



Fungal Planet description sheets: 785–867

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Key words

ITS nrDNA barcodes
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Abstract Novel species of fungi described in this study include those from various countries as follows: **Angola**, *Gnomoniopsis angolensis* and *Pseudopithomyces angolensis* on unknown host plants. **Australia**, *Dothiora corymbiae* on *Corymbia citriodora*, *Neoeucasphaeria eucalypti* (incl. *Neoeucasphaeria* gen. nov.) on *Eucalyptus* sp., *Fumagopsis stellae* on *Eucalyptus* sp., *Fusculina eucalyptorum* (incl. *Fusculinaceae* fam. nov.) on *Eucalyptus socialis*, *Harknessia corymbiicola* on *Corymbia maculata*, *Neocelosporium eucalypti* (incl. *Neocelosporium* gen. nov., *Neocelosporiaceae* fam. nov. and *Neocelosporiales* ord. nov.) on *Eucalyptus cyanophylla*, *Neophaeomoniella corymbiae* on *Corymbia citriodora*, *Neophaeomoniella eucalyptigena* on *Eucalyptus pilularis*, *Pseudoplagiostoma corymbiicola* on *Corymbia citriodora*, *Teratosphaeria gracilis* on *Eucalyptus gracilis*, *Zasmidium corymbiae* on *Corymbia citriodora*. **Brazil**, *Calonectria hemileiae* on pustules of *Hemileia vastatrix* formed on leaves of *Coffea arabica*, *Calvatia caatinguensis* on soil, *Cercospora solani-betacei* on *Solanum betaceum*, *Clathrus natalensis* on soil, *Diaporthe poincianellae* on *Poincianella pyramidalis*, *Geastrum piquiriunense* on soil, *Geosmithia carolliae* on wing of *Carollia perspicillata*, *Henningsia resupinata* on wood, *Penicillium guabinense* from soil, *Periconia caespitosa* from leaf litter, *Pseudocercospora styracina* on *Styrax* sp., *Simplicillium filiforme* as endophyte from *Citrullus lanatus*, *Thozetella pindobacuensis* on leaf litter, *Xenosonderhenia coussapoeae* on *Coussapoa floccosa*. **Canary Islands (Spain)**, *Orbilia amarilla* on *Euphorbia canariensis*. **Cape Verde Islands**, *Xylodon jacobaeus* on *Eucalyptus camaldulensis*. **Chile**, *Colletotrichum arboricola* on *Fuchsia magellanica*. **Costa Rica**, *Lasiosphaeria miniovina* on tree branch. **Ecuador**, *Ganoderma chochoense* on tree trunk. **France**, *Neofitzroyomyces nerii* (incl. *Neofitzroyomyces* gen. nov.) on *Nerium oleander*. **Ghana**, *Castanediella tereticornis* on *Eucalyptus tereticornis*, *Falcocladium africanum* on *Eucalyptus brassiana*, *Rachicladosporium corymbiae* on *Corymbia citriodora*. **Hungary**, *Entoloma silvae-frondosae* in *Carpinus betulus*-*Pinus sylvestris* mixed forest. **Iran**, *Pseudopyricularia persiana* on *Cyperus* sp. **Italy**, *Inocybe roseascens* on soil in mixed forest. **Laos**, *Ophiocordyceps houaynhangensis* on Coleoptera larva. **Malaysia**, *Monilochaetes melastomae* on *Melastoma* sp. **Mexico**, *Absidia terrestris* from soil. **Netherlands**, *Acaulium pannemaniae*, *Conioscypha boutwelliae*, *Fusicolla septimanifinifiscentiae*, *Gibellulopsis simonii*, *Lasionectria hilhorstii*, *Lectera nordwiniana*, *Leptodiscella rintelii*, *Parasarocladium debryunii* and *Sarocladium dejongiae* (incl. *Sarocladiaceae* fam. nov.) from soil. **New Zealand**, *Gnomoniopsis rosae* on *Rosa* sp. and *Neodevriesia metrosideri* on *Metrosideros* sp. **Puerto Rico**, *Neodevriesia coccolobae* on *Coccoloba uvifera*, *Neodevriesia tabebuiae* and *Alfaria tabebuiae* on *Tabebuia chrysantha*. **Russia**, *Amanita paludosa* on bogged soil in mixed deciduous forest, *Entoloma tiliae* in forest of *Tilia x europaea*, *Kwonionella endophytica* on *Pyrus communis*. **South Africa**, *Coniella diospyri* on *Diospyros mespiliformis*, *Neomelanconiella combreti* (incl. *Neomelanconiellaceae*

Abstract (cont.)

fam. nov. and *Neomelanconiella* gen. nov.) on *Combretum* sp., *Polyphialoseptoria natalensis* on unidentified plant host, *Pseudorobillarda bolusanthi* on *Bolusanthus speciosus*, *Thelonectria pelargonii* on *Pelargonium* sp. **Spain**, *Vermiculariopsiella lauracearum* and *Anungitopsis lauri* on *Laurus novocanariensis*, *Geosmithia xerotolerans* from a darkened wall of a house, *Pseudopenidiella gallaica* on leaf litter. **Thailand**, *Corynespora thailandica* on wood, *Lareunionomyces loeiensis* on leaf litter, *Neocochlearomyces chromolaenae* (incl. *Neocochlearomyces* gen. nov.) on *Chromolaena odorata*, *Neomyrmecridium septatum* (incl. *Neomyrmecridium* gen. nov.), *Pararamichloridium caricicola* on *Carex* sp., *Xenodactylaria thailandica* (incl. *Xenodactylariaceae* fam. nov. and *Xenodactylaria* gen. nov.), *Neomyrmecridium asiaticum* and *Cymostachys thailandica* from unidentified vine. **USA**, *Carolinigaster bonitoi* (incl. *Carolinigaster* gen. nov.) from soil, *Penicillium fortuitum* from house dust, *Phaeotheca shathenatiana* (incl. *Phaeothecaceae* fam. nov.) from twig and cone litter, *Pythium wohlseniorum* from stream water, *Superstratomyces tardicrescens* from human eye, *Talaromyces iowaense* from office air. **Vietnam**, *Fistulinella olivaceoalba* on soil. Morphological and culture characteristics along with DNA barcodes are provided.

