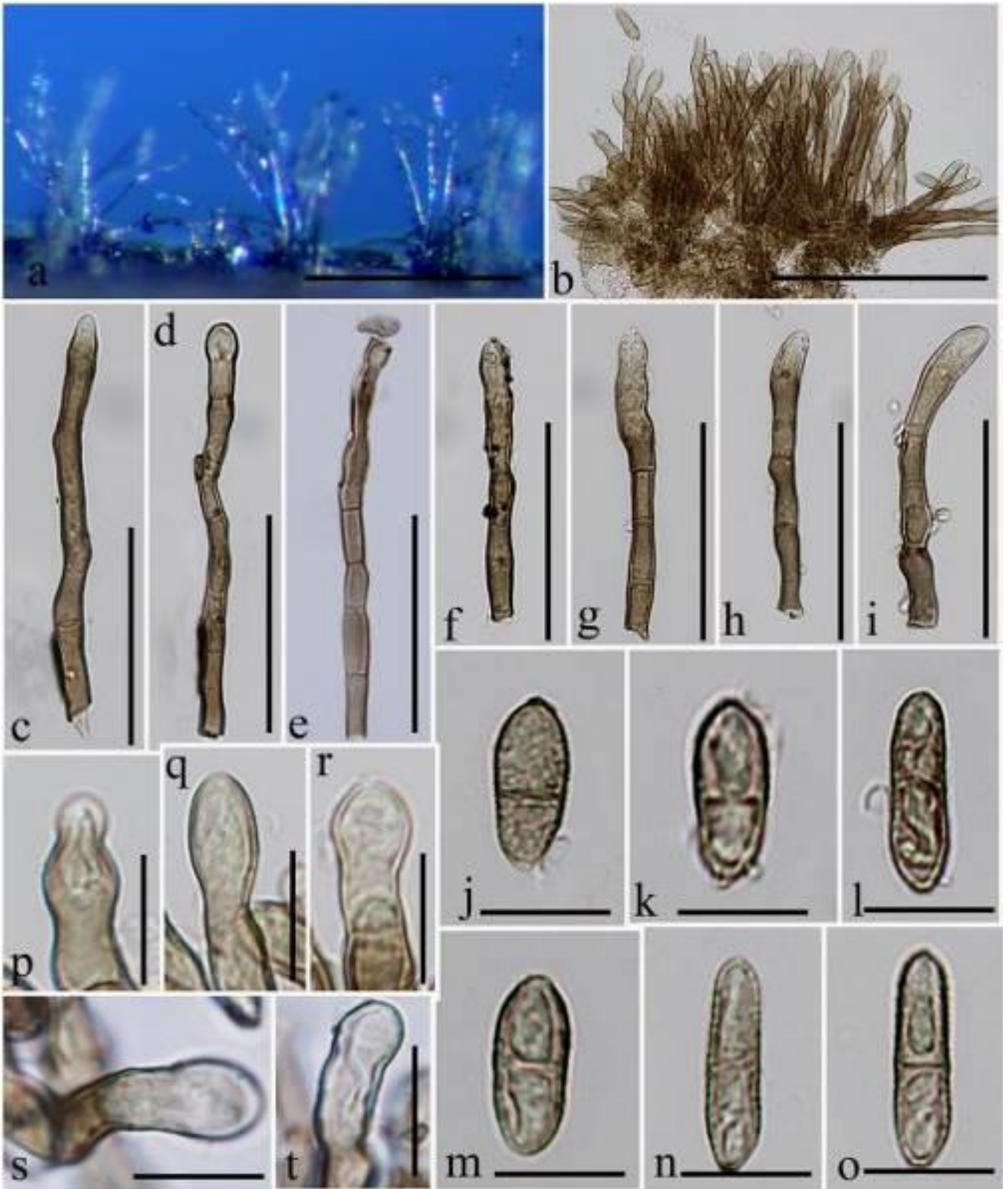


Fig. 15 – *Cladosporium cucumerinum*. a. Colonies on host tissue. b. Conidioma. c-f. Conidiophores. f-i. Conidiophores with conidiogenous cells. j-o. Conidia. p-t. Conidiogenous cells. Scale bars: a–b=500 μ m, c–i=100 μ m, j–t=50 μ m.

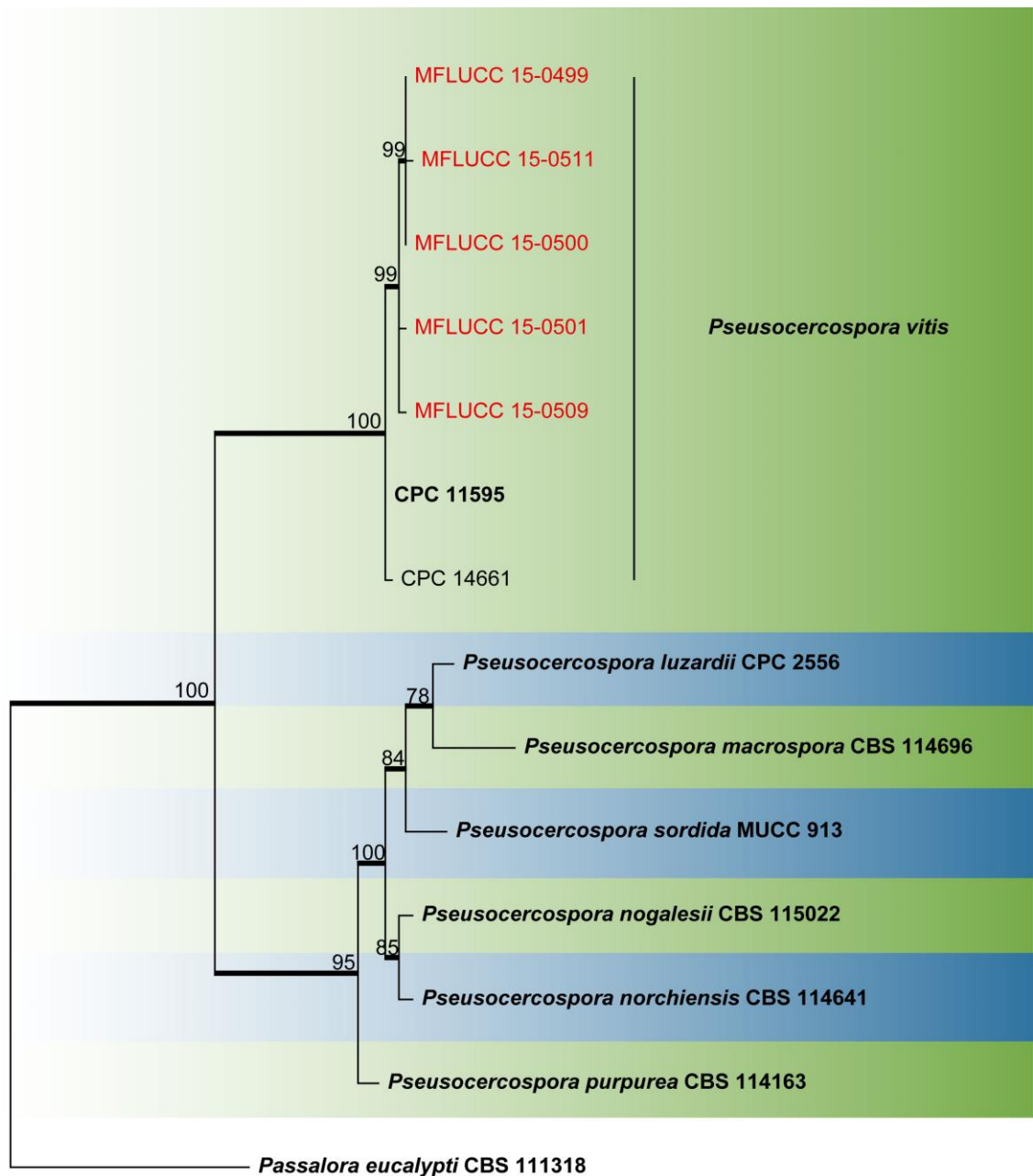


Fig. 16 – One of the ten most parsimonious trees obtained from a heuristic search of combined ITS and ACT sequence data of taxa of *Pseudocercospora*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. The ex-type strains are in bold. Strains obtained in this study are in blue. The tree is rooted with *Pseudocercospora eucalypti* CBS 111318.

Pseudocercospora vitis (Lév.) Speg., Anal. Mus. nac. B. Aires, Ser. 3 13: 438 (1911)

Facesoffungi number: FoF03597

Pathogen on leaves of *Vitis* sp. **Sexual morph:** Not observed. **Asexual morph:** *Conidiophores* 93–267 \times 2–5 μm (\bar{x} =165 \times 4 μm , n=30), synnematosus, brown, smooth, unbranched, straight to curved, sub-cylindrical. *Conidiogenous* cells up to 32 μm long, terminal, brown, smooth, proliferating sympodially. *Conidia* 17–45 \times 3–8 μm (\bar{x} =31 \times 5 μm , n=30), solitary, simple, pale to mild brown, smooth or rugulose, obclavate, apex subobtuse, base obconically truncate, straight to gently curved, 2–6-septate.



Fig. 17 – *Pseudocercospora vitis*. a. Lesions on *Vitis* sp. b-c. Conidiophores. d-f. Conidia. g. Upper view of colony after 14 days. h. Reverse view of colony after 14days. Scale bars: b–c=20 μ m, d–f=10 μ m.

Cultural characteristics — Colonies on PDA reaching 40 mm diam. after 18 days at 25° C, with undulate edge, effuse, tufted, centre greyish white becoming olivaceous brown with age, dull green towards the edge, reverse dull green.

Material examined — THAILAND, Chiang Sean, on leaves of *Vitis* sp., 7 March 2015, Ruvishika S. Jayawardena LCS04, LCS01, LSC02 (MFLU 15-0684, 15-0682, 15-0681); living culture, MFLUCC 15-0499, 15-0500 and 15-0501; THAILAND, Golden Triangle, Chiang Sean, on leaves of *Vitis* sp., 7 March 2015, K.C. Mallikarathna LGT03, LGT04 (MFLU 15-0669, 15-0668); living culture, MFLUCC 15-0511 and 15-0509.

Notes — *Pseudocercospora vitis* is a pathogen of *Vitis* sp. causing leaf spots. This species appears to be host-specific (Crous et al. 2013). *Pseudocercospora riachueli* var. *horiana* (Togashi & Katsuki) U. Braun & Crous has been recorded from Thailand, but *P. vitis* was not recorded (Pheng et al. 2013). Therefore, this study provides the first report of *P. vitis* associated with *Vitis* sp. in Thailand.

Dothideales Lindau, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 373 (1897)

Sacrotheciaceae Bonord., Abh. naturforsch. Ges. Halle 8: 82 (1864)

Species of this family are parasitic or saprobic. This family can be distinguished by having immersed to erumpent, uniloculate ascostromata and aseptate to many-septate hyaline ascospores (Thambugala et al. 2014).

Aureobasidium Viala & G. Boyer, Rev. gén. Bot. 3: 371 (1891)

This genus was introduced by Viala and Boyer (1891). Species of this genus are known to be pathogens and saprotrophs (Thambugala et al. 2014). Thambugala et al. (2014) placed this genus in the *Aureobasidiaceae*. Liu et al. (2015) synonymized this family under *Sacrotheciaceae*. Strains isolated in this study clustered together with the type strain of *Aureobasidium pullulans* (Fig. 18).

Aureobasidium pullulans (de Bary) G. Arnaud var. *pullulans*, Annales École Nat. Agric. Montpellier 16: 39, 1918

Facesoffungi number: FoF00099

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** not observed.

Asexual morph: *Conidiomata* acervular to sporodochial, amphigenous, substomatal, subepidermal, pulvinate, dry or crystalline in appearance, pale brown, discrete. *Conidiogenous cells* undifferentiated, intercalary or terminal on hyaline hyphae or arising as short lateral branches. *Conidia* 8–16×4–7 µm (\bar{x} =10×5 µm, n= 40), blastic, hyaline, smooth-walled, aseptate, straight, ellipsoidal to sphaerical, reniform to sickle-shaped, sometimes cylindrical with obtuse ends and occasionally with a slightly truncate base, rather variable in shape and size.

Culture characteristics — Colonies on PDA attaining 30mm diam. at 25° C after 7 d appearing smooth and slimy due to abundant sporulation. No aerial mycelium. Pink to yellow culture, yellow to light yellow in reverse view. After 14days black sectors composed of dark pigmented hyphae.

Material examined — ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 15 February 2015, Erio Camporesi IT 2378 (MFLU 15-1084); culture, MFLUCC 17-1218; ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 16 February 2015, Erio Camporesi IT 2382 (MFLU 15-1086); living culture, MFLUCC 17-1221, MFLUCC 17-1222; ITALY, Province of Forlì-Cesena, near Meldola, on dead and aerial branch of *Vitis vinifera*, 2 February 2016, Erio Camporesi IT 2800 (MFLU 16-0652) culture, MFLUCC 17-1256; ITALY, Province of Forlì-Cesena, Tessello - Cesena, on dead and aerial branch of *Vitis vinifera*, 5 March 2015, Erio Camporesi IT 2404 (MFLU 15-3513), culture, MFLUCC 17-1231; ITALY, Province of Forlì-Cesena, Farazzano - Forlì, on dead and aerial branch of *Vitis vinifera*, 10 November 2016, Erio Camporesi IT 3146 (MFLU 16-2813).

Notes — Isolates found in this study are morphologically similar to the type species of *A. pullulans* and phylogenetic analysis of combined LSU, SSU and ITS gene regions clustered them with *A. pullulans* (Fig.17). *Aureobasidium pullulans* has been recorded as an endophyte on *Vitis* sp. (Mulencko et al. 2008, Gonzalez & Tello 2011, Sanoamuang et al. 2013, Fischer et al. 2016). This study provides the first record of this species as a saprotroph on *V. vinifera* in Italy.

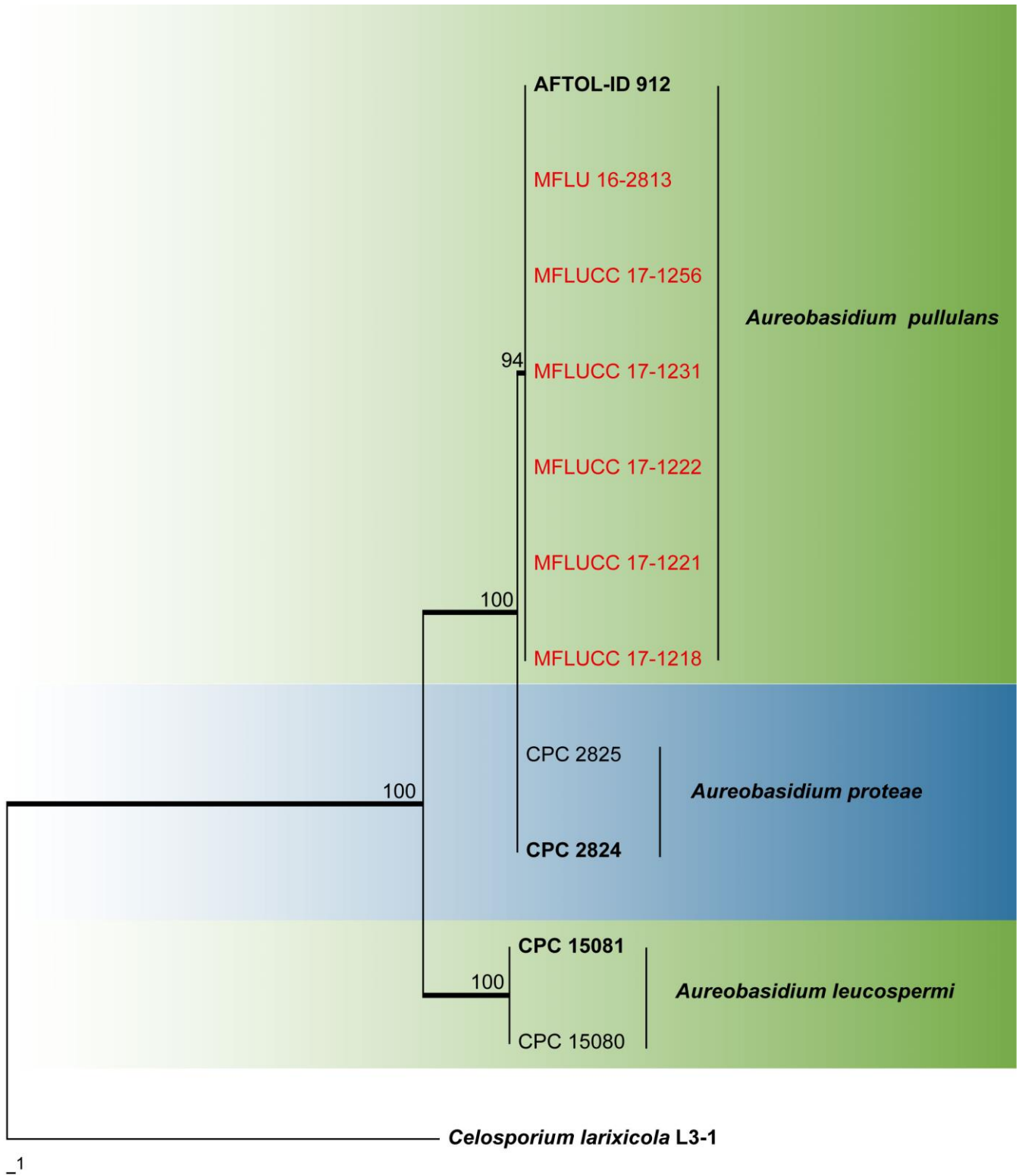


Fig. 18 – One of ten most parsimonious trees obtained from a heuristic search of combined LSU, SSU and ITS sequence data of taxa of *Aureobasidium*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Celosporium larixicola* L3-1.

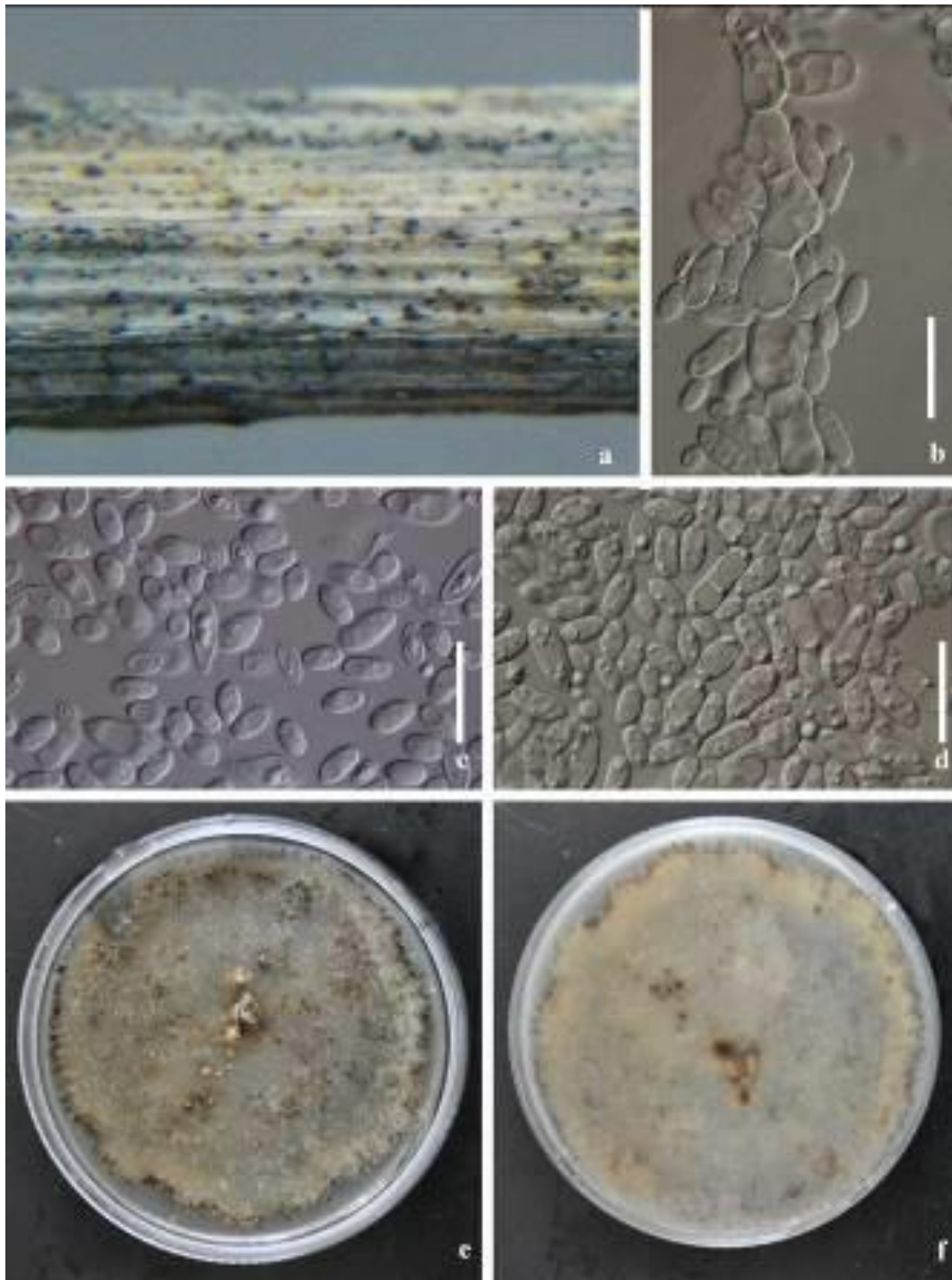


Fig. 19 – *Aureobasidium pullulans*. a. Fruiting bodies on host tissue. b. Conidiophore and conidiogenesis. c-d. Conidia. e. Surface view of colony after 7 weeks. f. Reverse view of colony after 7 weeks. Scale bars: b–d=10 μ m.

Pleosporales Luttr. ex M.E. Barr, Prodr. Cl. Loculoasc. (Amherst): 67 (1987)

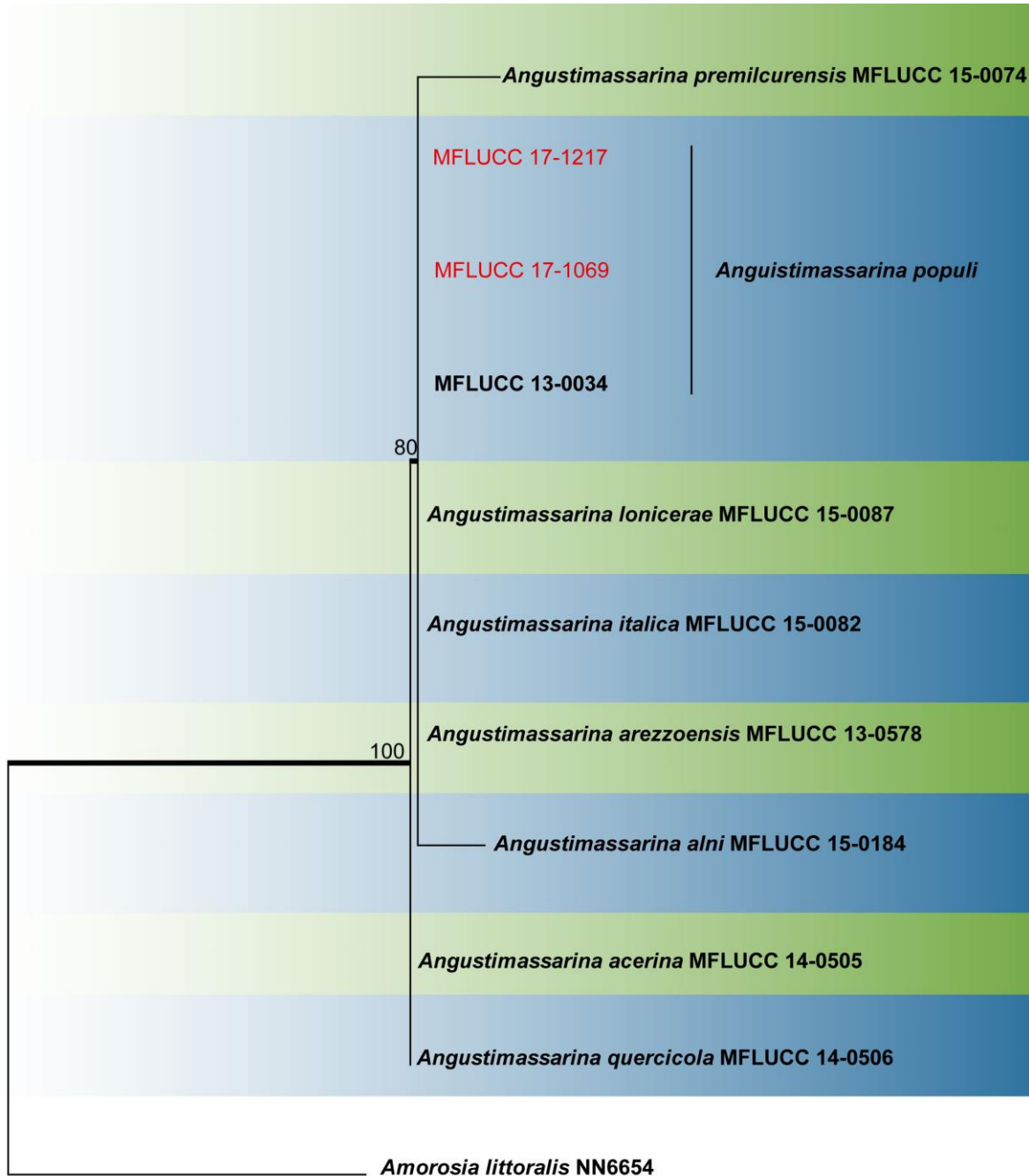
Amorosiaceae Thambugala & K.D. Hyde, in Thambugala et al., Fungal Diversity: 10.1007/s13225-015-0348-3, [54] (2015)

Amorosiaceae was introduced by Thambugala et al. (2015). This family is characterized by hyphomycetous asexual morphs and appears to grow within ascomata of other ascomycetes (Thambugala et al. 2015). Currently this family comprises two genera. An updated family tree is

provided in Hyde et al. (2017), while in this paper a tree to show the placement of our isolates is given (Fig. 20).

Angustimassarina Thambug., Kaz. Tanaka & K.D. Hyde, in Thambugala et al., Fungal Diversity: 10.1007/s13225-015-0348-3, [55] (2015)

Species of this genus are considered to be mainly fungicolous and appear to grow within ascomata of other ascomycetes. Currently there are eight species in the genus (Index Fungorum, 2018).



¹
Fig. 20 – One of the eight most parsimonious trees obtained from a heuristic search of combined ITS, LSU, SSU and TEF1 sequence data of taxa from the *Angustimassarina*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Amorosia littoralis* NN 6654n.

Angustimassarina populi Thambug. & K.D. Hyde, in Thambugala et al., Fungal Diversity: 10.1007/s13225-015-0348-3, [56] (2015)

Facesoffungi number: FoF01086

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** *Ascomata* 150–170 µm high, 110–120 µm (\bar{x} =160×138 µm, n=10) diam., solitary, immersed, becoming erumpent, coriaceous, black, globose to subglobose, uniloculate, ostiolate. *Ostiole* crest-like, rounded, papillate, with a pore-like opening. *Peridium* 13–30 µm (\bar{x} =21 µm, n=10) wide, composed of dark brown to hyaline cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, septate, unbranched, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 82–95×9–14 µm (\bar{x} =88×12 µm, n=20), 8-spored, bitunicate, fissitunicate, cylindrical, pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 18–24×3–6 µm (\bar{x} =21×4 µm, n=20), uni- to bi-seriate, partially overlapping, hyaline, fusiform, 1-septate, constricted at the septum, filled with a different sized guttule in each cell, surrounded by a mucilaginous sheath. **Asexual morph:** Not observed.

Culture characteristics — Colonies on PDA attaining 45 mm diam. Mycelium well developed, superficial. Chlamydospores not observed. At 25° C, after 5 weeks, flat, greyish brown, with reverse dark greyish, with crenate edge.

Material examined — ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 15 February 2015, Erio Camporesi IT 2378 (MFLU 15-1083); culture, MFLUCC 17-1217; ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 21 February 2015, Erio Camporesi IT 2383 (MFLU 15-3508); culture, MFLUCC 17-1069.

Notes — This species is morphologically similar to *A. populi* and in the phylogenetic analysis of combined ITS, LSU, SSU and TEF1 sequence data, the isolates cluster with *A. populi* (Fig. 20). This study provides the first report of *A. populi* from *Vitis* species.

Didymellaceae Gruyter, Aveskamp & Verkley, Mycol. Res. 113(4): 516 (2009)

This family was introduced to accommodate *Didymella* and phoma-like genera (Tibpromma et al. 2017). *Didymellaceae* consists of pathogens, endophytes and saprotrophs of many hosts (Chen et al. 2015). Chen et al. (2015) revised the family based on multi-gene (ITS, LSU, RPB2 and tub2) phylogenetic analysis and morphological observations.

Didymella Sacc., Michelia 2(no. 6): 57 (1880)

Didymella is a poorly understood genus and appears to be polyphyletic. Chen et al. (2015) amended this genus to accommodate *Peyronellaea* and several other associated phoma-like species. Most species in this genus produced chlamydospores in culture. A phylogenetic tree showing the placement of our strains is given (Fig. 22).

Didymella negeriana (Thüm.) Q. Chen & L. Cai, in Chen, Jiang, Zhang, Cai & Crous, Stud. Mycol. 82: 178 (2015)

Facesoffungi number: FoF 03830

Opportunistic pathogen on stems of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* on PDA 75–200 µm (\bar{x} =120 µm, n=10) diam., pycnidial, solitary or confluent, scattered, globose or irregular, glabrous, initially citrine-honey to sienna-olivaceous, but later turn black. *Pycnidial wall* thin-layered, pigmented. Conidial exudate saffron to pale vinaceous. *Conidiogenous cells* 6–10×3–7 µm (\bar{x} =8×5 µm, n=20), hyaline, smooth-walled, globose to bottle-shaped. *Conidia* 5–7×3–5 µm (\bar{x} =6×3µm, n=30), ellipsoid to oblong, straight or slightly curved, initially hyaline, smooth-walled, acutely rounded at both ends, with several guttules.

Culture characteristics — Colonies on PDA, regular, floccose to woolly, circular, smoke grey aerial mycelium on the surface, reverse olivaceous grey, slow growing, reach 5 cm diam. after 7 days at 20 °C.

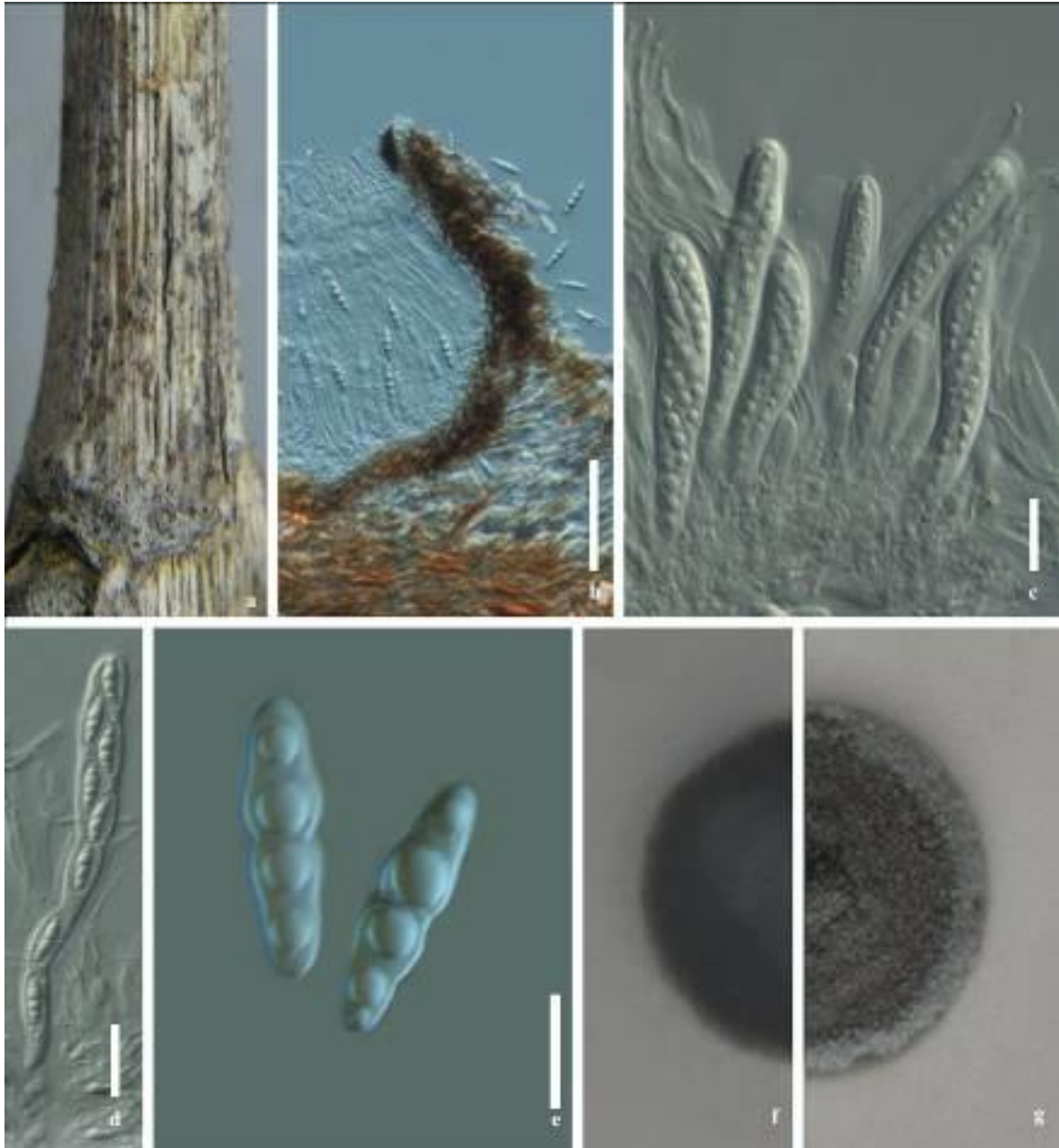


Fig. 21 – *Angustimassarina populi*. a. Appearance of immersed ascomata on host surface. b. Section through ascoma. c. Immature asci. d. Mature bitunicate ascus. e. Ascospores. f, g. Culture on PDA. Scale bars: b=100 μ m, c–d=20 μ m, e=10 μ m.

Material examined — ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 16 February 2016, Erio Camporesi (MFLU 15–1086), ex-type living culture, MFLUCC 16–1394.

Notes — According to our phylogenetic analyses of combined LSU, ITS, RPB2 and β -tubulin sequence data of *Didymella* species (Fig. 22), our isolates cluster together in a well-defined clade with *Didymella negriana* (CBS 358.71) with relatively high bootstrap and Bayesian probabilities (100% MP/1.00 PP). This species has been reported as a common opportunistic pathogen associated with disease symptoms on leaves, fruits, and stems of *Vitis vinifera* in southern Europe. The pathogen is often misidentified as *Phoma viticola* (currently known as *Diaporthe ampelina*), another pathogen of grapevine (de Gruyter et al. 1998).

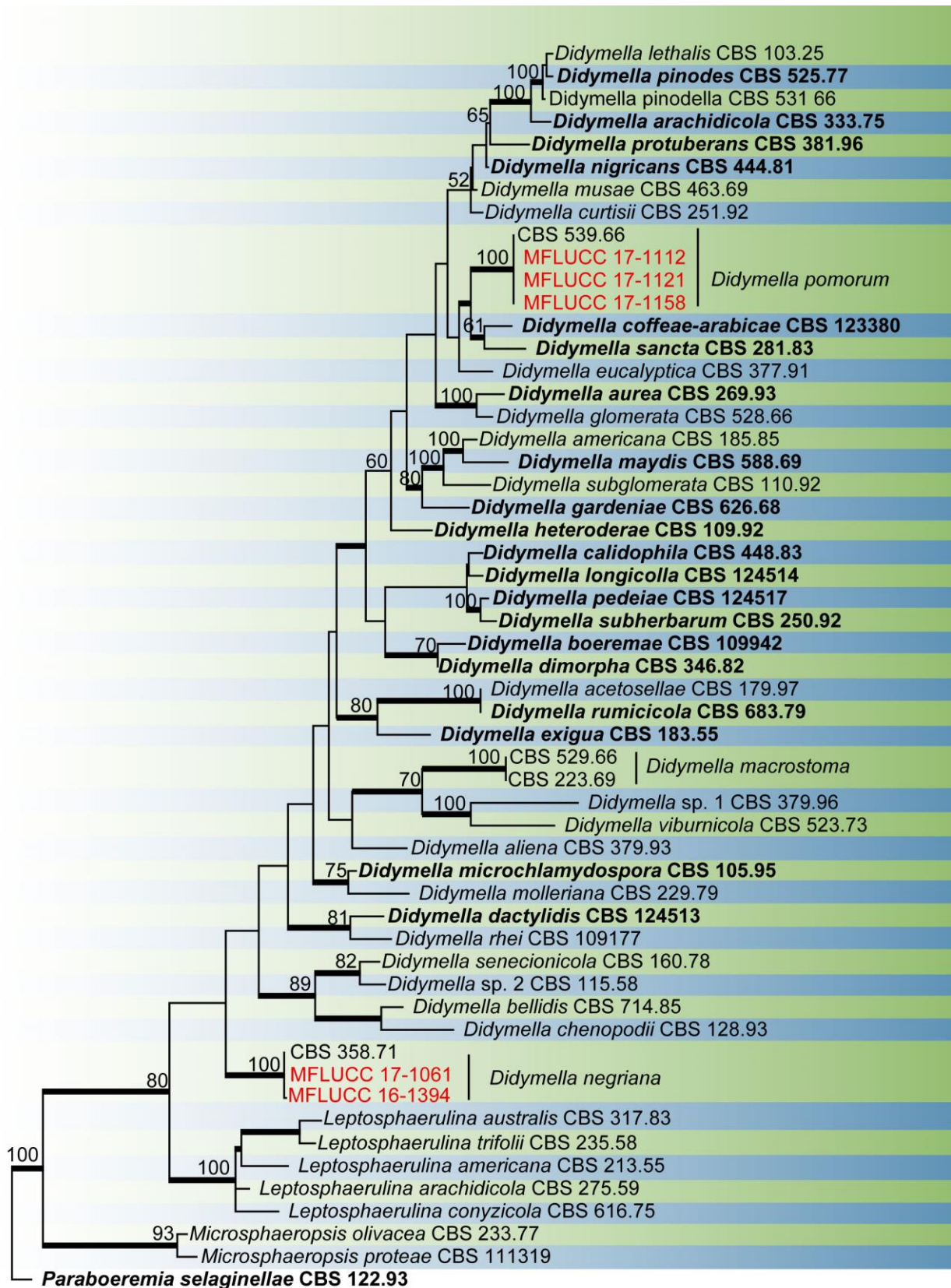


Fig. 22 – One of the equally most parsimonious trees obtained from combined analyses set of LSU, ITS, RPB2 and β -tubulin sequence data for *Didymella* species. MP values (>70 %) resulting from 1000 bootstrap replicates and Bayesian posterior probabilities above 0.95 are given at the nodes. The tree is rooted to *Paraboeremia selaginellae* (CBS 122.93). Ex-type strains are in bold and species from the current study are in red.

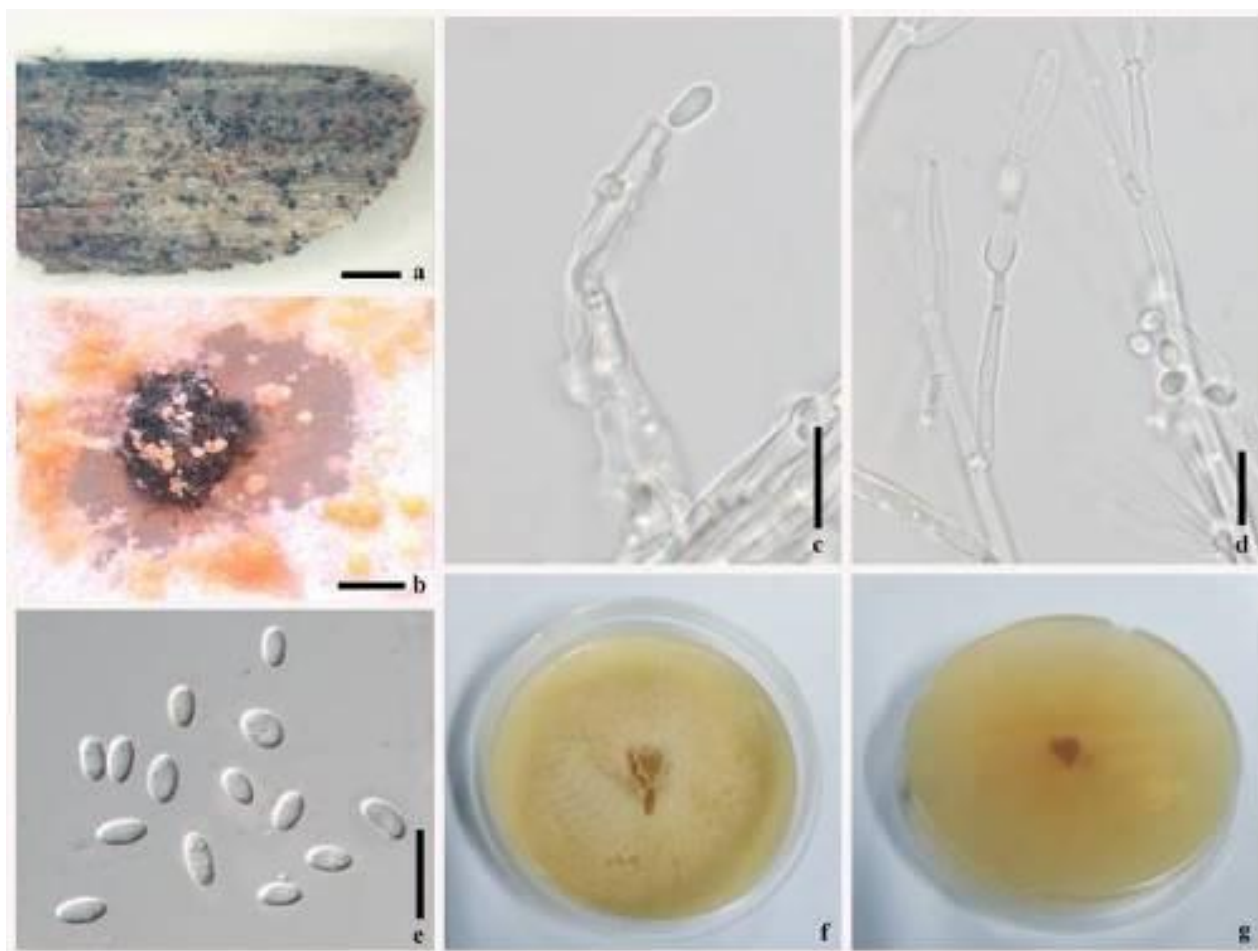


Fig. 23 – *Didymella negeriana*. a. Host tissue from which the species was isolated b. Saffron to pale vinaceous conidial mass on PDA c. Conidiogenesis d. Hyphae e. Conidia f–g. Upper view (f). and reverse view (g). of colony on PDA. Scale bars: a=1 mm, b=2 mm, c–e=10 μ m.

Didymella pomorum (Thüm.) Q. Chen & L. Cai, Stud. Mycol. 82: 179 (2015)

Facesoffungi number: FoF 03829

Saprotrophic on dead root, shoot and leaves of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Pycnidia* mostly 100–200 μ m diam., usually subglobose-ampulliform with a distinct ostiole, and often furrowed surface, solitary, but frequently confluent in groups up to 1000 μ m diam. Conidial exudate usually whitish to cream, often later darkening to olivaceous brown. Fertile micropycnidia frequently occur. *Conidia* 4–8 \times 2–3 μ m (\bar{x} =6 \times 2 μ m, n=40), variable in shape and dimensions, mostly ovoid-ellipsoidal, frequently with one large guttule and several smaller ones, hyaline, but with age becoming light brown. *Chlamydospores* solitary or in long chains or as dictyochlamydospores.

Culture characteristics — Colonies on PDA, regular, floccose to woolly, circular, smoke grey aerial mycelium on the surface, pale to olivaceous at centre, white at edge, with reverse brownish to blackish beneath dense mycelium, reaching 5 cm diam. after 7 days at 25 °C.

