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Nomenclatural novelties: Yu Pei Tan & Roger G. Shivas

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Cercophora trotae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

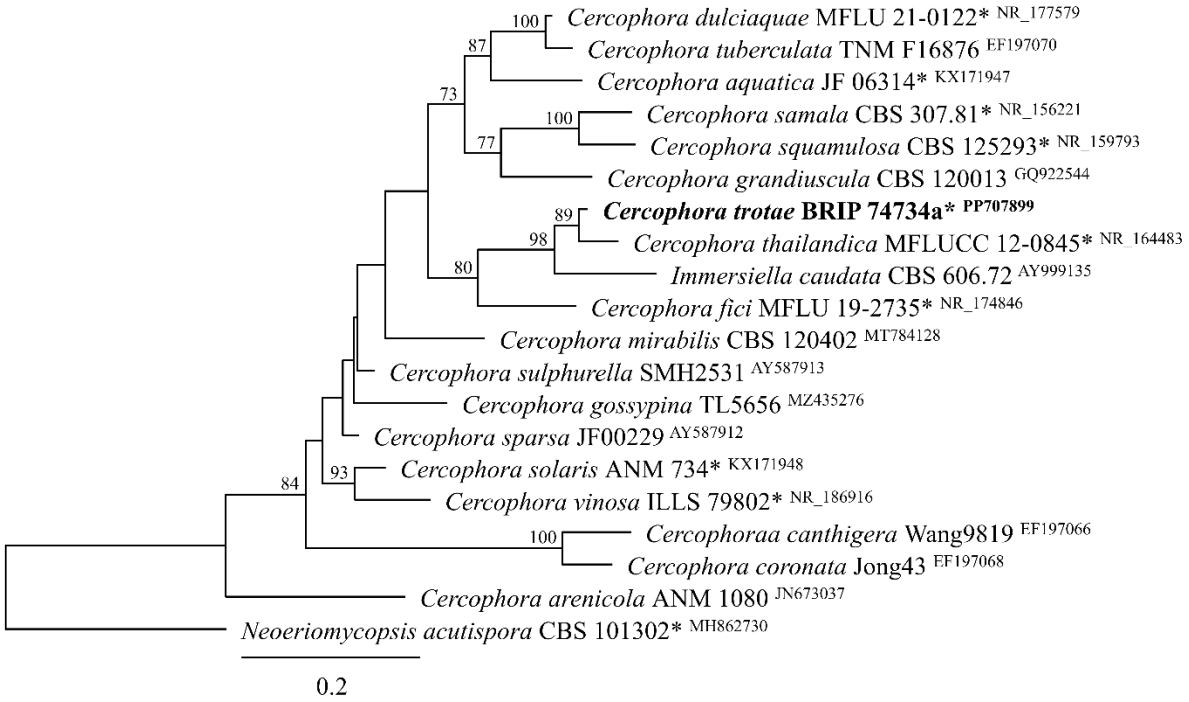
IF 902087

Classification — *Neoschizotheciaceae*, *Sordariales*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA describe *Cercophora trotae*, and are available under the accessions PP707899 (ITS), and PP707918 (LSU). *Cercophora trotae* differs from *C. thailandica* (ex-type strain MFLUCC 12-0845) by sequence comparison of the ITS region (GenBank NR_164483; Identities 351/365 (96%), three gaps; unique nucleotide at positions 261(G), 262(C), 288(C), 419(T), 470(C), 508(T), 514(C), 532(C), 566(G), 567(C), 597(A)), and LSU (GenBank KU863127; Identities 835/843 (99%), one gap; unique nucleotide at positions 146(C), 151(T), 465(C), 483(T), 501(G), 713(A), 755(A)). *Cercophora trotae* differs from *Immersiella caudata* (strain CBS 606.72) by sequence comparison of the ITS region (GenBank AY999135; Identities 490/535 (91%), 10 gaps; unique nucleotide at positions 196(C), 197(G), 201(C), 202(T), 203(A), 204(C), 226(T), 233(C), 248(A), 249(T), 261(G), 262(C), 268(A), 270(T), 271(A), 279(T), 282(C), 285(A), 287(T), 288(C), 292(A), 294(G), 296(T), 359(A), 419(T), 422(T), 424(T), 513(T), 549(T), 552(A), 579(G), 581(T), 597(A), 602(C), 604(C)), and LSU (GenBank AY999113; Identities 819/832 (98%), two gaps; unique nucleotide at positions 119(A), 151(T), 170(G), 180(T), 369(A), 449(C), 466(A), 472(T), 510(A), 713(A), 755(A)).