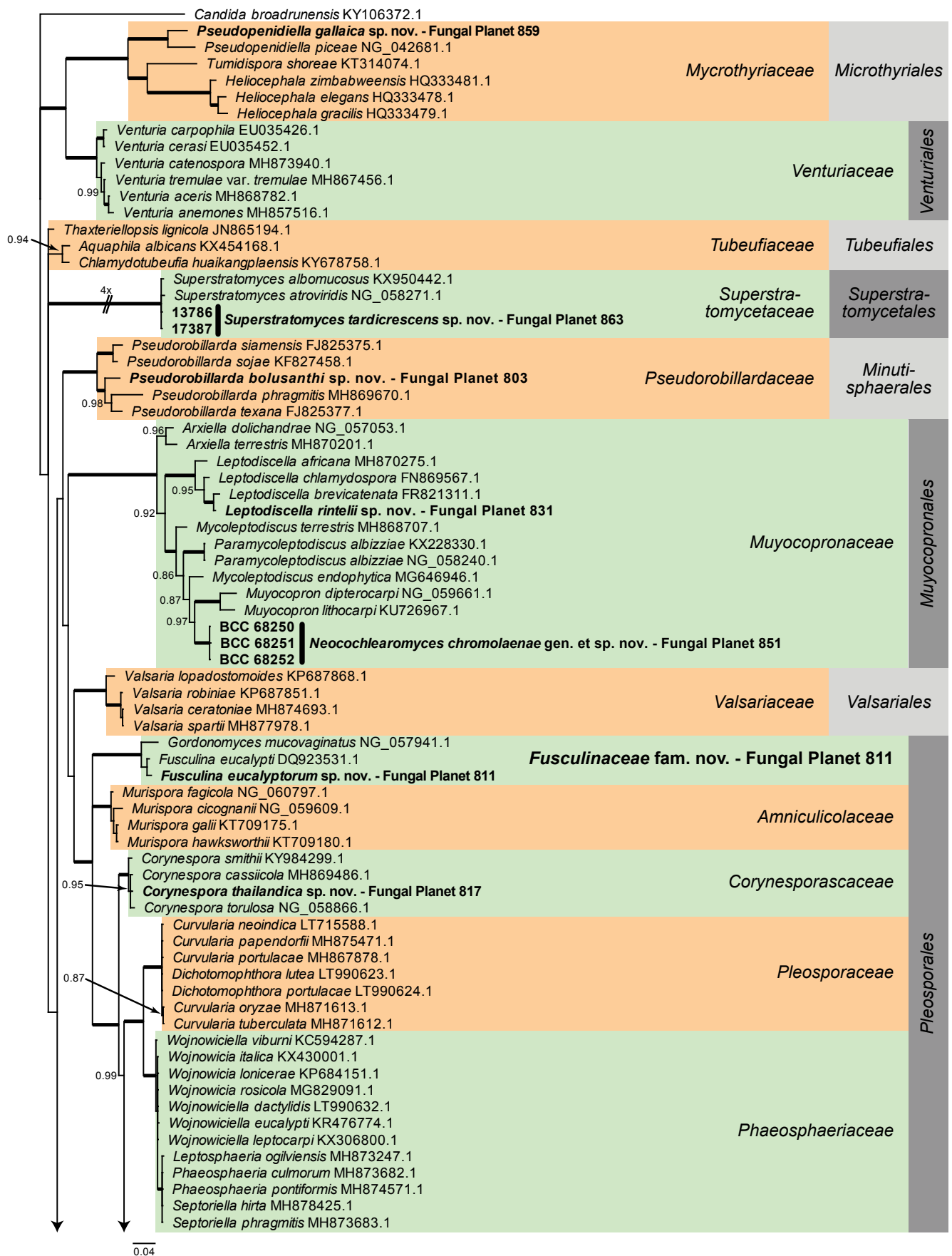
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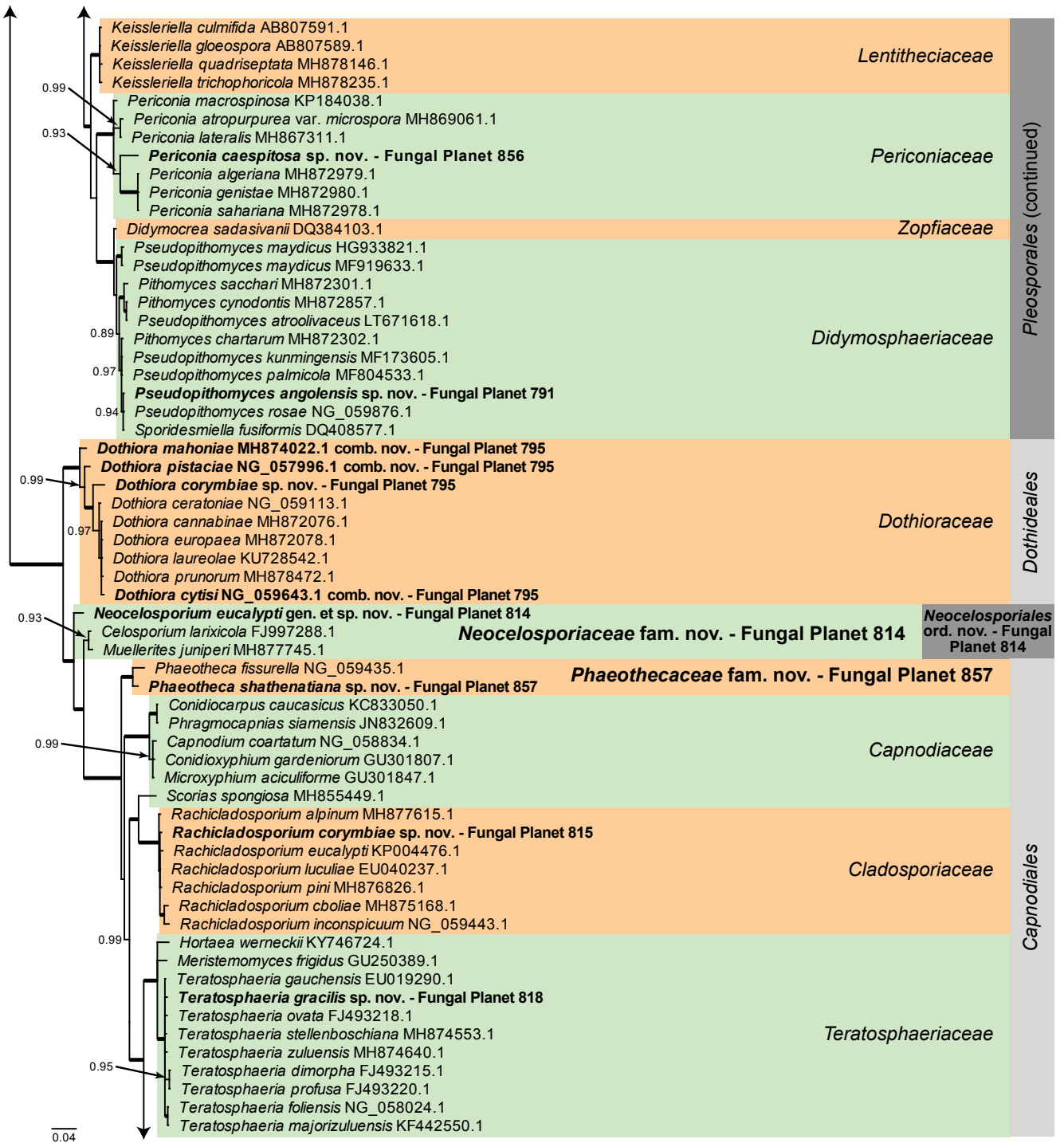
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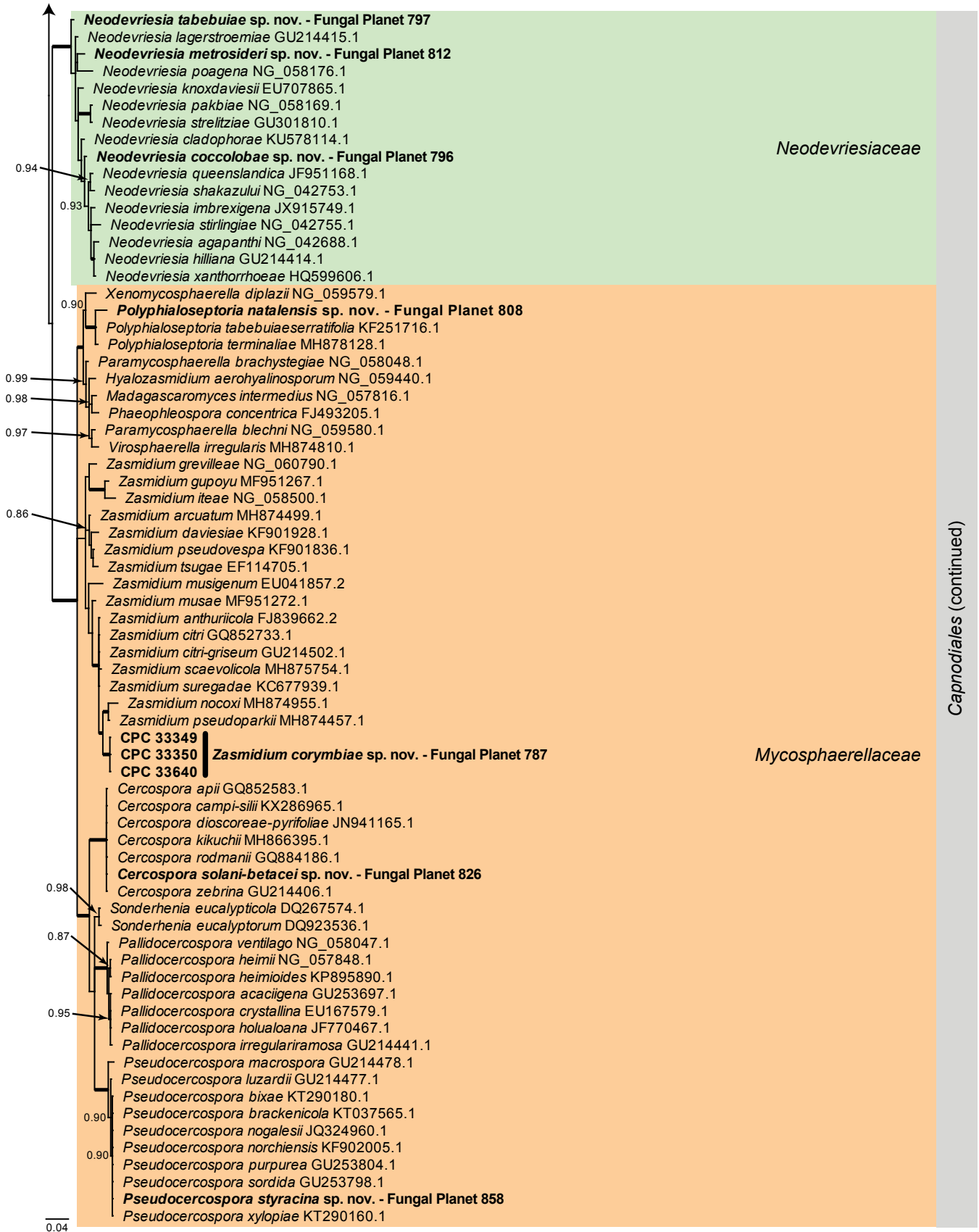


