

Nomenclatural novelties: Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson & R.G. Shivas

*Cladosporium heteropogonicola* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559375

Holotype BRIP 72465a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72465a and are available in GenBank under the accessions OL307932 (ITS region), OL332743 (actin), and OL332742 (tef1). *Cladosporium heteropogonicola* differs from *C. funiculosum* (ex-type strain CBS 12219) by sequence comparison of act (GenBank HM148583.1; Identities 208/217(96%); unique nucleotide at positions 53(T), 54(G), 55(A), 78(A), 99(C), 102(T), 163(A), 178(T), and 185(T)), and tef1 (GenBank HM148338.1; Identities 344/374(92%), Gaps 3/374). *Cladosporium heteropogonicola* differs from *C. pseudocladosporioides* (ex-type strain CBS 12219) by sequence comparison of act (GenBank HM148647.1; Identities 207/217(95%); unique nucleotide at positions 54(G), 82(T), 150(T), 154(A), 161(C), 162(C), 163(A), 173(G), 177(T), and 178(T)), and tef1 (GenBank HM148402.1; Identities 293/314(93%), Gaps 2/314).

Specimen examined: Australia, Queensland, Undara Volcanic National Park, on leaf of *Heteropogon* sp. (Poaceae), 21 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72465a.

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

*Cladosporium queenslandicum* Y.P. Tan & R.G. Shivas, sp. nov.