Material examined — CHINA, Beijing, on dead root of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17–1112; CHINA, Beijing, on dead shoot of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17–1121; CHINA, Beijing, on dead leaves of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17–1158.

Notes — *Didymella pomorum* has been recorded as a saprotroph from *Dendrobium fimbriata*, *Gentiana stramineae*, *Heracleum dissectum*, *Polygonum tataricum* and *Triticum* sp. (Chen et al. 2017). This study provides the first report of this species associated with *Vitis* species.

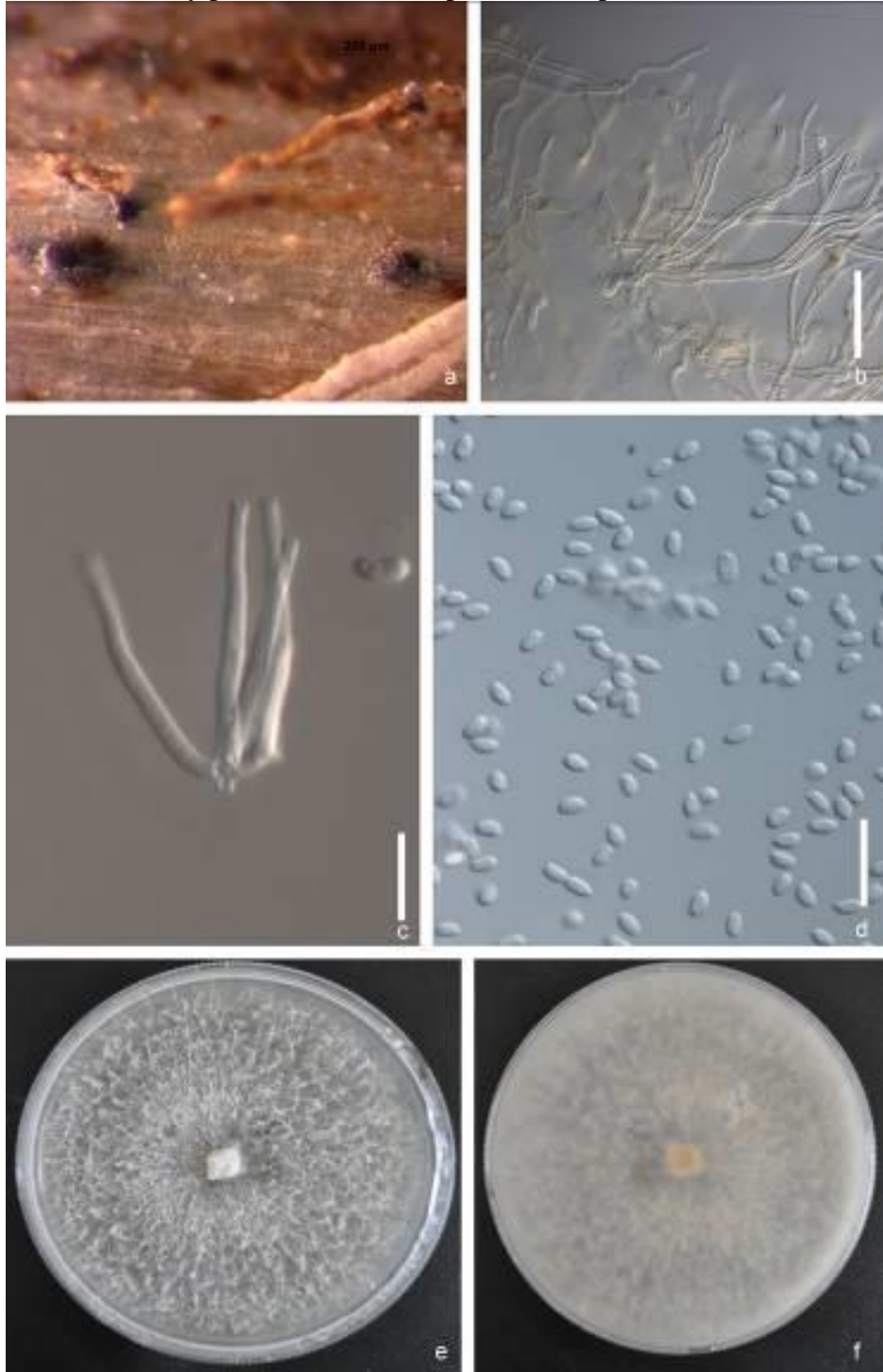
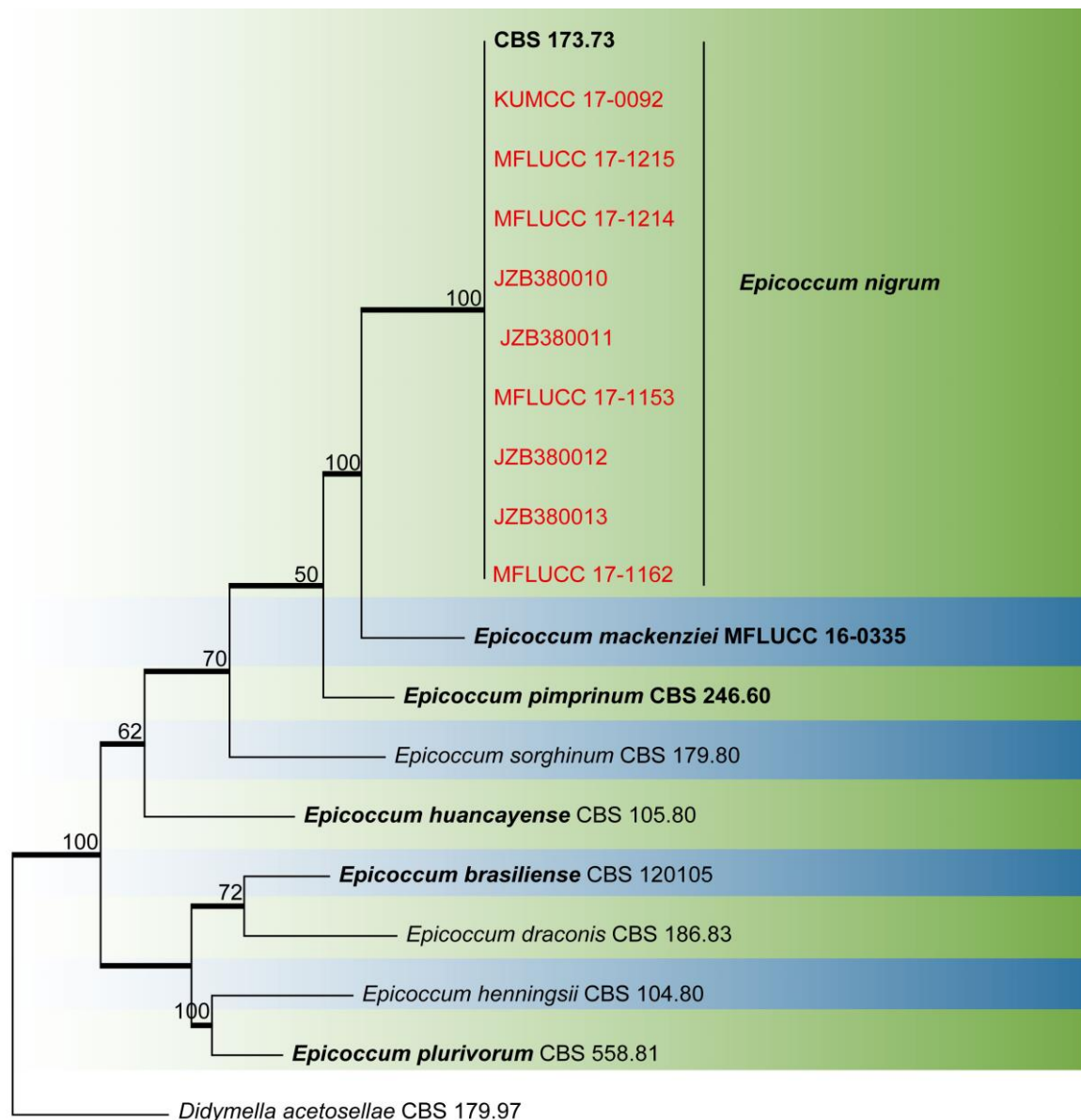


Fig. 24 – *Didymella pomorum*. a. Host tissue from which the species was isolated b. Hyphae c. Conidiophores d. Conidia e. Upper view of colony on PDA after 7 days f. Reverse view of colony on PDA after 7 days. Scale bars: b–d=10 µm.

Epicoccum Link, Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816) [1815]

This genus belongs in the *Didymellaceae* (Aveskamp et al. 2010) and is characterized by epicoccoid and sub-cylindrical conidia (Chen et al. 2015). According to the combined gene phylogenetic analysis of LSU, ITS, RPB2 and β -tubulin sequence data, our strains clustered with *E. nigrum*, a common saprotroph associated with *Vitis* species (Fig. 25).



¹⁰
Fig. 25 – One of the eight most parsimonious trees obtained from a heuristic search of combined LSU, ITS, RPB2 and β -tubulin sequence data of taxa of *Epicoccum*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Didymella acetosellae* CBS 179.97.

Epicoccum nigrum Link, Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816) [1815]

Facesoffungi number: FoF02685

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 250–700 μm (\bar{x} =500 μm , n=10), pycnidial, mainly solitary, globose to irregularly shaped. *Pycnidial wall* pseudoparenchymatous, composed of 5–9 layers, outer wall olivaceous brown. *Conidiogenous cells* 4–5 \times 3–4 μm (\bar{x} =2 \times 3 μm , n=20), phialidic, hyaline, smooth, globose to flask-shaped. *Conidia* 3–6 \times 1–3 μm (\bar{x} = 4 \times 2 μm , n=84), hyaline, unicellular, ovoid, ellipsoidal to oblong, or sub-cylindrical. *Chlamydospores* 7–21 \times 6–16 μm (\bar{x} =12 \times 10 μm , n=20), multicellular, globose or irregularly shaped, dictyosporous, solitary or in chains, smooth, verrucose, pale brown to dark brown.

Culture characteristics — Colonies on PDA reaching 65–75 mm in 7 days at 25 °C entire margin, immersed mycelium completely covered by a mycelial mat which is densely floccose, bright yellow, reverse with orange center, becoming yellow towards the margin.

Material examined — ITALY, Province of Forlì-Cesena, near Pieve di Rivoschio, on dead and aerial branch of *Vitis vinifera*, 2 February 2015, Erio Camporesi IT 2363-3a, IT 2363-3b, (MFLU 15-1082); culture, MFLUCC 17-1214 and 17-1215; ITALY, Province of Forlì-Cesena, Fiumana - Predappio, on dead and aerial branch of *V. vinifera*, 13 February 2016, Erio Camporesi IT 2831-L, (MFLU 16-0879); culture, KUMCC 17-0092; CHINA, Beijing, on dead leaves of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika S. Jayawardena, culture JZB380010; CHINA, Beijing, on dead leaves of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika S. Jayawardena, culture JZB380011; CHINA, Beijing, on dead shoots of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika S. Jayawardena, culture JZB380012; CHINA, Beijing, on dead shoots of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika S. Jayawardena, culture JZB380013.

Notes — *Epicoccum nigrum* is a common saprotroph that can be found on many hosts (Aveskamp et al. 2010). This species has been recorded to be associated with *Vitis* sp. as an endophyte as well as a saprotroph in Spain and Switzerland (Gonzales & Tello 2011, Garcia Benavides et al. 2013, Casieri et al. 2009). There are no records of *E. nigrum* associated with *Vitis* sp. in China or Italy in the SMML database.

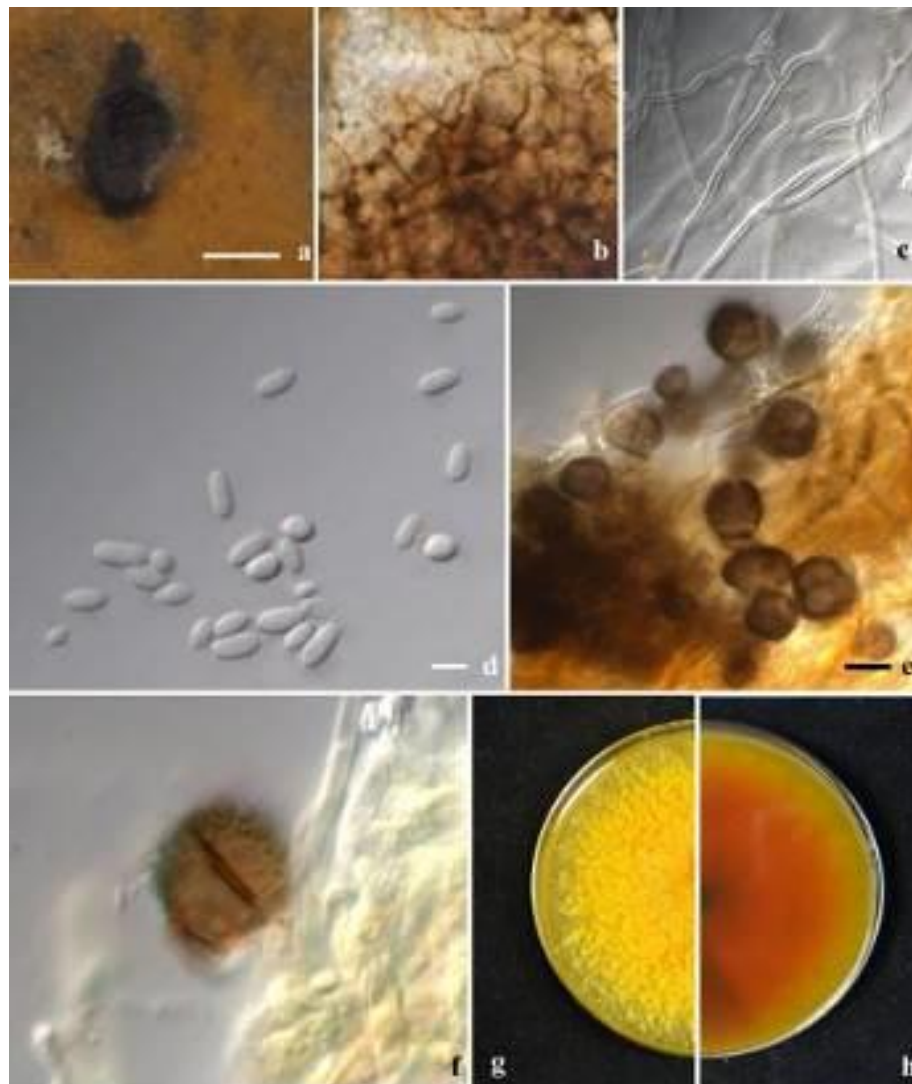


Fig. 26 – *Epicoccum nigrum*. a. Pycnidium. b. Section of pycnidial wall. c. Septate, branching hyaline to olivaceous-grey hyphae. d. Conidia. e–f. Chlamydospores. g. Upper view of 7 day old culture. h. Reverse view of 7 day old culture. Scale bars: a=50 µm, e=20 µm, d=10 µm scale bar of d applies to f, and scale bar of e applies to b–c.

Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953)

Didymosphaeriaceae was introduced to accommodate species with 1-septate ascospores and trabeculate pseudoparaphyses (Liew et al. 2001, Ariyawansa et al. 2014, Tibpromma et al. 2017). Ariyawansa et al. (2014) synonymized *Montagnulaceae* under *Didymosphaeriaceae*. This family consists of saprotrophs, endophytes and pathogens.

Pseudocamarosporium Wijayaw. & K.D. Hyde, in Wijayawardene, Hyde, Bhat, Camporesi, Schumacher, Chethana, Wikee, Bahkali & Wang, Cryptog. Mycol. 35(2): 185 (2014)

Pseudocamarosporium was established by Wijayawardene et al. (2014b) for some camarosporium-like species grouping in *Didymosphaeriaceae*. This genus shows similar conidial morphology with *Camarosporium sensu stricto*, but differs in having paraphyses and microconidia (Wijayawardene et al. 2014b). We collected *P. propinquum* associated with dead branches of *Vitis vinifera* in Italy and it matched the epitype description (Wijayawardene et al. 2014b) and clustered together with the ex-type strain (Fig. 27).

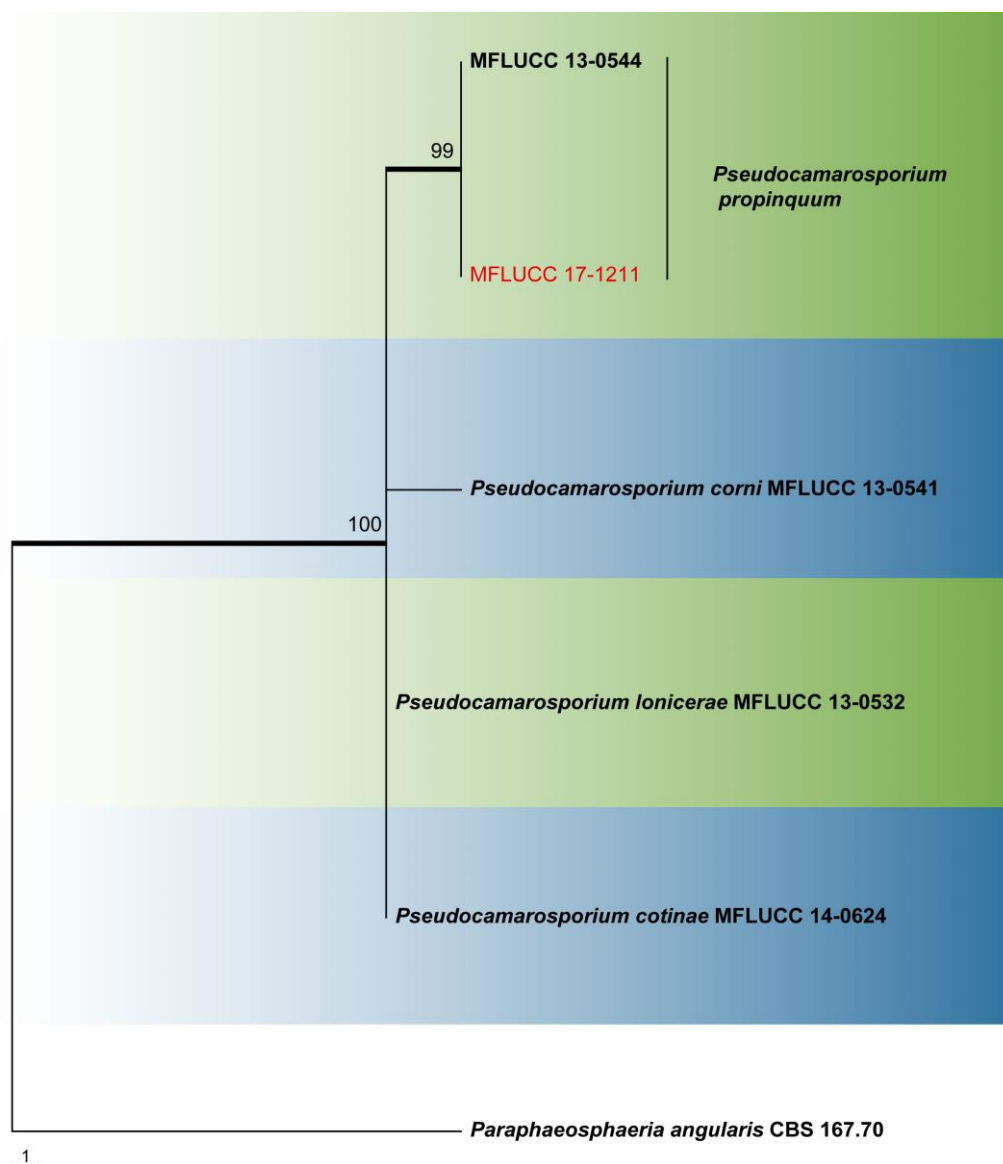


Fig. 27 – One of the ten most parsimonious trees obtained from a heuristic search of combined LSU, SSU and ITS sequence data of taxa of *Pseudocamarosporium*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Paraphaeosphaeria angularis* CBS 167.70.

Pseudocamarosporium propinquum (Sacc.) Wijayaw., Camporesi & K.D. Hyde, in Wijayawardene, Hyde, Bhat, Camporesi, Schumacher, Chethana, Wikee, Bahkali & Wang, Cryptog. Mycol. 35(2): 191 (2014)

Facesoffungi number: FoF02162

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiomata* pycnidial 350–580 μm diam, 100–180 μm high (\bar{x} =465 \times 168 μm , n=10), solitary, scattered, black, immersed to sub-immersed, sub-globose or irregular in shape, ostiolate. *Pycnidial wall* 15–30 μm , multi-layered, with inner most thin, hyaline layer, with 3–5 outer layers of brown-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–16 \times 6–7 (\bar{x} =13 \times 6 μm , n=20), with percurrent phialidic development, smooth, short, hyaline, formed from the inner layer of the pycnidial wall. *Conidia* 10–14 \times 6–8 μm (\bar{x} =12 \times 4 μm , n=40), oblong to ellipsoidal, initially hyaline, aseptate, becoming muriform, with 3 transverse septa and 1–2 longitudinal septa, pale brown to dark brown, smooth-walled.

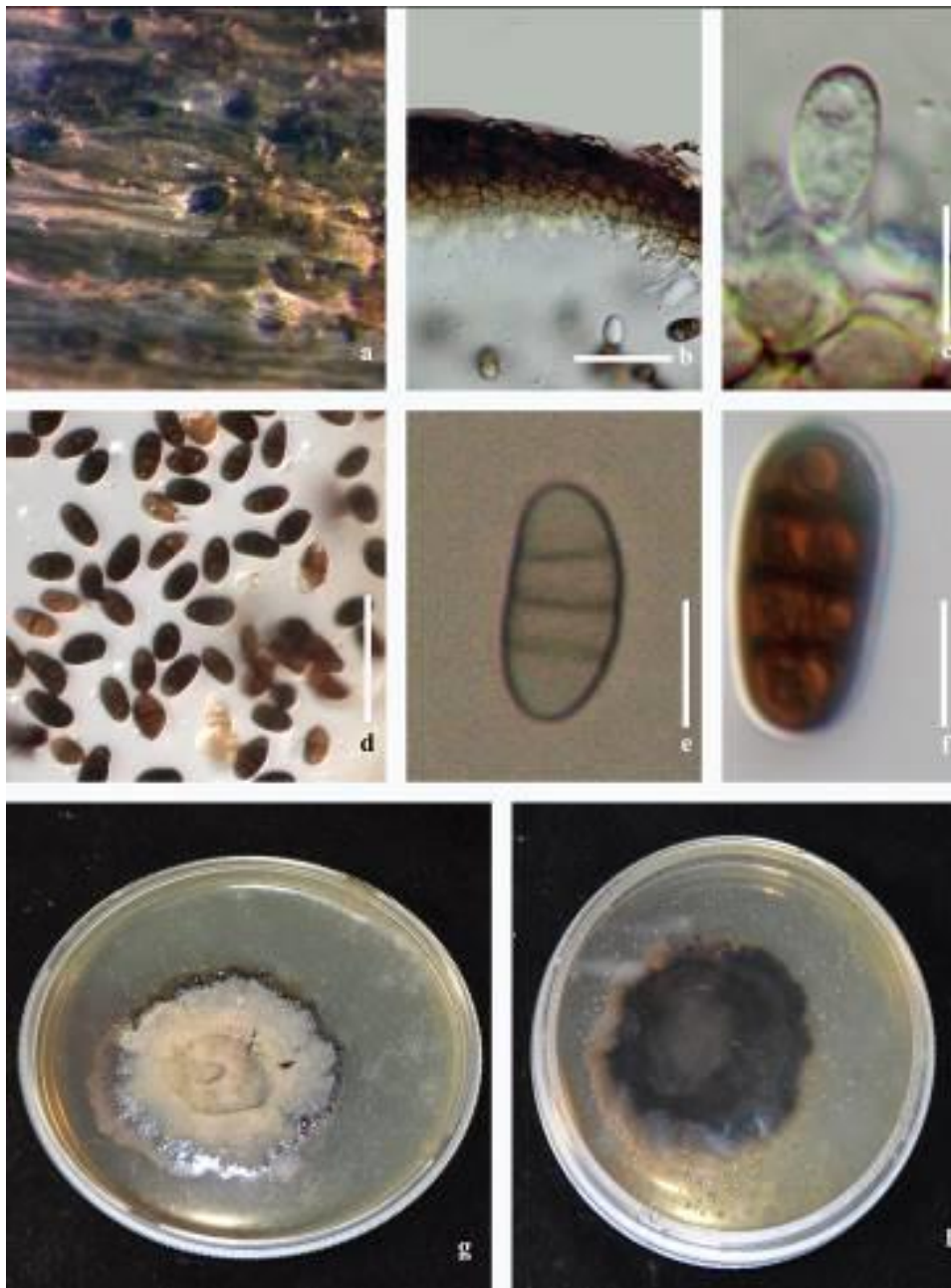


Fig. 28 – *Pseudocamarosporium propinquum* a Conidiomata on host tissue. b Cell wall of conidioma. c Conidiogenous cell. d-f Conidia. g Upper view of 14 day old culture. h Reverse view of 14 day old culture. Scale bars b=50 μm , c-f=10 μm .

Culture characteristics — Colonies on PDA at 25 °C reaching 50 mm after 14 days, circular, flat, moderately dense, surface greenish olivaceous, white at the margin, becoming dark olive, reverse black, entire to slightly undulate edge.

Material examined — ITALY, Forlì-Cesena Province, Tontola - Predappio, on dead and aerial branch of *Vitis vinifera*, 11 April 2016, E. Camporesi, IT 2931 (MFLU 16-1167); culture, KUMCC 17-0041, MFLUCC 17-1282. ITALY, Province of Forlì-Cesena, near Pieve di Rivoschio, on dead and aerial branch of *V. vinifera*, 2 February 2015, Erio Camporesi IT 2363 (MFLU 15-1082); living culture, MFLUCC 17-1211.

Notes — There are no previous records of the genus *Pseudocamarosporium* on *Vitis* sp. Therefore, we provide the first report of this species associated with *Vitis vinifera* in Italy as well as in the world.

Lophiostomataceae Sacc. [as 'Lophiostomaceae'], Syll. fung. (Abellini) 2: 672 (1883)

Based on the formation of a slit-like ostiolar opening on a laterally compressed papilla, Nitschke (1869) introduced *Lophiostomataceae*. This family was designated as a separate family in the Pleosporales by Saccardo (1883). The family has been treated by Thambugala et al. (2014) and several new species have been described in recent publications (e.g. Thambugala et al. 2014, Hyde et al. 2017, Tibpromma et al. 2017).

Lophiostoma Ces. & De Not., Comm. Soc. crittog. Ital. 1(fasc. 4): 219 (1863)

Lophiostoma was established by Cesati & De Notaris (1863) to accommodate *L. macrostomum*. There are 446 epithets under this genus in Index Fungorum (2018). Strains obtained in this study clustered with the other representative strains of *L. macrostomum* with high bootstrap support (Fig. 38).

Lophiostoma macrostomum (Tode) Ces. & De Not., Symbolae Mycologicae: 7 (1870)

Facesoffungi number: FoF03831

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** *Ascomata* 450–500 µm high, 510–550 µm diam. (\bar{x} = 500×540 µm, n=10), scattered to gregarious, semi-immersed to densely erumpent, carbonaceous, dark brown to black, globose to subglobose. *Ostiole* slit-like with a small to large flat crest-like apex composed of pseudoparenchymatous cells. *Peridium* 30–50 µm wide (\bar{x} = 37µm, n=12), thick at the sides, broad at the apex and thinner at the base, inner layer composed of hyaline *textura angularis* cells, outer layer dark brown to black. *Hamathecium* of septate, long, hyaline, anastomosing and branched, cellular pseudoparaphyses, embedded in gelatinous matrix between and above the asci. *Asci* 90–120×10–13 µm (\bar{x} = 110×12 µm, n=10), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with furcate pedicel, rounded at the apex with a minute ocular chamber. *Ascospores* 28–35×4–6 µm (\bar{x} = 32×5 µm, n=20), uniseriate or partially biseriata, narrowly fusiform with acute ends, 1–3-septate and slightly constricted at septa, with a distinct oil drop in each cell, smooth-walled, hyaline. **Asexual morph:** Not observed.

Material examined — ITALY, Province of Forlì-Cesena, Trivella di Predappio, dead and aerial branch of *Vitis vinifera*, 30 December 2014, Erio Camporesi, IT 2323 (MFLU 15-1076); ITALY, Province of Forlì-Cesena, near Pieve di Rivoschio, dead and aerial branch of *V. vinifera*, 2 February 2015, Erio Camporesi, IT 2363 (MFLU 15-1082).

Notes — Species of this genus have been reported on *Vitis* species in different countries, but *Lophiostoma macrostomum* has been previously recorded only as an endophyte from *Vitis* sp. in Pakistan (Ahmad et al. 1997) and as a saprobe (Zhang et al. 2009). A culture is unavailable for the strain in this study and sequencing from fruiting bodies was conducted. This study provides the first report of *L. macrostomum* as a saprotroph as well as a new record from Italy associated with *V. vinifera*.

Massariaceae Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26: 73 (1869)

Massariaceae was introduced by Nitschke (1869) to accommodate *Massaria*.

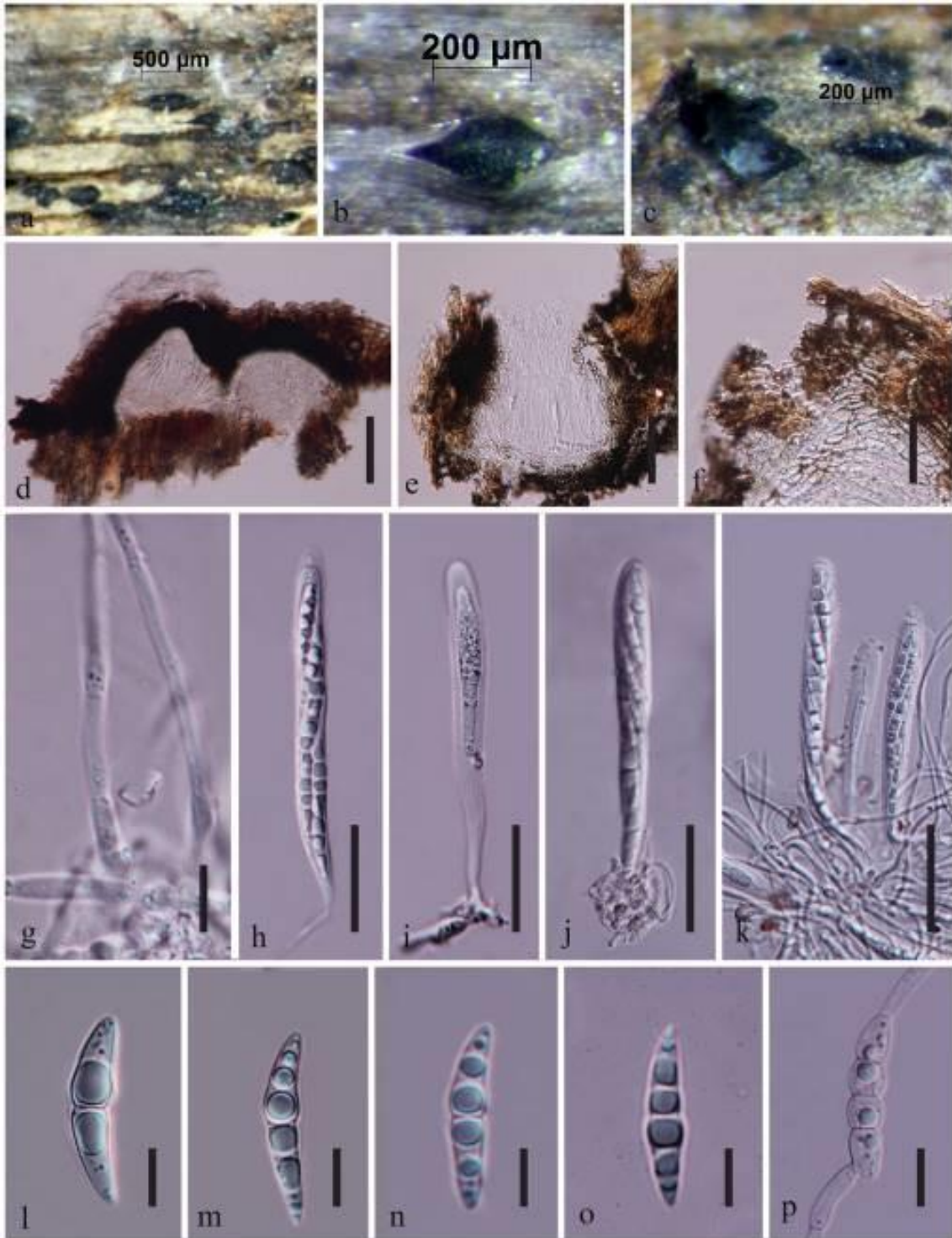
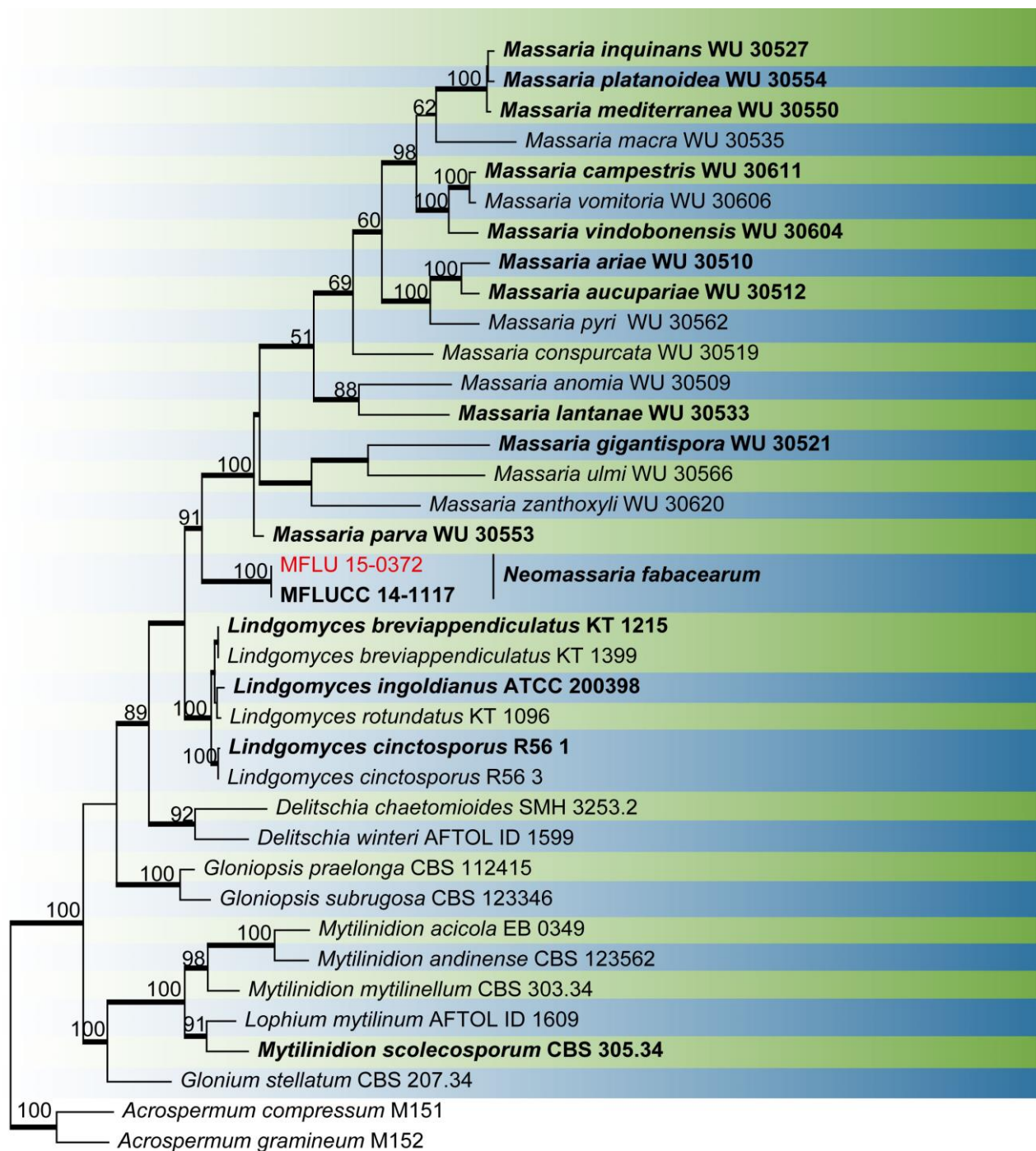


Fig. 29 – *Lophiostoma macrostomum* **a, b** Ascomata on host surface. **c** Section of ascoma. **d, e** Section through ascoma. **f** Peridium. **g** Pseudoparaphyses. **h-k** Asci. **l-o** Ascospores. **p** Germinated spore. Scale bars **d, e**=100 μm , **f, h-k**=30 μm , **g**=5 μm , **l-p**=10 μm .

Neomassaria Mapook, Camporesi & K.D. Hyde, in Hyde et al., Fungal Diversity: 10.1007/s13225-016-0373-x, [74] (2016)

This genus was introduced to accommodate *N. fabacearum* (Hyde et al. 2016) and has only one species epithet in Index Fungorum (2018). Our strain clustered with the type strain with high bootstrap support (Fig. 30).



10

Fig. 30 – One of ten most parsimonious trees obtained from a heuristic search of combined LSU, SSU and TEF1 sequence data of *Massariaceae*. Parsimony bootstrap support values $\geq 75\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. Ex-type strains are in bold. Strains isolated in this study are shown in red. The tree is rooted with *Acrospermum compressum* (M151) and *A. gramineum* (M152).

Neomassaria fabacearum Mapook, Camporesi & K.D. Hyde, in Hyde et al., Fungal Diversity: 10.1007/s13225-016-0373-x, [77] (2016)

Facesoffungi number: FoF02438

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** *Ascomata* 210–250 μm high, 215–245 μm diam. (\bar{x} =227 \times 235 μm , n=5), immersed, solitary or scattered, coriaceous, globose to subglobose, brown to dark brown, *Ostiole* central. *Peridium* 10–25 μm wide, comprising light brown cells of *textura angularis*. *Hamathecium* comprising 1–1.5 μm wide, cylindrical to filiform, septate, branched pseudoparaphyses. *Asci* 65–105 \times 10–15 μm (\bar{x} =86 \times 12 μm ,

n=10), 8-spored, bitunicate, oblong to cylindrical, short pedicellate, with a wide ocular chamber. *Ascospores* 19–21×5–6 μm (\bar{x} =20×5 μm , n=10), overlapping 1–2-seriate, hyaline, ellipsoid to broadly fusiform, 1-septate, constricted at the septum, surrounded by hyaline gelatinous sheath observed clearly when mounted in Indian ink. **Asexual morph:** Not observed.

Material examined — ITALY, Province of Forlì-Cesena, Dovadola, on dead aerial branch of *Vitis vinifera*, 17 January 2014, Erio Camporesi, IT 1653 (MFLU 15-0372).

Notes — A culture is not available for this strain, and sequencing from the fruiting bodies were conducted. *Neomassaria fabacearum* is a saprotroph on *Hippocrepis emerus* (Hyde et al. 2016), and this study provides the first record of this species as a saprotroph on *Vitis vinifera* as well as a new record from Italy.

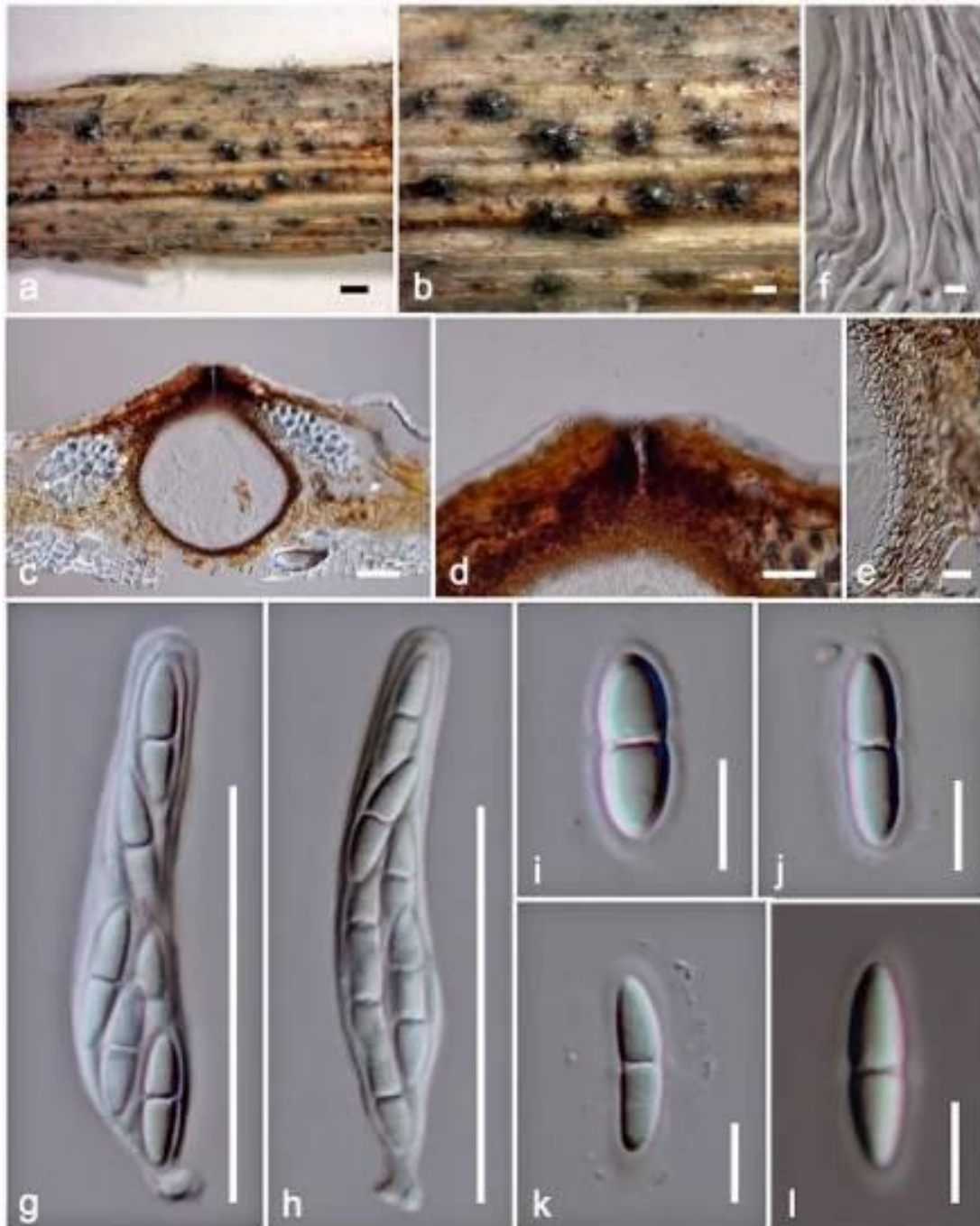


Fig. 31 – *Neomassaria fabacearum*. a, b. Appearance of ascomata on substrate. c. Section through ascoma. d. Ostiole. e. Peridium. f. Pseudoparaphyses. g, h. Asci. i–k. Ascospores. l. Ascospore surrounded by hyaline gelatinous sheath in Indian ink. Scale bars: a=500 μm , b=200 μm , c=100 μm , d, g–h=50 μm , e=20 μm , i–l=10 μm , f=5 μm .

Pleosporaceae Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26: 74 (1869)

Pleosporaceae is the largest family in Pleosporales and members of this family are pathogens or saprotrophs. Ariyawansa et al. (2015) revised the family and accepted 18 genera.

Alternaria Nees, Syst. Pilze (Würzburg): 72 (1816) [1816-17]

Alternaria was introduced by Nees (1816) and is a ubiquitous genus that includes saprobic, endophytic and pathogenic species associated with a wide variety of substrates (Woudenberg et al. 2013). Several species of this genus are known to be associated with grapevine. We provide accounts of *A. alternata* and *A. vitis* from *Vitis* sp. and a new species is introduced based on morphological traits and phylogeny (Fig. 32).