Overview Dothideomycetes phylogeny – part 1

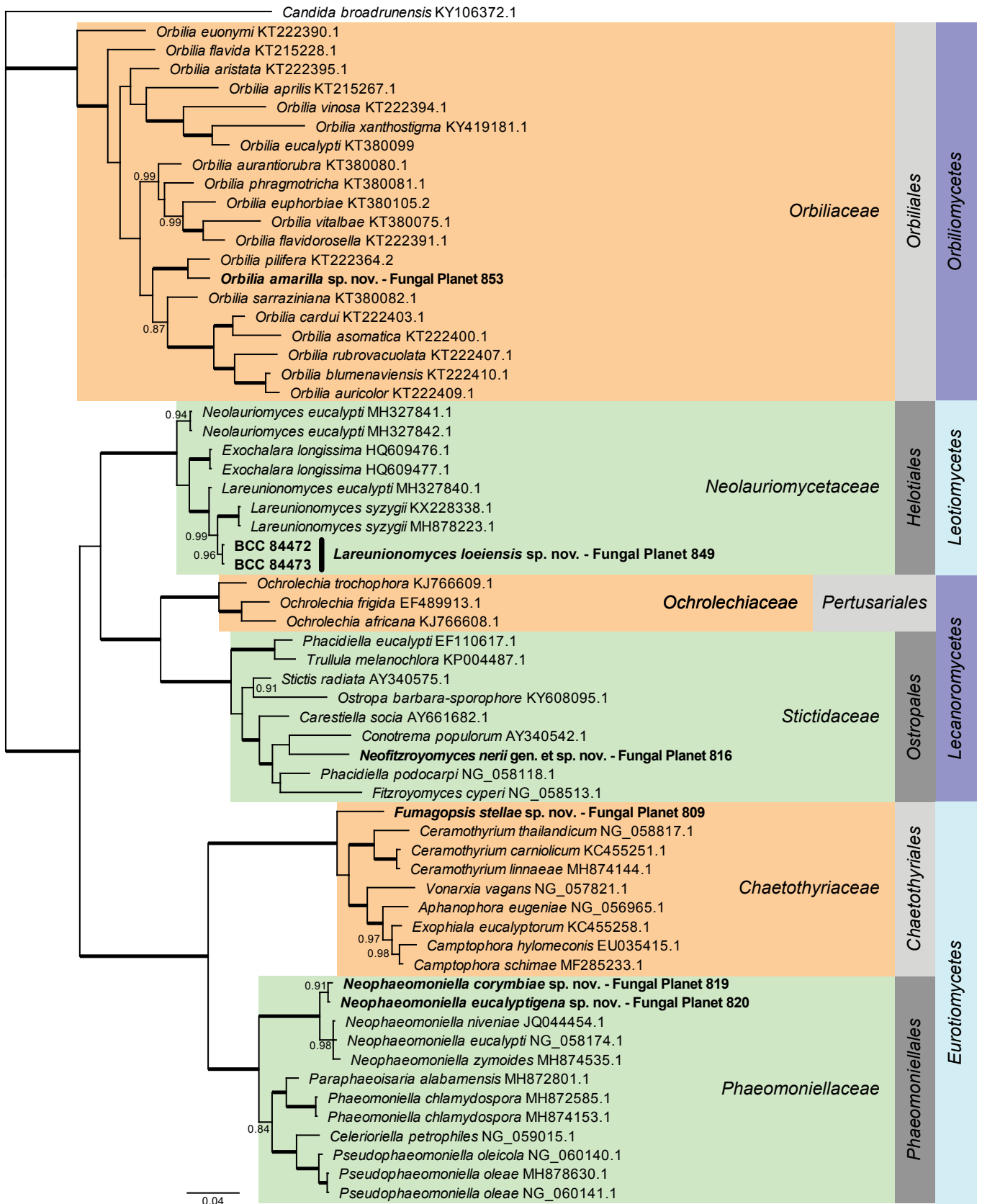
Consensus phylogram (50 % majority rule) of 2478 trees resulting from a Bayesian analysis of the LSU sequence alignment (206 taxa including outgroup; 801 aligned positions; 464 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown 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. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) 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 S23436).



