

Nomenclatural novelties : Y.P. Tan, Marney & R.G. Shivas

*Derxomyces odellii* Y.P. Tan, Marney & R.G. Shivas, sp. nov.

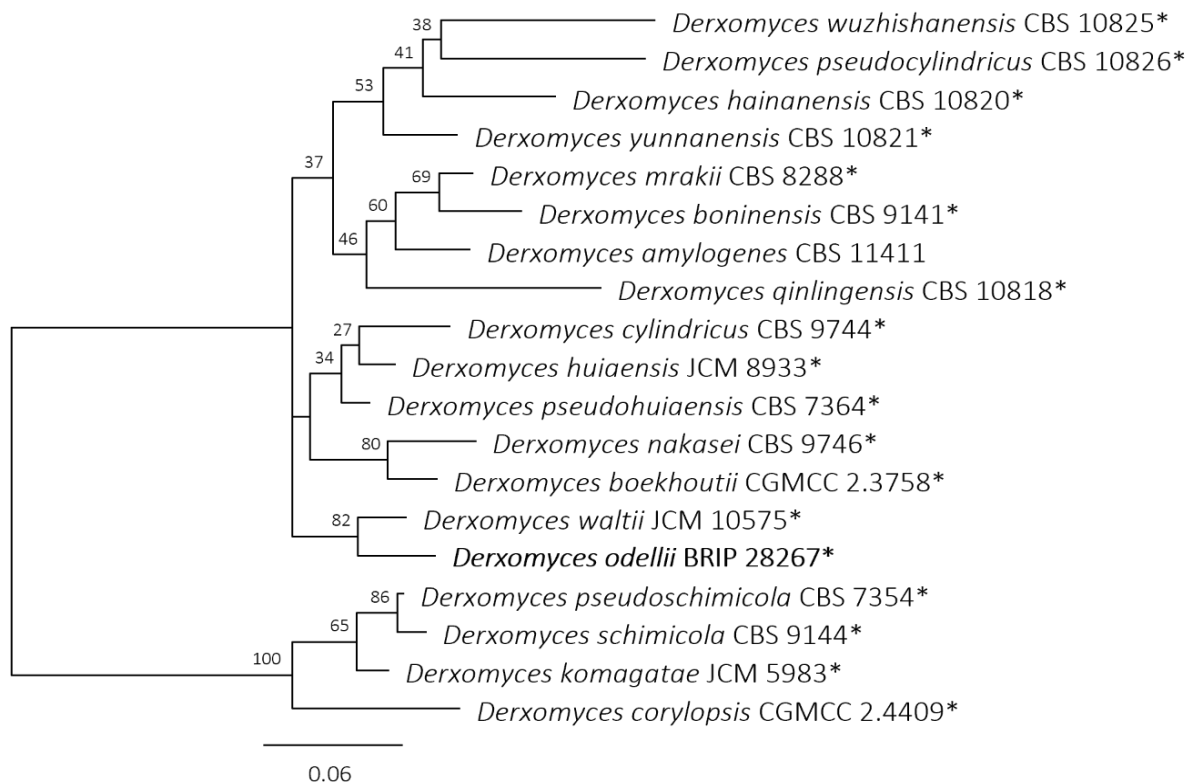
IF 558743

Holotype BRIP 28267

Diagnosis: Differing from *Derxomyces waltii* (ex-type strain JCM 10575) by sequence comparison of the ITS region (GenBank NR\_111014; Identities 466/489 (95%)).

Specimen examined: Australia, Queensland, North Stradbroke Island, Brown Lake, phylloplane on an unidentified tree, 22 Nov. 2001, T.S. Marney TSM061 (includes ex-type culture) (ITS sequence GenBank MZ749693).

Etymology: Named after Ryan Heath O'Dell, who has provided excellent research support for the Queensland Plant Pathology Herbarium for over a decade.



Phylogenetic tree based on a maximum likelihood analysis of an alignment of the ITS sequences from *Derxomyces* species. Analysis was performed on the Geneious Prime 2021 platform using RAxML v.8.2.11, based on the GTR substitution model with gamma-distribution rate variation. Bootstrap values are shown as percentages on the branches of the consensus tree that was inferred from 1 000 replicates. Branch lengths are proportional to substitutions per site. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (\*).

