Fungal Planet description sheets: 785–867

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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: Angola, Australia, Brazil, China, Costa Rica, Cuba, Ecuador, France, Ghana, Hungary, Italy, Laos, Malaysia, Mexico, Netherlands, New Zealand, Nigeria, Puerto Rico, South Africa, Thailand, United States, Venezuela, and Vietnam. The following taxa are described for the first time: Absidia terrestris in Peru; Afrophialinae in South Africa; Amanita paludosa in New Zealand; Aspergillus parasiticus in Costa Rica; A. rubescens in India; A. terrestris in China; A. xylinus in Ecuador; A. zatkovae in Italy; A. zonierantherae in South Africa; A. zonierantherae in Taiwan; A. zonierantherae in United States; A. zonierantherae in Vietnam; and A. zonierantherae in Australia. The following taxa are redescribed: A. terrestris (as Absidia terrestris) in Peru; A. terrestris (as Absidia terrestris) in China; A. terrestris (as Absidia terrestris) in Ecuador; A. terrestris (as Absidia terrestris) in India; A. terrestris (as Absidia terrestris) in Taiwan; A. terrestris (as Absidia terrestris) in United States; A. terrestris (as Absidia terrestris) in Vietnam; and A. terrestris (as Absidia terrestris) in Australia. The following taxa are reviewed: A. terrestris (as Absidia terrestris) in Peru; A. terrestris (as Absidia terrestris) in China; A. terrestris (as Absidia terrestris) in Ecuador; A. terrestris (as Absidia terrestris) in India; A. terrestris (as Absidia terrestris) in Taiwan; A. terrestris (as Absidia terrestris) in United States; A. terrestris (as Absidia terrestris) in Vietnam; and A. terrestris (as Absidia terrestris) in Australia.
Abstract (cont.)

fam. nov. and Neomelanconiella gen. nov.) on Combretum sp., Polyphialocephala natalensis on unidentified plant host, Pseudodibellaira bolusanthi on Bolusanthus speciosus, Thelonectra pelargonii on Pelargonium sp. Spain, Vermiculariopsiella lauraeaurum and Anungitopsis lauri on Laurus novocanariensis, Geosmithia xerotolerans from a darkened wall of a house, Pseudopediophila gallicata on leaf litter. Thailand, Corynespora thailandica on wood, Laneunomonospora loeiensis on leaf litter, Neocochlearomyces chromolaenae (incl. Neocochlearomyces gen. nov.) on Chromolena odorata, Neomymecridium septatum (incl. Neomymecridium gen. nov.), Pararamichloridium cariicolae on Carex sp., Xenodactylaria thailandica (incl. Xenodactylariae fam. nov. and Xenodactylaria gen. nov.), Neomymecridium aasiaticum and Cymostachys thailandica from unidentified vine, USA, Carolinigaster bonitoi (incl. Carolinigaster gen. nov.) from soil, Penicillium fortitum from house dust, Phaeotheca shathenatiana (incl. Phaeothecaeeae fam. nov.) from twig and cone litter, Pythium wohtseniorum from stream water, Superstratomyces tardicrescens from human eye, Talaromyces iowaense from office air, Vietnam, Fistulinella olivaeoalba on soil. Morphological and culture characteristics along with DNA barcodes are provided.

Article info
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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
| Name                                              | Accession       |
|---------------------------------------------------|-----------------|
| Neodevriesia tabebuiae sp. nov. - Fungal Planet 797 |                |
| Neodevriesia lagerstroemiae                       | GU214415.1      |
| Neodevriesia matroderi sp. nov. - Fungal Planet 812 |                |
| Neodevriesia poagena NG_058176.1                  |                |
| Neodevriesia knoxdaviesi EU707865.1               |                |
| Neodevriesia pakkiae NG_058169.1                  |                |
| Neodevriesia streilizei GU301810.1                |                |
| Neodevriesia cladorhopae KU578114.1               |                |
| Neodevriesia coccoloba sp. nov. - Fungal Planet 796 |                |
| Neodevriesia queenslandica JF951168.1             |                |
| Neodevriesia shakazului NG_042753.1               |                |
| Neodevriesia imbrexigena JX915749.1               |                |
| Neodevriesia stringiae NG_042755.1                |                |
| Neodevriesia agapanthi NG_042688.1                |                |
| Neodevriesia fallana GU214414.1                   |                |
| Neodevriesia xanthorrhoeae HQ599606.1             |                |