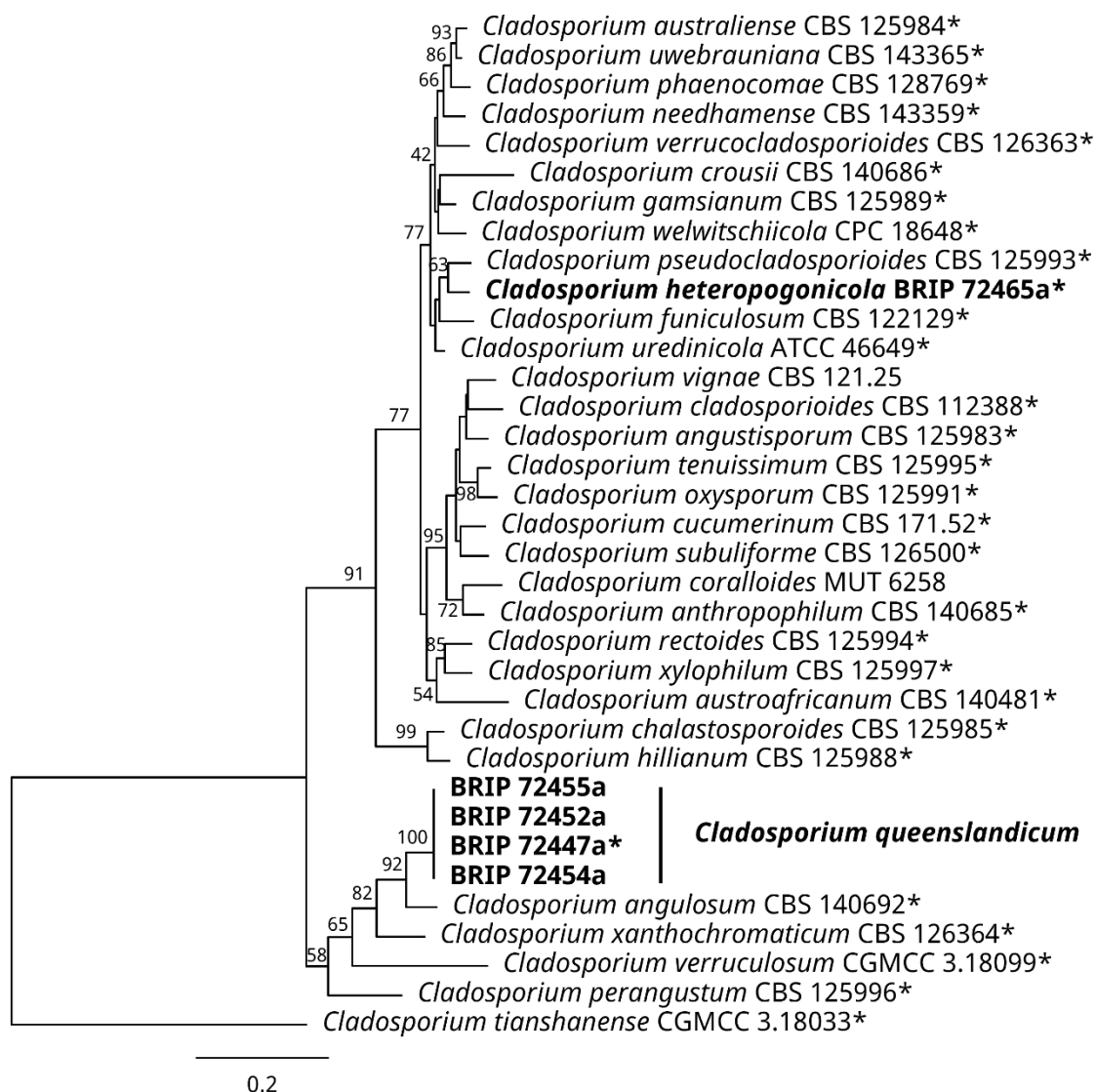
IF 559376

Holotype BRIP 72447a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72447a and are available in GenBank under the accessions OL307928 (ITS region), OL332736 (act), and OL332735 (tef1, translation elongation factor 1- $\alpha$ ). *Cladosporium queenslandicum* differs from *C. angulosum* (ex-type strain CBS 140692) by sequence comparison of act (GenBank LN834609.1; Identities 192/207(93%), Gaps 2/207; unique nucleotide at positions 70(C), 71(A), 86(T), 136(T), 141(C), 147(A), 160(G), 162(T), 163(C), 164(C), 167(C), 178(A), and 199(T)), and tef1 (GenBank LN834521.1; Identities 208/234(89%), Gaps 5/234(2%)).

Specimens examined: Australia, Queensland, Barwidgi, Ootann Road, leaf of *Arundinella nepalensis* (Poaceae), 20 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72447a; Petford, Burke Development Road, leaf of *Melinis repens* (Poaceae), 19 Apr. 2021, *ibid*, BRIP 72454a (ITS, and act sequences GenBank OL307930, and OL332739, respectively); *ibid*, *Rhynchospora heterochaeta* (Cyperaceae), *ibid*, BRIP 72452a (ITS, actin, and tef1 sequences GenBank OL307929, OL332738, and OL332737, respectively); Georgetown, sheath lesion of *Sorghum timorense* (Poaceae), 22 Apr. 2021, *ibid*, BRIP 72455a (ITS, actin, and tef1 sequences GenBank OL307931, OL332741, and OL332740, respectively).

Etymology: Named after the state of Queensland, where the fungus was collected.



Phylogenetic tree based on a maximum likelihood analysis of an alignment of concatenated multilocus alignment (act and tef1) from *Cladosporium cladosporioides* 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. *Cladosporium tianshanense* ex-type strain CGMCC 3.18033 was used as the outgroup. Novel Branch lengths are proportional to substitutions per site. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (\*).

*Curvularia angiewkeae* Y.P. Tan, sp. nov.

IF 559377

Holotype BRIP 72449a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72449a and are available in GenBank under the accessions OK638993 (ITS region), OK655929 (gapdh, glyceraldehyde-3-phosphate dehydrogenase), and OK655924 (tef1, translation elongation factor 1 alpha). *Curvularia angiewkeae* differs from *C. tuberculata* (ex-type strain CBS 146.63) by sequence comparison of the ITS region (GenBank NR\_138222; Identities 598/657(91%), Gaps 38/657(5%)), and gapdh (GenBank LT715830; Identities 457/489(93%), Gaps 6/489(1%)).