Overview Dothideomycetes phylogeny (cont.) – part 2

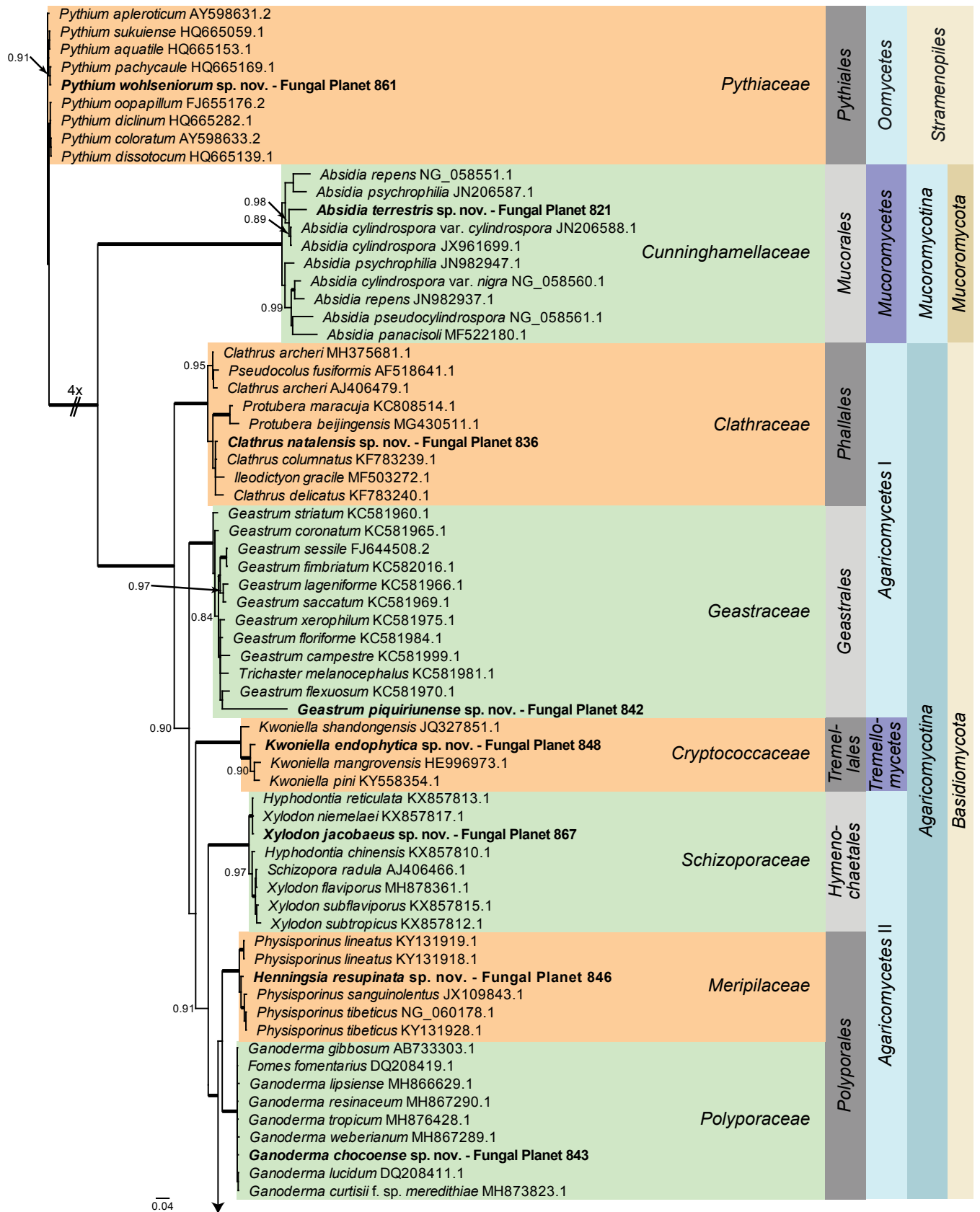


Overview Dothideomycetes phylogeny (cont.) – part 3



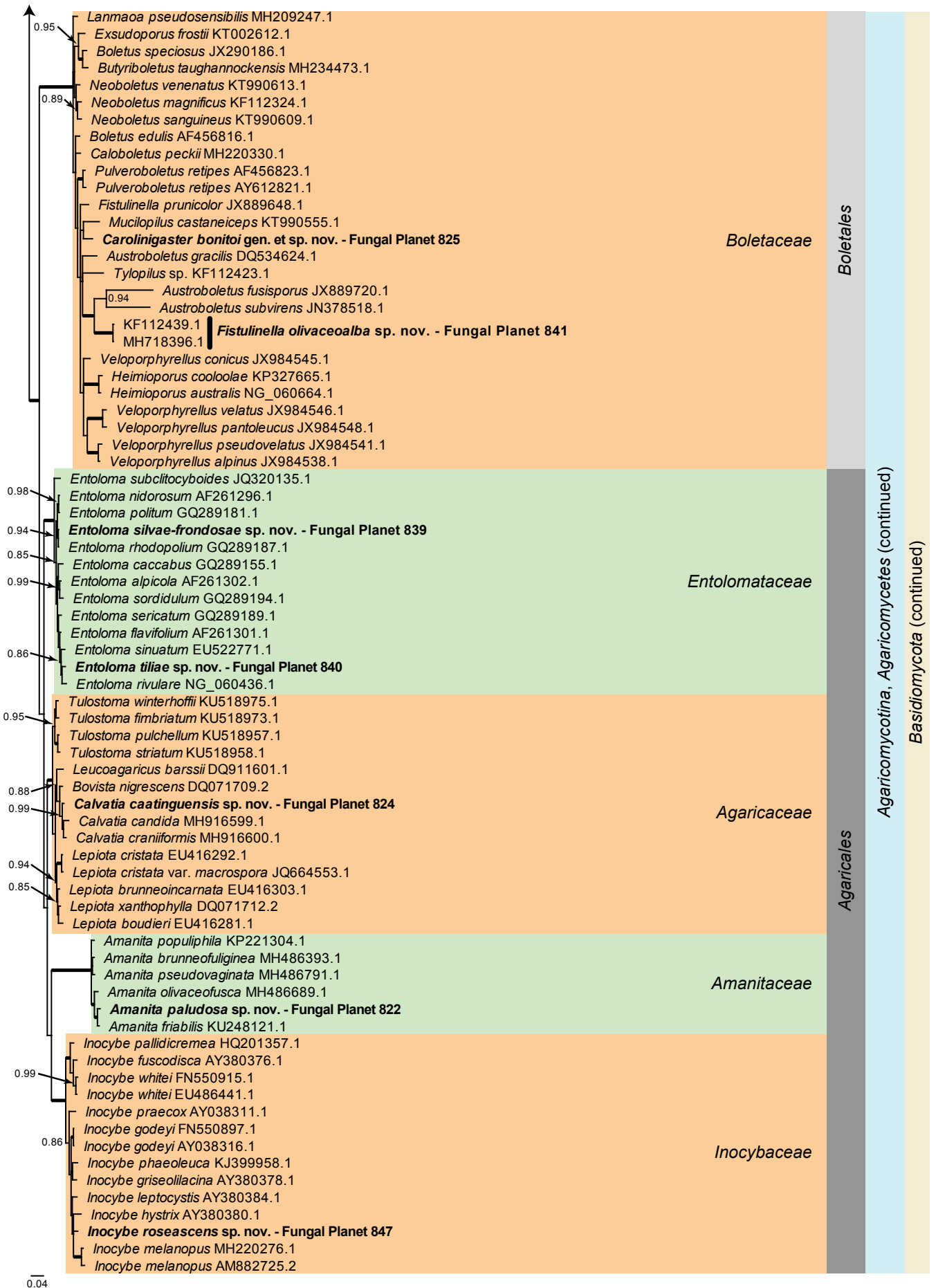
Overview Orbiliomycetes, Leotiomycetes, Lecanoromycetes and Eurotiomycetes phylogeny