**Mycosphaerellaceae**

| Name                                              | Accession       |
|---------------------------------------------------|-----------------|
| Zasmidium corymbiae                               |                |
| Zasmidium anthuriicola                            | FJ839662.2      |
| Zasmidium citri                                  | GQ852733.1      |
| Zasmidium citrigreum                             | GU214499.1      |
| Zasmidium musae                                   | MF951272.1      |
| Zasmidium arthunicola                            | FJ839662.2      |
| Zasmidium ctenii                                 | GU214499.1      |
| Zasmidium cteni-griseum                          | GU214499.1      |
| Zasmidium scabrolium                             | MH875754.1      |
| Zasmidium senegalense                            | K677939.1       |
| Zasmidium nocoxi                                 | MH874955.1      |
| Zasmidium pseudoparkii                           | MH874457.1      |

| Name                                              | Accession       |
|---------------------------------------------------|-----------------|
| CPC 33349 Zasmidium corymbiae sp. nov. - Fungal Planet 787 |                |
| CPC 33350 Zasmidium corymbiae sp. nov. - Fungal Planet 787 |                |
| CPC 33640 Zasmidium corymbiae sp. nov. - Fungal Planet 787 |                |
| Cercoспорa api                                     | GQ852583.1      |
| Cercoспорa campi-sali                              | KX286965.1      |
| Cercoспора diloсореa-pyrнфоlе                         | JN941165.1      |
| Cercoспора kikuclhi                                 | MH86395.1       |
| Cercoспора rodmanii                                | HQ84186.1       |

| Name                                              | Accession       |
|---------------------------------------------------|-----------------|
| Cercospora solani-betacea sp. nov. - Fungal Planet 826 |                |
| Cercospora zebrina                                | GU214406.1      |
| Sonderhenia eucalypticina                         | DQ267574.1      |
| Sonderhenia eucalyptorum                          | DQ923536.1      |
| Pallidocercospora ventiNago NG_058047.1           |                |
| Pallidocercospora heinmi NG_05848.1               |                |
| Pallidocercospora heinmiodes KF935890.1           |                |
| Pallidocercospora acaciens GU253897.1             |                |
| Pallidocercospora crystallina EU167579.1          |                |
| Pallidocercospora holalaoana JF770467.1           |                |
| Pallidocercospora irregularramosa GU214441.1      |                |
| Pseudocercospora macrospora GU214478.1            |                |
| Pseudocercospora luzardi GU214477.1               |                |
| Pseudocercospora bicae KT290180.1                 |                |
| Pseudocercospora trachynkoko KT037565.1           |                |
| Pseudocercospora nogaeksi JQ324960.1              |                |
| Pseudocercospora norchensis KF902005.1            |                |
| Pseudocercospora purpurea GU253804.1              |                |
| Pseudocercospora sordida GU253798.1               |                |

**Overview Dothideomycetes phylogeny** (cont.) – part 3
Overview Orbiliomycetes, Leotiomycetes, Lecanoromycetes and Eurotiomycetes phylogeny

Consensus phylogram (50 % majority rule) of 12 452 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 phylolgy – 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. 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

- Boletus speciosus
- Butyriboletus taughannokensis
- Caloboletus peckii
- Pulveroboletus retipes
- Fistulinella prunicolor

- Mucilopilus castaneiceps
- Carolinigaster bonitoi gen. et sp. nov. - Fungal Planet 825

- Amanita paludosa sp. nov. - Fungal Planet 822
- Amanita triabils KU248121.1

- Inocybe pallidicremea HJ2201357.1
- Inocybe fuscofusca AY830376.1
- Inocybe whitei FNS50915.1
- Inocybe whitei EU486441.1
- Inocybe praeox AY038311.1
- Inocybe godeyi FNS50897.1
- Inocybe godeyi AY038316.1
- Inocybe phaeoleuca KJ399958.1
- Inocybe griseolilacina AY380378.1
- Inocybe whitei AY380384.1
- Inocybe hystrix AY380380.1
- Inocybe roseascens sp. nov. - Fungal Planet 847
- Inocybe melanopus MH220276.1
- Inocybe melanopus AM892725.2

- Falkomycota, Agaricomycotina (continued)
- Boletales
- Agaricales
- Agaricaceae
- Amanitaceae
- Inocybaceae

- Fungi
- Basidiomycota (continued)

- Fusarium oxysporum
- Aspergillus niger
- Penicillium chrysogenum
- Trichoderma viride
- Neurospora crassa
- Rhizopus oryzae

- Mucoromycota
- Stramenopiles

- Carcinocystis tumefaciens
- Eremothecium ashbyii
- Cryptococcus neoformans
- Saprolegnia ferax
- Chytridiomycota
- Oomycota

- Overview

- Boletaceae
- Entolomataceae
- Agaricaceae
- Amanitaceae
- Inocybaceae
Overview Diaporthales (Sordariomycetes) phylogeny

Consensus phylogram (50 % majority rule) of 1 052 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 after 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 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).
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
Clathrus natalensis
Clathrus natalensis  
G.S. Medeiros, Melanda, T.S. Cabral, B.D.B Silva & Baseia, sp. nov.

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

Classification — Clathraceae, Phallales, Phallomyceciidae.

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 (BB3–BA2), transverse section of an arm shows 3–4 tubes subglobose, elongated to piriiform. Pseudostipe absent. Gloe vaginae, 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 crisatus 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. crysomycei us 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.

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.

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.

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