Specimen examined: Australia, Queensland, Petford, Burke Development Road, on leaf of *Scleria* sp. (Cyperaceae), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72449a.

Etymology: Named after Ang Siew Kee (1956–2009), beloved late mother of Yu Pei Tan.

*Curvularia chuasoengiae* Y.P. Tan, sp. nov.

IF 559378

Holotype BRIP 72482a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72482a and are available in GenBank under the accessions OK638997 (ITS region), and OK655933 (gapdh). *Curvularia chuasoengiae* differs from *Curvularia angiewkeae* (ex-type strain BRIP 72449a) by sequence comparison of the ITS region (GenBank OK638993; Identities 678/681(99%), Gaps 1/681; unique nucleotide at positions 505(T), and 613(T)), and gapdh (GenBank OK655929; Identities 558/567(98%); unique nucleotide at positions 177(G), 191(C), 201(C), 202(T), 204(C), 222(A), 230(T), 238(G), and 471(G)).

Specimen examined: Australia, Queensland, Petford, Burke Development Road, eye spot on leaf of *Scleria* sp. (Cyperaceae), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72482a.

Etymology: Named after Chua Soo Eng (1927–2018), beloved late grandmother of Yu Pei Tan.

*Curvularia frankliniae* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559379

Holotype BRIP 72476a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72476a and are available in GenBank under the accessions OK638995 (ITS region), OK655931 (gapdh), and OK655926 (tef1). *Curvularia frankliniae* differs from *C. eragrosticola* (ex-type strain BRIP 12538) by sequence comparison of the ITS region (GenBank NR\_158446.1; Identities 617/625(99%), Gaps 2/625; unique nucleotide at positions 198(T), 209(T), 217(T), 209(T), 612(T), and 642(T)), gapdh (GenBank MH433643.1; 507/541(94%), Gaps 2/541), and tef1 (GenBank MH433661.1; Identities 856/869(99%); unique nucleotide at positions 255(T), 320(C), 411(C), 416(C), 447(T), 450(T), 489(C), 513(T) 600(T), 612(A), 717(T), 807(C), and 870(T)).

Specimen examined: Australia, Queensland, Barwidgi, Ootann Road, on leaf of *Sorghum timorense* (Poaceae), 20 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72476a.

Etymology: Named after Rosalind Franklin (1920–1958), a chemist and X-ray crystallographer whose work at King's College London in 1951 was central to the discovery of the double helix structure of deoxyribonucleic acid.

*Curvularia hustoniae* Y.P. Tan, sp. nov.

IF 559380

Holotype BRIP 72486a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72486a and are available in GenBank under the accessions OK638999 (ITS region), OK655935 (gapdh), and OK655928 (tef1). *Curvularia hustoniae* differs from *C. akaiensis* (ex-type strain BRIP 16080) by sequence comparison of gapdh (GenBank KJ415407.1; Identities 529/535(99%); unique nucleotide at positions 69(G), 168(C), 174(T), 281(T), 335(G), and 356(T), and tef1 (GenBank KJ415453.1; Identities 800/804(99%); unique nucleotide at positions 152(T), 221(T), 620(T), and 731(T)). *Curvularia hustoniae* differs from *bothriochloae* (ex-type strain BRIP 12522) by sequence comparison of the ITS region (GenBank KJ415543.1; Identities 393/395(99%), Gaps 1/395; unique nucleotide at position 539(T)), gapdh (GenBank KJ415403.1; Identities 521/532(98%); unique nucleotide at positions 40(G), 53(A), 69(G),

159(C), 160(C), 173(T), 309(C), 336(G)357(T), and 462(C)), and *tef1* (GenBank KJ415449.1; Identities 799/804(99%); unique nucleotide at positions 152(T), 221(T), 316(C), 443(C), and 731(T)).

Specimen examined: Australia, Queensland, Hughenden, Flinders Highway, inflorescence of *Heteropogon triticeus* (Poaceae), 24 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72486a.

