Fungal Planet description sheets: 1182–1283

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Key words
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Abstract. Novel species of fungi described in this study include those from various countries as follows: Algeria, Phaeoacremonium adelophialidum from Vitis vinifera. Antarctica, Coniochaeta salicifolia as endophyte from healthy leaves of Geijera salicifolia, Eremothecium peggi in fruit of Citrus australis. Microdochium rataeicola from stem of Sporobolus natalensis, Neocalospora rurecinae on stems of Corymbia variegata, Phytophthora kermitii from rhizosphere soil of Pitlitos pyramidalus, Pseudosclerospora endophytes from live leaves of Backhousia citriodora, Pseudosclerospora indica, Pseudosclerospora louiceottiacae and Pseudosclerospora queenslandica on living leaves of Eucalyptus sp. Brazil, Abisidia montepaacoisalis from soil of Chile, Ilyonectria zarorii from soil under Maytenus boaria. Costa Rica, Colletotrichum filamentosum from an unidentified fern. Croatia, Mollisia endogranaulata on deteriorated hardwood. Czech Republic, Acreolus navicularis from tea tag with fruit tea, Neospathotheca buxi as endophyte from Buxus sempervirens, Xeromyces boehmiensis from surface of biscuits with chocolate glaze and filled with jam. France, Entoloma cyanobasale on basic to calcareous soil, Fusarium aconidioides from Trichium aestivum, Fusarium juglandicola from buds of Juglans regia. Germany, Tetrapyla endophytica as endophyte from Microthlaspi perfoliatum roots. India, Castanediella ambae on leaves of Mangifera indica, Lactifluus kandali on soil under Casanopas sp., Penicillium uratokhendenses from soil of Italy, Penicillium ferrariae from compost. Namibia, Beznizeryomyces gobabebensis on leaves of unidentified succulent, Cladosporium stipagrostidis from leaves of Stipa argiotes, Cystoschyzomyces euphratieae from leaves of Euphoria sp., Dematilleta hypolithi from hypolith under a rock, Hysterobrevium walvisbaylicola on leaves of unidentified tree, Knufia hypolithi and Knufia walvisbaylicola from hypolith under a rock, Lapidomyces stipagrostidis from leaves of Stipa argiotes sp., Nothophaeotheca mirabellinas (incl. Nothophaeotheca gen. nov.) on persistent inflorescence remains of Bleschris obmitrata, Paramyrtathomostelea salvaoreae on twigs of Salvadora persica, Preussia procavicaulis on dune of Procvia sp., Sordaria equinica on zebra dung, Volutella salvaoreae on stems of Salvadora persica. Netherlands, Entoloma ammophorum on sandy soil, Entoloma pseudocentrum on nutrient poor (acid) soil, Entoloma pudens on plant debris, amongst grasses. New Zealand, Amorocoleopilomyces neoregeliae from leaf spots of Neoregelia sp., Aquilomyces metrosideri and Septoria callistemonis from stem discoloration and leaf spots of Metrosporidium sp., Cadophora neoregeliae from leaf spots of Neoregelia sp., Flexurozymes asellae (incl. Flexurozymes gen. nov.) and Mollisia asellae from leaf spots of Astelia chathamica, Ophioceras freycinetiae from leaf spots of Freycinetia

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Abstract (cont.)

