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Nomenclatural novelties: Y.P. Tan, S.L. Bishop-Hurley, T.S. Marney & R.G. Shivas

Aspergillus montoensis Y.P. Tan, Bishop-Hurley, S.M. Thompson & R.G. Shivas, sp. nov.

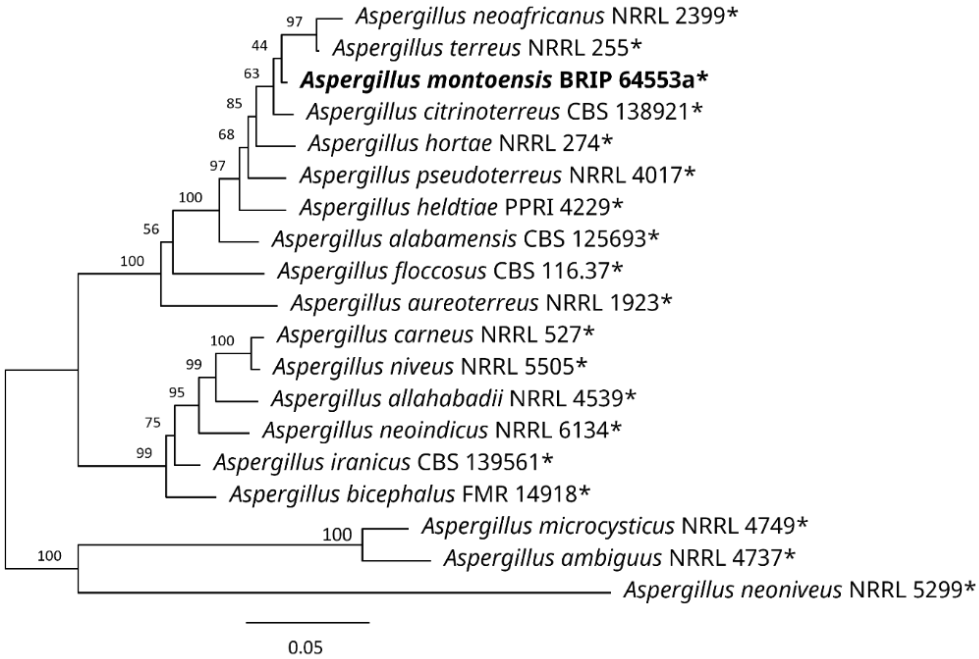
IF 558828

Holotype BRIP 64553a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nDNA describe the type BRIP 71717 and are available in GenBank under the accessions OK441076 (ITS region), OK509073 (tub2, β-tubulin), and OK533535 (rpb2, RNA polymerase II gene). Aspergillus montoensis differs from A. citrinoterreus (ex-type strain CBS 138921) by sequence comparison of tub2 (GenBank LN680657.1; Identities 456/469(97%), Gaps 3/474; unique nucleotide at positions 290(C), 337(A), 459(G), 464(T), 470(C), 579(G), 602(G), 611(A), 629(T), and 724(C)), and rpb2 (GenBank LT827022.1; Identities 853/859(99%); unique nucleotide at positions 86(T), 299(G), 374(C), 455(T), 949(T), and 961(T)). Aspergillus montoensis differs from A. terreus (ex-type strain NRRL 255) by sequence comparison of tub2 (GenBank EF669519.1; 514/515(99%); unique nucleotide at position 88(C)), and rpb2 (GenBank EF669628.1; Identities 838/859(98%); unique nucleotide at positions 66(T), 279(T), 305(G), 344(T), 374(C), 395(T), 397(C), 446(G), 490(C), 482(G), 503(C), 512(C), 536(T), 548(T), 572(G) 668(T) 746(C), 806(T), 815(G), 833(C), and 848(C)).

Specimen examined: Australia, Queensland, Monto, from root of Vigna radiata, 2016, S.M. Thompson & K. Buller, BRIP 64553a.

