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RESEARCH ARTICLE

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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**, *Comoclathris antarctica* from soil. **Australia**, *Coniochaeta salicifolia* as endophyte from healthy leaves of *Geijera salicifolia*, *Eremothecium peggii* in fruit of *Citrus australis*, *Microdochium ratticaudae* from stem of *Sporobolus natalensis*, *Neocelosporium corymbiae* on stems of *Corymbia variegata*, *Phytophthora kelmanii* from rhizosphere soil of *Ptilotus pyramidatus*, *Pseudosydowia backhousiae* on living leaves of *Backhousia citriodora*, *Pseudosydowia indooroopillyensis*, *Pseudosydowia louisecottisiae* and *Pseudosydowia queenslandica* on living leaves of *Eucalyptus* sp. **Brazil**, *Absidia montepascoalis* from soil. **Chile**, *Ilyonectria zarorii* from soil under *Maytenus boaria.* **Costa Rica**, *Colletotrichum filicis* from an unidentified fern. **Croatia**, *Mollisia endogranulata* on deteriorated hardwood. **Czech Republic**, *Arcopilus navicularis* from tea bag with fruit tea, *Neosetophoma buxi* as endophyte from *Buxus sempervirens*, *Xerochrysium bohemicum* on surface of biscuits with chocolate glaze and filled with jam. **France**, *Entoloma cyaneobasale* on basic to calcareous soil, *Fusarium aconidiale* from *Triticum aestivum*, *Fusarium juglandicola* from buds of *Juglans regia*. **Germany**, *Tetraploa endophytica* as endophyte from *Microthlaspi perfoliatum* roots. **India**, *Castanediella ambae* on leaves of *Mangifera indica*, *Lactifluus kanadii* on soil under *Castanopsis* sp., *Penicillium uttarakhandense* from soil. **Italy**, *Penicillium ferraniaense* from compost. **Namibia**, *Bezerromyces gobabebensis* on leaves of unidentified succulent, *Cladosporium stipagrostidicola* on leaves of *Stipagrostis* sp., *Cymostachys euphorbiae* on leaves of *Euphorbia* sp., *Deniquelata hypolithi* from hypolith under a rock, *Hysterobrevium walvisbayicola* on leaves of unidentified tree, *Knufia hypolithi* and *Knufia walvisbayicola* from hypolith under a rock, *Lapidomyces stipagrostidicola* on leaves of *Stipagrostis* sp., *Nothophaeotheca mirabibensis* (incl. *Nothophaeotheca* gen. nov.) on persistent inflorescence remains of *Blepharis obmitrata*, *Paramyrothecium salvadorae* on twigs of *Salvadora persica*, *Preussia procaviicola* on dung of *Procavia* sp., *Sordaria equicola* on zebra dung, *Volutella salvadorae* on stems of *Salvadora persica*. **Netherlands**, *Entoloma ammophilum* on sandy soil, *Entoloma pseudocruentatum* on nutrient poor (acid) soil, *Entoloma pudens* on plant debris, amongst grasses. **New Zealand**, *Amorocoelophoma neoregeliae* from leaf spots of *Neoregelia* sp., *Aquilomyces metrosideri* and *Septoriella callistemonis* from stem discolouration and leaf spots of *Metrosideros* sp., *Cadophora neoregeliae* from leaf spots of *Neoregelia* sp., *Flexuomyces asteliae* (incl. *Flexuomyces* gen. nov.) and *Mollisia asteliae* from leaf spots of *Astelia chathamica*, *Ophioceras freycinetiae* from leaf spots of *Freycinetia*

Abstract (cont.)

banksii, *Phaeosphaeria caricis-sectae* from leaf spots of *Carex secta*. **Norway**, *Cuphophyllus flavipesoides* on soil in semi-natural grassland, *Entoloma coracis* on soil in calcareous *Pinus* and *Tilia* forests, *Entoloma cyaneolilacinum* on soil semi-natural grasslands, *Inocybe norvegica* on gravelly soil. **Pakistan**, *Butyriboletus parachinarensis* on soil in association with *Quercus baloot*. **Poland**, *Hyalodendriella bialowiezensis* on debris beneath fallen bark of Norway spruce *Picea abies*. **Russia**, *Bolbitius sibiricus* on a moss covered rotting trunk of *Populus tremula*, *Crepidotus wasseri* on debris of *Populus tremula*, *Entoloma isborscanum* on soil on calcareous grasslands, *Entoloma subcoracis* on soil in subalpine grasslands, *Hydropus lecythiocystis* on rotted wood of *Betula pendula*, *Meruliopsis faginea* on fallen dead branches of *Fagus orientalis*, *Metschnikowia taurica* from fruits of *Ziziphus jujube*, *Suillus 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*, *Castanediella senegaliae* on dead pods of *Senegalia ataxacantha*, *Cladophialophora behniae* on leaves of *Behnia* sp., *Colletotrichum cliviigenum* on leaves of *Clivia* sp., *Diatrype dalbergiae* on bark of *Dalbergia armata*, *Falcocladium heteropyxidicola* on leaves of *Heteropyxis canescens*, *Lapidomyces aloidendricola* as epiphyte on brown stem of *Aloidendron dichotomum*, *Lasionectria sansevieriae* and *Phaeosphaeriopsis sansevieriae* on leaves of *Sansevieria 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*, *Paracymostachys euphorbiae* (incl. *Paracymostachys* gen. nov.) on leaf litter of *Euphorbia ingens*, *Paramycosphaerella pterocarpi* on leaves of *Pterocarpus angolensis*, *Paramycosphaerella syzygii* on leaf litter of *Syzygium chordatum*, *Parateichospora phoenicicola* (incl. *Parateichospora* gen. nov.) on leaves of *Phoenix reclinata*, *Seiridium syzygii* on twigs of *Syzygium chordatum*, *Setophoma syzygii* on leaves of *Syzygium* sp., *Starmerella xylocopis* from larval feed of an Afrotropical bee *Xylocopa caffra*, *Teratosphaeria combreti* on leaf litter of *Combretum kraussii*, *Teratosphaericola leucadendri* on leaves of *Leucadendron* sp., *Toxicocladosporium pterocarpi* on pods of *Pterocarpus angolensis*. **Spain**, *Cortinarius bonachei* with *Quercus ilex* in calcareus soils, *Cortinarius brunneovolvatus* under *Quercus ilex* subsp. *ballota* in calcareous soil, *Extremopsis radicicola* (incl. *Extremopsis* gen. nov.) from root-associated soil in a wet heathland, *Russula quintanensis* on acidic soils, *Tubaria vulcanica* on volcanic lapilii material, *Tuber zambonelliae* in calcareus soil. **Sweden**, *Elaphomyces borealis* on soil under *Pinus sylvestris* and *Betula pubescens*. **Tanzania**, *Curvularia tanzanica* on inflorescence of *Cyperus aromaticus*. **Thailand**, *Simplicillium niveum* on *Ophiocordyceps camponoti-leonardi* on underside of unidentified dicotyledonous leaf. **USA**, *Calonectria californiensis* on leaves of *Umbellularia californica*, *Exophiala spartinae* from surface sterilised roots of *Spartina alterniflora*, *Neophaeococcomyces oklahomaensis* from outside wall of alcohol distillery. **Vietnam**, *Fistulinella aurantioflava* on soil. Morphological and culture characteristics are supported by DNA barcodes.