Specimen examined: Australia, Queensland, Bunya Mountains, *Sporobolus pyramidalis* (*Poaceae*), 24 Mar. 2022, *J.S. Vitelli, D. Officer, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 74734a permanently preserved in a metabolically inactive state).

Etymology: Named after Trota of Salerno (fl. 12th century), a medical practitioner and author, known for her practical texts on gynaecology and obstetrics. Trota also advocated the importance of exercise, a good diet, stress reduction, and cleanliness in daily life.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of ITS sequences from species of *Cercophora*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Neoeriomycopsis acutispora* (ex-type strain CBS 101302) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Collybiopsis tayloriae Y.P. Tan & Bishop-Hurley, *sp. nov.*

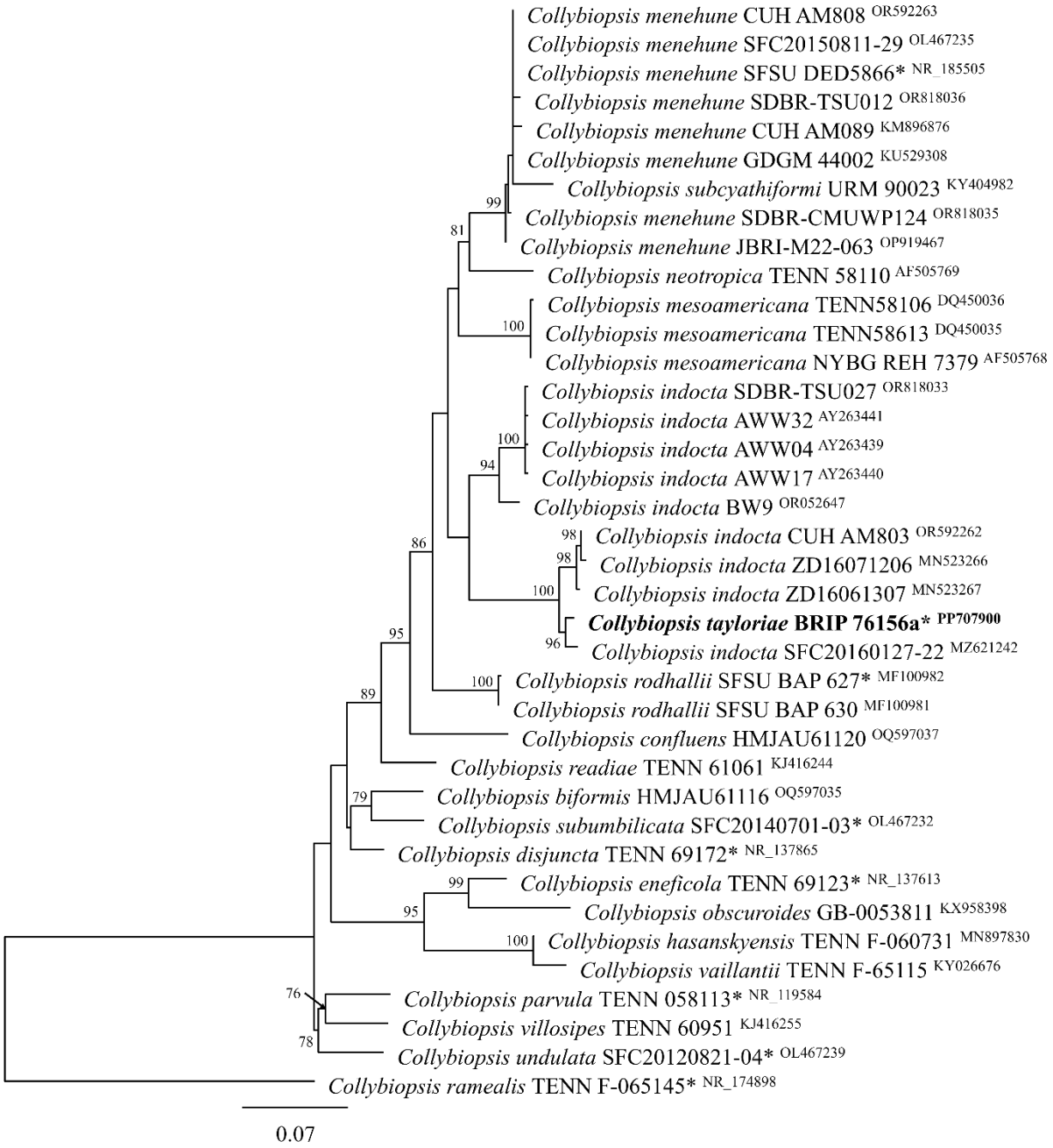
IF 902088

Classification — *Omphalotaceae, Agaricales, Agaricomycetes*

Diagnosis: Sequences from the rDNA describe *Collybiopsis tayloriae,* and are available under the accessions PP707900 (ITS), and PP707919 (LSU). *Collybiopsis tayloriae* differs from *C. indocta* (strain SFC20160127-22) by sequence comparison of the ITS region (GenBank MZ621242; Identities 693/701 (99%); unique nucleotide at positions 135(T), 226(T), 608(T), 610(C), 640(T), 706(T), 732(T), 755(T)).

Specimen examined: Australia, Queensland, Samford Valley, from dead branch of *Acacia* sp. (*Fabaceae*), 12 Sep. 2023, *S.L. Bishop-Hurley* (holotype BRIP 76156a permanently preserved in a metabolically inactive state).

Etymology: Named after Grace Marie Taylor (née Bulmer; 1930–1999), a mycologist and botanist, who described several new species of fungi, and illustrated books on New Zealand fungi and plants.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of ITS sequences from species of *Collybiopsis*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Collybiopsis ramealis* (type specimen TENN F-065145) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains or type specimens are marked by an asterisk (*).