*Gjaerumia marneyi* Y.P. Tan, Bishop-Hurley & R.G. Shivas, sp. nov.

IF 558680

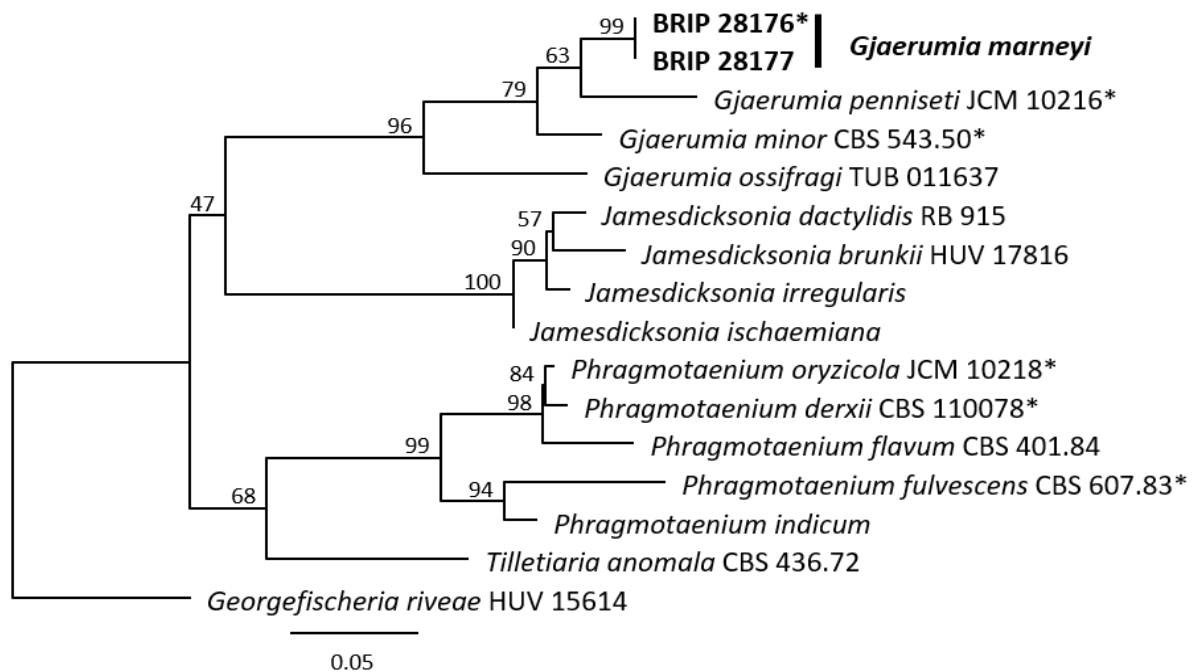
Holotype BRIP 28176

Diagnosis: Differing from *Gjaerumia minor* (ex-type strain CBS 543.50) by sequence comparison of ITS (GenBank KP322989; Identities 539/605 (89%)), and LSU (GenBank MH868274; Identities 828/840 (99%)), and from *G. penniseti* (ex-type strain JCM 10216) by sequence comparison of LSU (GenBank NG\_059383; Identities 567/589 (96%)).

Specimens examined: Australia, Queensland, Brisbane (Indooroopilly), phylloplane of *Hibiscus tiliaceus* (Malvaceae), 13 Sep. 2001, T.S. Marney TSM023 (includes ex-type culture) (ITS and LSU sequences GenBank MZ766446 and MZ766448, respectively). ditto, T.S. Marney TSM024, BRIP 28177 (ITS and LSU sequences GenBank MZ766447 and MZ766449, respectively).

Etymology: Named after the collector, Thomas Stephen Marney, who collected, isolated, and preserved this fungus.

Notes: *Gjaerumia marneyi* (Gjaerumiaceae, Georgefischeriales, Basidiomycota) is the fifth species in the genus according to Index Fungorum. Species of *Gjaerumia* include yeasts, as well as plant-infecting smut fungi. *Gjaerumia marneyi* is only known as an asexual culturable yeast species.



Phylogenetic tree based on a maximum likelihood analysis of a combined multilocus alignment (LSU and ITS) from species within the Georgefischeriales. Analysis was performed on the Geneious Prime 2021 platform using RAxML v.8.2.11, based on the GTR substitution model with gamma-distribution rate variation. Bootstrap values are shown as percentages on the branches of the consensus tree that was inferred from 1 000 replicates. Branch lengths are proportional to substitutions per site. *Georgefischeria riveae* HUV 15614 was used as outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (\*).