Etymology: Named after Wilhemina (Willa) M. Huston, an Australian molecular microbiologist in recognition on her research on human of intracellular pathogens, especially *Chlamydia* and *Legionella*, and mentorship of Australian microbiologists, including the lead author.

*Curvularia templetoniae* Y.P. Tan, sp. nov.

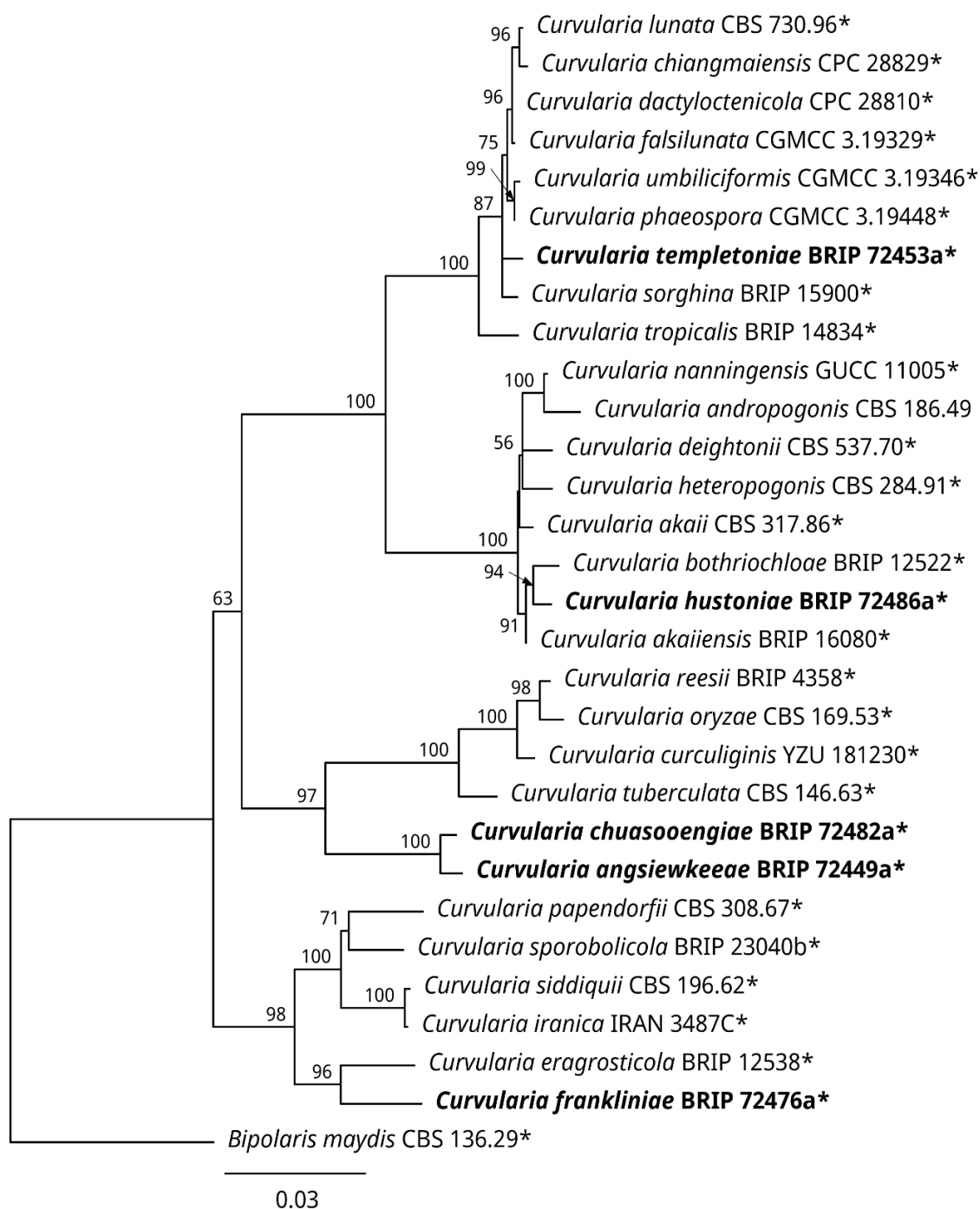
IF 559381

Holotype BRIP 72453a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72453a and are available in GenBank under the accessions OK442370 (ITS region), OK655930 (*gapdh*), and OK655925 (*tef1*). *Curvularia templetoniae* differs from *C. Chiangmaiensis* (ex-type strain CPC 28829) by sequence comparison of the ITS region (GenBank MF490814.1; unique nucleotide at position 279(T)), *gapdh* (GenBank MF490836.1; Identities 536/547(98%); unique nucleotide at positions 67(C), 172(C), 184(C), 204(T), 230(G), 250(T), 254(G), 513(T), 525(T), and 561(T)), and *tef1* (GenBank MF490857.1; Identities 887/893(99%); unique nucleotide at positions 321(C), 375(T), 378(T), 426(T), 564(T), and 851(T)). *Curvularia templetoniae* differs from *C. dactyloctenicola* (ex-type strain CPC 28810) by sequence comparison of *gapdh* (GenBank MF490837.1; Identities 542/550(99%); unique nucleotide at positions 67(C), 184(C), 204(T), 230(G), 254(G), 513(T), 525(T), and 561(T)), and *tef1* (GenBank MF490858.1; Identities 926/930(99%); unique nucleotide at positions 375(T), 378(T), 426(T), and 564(T)). *Curvularia templetoniae* differs from *C. falsilunata* (ex-type strain CGMCC 3.19329) by sequence comparison of *gapdh* (GenBank MN264093.1; Identities 543/552(98%); unique nucleotide at positions 67(C), 184(C), 204(T), 230(G), 254(G), 498(T), 513(T), 525(T), and 