Alternaria alternata (Fr.) Keissl., Beih. bot. Zbl., Abt. 2 29: 434 (1912)

Facesoffungi number: FOF03825

Saprotrophic on dead stems and inflorescence of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiophores* 40–50×3–6 µm (\bar{x} =26×5 µm, n=20) solitary to clustered, simple or branched, straight or flexuous, sometimes geniculate, pale, olivaceous or golden brown, smooth. *Conidia* 20–63×9–18 µm (\bar{x} =43×12 µm, n=40), produced in single or branched chains on short conidiophores, obclavate, obpyriform, ovoid or ellipsoidal, pale to mid golden brown, 3–8 transverse and longitudinal septa, verruculose, tapering in the lower half into a narrow tail extension, upper part with a very short rounded beak ending abruptly. On PDA, *conidia* 22–38×6–11 µm (\bar{x} =31×7 µm, n=40), in long and sometimes branched chains of 8–12 spores, obclavate, dark olive brown, 4–8 transverse and 0–2 longitudinal or oblique septa.

Culture characteristics — Colonies growing on PDA reaching 60 mm in 7 days at 25° C, initially greyish with a very thin white margin and cottony texture, later becoming dark olive green to dark brown, mycelium superficial, effuse, radially striate, with irregular edge, brown to dark brown coloured hyphae.

Material examined — ITALY, Province of Forlì-Cesena, near Teodorano - Meldola, on dead aerial branch of *Vitis vinifera*, 15 February 2015, Erio Camporesi, IT 2380 (MFLU 15-0372), culture MFLUCC 17-1219 (KUMCC 17-0118); CHINA, Yunnan, on dead shoot of *V. vinifera* cv. Carbanate Gernischet, 11 June 2015, X. H. Li, culture MFLUCC 17-1187; CHINA, Beijing, on dead shoot of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17-1118, MFLUCC 17-1129, MFLUCC 17-1150, MFLUCC 17-1151; CHINA, Beijing, on dead inflorescence of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17-1122, MFLUCC 17-1130

Notes — *Alternaria alternata* is a well-known pathogen throughout the world causing various diseases on economically important crops. This species is known to cause a fruit rot of grapevine. *Alternaria alternata* has been also recorded as an endophyte and a saprotroph from grapevine worldwide (Jayawardena et al. 2018).

Alternaria italica J.F. LI, Camporesi & K.D. Hyde *sp. Nov.*

Index Fungorum numbers: IF553987 *Facesoffungi* number: FoF 03880

Holotype: HKAS 100717

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Mycelium* superficial on substrate, composed of septate, branched, smooth, thin-walled, brown to dark brown hyphae. *Conidiophores* 250–300×17–21 µm (\bar{x} =278×18 µm, n=100), macronematous, mononematous, light brown to brown, thick-walled, smooth, septate, branched at the base, straight or flexuous, cylindrical. *Conidiogenous cells* 8–13×9–15 µm (\bar{x} =10×11 µm, n=100), cicatrized, monoblastic, integrated, terminal, determinate or percurrent, cylindrical, doliiform, subhyaline, smooth, thin-walled. *Conidia* 76–98×23–39 µm (\bar{x} =86×32 µm, n=100), acrogenous, holoblastic, solitary, light grey to brownish grey, 8–11-septate or more, dry, simple, straight, curved, fusiform, obpyriform, obturbinate or subglobose, catenate, sometimes rostrate, smooth, thin-walled.

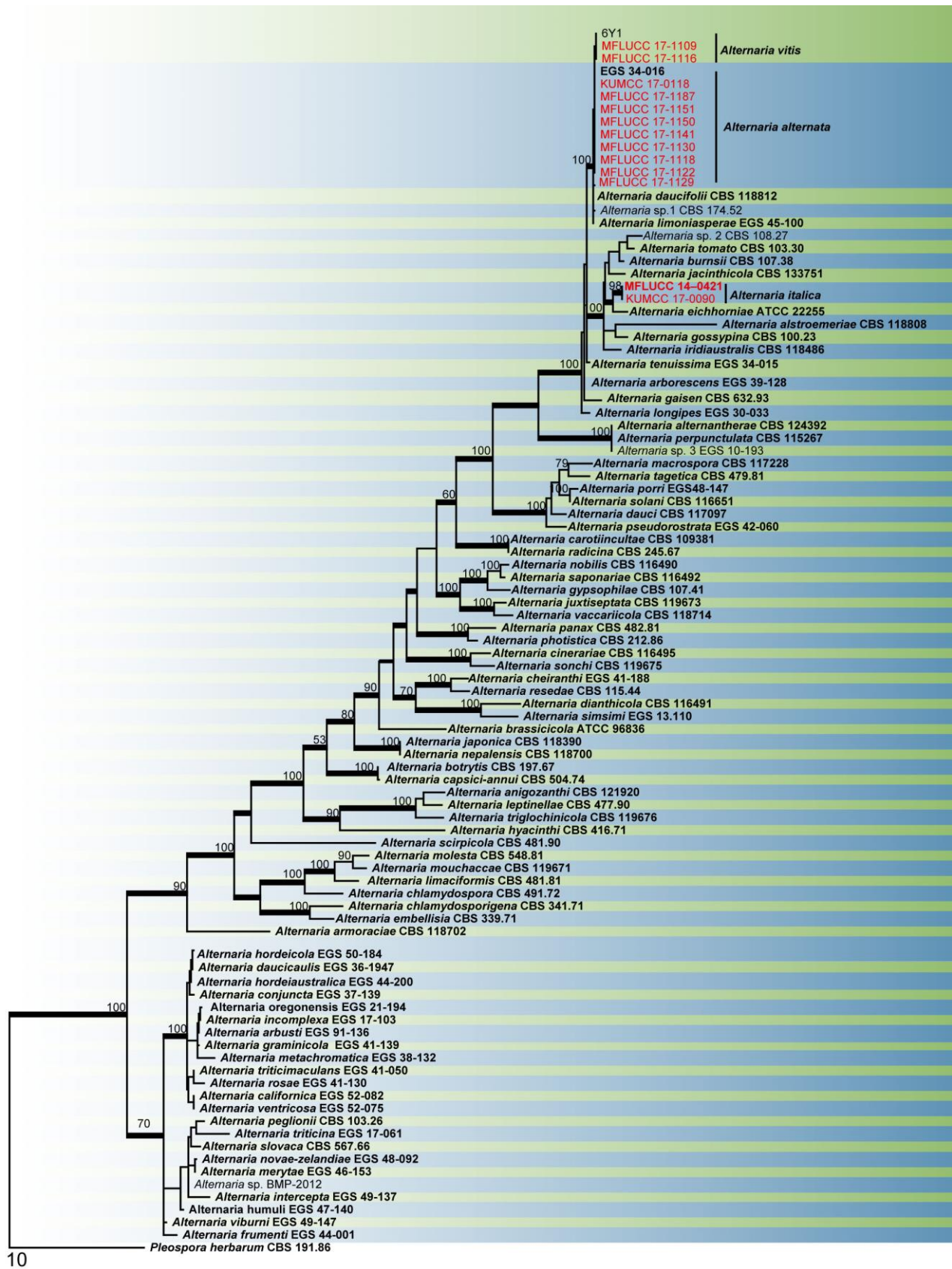


Fig. 32 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, LSU, GAPDH, RPB2 and TEF1 sequence data of taxa from *Alternaria*. Parsimony bootstrap support values $\geq 75\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.95 given in bold. Ex-type strains are in bold. Strains of this study are in red. The tree is rooted with *Pleospora herbarum* CBS 191.86.

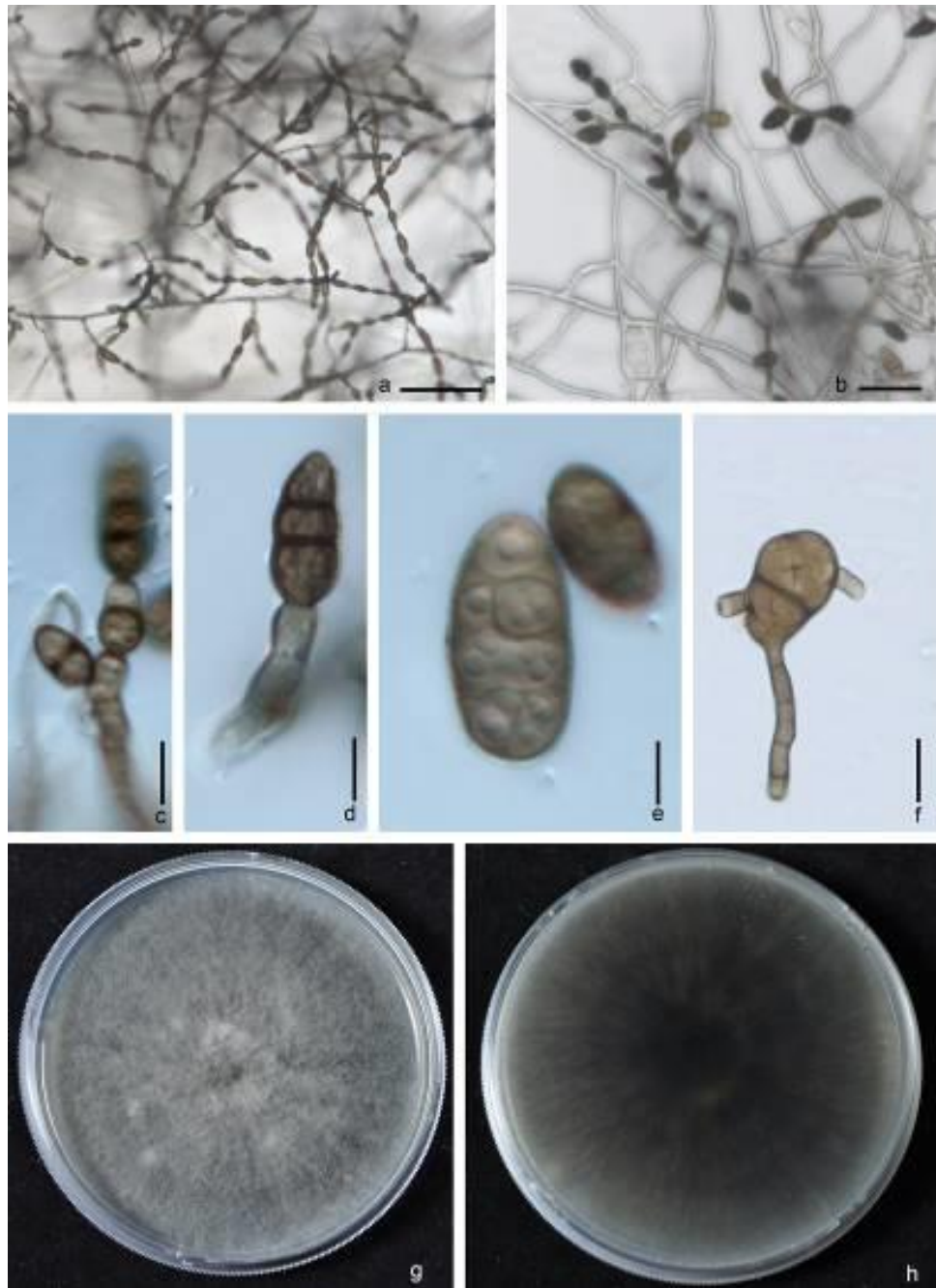


Fig. 33 – *Alternaria alternata*. a-b. Conidial chains. c-d. Conidiophores. e. Conidia. f. Germinated conidium g. Upper view of the culture on PDA. h. Reverse view of the culture on PDA. Scale bars: a–b=100 μ m, c–f=20 μ m.

Cultural characteristics — Conidia germinating on PDA within 14 hours and germ tubes produced from all cells. Colonies growing on PDA, hairy or cottony, brown to dark brown, reaching 5 mm in 20 days at 25 °C, mycelium superficial, effuse, radially striate, with irregular edge, brown to dark brown hyphae; asexual spores and sexual spores not formed within 60 days.

Material examined — ITALY, Province of Forlì-Cesena, Via Pietro Nenni – Forlì, on dead and aerial branch of *Vitis vinifera*, 12 November 2013, Erio Camporesi, IT 1513 (HKAS 100717 - holotype), culture MFLUCC 14–0421= KUMCC 17-0123.

Notes — Based on morphology and multigene phylogenetic support we introduce *A. italica* to accommodate the new taxon.

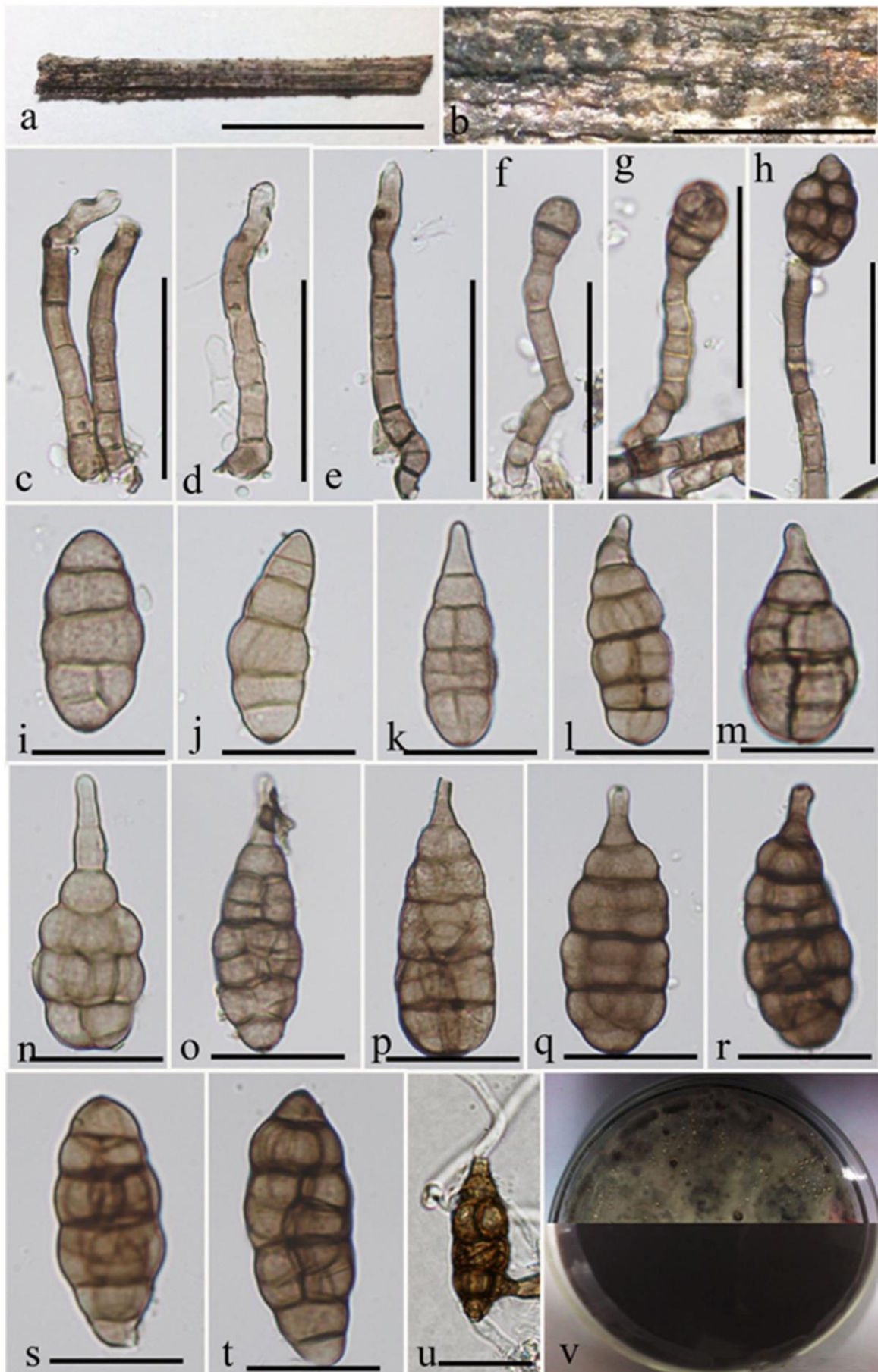


Fig. 34 – *Alternaria italica*. a. Host tissue. b. Colonies on dead branch. c-e. Conidiophores. f-h. Conidiophores with conidiogenous cells. i-t. Conidia. u. Germinated conidium. v. Culture on PDA. Scale bars: a=1 cm, b=1000 µm, c-h=100 µm, i-u=20 µm.

Alternaria vitis Cavara, Atti Ist. bot. R. Univ. Pavia, 2 Sér. 1: 319 (1888)

Facesoffungi number: FOF03826

Saprotrophic on dead stems and roots of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiophores* simple or branched, dark brown. Conidia 25–66×10–18 μm (\bar{x} =39×15 μm , n=40), brown, usually producing single conidia, chains rarely observed, slightly verrucose, swollen at the base and gradually tapering towards end, apex filiform, lighter than the rest of the spores and ending in a straight false beak.

Culture characteristics — Colonies growing on PDA reaching 60 mm in 7 days at 25° C, initially white colonies with cottony texture appear, later becoming greyish to dark olive brown, mycelium superficial, effuse, and radially striate, with irregular edge, sometimes sectoring can be observed.

Material examined — CHINA, Beijing, on dead root of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17-1109; CHINA, Beijing, on dead shoot of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17-1116.

Notes — *Alternaria vitis* is a well-known pathogen in grape growing regions due it causing fruit rots and leaf blights. Based on morphology, Zhang (2003) and Zhuang (2005) reported this species from China. In this study we identified this species as a saprotroph of *V. vinifera* based on morphology as well as sequence data.



Fig. 35 – *Alternaria vitis*. a-d. Conidia. e. Conidiophore. f. Upper view of the culture on PDA. g. Reverse view of the culture on PDA. Scale bars: a–e=20 μm .

Bipolaris Shoemaker, Can. J. Bot. 37(5): 882 (1959)

Bipolaris was introduced by Shoemaker (1959) and it is considered an important plant pathogen associated with over 60 host genera (Manamgoda et al. 2011, Hyde et al. 2014). Our saprotrophic strains clustered with the type strain of *B. maydis* with a high bootstrap support in the phylogenetic analysis (Fig. 36).

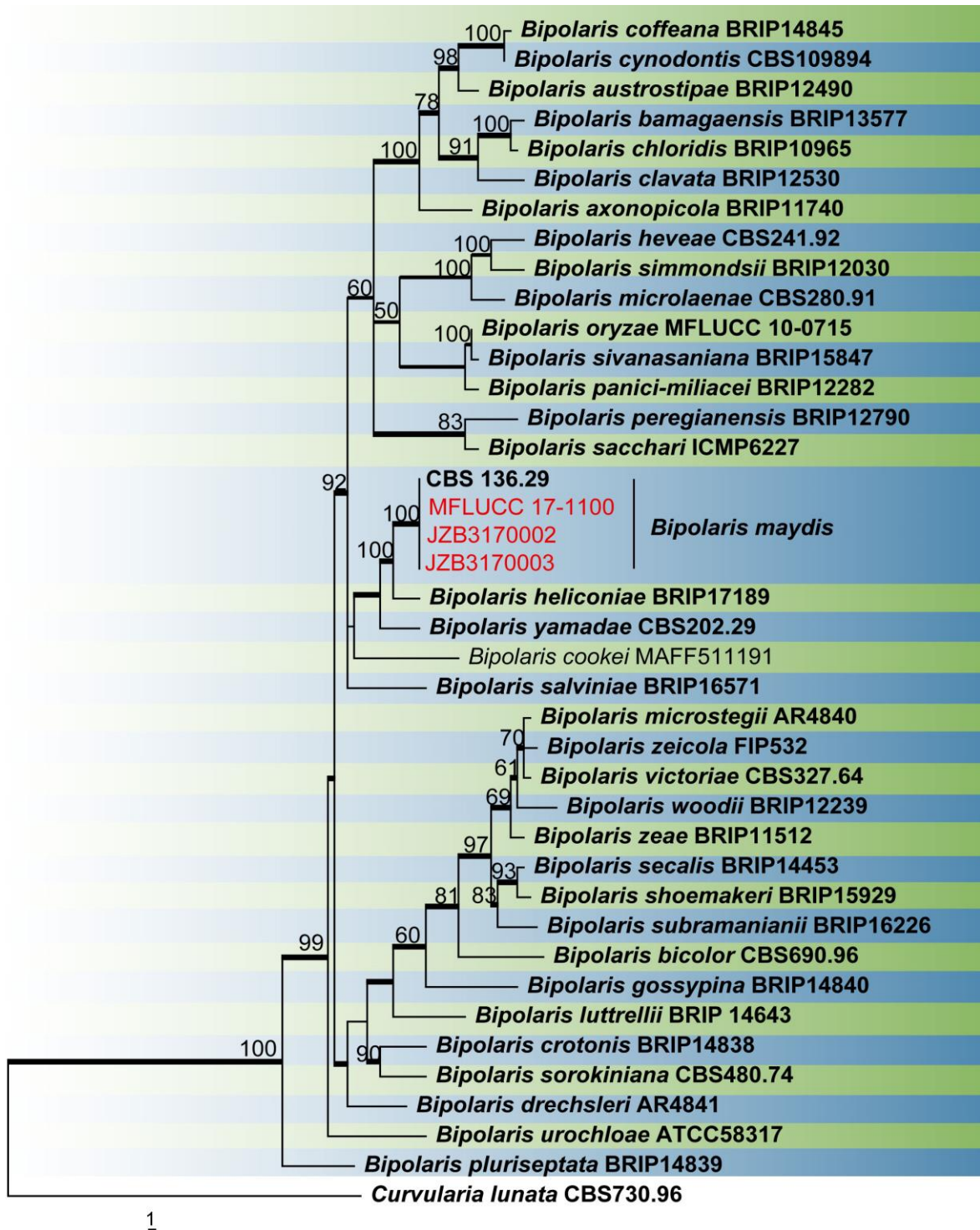


Fig. 36 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, and GAPDH sequence data of taxa of *Bipolaris*. Parsimony bootstrap support values $\geq 75\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.95 given in bold. Ex-type strains are in bold. The tree is rooted with *Curvularia lunata* CBS 730.96.

Bipolaris maydis (Y. Nisik. & C. Miyake) Shoemaker, Can. J. Bot. 33: 882 (1959)

Facesoffungi No: FoF00504

Saprotrophic on dead shoots of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiophores* 90–690×5–7 μm (\bar{x} =272×5 μm, n=50), usually arising singly or in small groups, simple or rarely branched, septate, straight or flexuous, geniculate at upper part, olivaceous brown. *Conidiogenous nodes* dark brown, distinct. *Conidia* 60–150×12–18 μm (\bar{x} =94×13 μm, n=40), pale to mid dark brown, smooth, slightly curved, fusiform, distoseptate. *Hilum* distinct, 3–5 μm wide, germination tubes arising from both ends of conidia.

Cultural characteristics — Colonies on PDA reaching 70mm in 7 days at 25 °C, greyish white when young, becoming blackish when mature.

Material examined — CHINA, Beijing, on dead shoots of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17-1100, JZB317002, JZB317003.

Notes — *Bipolaris maydis* is a well-known pathogen that causes Southern leaf blight in maize (Manamgoda et al. 2014). This study provides the first record of *B. maydis* on *Vitis vinifera* as well as a new record from China.

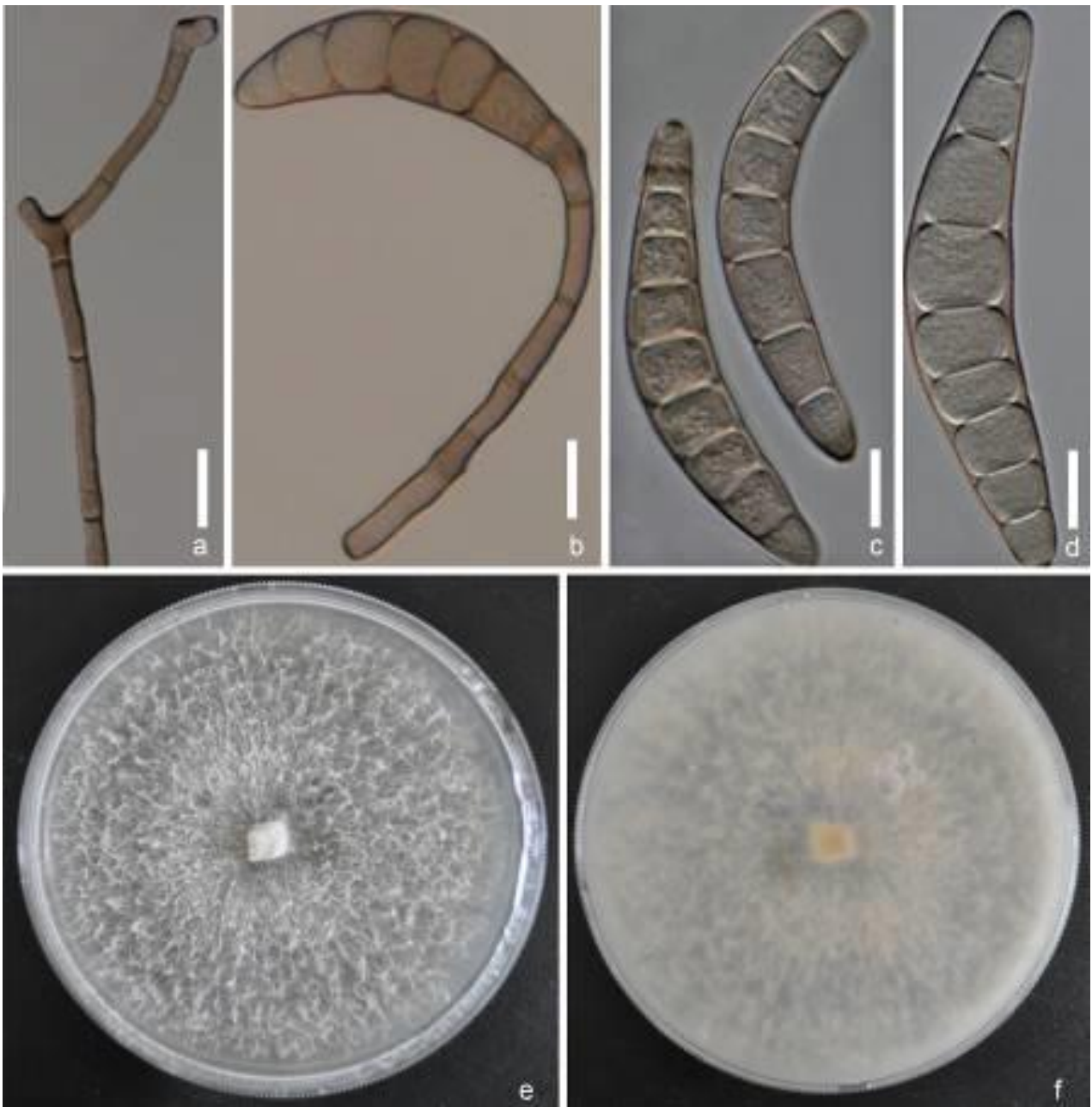


Fig. 37 – *Bipolaris maydis*. a-b. Conidiophores. c-d. Conidia. e. Surface view of colony on PDA. f. Reverse view of colony on PDA. Scale bars: a–d = 10 μm.

Teichosporaceae M.E. Barr, Mycotaxon 82: 374 (2002)

This family was introduced by Barr (2002) to accommodate *Teichospora* Fuckel. Jaklitsch et al. (2016) provided the basis for the classification of this family and synonymized *Floricolaceae* Thambugala, Kaz. Tanaka & K.D. Hyde.

Floricola Kohlm. & Volkm.-Kohlm., Bot. Mar.43(4): 385 (2000)

Floricola was introduced as a monotypic genus by Kohlmeyer & Volkmann-Kohlmeyer (2000) with *F. striata* JK5603K as the type species. Species of *Floricola* are saprotrophs with a cosmopolitan distribution (Thambugala et al. 2015). Jaklitsch et al. (2016) synonymized this genus under *Teichospora*. However, Wijayawardene et al. (2017) maintained *Floricola* as a distinct genus. There are only two epithets under this genus. Our strain clustered with the type strain of *F. viticola* in the multigene phylogenetic analysis (Fig. 38).

Floricola viticola Phukhams., Camporesi & K.D. Hyde, in Ariyawansa et al., Fungal Diversity: 10.1007/s13225-015-0346-5, [45] (2015)

Facesoffungi number: FoF03822

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 220–239×154–202 μm (\bar{x} =237×177 μm , n=10) diam., solitary, pycnidial, unilocular, scattered, immersed to erumpent, subglobose, dark brown to black. *Pycnidial wall* 13–35 μm (–40 μm at apex), merging with host tissues externally, composed of brown cells of *textura angularis* with hyaline inner lining bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–10×2–9 μm (\bar{x} =4×5 μm , n=20), enteroblastic, phialidic, determinate, solitary, doliiiform, smooth-walled, hyaline. *Conidia* 7–12×2–6 μm (\bar{x} =9×4 μm , n=50), initially hyaline, dark brown at maturity, oblong, sub-fusiform, occasionally curved at the apex, with slight abscission scar at base, with 1–3-longitudinal septa, constricted at some septa, narrowly rounded at both ends, smooth-walled.

Cultural characters — Colonies on PDA 20 mm diam. after 4 weeks at 16 °C, cream to orangish white at the margins; reverse white to cream and orangish white at the center, medium dense, circular, umbonate, fimbriate, fluffy, slightly radiating, without diffusible pigments.

Material examined — ITALY, Province of Forlì-Cesena, near Galeata, on dead and aerial branch of *Vitis vinifera*, 16 October 2014, E. Camporesi IT2178 (MFLU 15–1404), culture, MFLUCC 15–0039.

Notes —*Floricola viticola* has been recorded only from Italy as a saprotroph on *Vitis vinifera*.

Sordariomycetes

The class Sordariomycetes has been treated by Maharachchikumbura et al. (2015, 2016) and the taxonomic arrangements used by these authors and Wijayawardene et al. (2017) are followed here.

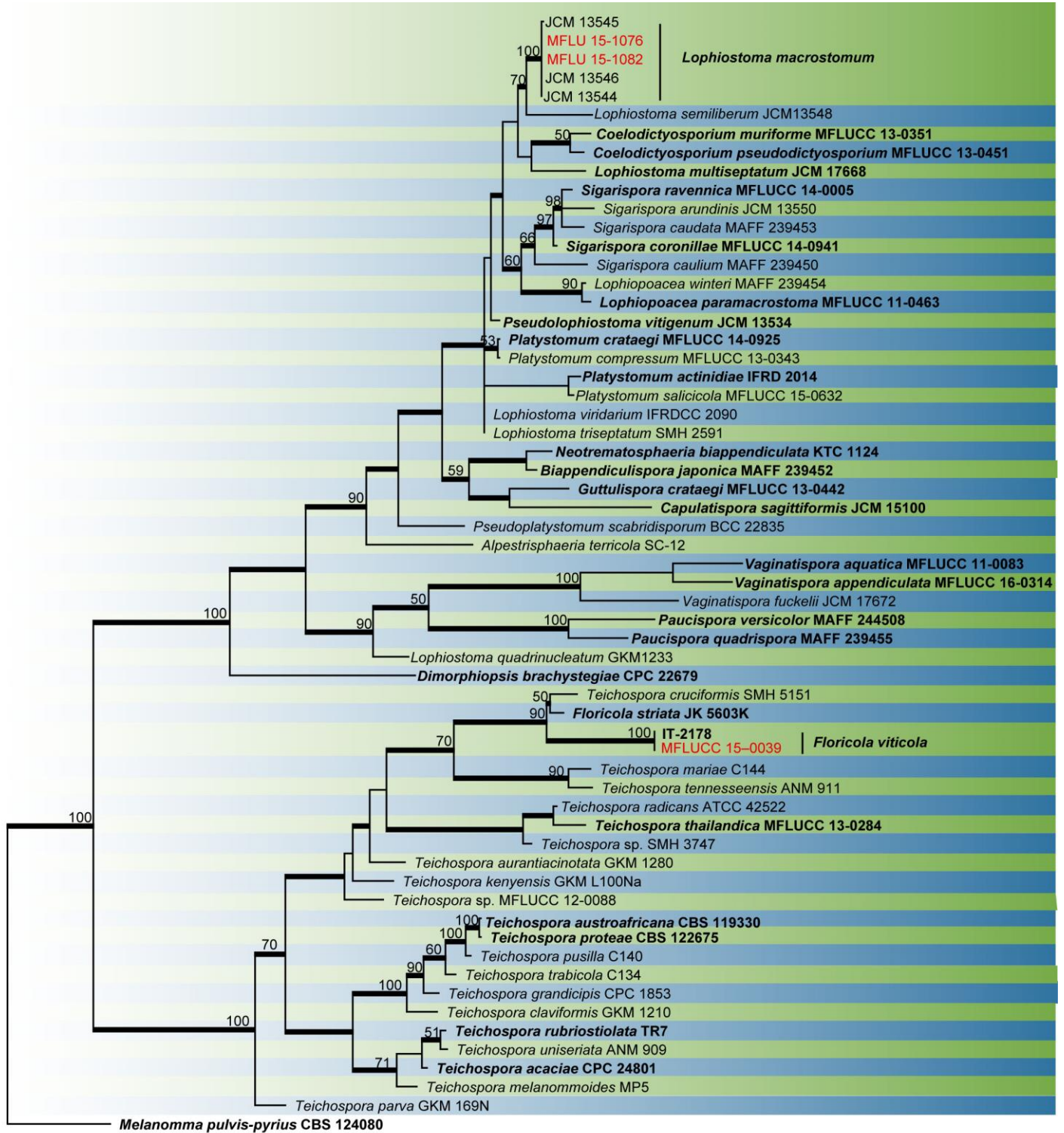
Amphisphaeriales D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 177 (1986)

Sporocadaceae Corda, Icon. Fungorum (Prague) 5: 34. 1842

Members of this family are endophytes and saprobes, as well as foliar pathogens (Nag Raj 1993). Maharachchikumbura et al. (2016) synonymized *Discosiaceae* under this family.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 135 (2014)

Species of this genus can be easily distinguished by their versicolourous median cells (Maharachchikumbura et al. 2014). Strains in this study clustered together with the type strains of *N. clavispora* and *N. vitis*, respectively (Fig. 42).



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Fig. 38 – RAxML phylogram obtained from the combined LSU, SSU ITS and TEF1 sequence data of species of *Teichosporaceae* and *Lophiostomataceae*. The species isolated in this study are shown in red. RAxML bootstrap support (BS) values $\geq 50\%$ are shown at the nodes and branches with Bayesian posterior probability scores ≥ 0.90 are given in bold. The tree is rooted with *Melanomma pulvis-pyrius* (CBS 124080).

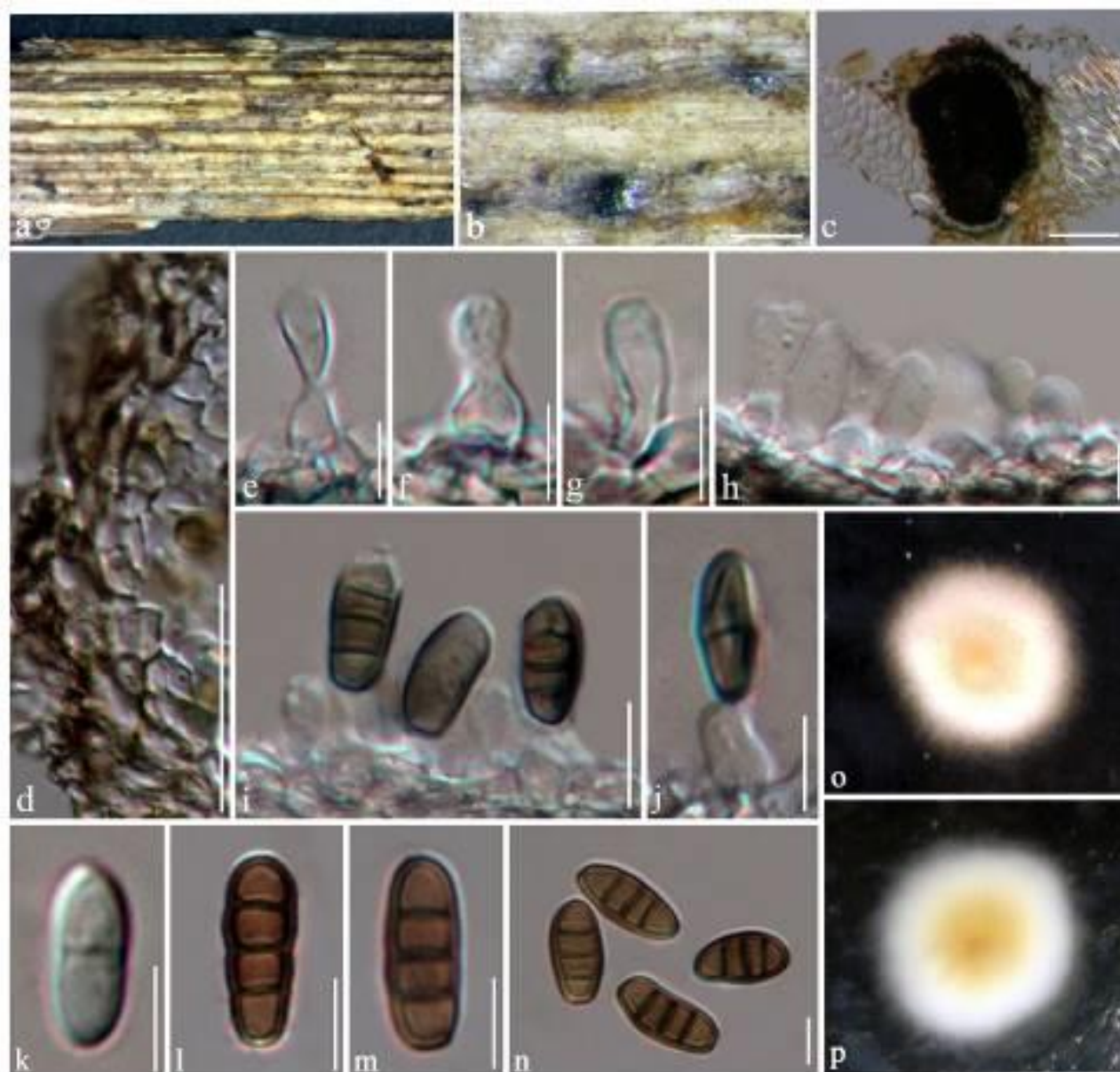


Fig. 39 – *Floricola viticola*. a. Fruiting bodies on host tissue. b. Close up of conidiomata below surface of host. c. Vertical section through conidioma. d. Part of peridium. e-j. conidiogenous cells with developing conidia. k-n. Conidia. o. Upper view of the culture on PDA. p. Reverse view of the culture on PDA Scale bars: b=200 μ m, c=100 μ m, d=50 μ m, e–n=5 μ m.

Neopestalotiopsis clavispora (G.F. Atk.) Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 138 (2014)

Facesoffungi number: FoF 03819

Saprotrophic on root and shoots of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* pycnidial in culture on PDA, 150–250 μ m in diam., black, numerous, scattered. *Conidia* 18–26 \times 6–8 μ m (\bar{x} = 21 \times 8 μ m, n=40), fusiform, 4-septate, straight or slightly curved; basal cell long and conic, hyaline, thin and verruculose, with three median cells 13–15 μ m long, dark brown to olivaceous, septa and periclinal walls darker than the rest of the cell, versicoloured, second cell from base pale brown, 4–5 μ m long; third cell darker brown, 5–7 μ m long; fourth cell darker, 5–6 μ m long; apical cell 3–4 μ m long, short, broad conic, hyaline, subcylindric; with 2–3 (rarely 2) apical appendages, 19–30 μ m long, tubular, ; with basal, filiform appendage.

Culture characteristics — Colonies on PDA reaching 70 mm after 7 days at 25° C, edge undulate, whitish, aerial mycelium on surface, fruiting bodies black, concentric; reverse pale luteous.

Material examined — CHINA, Beijing, on dead shoot of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-1117, MFLUCC 17-1120, MFLUCC 35, JZB340031, JZB340033 and JZB340034; CHINA, Beijing, on dead root of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, JZB340032.

Notes — *Neopestalotiopsis clavispora* is known as a saprotroph on *Magnolia* sp. and *Quercus rubra* (Maharachchikumbura et al. 2014). This study provides the first record of *N. clavispora* on *Vitis vinifera*.

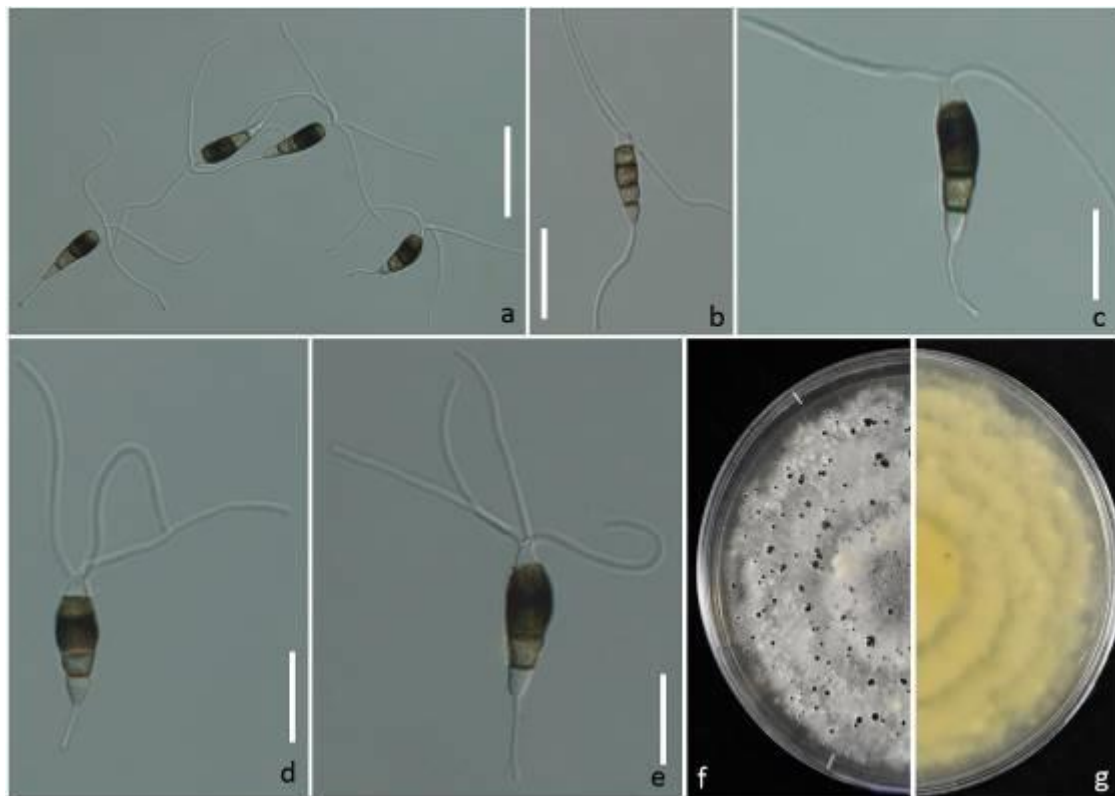


Fig. 40 – *Neopestalotiopsis clavispora*. a-e. Conidia. f. Upper view of the colony g. Reverse view of the colony. Scale bars a–e=10 µm.

Neopestalotiopsis vitis Jayawardena, Maharachch., Yan, Li & Hyde, in Jayawardena, Liu, Maharachchikumbura, Zhang, Xing, Hyde, Nilthong, Li & Yan, Phytotaxa 258(1): 69 (2016)

Facesoffungi number: FoF01110

Saprotrophic on dead bark, root and shoots of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose to oval, solitary or aggregated in clusters, semi-immersed, black, 120–550 µm diam.; exuding globose, black, glistening, conidial masses. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* discrete, fusiform, hyaline, cylindrical to subcylindrical or ampulliform to lageniform, rugose-walled, simple, 2–11×1–5 µm. *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, 20–28×5–10 µm (\bar{x} =22×7 µm, n=40); basal cell conic to acute with a truncate base, hyaline, rugose, thin-walled, 3–7 µm long, three median cells, doliiform, 13–18 µm long, wall rugose, versicoloured, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base pale brown to olivaceous, 4–6 µm long; third cell olivaceous to darker brown, 4–7 µm long; fourth cell brown, 4–6 µm long; apical cell 3–5 µm long, hyaline, cylindrical to subcylindrical, thin and smooth walled, with 2–4 tubular apical appendages (mostly 3), arising from

the apical crest, flexuous, unbranched, 12–45 μm long, basal appendage 1–2, tubular, unbranched, centric, 2–7 μm long.

Culture characteristics — Colonies on PDA reaching 50–60 mm in diam. after 7 days at 25 $^{\circ}\text{C}$, with lobate edge, whitish to pale honey coloured, with dense aerial mycelium on the surface with black, concentric conidiomata, reverse pale yellow.