Fusarium peseshetiae Y.P. Tan & Bishop-Hurley, *sp. nov.*

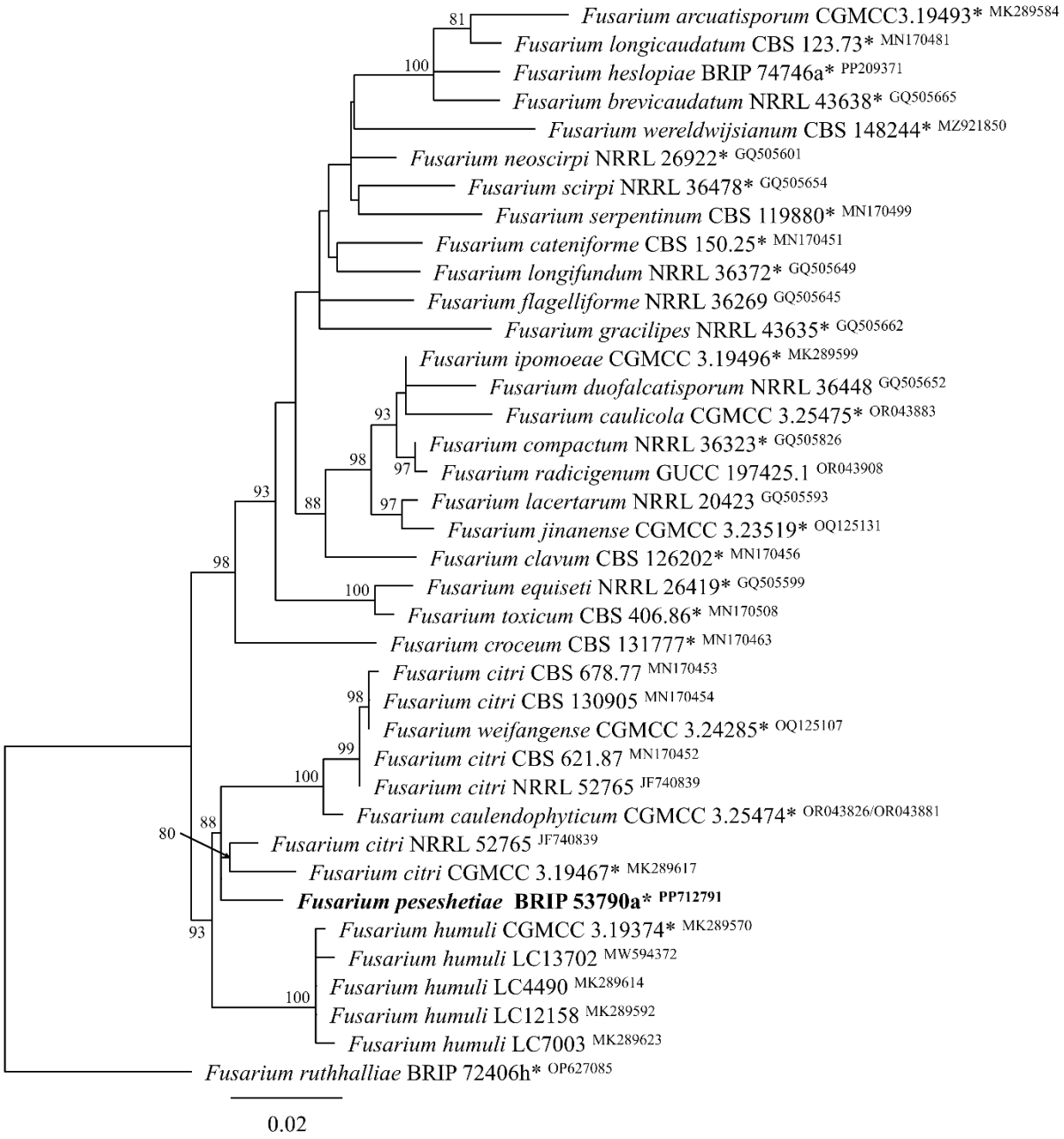
IF 902089

Classification — *Nectriaceae, Hypocreales, Sordariomycetes*

Diagnosis: Sequences from the nrDNA describe *Fusarium peseshetiae*, and are available under the accessions PP712790 (*rpb2*), and PP712791 (*tef1a*). *Fusarium peseshetiae* differs from *F. citri* (ex-type strain CGMCC 3.19467) by sequence comparison of *rpb2* (GenBank MK289771; Identities 826/837 (99%); unique nucleotide at positions 153(T), 359(T), 374(G), 383(T), 536(C), 389(A), 725(G), 743(C), 809(C), 824(C), 869(C)), and *tef1a* (GenBank MK289617; Identities 456/471 (97%), three gaps; unique nucleotide at positions 31(C), 41(T), 51(C), 56(T), 57(T), 69(C), 78(C), 247(C), 270(T), 404(A), 414(C), 420(T)). *Fusarium peseshetiae* differs from *F. citri* (ex-type strain CGMCC 3.19374) by sequence comparison of *rpb2* (GenBank MK289724; Identities 820/837 (98%); unique nucleotide at positions 251(A), 263(T), 302(C), 374(G), 494(G), 507(T), 512(A), 545(A), 578(T), 602(T), 614(G), 689(A), 743(C), 791(G), 824(C), 869(C)), and *tef1a* (GenBank MK289570; Identities 449/469 (96%), four gaps; unique nucleotide at positions 31(C), 41(T), 43(C), 44(A), 56(T), 78(C), 87(G), 134(T), 200(T), 394(G), 400(A), 406(T), 413(T), 416(T), 420(T), 422(C)).

Specimen examined: Australia, Queensland, Brisbane, from leaf blotch of *Aspidistra* sp. (*Asparagaceae*), 25 Jul. 1972, *H.J. Ogle* (holotype BRIP 53790a permanently preserved in a metabolically inactive state).

Etymology: Named after Peseshet (ca. 2686–2181 BCE), who is likely the earliest known female physician. Peseshet lived during the Fourth Dynasty of ancient Egypt, at the time of the building of the Great Pyramids.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of *tef1a* sequences from species of the *Fusarium incarnatum-equiseti* species complex. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Fusarium ruthhalliae* (ex-type strain BRIP 72406h) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Lecanicillium sotirae Y.P. Tan, Bishop-Hurley & Marney, *sp. nov.*