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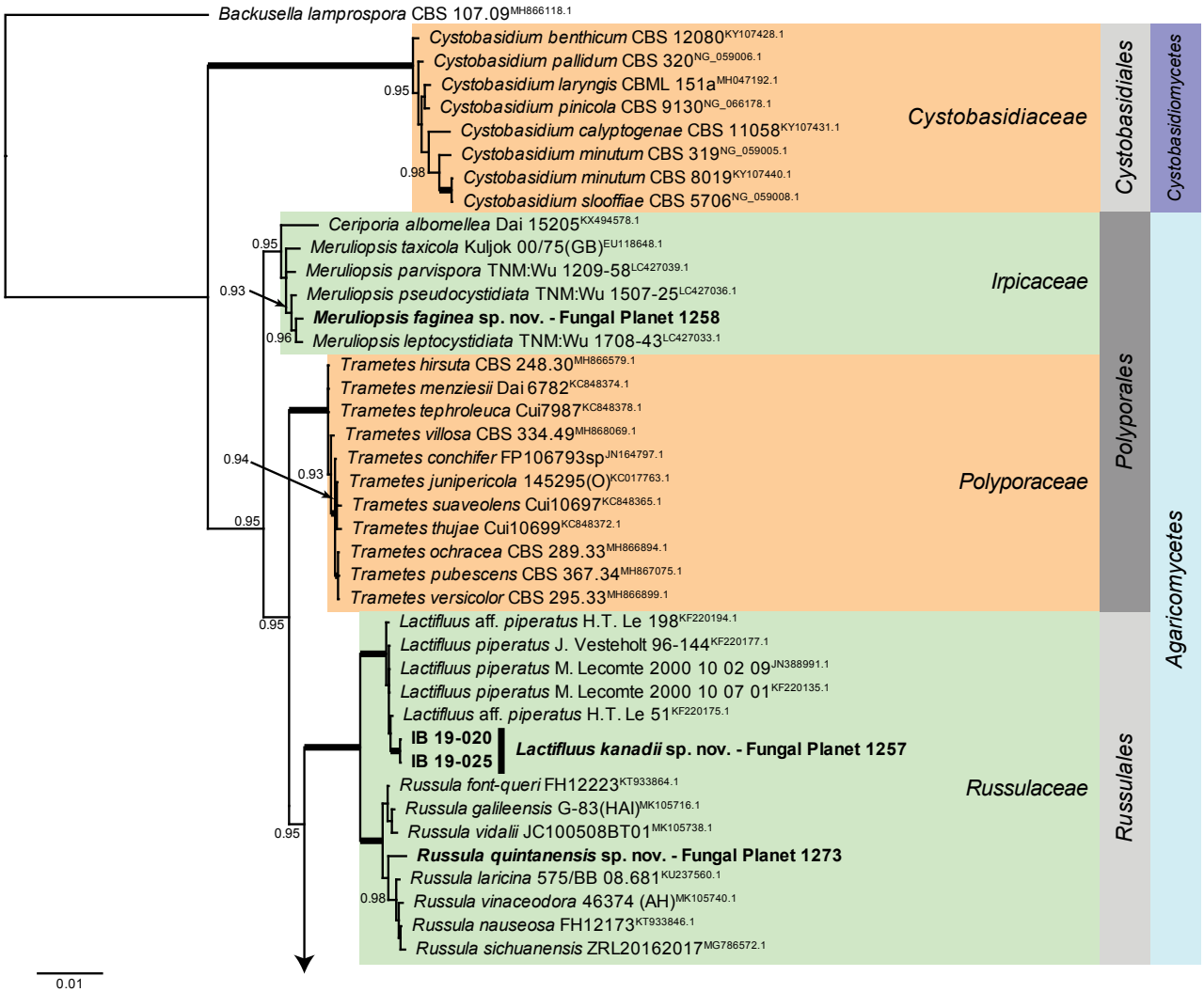
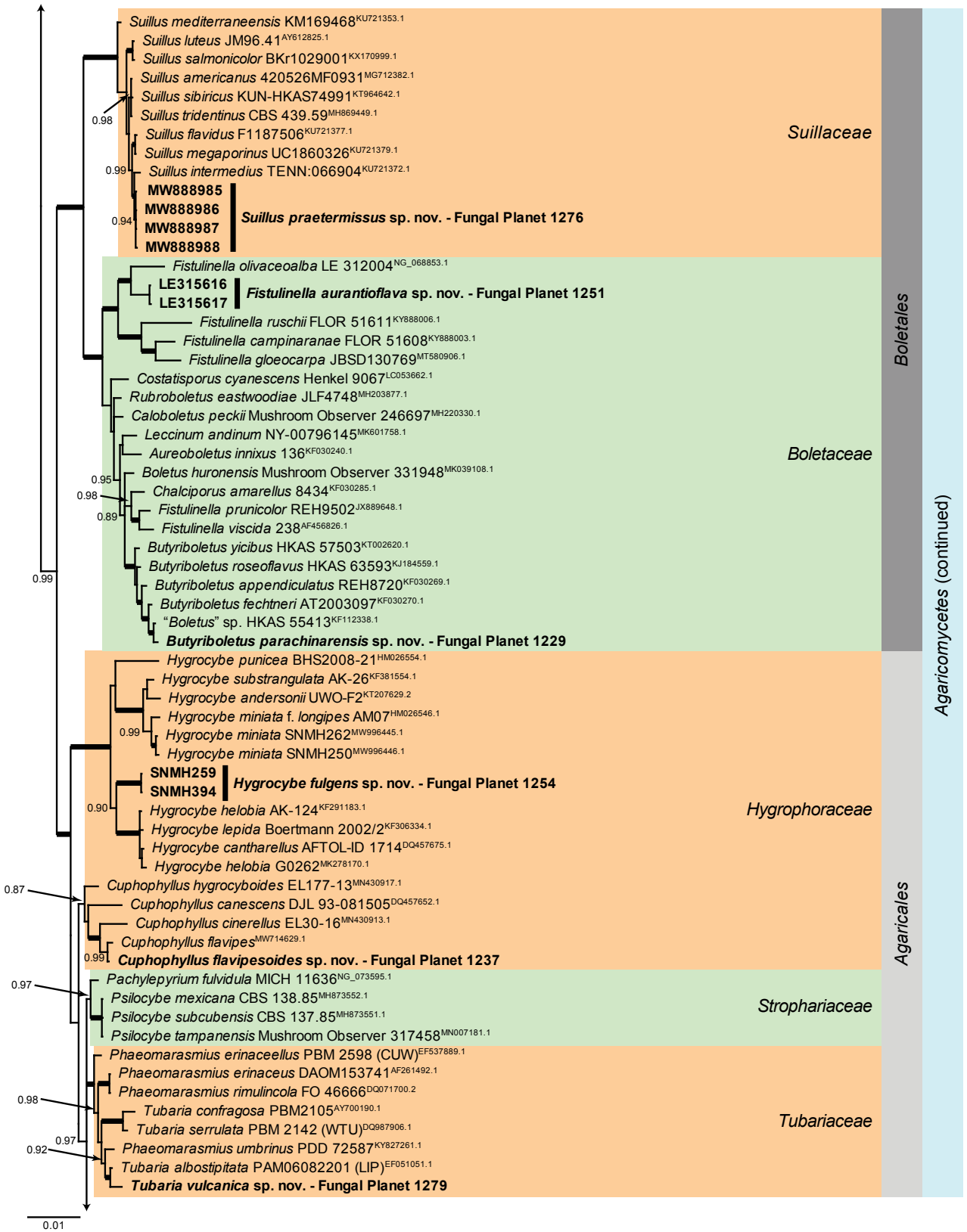
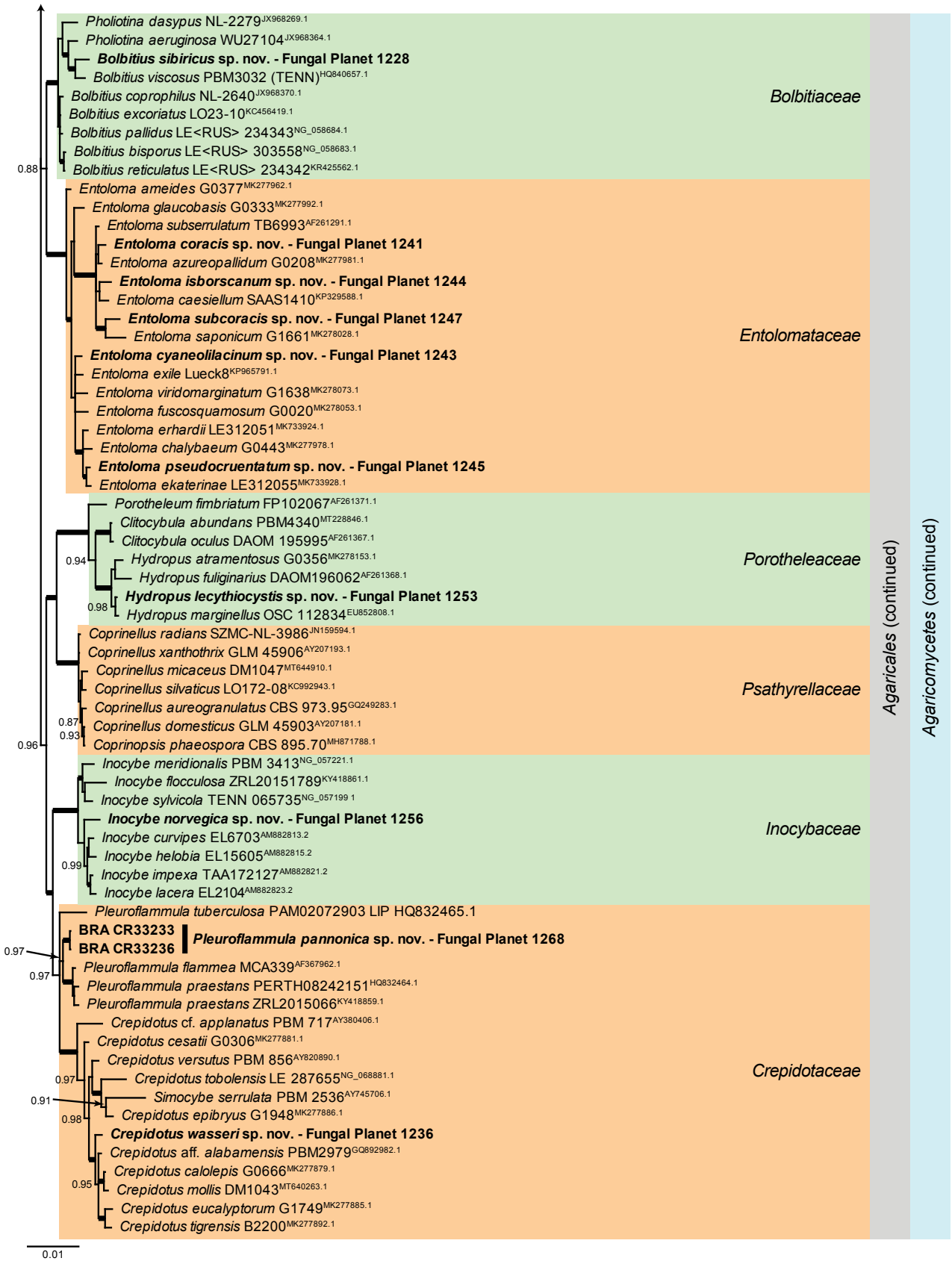