Etymology: Named after Monto, the town where this fungus was collected.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (tub2 and rpb2) of Aspergillus ser. Terrei 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. Three species from Aspergillus ser. Ambigui (A. ambiguous, A. microcysticus, and A. neoniveus) were

used as the outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (*).

Bannoa macarangae Y.P. Tan, Marney & R.G. Shivas, sp. nov.

IF 558829

Holotype BRIP 28272 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA region describe the type BRIP 28272 and are available in GenBank under the accessions OK001795 (ITS region) and OK036710 (LSU). Bannoa macarangae differs from B. syzygii (ex-type strain CBS 9040) by sequence comparison of ITS (GenBank NR_154870; Identities 547/561(98%), Gaps 2/561; unique nucleotide at positions 16(T), 36(G), 114(A), 124(G), 273(C), 333(A), 341(T), 343(T), 481(C), 502(A), and 510(T)) and LSU (GenBank KY106156; Identities 809/819(99%), Gaps 4/819; unique nucleotide at positions 74(A), 350(C), 414(T), 446(A), 451(C), 474(A)).

Specimen examined: Australia, Queensland, Dunwich, Myora Springs, from phylloplane of Macaranga tanarius, Nov. 2001, T.S. Marney TSM 066, BRIP 28272.

Etymology: Named after Macaranga, the plant genus from which this fungus was isolated.

Notes: Bannoa macarangae (Erythrobasidiaceae) is the eighth species described in this genus of red to orange ballistosporogenous yeasts. All species are associated with living or dead leaves.

Erythrobasidium leptospermi Y.P. Tan, Gogorza Gondra & R.G. Shivas, sp. nov.

IF 558830

Holotype BRIP 66853 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA region describe the type BRIP 66853 and are available in GenBank under the accessions OK360957 (ITS region) and OK393708 (LSU). Erythrobasidium leptospermi differs from E. elongatum (ex-type strain CBS 8080) by sequence comparison of the ITS region (GenBank NR_073306.1; Identities 541/620(87%), Gaps 24/620) and LSU (GenBank NG_059254.1; Identities 833/870(96%), Gaps 1/870).

Specimen examined: Australia, Queensland, Bribie Island, from phylloplane of Leptospermum speciosum, 7 Mar. 2018, A.R. Gogorza Gondra, V.N. Wolter, M.D.E. Shivas & R.G. Shivas, BRIP 66871, isotype strain CBS 16060.

Etymology: Named after Leptospermum, the plant genus from which this fungus was isolated.

Erythrobasidium proteacearum Y.P. Tan, Gogorza Gondra & R.G. Shivas, sp. nov.

IF 558832

Holotype BRIP 66871 (permanently preserved in a metabolically inactive state)