Material examined — CHINA, Beijing, on dead bark of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-1108, JZB340029; CHINA, Beijing, on dead shoots of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-1108, JZB340027, JZB340028; CHINA, Beijing, on dead roots of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, JZB340030. CHINA, Yunnan, on dead shoots of *Vitis vinifera* cv. CarbanateGernischet, 11 June 2015, XH. Li, culture, MFLUCC 17-1167.

Notes — Jayawardena et al. (2016a) introduced *N. vitis* to accommodate a pathogen that causes leaf spot, fruit rots and cankers of grapevine in China. This study provides the first record of this species as a saprotroph on *V. vinifera*.

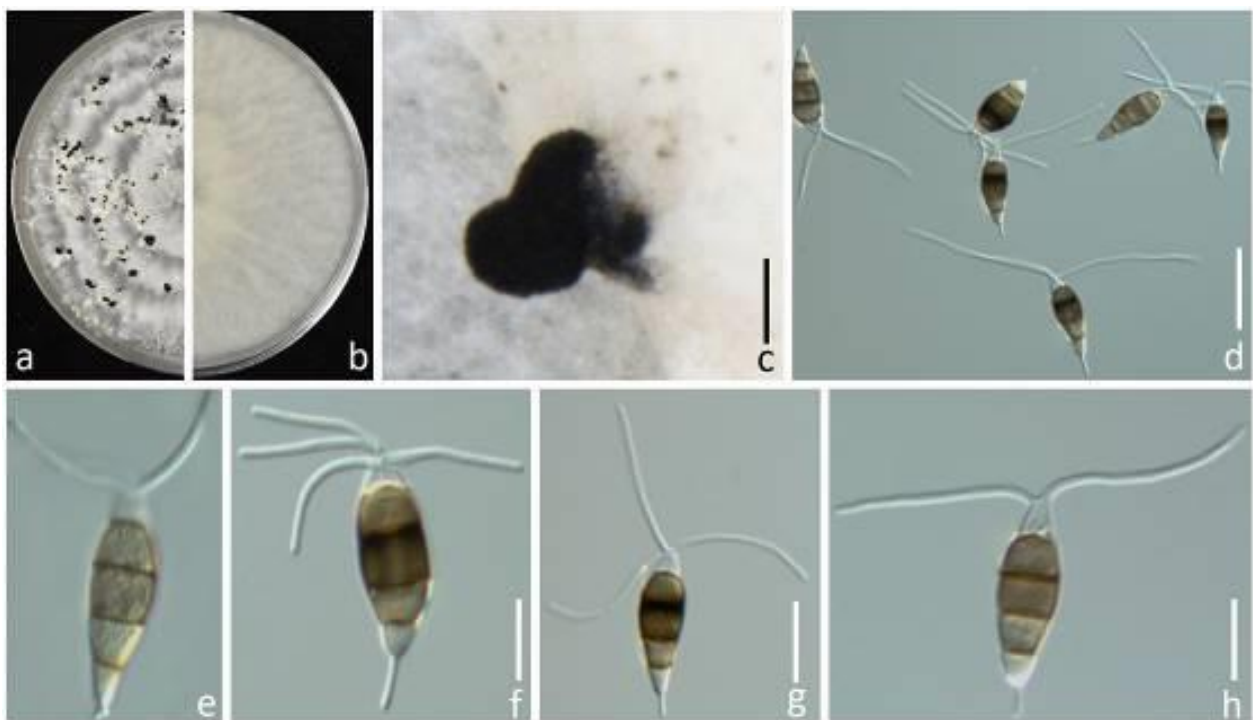


Fig. 41 – *Neopestalotiopsis vitis*. a. Upper view of the colony b. Reverse view of the colony. c. Black exude on PDA. d-h. Conidia. Scale bars: d–h=10 μm c=100 μm .

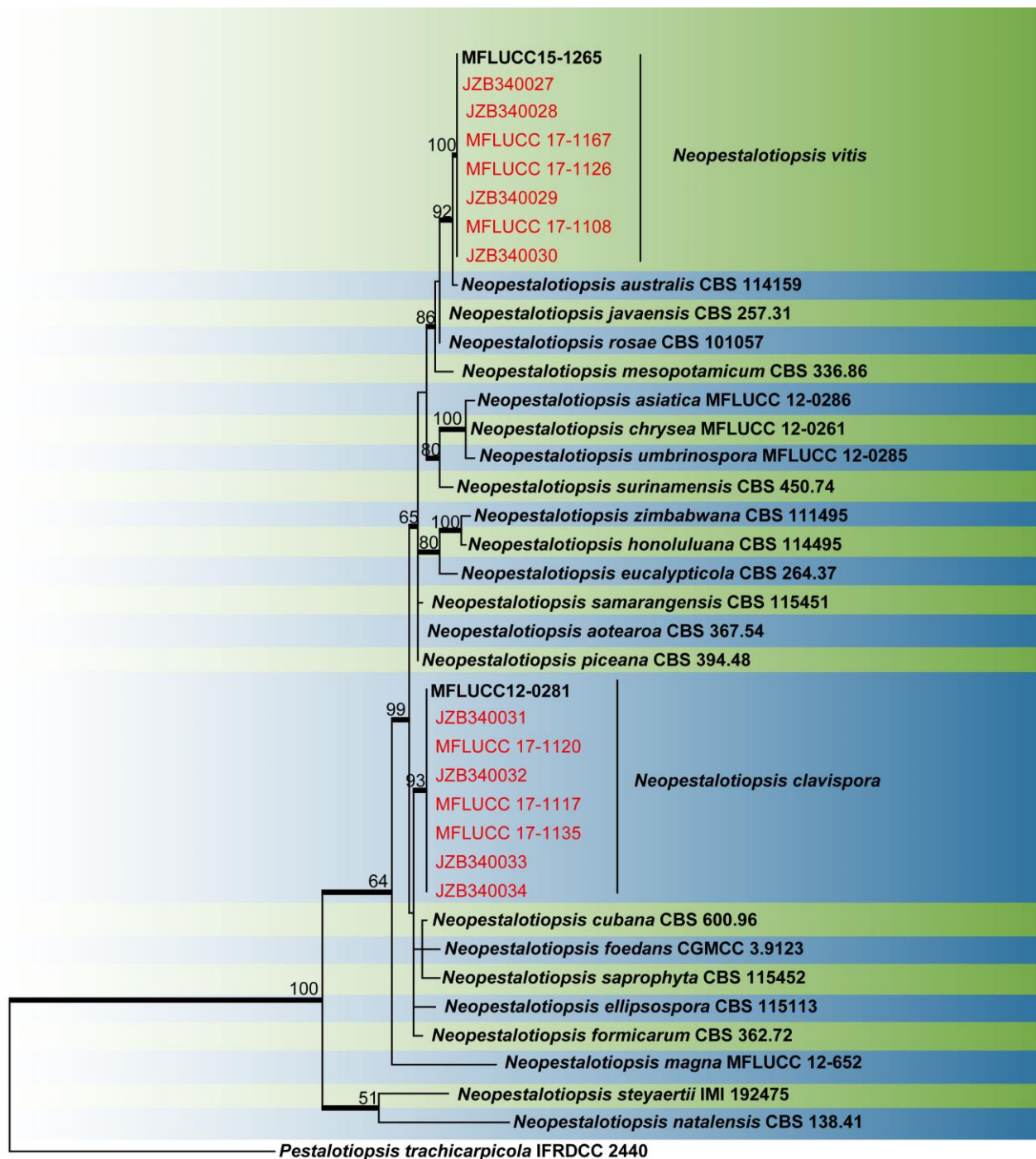
Pestalotiopsis Steyaert, Bull. Jard. bot. État Brux. 19: 300 (1949)

Pestalotiopsis was introduced to accommodate species with 5-celled conidia and has been relatively well-studied (Maharachchikumbura et al. 2012, 2014). Species of this genus have been often isolated as endophytes (Maharachchikumbura et al. 2011, 2012). In this study we provide accounts for *P. chamaeropsis* and a *Pestalotiopsis* sp., based on morphology and phylogenetic analysis (Fig. 45).

Pestalotiopsis chamaeropsis Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 158 (2014)

Facesoffungi number: FoF03818

Saprotrophic on dead branch of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** Coelomycetous. *Conidiomata* 140–210 μm diam., 85–100 μm high, slightly raised, black, solitary to aggregated, semi-immersed, becoming erumpent at maturity, pycnidoid, globose to



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Fig. 42 – One of eight most parsimonious trees obtained from a heuristic search of combined ITS, TUB2 and TEF1 sequence data of taxa of *Neopestalotiopsis*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Pestalotiopsis trachicarpicola* IFRDCC 2440.

subglobose, unilocular, glabrous. *Conidiomata wall* 8–15 μm wide, composed of thin-walled, outer, light brown cells of *textura prismatica* and inner, hyaline cells of *textura angularis* to *textura globulosa*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–13 μm long, 1–4 μm wide, hyaline, enteroblastic, subcylindrical, arising from the cells lining the inner wall of the pycnidium. *Conidia* 20–30 \times 8–10 μm (\bar{x} =25 \times 8 μm , n=50), fusiform, 4-septate, straight or slightly curved, bearing tubular, unbranched, flexuous appendages at both ends, basal cell 3–5 μm (\bar{x} =4

μm) long, hyaline, cuneiform, 3 median cells, together 15–20 μm long (second cell from base 4–7 μm (\bar{x} =5 μm), third cell 4–7 μm (\bar{x} =6 μm), fourth cell 4–7 μm (\bar{x} =5 μm)), cylindrical to doliiform, medium brown to dark brown and mostly concolourous, third cell from base darker in mature conidia at times, septa and periclinal walls thicker, apical cell 3–5 μm (\bar{x} =4 μm) long, hyaline, conical, with 4(–5) apical appendages, 5–20 μm (\bar{x} =11 μm) long, with independent loci of origin at apical end of the cell, basal appendage 2–5 μm (\bar{x} =4 μm) long, single, eccentric, unbranched.

Material examined — ITALY, Province of Forlì-Cesena, San Lorenzo in Noceto - Forlì on dead aerial branch of *Vitis vinifera*, 29 April 2014, Erio Camporesi, IT 1838 (MFLU 15-0794).

Notes — A culture is not available for this species. Therefore, sequencing was carried out using fruiting bodies. This species is only known from leaves of *Chamaerops humilis* from Italy. This study provides the first record of *P. chamaeropsis* as a saprotroph on *V. vinifera*.



Fig. 43 – *Pestalotiopsis chamaeropsis*. a. Appearance of conidiomata on host surface. b. Close up of a conidioma. c, d. Vertical sections through conidiomata. e, f. Conidia arising from conidiogenous cells. g–k. Conidia. Scale bars: a=1000 μm , b=200 μm , c, d=50 μm , e–k=10 μm .

***Pestalotiopsis* sp.**

Facesoffungi number: FoF 03879

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 88–118 μm high, 99–163 μm diam. (\bar{x} =100×129 μm , n=5), gregarious to scattered, semi-immersed to erumpent through the host surface, sub-globose to

ampulliform, dark brown to black, unilocular, pycnidial, ostiole central with distinct papilla. *Pycnidial wall* 15–21 μm , thick-walled with equal thickness, composed of 6–7 layers of pseudoparenchymatous cells, outer layer with thick-walled dark brown to black, *textura angularis* to *textura globose*, inner layer with thin-walled light brown to hyaline *textura angularis* to *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–7 \times 2–3 μm (\bar{x} =5 \times 2 μm , n=10), discrete, cylindrical, swollen at the base, hyaline, smooth, thin-walled, producing a single conidium at the apex. *Conidia* 24–28 \times 8–10 μm (\bar{x} =26 \times 9 μm , n=20), fusoid, ellipsoid, straight to slightly curved, 4-septate; basal cell conic with a truncate base, hyaline, rugose and thin-walled, 3–6 μm long; three median cells doliiform, 16–20 μm long (\bar{x} =17 μm), wall verruculose, concolourous, olivaceous, (second cell from the base 4–7 μm (\bar{x} =5 μm); third 5–7 μm (\bar{x} =6 μm); fourth cell 4–7 μm (\bar{x} =5 μm); apical cell 3–5 μm (\bar{x} =4 μm) long, hyaline, sub-cylindrical, rugose and thin-walled; with 4–5 tubular apical appendages, arising from the apical crest, unbranched, filiform, flexuous, 9–23 μm long (\bar{x} =17 μm); basal appendage single, tubular, unbranched, centric, 4–9 μm (\bar{x} =6 μm) long.

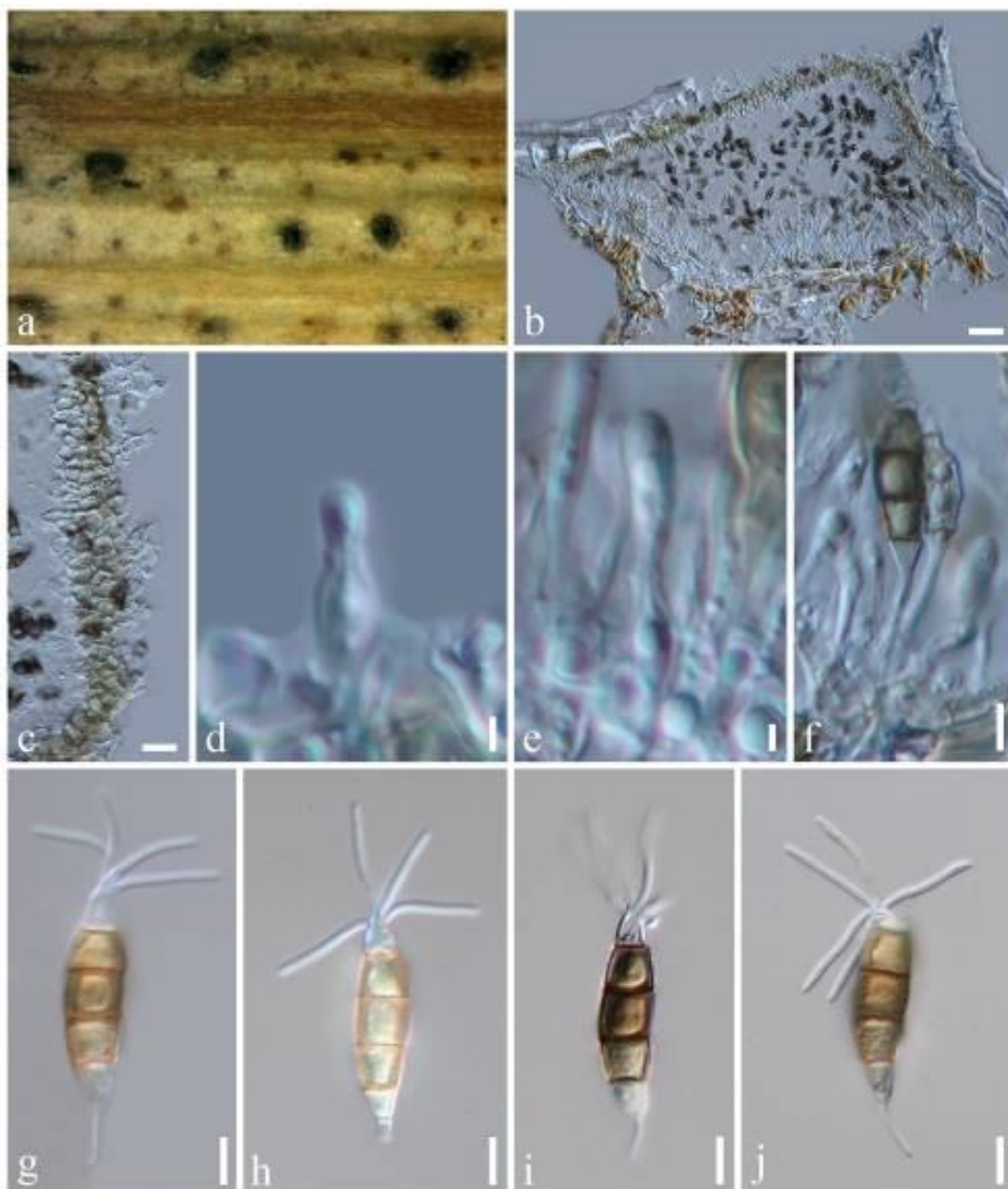
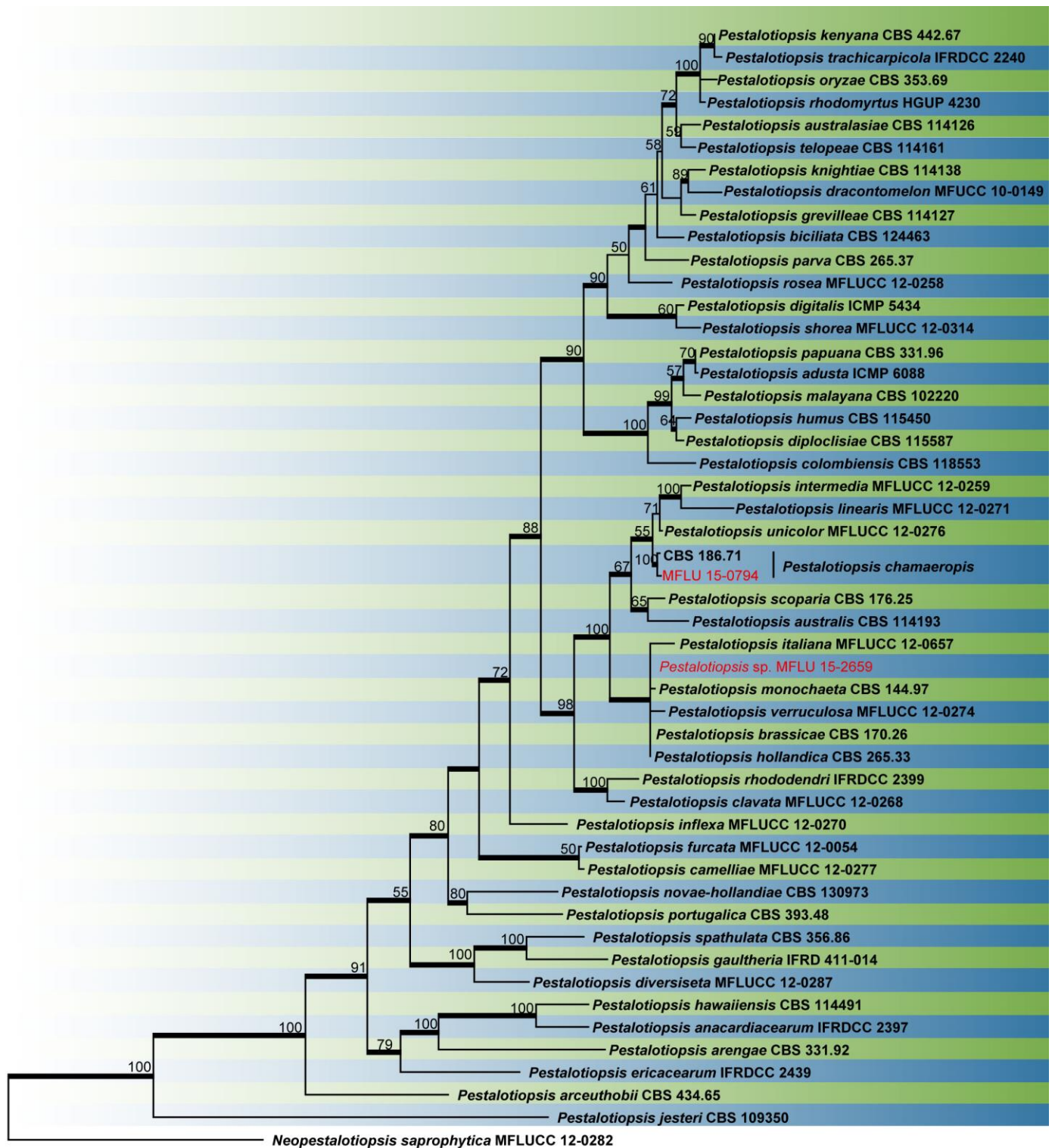


Fig. 44 – *Pestalotiopsis* sp. a. Appearance of conidioma on host surface. b. Longitudinal section of conidioma. c. Peridium. d-f. Conidiogenous cells. g-j Conidia. Scale bars: b=50 μm , c–e=20 μm , f–j=10 μm .



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Fig. 45 – One of the ten most parsimonious trees obtained from a heuristic search of combined ITS, TUB2 and TEF1 sequence data of taxa of *Pestalotiopsis*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Neopestalotiopsis saprophytica* MFLUCC 12-0282.

Material examined — ITALY, Province of Forlì-Cesena, San Lorenzo in Noceto- Forlì, on dead and aerial branch of *Vitis vinifera*, 29 April 2014, Camporesi Erio (MFLU 15-2659).

Notes — Several species of *Pestalotiopsis* have been recorded to be associated with *V. vinifera* in grape growing regions (Nag Raj 1993, Jayawardena et al. 2015, Maharachchikumbura et al. 2016b). Only ITS sequence data is available for this species, and in our phylogenetic tree it is placed in the clade with *P. italiana*, *P. monochaeta*, *P. verruculosa*, *P. brassicae* and *P. hollandica*. Due to the lack of protein coding regions that are useful for better resolution in *Pestalotiopsis*, we decided to keep it as an un-named *Pestalotiopsis* sp.

Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 180 (2014)

This genus was introduced to accommodate species with dark concolorous median cells and knobbed apical appendages (Maharachchikumbura et al. 2014). Combined gene phylogenetic analysis showed that our strain belongs with *P. camelliae-sinensis* (Fig. 47).

Pseudopestalotiopsis camelliae-sinensis F. Liu & L. Cai, Scientific Reports 7: 866: 12 (2017)

Facesoffungi number: FoF 01629

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose or clavate, aggregated, dark brown to black, up to 500 µm diam; exuding globose, dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete or integrated, ampulliform, subcylindrical or nearly globose, hyaline, smooth or minutely verruculose, 9–18×3–6 µm. *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, 25–34×6–9 µm (\bar{x} =28×8 µm, n=40); basal cell conic or obconic with a truncate base, hyaline, rugose and thin-walled, 3–6 µm long; three median cells doliiform or subcylindrical, 16–19 µm long, verruculose, concoloured, septa darker than the rest of cell and conidium constricted at septa; second cell from base, 5–8 µm long; third cell 4–7µm long; fourth cell 5–8µm long; apical cell 3–6 µm long, hyaline, subcylindrical or obconic with a truncate base, thin-walled, slightly rugose; with 2–3 tubular apical appendages (rarely 4), arising from the apical crest, unbranched, filiform, 24–53 µm long; basal appendage single, tubular, centric or uncentred, 6–9 µm long.

Culture characteristics — Colonies on PDA attaining 70–80 mm diam after 7 days at 25 °C, with lobate edge, whitish to pale honey-coloured, reverse whitish to pale honey.

Material examined — ITALY, Province of Forlì-Cesena, near Teodorano - Meldola, on dead aerial branch of *Vitis vinifera*, 15 February 2015, Erio Camporesi, IT 2380 (MFLU 15-0372), culture MFLUCC 17-1220 (KUMCC 17-0064).

Notes — Maharachchikumbura et al. (2016) proposed *Ps. camelliae* nomenclaturally as *Ps. ignota*, but in other parts of the same paper cited it as *Ps. camelliae*. Therefore, the name *Ps. camelliae* is considered as invalid. Liu et al. (2017) described a new species named *Ps. camelliae-sinensis* and our isolate clusters together with the type species of this new species. This study provides the first record of *Ps. camelliae-sinensis* as a saprotroph on *V. vinifera*.

Seimatosporium Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 3(13): 79 (1833)

Seimatosporium was introduced by Corda (1833) based on *S. rosae*. Species of this genus are known to be saprotrophs. Strains in this study clustered together with the type strain of *S. vitis* (Fig. 48).

Seimatosporium vitis Y.P. Xiao, Camporesi & K.D. Hyde, in Senanayake et al., Fungal Diversity 73: 102 (2015)

Facesoffungi number: FoF02938

Saprobic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 290–542 µm diam. (\bar{x} =466 µm, n=10), solitary or gregarious, semi-immersed, elongate to rounded, dark brown to black. *Pycnidial wall* light brown, thin-walled cells of *textura*

angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 15–32×1–3 μm (\bar{x} =20×2 μm, n=20), holoblastic, cylindrical, hyaline to pale brown, smooth-walled. *Conidia* 12–18×2–7 μm (\bar{x} =15×5 μm, n=40), ellipsoid or fusiform, straight or slightly curved, pale to dark brown, smooth-walled, 3-septate, constricted at septa, guttulate, apical cells conical with acutely rounded apex, base cells obconical, rounded at the base, bearing appendage at both ends. *Appendages* 7–14 μm (\bar{x} =11 μm, n=40), central or eccentric, single, unbranched, cylindrical, occur at both ends.

Culture characteristics — Colonies on PDA, circular, flat, entire-edged, dark brown centre on the surface, with white to smoke grey margin, dark brown centre on reverse, with grey olivaceous to white near the margin, reaching 8 cm diam. after 2 weeks at 20°C.

Material examined — ITALY, Province of Forlì-Cesena, Via Nenni - Forlì, on dead and aerial branch of *Vitis vinifera*, 9 March 2016, Erio Camporesi (MFLU 16–0998), culture MFLUCC 17-1060; ITALY, Province of Forlì-Cesena, Meldola, Teodorano, on dead and aerial branch of *V. vinifera*, 14 February 2015, Erio Camporesi, IT2377 (MFLU 15–0204).

Notes — The first *Seimatosporium* species identified from *Vitis* was *Seimatosporium vitis* (Senanayake et al. 2015). According to our phylogenetic analyses of combined LSU and ITS sequence data (Fig. 47), our isolates clade together with the type species of *S. vitis* (MFLUCC 14–0052) with relatively high bootstrap and Bayesian probabilities (99 % MP/ 1.00 PP). However, our isolate deviates from the type species by having larger conidiomata, smaller conidia, and by having appendages at both ends (Senanayake et al. 2015). Since phylogenetic evidence does not support our isolate to be a new species, we determine our isolate as *Seimatosporium vitis*.

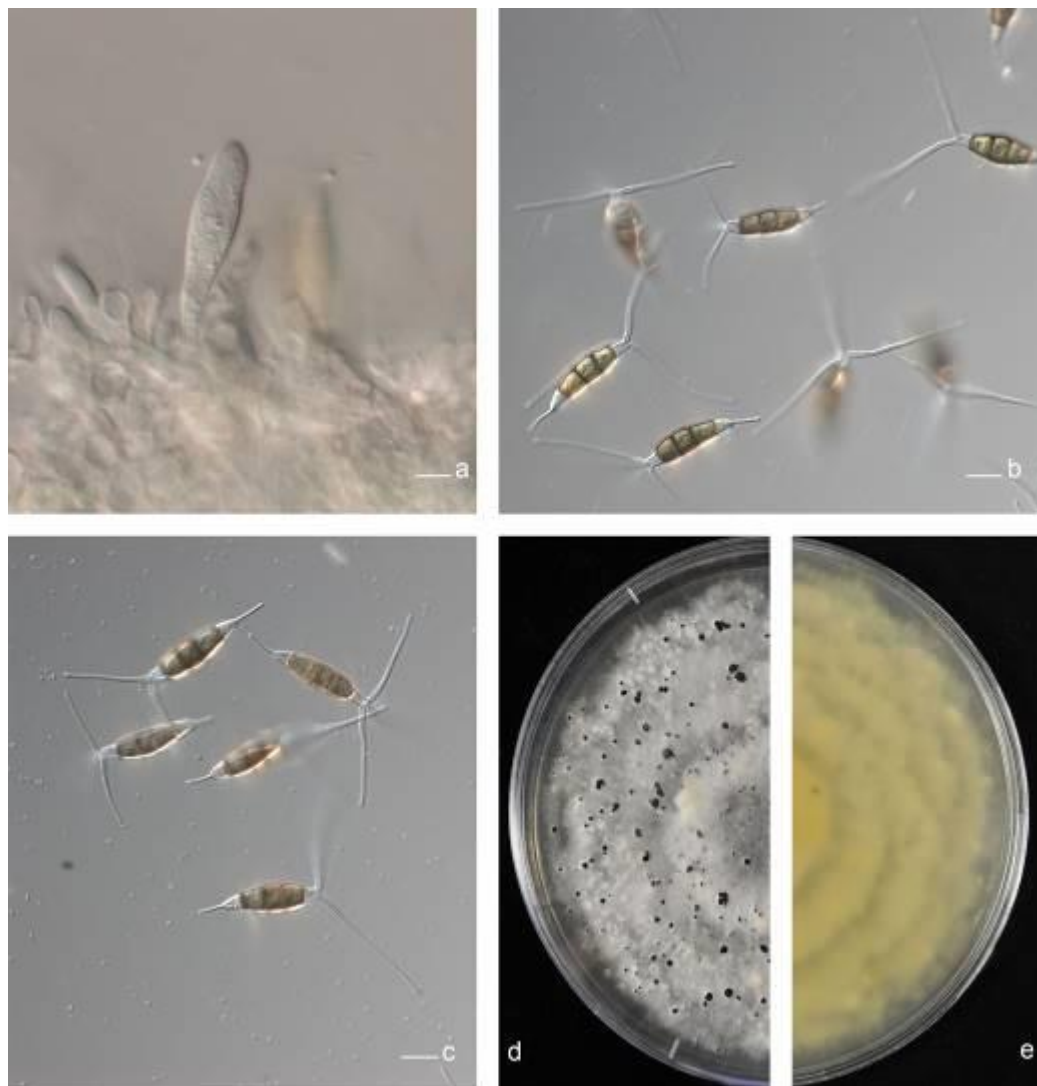


Fig. 46 –*Pseudopestalotiopsis camelliae-sinensis*. a. Conidiogenous cells. b-c. Conidia. d. Upper view of the colony. e. Reverse view of the colony. Scale bars: a–c=20 μm.

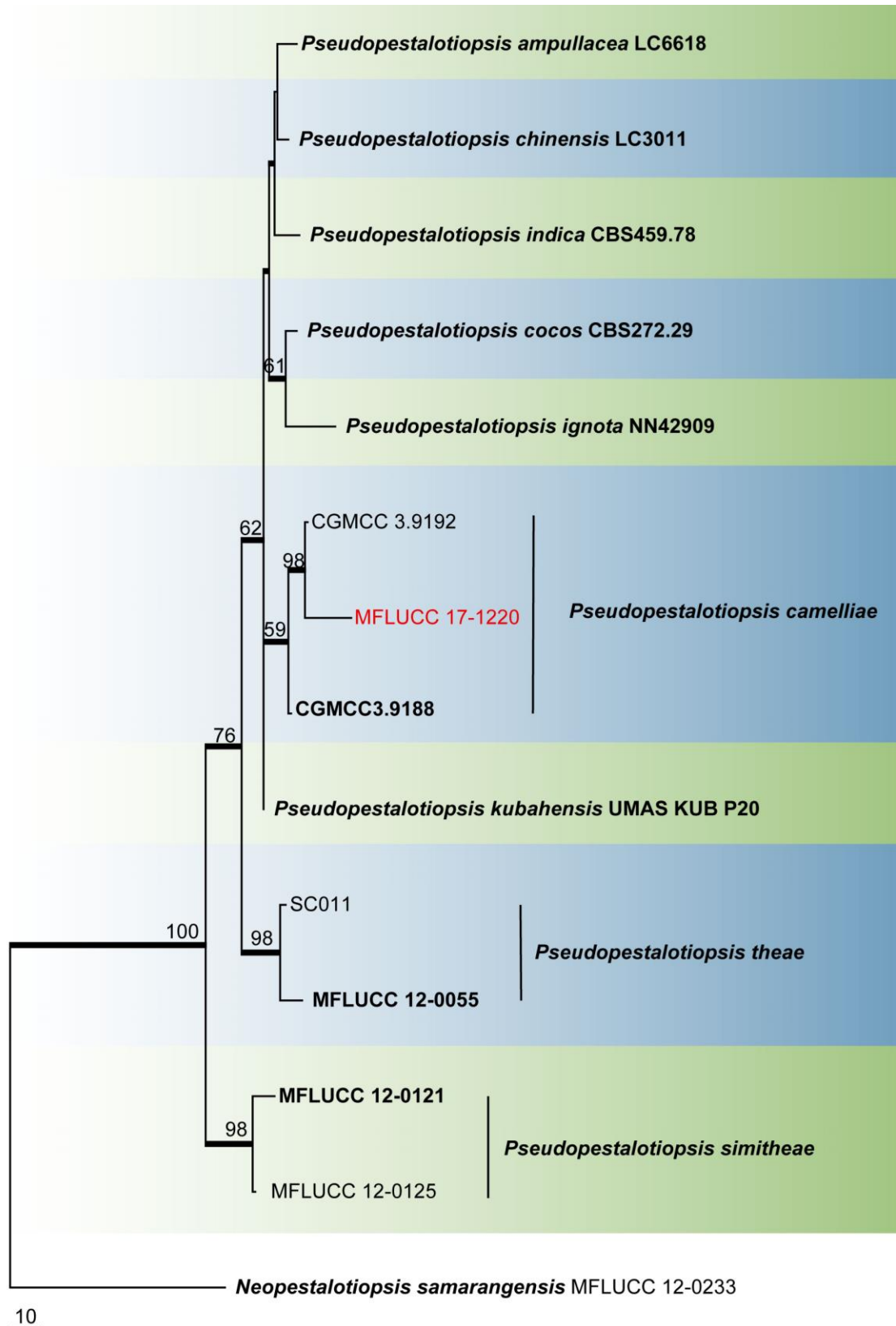


Fig. 47 – One of seven most parsimonious trees obtained from a heuristic search of combined ITS, TUB2 and TEF1 sequence data of taxa of *Pseudopestalotiopsis*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Neopestalotiopsis samarangensis* MFLUCC 12-0233.

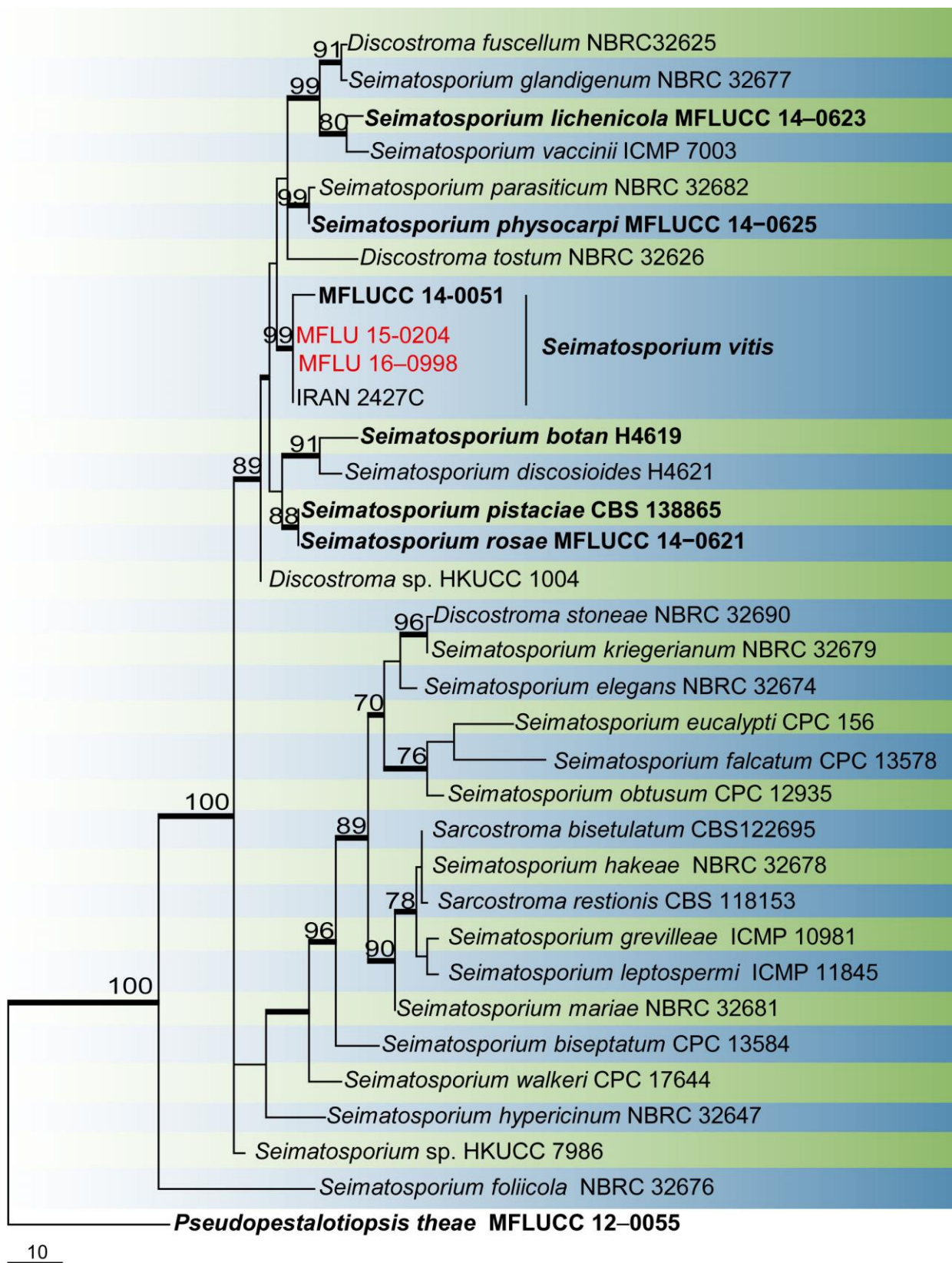


Fig. 48 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS and LSU sequence data of taxa from the *Seimatosporium*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.75 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Pseudopestalotiopsis theae* MFLUCC 12-0055.

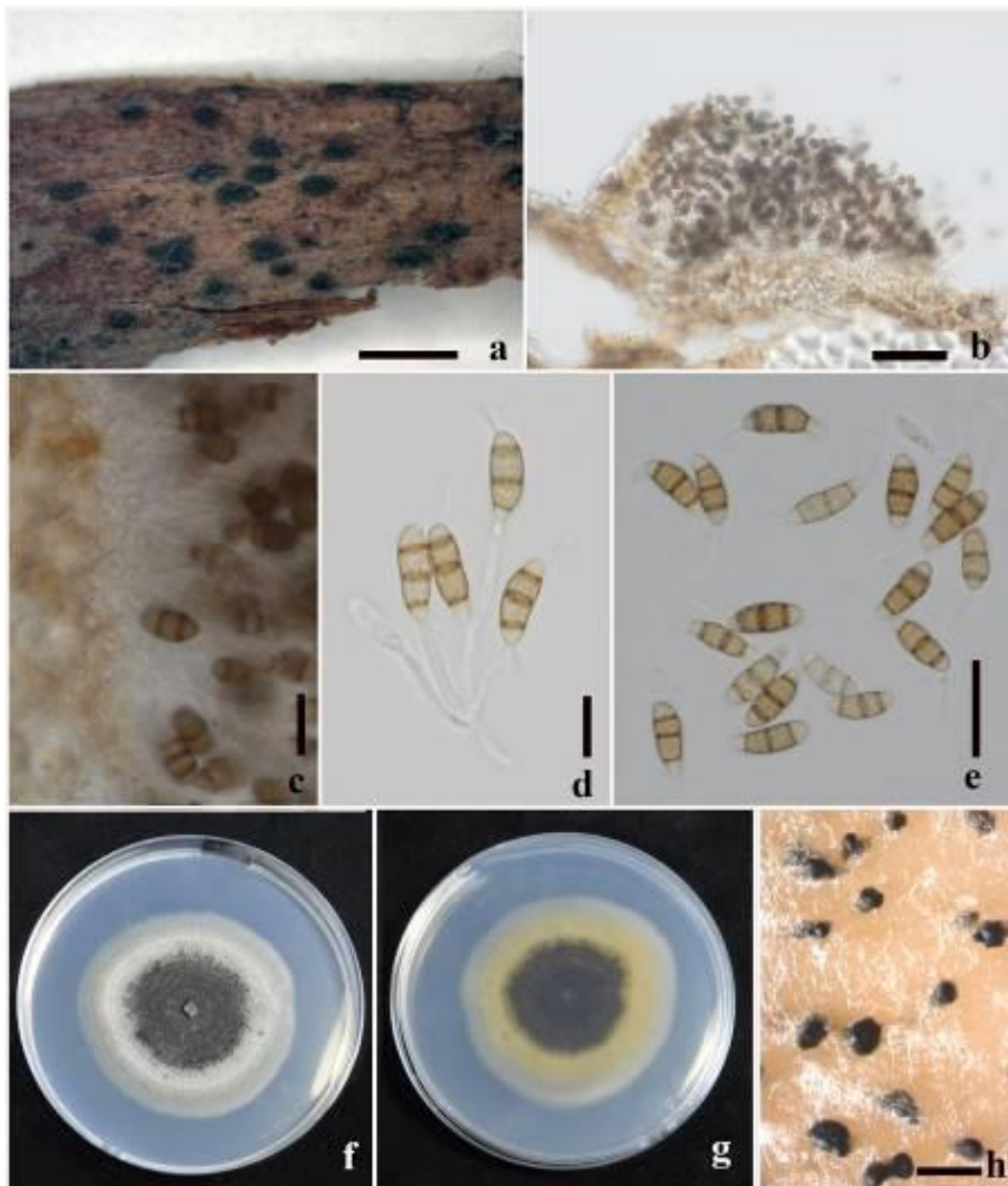


Fig. 49 – *Seimatosporium vitis*. a. Conidiomata on dead branch of *Vitis vinifera* b. Longitudinal section of a conidioma c. Longitudinal section of a conidioma wall d. Different stages of conidiogenesis e. Conidia f–g. Upper view (f), and the reverse view (g), of the colony on PDA h. Conidiomata on PDA. Scale bars: a=1000 μ m, b=50 μ m, c, d=10 μ m, e=20 μ m, h=2000 μ m.

Sordariales Chadev. ex D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 182 (1986)

Chaetomiaceae G. Winter, Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 153 (1885)

Chaetomiaceae was introduced by Winter (1885) and is typified by *Chaetomium* (Grunow et al. 1887). Twenty genera are presently placed in the family (Maharachchikumbura et al. 2015).

Chaetomium Kunze, in Kunze & Schmidt, Mykologische Hefte (Leipzig) 1: 15 (1817)

Chaetomium is a cosmopolitan genus with more than 150 species. Special characteristics of *Chaetomium* are ascomata covered with hairs or setae, clavate or fusiform or sometimes cylindrical thin-walled asci, lack of paraphyses before ascomata mature and 1-celled, brown or grey-brown ascospores with germ pores (Hawksworth & Wells 1973, von Arx et al. 1986). Strains in this study clustered together with the type strain of *C. globosum* (Fig. 50).