Overview *Agaricomycetes* phylogeny – part 1

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 lamprospora* (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).



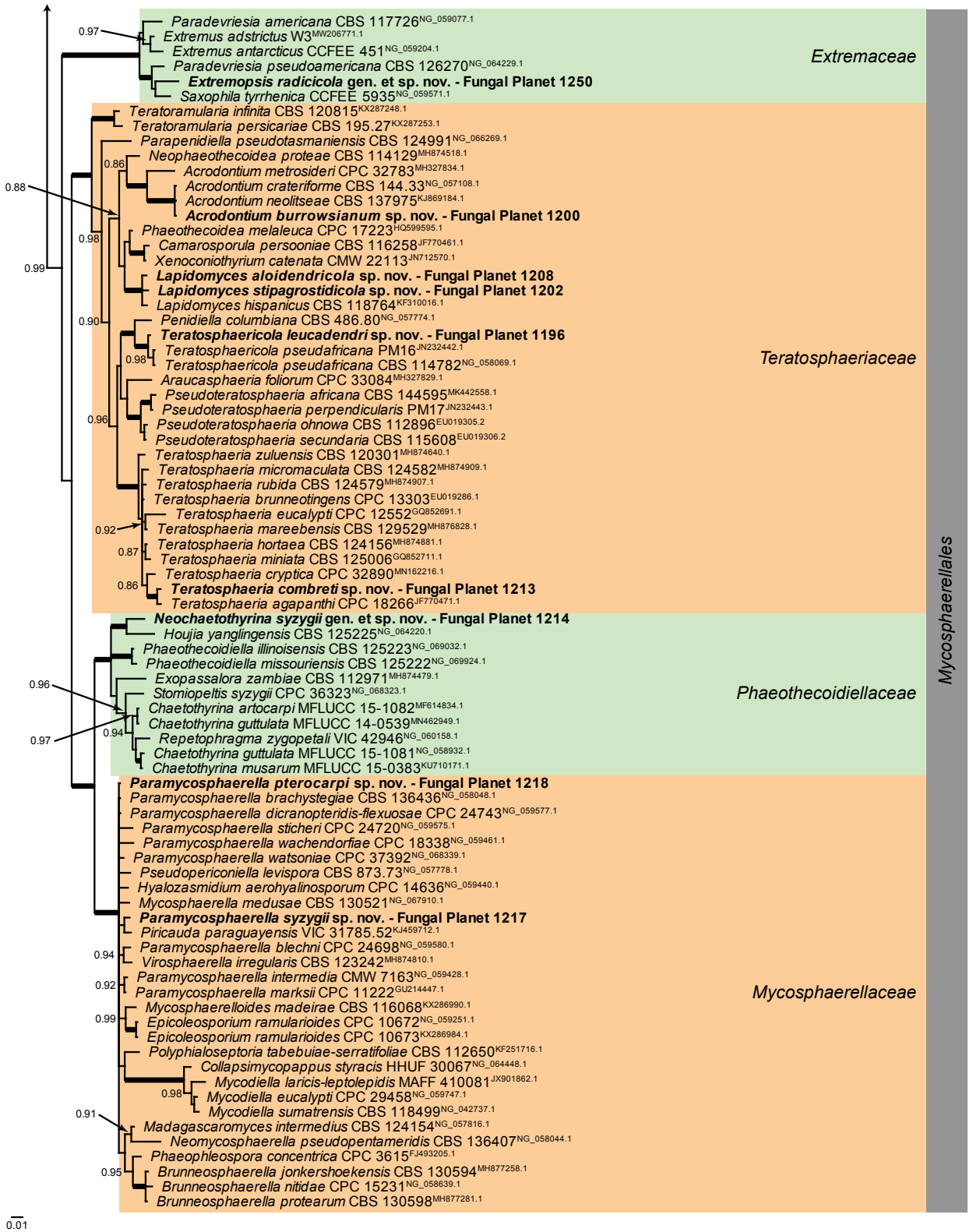
Overview *Agaricomycetes* phylogeny (cont.) – part 2