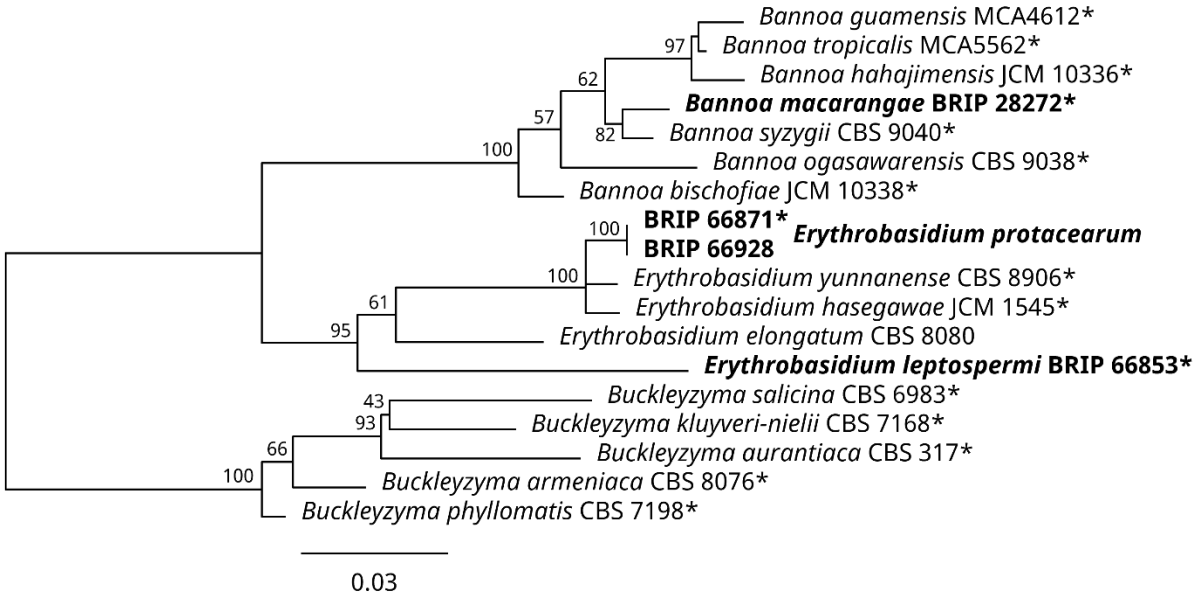
Diagnosis: Sequences from the rDNA region describe the type BRIP 66871 and are available in GenBank under the accessions OK360958 (ITS region) and OK393709 (LSU). Erythrobasidium proteacearum differs from E. yunnanense (ex-type strain CBS 8906) by sequence comparison of the ITS region (GenBank NR_155098.1; Identities 548/554(99%), Gaps 3/554; unique nucleotide at positions 128(C), 143(C), and 516 (T)) and LSU (GenBank GenBank KY107682.1; Identities 515/524(98%), Gaps 1/524; unique nucleotide at positions 99(T), 124(T), 374(T), 385(G), 401(C), 403(A), 424(A), and 426(G)). Erythrobasidium proteacearum differs from E. hasegawianum (ex-type strain JCM 1545) by sequence comparison of the ITS region (GenBank AB030352.1; Identities 564/575(98%), Gaps 2/575; unique nucleotide at positions 71(C), 128–129(CA), 143–144 (CT), 346(T), 393(G), 437(T), and 515(T)), and LSU (GenBank AF131058.1; Identities 557/564(99%); unique nucleotide at positions 374(T), 385(G), 387(A), 401(C), 403(A), 424(A), and 426(G)).

Specimens examined: Australia, Queensland, Bribie Island, from phylloplane of Banksia aemula, 7 Mar. 2018, A.R. Gogorza Gondra, V.N. Wolter, M.D.E. Shivas & R.G. Shivas, BRIP 66871, isotype strain

CBS 16074; Doonan, from phylloplane of Conospermum taxifolium, 12 Mar. 2018, A.R. Gogorza Gondra, V.N. Wolter, M.D.E. Shivas & R.G. Shivas, BRIP 66928 (ITS and LSU sequences GenBank OK360959 and OK393710, respectively).

Etymology: Named after Proteaceae, the plant family from which this fungus was isolated.

Notes: Erythrobasidium leptospermi and E. proteacearum (Erythrobasidiaceae) are the fourth and fifth species described in this genus of orange-red ballistosporogenous yeasts.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (LSU and ITS) of Erythrobasidiaceae 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. Bucklezyma species were used as the outgroup. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (*).

Brunneofusispora sennae-torae Y.P. Tan, Bishop-Hurley, T. Taylor, Comben & R.G. Shivas, sp. nov.