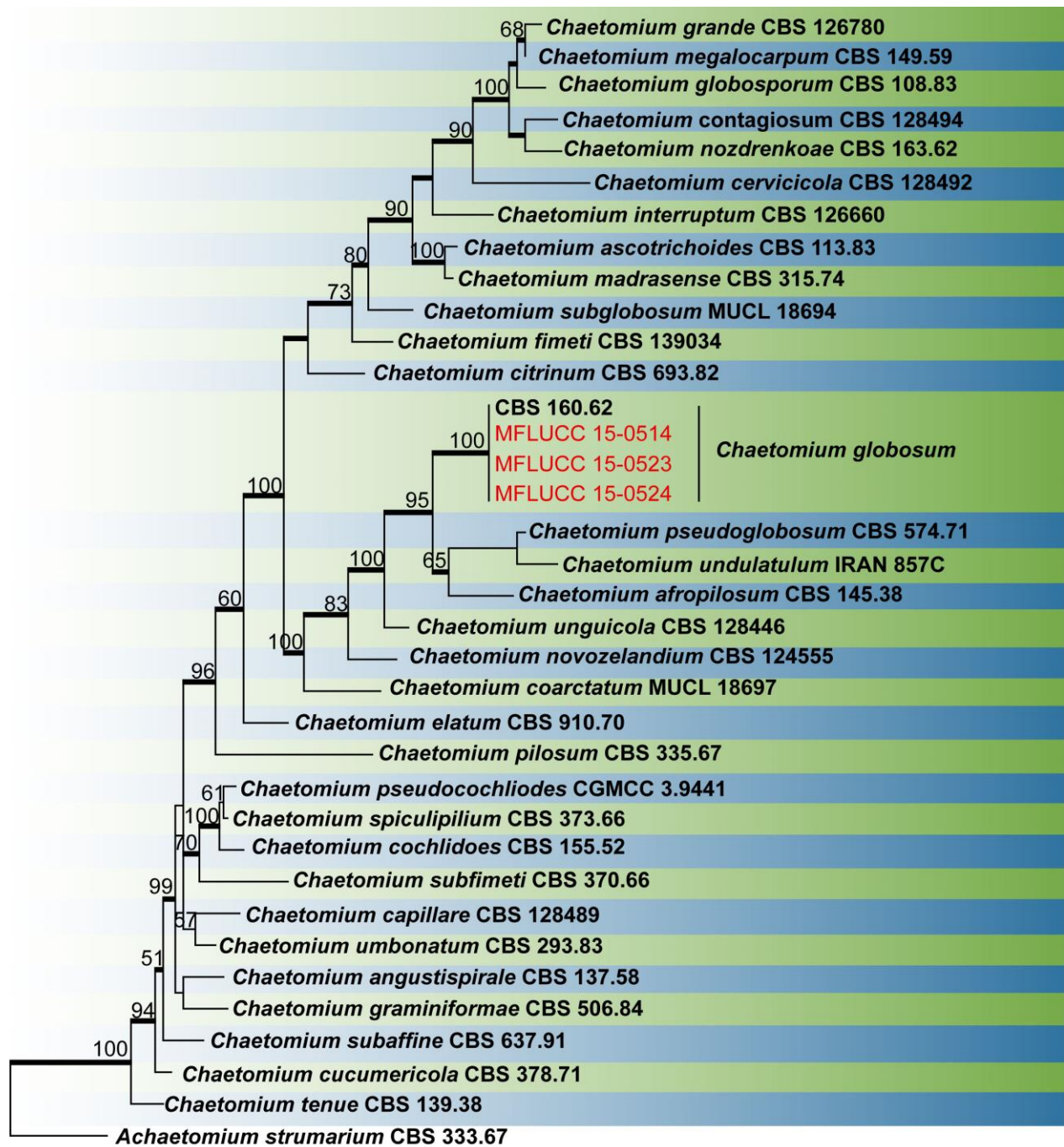


Fig. 50 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, LSU and TEF1 sequence data of taxa from the *Chaetomium*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.75 given in bold. Ex-type strains are in bold. Strains obtained in this study are in blue. The tree is rooted with *Achaetomium strumarium* CBS 333.67.

Chaetomium globosum Kunze, in Kunze & Schmidt, Mykologische Hefte (Leipzig) 1: 16 (1817)

Facesoffungi number: FoF03614

Saprotrophic on dead and aerial branch of *Vitis* sp. **Sexual morph:** *Ascomata* superficial, ostiolate, greenish olivaceous or slightly dark olivaceous buff to grey in reflected light owing to ascomatal hairs, globose, ellipsoid, ovate or obovate, 160–300×130–220 μm. *Ascomatal wall* brown, composed of hypha-like or amorphous cells, *textura intricata* in surface view. *Terminal hairs* abundant, finely verrucose, brown, tapering and fading towards the tips, 3–5 μm diam. near the base, flexuous, undulate to loosely coiled with erect or flexuous lower part, usually unbranched.

Lateral hairs brown, flexuous, fading and tapering towards the apices. *Asci* fasciculate, fusiform or clavate, spore-bearing part 28–40×10–15 µm, stalks 18–25 µm long, with eight biseriate ascospores, evanescent. *Ascospores* olivaceous brown when mature, limoniform, usually biapiculate, bilaterally flattened, 8–11×6–7 µm, with an apical germ pore. **Asexual morph:** Not observed (see Maharachchikumbura et al. 2016 for description).

Culture characteristics — Colonies on PDA reaching 50 mm in 7 days at 25 °C, brown or orange or white, woolly, border even, reverse buff-coloured to brown, aerial mycelium cottony or felty, with funiculose setae and hyphae. Mycelium abundant, intramatrical and aerial, composed of hyaline or dark brown, septate, hyphae.

Material examined — ITALY, Province of Forli-Cesena, Marsignano – Predappio, on dead and aerial branch of *Vitis* sp., 29 December 2014, Erio Camporesi IT2321 (MFLU 15-0687); living culture, MFLUCC 15-0514, 16-0523, 16-0524.

Notes — *Chaetomium globosum* is known as a pathogen causing soft rot of beechwood (Levi et al. 1965). This species is also known for its biological control properties (Wang et al. 2012). This species has been reported from *V. vinifera* as an endophyte in Spain and Switzerland (Casieri et al. 2009; Gonzalez & Tello 2011). This study provides the first report of *C. globosum* as a saprotroph associated with *Vitis* sp. in Italy.

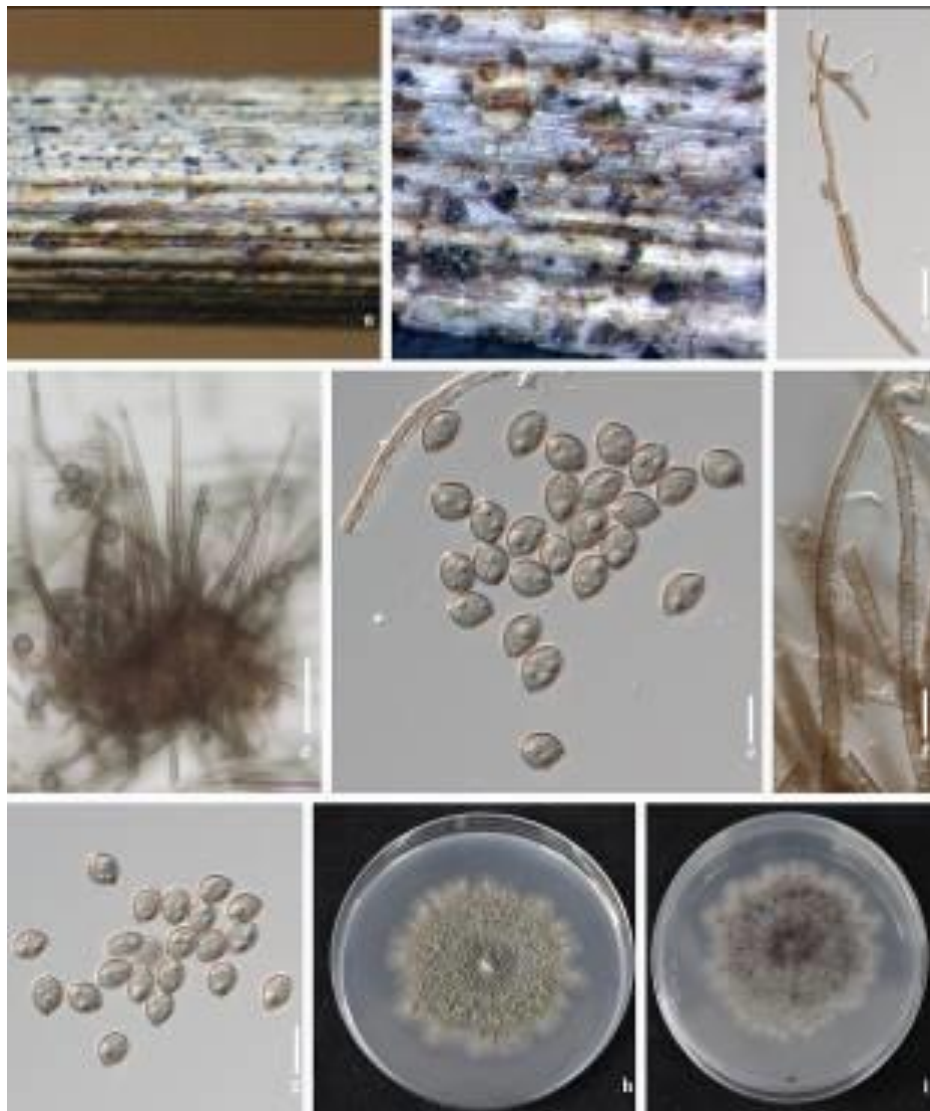


Fig. 51 – *Chaetomium globosum*. a, b. Conidiomata on host surface. c, f. Terminal ascomatal hairs. d. Ascoma. e, g. Conidia. h. Upper view of 7day old culture. g. Reverse view of 7 day old culture. Scale bars: d=100 µm, c, e–g=10 µm.

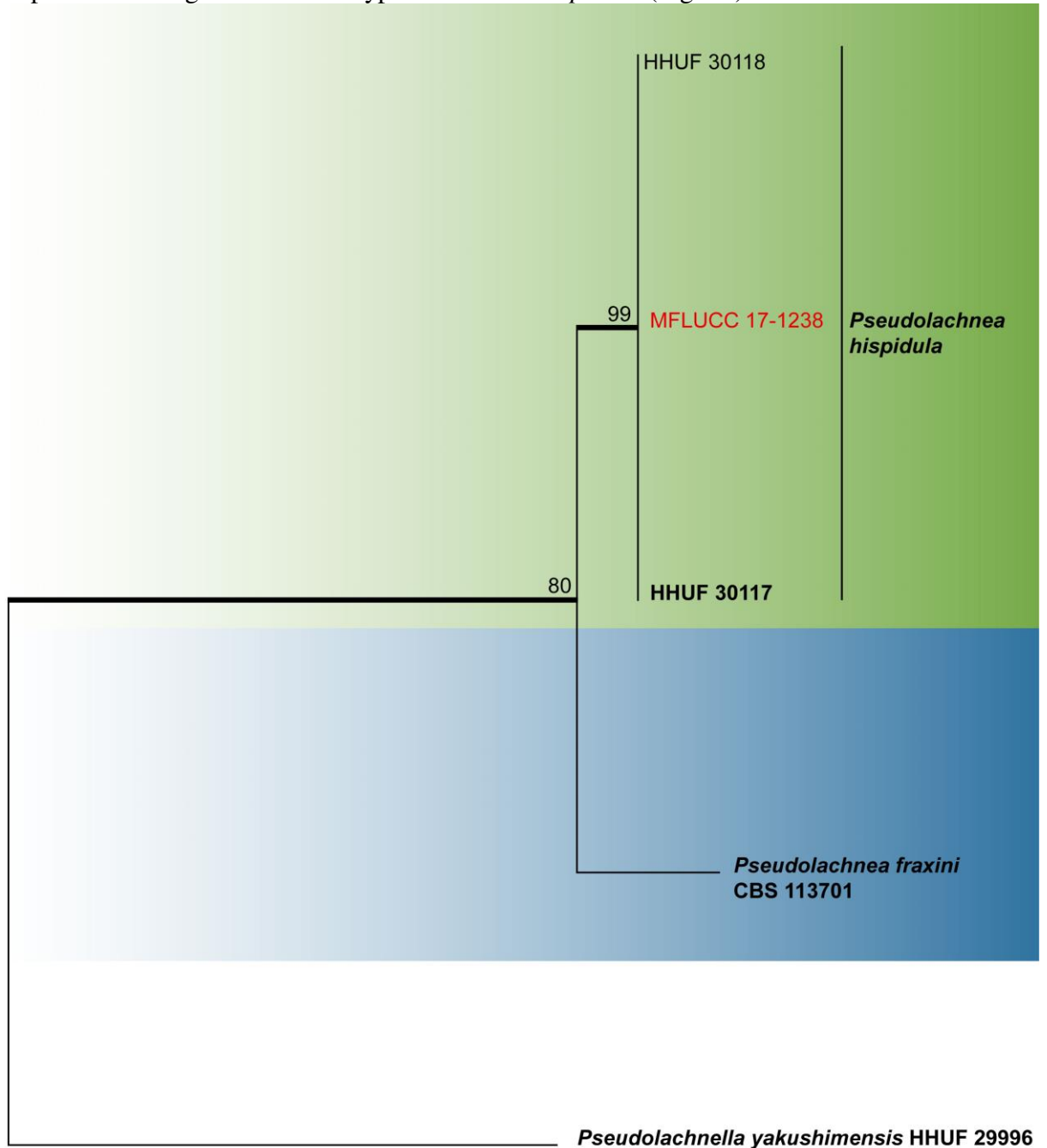
Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96(2): 378 (2004)

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels, Sydowia 51(1): 56 (1999)

The family is composed of morphologically diverse genera. *Chaetosphaeriaceae* is a family that needs molecular data to support the accepted genera (Maharachchikumbura et al. 2016).

Pseudolachnea Ranoj., Anns mycol. 8(3): 393 (1910)

Pseudolachnea is a genus with conidial appendages. There are only 21 epithets of this genus in Index Fungorum and a revision of this genus is needed (Index Fungorum 2018). Our strain from *Vitis* sp. clustered together with the type strain of *P. hispidula* (Fig. 52).



¹
Fig. 52 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS and LSU sequence data of taxa from the *Pseudolachnea*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in blue. The tree is rooted with *Pseudolachnella yakushimensis* HHUF 29996.

Pseudolachnea hispidula (Schrad.) B. Sutton, Mycol. Pap. 141: 167 (1977)

Facesoffungi number: FoF03615

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiomata* stromatic, acervular, cupulate, setose, ellipsoid, 180–700 µm diam. *Setae* 100–200 µm long, acute and 2–3 µm wide at the apex, 4–8 µm wide at the base. *Conidiophores* up to 16 µm long. *Conidiogenous cells* 8–10×1–2 µm (\bar{x} =9×1 µm, n=20). *Conidia* 11–17×2–3 µm (\bar{x} =15×2 µm, n=40), 1-septate, fusiform, slightly curved, hyaline, bearing an unbranched appendage, 1–3 µm long (\bar{x} =2 µm, n=40), at each end.

Culture characteristics — Colonies on PDA attaining 40 mm diam. in 7 day at 25 °C in the dark, floccose, straw coloured mycelium.

Material examined — ITALY, Province of Forlì-Cesena, Montegelli - Sogliano al Rubicone, on dead and aerial branch of *Vitis vinifera*, 31 March 2015, Erio Camporesi IT 2429 (MFLU 17-1250); living culture, MFLUCC 17-1238.

Notes — Our strain is morphologically similar to the type strain *P. hispidula* and the combined phylogenetic analysis of ITS and LSU sequence data established this. There are no records of species of this genus associated with *Vitis* sp. This study provides the first record of a *Pseudolachnea* species associated with *Vitis vinifera*.

Diaporthales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 53 (1932)

Diaporthaceae Höhn. ex Wehm., Am. J. Bot. 13: 638 (1926)

This family contains pathogens, endophytes and saprotrophs and has a worldwide distribution (Maharachchimbura et al. 2016). In this study we provide accounts of *D. ampelina*, *D. eres* and *D. rudis* from *Vitis* sp. and a new species is introduced based on morphological traits and phylogeny (Fig. 54).

Diaporthe Nitschke, Pyrenomyc. Germ. 2: 240 (1870)

Species of this genus are plant pathogens, endophytes or saprotrophs, commonly isolated from a wide range of hosts (Udayanga et al. 2012, 2014, Hyde et al. 2014). The phylogeny and taxonomy of the genus has been addressed in recent studies (Udayanga et al. 2012, 2014, 2015).

Diaporthe ampelina (Berk. & M.A. Curtis) R.R. Gomes, Glienke & Crous, Persoonia 31: 14 (2013)

Facesoffungi number: FoF03516

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiomata* up to 350 µm diam, 200–300 µm high, pycnidial, globose, unilocular, black, erumpent, walls consisting of two regions of *textura angularis*; the outer region brown, 2–3 cells thick, inner region brown 3–4 cells thick, with the outside cells compressed. *Alpha conidiophores* 8–30×1–3 µm (\bar{x} =24×2 µm, n=10), hyaline, smooth, densely aggregated, cylindrical, straight to sinuous. *Alpha conidiogenous cells* 4–15×1–2 µm (\bar{x} =11×2 µm, n=20), phialidic, subcylindrical, terminal and lateral, slightly tapering towards apex. *Paraphyses* not observed. *Alpha conidia* 7–12×1–4 µm (\bar{x} =8×3 µm, n=40), commonly found, aseptate, hyaline, smooth, guttulate, fusoid to ellipsoid, apex acutely rounded, base obtuse to subtruncate. *Beta conidia* 18–25×1–2 µm (\bar{x} =21×1 µm, n=20), straight, curved. *Gamma conidia* 13–16×1–2 µm (\bar{x} =15×1 µm, n=20).

Culture characteristics — Colonies on PDA attain 40 mm in 7 day, with fluffy white aerial mycelium with patches of saffron, reverse luteous to olivaceous-grey.

Material examined — ITALY, Province of Forlì-Cesena, Fiumana - Predappio, on dead and aerial branch of *Vitis vinifera*, 13 February 2016, Erio Camporesi IT 2831 (MFLU 16-0879); living culture, MFLUCC 17-1270, 17-1271; ITALY, Province of Forlì-Cesena [FC], Teodorano - Meldola, on dead branch of *Vitis vinifera*, 21 February 2015, Erio Camporesi IT 2384 (MFLU 15-3508); living culture MFLUCC 16-0960.

Notes — *Diaporthe ampelina* is known to causes cane and leaf spot and infection of pruning wounds of *Vitis* sp. (Dissanayake et al. 2017). Our strains show similar morphology to the type species of *D. ampelina* and clustered together with the type.

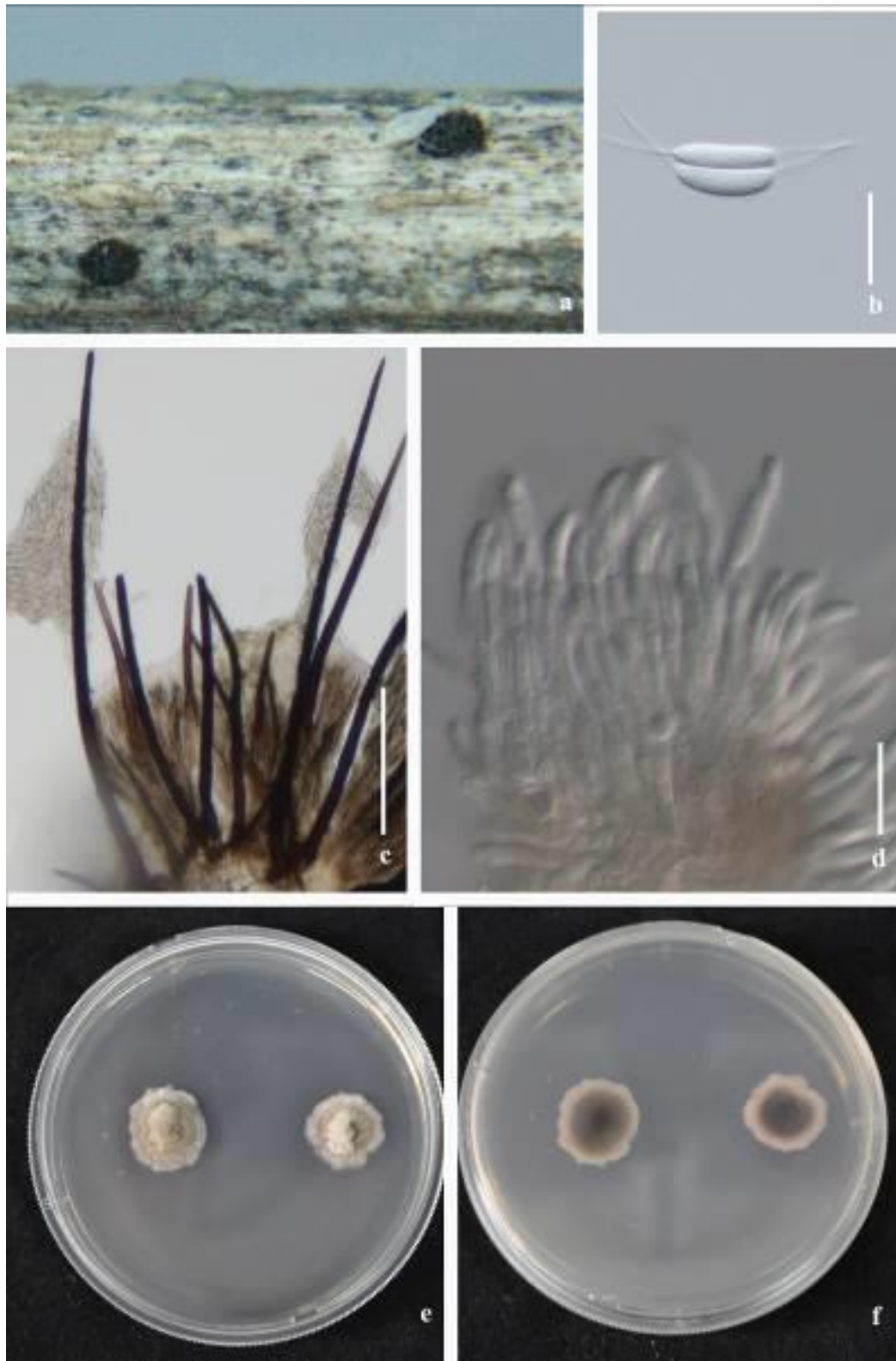
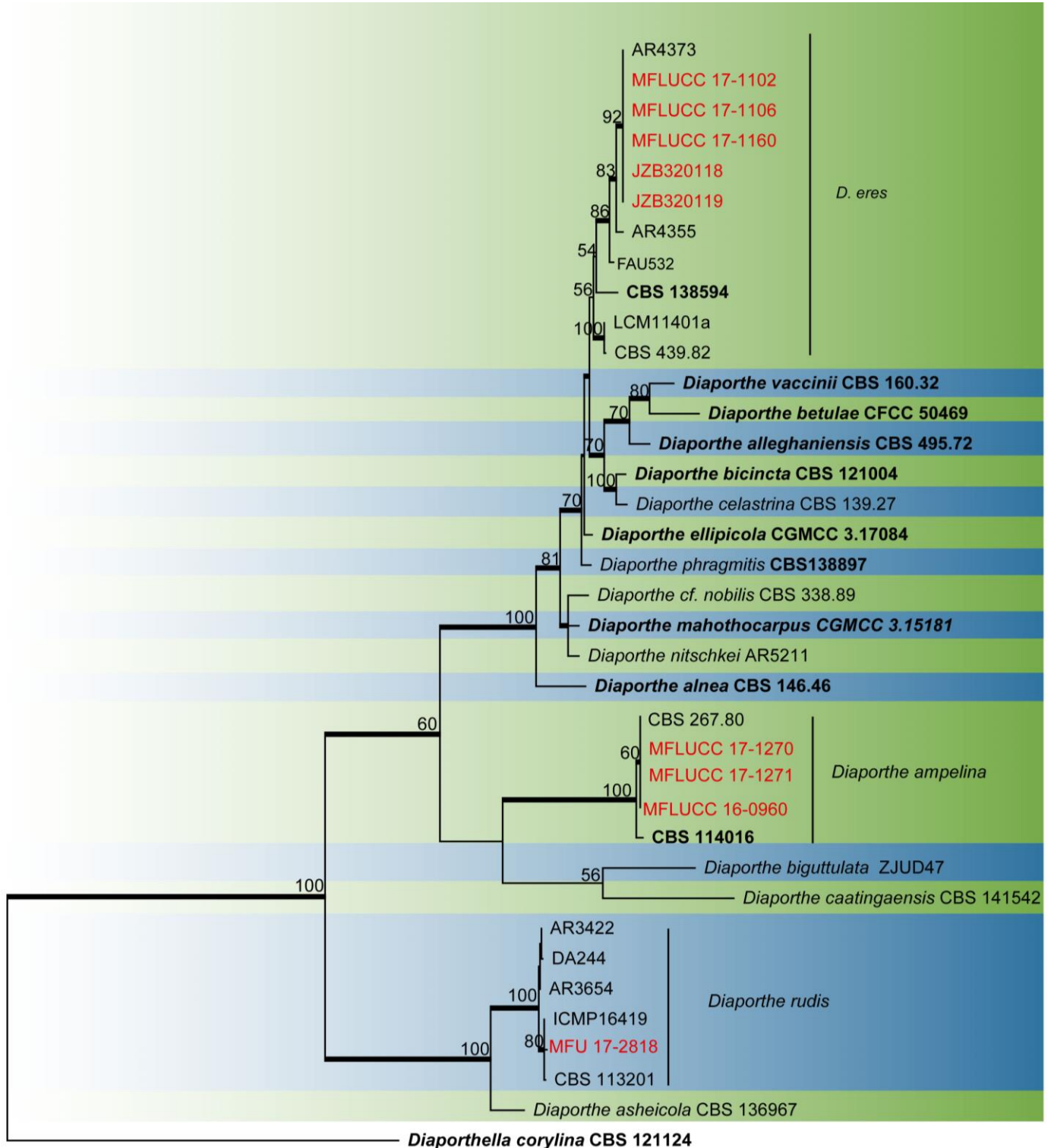


Fig. 53 – *Pseudolachnea hispidula*. a. Conidiomata on host. b. Conidia. c. Setae. d. Conidiophores and conidiogenous cells. e. Upper view of 7 day old culture. f. Reverse view of 7 day old culture. Scale bars: c=50 μ m, b, d=10 μ m.



10

Fig. 54 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, TUB2, TEF1 and CAL sequence data of taxa from *Diaporthe*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.75 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Diaporthe foeniculiana* CBS 111553.

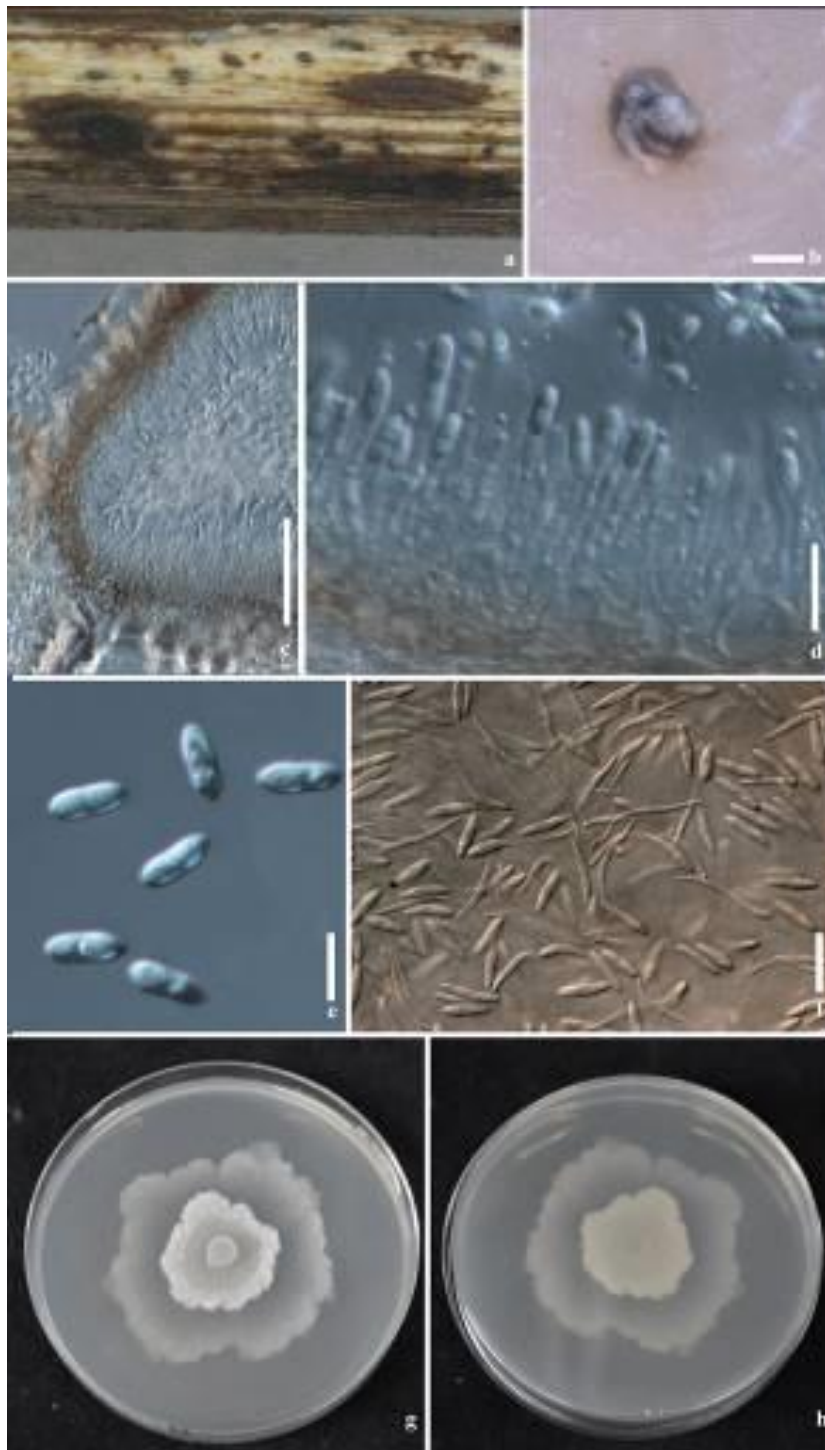


Fig. 55 – *Diaporthe ampelina*. a. Conidiomata on host tissue. b. Conidioma on PDA. c. Section of conidioma. d. Conidiophores. e. Alpha conidia. f. Beta and gamma conidia. g. Upper view of 7 day old culture. h. Reverse view of 7 day old culture. Scale Bars: c=50 μ m, d=20 μ m b, e, f=10 μ m.

Diaporthe eres Nitschke, Pyrenomyc. Germ. 2: 245 (1870)

Facesoffungi number: FoF02182

Saprotrophic on dead shoots of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Pycnidia* 200–250 μ m diam, globose, black, elongated neck, often with yellowish conidial cirrus extruding from ostiole, walls parenchymatous, consisting of 3–4 layers of medium brown cells of *textura angularis*. *Conidiophores* 10–15 \times 2–3 μ m (\bar{x} =12 \times 2, n=10), hyaline, smooth, unbranched, ampulliform. *Conidiogenous cells* 0.5–1 μ m diam, phialidic, cylindrical, terminal, slightly tapering towards the apex. *Paraphyses* absent. *Alpha conidia* 7–9 \times 3–4 μ m (\bar{x} =8 \times 3, n=40), abundant, aseptate, hyaline, smooth, ovate to ellipsoidal, often biguttulate, base

sub-truncate. *Beta conidia* 22–29×1–2 μm (\bar{x} =25×1, n=30), aseptate, hyaline, smooth, fusiform to hooked, base sub-truncate.

Cultural characteristics — Colonies on PDA reaching 70 mm in 14 days, white, aerial, fluffy mycelium, reverse iron-grey to black.

Material examined — CHINA, Beijing, on dead shoots of *Vitis vinifera*, 3 June 2015, Ruvishika Jayawardena, culture MFLUCC 17-1102, 17-1106 and 17-1160.

Notes — *Diaporthe eres* is a common pathogen of grapevine causing cankers (Fischer et al. 2016). This species is also a saprotroph (Udayanga et al. 2015). Our isolates clustered with the type of *D. eres* with high bootstrap support.

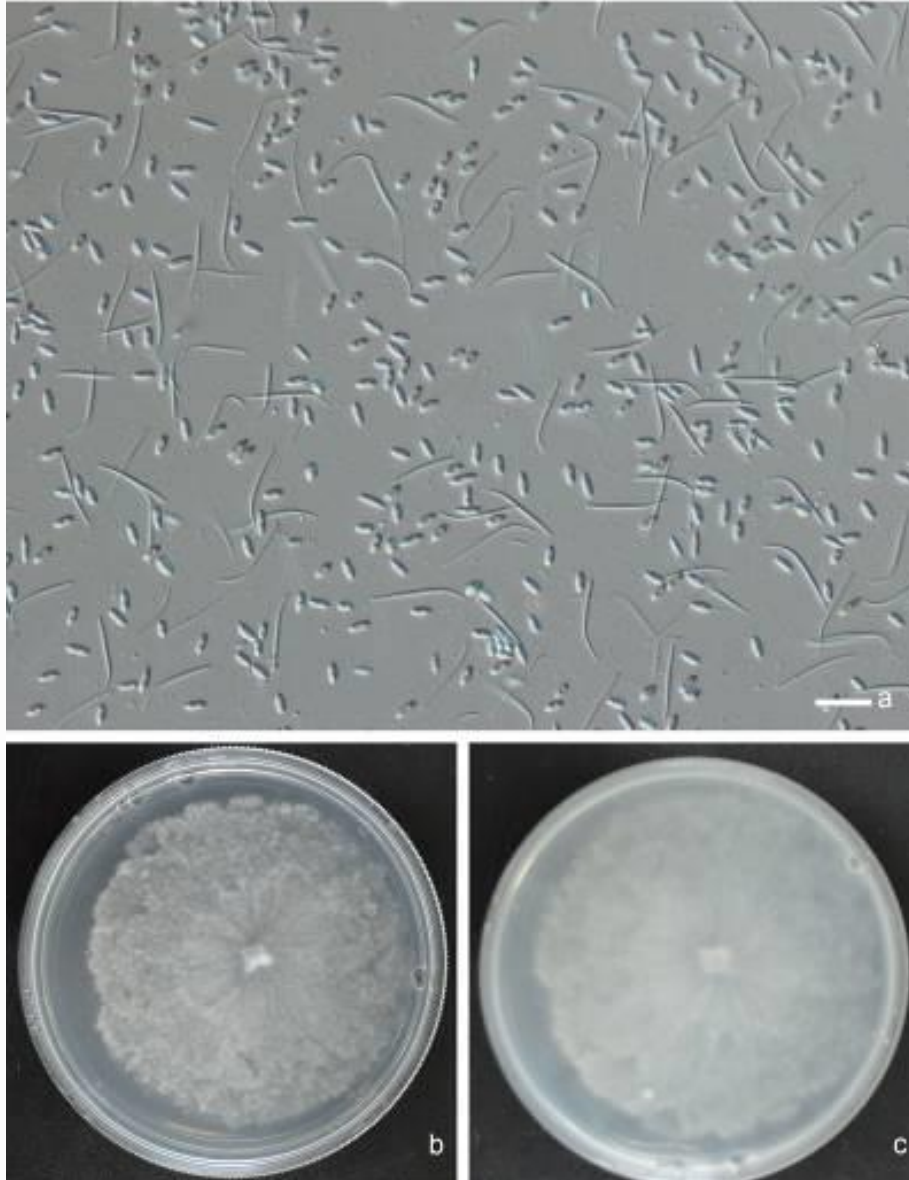


Fig. 56 – *Diaporthe eres*. a. Alpha and beta conidia. b. Upper view of 7 day old culture. c. Reverse view of 7 day old culture. Scale Bars: a=10 μm.

Diaporthe rudis (Fr.) Nitschke, Pyrenomyc. Germ. 2: 282 (1870)

Facesoffungi number: FoF03821

Saprotrophic on dead branch of *Vitis vinifera*. **Sexual morph:** *Ascomata* 300–340 μm high, 125–270 μm diam., (\bar{x} =330×250 μm, n=10), solitary or rarely aggregated, scattered, immersed to erumpent, globose to subglobose, black, coriaceous, ostiolate, papillate. *Papilla* 150–170 μm high, 65–70 μm wide (\bar{x} =160×75 μm, n=10), asymmetrical, short, internally covered by periphyses. *Peridium* inner, hyaline, thick-walled, compressed cells of *textura angularis* and outer, brown,

thick-walled, compressed cells of *textura angularis*. *Hamathecium* paraphysate. *Asci* 55–60×10–13 μm (\bar{x} =57×13 μm , n=20), 8-spored, unitunicate, ellipsoid to fusiform, sessile, apex with characteristic J-, apical ring. *Ascospores* 9–13×3–4 μm (\bar{x} =13×3 μm , n =20), biseriate, ellipsoid to fusiform, 1-septate, slightly constricted at the septa, ends pointed, sometimes upper cell narrowed towards the ends. **Asexual morph:** Not observed.

Material examined — ITALY, Province of Forlì-Cesena, Marsignano, Predappio, on dead and aerial branch of *Vitis vinifera*, 7 February 2014, Erio Camporesi, IT 1709, (MFLU 14–0xxxx).

Notes — A culture is not available for this species, direct sequencing of fruiting bodies was conducted. *Diaporthe rudis* is known as a pathogen on *Vitis vinifera* from several countries. This study provides the sexual morph of this species and reports this species as a saprotroph on *V. vinifera* in Italy.

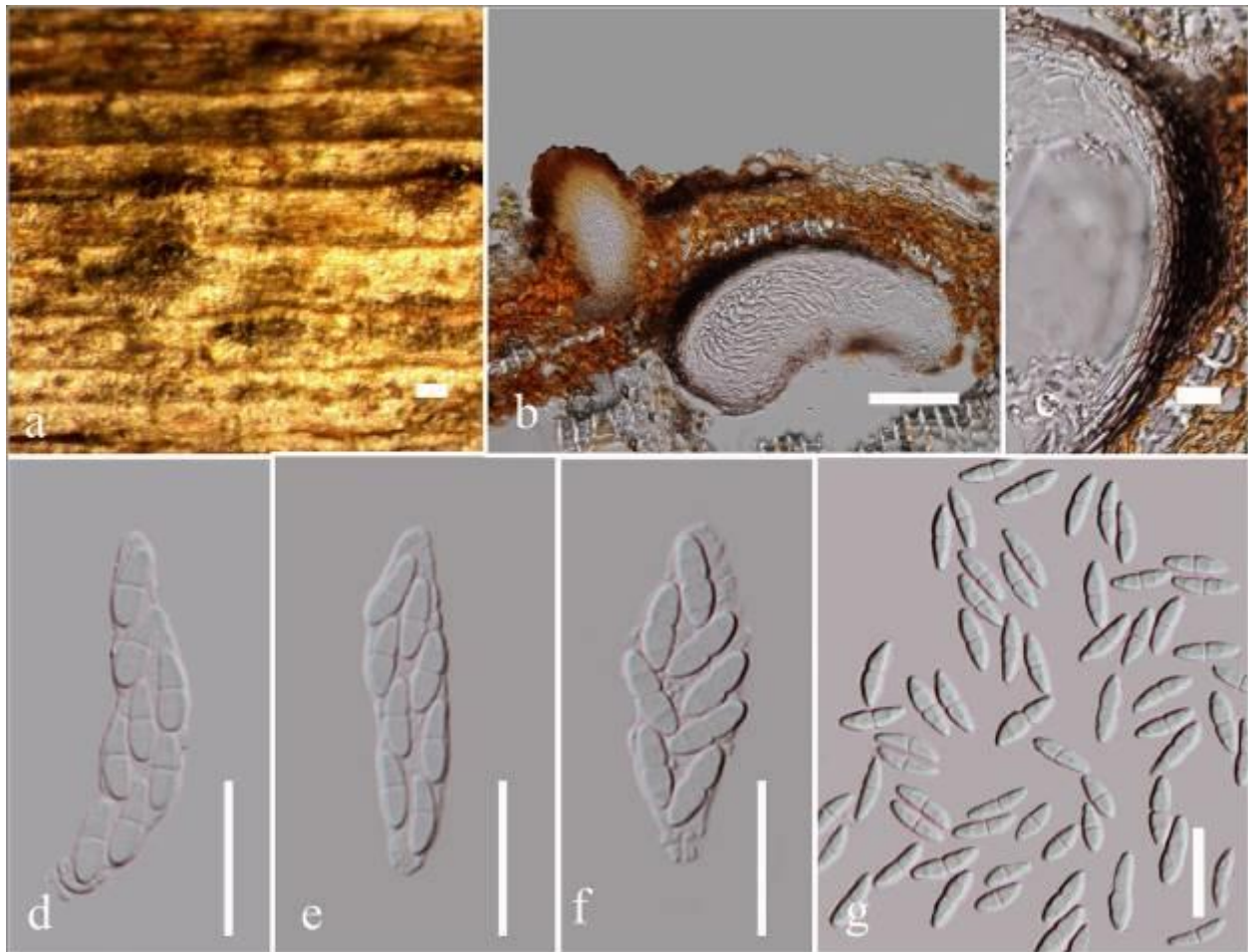


Fig. 57– *Diaporthe rudis*. a. Ascomata on substrate. b. Cross section of ascoma. c. Peridium. d–f. Asci. g. Ascospores. Scale bars: a=200 μm , b=100 μm , c=20 μm , d–g=10 μm .

Schizoparmaceae Rossman, D.F. Farr & Castl. [as 'Schizoparmeaceae'], Mycoscience 48(3): 137 (2007)

This family was introduced to accommodate *Schizoparme* and the asexual morph genus *Coniella* (Maharachchikumbura et al. 2016). Species of this family are pathogens or saprotrophs.

Coniella Höhn., Ber. dt. bot. Ges. 36(7): 316 (1918)

Coniella was introduced to accommodate *C. pulchella* Höhn. Species of *Coniella* are commonly associated with a wide variety of woody and herbaceous hosts (van Niekerk et al. 2004). Our strains clustered together with the type species of *C. vitis* (Fig. 59).

Coniella vitis Chethana, Yan, Li & K.D. Hyde, Chethana et al. Plant Diversity 101(12):2129(2017)
Facesoffungi number: FoF02722
See Chethana et al. (2017) for description.

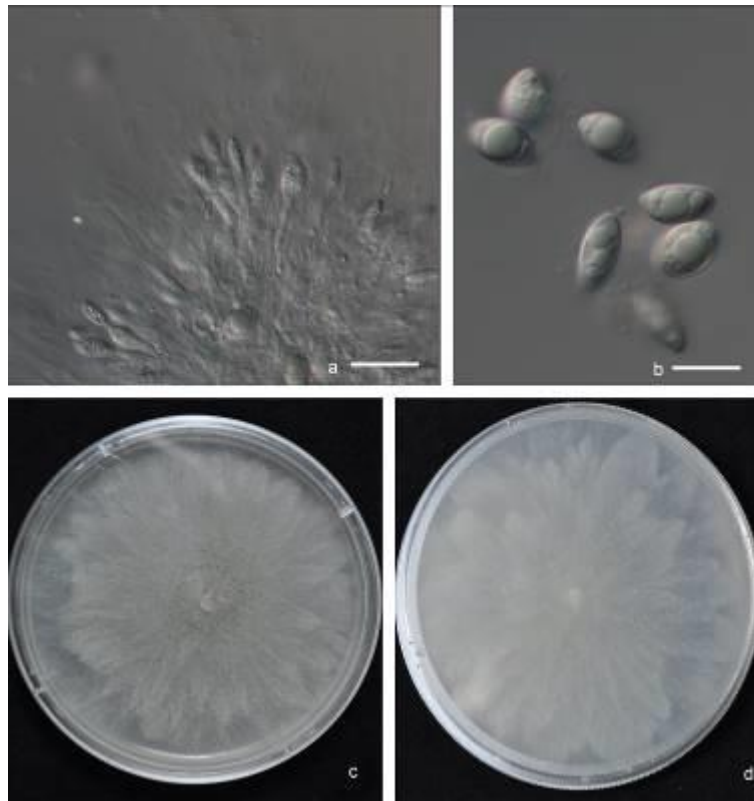


Fig. 58 – *Coniella vitis*. a. Conidiogenous cells. b. Conidia c. Upper view of 7 day old culture. d. Reverse view of 7 day old culture. Scale Bars: a–b=10 μ m.

Material examined — CHINA, Beijing, on dead leaves of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-1113, JZB370026; CHINA, Beijing, on dead bark of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-1123, MFLUCC 17-1138; CHINA, Beijing, on dead shoot of *V. vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-1125, JZB370014, JZB370009.

Notes — *Coniella vitis* was introduced by Chethana et al. (2017) to accommodate the white rot pathogen in Chinese vineyards. Our strains clustered with the type strain of this species. This study provides the first record of *C. vitis* as a saprotroph on *V. vinifera* in China.