Overview *Agaricomycetes* phylogeny (cont.) – part 3

Overview *Dothideomycetes* (Other orders) phylogeny – part 1

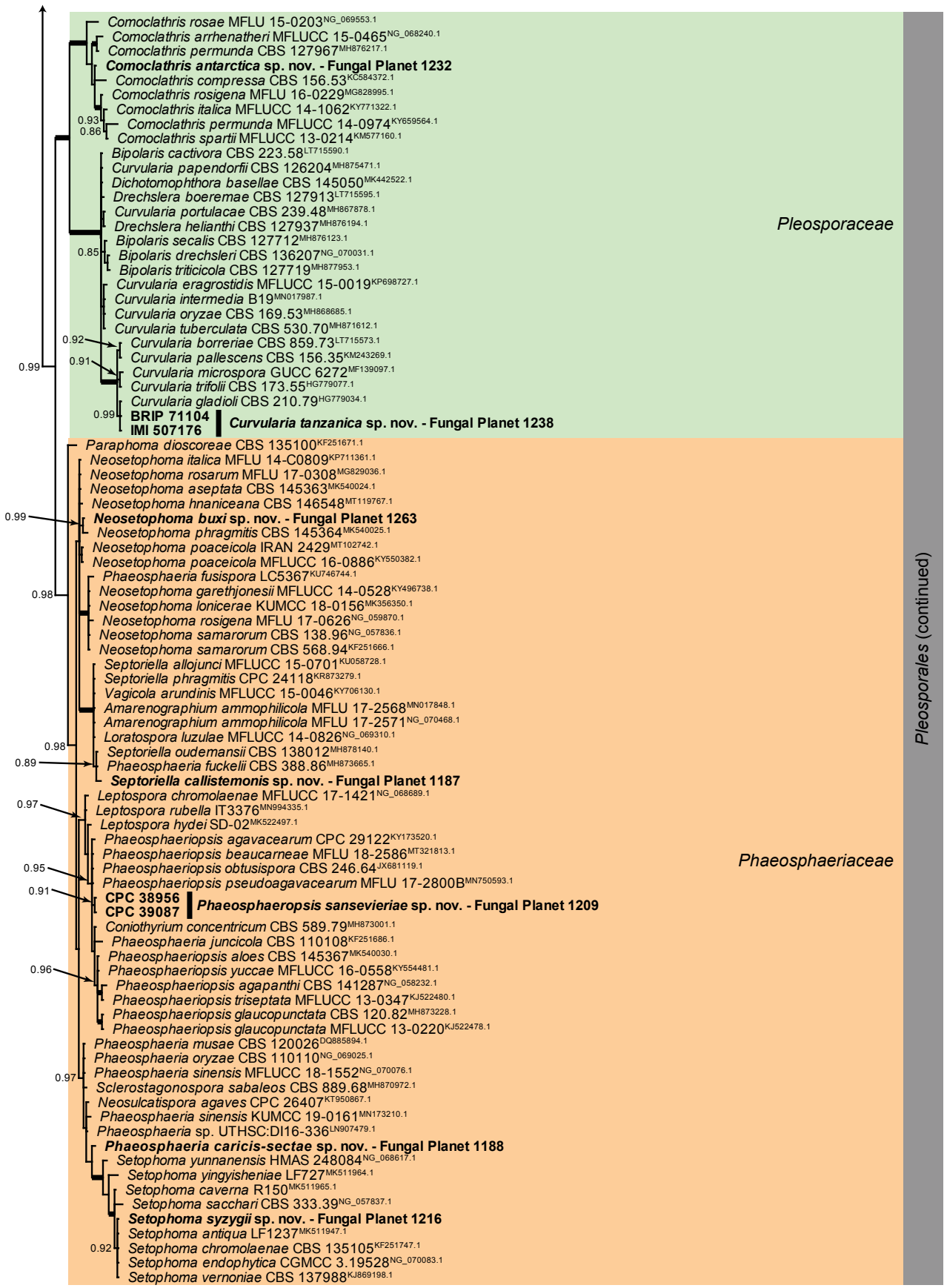
Consensus phylogram (50 % majority rule) of 56 102 trees resulting from a Bayesian analysis of the LSU sequence alignment (179 sequences including outgroup; 832 aligned positions; 378 unique site patterns; 3 740 000 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist 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 *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 most basal branched was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).



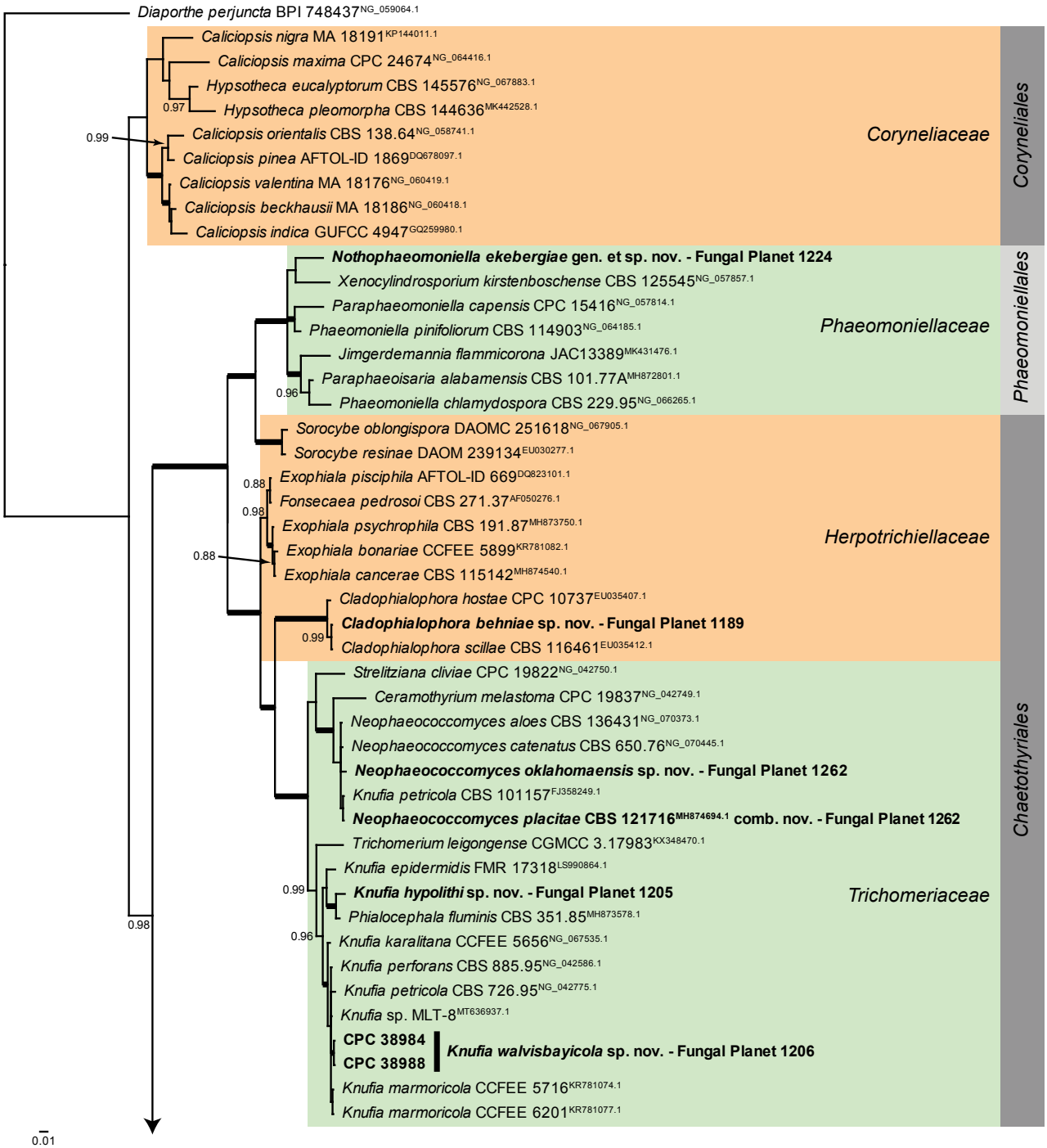
Overview *Dothideomycetes* (Other orders) phylogeny – part 2

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; 6 075 000 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 *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).