banksi, Phaeosphaeria caricis-seciae from leaf spots of Carex secta. Norway, Cuphophyllum flavipesoides on soil in semi-natural grassland, Entoloma coracis on soil in calcareous Pinus and Tilia forests, Entoloma cyanellacinum on soil semi-natural grasslands, Inocybe norvegica on gravelly soil. Pakistan, Butynoateus pararchinenaris on soil in association with Quercus baloot. Poland, Hyalodendriella bialowiwienzis on debris beneath fallen bark of Norway spruce Picea abies. Russia, Boblitus sibiricus on a moss covered rotting trunk of Populus tremula, Crepidotus wasseri on debris of Populus tremula, Entoloma isoboscanum on soil on calcareous grasslands, Entoloma subcoracias on soil in subalpine grasslands, Hydropus lyciophyti on rotted wood of Betula pendula, Merulipos faginea on fallen dead branches of Fagus orientalis, Metyltrombokia taurica from fruits of Ziziphus jujube, Sullusta praetermissus on soil, Teunia lichenophila as endophyte from Cladonia rangiferina. Slovakia, Hygrocybe fulgens on mowed grassland, Pleuroflammula pannonica from corticated branches of Quercus sp. South Africa, Acrodontium burrowsianum on leaves of unidentified Poaceae, Castaneidiella senegaliae on dead pods of Senegalia axatacantha, Cladophalohora behniae on leaves of Behnia sp., Colлетistrichum clivigenum on leaves of Clivia sp., Diatrype dalbergiae on bark of Dalbergia armata, Falcocladium heteropyricola on leaves of Heteropyxis canescens, Lopadomyces airoidendri as epiphyte on brown stem of Aloidendron dichotomum, Lasonectria sanvieriae and Phaeosphaeropsis sanvieriae on leaves of Sanvieria hyacinthoides, Lylea dalbergiae on Diatrype dalbergiae on bark of Dalbergia armata, Neochaetothyrina syzygii (incl. Neochaetothyrina gen. nov.) on leaves of Syzygium chordatum, Nothophaeomoniella ekebergiae (incl. Nothophaeomoniella gen. nov.) on leaves of Ekebergia pterophylla, Paracycomastochys euphorbiae (incl. Paracycomastochys gen. nov.) on leaf of Euphorbia ingens, Paramycosphaerella pterocarpi on leaves of Pterocarpus angolensis, Paramycosphaerella syzygii on leaf litter of Syzygium chordatum, Pareiteichospora phoenicicola (incl. Pareiteichospora gen. nov.) on leaves of Phoenix reclinata, Seiridium syzygii on leaves of Syzygium sp., Starmella xylofopis from larval feed of an Afrotropical bee Xylocoopa calida, Teratosphaeria comberti on leaf of Combretum kraussii, Teratosphaeria leucaenidii on leaves of Leucaenodon sp., Toxicodiplacium pterocarpi on pods of Pterocarpus angolensis. Spain, Cortinarius bonachei with Quercus ilex in calcareous soils, Cortinarius brunneovolvatus under Quercus ilex subsp. ballota in calcareous soil, Extremopsis radicola (incl. Extremopsis gen. nov.) from root-associated soil in a wet heathland, Russula quintanensis on acidic soils, Tubaria vulcanica on volcanic lapilli material, Tuber zambonelliae on leaf litter of Pinus sylvestris and Betula pubescens. Tanzania, Curvularia tanzanica on insole surface of Cyperus aromaticus. Thailand, Simplicillium niveum on Ophiocordyceps camponoti-leonardi, on underside of unidentified dichotyledon leaf. USA, Calonecrtia californiensis on leaves of Umbellularia californica, Exophiala spinariae from surface sterilised roots of Spartina alterniflora, Neophaeocorymomyces oklahomaensis from outside wall of alcohol distillery. Vietnam, Fistulinella aurantiolavata on soil. Morphological and culture characteristics are supported by DNA barcodes.

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Overview *Agaricomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 279752 trees resulting from a Bayesian analysis of the LSU sequence alignment (170 sequences including outgroup; 948 aligned positions; 553 unique site patterns; 1865000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Backusella lamprospera (GenBank MH866118.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Agaricomycetes phylogeny (cont.) – part 2

Suillaceae

Boletaceae

Agaricales

Boletales

Agaricomycetes (continued)
### Overview Agaricomycetes phylogeny (cont.) – part 3