*Hannaella xanthorrhoeae* Y.P. Tan, Marney & R.G. Shivas, sp. nov.

IF 558681

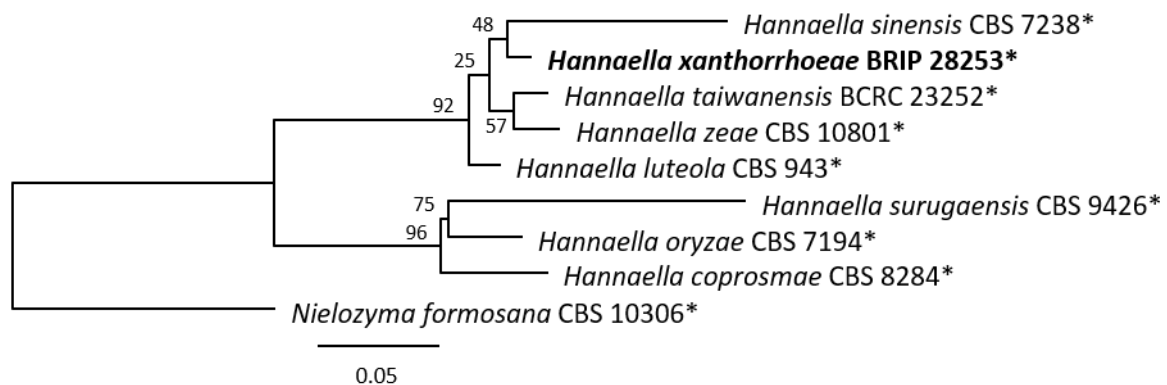
Holotype BRIP 28253

Diagnosis: Differing from the following three species of *Hannaella* by sequence comparison of ITS: *H. sinensis* (ex-type strain CBS 7238; GenBank NR\_111075; Identities 387/405 (96%)), *H. taiwanensis* (ex-type strain BCRC 23252; GenBank NR\_172728; Identities 430/448 (96%)); and *H. zae* (ex-type strain CBS 10801; GenBank NR\_144771; Identities 425/444 (96%)).

Specimen examined: Australia, Queensland, North Stradbroke Island, Brown Lake, phylloplane of *Xanthorrhoea preissii*, 22 Nov. 2001, T.S. Marney TSM047 (includes ex-type culture) (ITS sequence GenBank MZ766445).

Etymology: Named after the host genus, *Xanthorrhoea*, from which the fungus was isolated.

Notes: *Hannaella xanthorrhoeae* (Bulleribasidiaceae, Tremellales, Basidiomycota) is the seventh species in the genus according to Index Fungorum. *Hannaella* contains species that were formerly classified in the *Bullera sinensis* clade. Species of *Hannaella* have been reported from diverse habitats worldwide, including the phylloplane of several plant species.



Phylogenetic tree based on a maximum likelihood analysis of an alignment of the ITS sequences from validly published *Hannaella* species. Analysis was performed on the Geneious Prime 2021 platform using RAxML v.8.2.11, based on the GTR substitution model with gamma-distribution rate variation. Bootstrap values are shown as percentages on the branches of the consensus tree that was inferred from 1 000 replicates. Branch lengths are proportional to substitutions per site. *Nielozyma formosana* strain CBS 10306 was used as outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (\*).

*Naganishia brisbanensis* Y.P. Tan, Marney & R.G. Shivas, sp. nov.