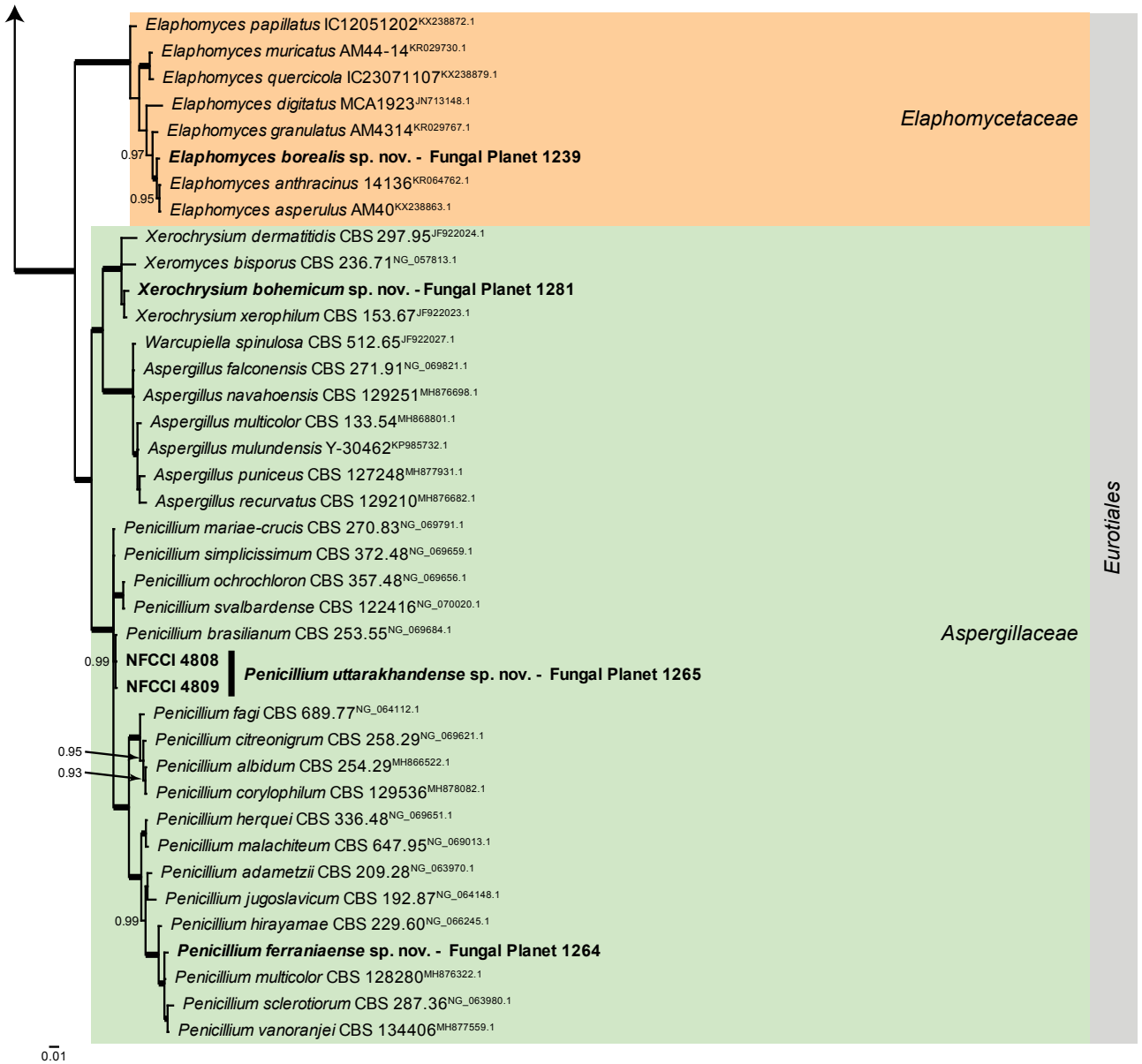


Overview *Dothideomycetes* (*Pleosporales*) phylogeny – part 2

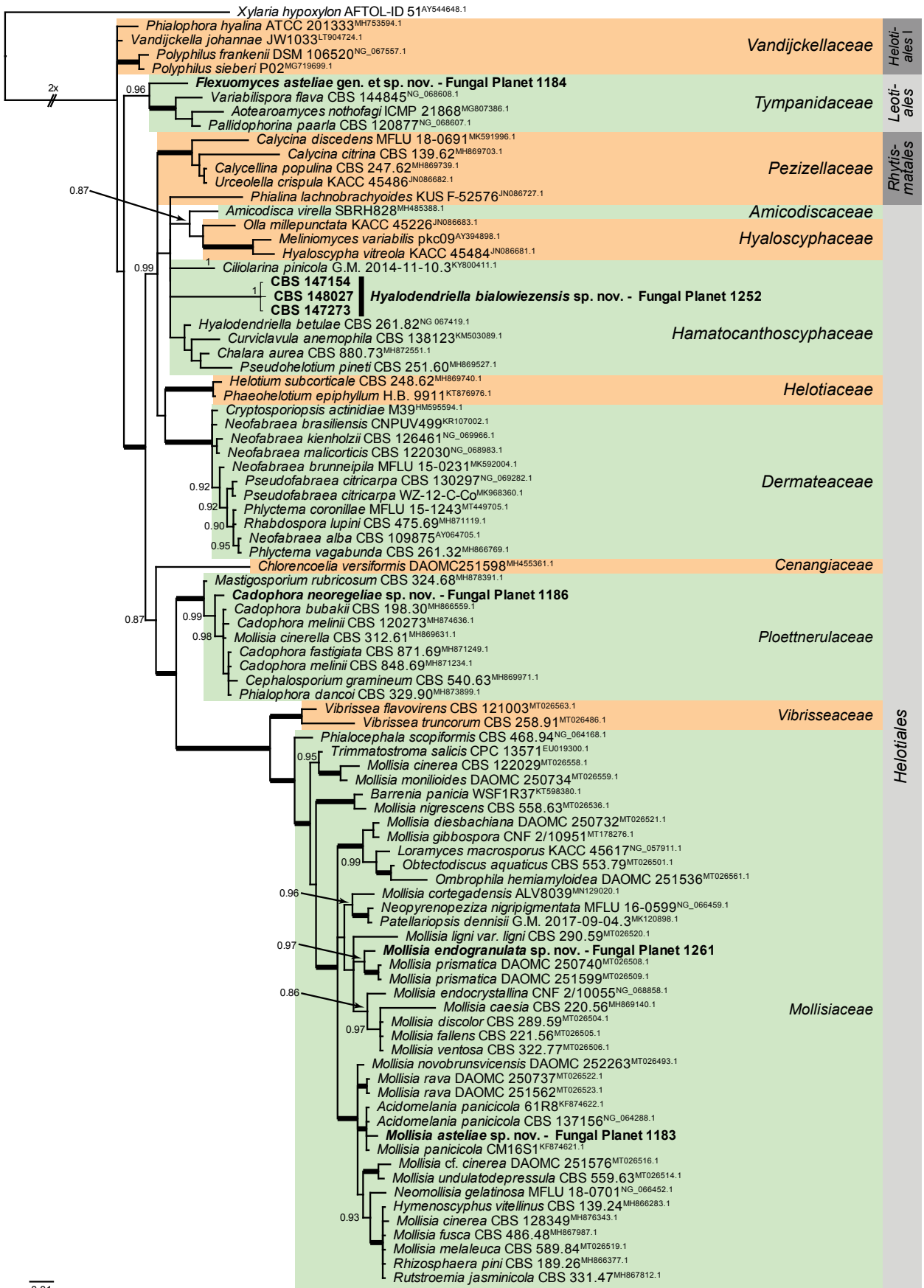


Overview *Eurotiomycetes* phylogeny – part 1

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; 1 010 000 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