561(T)), and *tef1* (GenBank MN263954.1; Identities 922/926(99%); unique nucleotide at positions 375(T), 378(T), 426(T), and 564(T)). *Curvularia templetoniae* differs from *C. lunata* (ex-type CBS 730.96) by sequence comparison of *gapdh* (GenBank JX276441.1; Identities 472/482(98%); unique nucleotide at positions 172(C), 183(C), 204(T), 230(G), 249(T), 253(G), 513(T), 516(C), 525(T), and 561(T)), and *tef1* (GenBank JX266596.1; Identities 896/901(99%); unique nucleotide at positions 375(T), 378(T), 426(T), 564(T), and 732(C)). *Curvularia templetoniae* differs from *C. phaeospora* (ex-type strain CGMCC 3.19448) by sequence comparison of *gapdh* (GenBank MN264118.1; Identities 543/552(98%); unique nucleotide at positions 67(C), 133(G), 190(C), 204(T), 208(G), 254(G), 513(T) 525(T), and 561(T)), and *tef1* (GenBank MN263980.1; Identities 922/926(99%); unique nucleotide at positions 375(T), 378(T), 426(T), and 564(T)). *Curvularia templetoniae* differs from *C. sorghina* (ex-type strain BRIP 15900) by sequence comparison of *gapdh* (GenBank KJ415388.1; Identities 538/546(99%); unique nucleotide at positions 75(T), 178(C), 198(G), 204(T), 210(A), 513(T), 525(T), and 561(T)), and *tef1* (GenBank KJ415435.1; Identities 800/804(99%); unique nucleotide at positions 375(T), 378(T), 425(T), and 561(T)). *Curvularia templetoniae* differs from *C. umbiliciformis* (ex-type strain CGMCC 3.19346) by sequence comparison of *gapdh* (GenBank MN264142.1; Identities 543/552(98%); unique nucleotide at positions 67(C), 133(G), 190(C), 204(T), 208(G), 254(G), 513(T) 525(T), and 561(T)), and *tef1* (GenBank MN264004.1; Identities 920/926(99%); unique nucleotide at positions 375(T), 379(G), 426(T), 564(T), 591(C), and 603(C)).