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert, Stud. Mycol. 68: 170 (2011)

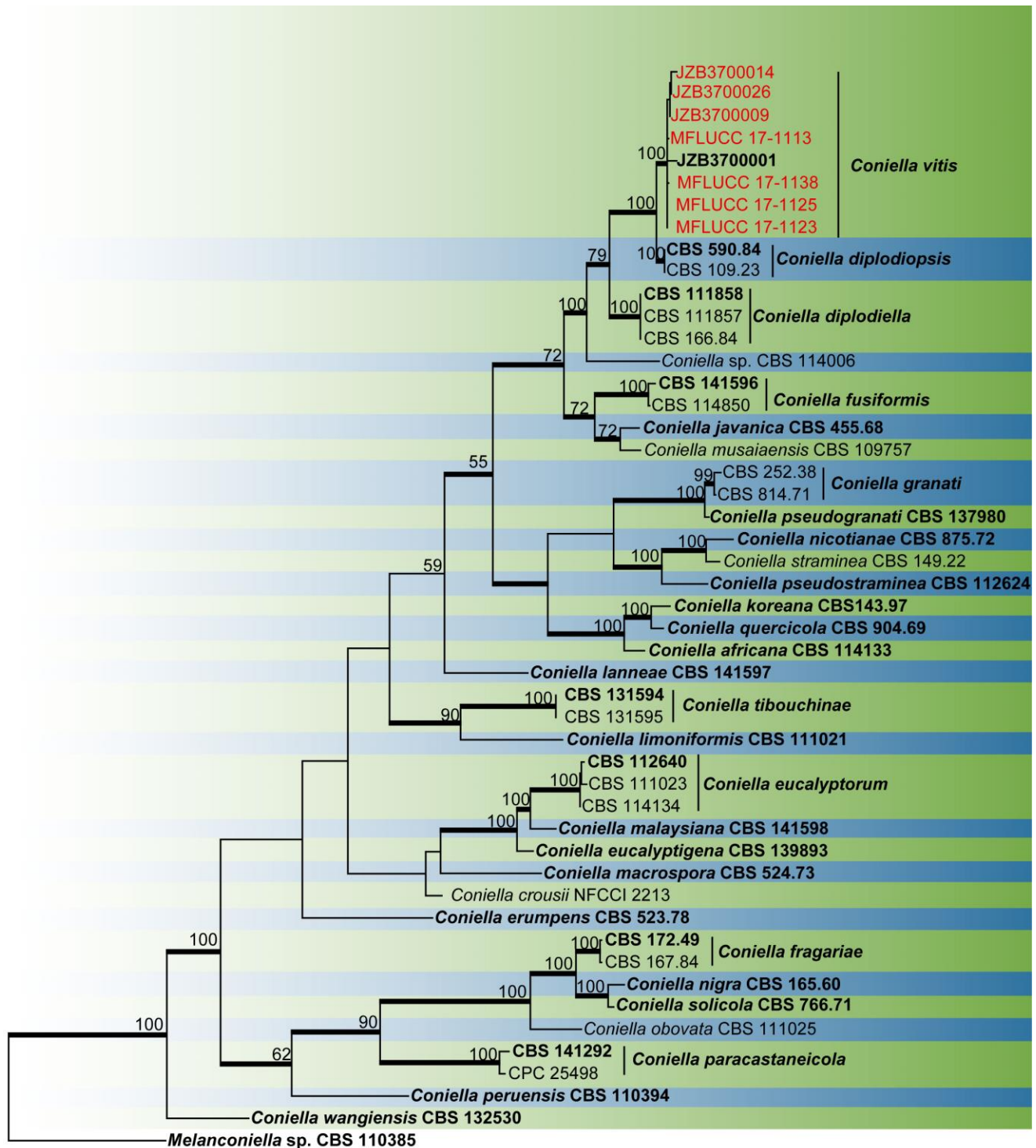
Glomerellaceae Locq. ex Seifert & W. Gams, in Zhang, Castlebury, Miller, Huhndorf, Schoch, Seifert, Rossman, Rogers, Kohlmeyer, Volkmann-Kohlmeyer & Sung, Mycologia 98(6): 1083 (2007) [2006]

Glomerellaceae is a monotypic family, mainly comprised of pathogens. The family was invalidly published by Locquin (1984) and was validated in Zhang et al. (2006). This family was accepted as one of the three families of *Glomerellales* in Réblová et al. (2011). This family is characterized by the *Colletotrichum* asexual morph and the *Glomerella* sexual morph, the latter was synonymized under *Colletotrichum* (Hyde et al. 2014, Maharachchikumbura et al. 2016a).

Colletotrichum Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 3(12): 41 (1831)

This genus was introduced by Corda (1831) for *C. lineola* Corda and until recent studies used a polyphasic approach including multigene phylogenetic analysis, the genus was highly confused (Cai et al. 2009, Hyde et al. 2009a,b). *Colletotrichum* is comprised mainly of pathogens,

but some species are endophytes or saprotrophs (Hyde et al. 2014, Jayawardena et al. 2016b). Kirk et al. (2001, 2008), Réblová et al. (2011) placed *Colletotrichum* in *Glomerellaceae* and this placement was confirmed by Maharachchikumbura et al. (2016a). We provide accounts for *C. dematium*, *C. godetiae*, *C. hebeiense*, *C. siamense*, *C. truncatum* and *C. viniferum* based on morphology and multigene phylogenetic analysis.



10

Fig. 59 – One of seven most parsimonious trees obtained from a heuristic search of combined ITS, LSU, histone and TEF1 sequence data of taxa of *Coniella*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Melanconiella* sp. CBS 110385.

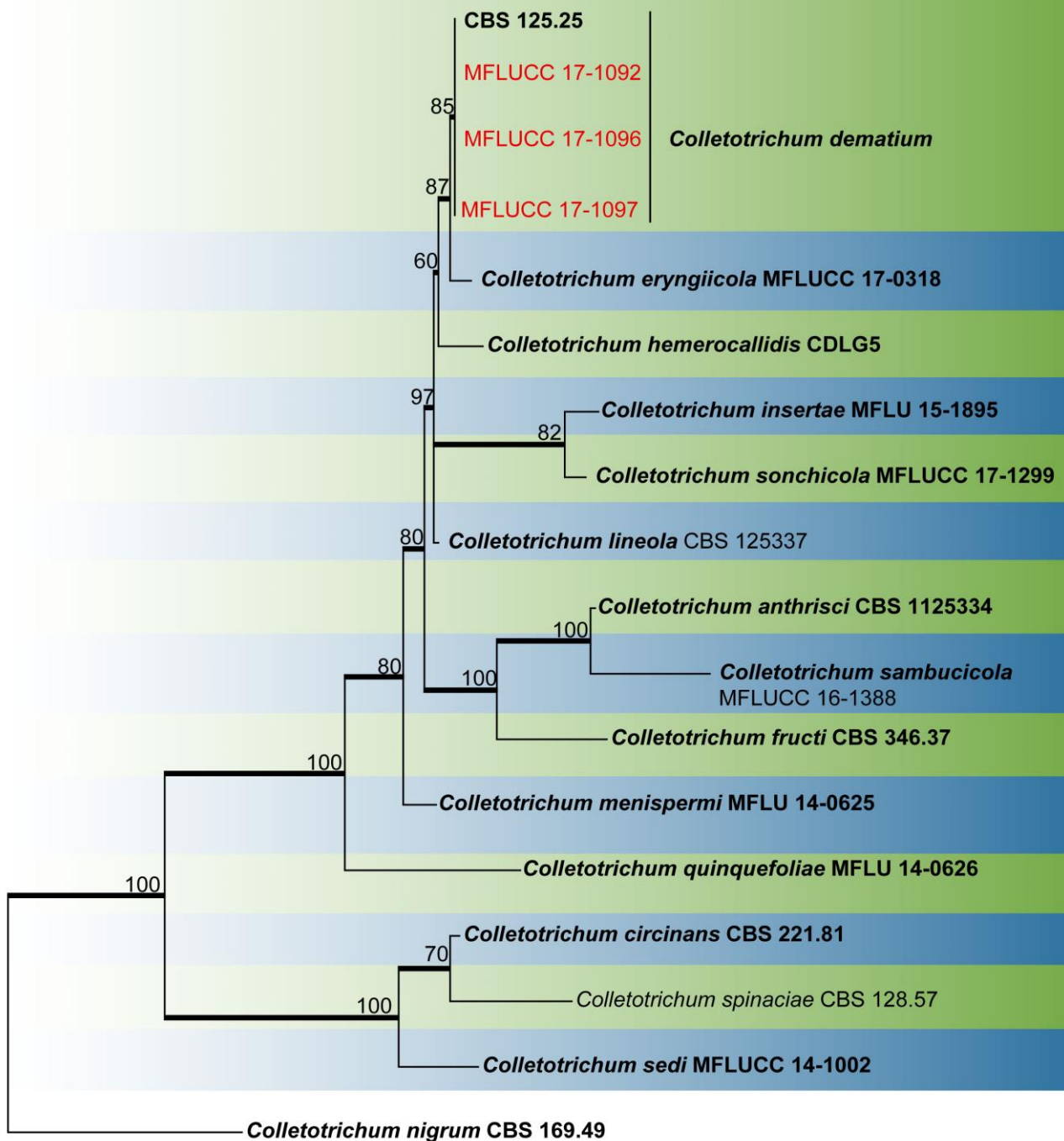


Fig. 60 – One of eight most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS, ACT and TUB2 sequence data of taxa for the dematium species complex. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in blue. The tree is rooted with *Colletotrichum nigrum* CBS 169.49.

Colletotrichum dematium (Pers.) Grove, J. Bot., Lond. 56: 341 (1918)

Facesoffungi number: FoF03598

Saprotrophic on dead and dying twigs of *Vitis vinifera*. **Sexual morph:** Not observed.

Asexual morph: *Conidiomata* 130–400 μm (\bar{x} =270 μm , n=10) diam., black, acervulus, oval, solitary, gregarious. *Setae* straight or \pm bent, rarely observed, dark brown, becoming paler towards the apex, opaque, smooth-walled, 1–6-septate, 30–145 μm long, base cylindrical, slightly inflated,

7–11 μm diam., tip acute to rounded, smooth. *Conidiophores* simple, to 20 μm long, hyaline to pale brown, septate. *Conidiogenous cells* enteroblastic, 5–16 \times 2–4 μm (\bar{x} =12 \times 3 μm , n=20), hyaline, smooth-walled, cylindrical to slightly inflated, opening 0.5–1 μm wide, collarette or periclinal thickening observed. *Conidia* 17–25 \times 3–5 μm (\bar{x} =18 \times 4 μm , n=15), L/W ratio=5, hyaline, smooth or verruculose, aseptate, curved, both sides gradually tapering towards the round to slightly acute apex and truncate base, guttulate. *Appressoria* not observed.

Cultural characteristics — Colonies on PDA, reaching 40–55 mm in 7 days at 25 °C, flat with entire margin, aerial mycelium sparse, short, pale olivaceous-grey, colony surface buff, some sectors dark grey-olivaceous to dark olivaceous-grey, iron-grey acervuli can be observed mainly on the edge of the colony. Reverse olivaceous-green, concentric rings clearly observed.

Material examined — RUSSIA, Rostov region, Shakhty city, urban green area, on dead and dying twigs of *Vitis vinifera*, 1 March 2016, Timur S. Bulgakov T-1209 (MFLU 16-1308), culture, MFLUCC 16-1388=KUMCC 16-0127, MFLUCC 17-1092, MFLUCC 17-1096, MFLUCC 17-1097.

Notes — *Colletotrichum dematium* species complex is mainly characterized by having curved conidia (Jayawardena et al. 2016b). The strains used in this study cluster together with the type species of *C. dematium* (Fig. 58). *Colletotrichum dematium* has been reported as an endophyte in *Vitis* sp. (Jayawardena et al. 2016b). This study provides the first report of *C. dematium* as a saprotroph on *Vitis* sp.

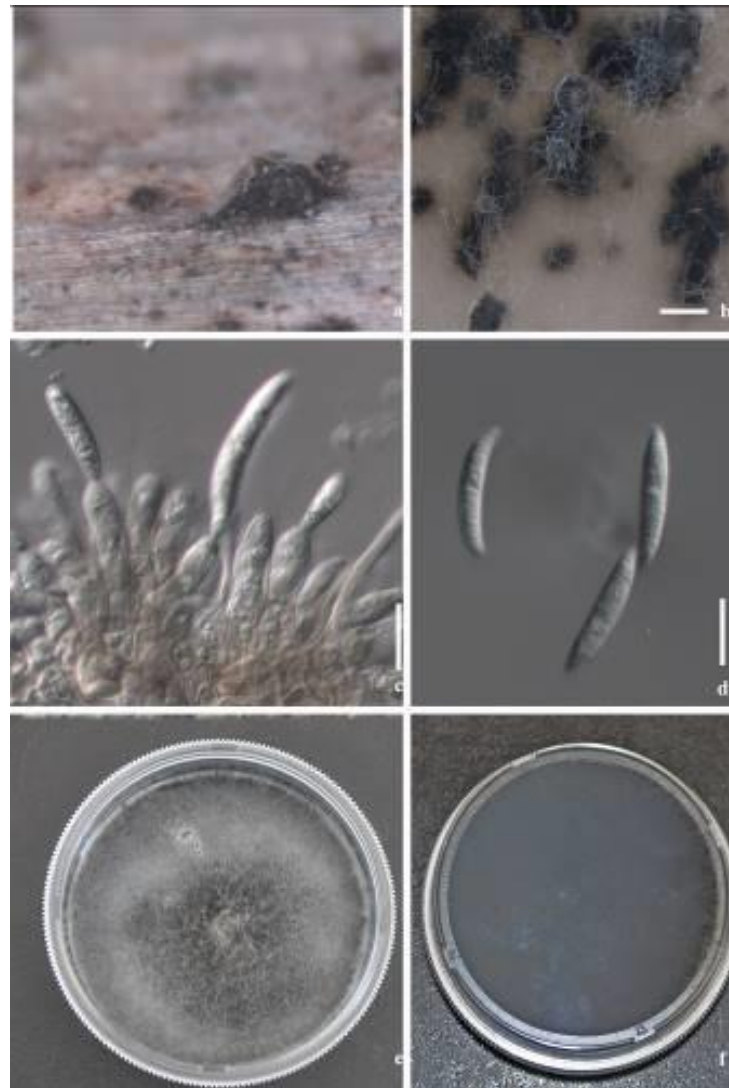


Fig. 61 – *Colletotrichum dematium*. a. Conidiomata on host. b. Conidiomata on PDA. c. Conidiophores and conidiogenous cells. d. Conidia. e. Upper view of 7 day old culture. f. Reverse view of 7 day old culture. Scale bars: b–d=10 μm .

Colletotrichum godetiae Neerg., Friesia 4(1–2): 72. 1950.

Facesoffungi number: FoF 03881

Saprotrophic on dead and aerial branch of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** On PDA, *Conidiomata* absent, conidiophores form directly on hyphae. *Vegetative hyphae* 1–7 µm, hyaline to pale brown, septate, branched, smooth-walled. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, simple. *Conidiogenous cells* 5–11×3–7 µm (\bar{x} =7×4 µm, n=20), hyaline, smooth-walled, cylindrical, often with short neck. *Conidia* 11–17×4–6 µm (\bar{x} =14×5 µm, n=30), L/W ratio= 2.8, cylindrical to fusiform, straight, hyaline, smooth-walled, acute at both ends or rarely one end rounded and one end slightly acute, aseptate. Conidial exudate salmon to orange.

Culture characteristics — Colonies on PDA, circular, flat, entire margin, initially white aerial mycelium, at maturity turns dark olivaceous-grey in the margin and white towards the centre, reverse greyish brown towards the margin and dark vinaceous buff to grey towards centre, reaching 3 cm diam. after 7 days at 20 °C.

Material examined — ITALY, Province of Forlì-Cesena, Fiumana – Predappio, on dead and aerial branch of *Vitis vinifera*, 13 February 2016, Erio Camporesi IT 2831 (MFLU 16-0879), culture, MFLUCC 16-1395, MFLUCC 17-1062.

Notes — *Colletotrichum godetiae* clustered in the *Colletotrichum acutatum* species complex (Jayawardena et al. 2016b). This species was invalidly described by Neergaard, from seeds of *Clarkia hybrida* cv. Kelvedon Glory., and later validated with a Latin description (Neergaard 1950). In our phylogenetic analyses of combined ITS, GDPH, CHS, ACT and β-tubulin sequence data (Fig. 61), our isolates are in a well-defined clade with the type species of *C. godetiae* (CBS 133.44) with relatively high bootstrap and Bayesian probabilities (100% MP/ 1.00 PP). Similar morphology was observed between our isolate and the type species of *C. godetiae* (CBS 133.44). The species has been mainly recorded from Europe, but it is also found in a few other countries, causing fruit, leaf and stem diseases (Jayawardena et al. 2016b). It was reported to cause anthracnose disease on *Vitis vinifera* (Baroncelli et al. 2014). This study provides the first record of *C. godetiae* as a saprotroph on *V. vinifera* in Italy.

Colletotrichum hebeiense X.H. Li, Y. Wang, K.D. Hyde, M.M.R.S. Jayawardena & J.Y. Yan, in Yan, Jayawardena, Goonasekara, Wang, Zhang, Liu, Huang, Wang, Shang, Peng, Bahkali, Hyde & Li, Fungal Diversity 71: 241 (2015)

Facesoffungi number: FoF 03828

Saprotrophic on dead shoots of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Vegetative hyphae* 2 µm in diam, hyaline, smooth-walled, septate, branched. *Conidiomata* and *setae* not observed. *Conidiogenous cells* 6–25×1–3 µm (\bar{x} =15×3 µm, n=10), hyaline, smooth-walled, cylindrical, opening 0.5–2 µm diam, collarette < 0.4 µm long, periclinal thickening visible to conspicuous. *Conidia* 12–15×4–7 µm (\bar{x} =14×5 µm, n=40), hyaline, smooth-walled, aseptate, straight, cylindrical to clavate, apex rounded, base rounded, L/W ratio=2.6. *Appressoria* not observed.

Culture characteristics — Colonies grown from single conidia on PDA white becoming grey, reverse yellow and becoming black, reaching a maximum of 80 mm diam. in 7 days at 28 °C.

Material examined — CHINA, Beijing, on dead shoot of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, JZB330117.

Notes — *Colletotrichum hebeiense* is described as a ripe rot pathogen of grapes in China (Yan et al. 2015). Our strain clustered with the type strain of *C. hebeiense* with a high bootstrap support (Fig. 67). This study provides the first record of *C. hebeiense* as a saprotroph on *V. vinifera* in China.

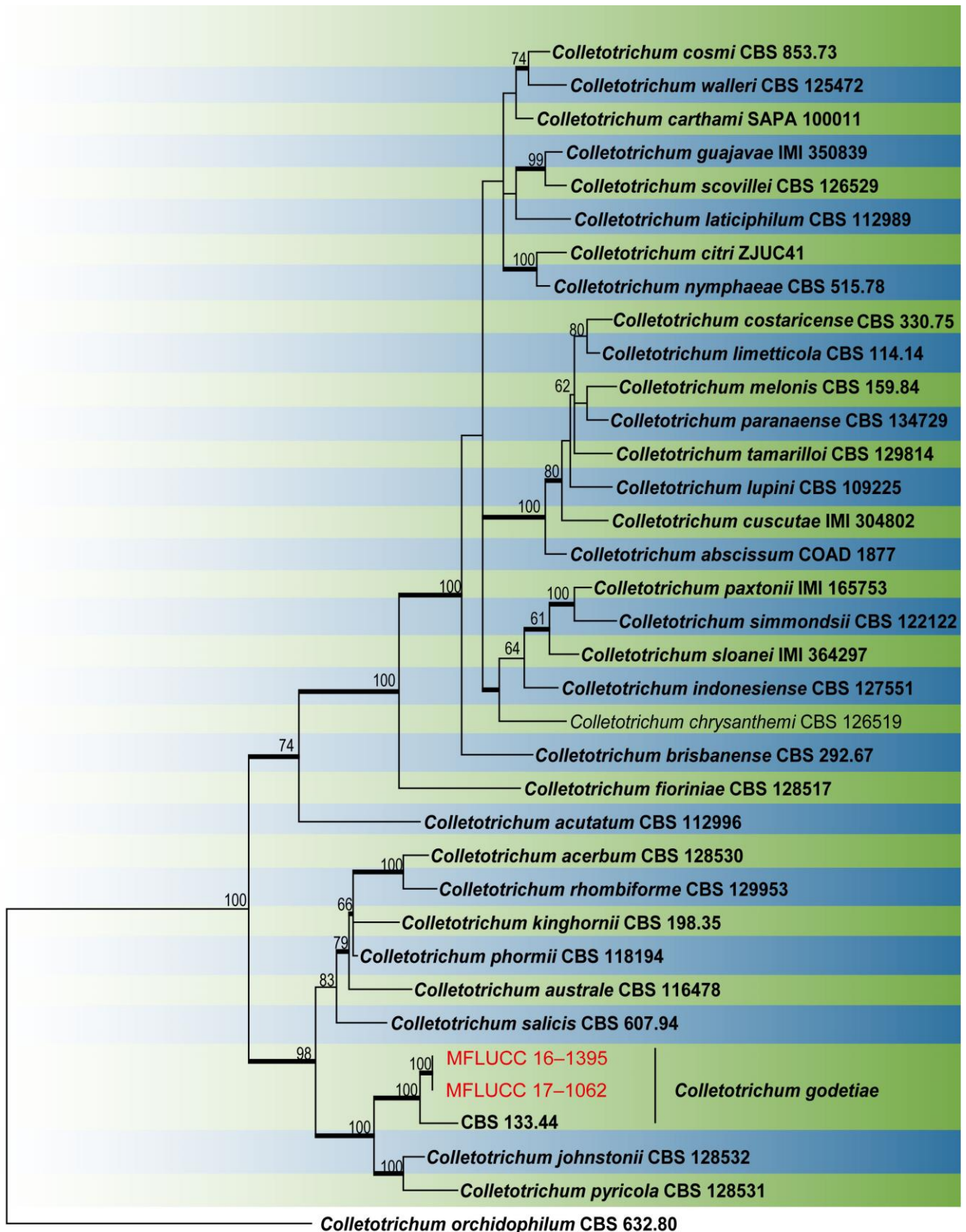
Colletotrichum siamense Prihast., L. Cai & K.D. Hyde, in Prihastuti, Cai, Chen, McKenzie & Hyde, Fungal Diversity 39: 98 (2009)

Facesoffungi number: FoF03599

Saprotrophic on dead and aerial branches of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 70–143 μm diam., brown to dark brown, acervulus, oval, solitary to aggregated. *Setae* absent. *Conidiophores* hyaline, cylindrical or clavate, smooth-walled, simple, to 80 μm long. *Conidiogenous cells* 10–14 μm long, enteroblastic, hyaline, smooth-walled, cylindrical to slightly inflated, *Collarlette* 0.5–1 μm long, periclinal thickening visible. *Conidia* 7–19 \times 3–4 μm (\bar{x} =11 \times 4 μm , n=40) hyaline, smooth or verruculose, aseptate, guttulate, fusiform, ovoid to cylindrical or clavate with rounded apices. *Appressoria* not observed.



Fig. 62 – *Colletotrichum godetiae*. a. Host tissue from which the species was isolated. b. Orange coloured conidial exudate. c. Conidiogenesis. d. Conidia. e. Upper view. f. Reverse view of colony on PDA. Scale bars: a=1 mm, b=2 mm, c=10 μm , d=20 μm .



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Fig. 63 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS, ACT and TUB2 sequence data of taxa for the *acutatum* species complex. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in blue. The tree is rooted with *Colletotrichum orchidophilum* CBS 632.80.



Fig. 64 – *Colletotrichum hebeiense*. a. Conidiophore. b. Conidia. c. Upper view of the colony. d. Reverse view of the colony. Scale bars: a–b= 10 μ m.

Culture characteristics — *Colonies* on PDA reaching a maximum of 80 mm diam. in 7 days at 25 °C, at first white and becoming pale brownish to pinkish, reverse pale yellowish to pinkish, aerial mycelium greyish white, dense, cottony. Vegetative hyphae 2.1 μ m hyaline, smooth-walled, septate, branched.

Material examined — ITALY, Province of Forlì-Cesena, Teodorano - Meldola, on dead and aerial branch of *Vitis vinifera*, 15 February 2015, Erio Camporesi IT 2379 (MFLU 15-1085), culture, MFLUCC 17-1219.

Notes — *Colletotrichum siamense* has been recorded from USA associated with grape ripe rot (Weir et al. 2012). A strain in this study clustered with the type species of *C. siamense* (Fig. 67). This is the first record of *C. siamense* as a saprotroph of *Vitis vinifera*.

Colletotrichum viniferum L.J. Peng, L. Cai, K.D. Hyde & Zi Y. Ying, *Mycoscience* 54(1): 36 (2013)

Facesoffungi number: FoF03600

Pathogen on cluster stems and fruits. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 48–143 μ m diam., black, acervulus, oval, solitary to aggregated. *Setae* absent. *Conidiophores* hyaline to light brown, cylindrical or clavate, smooth-walled, simple, wide at the

base, to 46 μm long, occurring in densely arranged clusters. *Conidiogenous cells* enteroblastic, hyaline, smooth-walled, cylindrical to slightly inflated, collarete 0.5–1 μm long, periclinal thickening visible, *Conidia* 7–12 \times 2–6 μm (\bar{x} =7 \times 4 μm , n=40), hyaline, smooth or verruculose, aseptate, ovoid to cylindrical or clavate with rounded apices. *Appressoria* formed in culture 9–16 \times 5–6 μm (\bar{x} =13 \times 5 μm , n=10), solitary to aggregated, in small groups or short chains, medium to dark brown, smooth-walled, round, oval or irregular.

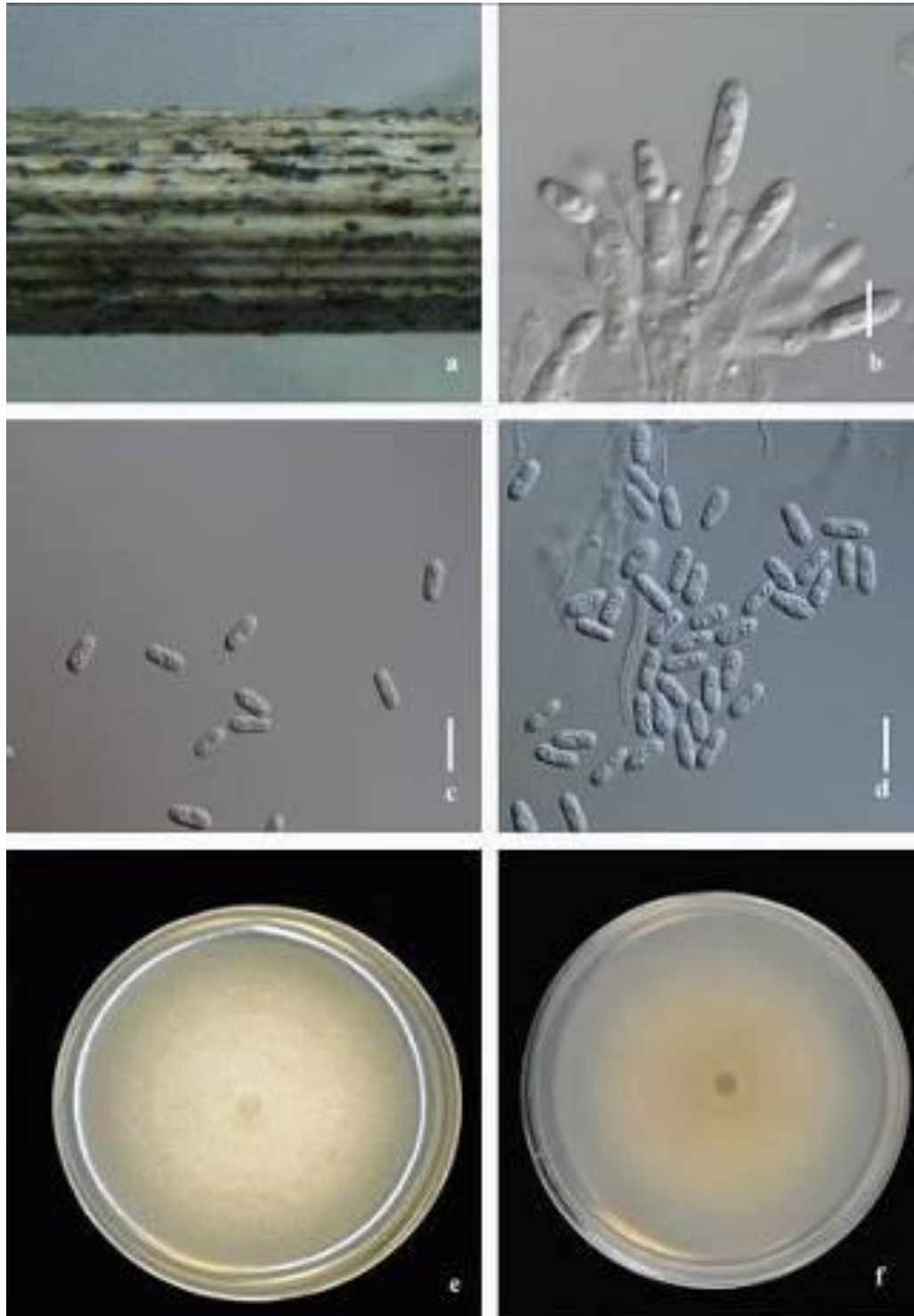


Fig. 65 – *Colletotrichum siamense*. a. Conidiomata on host. b. Conidiophores and conidiogenous cells. c-d. Conidia. e. Upper view of 7 day old culture on PDA. f. Reverse view of 7 day old culture on PDA. Scale bars: b–d=10 μm .

Culture characteristics — *Colonies* on PDA reaching 75 mm diam. in 7 day at 25 °C, at first white becoming dark grey, reverse pale yellowish, aerial mycelium greyish white, dense, cottony, vegetative hyphae 2.1 µm hyaline, smooth-walled, septate, branched.

Material examined — CHINA, Sichuan Province, Chengdou City, on cluster stem of *Vitis labruscana*, 12 August 2014, Liu Xiao SCCD7 (MFLU 15-0794), culture, MFLUCC 14-1213=CGMCC 3.17465; CHINA, Sichuan Province, Chengdou City, on cluster stem of *V. labruscana*, 12 August 2014, Liu Xiao SCCD2, SCCD3 and SCCD4 living cultures MFLUCC 14-1214, MFLUCC 14-1215 and MFLUCC 14-1216 respectively.

Notes — *Colletotrichum viniferum* was introduced by Peng et al. (2013). This species is a known pathogen causing grape ripe rot in China (Yan et al. 2015). Our strains clustered with the type species of *C. viniferum* with high bootstrap support (Fig. 67). This study provides the first report of *C. viniferum* as a pathogen on cluster stems.

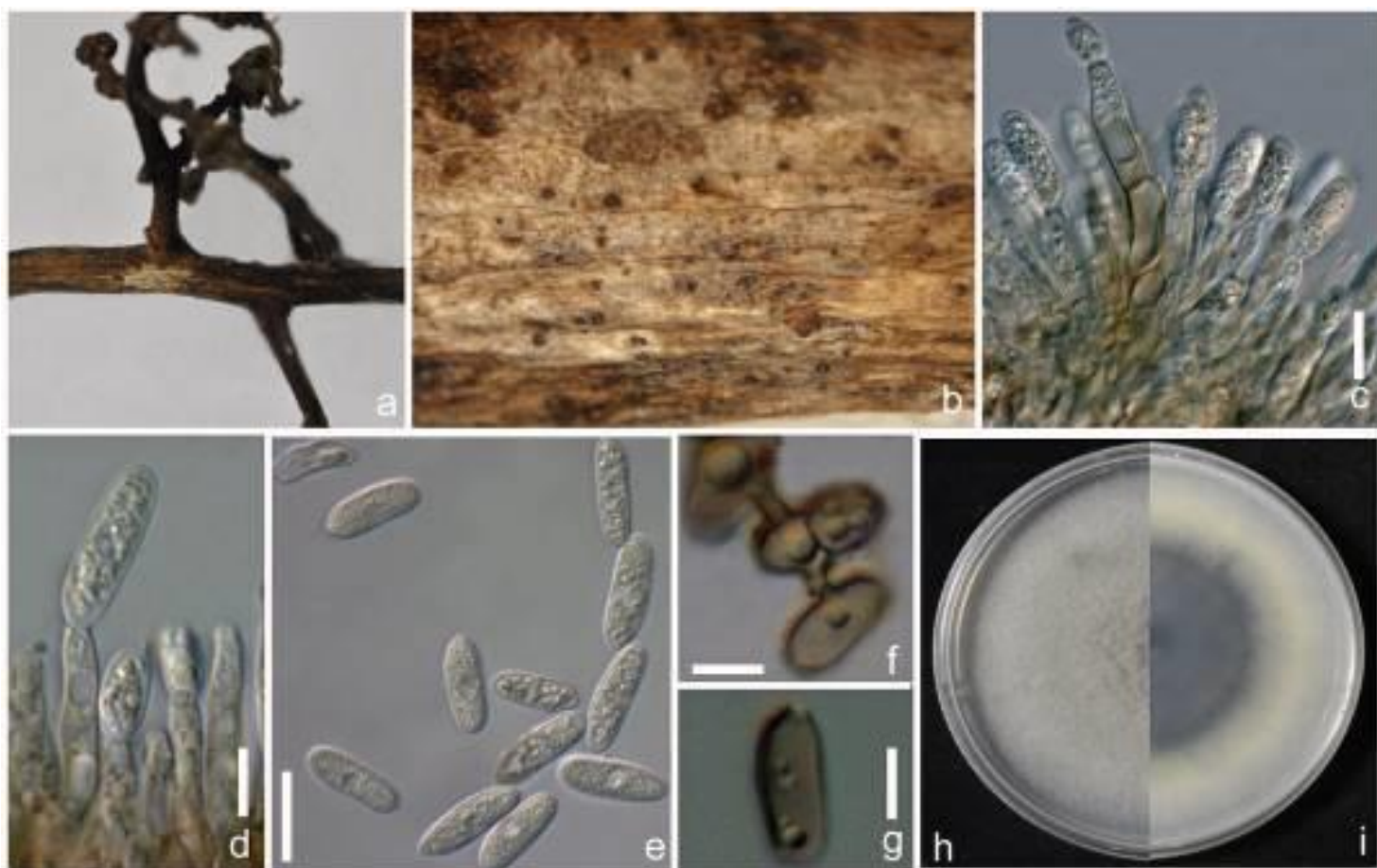


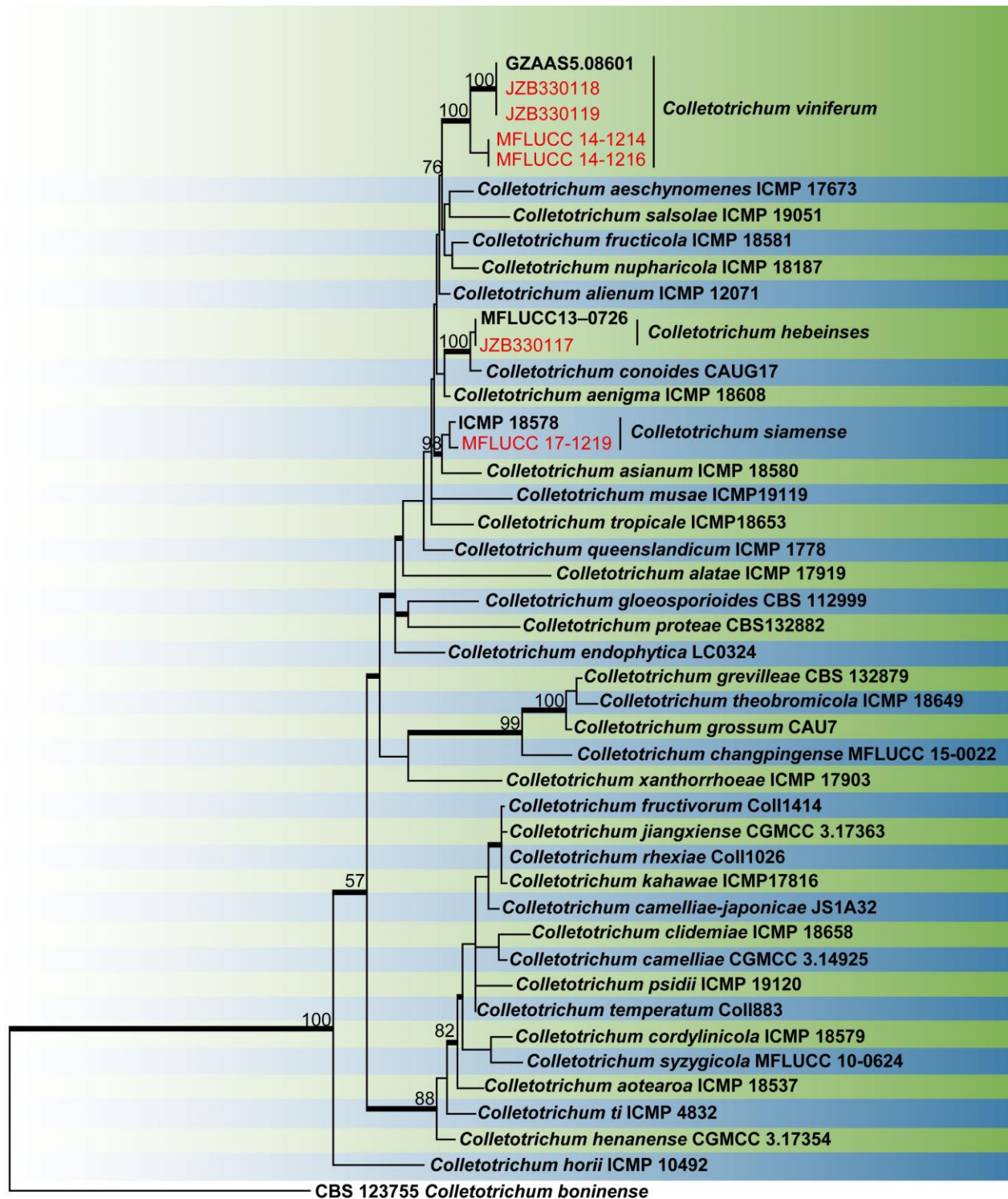
Fig. 66 – *Colletotrichum viniferum*. a. Bleached necrotic lesion on a cluster stem. b. Conidiomata. c-d. Conidiophores and conidiogenous cells. e. Mature conidia. f-g. Appressoria. h. Upper view of 7 day old culture. i. Reverse view of 7 day old culture. Scale bars: c–g=5 µm.

Colletotrichum truncatum (Schwein.) Andrus & W.D. Moore, Phytopathology 25: 121 (1935)

Facesoffungi number: FoF03827

Saprotrophic on dead shoot of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* acervular, conidiophores and setae formed directly on hyphae. *Setae* hyaline to pale brown, smooth to verruculose, 80–130 µm long, 2–5-septate, tapering slightly towards the slightly acute to round tip, base cylindrical to conical, 4–5 µm diam. *Conidiophores* hyaline to pale brown, septate, strongly branched, densely clustered, up to 90 µm long. *Conidiogenous cells* enteroblastic, hyaline to pale brown, cylindrical, 4–20×2–4 µm, opening 1.5–2 µm diam, collarette

rarely visible, periclinal thickening not observed. *Conidia* hyaline, smooth-walled to verruculose, aseptate, long central part of conidia usually slightly curved with parallel walls, ending abruptly at the round and truncate base, tapering towards the acute and more strongly curved apex, 17–30×3–4 µm, (\bar{x} = 22×4) L/W ratio = 5.7.



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Fig. 67 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS, ACT and TUB2 sequence data of taxa for the gloeosporioides species complex. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in blue. The tree is rooted with *Colletotrichum boninense* CBS 123755.

Culture characteristics — *Colonies* on PDA reaching a maximum of 50 mm diam. in 7 days at 25 °C, flat with an entire margin.

Material examined — CHINA, Beijing, on dead shoot of *Vitis vinifera* cv. Red Globe, 3 June 2015, Ruvishika Jayawardena, culture, MFLUCC 17-2380.

Notes — *Colletotrichum truncatum* is a pathogen of *Capsicum* sp. as well as on other economically important crops (Jayawardena et al. 2016b). This species has been recorded from Italy and Switzerland as a pathogen causing grape ripe rot (Pan et al. 2016), and as an endophyte from India (Farr 1973). Our strain clustered with the type strain of *C. truncatum* (Fig. 69). This is the first record of *C. truncatum* as a saprotroph on *Vitis vinifera* in China.

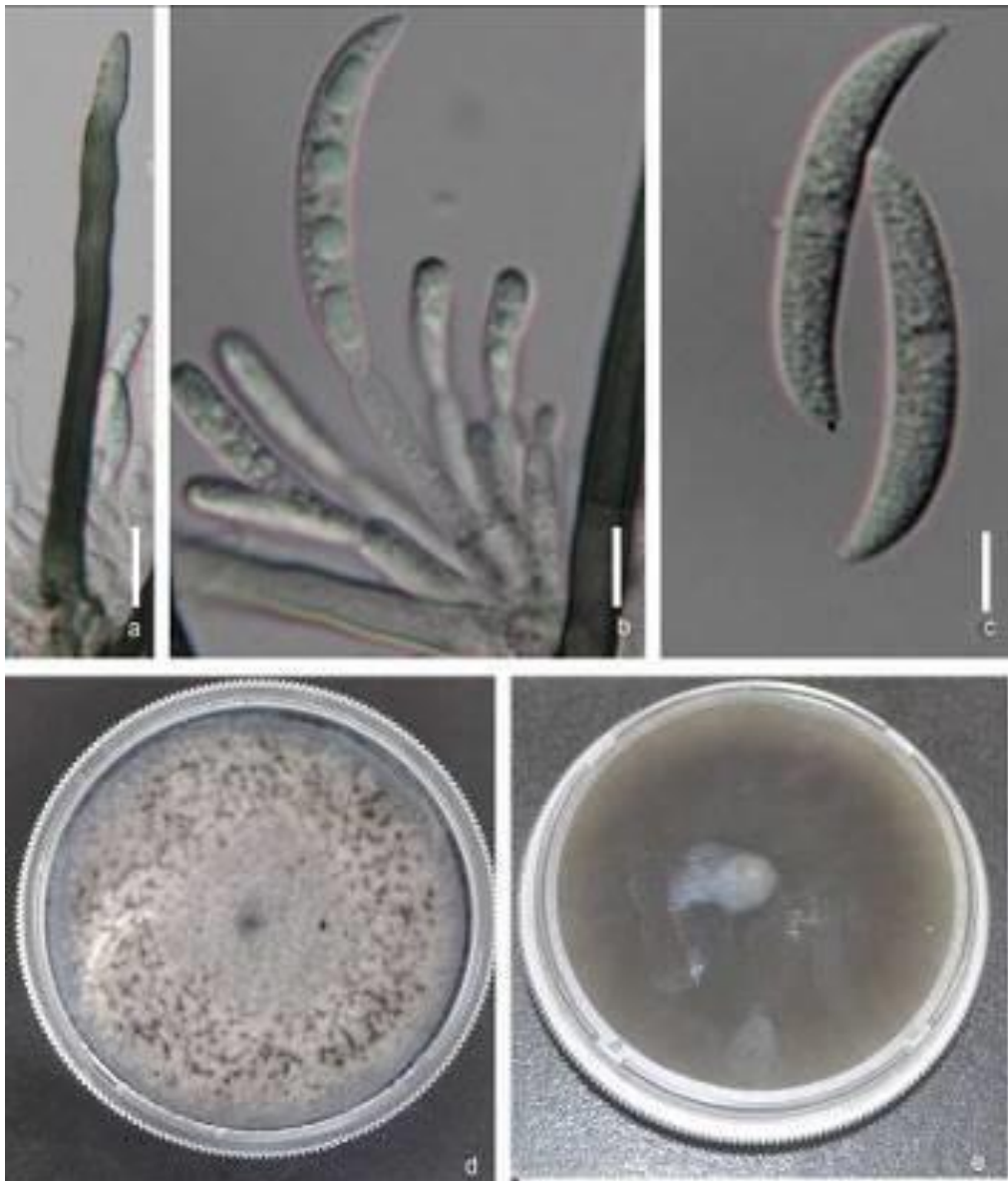


Fig. 68 – *Colletotrichum truncatum*. a. Seta. b. Conidiophore and conidiogenous cells. c. Conidia. d. Upper view of colony on PDA. e. Reverse view of colony on PDA. Scale bars: a=10 µm.

Xylariales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 66 (1932)

Diatrypaceae Nitschke [as 'Diatrypeae'], Verh. naturh. Ver. preuss. Rheinl. 26: 73 (1869)

Diatrypaceae was introduced to accommodate *Diatrype*. Fungal taxa belonging to this family can produce extracellular ligninolytic enzymes, showing a physiological capacity in decaying wood (Trouillas et al. 2011). Currently this family comprises 15 genera (Maharachchikumbura et al. 2016a, Wijayawardene et al. 2018). Several genera in the

Diatrypaceae (*Cryptovalsa*, *Diatrype*, *Diatrypella*, *Eutypa* and *Eutypella*) are known to occur on grapevines worldwide (Luque et al. 2005).