Consensus phylogram (50 % majority rule) of 12452 trees resulting from a Bayesian analysis of the LSU sequence alignment (78 taxa including outgroup; 829 aligned positions; 360 unique site patterns) using MrBayes v. 3.2.6 (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. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) 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 S23436).

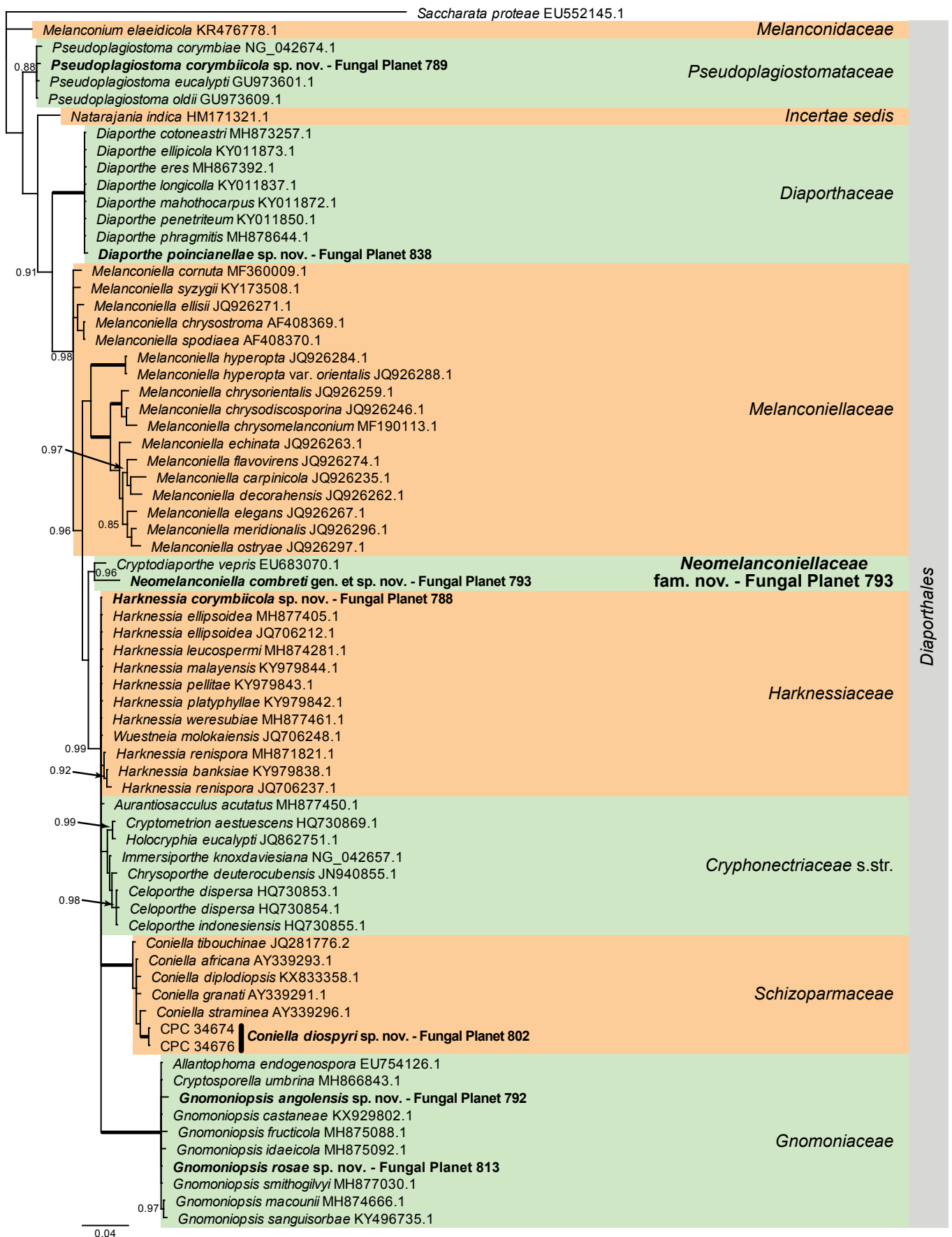


Overview Stramenopiles, Mucoromycota and Basidiomycota phylogeny – part 1

Consensus phylogram (50 % majority rule) of 113 852 trees resulting from a Bayesian analysis of the LSU sequence alignment (141 taxa including outgroup; 980 aligned positions; 654 unique site patterns) using MrBayes v. 3.2.6 (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, classes, subdivisions and phyla are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to the *Stramenopiles* clade 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 S23436).