Specimen examined: Australia, Queensland, Petford, Burke Development Road, on leaf of *Hyparrhenia hirta* (Poaceae), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72453a.

Etymology: Named after Jillian M. Templeton, an Australian microbiologist for her research into food safety pathogens, such as *Campylobacter* and *Salmonella*, and mentorship of the lead author.



Phylogenetic tree based on a maximum likelihood analysis of an alignment of concatenated multilocus alignment (ITS, gapdh and tef1) from phylogenetically related Curvularia 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. Bipolaris maydis ex-type strain CBS 136.29 was used as the outgroup. Novel Branch lengths are proportional to substitutions per site. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (\*).

*Epicoccum andropogonearum* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559382

Holotype BRIP 72450a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72450a and are available in GenBank under the accessions OK442369 (ITS region) and OK557942 (rpb2). *Epicoccum andropogonearum* differs from *E. camelliae* (ex-type strain CGMCC 3.18343) by sequence comparison of rpb2 (GenBank KY742170.1; Identities 586/596(98%); unique nucleotide at positions 183(T), 195(T), 231(T), 291(T), 333(T), 405(T), 468(T), 591(T), 678(T), and 720(G)). *Epicoccum andropogonearum* differs from *E. variabile* (ex-type strain CBS 119733) by sequence comparison of rpb2 (GenBank MT018103.1; Identities 587/596 (98%); unique nucleotide at positions 243(T), 291(T), 372(C), 405(T), 408(G), 468(T), 600(C), 601(A), and 678(T)). *Epicoccum andropogonearum* differs from *E. viticis* (ex-type strain CGMCC 3.18344) by sequence comparison of rpb2 (GenBank KY742186.1; Identities 587/596 (98%); unique nucleotide at positions 195(T), 291(T), 405(T), 468(T), 555(T), 591(T), 678(T), and 687(A)).

Specimens examined: Australia, Queensland, Petford, Burke Development Road, from leaf spot of *Cymbopogon refractus* (Poaceae), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72450a; *ibid*, from leaf spot of *Hyparrhenia hirta* sp. (Poaceae), *ibid*, culture BRIP 72453b (GenBank accessions OK442370 for ITS region, and OK557943 for rpb2).

Etymology: Named after the tribe, Andropogoneae, in which the host genera *Cymbopogon* and *Hyparrhenia* belong.

*Epicoccum chloridis* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559383

Holotype BRIP 72460a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72460a and are available in GenBank under the accessions OK442371 (ITS region) and OK557944 (rpb2). *Epicoccum chloridis* differs from *E. ovisporum* (ex-type strain CBS 180.80) by sequence comparison of ITS region (GenBank NR\_158228; Identities 468/483(97%), Gaps 4/483(0%); unique nucleotide at positions 238(C), 243(C), 249(G), 261(T), 300(A), 301(C), 522(C), 564(G), 582(T), 583(T) and 590(G)), and rpb2 (GenBank LT623252; Identities 881/936(94%), Gaps 1/936(0%)).

Specimen examined: Australia, Queensland, Hervey Range, from leaf spot of *Chloris gayana* (Poaceae), 25 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72460a.

Etymology: Named after *Chloris*, the plant from which this fungus was isolated.