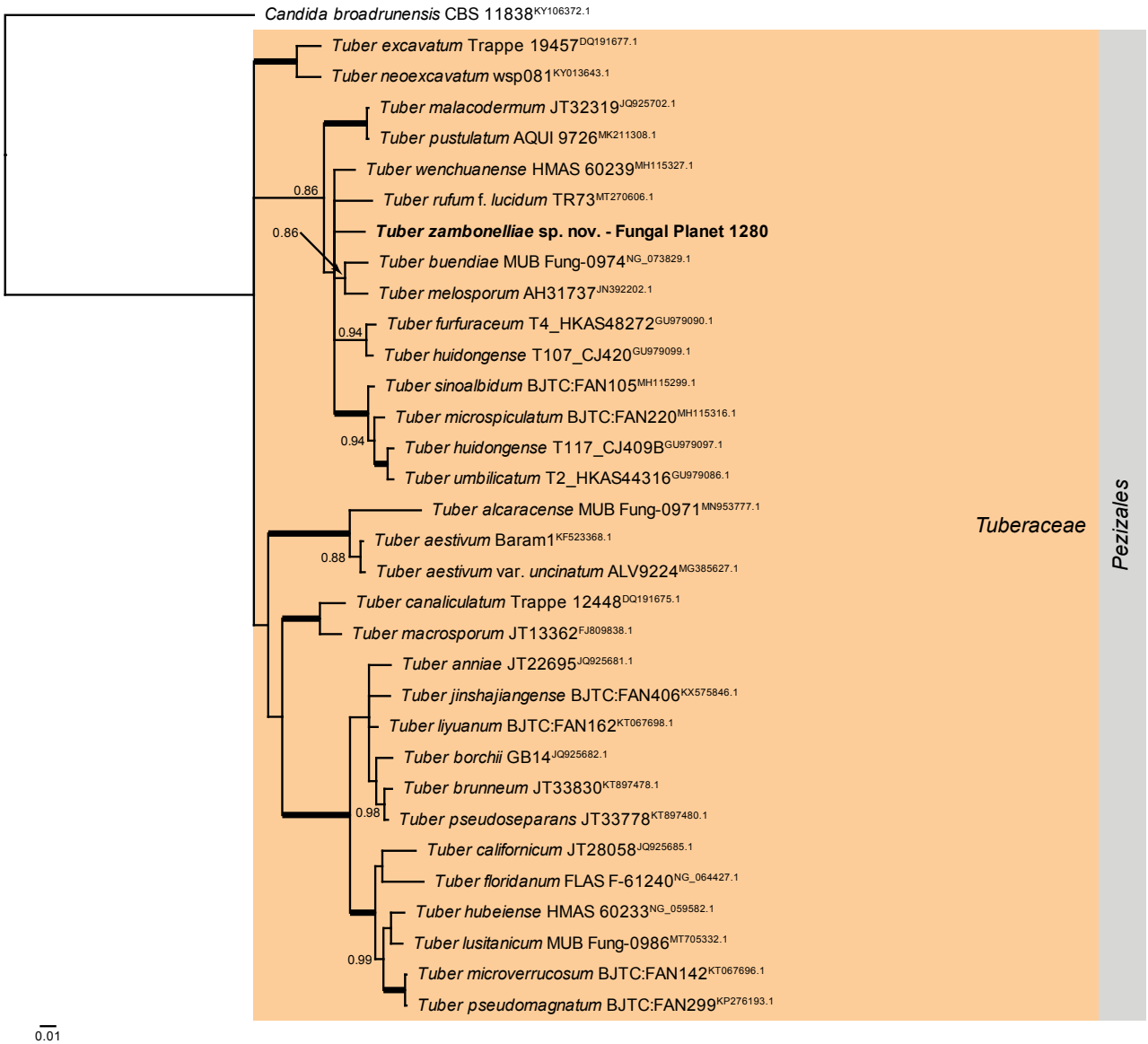


Overview *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 408 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (90 sequences including outgroup; 826 aligned positions; 283 unique site patterns; 2 720 000 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) 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 branched was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

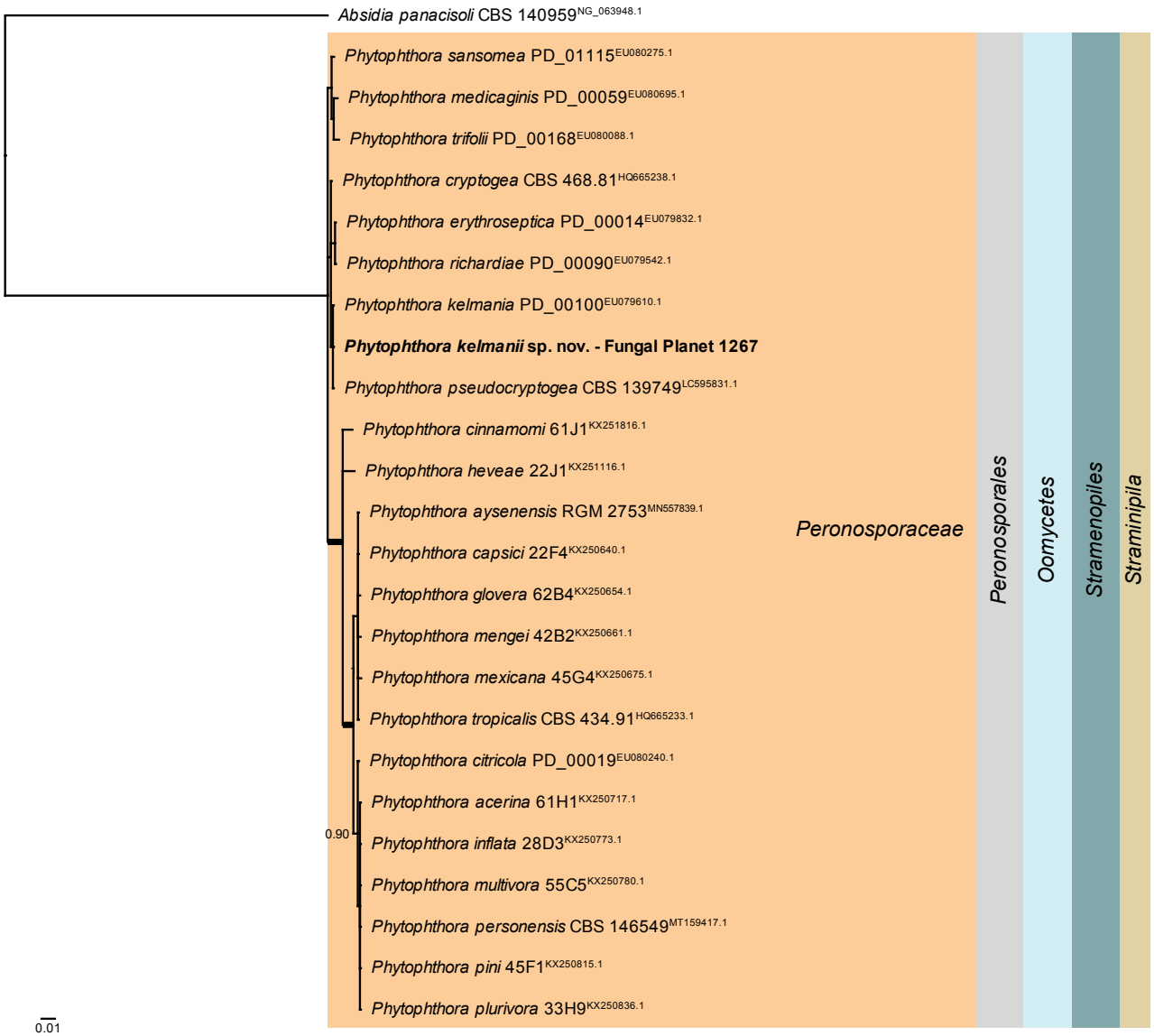
Overview *Mucoromycetes* phylogeny

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).