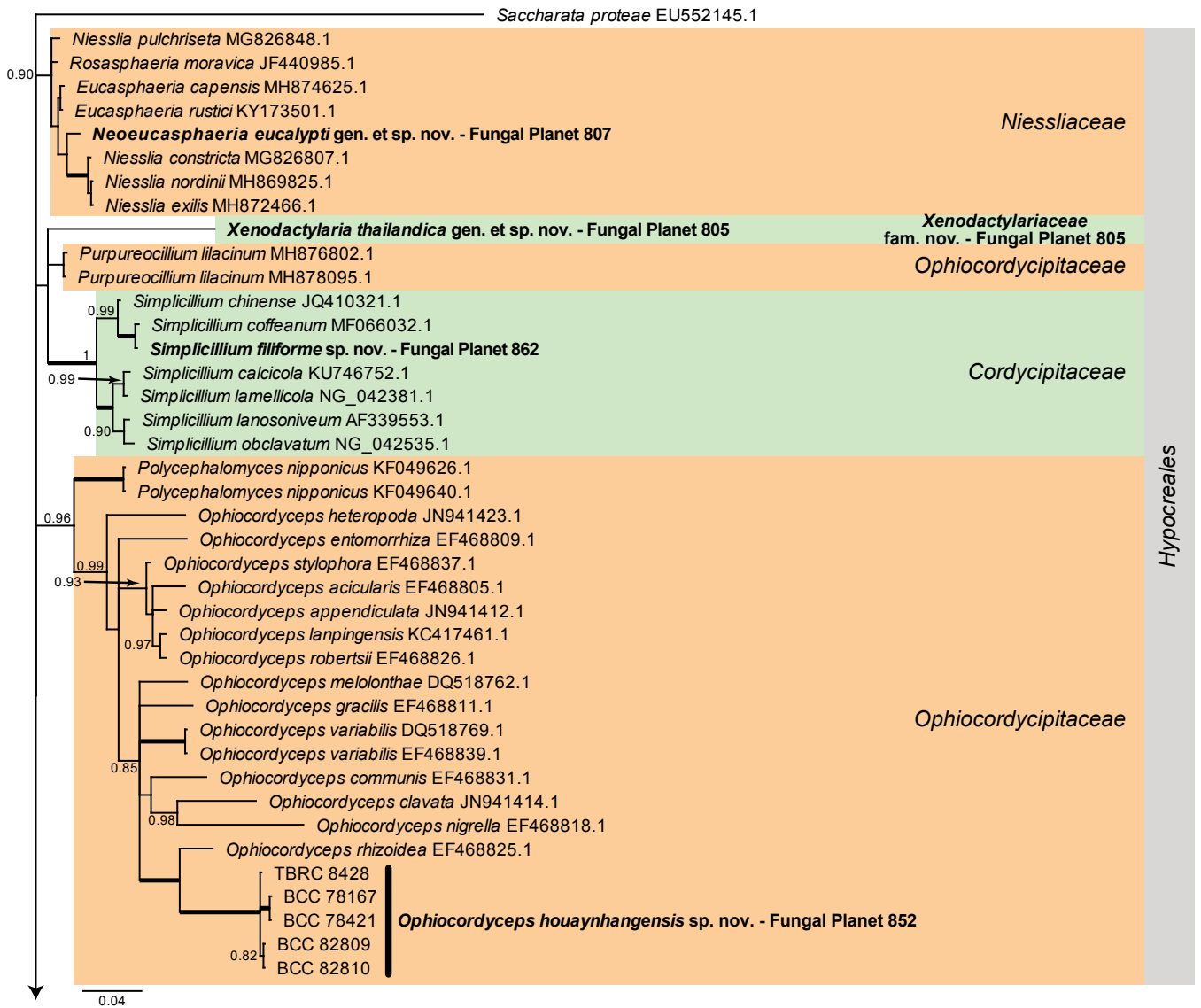


Overview Stramenopiles, Mucoromycota and Basidiomycota phylogeny (cont.) – part 2



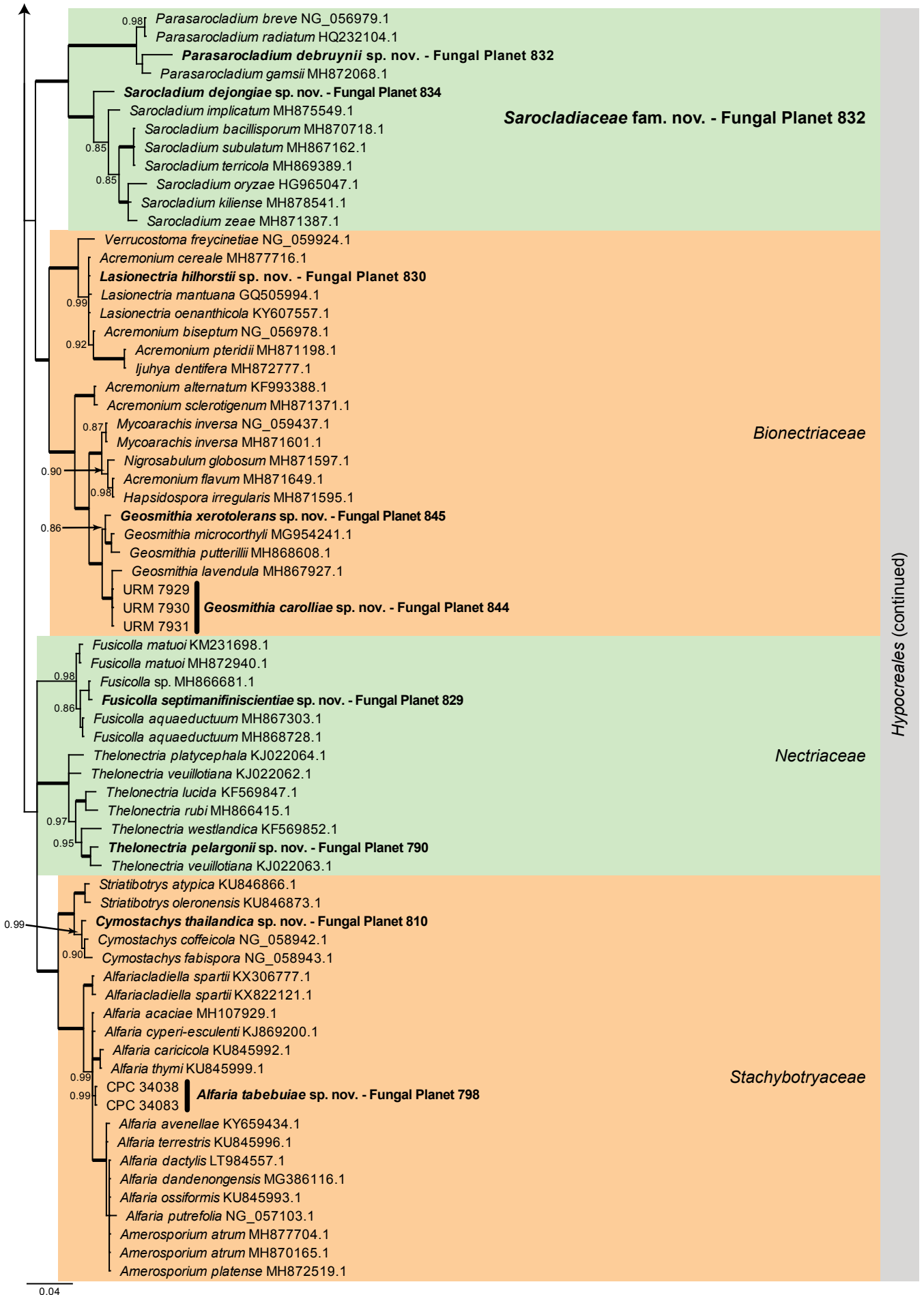
Overview Diaporthales (Sordariomycetes) phylogeny

Consensus phylogram (50 % majority rule) of 1052 trees resulting from a Bayesian analysis of the LSU sequence alignment (71 taxa including outgroup; 768 aligned positions; 176 unique site patterns) using MrBayes v. 3.2.6 (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. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree is rooted to *Saccharata proteae* (GenBank EU552145.1) 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 S23436).