#### Bolbitiaceae
- **Pholotina dasypus** NL-2279
- **Pholotina aeruginosa** WJ27104
- **Bolbitius sibiricus** sp. nov. - Fungal Planet 1228
- **Bolbitius viscosus** PBM3032 (TENN)
- **Bolbitius coprophilus** NL-2640
- **Bolbitius excoriatus** LO23-19
- **Bolbitius paldius** LE<BRUS>
- **Bolbitius bisporus** LO23-10
- **Bolbitius reticulatus** LE<BRUS>
- **Entoloma ameides** G0377
- **Entoloma gleocobasis** G0333
- **Entoloma subserenatum** TB693
- **Entoloma coracis** sp. nov. - Fungal Planet 1241
- **Entoloma azureopallidum** G0348
- **Entoloma saponicum** G1661
- **Entoloma exile** Lueck
- **Entoloma ekaterinae**
- **Porotheleum fimbriatum** FP102067
- **Clitocybula abundans** PBM4340
- **Clitocybula oculus** DAOM 195995
- **Hydropus atramentosus** G0356
- **Hydropus fuliginarius** DAOM196062
- **Hydropus lecythiocystis** sp. nov. - Fungal Planet 1253
- **Hydropus marginellus** OSC 112834
- **Coprinellus radians** SZMC-NL-3986
- **Coprinellus xanthothrix** GLM 45906
- **Coprinellus micaceus** DM1047
- **Coprinellus silvicus** LO17-2
- **Coprinellus aureogranulatus** CBS 973.95
- **Coprinellus domesticus** GLM 45903
- **Coprinellus phaeospora** CBS 895.70
- **Pleuroflammula tuberculosa** PAM02072903
- **Inocybe meridionalis** PBM 3413
- **Inocybe flocculosa** ZRL201517
- **Inocybe sylvicola** TAA172127
- **Inocybe lacera** EL2104
- **Pleuroflammula aberrans** PAM02072903
- **Crepidotus cf. applanatus** PBM 717
- **Crepidotus cesatii** G0306
- **Crepidotus versutus** PBM 856
- **Crepidotus albifrons** LE 287655
- **Crepidotus toboiensis** LE 287655
- **Crepidotus mollis** DM1043
- **Crepidotus euclaytorum** G1749
- **Crepidotus irrigens** B2200

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Overview Dothideomycetes (Other orders) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 56 102 trees resulting from a Bayesian analysis of the LSU sequence alignment (179 sequences including outgroup; 832 aligned positions; 37 400 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Diaporthaceae sp. (GenBank NG_059864.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The most basal branch was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Dothideomycetes (Pleosporales) phylogeny – part 1

Consensus phylogram (50% majority rule) of 91,128 trees resulting from a Bayesian analysis of the LSU sequence alignment (170 sequences including outgroup; 799 aligned positions; 295 unique site patterns; 607,500 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.0. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession group; 799 aligned positions; 295 unique site patterns; 607,500 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012).
Overview Dothideomycetes (Pleosporales) phylogeny – part 2
Overview Eurotiomycetes phylogeny – part 1

Consensus phylogram (50 % majority rule) of 146 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (85 sequences including outgroup; 847 aligned positions; 357 unique site patterns; 101 000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Diaporthe perjuncta (GenBank NG_059064.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Eurotiomycetes phylogeny – part 2
Overview Leotiomycetes phylogeny

Consensus phylogram (50 % majority rule) of 408002 trees resulting from a Bayesian analysis of the LSU sequence alignment (90 sequences including outgroup; 826 aligned positions; 283 unique site patterns; 2720000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Xylaria hypoxylon (GenBank AY544648.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The most basal branch was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
**Overview Mucoromycetes phylogeny**

Consensus phylogram (50 % majority rule) of 141,002 trees resulting from a Bayesian analysis of the LSU sequence alignment (22 sequences including outgroup; 660 aligned positions; 319 unique site patterns; 470,000 generations with trees sampled every five generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher taxonomic classification is indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Chytridium lagenaria* (GenBank FJ804156.1) and the taxonomic novelty described in this study for which LSU sequence data were available is indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Pezizomycetes phylogeny

Consensus phylogram (50% majority rule) of 87,002 trees resulting from a Bayesian analysis of the LSU sequence alignment (33 sequences including outgroup; 792 aligned positions; 203 unique site patterns; 290,000 generations with trees sampled every five generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The family and order are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Candida broadrunensis (GenBank KY106372.1) and the taxonomic novelty described in this study for which LSU sequence data were available is indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Phytophthora phylogeny

Consensus phylogram (50 % majority rule) of 64,502 trees resulting from a Bayesian analysis of the LSU sequence alignment (25 sequences including outgroup; 1,110 aligned positions; 68 unique site patterns; 215,000 generations with trees sampled every five generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher taxonomic classification is indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Absidia panacisoli (GenBank NG_063948.1) and the taxonomic novelty described in this study for which LSU sequence data were available is indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Saccharomycetes and Tremellomycetes phylogeny