IF 558833

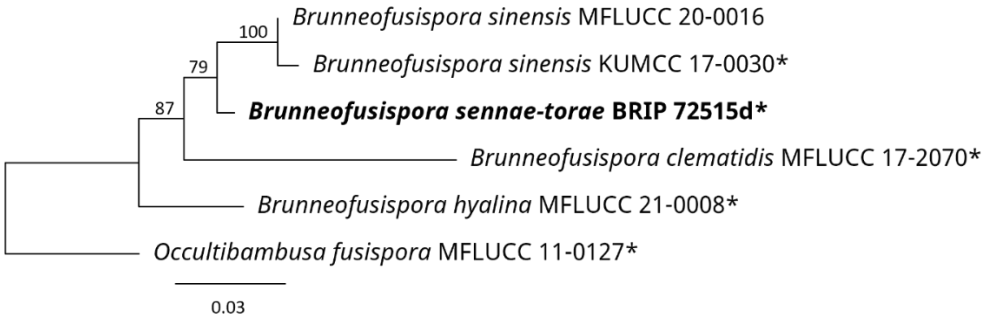
Holotype BRIP 72515d (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA region describe the type BRIP 72515d and are available in GenBank under the accessions OK493236 (ITS region) and OK493235 (LSU). Brunneofusispora sennae-torae differs from B. sinensis (ex-type strain KUMCC 17-0030) by sequence comparison of the ITS region (GenBank MH393558; Identities 506/538(94%), Gaps 11/538), and LSU (GenBank MH393557.1; Identities 774/783(99%), Gaps 2/783; unique nucleotide at positions 88(C), 196(C), 470(C), 539(T), 677(G), 763(G), and 816 (T)).

Specimen examined: Australia, Queensland, Cooktown, from leaf spot of Senna tora, 25 May 2021, D.F. Comben, M.D.E. Shivas & R.G. Shivas, BRIP 72515d.

Etymology: Named after the host plant, Senna tora, from which the fungus was isolated.

Notes: Brunneofusispora sennae-torae is the fourth species, and the first record from Australia of this genus of saprobic terrestrial fungi found on dead and decaying wood.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (LSU and ITS) of Brunneofusispora 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. Occultibambusa fusispora ex-type strain MFLUCC 11-0127 was used as the outgroup. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (*).

Fusarium dhileepanii Y.P. Tan, Bishop-Hurley & R.G. Shivas, sp. nov.

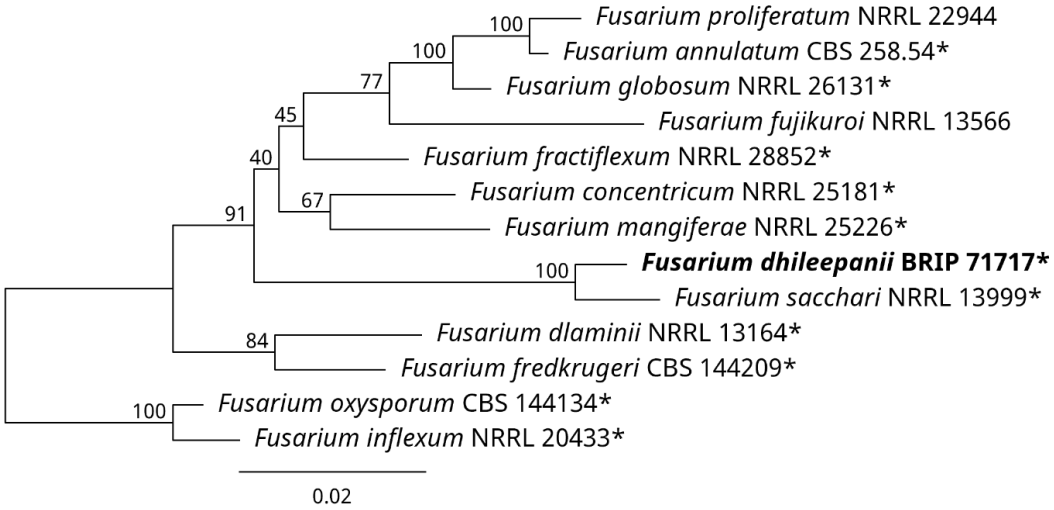
IF 558834

Holotype BRIP 71717 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the nDNA describe the type BRIP 71717 and are available in GenBank under the accessions OK509072 (tef1α, translation elongation factor 1 alpha) and OK533536 (rpb2). Fusarium dhileepanii differs from F. sacchari (ex-type strain NRRL 13999) by sequence comparison of tef1α (GenBank AF160278.1; Identities 619/630(98%); unique nucleotide at positions 67(T), 102(G), 115(A), 117(G), 122–123(TG), 133(C), 137(T), 362(T), 417(T), and 423(C)), and rpb2 (GenBank JX171580.1, Identities 892/902(99%); unique nucleotide at positions 24(T), 180(C), 246(T), 291(C) 369(A), 396(T), 630(G), 636(G), 747(T), and 828(G)).