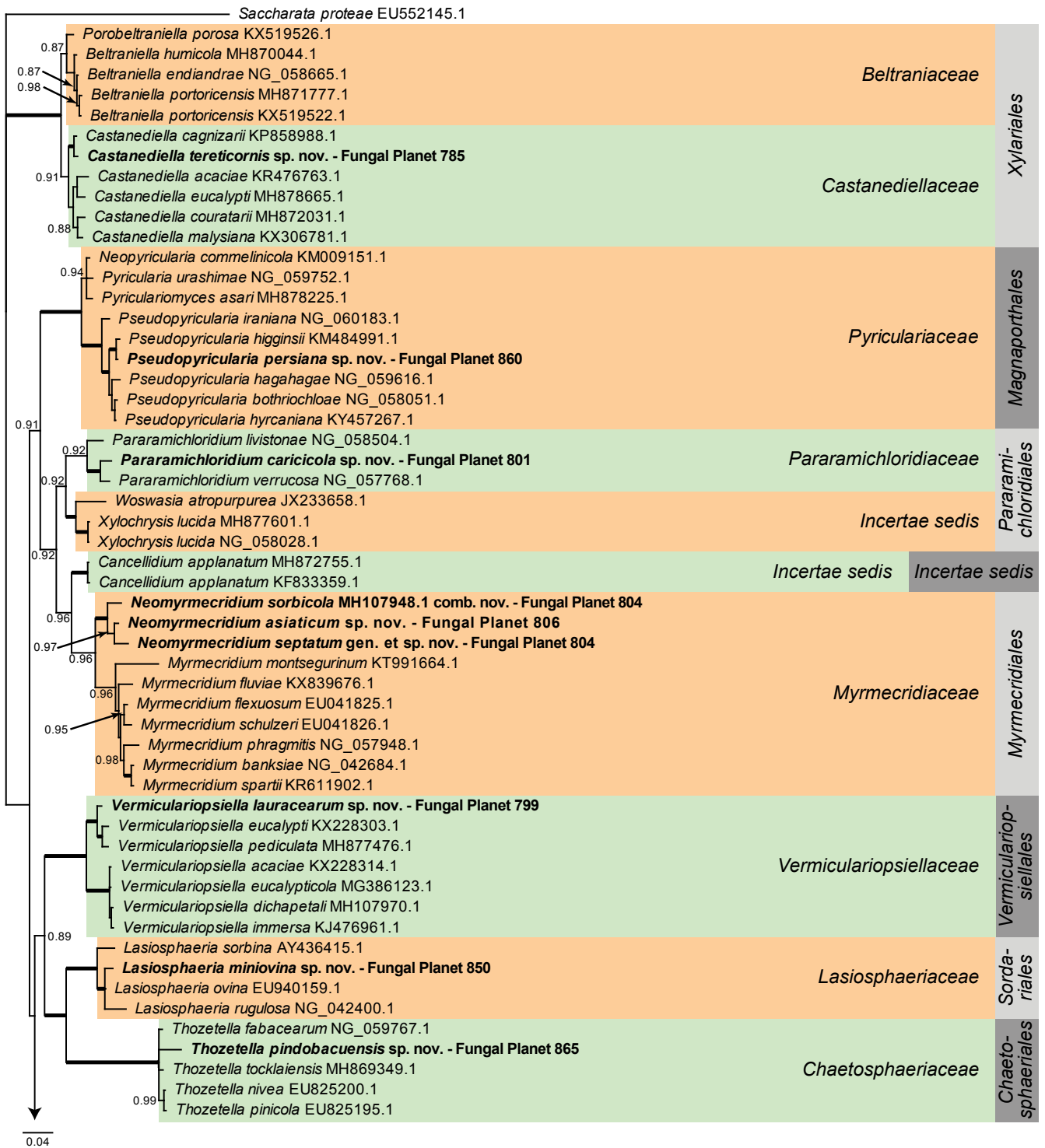
Overview Hypocreales (Sordariomycetes) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 3078 trees resulting from a Bayesian analysis of the LSU sequence alignment (110 taxa including outgroup; 820 aligned positions; 339 unique site patterns) using MrBayes v. 3.2.6 (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. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) 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 S23436).



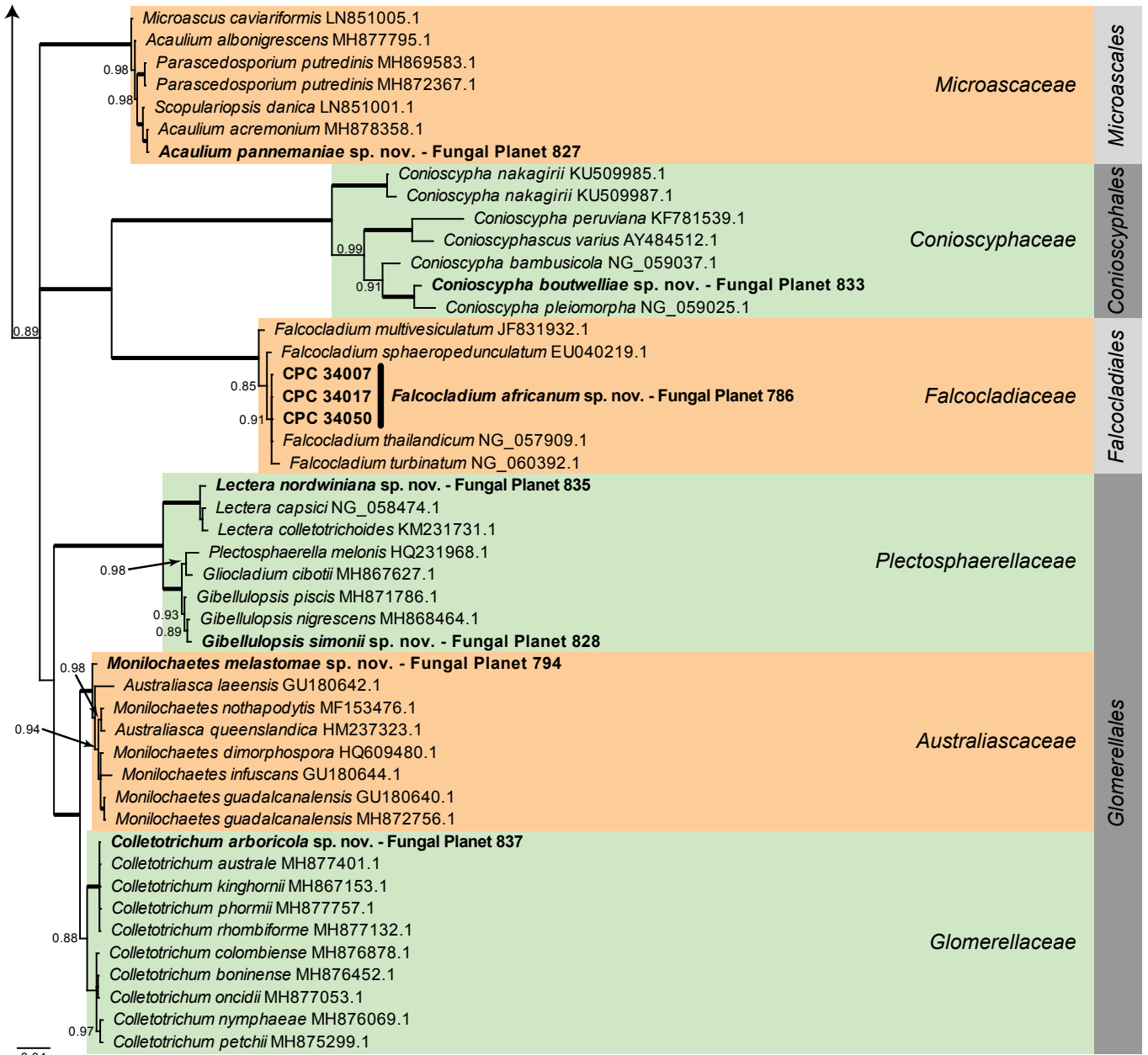
Hypocreales (continued)

Overview *Hypocreales* (*Sordariomycetes*) phylogeny (cont.) – part 2



Overview other orders (Sordariomycetes) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 452 trees resulting from a Bayesian analysis of the LSU sequence alignment (102 taxa including outgroup; 782 aligned positions; 396 unique site patterns) using MrBayes v. 3.2.6 (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. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) 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 S23436).