IF 558748

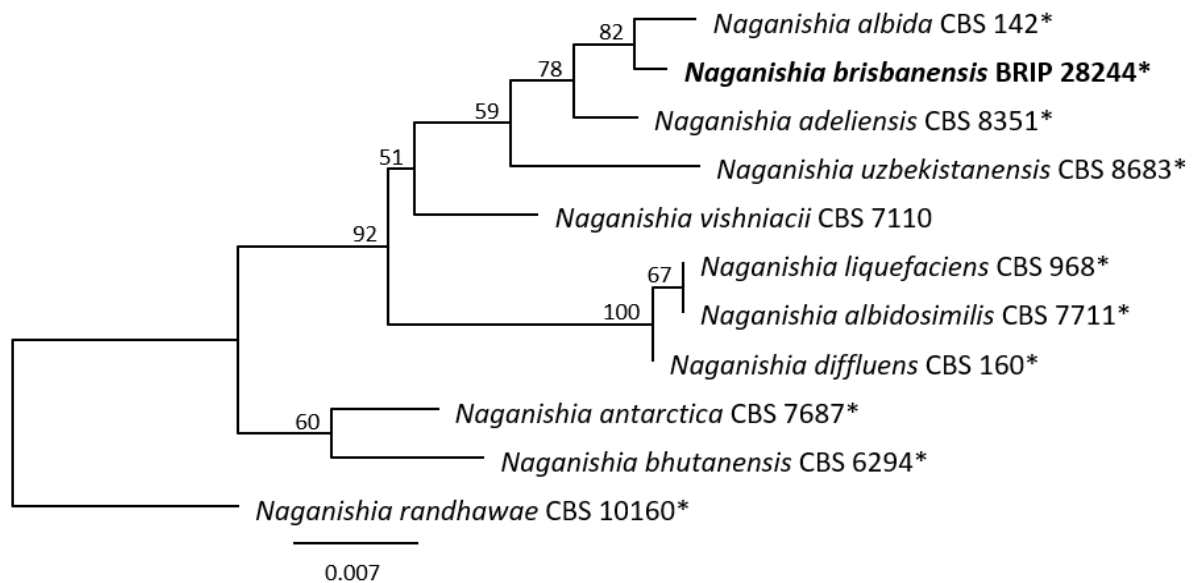
Holotype BRIP 28244

Diagnosis: Differing from its closest phylogenetic relative, *Naganishia albida* (ex-type strain CBS 142) by sequence comparison of ITS (GenBank NR\_111046; Identities 588/597(98%)).

Specimen examined: Australia, Queensland, Brisbane, Chapel Hill, phylloplane of *Backhousia citridora*, 28 Aug. 2001, T.S. Marney TSM038 (includes ex-type culture) (ITS sequence GenBank MZ766444).

Etymology: Named after Brisbane, the city from which the fungus was collected.

Notes: *Naganishia brisbanensis* (Cryptococcaceae, Tremellales, Basidiomycota) is the nineteenth species in the genus according to Index Fungorum. *Naganishia* was formerly classified as the *Cryptococcus albidus* clade. Species of *Naganishia* have been reported from diverse habitats, including on plant surfaces, soil, and water, often in extreme conditions of temperature (hot and cold), dryness and UV radiation.



Phylogenetic tree based on a maximum likelihood analysis of an alignment of the ITS sequences of *Naganishia* species. Analysis was performed on the Geneious Prime 2021 platform using RAxML v.8.2.11, based on the GTR substitution model with gamma-distribution rate variation. Bootstrap values are shown as percentages on the branches of the consensus tree that was inferred from 1000 replicates. Branch lengths are proportional to substitutions per site. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (\*).

*Symmetrospora eucalypti* Y.P. Tan, Marney & R.G. Shivas, sp. nov.

IF 558749

Holotype BRIP 28188

Diagnosis: Differing from *Symmetrospora marina* (ex-type strain CBS 2365) by sequence comparison of ITS (GenBank NR\_073272.1; Identities 524/566(93%)), and LSU (GenBank KY109809.1; Identities 551/570(97%)), and from *S. pseudomarina* (ex-type strain CBS 14057) by sequence comparison of ITS (GenBank NR\_171799.1; Identities 526/566(93%)) and LSU (GenBank KJ701217.1; 1316/1342(98%)).

Specimens examined: Australia, Queensland, Brisbane, Indooroopilly, phylloplane of *Eucalyptus* sp. (Myrtaceae), 13 Sept. 2001, T.S. Marney TSM035, holotype (ITS and LSU sequences GenBank MZ930249 and MZ930244, respectively); ditto, T.S. Marney TSM034, BRIP 28187 (ITS sequence GenBank MZ930248).

Etymology: Named after the genus of the host plant from which the fungus was isolated.

*Symmetrospora proteacearum* Y.P. Tan, Marney & R.G. Shivas, sp. nov.