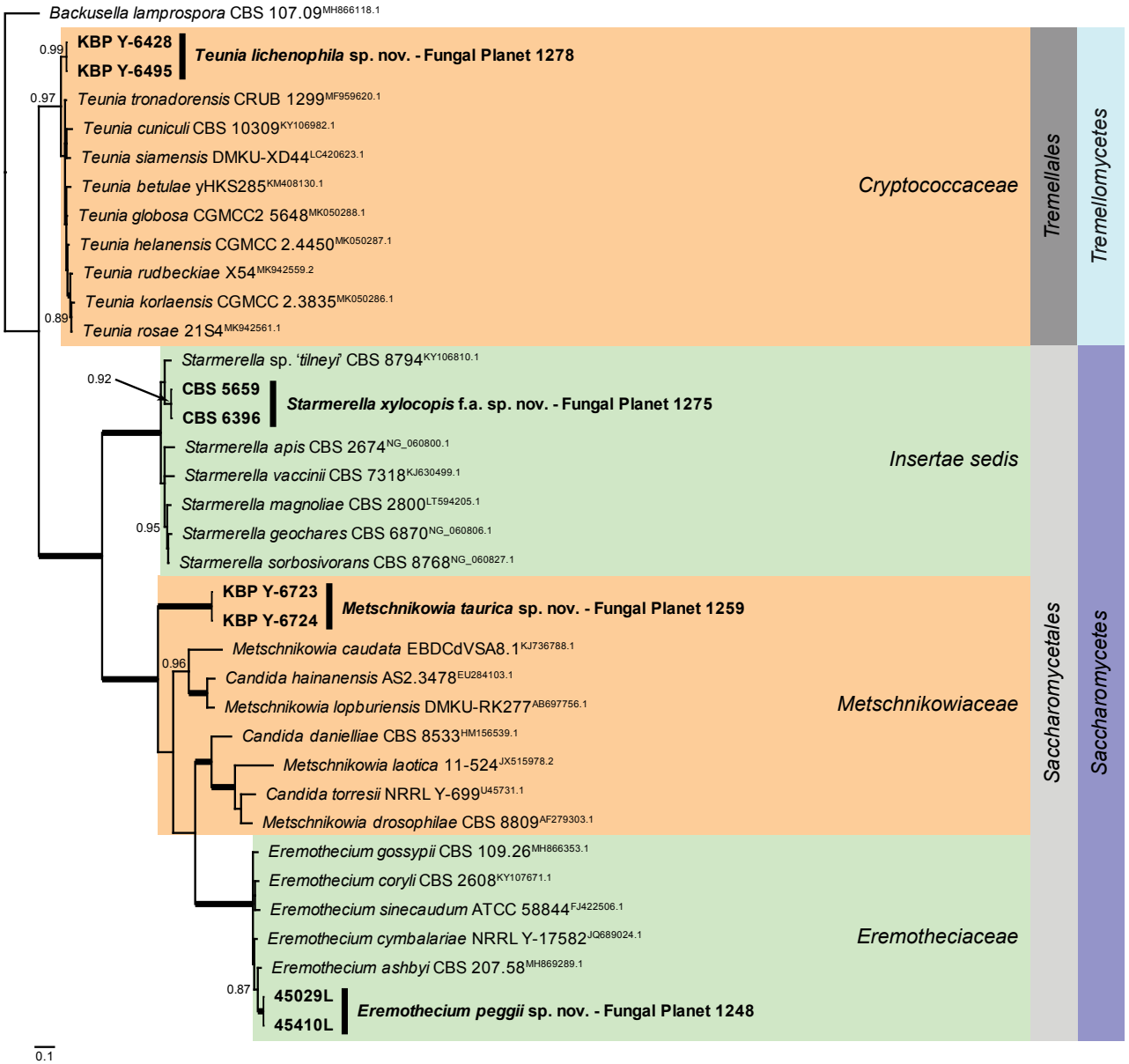
Overview *Pezizomycetes* phylogeny

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).

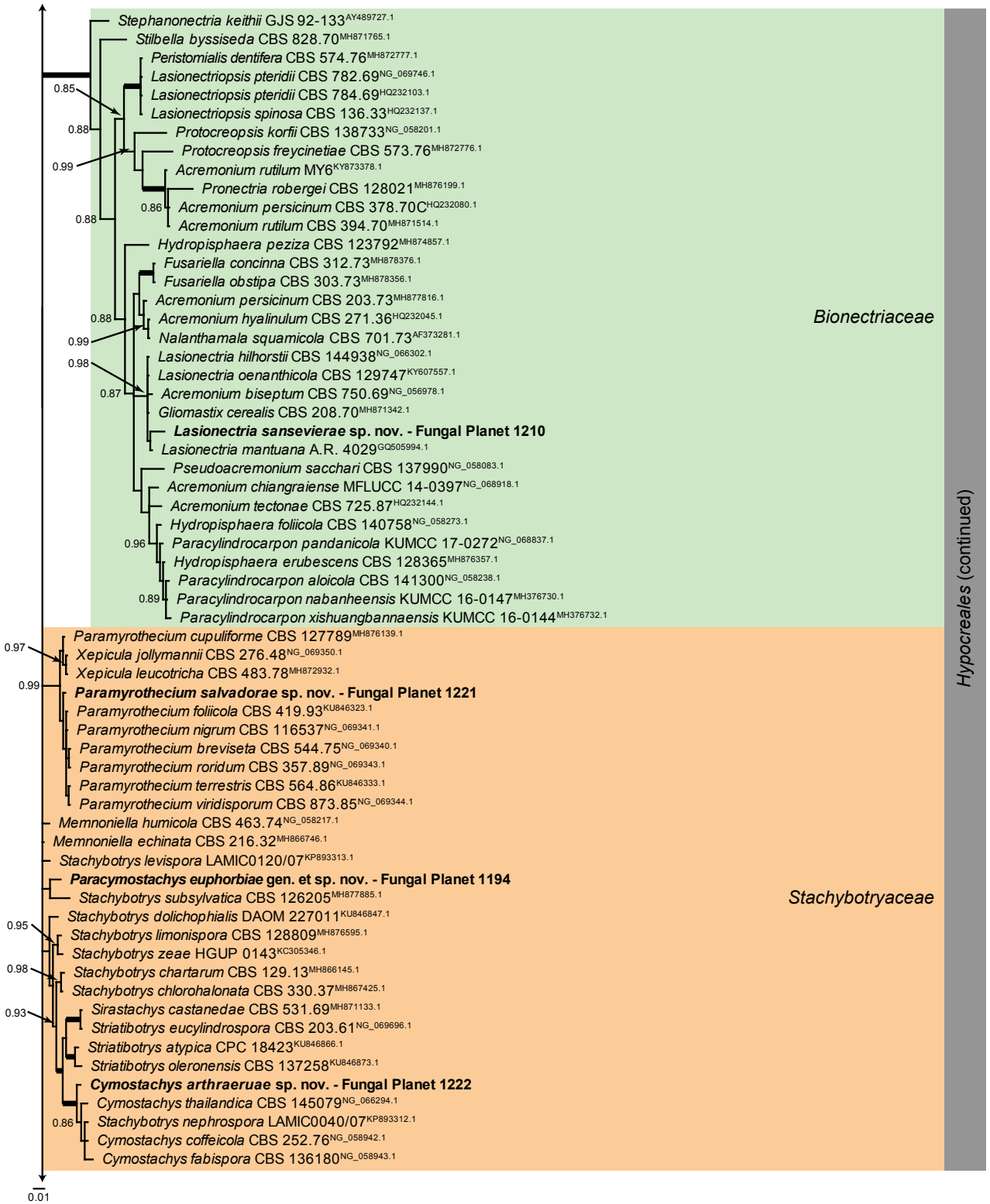


Overview *Saccharomycetes* and *Tremellomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 136 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (36 sequences including outgroup; 667 aligned positions; 432 unique site patterns; 910 000 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. 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 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).

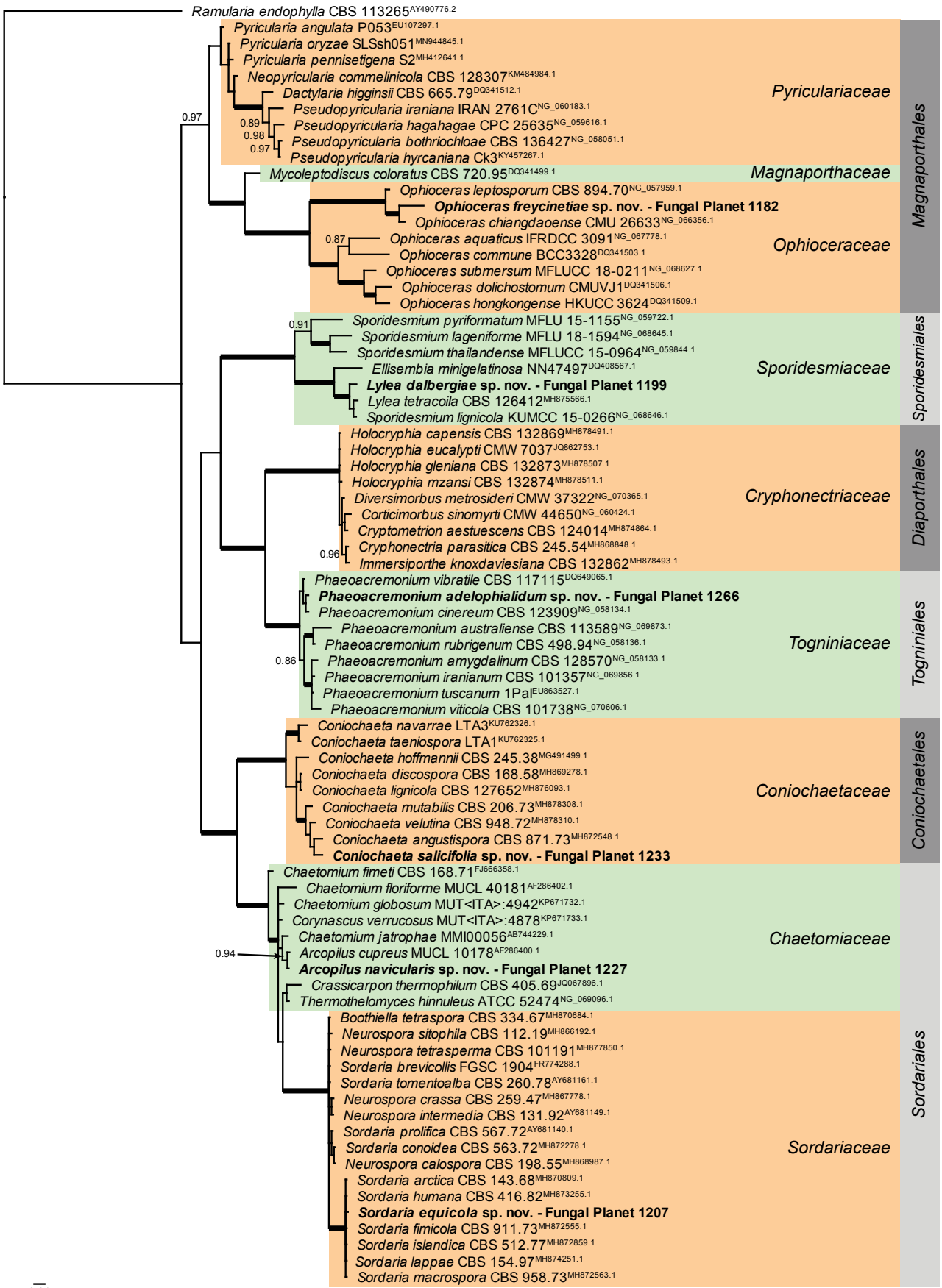
Overview *Sordariomycetes* (*Falcocladiales*, *Glomerellales* and *Hypocreales*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 846 978 trees resulting from a Bayesian analysis of the LSU sequence alignment (194 sequences including outgroup; 816 aligned positions; 310 unique site patterns; 56 465 000 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).