*Epicoccum mnesitheae* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559384

Holotype BRIP 72463b (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nrDNA describe the type BRIP 72463b and are available in GenBank under the accessions OK442372 (ITS region) and OK557945 (rpb2). *Epicoccum mnesitheae* differs from *E. camelliae* (ex-type strain CGMCC 3.18343) by sequence comparison of ITS region (GenBank KY742091.1; Identities 476/479(99%); unique nucleotide at positions 301(C), 302(T), and 523(C)), and rpb2 (GenBank KY742170.1; Identities 582/596(98%); unique nucleotide at positions 174(T), 177(T), 201(T), 222(T), 225(T), 224(T), 400(A), 477(G), 549(T), 618(T), 619(G), 657(C), and 711(G)). *Epicoccum mnesitheae* differs from *E. variabile* (ex-type strain CBS 119733) by sequence comparison of the ITS region (GenBank MN973501.1; Identities 440/443(99%); unique nucleotide at positions 301–302(CT), and 523(C)), and rpb2 (GenBank MT018103.1; Identities 583/596(98%); unique nucleotide at positions 177(T), 186(C), 201(T), 225(T), 234(T), 363(C), 477(G), 549(T), 591(C), 592(A), 618(T), 619(G), and 657(C)). *Epicoccum mnesitheae* differs from *E. viticis* ex-type strain CGMCC 3.18344) by sequence comparison of ITS region (GenBank NR\_158267.1;

Identities 476/479(99%); unique nucleotide at positions 301(C), 302(T), and 523(C)), and rpb2 (GenBank KY742186; Identities 583/596(98%); unique nucleotide at positions 177(T), 201(T), 235(T), 477(G), 546(C), 549(T), 582(T), 618(T), 619(G), 657(C), 678(A), and 711(G)).

Specimen examined: Australia, Queensland, Mount Surprise, from leaf spot of *Mnesithea rottboellioides* (Poaceae), 21 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72463b.

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

*Epicoccum rhynchosporae* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559385

Holotype BRIP 72439a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nDNA describe the type BRIP 72439a and are available in GenBank under the accessions OK442367 (ITS region) and OK557940 (rpb2). *Epicoccum rhynchosporae* differs from *E. chloridis* (ex-type strain BRIP 72460a) by sequence comparison of ITS region (GenBank OK442371; unique nucleotide position 199(C)), and rpb2 (GenBank OK557944; Identities 923/930(99%); unique nucleotide at positions 51(T), 102(G), 111(G), 603(C), 678(T), and 753(T)).

Specimen examined: Australia, Queensland, Petford, Burke Development Road, from leaf spot of *Rhynchospora heterochaeta* (Cyperaceae), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72439a.

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

*Epicoccum sorghicola* Y.P. Tan & R.G. Shivas, sp. nov.

IF 559386

Holotype BRIP 72441a (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nDNA describe the type BRIP 72441a and are available in GenBank under the accessions OK442368 (ITS region) and OK557941 (rpb2). *Epicoccum sorghicola* differs from *E. hordei* (ex-type strain CGMCC 3.18360) by sequence comparison of the ITS region (GenBank NR\_158263.1; position 532 (T)), and rpb2 (GenBank MT018102.1; Identities 567/596 (95%)).

Specimen examined: Australia, Queensland, Georgetown, from sheath spot of *Sorghum timorense* (Poaceae), 22 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72441a.

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

*Epicoccum triodiae* Y.P. Tan & R.G. Shivas, sp. nov.