Specimen examined: Australia, Queensland, Daintree, from leaf of Cyperus aromaticus, 3 Sept. 2020, K. Dhileepan, M.D.E. Shivas & R.G. Shivas, BRIP 71717.

Etymology: Named after Kunjithapatham Dhileepan, who has enthusiastically led the search for fungi and insects as potential biological control agents for invasive plants in Australia.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (tef1α and rpb2) of Fusarium fujikuroi species complex. 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. Fusarium inflexum ex-type strain NRRL 20433 and F. oxysporum ex-type strain CBS 144134 were used as the outgroup. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (*).

Setophoma atkinsoniorum Y.P. Tan, Grice, Trevorrow, Bishop-Hurley & R.G. Shivas, sp. nov.

IF 558835

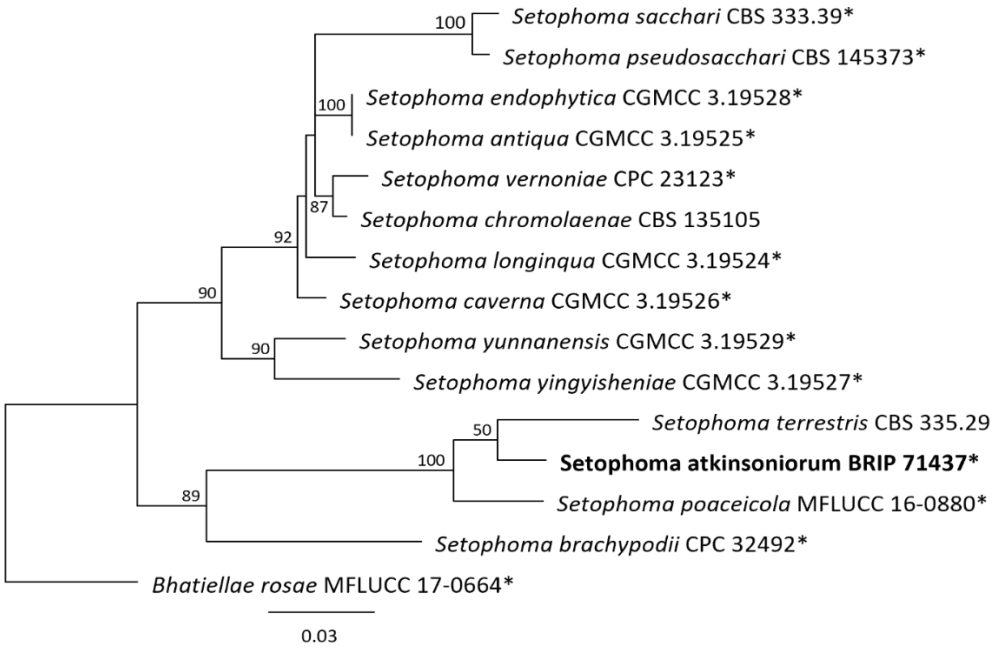
Holotype BRIP 71437 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA describe the ex-type strain BRIP 71437 and are available in GenBank under the accessions OK349508 (ITS region) and OK349509 (LSU). Setophoma atkinsoniorum differs from S. poaceicola (ex-type strain MFLUCC 16-0880) by sequence comparison of the ITS region (KY568988; Identities 478/512(93%), Gaps 9/516)), and LSU (GenBank KY550386.1; Identities 784/788(99%); unique nucleotide at positions 202(C), 205(G), 435(T), and 500(T)). Setophoma atkinsoniorum differs from *S. terrestris* (strain CBS 335.29) by sequence comparison of the ITS region (GenBank and GenBank KF251246; Identities 476/499(95%), Gaps 6/504), and LSU (GenBank GQ387587.1; Identities 852/869(98%); unique nucleotide at positions 122(C), 130(C), 132(T), 134(G), 136–137(CA), 144(C), 188(C), 199–202(GCCC), 205(G), 500–501(TC), 529(A), and 532(G)).