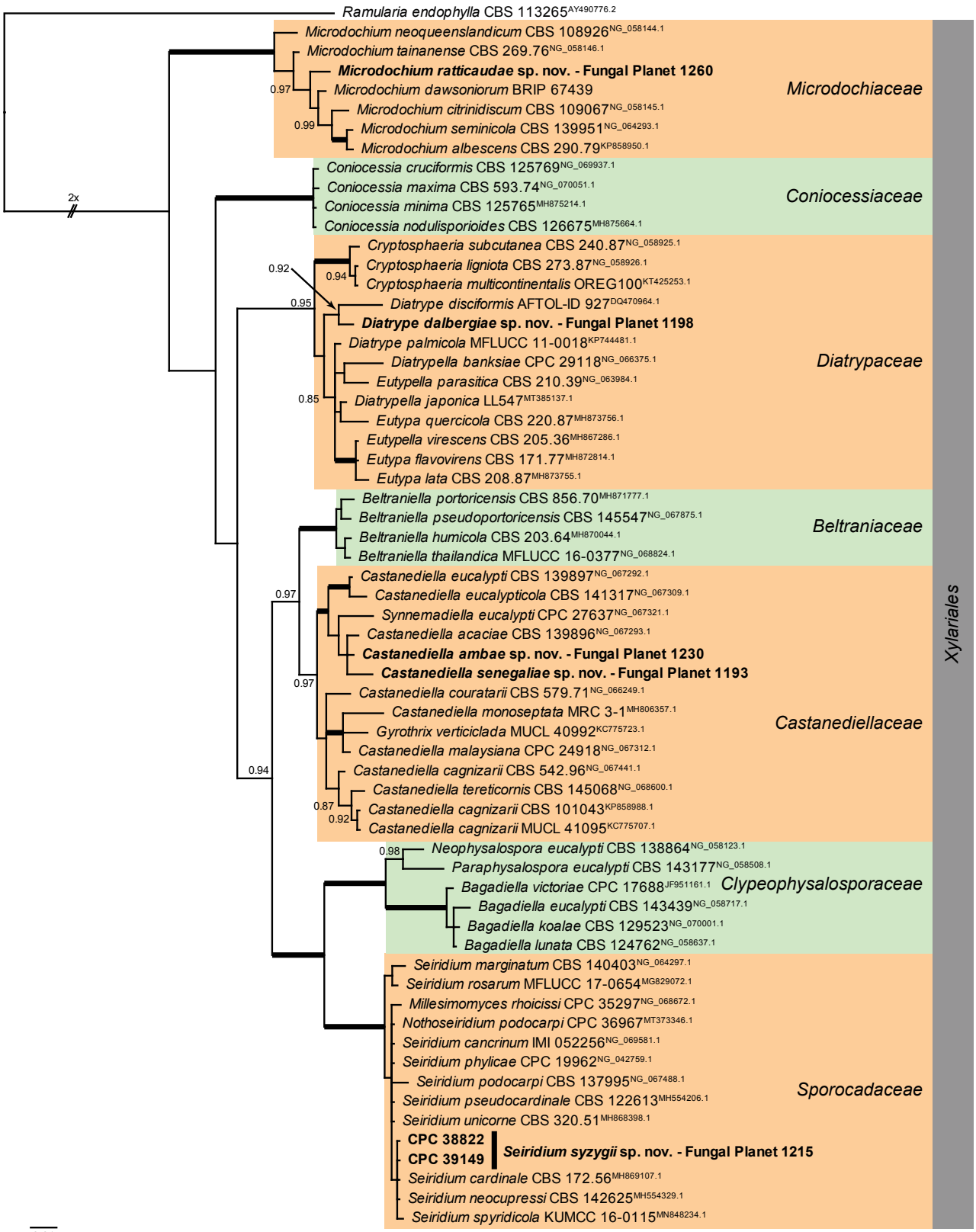
Overview *Sordariomycetes* (*Falcocladiales*, *Glomerellales* and *Hypocreales*) phylogeny (cont.) – part 2

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; 813 aligned positions; 293 unique site patterns; 1 530 000 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 *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* (*Xylariales*) phylogeny

Consensus phylogram (50 % majority rule) of 118 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (63 sequences including outgroup; 800 aligned positions; 192 unique site patterns; 790 000 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 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 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 most basal branched was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).


Curvularia tanzanica

Fungal Planet 1238 – 13 July 2021

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 at the apex, 21–32 × 8–12 µm, 3(–4)-distoseptate, brown to dark brown, end cells paler than others, third cell from base sometimes larger and darker than others; *hila* conspicuous, protuberant, thickened, darkened, 2–3 µm wide.

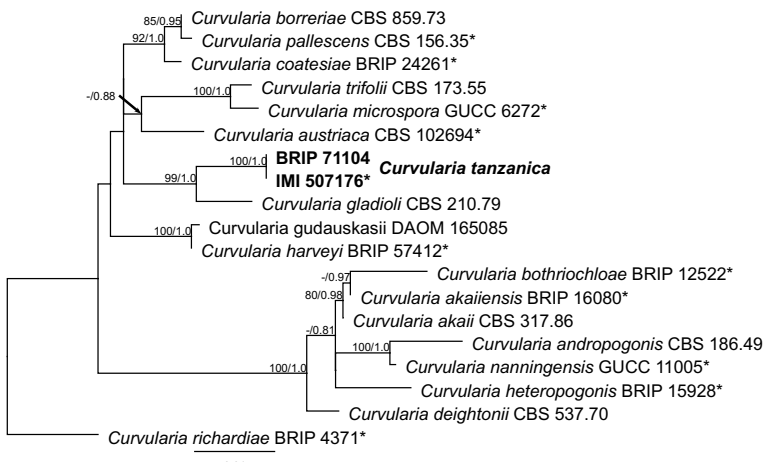
Culture characteristics — Colonies on potato dextrose agar approx. 4 cm diam after 7 d at 25 °C, surface with little aerial mycelium, dark brown to black.

Typus. Tanzania, Korogwe, Msambiasi, S05°07'57" E038°23'10", on 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, MycoBank MB 838305).

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.

Notes — *Curvularia tanzanica* is only known from collections on *Cyperus aromaticus* (syn: *Kyllinga polyphylla*) (*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. (Luttrell 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).



Phylogenetic tree of selected *Curvularia* species based on a maximum likelihood analysis of a combined multilocus alignment (ITS and *gapdh*). Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis 2014) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Curvularia richardiae* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

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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