IF 558750

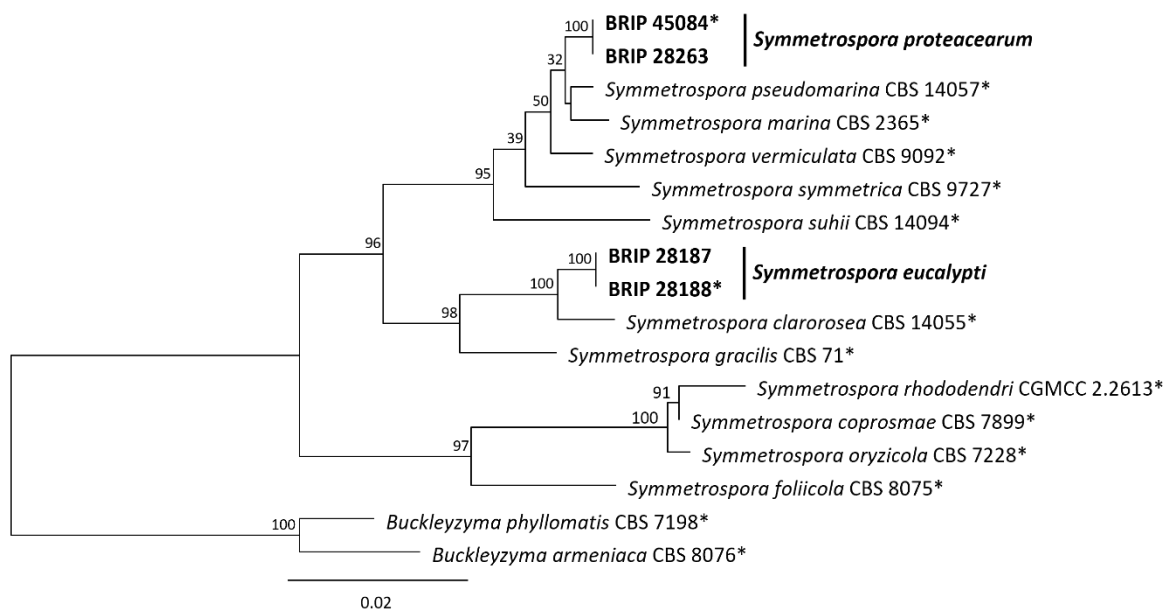
Holotype BRIP 45084

Diagnosis: Differing from *S. clarorosea* (ex-type strain CBS 14055) by sequence comparison of ITS (GenBank KJ701231.1; Identities 531/571(93%)), and LSU (GenBank NG\_075192.1; Identities 984/1010(97%)).

Specimens examined: Australia, Queensland, Brisbane, Indooroopilly, phylloplane of *Grevillea* sp. (Proteaceae), 4 Aug. 2004, T.S. Marney (includes ex-type culture) (ITS and LSU sequences GenBank MZ930246 and MZ930245, respectively); ditto, Dunwich, Brown Lake, phylloplane of *Banksia* sp. (Proteaceae), 22 Nov. 2001, T.S. Marney TSM057, BRIP 28263 (ITS sequence GenBank MZ930247).

Etymology: Named after the family of the host plant from which the fungus was isolated.

Notes: *Symmetrospora eucalypti* and *S. proteacearum* (Symmetrosporaceae, Pucciniomycotina, Basidiomycota) are the twelfth and thirteenth species in the genus according to Index Fungorum. Species of *Symmetrospora* are red ballistosporogenous yeasts mostly found on leaf surfaces, of which five species were previously classified in *Sporobolomyces*. The discovery and morphology-based description of *Symmetrospora foliicola* (as *Sporobolomyces foliicola*) from leaves of *Banksia collina* in Australia in 1983 ultimately led to this molecular-based taxonomic reinvestigation of some Australian phylloplane yeasts.



Phylogenetic tree based on a maximum likelihood analysis of a combined multilocus alignment (ITS and LSU). Analysis was performed on the Geneious Prime 2021 platform using RAxML v.8.2.11, based on the GTR substitution model with gamma-distribution rate variation. Bootstrap values are shown as percentages on the branches of the consensus tree that was inferred from 1 000 replicates. Branch lengths are proportional to substitutions per site. *Buckleyzyma armeniaca* strain CBS 8076 and *B. phyllomatis* strain CBS 7198 were used as outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (\*).