Specimen examined: Australia, Queensland, Mount Garnet, Pinnarendi Station, from dying plants of Cenchrus ciliaris, 22 Jun. 2020, R. Atkinson, B. English, K.R.E. Grice & P.R. Trevorrow, BRIP 71437.

Etymology: Named after Ronnie and Nadine Atkinson, who own and run Pinnarendi Station, a working cattle station, from where this fungus was collected.

Notes: Setophoma atkinsoniorum is the fourteenth species recognised in this genus that includes both saprobic and pathogenic species, including some that cause leaf spots, necrosis, and dieback on grasses.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (LSU and ITS) of Setophoma 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. Bhatiella rosae ex-type strain MFLUCC 17-0664 was used as the outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (*).

Sporobolomyces musae Y.P. Tan, Marney & R.G. Shivas, sp. nov.

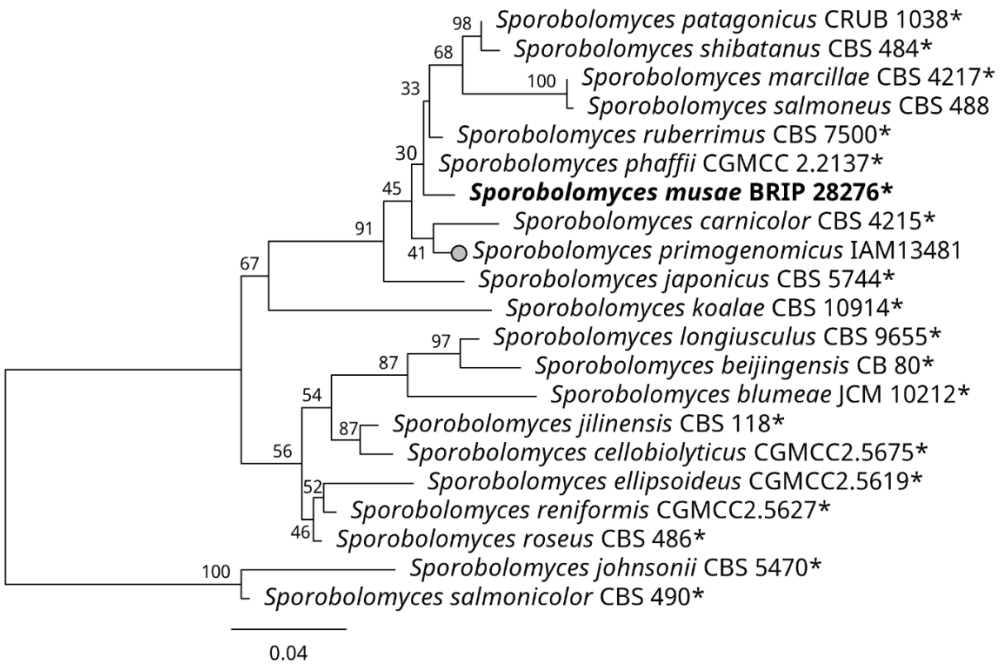
IF 558836

Holotype BRIP 28276 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA region describe the type BRIP 28276 and are available in GenBank under the accessions OK483138 (ITS region) and OK483137 (LSU). Sporobolomyces musae differs from S. phaffii (ex-type strain CGMCC 2.2137) by sequence comparison of the ITS region (GenBank NR_137660.1; Identities 535/540(99%); unique nucleotide at positions 130–131(TT), 344(T), 368(T), and 462(A)), and LSU (GenBank NG_068245.1; Identities 789/794(99%), Gaps 3/794; unique nucleotide at positions 406(C) and 470(T)). Sporobolomyces musae differs from S. rubberrimus (ex-type strain CBS 7500) by sequence comparison of the ITS region (GenBank AY015439.1, Identities 560/568(99%); unique nucleotide at positions 49(C), 80(A), 140–141(TT), 344(T), 361(C), 368(T), 462(A)), and LSU (GenBank NG_067252.1; Identities 519/539(99%), Gaps 1/539; unique nucleotide at positions 387(A), 389(C), 392–393(TT), 404(G), 406(C), 411(C), 424(T), 426–427(CC), 429(T), 470(T), 474–476(TGA), and 484–487(CTTA)).