Consensus phylogram (50 % majority rule) of 136502 trees resulting from a Bayesian analysis of the LSU sequence alignment (36 sequences including outgroup; 432 unique site patterns; 910000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The families, orders and classes are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Backusella lamprospora (GenBank MH866118.1) and the taxonomic novelities described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Sordariomycetes (Falcocladiales, Glomerellales and Hypocreales) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 846978 trees resulting from a Bayesian analysis of the LSU sequence alignment (194 sequences including outgroup; 816 aligned positions; 310 unique site patterns; 56465000 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Ramularia endophylla (GenBank AY490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Sordariomycetes (Falcocladiales, Glomerellales and Hypocreales) phylogeny (cont.) – part 2
Overview Sordariomycetes (Falcocladiales, Glomerellales and Hypocreales) phylogeny (cont.) – part 3
Overview Sordariomycetes (Other orders) phylogeny

Consensus phylogram (50 % majority rule) of 229,502 trees resulting from a Bayesian analysis of the LSU sequence alignment (79 sequences including outgroup; 81 aligned positions; 293 unique site patterns; 153,000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with colored blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Ramularia endophylla (GenBank AV490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Overview Sordariomycetes (Xylariales) phylogeny

Consensus phylogram (50 % majority rule) of 335 trees resulting from a Bayesian analysis of the LSU sequence alignment (63 sequences including outgroup; 800 aligned positions; 192 unique site patterns; 790000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and the order are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Ramularia endophyta (GenBank AV490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The most basal branch was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).
Curvularia tanzanica
Curvularia tanzanica Y.P. Tan, Dhileepan, Ntandu, Kurose & R.G. Shivas, sp. nov.

Etymology. Name refers to Tanzania, the country from which it was collected.

Classification — Pleosporaceae, Pleosporales, Dothideomycetes.

Hyphae pale brown, smooth or verruculose, branched and septate, up to 3–6 µm wide. Conidiophores erect, straight to flexuous, geniculate towards apex, brown, smooth, septate, 50–110 × 3–4 µm, lateral or terminal, unbranched or sparingly branched. Conidiogenous cells intercalary and terminal, brown, smooth to minutely verruculose, polytretic with darkened scars. Conidia cylindrical to narrowly ellipsoidal, straight, rounded.

Notes — Curvularia tanzanica is only known from collections on Cyperus aromaticus (syn: Kyllinga polyphyllya) (Cyperaceae) in Tanzania. Curvularia tanzanica was discovered while searching for plant pathogens on C. aromaticus in its native range in equatorial Africa. The aim of the surveys was to find plant pathogens that may have potential for the biological control of C. aromaticus in northern Queensland, Australia, where the sedge has become an invasive weed in pastures and sugar cane crops. Curvularia tanzanica colonised the floral parts of C. aromaticus that superficially resembled the darkened crustose inflorescences of Sporobolus spp. (Poaceae) covered (and sometimes destroyed) by certain species of Curvularia spp. (Luttrel 1976, Alcorn 1982, Tan et al. 2018).

The multilocus phylogenetic analysis of the ITS and gapdh loci placed C. tanzanica sister to C. gladioli strain CBS 210.79. Based on a blastn search, C. tanzanica differs from C. gladioli in ITS (GenBank LT631345; Identities 558/565 (99%), no gaps) and gapdh (GenBank LT715802; Identities 531/540 (98%), no gaps). Morphologically, C. tanzanica has straight conidia, which differentiates it from C. gladioli (illustrated in Parmelee (1956) as C. trifolii f. sp. gladioli) with curved conidia (the third cell from the base is swollen and convex on one side).

Typos. Tanzania, Korogwe, Msambiasi, S05°07'57" E038°23'10", from inflorescence of Cyperus aromaticus (Cyperaceae), 22 Dec. 2019, J.E. Ntandu, K. Dhileepan, M.D.E. Shivas & R.G. Shivas (holotype BRIP 71771, culture ex-type IMI 507176, ITS, LSU and gapdh sequences GenBank MW396857, MW396841 and MW388669).

Additional material examined. Tanzania, Korogwe, Msambiasi, S05°07'57" E038°23'10", from inflorescence of Cyperus aromaticus (Cyperaceae), 22 Dec. 2019, J.E. Ntandu, K. Dhileepan, M.D.E. Shivas & R.G. Shivas, BRIP 71104, ITS, LSU and gapdh sequences GenBank MW396856, MW396840 and MW388668.

Colour illustrations. Kunjithapatham Dhileepan in sedgeland, eastern Tanzania. Inflorescence of Cyperus aromaticus colonised by Curvularia tanzanica; conidiophores; conidia. Scale bars = 1 mm (inflorescence), 10 µm (others).
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