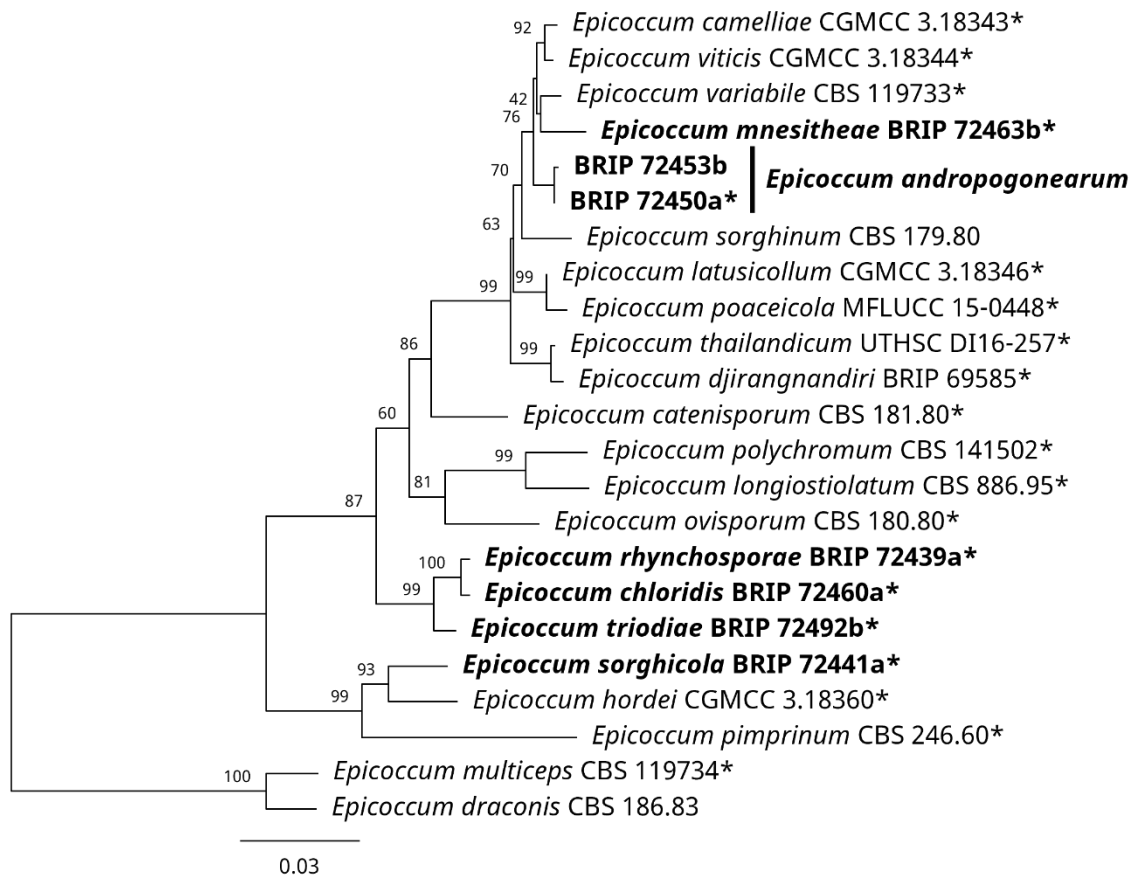
IF 559387

Holotype BRIP 72492b (permanently preserved in a metabolically inactive state)

Diagnosis: Sequences from the rDNA and nDNA describe the type BRIP 72492b and are available in GenBank under the accessions OK442373 (ITS region) and OK557946 (rpb2). *Epicoccum triodiae* differs from *E. chloridis* (ex-type strain BRIP 72460a) by sequence comparison of ITS region (GenBank OK442371; unique nucleotide at position 526(G)), and rpb2 (GenBank OK557944; Identities 921/936(98%); unique nucleotide at positions 107(G), 191(C), 201(T), 227(T), 296(T), 395(G), 398(T), 416(C), 539(T), 547(C), 608(C), 632(T), and 758(T)). *Epicoccum triodiae* differs from *E. rhynchosporae* (ex-type strain BRIP 72439a) by sequence comparison of ITS region (GenBank OK442367; Identities 579/581(99%); unique nucleotide at positions 198(T), and 526(G)), and rpb2 (GenBank OK557940; Identities 916/930(98%)).

Specimen examined: Australia, Queensland, Hughenden, from leaf spot of *Triodia pungens* (Poaceae), 24 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, BRIP 72492b.

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



Phylogenetic tree based on a maximum likelihood analysis of concatenated multilocus alignment (ITS and rpb2) from phylogenetically related *Epicoccum* 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. *Epicoccum draconis* strain CBS 186.83 and *E. multiceps* ex-type strain CBS 119734 were used as the outgroup. Novel taxa are indicated in bold. Ex-type strains are marked with an asterisk (\*).