Specimen examined: Australia, Queensland, Brisbane, St Lucia, on Musa acuminata, Nov. 1999, T.S. Marney, BRIP 28276.

Etymology: Named after Musa, the plant genus from which this fungus was isolated.



Phylogenetic tree based on a maximum likelihood analysis of a ITS region alignment of Sporobolomyces 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. Branch lengths are proportional to substitutions per site. Sporobolomyces johnsonii ex-type strain CBS 5470 and C. salmonicolor ex-type strain CBS 490 were used as the outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (*).

Synnemellisia acaciae Y.P. Tan, Bishop-Hurley, McTaggart & R.G. Shivas, sp. nov.

IF 558837

Holotype BRIP 71652 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA describe the ex-type strain BRIP 71652 are available in GenBank under the accessions OK342123 (ITS) and OK342124 (LSU). Synnemellisia acaciae differs from S. aurantia (ex-type strain COAD 2070) by sequence comparison of the ITS region (GenBank NR_154444.1; Identities 583/602(97%), Gaps 9/608; unique nucleotide positions 148–149(AC), 171(C), 403(C), 406(G), 463(C), 502–503(AC), 556–557(AC)), and LSU (GenBank NG_059728.1; Identities 830/845(98%), Gaps 15/845).

Specimen examined: Australia, Queensland, Wonga Beach, Dayman Point Boat Ramp, Mossman Daintree Road, on Acacia sp., 30 Aug. 2020, A.R. McTaggart, M.D.E. Shivas & R.G. Shivas, BRIP 71652.

Etymology: Named after Acacia, the host genus from which the holotype was isolated.

Synnemellisia urenae Y.P. Tan, Bishop-Hurley, McTaggart & R.G. Shivas, sp. nov.

IF 558838

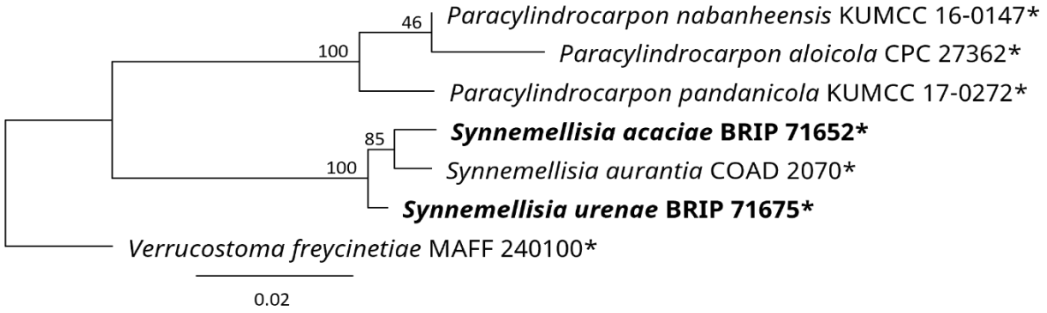
Holotype BRIP 71675 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA describe the ex-type strain BRIP 71675 and are available in GenBank under the accessions OK342124 (ITS) and OK342135 (LSU). *Synnemellisia urenae* differs from *S. aurantia* (ex-type strain COAD 2070) by sequence comparison of the ITS region (GenBank NR_154444.1; Identities 589/608(97%), Gaps 11/608; unique nucleotide at positions 87(A), 108(A), 121(T), 148(C), 186(T), 348(C), 500(A), and 557(C)), and LSU (GenBank NG_059728.1; Identities 829/845(98%), Gaps 15/845; unique nucleotide at position 644(G)). *Synnemellisia urenae* differs from *S. acaciae* (ex-type strain BRIP 71652) by sequence comparison of the ITS region (GenBank OK342123; Identities 586/602(97%), Gaps 2/608; unique nucleotide at positions 78(A), 109(A), 122(T), 137(A), 148(C), 187(A), 349(C), 403(T), 463(G), 503(A), 556–557(TT), and 559(C)), and LSU (GenBank OK342124; Identities 873/874(99%); unique nucleotide at position 644(G)).