Overview other orders (Sordariomycetes) phylogeny (cont.) – part 2



Fungal Planet 836 – 13 December 2018

Clathrus natalensis G.S. Medeiros, Melanda, T.S. Cabral, B.D.B Silva & Baseia, *sp. nov.*

Etymology. Named in reference to the type locality, Natal City.

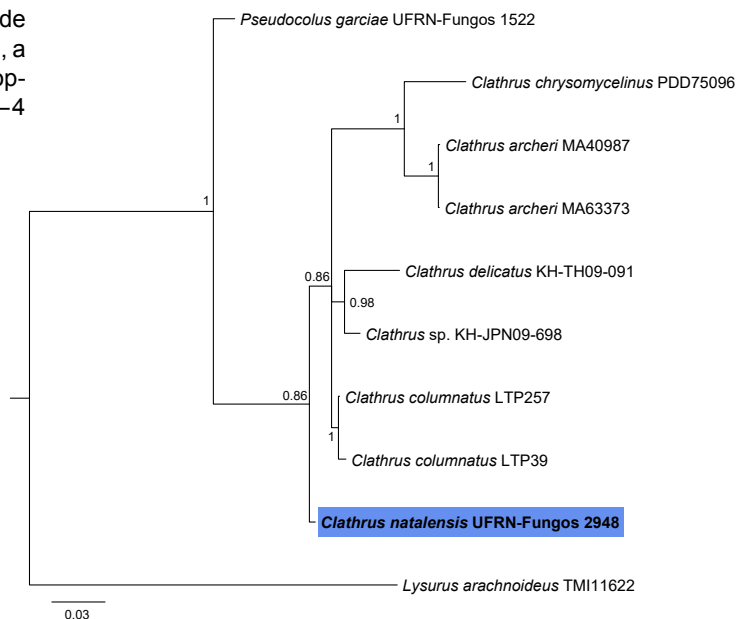
Classification — *Clathraceae*, *Phallales*, *Phallomycetidae*.

Immature *basidiomata* subglobose, 13–18 × 16–22 mm, greyish white (12A1–12B1 KW) with a single and thick rhizomorph greyish white (12A1–12B1 KW). Expanded basidiomata obovate to subglobose 46–95 × 24–71 mm. *Arm meshes* pentagonal to hexagonal, rugose at the beginning of development, becoming smooth afterwards, 32–90 × 20–70 mm, dull red to pinkish white (8B3–8A2), transverse section of an arm shows 3–4 tubes subglobose, elongated to pyriform. *Pseudostipe* absent. *Gleba* mucilaginous, in all inner part of arms, olive brown (KW 4F4), with an unpleasant smell. *Volva* 50–140 × 10–40 mm, greyish white (12A1–12B1 KW), with thick rhizomorph, greyish white (12A1–12B1 KW). *Basidiospores* cylindrical, 4.6–5.6 × 1.9–2.7 μm (5.2 ± 0.4 × 2.3 ± 0.3 μm; Qm = 2.29; n = 30 spores), wall ≤ 0.7 μm, smooth, hyaline in KOH. Arms exhibiting subglobose to globose and pyriform cells, 19.5–45.6 × 13–33.5 μm, wall ≤ 2.2 μm diam, hyaline. *Volva* composed of filamentous hyphae, 2.7–5.2 μm diam, wall ≤ 1.1 μm diam. *Rhizomorph* composed of filamentous hyphae, 3.2–4.7 μm diam, wall ≤ 0.9 μm diam.

Typus. BRAZIL, Rio Grande do Norte, Natal, Centro de Biociências, on soil with litter, 5 Apr. 2017, G.S. Medeiros (holotype UFRN-Fungos 2948, isotype UFRN-Fungos 2947, paratype UFRN-Fungos 2946, ITS and LSU sequences GenBank MH107232 and MH107235, MycoBank MB824737).

Notes — *Clathrus natalensis* was found in a remnant of Atlantic rainforest at the Universidade Federal do Rio Grande do Norte (UFRN) and is characterised by robust basidiomata, a pale red colouration, rugose arms at the beginning of development, becoming smooth afterwards, with the presence of 3–4

tubes in transverse section. This species presents similarities with *Clathrus cristatus* with the colour of the arms and mesh arrangement, but that presents basidiomata with crests along the arm edges (Fazolino et al. 2010), a characteristic absent in *C. natalensis*. In a BLASTn search, the ITS sequence obtained in this study has 94 % similarity to *Clathrus ruber* (GenBank GQ981501). However, *C. ruber* can easily be distinguished by the bright red colour, smaller meshes, and the immature basidiome marked by reticulations (Dring 1980). In the phylogenetic analysis, *C. natalensis* does not group with any species available on GenBank; in fact, they are clearly morphologically different. *Clathrus columnatus* and *C. archeri* show distinct receptacle arrangements, columnar in the first, and united arms below with pointed tips initially attached in the latter (Bosc 1811, Dring 1980); *C. crysomycelinus* and *C. delicatus* have white basidiomata, the first differs by a glebifer attached at the junction of the arms, and the second by a smaller receptacle (up to 25 mm high × 15 mm wide) and deep grooves in the outer face of the arms (Möller 1895, Dring 1980) – characteristics absent in *C. natalensis*. Thus, both morphological characters and the phylogenetic analysis separate *C. natalensis* from the already known species.



Colour illustrations. Brazil, Universidade Federal do Rio Grande do Norte, Centro de Biociências, locality where the type species was collected; basidiomata, transverse section of an arm showing the tubes, subglobose to globose and pyriform cells on arm, smooth spores, and filamentous hyphae in the rhizomorph. Scale bars = 20 mm (basidiomata), 2 mm (tubes), 10 μm (cells on arm, spores and rhizomorph hyphae). All morphology photos from the holotype UFRN-Fungos 2948.

Phylogenetic tree obtained with MrBayes v. 3.1.2. (Huelsenbeck & Ronquist 2001) using ITS, nuc-LSU and *atp6* (MK035869), under GTR+G (ITS/nucLSU) and HKY+G models (*atp6*), for 20 M generations. The type specimen is marked with a rectangle. Posterior probability values are indicated on the branches. TreeBASE submission ID 22520.

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