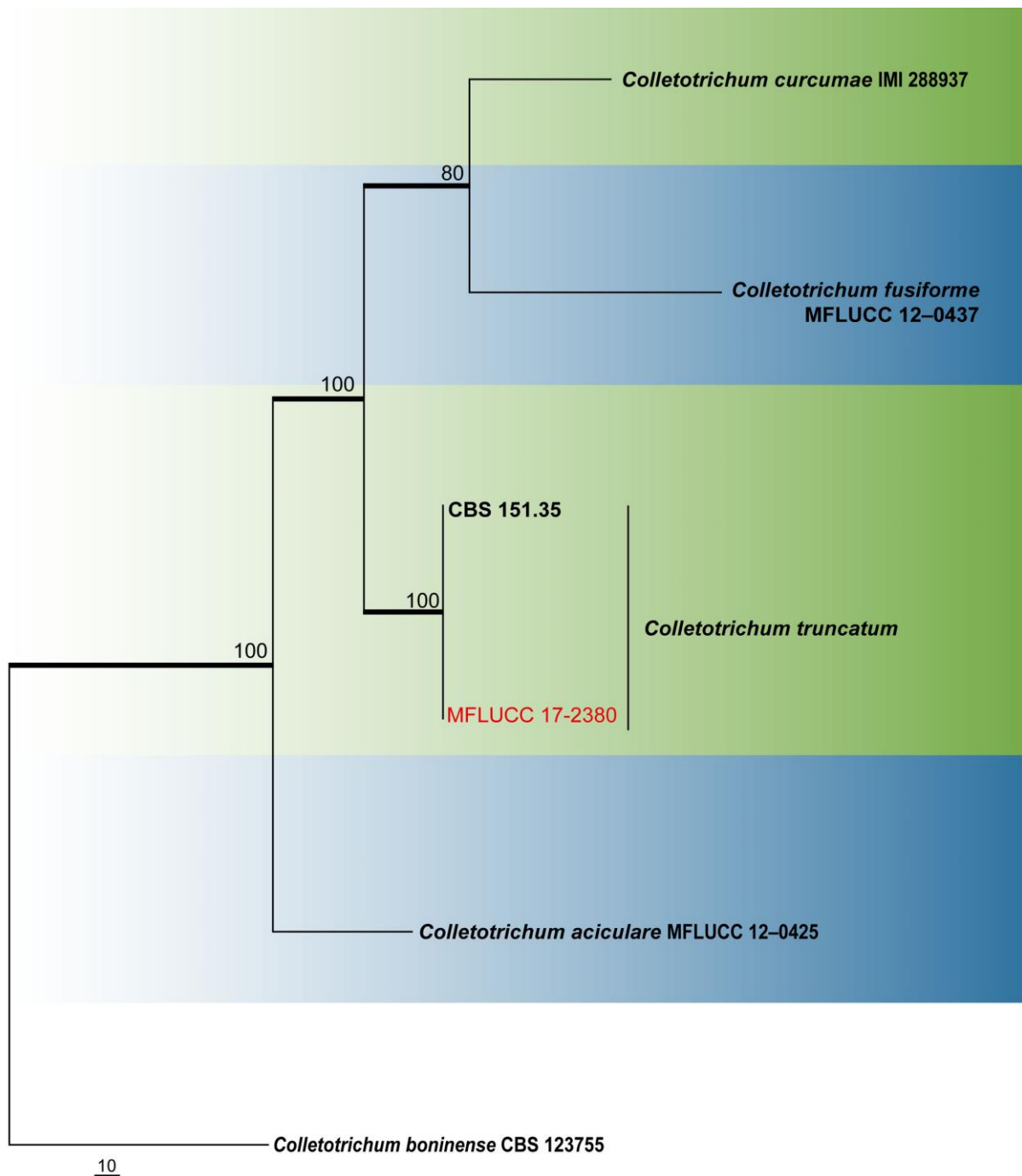


Fig. 69 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS, ACT and TUB2 sequence data of taxa for the gloeosporioides species complex. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Colletotrichum boninense* CBS 123755.

Cryptovalsa Ces. & De Not. ex Fuckel, Jb. Nassau. Ver. Naturk. 23-24: 212 (1870) [1869-70]

Species of *Cryptovalsa* are saprotrophs or pathogens worldwide (Wijayawardene et al. 2017). This is a common genus occurring on grapevine. *Cryptovalsa* is characterized by eutypoid ascostromata, polysporous asci and allantoid ascospores (Spooner 1981). Our strains clustered with the reference sequence of *C. ampelina* (Fig. 70). We provide a description of both the sexual and asexual morph of this species.

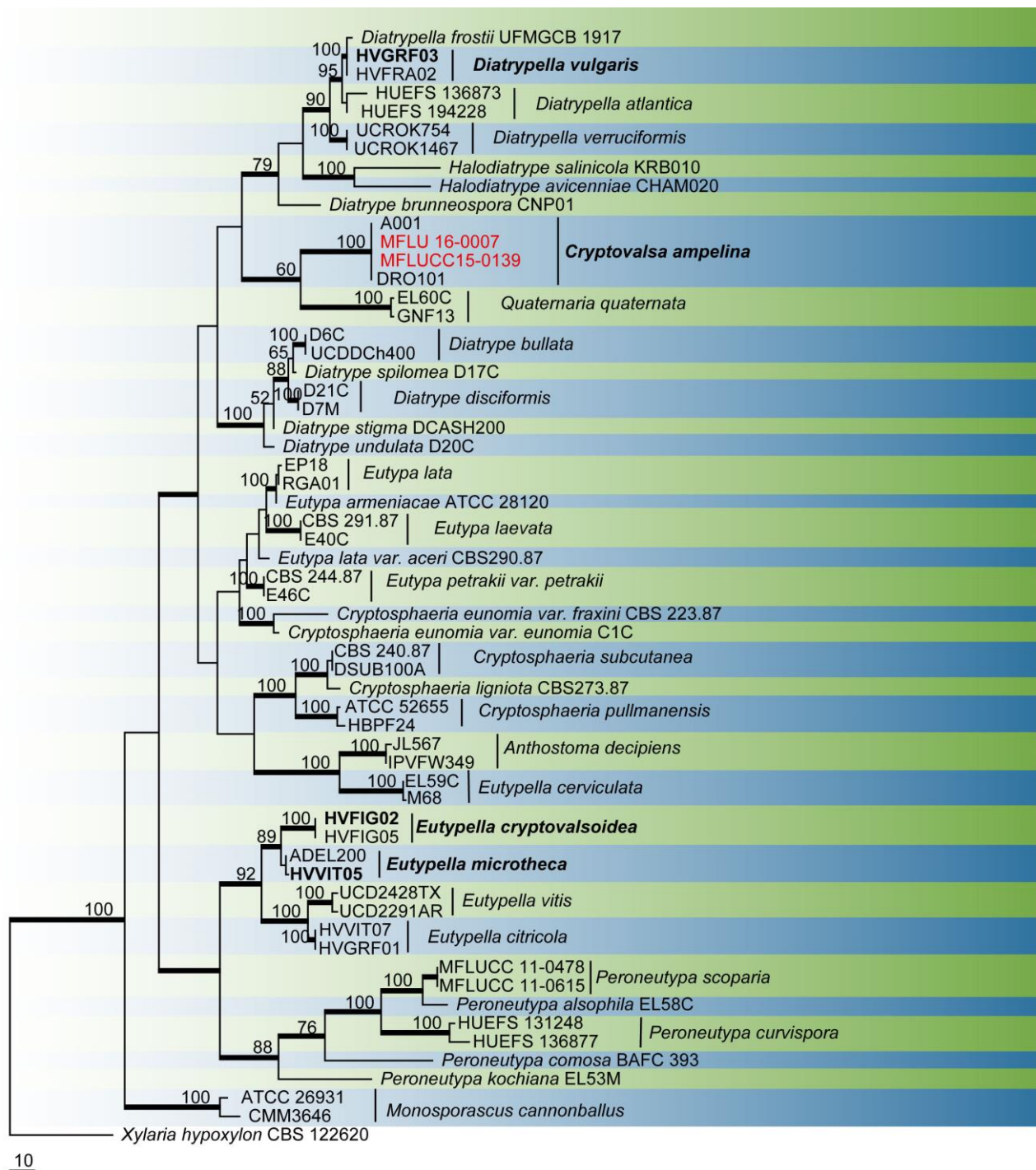


Fig.70 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS and TUB2 sequence data of taxa from the *Diatripaceae*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.75 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Diaporthe foeniculiana* CBS 111553.

Cryptovalsa ampelina (Nitschke) Fuckel, Jb. nassau. Ver. Naturk. 23–24: 212 (1870) [1869–70]
Facesoffungi number: FoF 01800

Saprotrophic on dead stem of *Vitis vinifera*. **Sexual morph:** *Stromata* poorly developed, immersed in bark, occasionally with protruding perithecial necks, single or in groups, irregularly scattered. *Ascomata* 350–380 µm high×130–170 µm diam. (\bar{x} =360×260 µm, n=10), solitary to gregarious, immersed, dark brown to black, globose to pyriform, raising above the epidermis and forming black, blister-like areas, often compressed, ostiolate. *Papilla* 125–140 µm high, 90–100

μm wide ($\bar{x}=138\times 96 \mu\text{m}$, $n=10$), central, long, internally covered by periphyses. *Peridium* 20–26 μm wide ($\bar{x}=25 \mu\text{m}$, $n=10$). *Peridium* 35–45 μm wide, composed of two types of layers; 9–11 outer layers, thick, with dark brown to black cells of *textura angularis* and 3–5 inner layers of hyaline cells. *Hamathecium* composed of dense, 2–4 μm wide, hyaline, aseptate, anastomosing paraphyses. *Asci* 120–135 \times 10–13 μm ($\bar{x}=130\times 13 \mu\text{m}$, $n=20$), unitunicate, 32 ascospores per ascus, elongate-clavate, with long pedicel, with J+ apical ring. *Ascospores* 10–15 \times 2–4 μm ($\bar{x}=12\times 3 \mu\text{m}$, $n=20$), overlapping to irregular, yellowish to light brown at maturity, allantoid, 1-celled, smooth-walled, with small guttules. **Asexual morph:** Coelomycetous, occurring in culture as pycnidia. *Conidiomata* superficial, solitary or aggregated, dark brown to black, globose to subglobose, with yellow to light brown interwoven, thick-walled hyphae. *Conidiophores* septate, bicellately to verticillately branch, arranged in dense palisades, cylindrical, hyaline, smooth, arising from the base. *Conidiogenous cells* 5–16 \times 1–2 μm ($\bar{x}=12\times 1 \mu\text{m}$, $n=20$), holoblastic, straight or curved, apically distorted on conidial secession. *Conidia* 17–30 \times 1–1.5 ($\bar{x}=22\times 1 \mu\text{m}$, $n=30$), filiform, curved, or rarely straight with flattened base and blunt apex, hyaline.

Cultural characteristics — Ascospores germinating on MEA within 24 hours. Germ tubes produced at germ pore. Colonies on MEA reaching 4.0 mm diam after 7 days at 25 °C, edge entire, flat or effuse or umbonate.

Material examined — ITALY, Province of Forlì-Cesena, Fiumana di Predappio, on dead stem of *Vitis vinifera*, 4 February 2014, Erio Camporesi, IT 1698 (MFLU 16-0007), living culture, MFLUCC15-0139.

Notes — *Cryptovalsa ampelina* is associated with Eutypa dieback in major grape growing countries (Trouillas et al. 2010). This is the most studied species in the genus and the only species to have molecular data available.

Hypocreales Lindau, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 343 (1897)

Hypocreaceae De Not., G. bot. ital. 2(1): 48 (1844)

Seaver (1909, 1911) divided Hypocreales into two families, *Nectriaceae* and *Hypocreaceae* Maharachchikumbura et al. (2016a) listed 18 genera under *Hypocreaceae*.

Trichoderma Pers., Neues Mag. Bot. 1: 92 (1794)

Members of this genus are saprotrophs or hypersaprotrophs on various plants and on other fungi (Maharachchikumbura et al. 2016a). *Hypocrea* has been synonymized under this genus.

Trichoderma atroviride P. Karst., Bidr. Känn. Finl. Nat. Folk 51: 363 (1892)

This study provides the first record of *T. atroviride* on *V. vinifera* as a saprotroph.

Trichoderma lixii (Pat.) P. Chaverri, in Chaverri, Branco Rocha, Jaklitsch, Gazis, Degenkolb & Samuels, Mycologia 107(3): 578 (2015)

This is the first record of *T. lixii* on *V. vinifera* as a saprotroph.

Trichoderma harzianum Rifai, Mycol. Pap. 116: 38 (1969)

Trichoderma harzianum has been recorded from *V. vinifera* as an endophyte from Spain (Gonzalez & Tello 2011). This is the first record of *T. harzianum* from *V. vinifera* as a saprotroph in China.

Nectriaceae Tul. & C. Tul. [as 'Nectriei'], Select. fung. carpol. (Paris) 3: 3 (1865)

Petch (1938) accepted *Nectriaceae* as a separate family in Hypocreales. *Nectriaceae* is characterized by uniloculate, pigmented ascomata and phialidic amerosporous to phragmosporous conidia (Maharachchikumbura et al. 2016a).

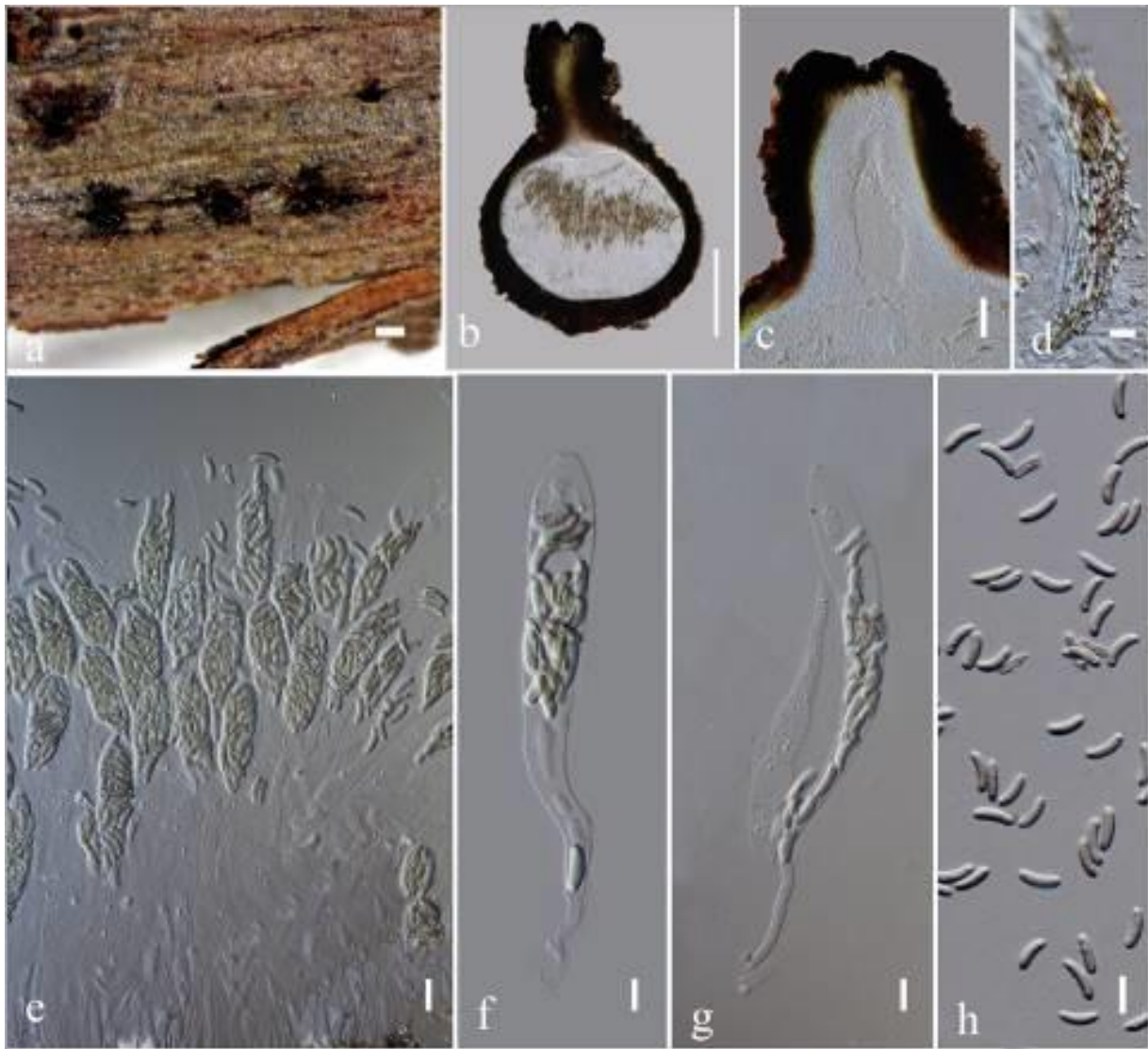


Fig. 71 – *Cryptovalsa ampelina*. a. Ascomata on substrate. b. Cross section of ascoma. c. Papilla d. Peridium e-g. Asci. h. Ascospores. Scale bars: a=200 μ m, b=100 μ m, c=50 μ m, d–h=10 μ m.

***Fusarium* Link**

Fusarium was described by Link (1809). Species belonging to this genus develop five distinct type of propagules. Strains from our study, based on ITS sequence data, appear to be *F. oxysporum* and *F. sambucinum* (Fig. 75)

***Fusarium oxysporum* Schldl., Fl. berol. (Berlin) 2: 139 (1824)**

Notes — *Fusarium oxysporum* is a well-known pathogen on grapevine (Gonzalez & Tello 2011, Jayawardena et al. 2018).

***Fusarium sambucinum* Fuckel, Jb. nassau. Ver. Naturk. 23-24: 167 (1870) [1869-70]**

Facesoffungi number: FoF03129

Saprotrophic on dead branch of woody host. **Sexual morph** Not observed. **Asexual morph** *Hyphae* hyaline, septate. *Conidiomata* not observed in culture. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal, cylindrical, variable in size. *Macroconidia* uncommon. *Microconidia* numerous, small terminal conidia, subglobose, 4–6 (\bar{x} =5, n=40)×2–4 (\bar{x} =3, n= 40) μ m, aseptate. Chlamydospores globose, 3.3 μ m in diam, solitary.

Culture characteristics — Colonies on PDA reaching 3–5 cm diam., after 5 days at 25 °C undulate, whitish puffy colonies on top view, reverse yellowish with white halo margin.

Material examined — Italy, Ontola - Predappio, Forlì-Cesena, on dead, aerial branch of *Vitis vinifera*, 11 April 2016, Erio Camporesi, IT 2931 (MFLU 16-1167), living culture MFLUCC 17-1057.

Notes — *Fusarium* includes species that are very important as plant pathogens. Several species or species complexes are involved in diseases of humans (Leslie & Summerell 2006). In phylogenetic analysis, the present isolates cluster together with *Fusarium sambucinum*, with 100% bootstrap support and 1.0 Bayesian posterior probability. Our isolate produced microconidia on PDA, which is a rare character for *F. sambucinum*. Another discrete character from type species is solitary chlamydoconidia. This study provides the first report of *F. sambucinum* associated with *V. vinifera* in Italy.

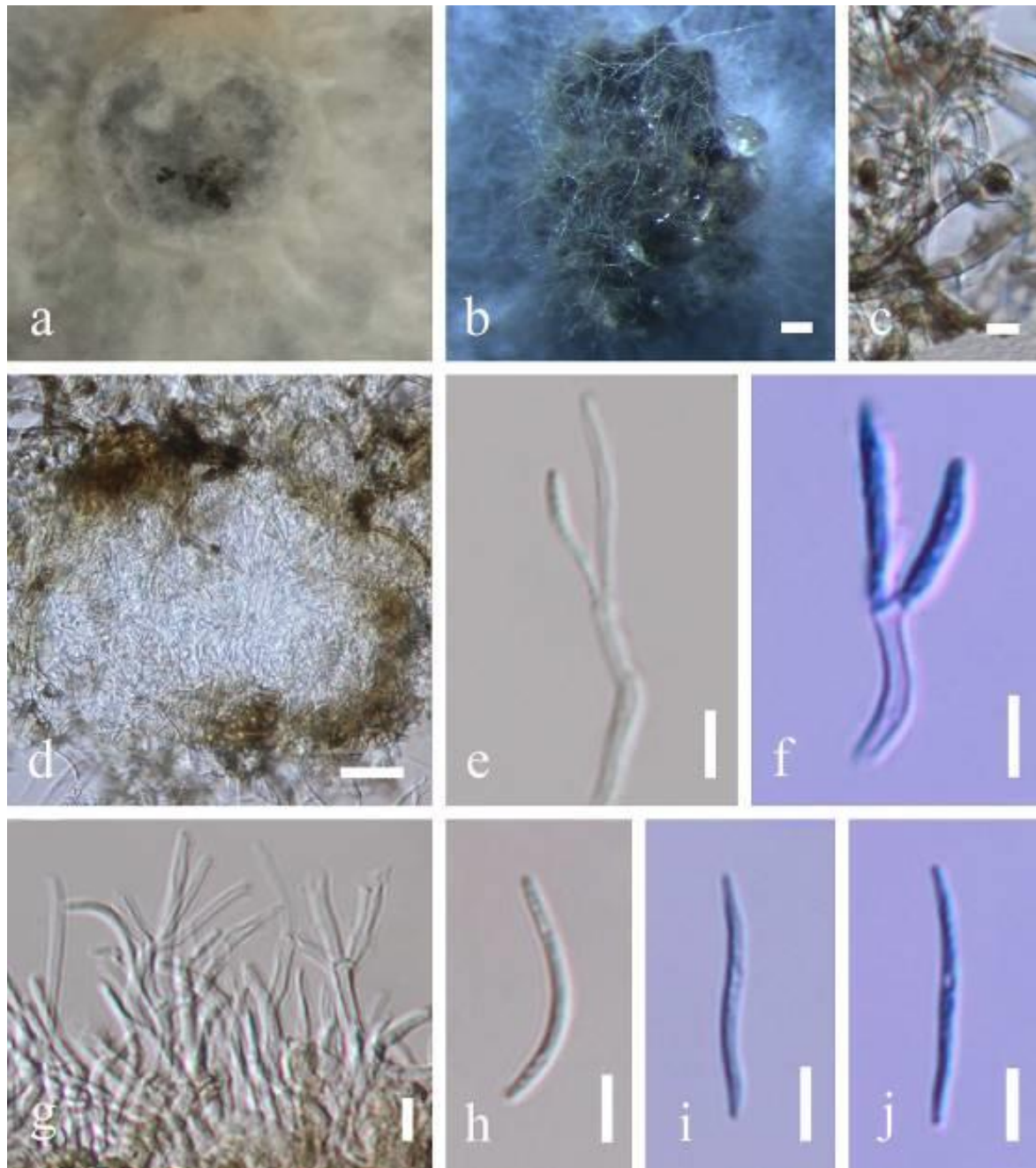


Fig. 72 – Culture on PDA *Cryptovalsa ampelina*. a, b. Conidiomata on the culture c. Hyphae on conidioma surface d. Section of conidioma e. Conidiophore with young conidium f. Conidiogenous cell with conidia g. Conidiophores h–j. Conidia. (note: f, i, j in cotton blue) Scale bars: b=200 µm, d=20 µm, c, e–j=5 µm.

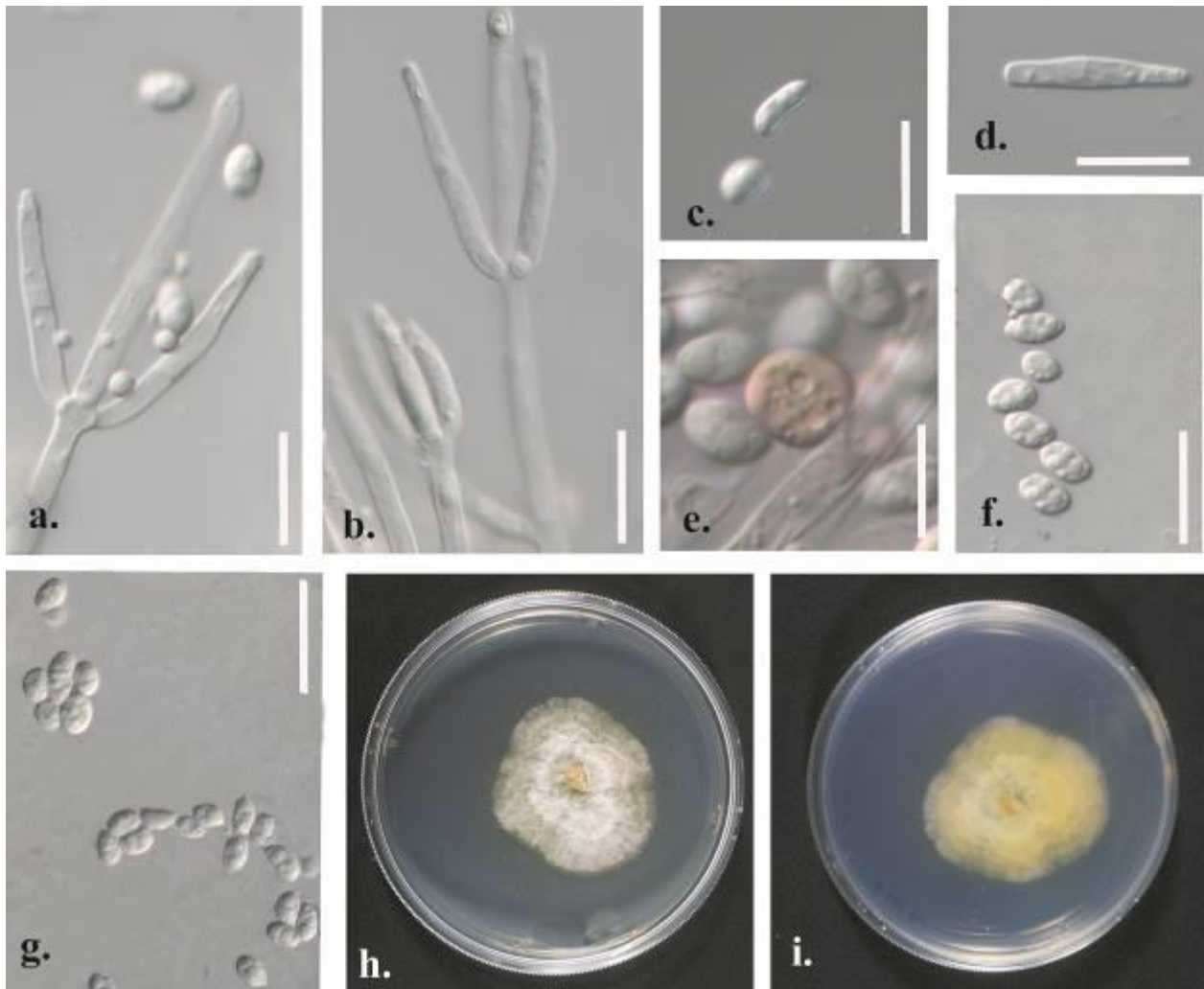


Fig. 76 – *Fusarium sambucinum*. a-b. Penicillate conidiogenous cells. c-d. Macroconidia. e. Chlamydospore. f-g. Conidia. h-i. Upper and reverse view on PDA. Scale bars: a–g=10 µm.

Stachybotryaceae L. Lombard & Crous, in Crous et al., *Persoonia*, *Mol. Phyl. Evol. Fungi* 32: 283 (2014)

Stachybotryaceae was introduced by Crous et al. (2014), in the order Hypocreales, to accommodate the genera *Myrothecium*, *Peethambara* and *Stachybotrys*.

Albifimbria L. Lombard & Crous, in Lombard, Houbraken, Decock, Samson, Meijer, Réblová, Groenewald & Crous, *Persoonia* 36: 177 (2016)

Members of *Albifimbria* are characterised by the formation of verrucose setae surrounding the sporodochia and conidia sometimes bearing a funnel-shaped mucoid appendage (Lombard et al. 2016). Our strains clustered with the type strains of *A. verrucaria* and *A. viridis* (Fig. 81).

Albifimbria verrucaria (Alb. & Schwein.) L. Lombard & Crous, in Lombard, Houbraken, Decock, Samson, Meijer, Réblová, Groenewald & Crous, *Persoonia* 36: 177 (2016)

Facesoffungi number: FoF03833

For description see Tulloch (1972).

Notes: This study is the first record of *A. verrucaria* as a saprotroph, on *V. vinifera* from China.

Albifimbria viridis L. Lombard & Crous, in Lombard, Houbraken, Decock, Samson, Meijer, Réblová, Groenewald & Crous, *Persoonia* 36: 178 (2016)

Facesoffungi number: FoF03834

For description see Lombard et al. (2016).

Notes: This study is the first record of *A. viridis* as a saprotroph, on *V. vinifera* from China.

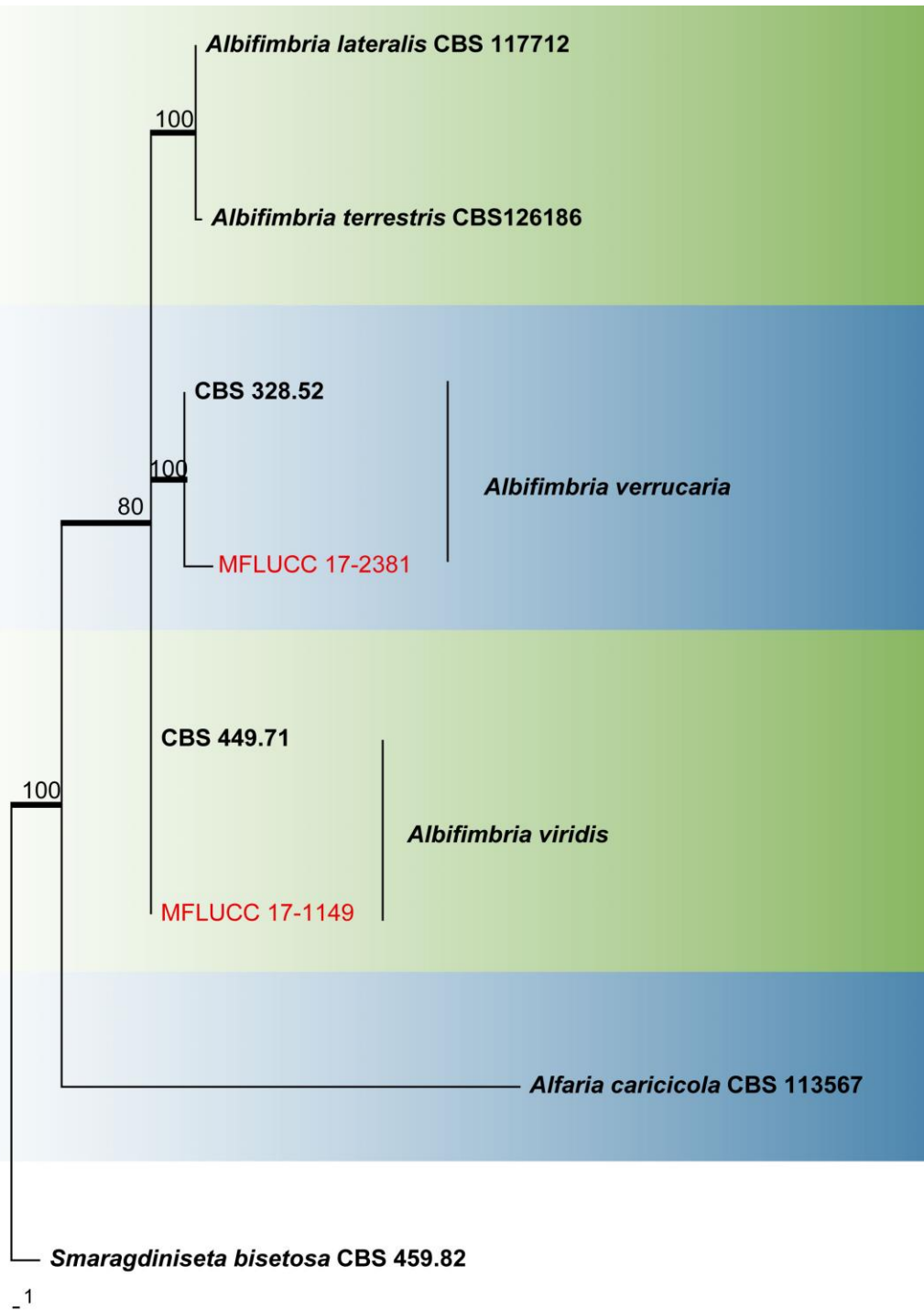


Fig. 77 – One of seven most parsimonious trees obtained from a heuristic search of combined ITS, and LSU sequence data of taxa of *Albifimbria*. Parsimony bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities ≥ 0.90 are given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Smaragdiniseta bisetosa* CBS 459.82.

***Hypocreales* genera incertae sedis**

Alfaria Crous, N.J. Montañó-Mata & García-Jim., in Crous et al., Persoonia 32: 239 (2014)

This genus was introduced by Crous et al. (2014) associated with leaf apical necrosis of *Cyperus esculentus*. In this study we describe the asexual morph of *A. cyperi-esculenti* and introduce a new species, *A. vitis* (Fig. 80).

Alfaria cyperi-esculenti Crous, Montañó-Mata & García-Jim., in Crous et al., *Persoonia* 32: 239 (2014)

Facesoffungi number: FoF03602

Saprotrophic on dead branches of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** Conidiomata sporodochial, stromatic, superficial, cupulate to discoid, scattered to gregarious, oval to elongate or irregular in outline, 150–450 µm diam, 35–80 µm deep. *Stroma* well-developed, hyaline, composed of cells of *textura globulosa* or *textura angularis*. *Setae* arising from the basal stroma of two kinds: Type I scattered among the conidiogenous cells, hypha-like, thin-walled, hyaline, septate, unbranched, smooth, flexuous, with obtuse or rounded apices, 50–70 µm long, 2–5 µm wide; and Type II originating from the fringe, thick-walled, pigmented towards the bottom third, smooth, 1–3-septate, unbranched, straight, narrowing to sharp apices, 60–100 µm long, 3–5 µm wide at the broadest part. *Conidiophores* arising from the basal stroma, unbranched or branched, hyaline, smooth, up to 40 µm long. *Conidiogenous cells* phialidic, cylindrical to elongate doliiform, hyaline, smooth, 6–18×1–3 µm (\bar{x} =11×2 µm, n=20), with conspicuous collarettes and periclinal thickenings, covered by an olivaceous green mucoid layer. *Conidia* aseptate, smooth, hyaline, ellipsoidal, 5–8×3–4 µm (\bar{x} =7×3µm, n=40).

Culture characteristics — Colonies on PDA attaining 30 mm diam. at 25° C after 7 days. White aerial mycelium and luteous to pale luteous mycelium; reverse yellow.

Material examined — ITALY, Province of Forlì-Cesena, San Lorenzo in Noceto - Forlì, on dead aerial branch of *Vitis vinifera*, 29 April 2014, Erio Camporesi IT 1838 (MFLU 15-0794, no culture is available), ITALY, Province of Forlì-Cesena, Trivella di Predappio, on dead aerial branch of *V. vinifera*, 8 March 2015, Erio Camporesi IT 2407 (MFLU 15-1084); living culture, MFLUCC 17-1233.

Notes — This genus was introduced to accommodate the leaf tip dieback and tuber rot pathogen of *Cyperus esculentus*. The two strains of this study clustered together with the type species *A. cyperi-esculenti* with high phylogenetic support. Crous et al. (2014) did not mention an asexual morph. Lin et al. (2017) introduced a new species of *Alfaria* based on phylogeny and asexual morphological characteristics and provided a backbone tree. This study provides the first report of *A. cyperi-esculenti* as a saprotroph on *Vitis* sp., as well as the first asexual morph description.

Alfaria vitis Manawasinghe, Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF553955; *Faces of fungi* number: FoF03132

Etymology: Name reflects the host genus *Vitis*, from which the species was isolated

Holotype: MFLU 15-1082

Saprotrophic on dead branch of *Vitis vinifera*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* not observed, *setae* not observed, *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, clustered, hyaline or greenish pigmented, smooth-walled. *Conidia* aseptate, green to mouse grey to black masses, elongated 9–6 µm (\bar{x} =7 µm, n=40) in length.

Culture characteristics — Colonies on PDA reach 3–5 cm diam. after 7 days at 25 °C, upper side on PDA whitish circular, filiform margin, reverse on PDA yellowish, filiform.

Material examined — Italy, Province of Forlì-Cesena, near Pieve di Rivoschio, on dead aerial branch of *Vitis vinifera*, 2 February 2015, Erio Camporesi IT 2363, (MFLU 15-1082); ex-type living culture, MFLUCC 17-1055= KUMCC 17-0139.

Notes — The combined phylogenetic analysis of ITS, LSU and EFa placed *Alfaria vitis* within the genus *Alfaria* in *Stachybotryaceae*. It forms a sister taxon with *A. putrifolia* with 66% bootstrap support and 0.95 Bayesian posterior probability values (Fig. 82). Compare to the sister

taxon, this species does not produce setae and conidiophores are reduced to conidiogenous cells. On PDA, *Alfaria putrifolia* culture was sterile, but *A. vitis* produced conidia.

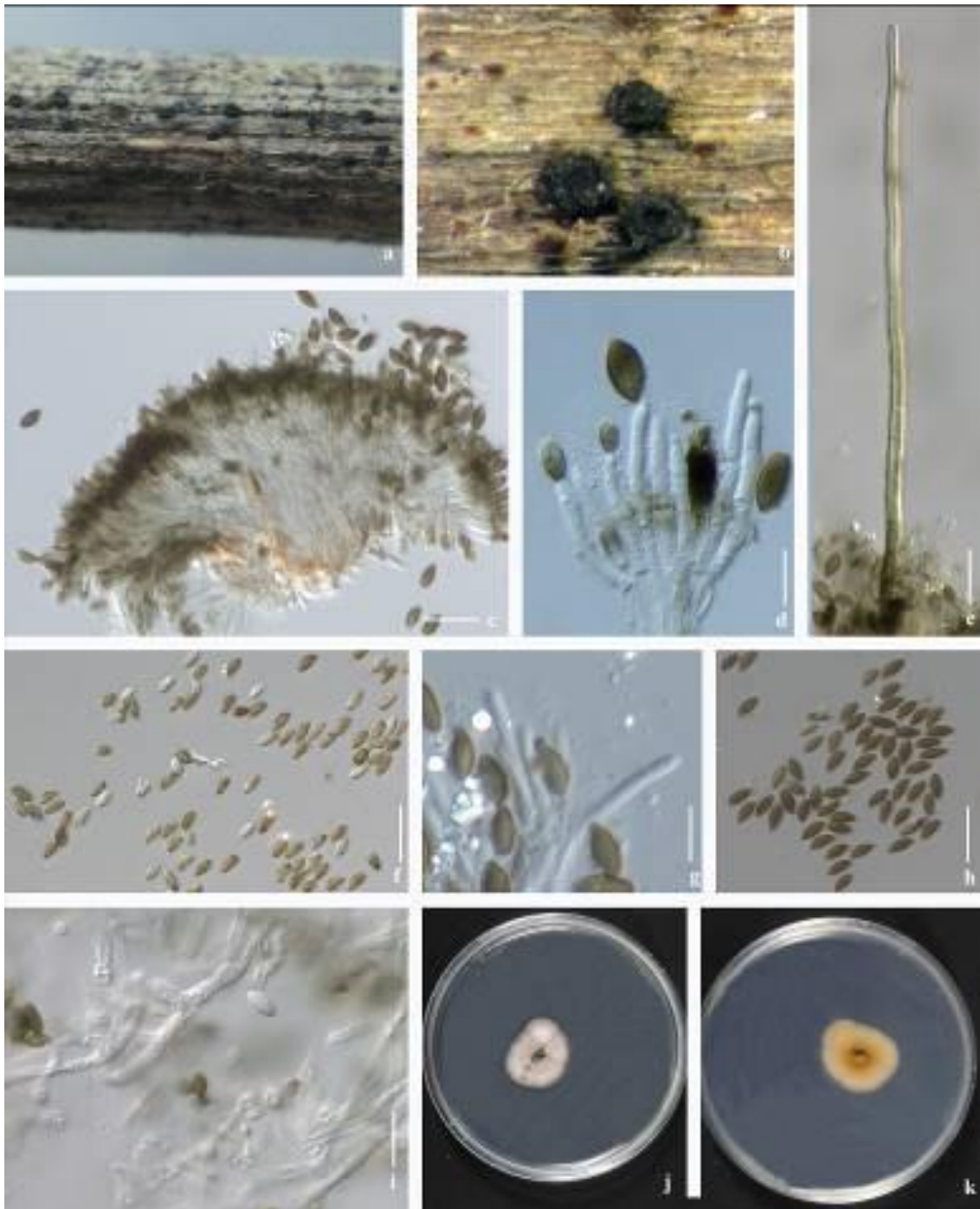


Fig. 78– *Alfaria cyperi-esculenti*. a, b. Conidiomata on host surface. c. Section of conidioma. d. Conidiophores and conidiogenous cells. e. Type II seta. f. Immature conidia. g. Type I setae. h. Mature conidia. i. Hyphae. j. Upper view of a 7 day old colony. k Reverse view of a 7 day old colony. Scale bars: c–i=20 μ m.

Xylariales genera incertae sedis

Neoanthostomella D.Q. Dai & K.D. Hyde, in Dai, Phookamsak, Wijayawardene, Li, Bhat, Xu, Taylor, Hyde & Chukeatirote, Fungal Diversity: 10.1007/s13225-016-0367-8, [84] (2016)

Neoanthostomella was introduced by Dai et al. (2016) to accommodate *N. pseudostromatica*. There are only two species in the genus (Index Fungorum 2018). A phylogenetic tree for *Xylariaceae* is given in Fig. 82.

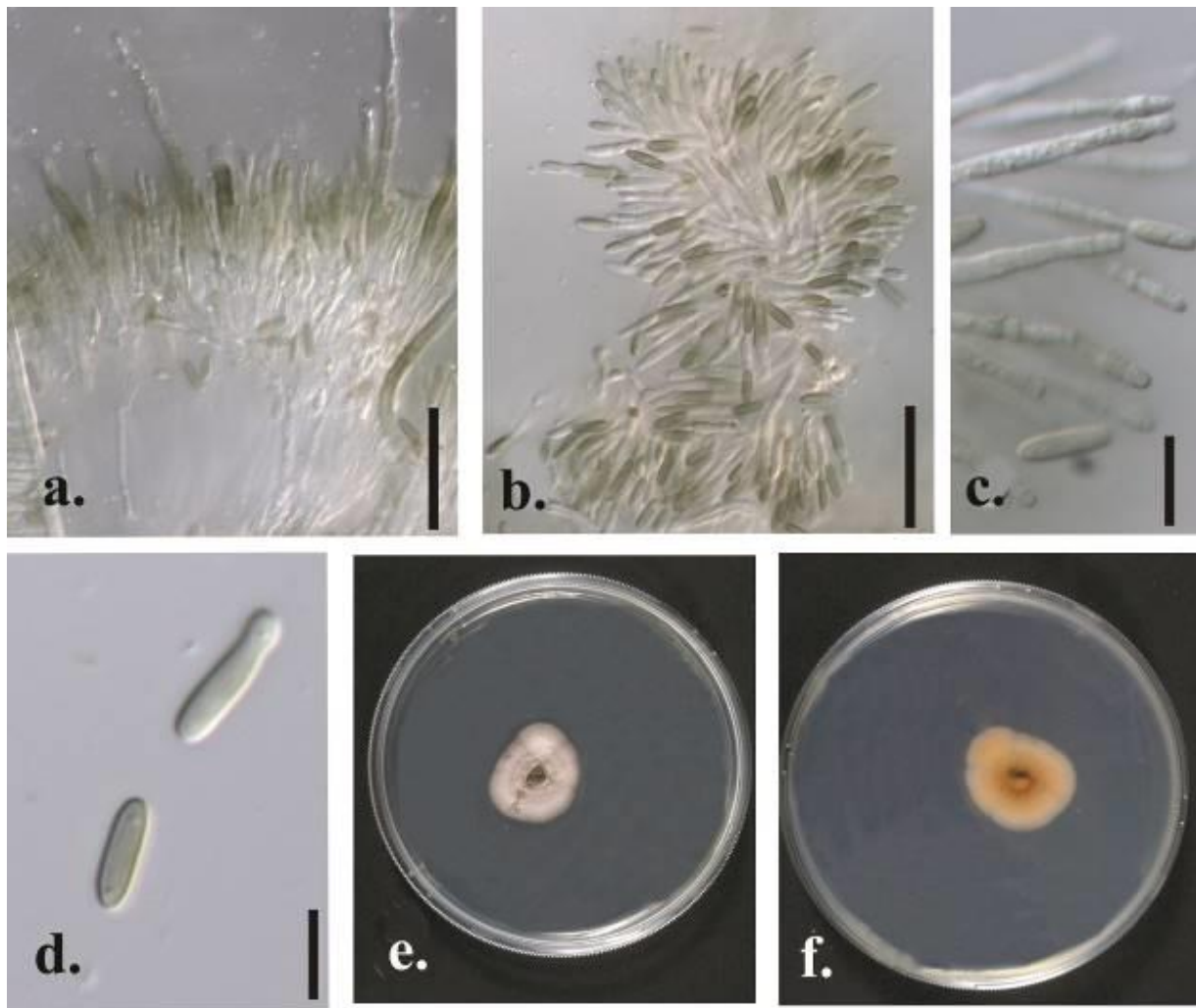


Fig. 79 – *Alfaria vitis*. a-b. Penicillate conidiophores. c. Conidiogenous cells d. Conidia. Scale bars: a–b=20 μm , c–d=10 μm .