Specimen examined: Australia, Queensland, East Russell, Krucknow Road, from stems of Urena lobata, 2 Sept. 2020, A.R. McTaggart, M.D.E. Shivas, R.G. Shivas, BRIP 71675.

Etymology: Named after Urena, the host genus from which the holotype was isolated.

Notes: Synnemellisia acacia and S. urenae are the second and third species of this bionectriaceous genus that occurs on dead stems.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (LSU and ITS) of Paracylindrocarpon and Synnemellisia 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. Branch lengths are proportional to substitutions per site. Verrucostoma freycinetiae ex-type strain MAFF 240100 was used as the outgroup. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (*).

Vishniacozyma insularis Y.P. Tan, Marney & R.G. Shivas, sp. nov.

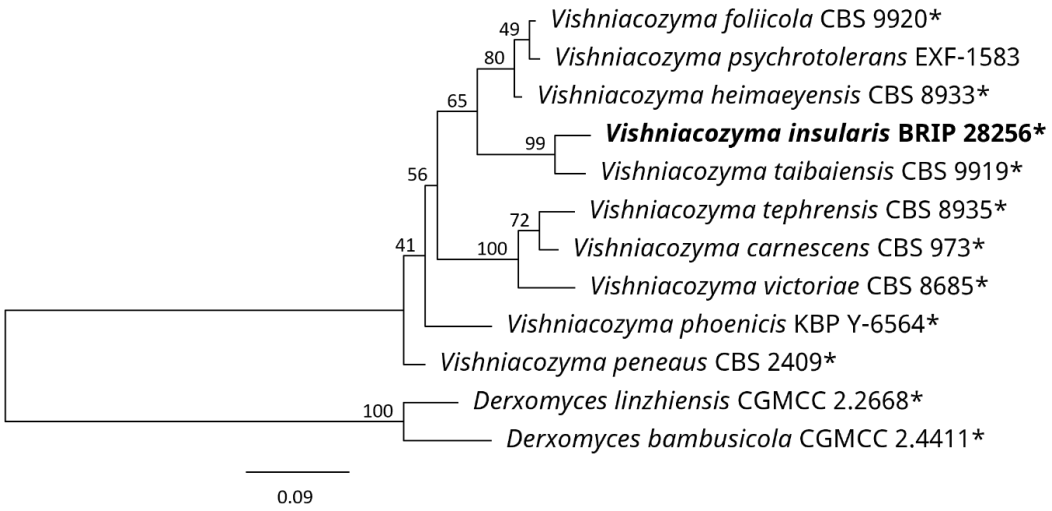
IF 558839

Holotype BRIP 28256 (permanently preserved in a metabolically inactive state)

Diagnosis: Sequence from the rDNA region describe the type BRIP 28256 and are available in GenBank under the accession OK442366 (ITS region). Vishniacozyma insularis differs from V. taibaiensis (ex-type strain 9919) by sequence comparison of the ITS region (GenBank NR_144810.1; Identities 482/511(94%), Gaps 6/511).

Specimen examined: Australia, Queensland, North Stradbroke Island, Brown Lake, from phylloplane of Banksia sp., 22 Nov. 2001, T.S. Marney, BRIP 28256.

Etymology: Name reflects the island location (= insularis, in Latin) where the fungus was collected.



Phylogenetic tree based on a maximum likelihood analysis of a ITS region alignment of Vishniacozyma 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. Branch lengths are proportional to substitutions per site. Derzomyces bambusicola ex-type strain CGMCC 2.4411 and C. linzhiensis ex-type strain CGMCC 2.2668 were used as the outgroup. Novel taxon is indicated in bold. Ex-type strains are marked with an asterisk (*).