Neoanthostomella viticola Daranagama, Camporesi & K. D. Hyde, in Daranagama, Camporesi, Jeewon, Liu, Stadler, Lumyong & Hyde, Cryptog. Mycol. 37(4): 524 (2016)

Facesoffungi number: FoF03817

Saprotrophic on dead branch of *Vitis vinifera*. **Sexual morph:** *Ascomata* 160–203 \times 180–225 μm (\bar{x} =186 μm \times 205 μm , n=10), immersed, visible as black, raised, conical-irregular shaped areas, coriaceous, clustered, rarely solitary, scattered, in cross section globose, with wide ostiolar neck. *Ostiole* 82–110 μm diam. at the base, 50–66 μm high (\bar{x} =102 \times 64 μm , n=10), grey, papillate, with a central periphysate ostiolar canal. *Peridium* 34–53 μm wide (\bar{x} =41 μm , n=10), with two cell layers, outwardly comprising thick-walled, compressed, light brown cells of *textura irregularis* and inwardly comprising thick-walled, several layers of hyaline cells of *textura angularis*. *Paraphyses* 3–3.4 μm wide at base (\bar{x} =3 μm , n=30), slightly longer than the asci, numerous, filamentous, septate. *Asci* 85–117 \times 5–7 μm (\bar{x} =92 \times 7 μm , n=20), 8-spored, unitunicate, cylindrical, long pedicellate, with apical apparatus. *Ascospores* 6–11 \times 3–5 μm (\bar{x} =9 \times 4 μm , n=20), uniseriate-overlapping uniseriate, ellipsoidal, with pointed ends, light brown, smooth-walled, germ slit spiral, 2/3 of the full-length. **Asexual morph:** Hyphomycetous. *Conidiophores* 60–80 \times 5–8 μm (\bar{x} =76 \times 6 μm , n=40), macronematous, septate, densely branched in the upper part, hyaline, smooth. *Conidiogenous cells* 9–12 \times 3–6 μm (\bar{x} =11 \times 5 μm , n=40), phialidic, with an apical collarette,

cylindrical, slightly wider at base, hyaline, smooth. *Conidia* 5–8×4–6 μm (\bar{x} =7×4 μm, n=20), hyaline, globose to ellipsoidal, slightly verruculose.

Culture characteristics — Colonies on Difco OA at 25–27 °C reaching 9 cm diam in 6 weeks, at first whitish, felty, azonate, with fluffy margins; reverse turning citrine light yellow after 2–3 weeks.

Material examined — ITALY, Province of Forlì-Cesena, Trivella di Predappio, on dead aerial branch of *Vitis vinifera*, 31 December 2014, Erio Camporesi, IT 2326 (MFLU 15-0691), cultures MFLUCC 16-0243, KUMCC 17-0102, MFLUCC 15-0517, MFLUCC 15-0518.

Notes — *Neoanthostomella viticola* was introduced by Daranagama et al. (2016) to accommodate a species isolated from *Vitis vinifera* in Italy.

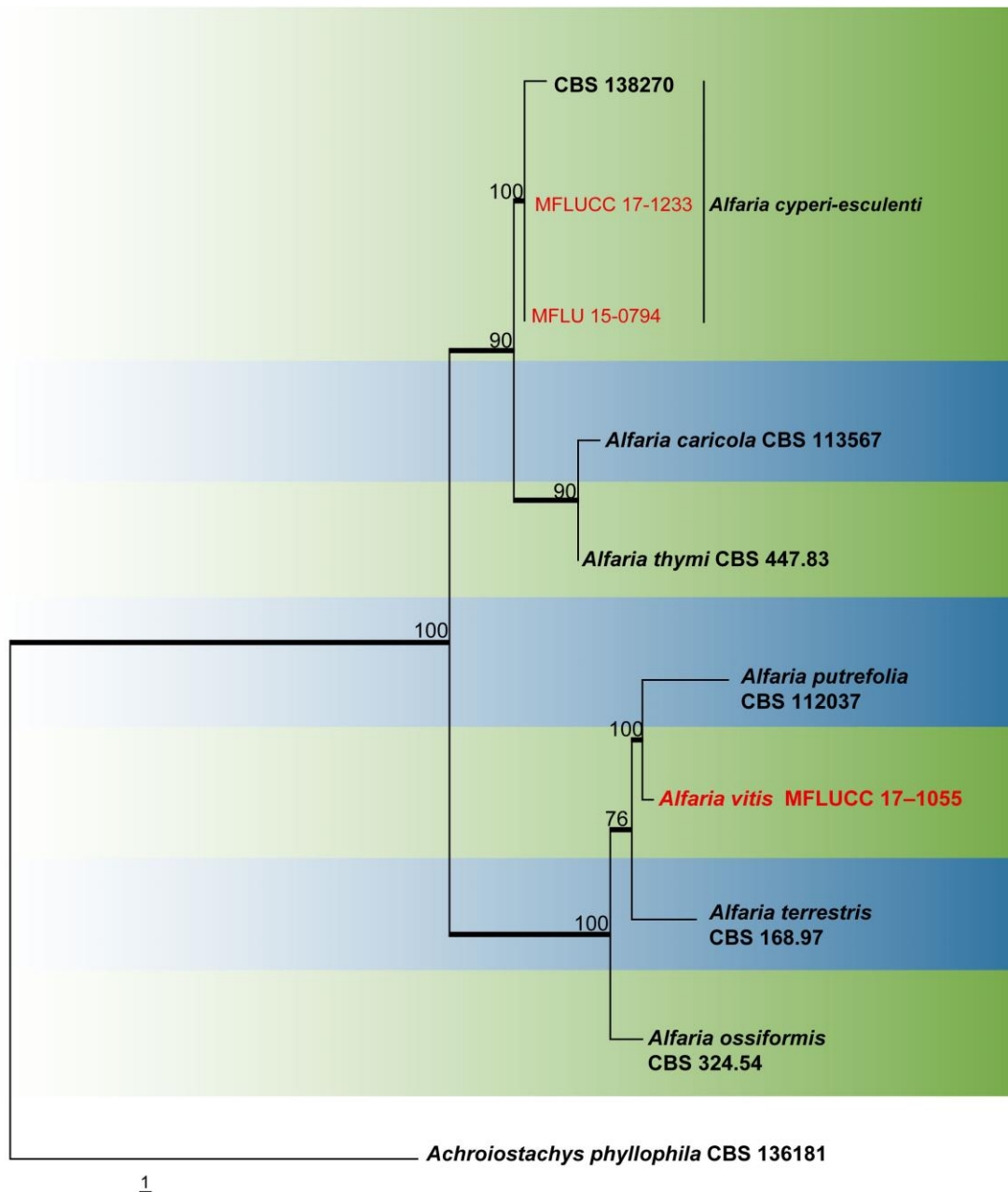


Fig. 80 – One of ten most parsimonious trees obtained from a heuristic search of combined ITS and LSU sequence data of taxa from *Alfaria*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.75 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Achroiostrachys phyllophila* CBS 136181.

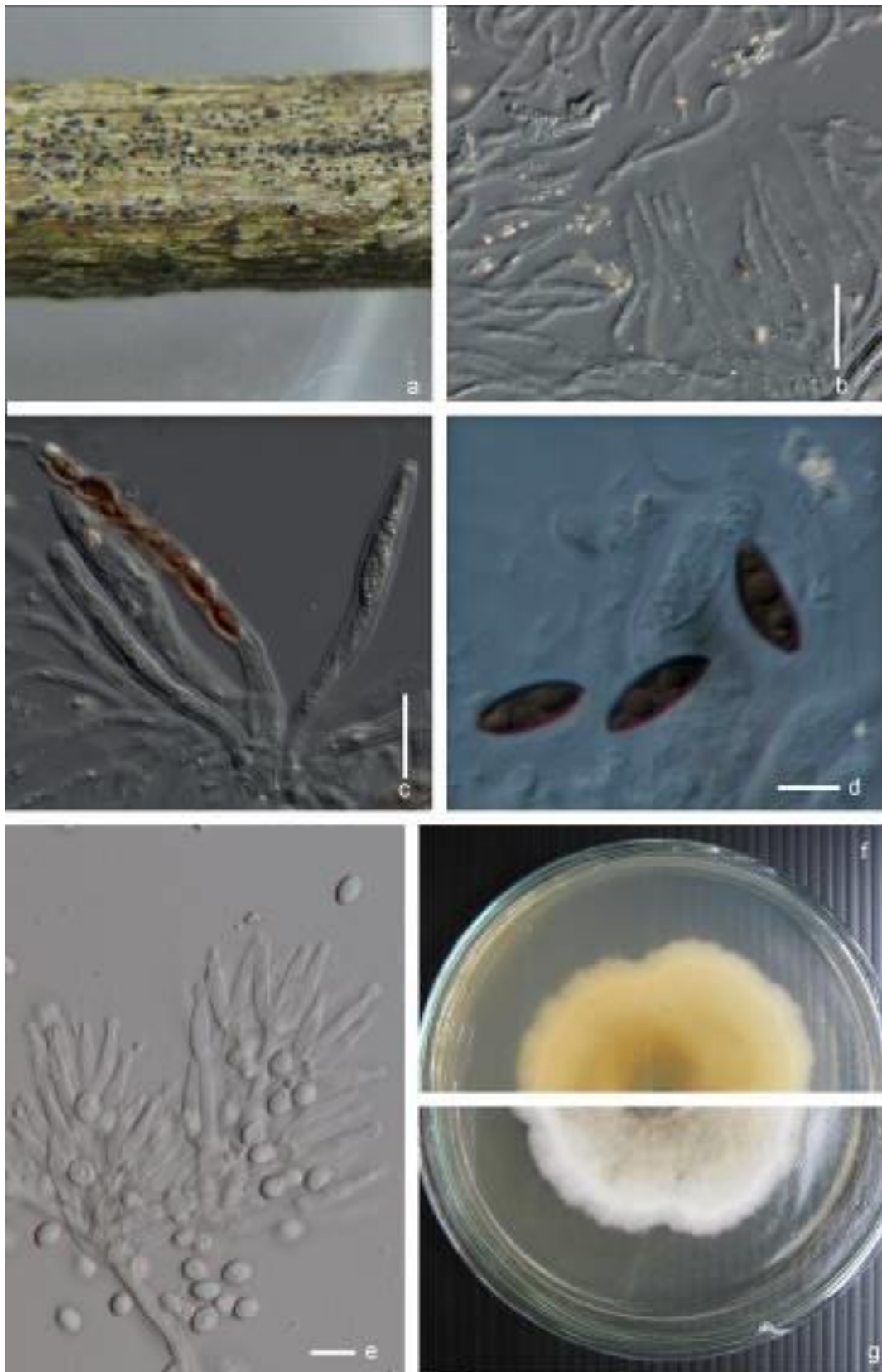


Fig. 81 – *Neoanthostomella viticola*. a. Fruiting bodies on host tissue. b. Paraphyses. c. Immature and mature asci. d. Ascospores. e. Conidiophores, conidiogenous cells and conidia f. Reverse view of colony on OA g. Upper view of the colony on OA. Scale bars: b–g=10 μ m.

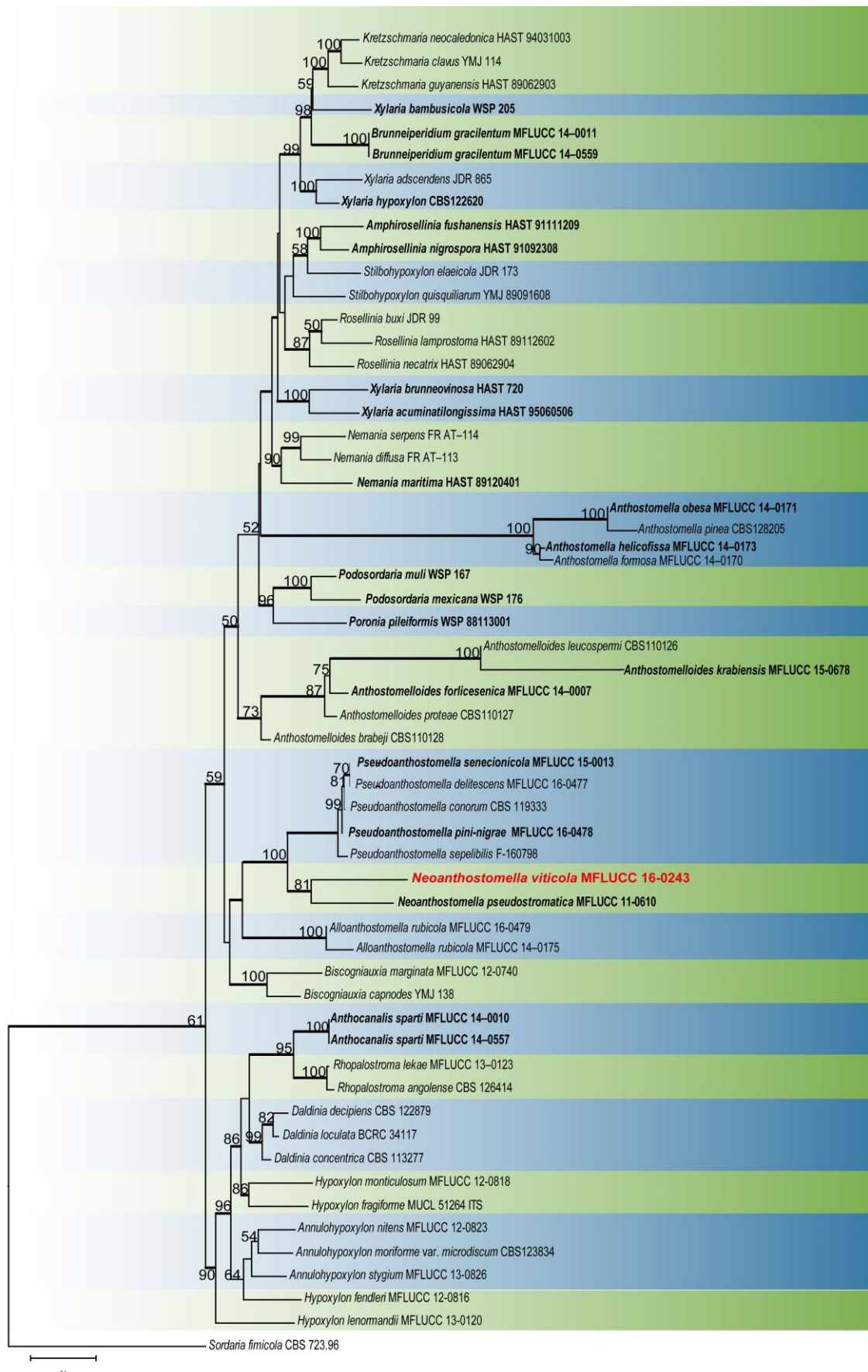


Fig. 82 – RAxML phylogram obtained from combined ITS, LSU, RPB2, TUB2 sequence data of *Xylariaceae*. Ex-type strains are in bold. Strains isolated in this study are shown in red. RAxML bootstrap support (BS) values $\geq 50\%$ are shown at the nodes and branches with Bayesian posterior probability scores ≥ 0.90 are given in bold. The tree is rooted with *Sordaria fimicola*.

Leotiomycetes

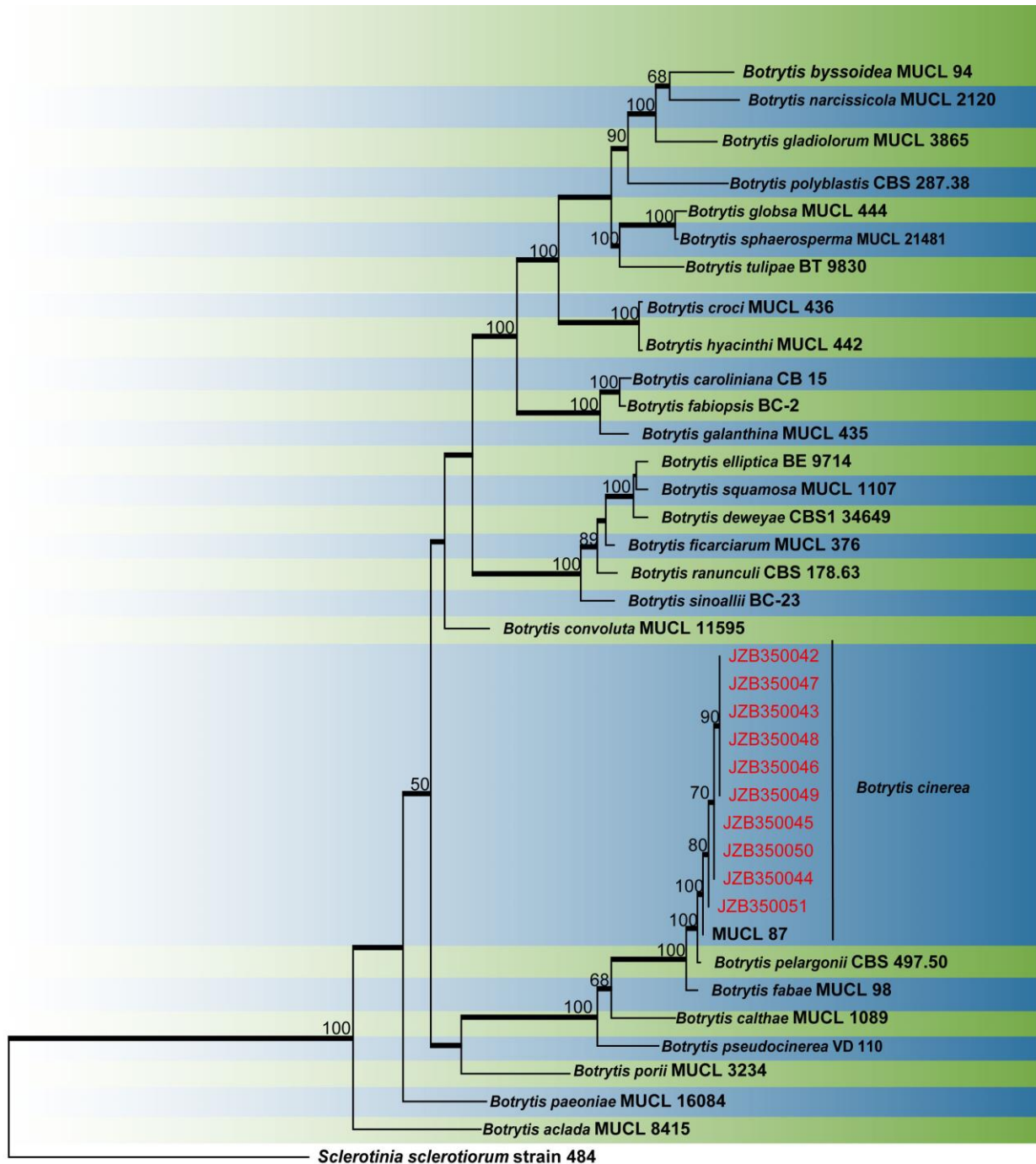
Helotiales Nannf. ex Korf & Lizoň, Mycotaxon 75: 501 (2000)

Sclerotiniaceae Whetzel, Mycologia 37(6): 652 (1945)

Botrytis cinerea Pers., Syn. meth. fung. (Göttingen) 2: 690 (1801)

Facesoffungi number: FoF:03822

Notes — This species is a well-known pathogen, endophyte and a saprotroph on *Vitis vinifera*. Phylogenetic analysis including the strains isolated in this study is given in Fig. 83.



10

Fig. 83 – One of ten most parsimonious trees obtained from a heuristic search of combined G3PDH, HSP60 and RPB2 sequence data of taxa from *Botrytis*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.75 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Sclerotinia sclerotiorum* strain 484.

Mucoromycetes

Mucorales Fr., Syst. mycol. (Lundae) 3(2): 296 (1832)

Mucoraceae Dumort., Comment. bot. (Tournay): 69 (1822)

Species of this family are mainly saprotrophs inhabiting soil, dung and dead plant material, although several are parasites on plants and on other fungi (Walther et al. 2013).

Actinomucor Schostak., Ber. dt. bot. Ges. 16: 155 (1898)

This genus is closely related to *Mucor*, but differs in having branched stolons which give rise to rhizoids and sporangiophores (Karimi et al. 2015). Strains from our study appeared to be *A. elegans*.

Actinomucor elegans (Eidam) C.R. Benj. & Hesselt., Mycologia 49: 241 (1957)

See Karimi et al. (2015) for the description.

Notes — *Actinomucor elegans* is recorded as a saprotroph on *Vitis vinifera* from China for the first time.

Mucor racemosus Bull., Hist. Champ. Fr. (Paris) 1: 104, tab. 504, fig. VII (1791)

Notes — *Mucor racemosus* has been recorded as an endophyte from Spain and Switzerland from *Vitis vinifera* (Casieri et al. 2009; Gonzalez & Tello 2011). This study provides the first report of this species as a saprotroph on *V. vinifera* from China. This species can be a secondary invader causing bunch rot of grapevine.

Mucor circinelloides Tiegh., Annls Sci. Nat., Bot., sér. 6 1: 94 (1875)

Notes — There is only one record of this species from *Vitis vinifera*. *Mucor circinelloides* has been recorded as a saprotroph from Switzerland (Casieri et al. 2009). This study provides the first report of this species as a saprotroph on *V. vinifera* from China.

Rhizopodaceae K. Schum., Lehrb. system. Bot. Phytopaläont. Phytogeogr. (Stuttgart): 70 (1894)

Rhizopus oryzae Went & Prins. Geerl., Verh. K. Akad. Wet., tweede sect. 4(2): 16 (1895)

Notes — This study provides the first record of *R. oryzae* associated with *V. vinifera*.

Eurotiomycetes

Eurotiales G.W. Martin ex Benny & Kimbr., Mycotaxon 12(1): 23 (1980)

Trichocomaceae E. Fisch., in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1: 310 (1897)

Aspergillus aculeatus Iizuka, J. agric. Chem. Soc. Japan 27: 806 (1953)

Notes — *Aspergillus aculeatus* is known to cause bunch rot of grapes in Canada (Jarvis & Traquair 1984). However, this species is considered as a secondary invader. *Aspergillus aculeatus* is recorded for the first time in China on *V. vinifera* as a saprotroph. A phylogenetic analysis of the strains isolated in this study is given in Fig. 84.

Aspergillus niger Tiegh., Annls Sci. Nat., Bot., sér. 5 8: 240 (1867)

Notes — This species is known to be associated with cankers as well as bunch rot of grapevine in grape growing regions (Gonzalez & Tello 2011). *Aspergillus niger* has been also recorded as a saprotroph and endophyte of *V. vinifera*.

Penicillium brevicompactum Dierckx, Ann. Soc. Sci. Bruxelles 25: 88 (1901)

Notes — This study provides the first record of *P. brevicompactum* associated with *V. vinifera*.

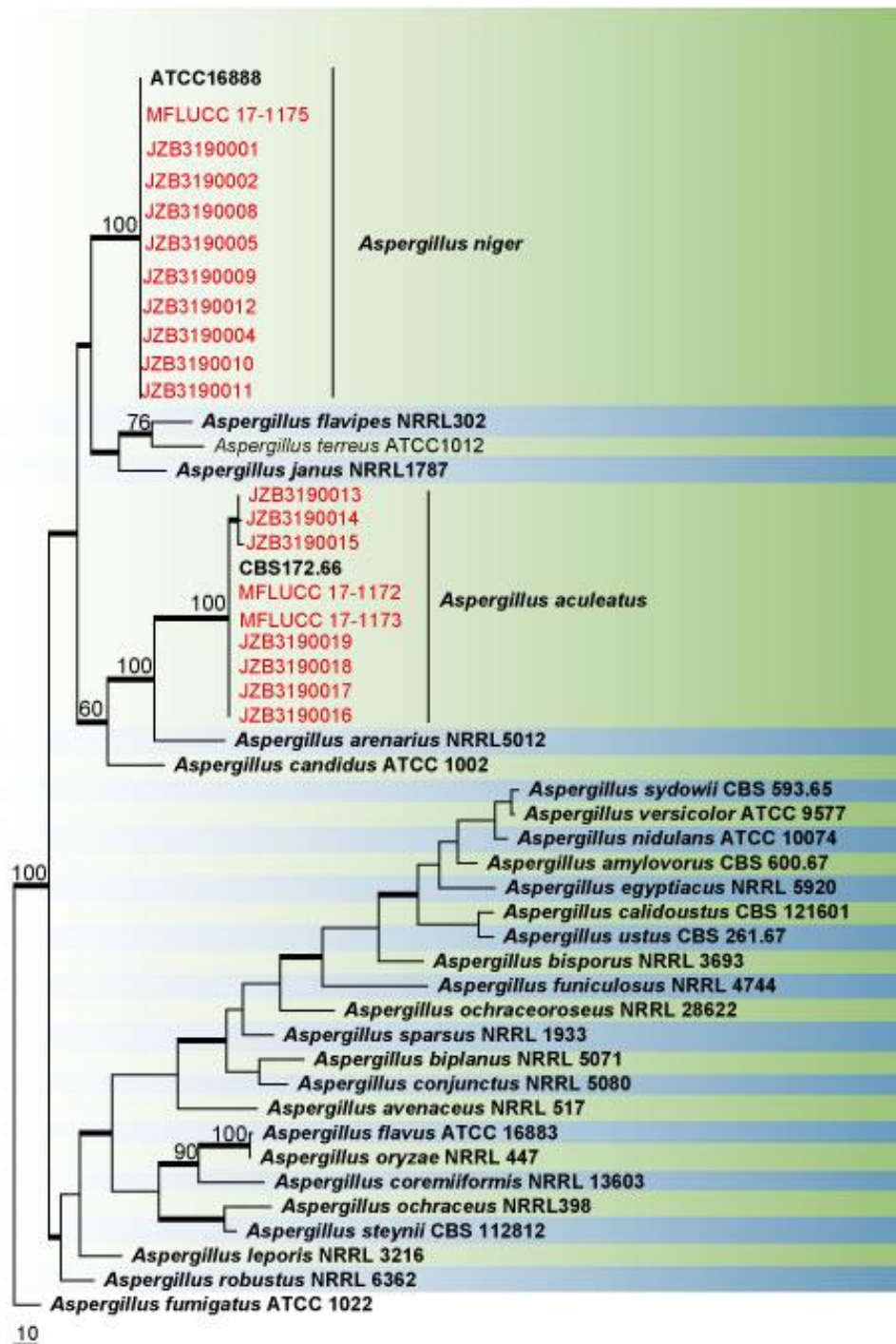


Fig. 84 – One of ten most parsimonious trees obtained from a heuristic search for ITS sequence data of taxa from *Aspergillus*. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.75 given in bold. Ex-type strains are in bold. Strains obtained in this study are in red. The tree is rooted with *Aspergillus fumigatus* ATCC 1022

Penicillium citrinum Thom, Bull. U.S. Department of Agriculture, Bureau Animal Industry 118: 61 (1910)

Notes — This study provides the first record of *P. citrinum* associated with *V. vinifera*.

Penicillium terrigenum Houbraken, Frisvad & Samson, Stud. Mycol. 70: 125 (2011)

Notes — *Penicillium terrigenum* was first described from soil. This study provides the first record of *P. terrigenum* associated with *V. vinifera*.

Talaromyces amestolkiae N. Yilmaz, Houbraken, Frisvad & Samson, in Yilmaz, Houbraken, Hoekstra, Frisvad, Visagie & Samson, *Persoonia* 29: 48 (2012)

Notes — *Talaromyces amestolkiae* was described from house dust in South Africa (Yilmaz et al. 2012). This study provides the first record of *T. amestolkiae* associated with *V. vinifera*.

Talaromyces pinophilus (Hedgc.) Samson, N. Yilmaz, Frisvad & Seifert, in Samson, Yilmaz, Houbraken, Spierenburg, Seifert, Peterson, Varga & Frisvad, *Stud. Mycol.* 70: 176 (2011)

Notes — *Talaromyces pinophilus* is recorded for the first time as a saprotroph from *Vitis vinifera*.

Talaromyces purpureogenus Samson, N. Yilmaz, Houbraken, Spierenb., Seifert, Peterson, Varga & Frisvad, in Samson, Yilmaz, Houbraken, Spierenburg, Seifert, Peterson, Varga & Frisvad, *Stud. Mycol.* 70: 177 (2011)

Notes — This study provides the first record of *T. purpureogenus* as a saprotroph on *V. vinifera* from China.

Agaricomycetes Doweld

Cantharellales Incertae sedis

***Minimedusa* sp.**

Notes — This study provides the first report of *Minimedusa* sp. as a saprotroph associated with *Vitis vinifera* in China as well as in the world.

Peniophoraceae Lotsy, *Vortr. bot. Stammesgesch.* 1: 687 (1907)

***Peniophora* sp.**

Notes — *Peniophora albomarginata* and *P. viticola* have been recorded as saprotrophs on *Vitis vinifera* in USA (Jayawardena et al. 2018). This study provides the first record of a *Peniophora* sp. associated with *V. vinifera* in China.

Oomycota Incertae sedis

Peronosporales E. Fisch., *Rabenh. Krypt.-Fl.*, Edn 2 (Leipzig) 1(4): 383 (1892)

Pythiaceae J. Schröt., *Nat. Pflanzenfam.* (Leipzig) 1(1): 104 (1893)

Pythium amasculinum Y.N. Yu, *Acta microbiol. sin.* 13(2): 118 (1973)

Notes — Species of *Pythium* are known to cause root rot of *V. vinifera* (Jayawardena et al. 2018). This study provides the first report of *P. amasculinum* as a saprotroph associated with *V. vinifera* in China.

Discussion

Numerous fungal species occur on *Vitis* species worldwide. In this study, we show the diversity and taxonomy of 67 fungal species associated with *Vitis* species, with molecular data and descriptions linked to morphological illustrations when possible. We hope that this research will stimulate interest in the collection and description of fungi associated with *Vitis* species other than pathogens. There are more than 500 fungal species recorded on *Vitis* spp. in the checklist provided by Jayawardena et al. (2018) and are likely to be thousands of species that are associated with *Vitis* species worldwide. Many of the saprotrophs are also well-known pathogens and they may be the primary source of inoculant in a vineyard. These taxa need to be collected, and where necessary epitypified and sequenced in order to have a better understanding about the host genus *Vitis*.

Species Name	Isolate No	ITS	LSU	SSU	RPB2	TUB2	TEF	CAL	ACT	CHS	GAPDH	Histone	HSP60
<i>Albifimbria verrucaria</i>	MFLUCC 17-2381	MG764005	MG792336										
<i>Albifimbria viridis</i>	MFLUCC 17-1149	MG764006	MG792337										
<i>Alfaria cyperi-esculenti</i>	MFLU 15- 0794	MG763956	MG812526										
	MFLUCC 17-1233	MG763957	MG812527										
<i>Alfaria vitis</i>	MFLUCC 17-1055	KY649631					KY926886						
<i>Alternaria alternata</i>	KUMCC 17- 0118	MG764010					MG818319						
	MFLUCC 17-1218	MG764015	MG818322		MG859740		MG818320				MG859751		
	MFLUCC 17-1222	MG764022	MG818326		MG859744		MG818321				MG859755		
	MFLUCC 17-1229	MG764019	MG818323		MG859741		MG818322				MG859752		
	MFLUCC 17-1230	MG764014	MG818327		MG859745		MG818323				MG859756		
	MFLUCC 17-1241	MG764013					MG818324						
	MFLUCC 17-1250	MG764012	MG818324		MG859742		MG818325				MG859753		
	MFLUCC 17-1251	MG764011	MG818325		MG859743		MG818326				MG859754		
	MFLUCC 17-1187	MG764009	MG818320		MG859739		MG818327				MG859750		
<i>Alternaria italica</i>	MFLUCC 14-0421	MG764018			MG859737								
	KUMCC 17- 0090	MG764019											
<i>Alternaria vitis</i>	MFLUCC 17-1109	MG764007	MG818319										
	MFLUCC 17-1116	MG764008											
<i>Angustimassarina populi</i>	MFLUCC 17-1069	MF409170	MF409166	MF409165			MF409163						
	MFLUCC 17-1217	MG763958	MG812609	MG812610			MG812528						
<i>Aspergillus aculeatus</i>	JZB3190013	MG764030											
	JZB3190014	MG764031											
	JZB3190015	MG764032											
	MFLUCC 17-1172	MG764033											
	MFLUCC 17-1173	MG764034											
	JZB3190016	MG764038											
	JZB3190017	MG764037											
	JZB3190018	MG764036											

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Species Name	Isolate No	ITS	LSU	SSU	RPB2	TUB2	TEF	CAL	ACT	CHS	GAPDH	Histone	HSP60
<i>Aspergillus niger</i>	JZB3190019	MG764035											
	MFLUCC 17-1175	MG764020											
	JZB3190001	MG764021											
	JZB3190002	MG764022											
	JZB3190004	MG764027											
	JZB3190005	MG764024											
	JZB3190008	MG764023											
	JZB3190009	MG764025											
	JZB3190010	MG764028											
	JZB3190011	MG764029											
	JZB3190012	MG764026											
	<i>Aureobasidium pullulans</i>	MFLU 16-2813	MG763964										
MFLUCC 17-1218		MG763959	MG812611	MG812616									
MFLUCC 17-1222		MG763961	MG812613	MG812618									
MFLUCC 17-1231		MG763962	MG812614	MG812619									
MFLUCC 17-1256		MG763963	MG812615	MG812620									
MFLUCC-17-1221		MG763960	MG812612	MG812617									
MFLUCC 17-1100		MG764039									MG859746		
<i>Bipolaris maydis</i>	JZB3170002	MG764040									MG859747		
	JZB317003	MG764041									MG859748		
<i>Botryosphaeria dothidea</i>	MFLUCC 17-0961	MF409167					MF409160						
	JZB310176	MG764042					MG859761						
<i>Botrytis cinerea</i>	JZB350042				MG859804						MG859814		MG859794
	JZB350043				MG859805						MG859815		MG859795
	JZB350044				MG859806						MG859816		MG859796
	JZB350045				MG859807						MG859817		MG859797
	JZB350046				MG859808						MG859818		MG859798
	JZB350047				MG859809						MG859819		MG859799
	JZB350048				MG859810						MG859820		MG859800
	JZB350049				MG859811						MG859821		MG859801
	JZB350050				MG859812						MG859822		MG859802
	JZB350051				MG859813						MG859823		MG859803
<i>Chaetomium globosum</i>	MFLUCC 15-0514	MG763966	MG812623				MG812562						
	MFLUCC 15-0523	MG763967	MG812624				MG812563						
	MFLUCC 15-0524	MG763968	MG812625				MG812564						
	MFLUCC 17-1056	KY926889								KY926887			
<i>Cladosporium cladosporioides</i>	MFLUCC 17-1133	MG764044					MG859786			MG859784			

Species Name	Isolate No	ITS	LSU	SSU	RPB2	TUB2	TEF	CAL	ACT	CHS	GAPDH	Histone	HSP60
	MFLUCC 17-1182	MG764043							MG859785				
<i>Cladosporium cucumerinum</i>	MFLU 14-0206	MG764045											
<i>Colletotrichum dematium</i>	MFLUCC 17-1092	MG763969				MG812538			MG812529	MG812532	MG812535		
	MFLUCC 17-1096	MG763970				MG812539			MG812530	MG812533	MG812536		
	MFLUCC 17-1097	MG763971				MG812540			MG812531	MG812534	MG812537		
<i>Colletotrichum godetiae</i>	MFLUCC 17-1062	KY632679				KY632673			KY632671	KY632675	KY632677		
	MFLUCC 17-1395	KY632680				KY632674			KY632672	KY632676	KY632678		
<i>Colletotrichum hebeiense</i>	JZB330117	MG763977				MG812546			MG812561	MG812549	MG812555		
<i>Colletotrichum siamense</i>	MFLUCC 17-1219	MG763974				MG812543			MG812558		MG812552		
<i>Colletotrichum truncatum</i>	MFLUCC 17-2380	MG764046				MG859758			MG859760	MG8597559	MG859757		
<i>Colletotrichum viniferum</i>	MFLUCC 14-1213	MG763972				MG812541			MG812556	MG812547	MG812550		
	MFLUCC 14-1214	MG763973				MG812542			MG812557	MG812548	MG812551		
	JZB330118	MG763976				MG812545			MG812560		MG812554		
	JZB330119	MG763975				MG812544			MG812559		MG812553		
<i>Coniella vitis</i>	JZB3700009	MG764053	MG837140				MG859783					MG859793	
	JZB3700014	MG764051	MG837138				MG859781					MG859791	
	JZB3700026	MG764052	MG837139				MG859782					MG859792	
	MFLUCC 1125	MG764049	MG837136				MG859779					MG859789	
	MFLUCC 17-1113	MG764047	MG837134				MG859777					MG859787	
	MFLUCC 17-1123	MG764048	MG837137				MG859780					MG859790	
	MFLUCC 17-1138	MG764050	MG837135				MG859778					MG859788	
<i>Cryptovalsa ampelina</i>	MFLUCC 15-0139	KU550094	KU550096	KU550095									
	MFLUC 16-007												
<i>Diaporthe ampelina</i>	MFLUCC 16-0960	MF409171				MF409159	MF409164	MF409172					
	MFLUCC 17-1270	MG763978				MG812588	MG812565	MG812586					
	MFLUCC 17-1271	MG763979				MG812589	MG812566	MG812587					
<i>Diaporthe eres</i>	MFLUCC 17-1102	MG763981					MG812568						
	MFLUCC 17-1106	MG763982				MG812591	MG812569	MG812583					

Species Name	Isolate No	ITS	LSU	SSU	RPB2	TUB2	TEF	CAL	ACT	CHS	GAPDH	Histone	HSP60
<i>Diaporthe rudis</i>	MFLUCC 17-1160	MG763980				MG812590	MG812567	MG812582					
	JZB320118	MG763983				MG812592	MG812570	MG812584					
	JZB320119	MG763984				MG812593	MG812571	MG812585					
	MFLU 17-2818	MG763985				MG812594	MG812572						
<i>Didymella negeriana</i>	MFLUCC 16-1394	KY632665	KY632667		KY632669	KY632663							
	MFLUCC 17-1061	KY632666	KY632668		KY632670	KY632664							
<i>Didymella pomorum</i>	MFLUCC 17-1112	MG763986	MG812603		MG812606	MG812595							
	MFLUCC 17-1121	MG763987	MG812604		MG812607	MG812596							
	MFLUCC 17-1158	MG763988	MG812605		MG812608	MG812597							
<i>Diplodia seriata</i>	MFLUCC 17-1251	MG763989					MG812577						
	MFLUCC 17-1252	MG763990					MG812578						
	MFLUCC 17-1253	MG763991					MG812579						
	MFLUCC 17-1264	MG763992					MG812580						
	MFLUCC 17-1265	MG763993					MG812581						
	MFLUCC 17-0964	MF409168					MF409161						
	MFLUCC 17-0962	MF409169					MF409162						
<i>Dothiorella sarmentorum</i>	MFLUCC 17-1212	MG763994					MG812573						
	MFLUCC 17-1213	MG763995					MG812574						
	JZB3150039	MG763996					MG812576						
<i>Epicoccum nigrum</i>	KUMCC 17-0092	MG807025	MG818842		MG859837	MG859828							
	MFLUCC 17-1214	MG807027	MG818843		MG859839	MG859830							
	MFLUCC 17-1215	MG807026	MG818844		MG859838	MG859829							
	JZB380010	MG807022	MG818845		MG859835	MG859826							
	JZB380011	MG807024	MG818846		MG859836	MG859827							
	MFLUCC 17-1153	MG807028	MG818847		MG859840	MG859831							
	JZB380012	MG807023	MG818848		MG859834	MG859825							
	JZB380013	MG807021	MG818849		MG859833	MG859824							
	MFLUCC 17-1162	MG807029	MG818850		MG859841	MG859832							
	MFLUCC 15-0039			MG837003	MG8370034								

Species Name	Isolate No	ITS	LSU	SSU	RPB2	TUB2	TEF	CAL	ACT	CHS	GAPDH	Histone	HSP60
<i>Fusarium oxysporum</i>	MFLUCC	MG807034											
	17-1103												
	MFLUCC	MG807033											
	17-1107												
	MFLUCC	MG807032											
	17-1124												
	MFLUCC	MG807031											
	17-1127												
	MFLUCC	MG807030											
<i>Fusarium sambucinum</i>	MFLUCC	MG807035											
	17-1184												
	MFLUCC	KY926891											
<i>Mucor circinelloides</i>	MFLUCC	MG807042											
	17-1111												
<i>Mucor racemosus</i>	MFLUCC	MG807041											
	17-1140												
	JZB3210021	MG807036											
	MFLUCC	MG807040											
	17-1163												
	MFLUCC	MG807039											
	17-1178												
MFLUCC	MG807038												
<i>Neanthostomella viticola</i>	MFLUCC	MG807037											
	17-1186												
	MFLUCC	KX505957	KX505958			KX789496	KX789495						
	16-0243												
	MFLUCC	15-0900											
	15-0900												
<i>Neofusicoccum italicum</i>	MFLUCC	MG763997							MG812525				
	17-1254												
<i>Neofusicoccum parvum</i>	MFLU	15-0372											
	15-0372												
<i>Neomassaria fabacearum</i>	MFLUCC	MG807058							MG859848	MG859768			
	17-1117												
	JZB340031	MG807056						MG859846	MG859766				
	JZB340032	MG807055						MG859845	MG859765				
	JZB340033	MG807054						MG859844	MG859764				
	JZB340034	MG807053						MG859843	MG859763				
	MFLUCC	MG807052						MG859842	MG859762				
	17-1120												
	MFLUCC	MG807057						MG859847	MG859767				
	17-1135												
<i>Neopestalotiopsis vitis</i>	MFLUCC	MG807045						MG859849	MG859769				
	17-1108												
	MFLUCC	MG807046						MG859850	MG859770				
	17-1126												
MFLUCC	MG807047						MG859851	MG859771					

Species Name	Isolate No	ITS	LSU	SSU	RPB2	TUB2	TEF	CAL	ACT	CHS	GAPDH	Histone	HSP60
	17-1167												
	JZB340027	MG807051				MG859855	MG859775						
	JZB340028	MG807050				MG859854	MG859774						
	JZB340029	MG807049				MG859853	MG859773						
	JZB340030	MG807048				MG859852	MG859772						
<i>Pestalotiopsis chamaeropsis</i>	MFLU 15-0794	MG807043				MG859857							
<i>Pestalotiopsis</i> sp.	MFLU 15-2659	MG807044											
<i>Pseudocamarosporium propinquum</i>	MFLUCC 17-1211	MG763965											
<i>Pseudocercospora vitis</i>	MFLUCC 15-0499	MG763998									MG812598		
	MFLUCC 15-0500	MG763999									MG812599		
	MFLUCC 15-0501	MG764000									MG812600		
	MFLUCC 15-0509	MG764001									MG812602		
	MFLUCC 15-0511	MG764002									MG812601		
<i>Pseudolachnea hispidula</i>	MFLUCC 17-1238	MG764003	MG812626										
<i>Pseudopestalotiopsis camelliae-sinensis</i>	MFLUCC 17-1220	MG807059				MG859856	MG859776						
<i>Pythium amasculinum</i>	JZB3220001	MG807060											
<i>Rhizopus oryzae</i>	MFLUCC 17-1104	MG807017											
	MFLUCC 17-1119	MG807018											
	MFLUCC 17-1166	MG807019											
	MFLUCC 17-1169	MG807020											
<i>Seimatosporium vitis</i>	MFLU 15-0204	MG764004	MG812627										
	MFLU 17-1060	KY632661	KY632662										

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