IF 902090

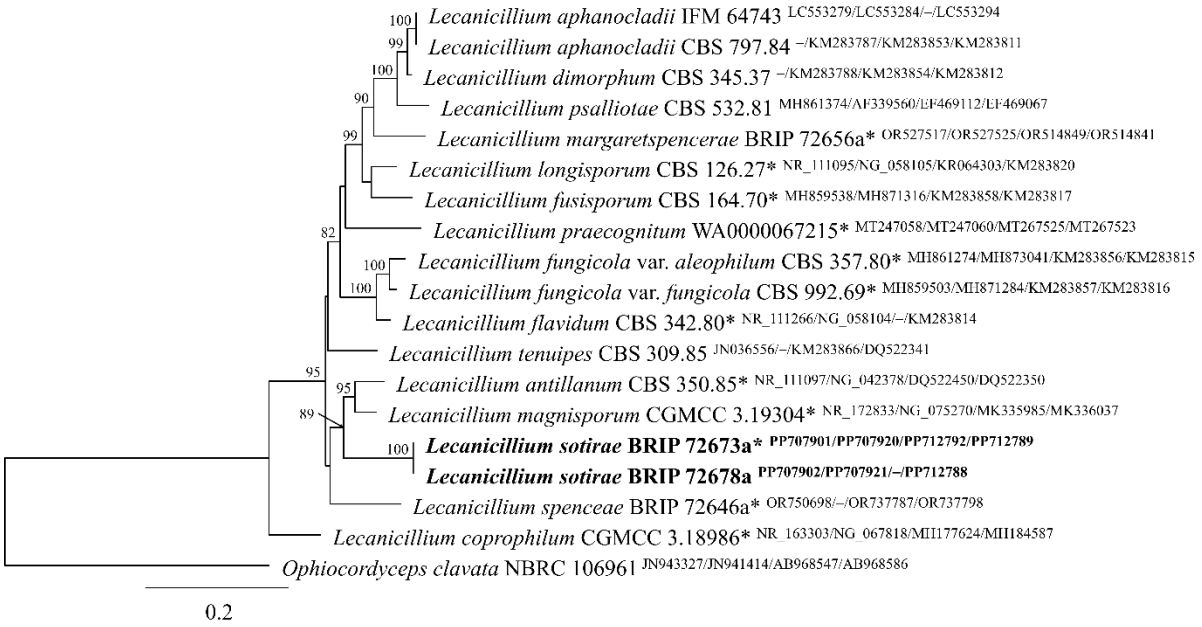
Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Lecanicillium sotirae*, and are available under the accessions PP707901 (ITS), PP707920 (LSU), PP712792 (*rpb2*), and PP712789 (*tef1a*). *Lecanicillium sotirae* differs from *L. antillanum* (ex-type strain CBS 350.85) by sequence comparison of the ITS region (GenBank NR_111097; Identities 503/534 (94%); eight gaps; unique nucleotide at positions 179(C), 194(T), 195(T), 196(T), 213(C), 216(T), 229(G), 232(A), 236(T), 240(T), 243(T), 257(A), 262(A), 297(A), 299(C), 311(A), 312(T), 509(C), 512(A), 605(T), 621(A), 623(C), 642(C)), and LSU (GenBank NG_042378; Identities 818/823 (99%); unique nucleotide at positions 90(A), 101(C), 181(T), 484(C)). *Lecanicillium sotirae* differs from *L. magnisporum* (ex-type strain CGMCC 3.19304) by sequence comparison of the ITS region (GenBank NR_172833; Identities 479/506 (95%), eight gaps; unique nucleotide at positions 179(C), 193(A), 194(T), 195(T), 213(C), 216(T), 229(G), 234(C), 236(T), 257(A), 262(A), 299(C), 313(A), 314(C), 331(C), 509(C), 512(A), 621(A), 623(C)), and LSU (GenBank NG_075270; Identities 829/836 (99%); unique nucleotide at positions 90(A), 101(C), 118(G), 465(A), 499(G), 509(C)).

Specimens examined: Australia, Queensland, Mission Beach, from an unidentified dead spider, 30 Apr. 2021, *T.S. Marney, Y.P. Tan, K.L. Bransgrove, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 72673a permanently preserved in a metabolically inactive state); ibid, from an unidentified dead spider, 30 Apr. 2021, *T.S. Marney, Y.P. Tan, K.L. Bransgrove, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas*, culture BRIP 72678a (ITS, LSU, and *tef1a* sequences GenBank PP707902, PP707921, and PP712788).

Etymology: Named after Sotira (fl. 1st century), a gynaecologist and obstetrician in ancient Greece.

Lecanicillium sotirae. Dead spiders from which cultures of *L. sotirae* were isolated (left, BRIP 72673a; right, BRIP 72678a). Scale bars = 1 mm.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of the combined ITS, LSU, *rpb2*, and *tef1* sequences from species of *Lecanicillium*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Ophiocordyceps clavata* (strain NBRC 106961) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/LSU/*rpb2*/*tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Neokalmusia deguarnae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

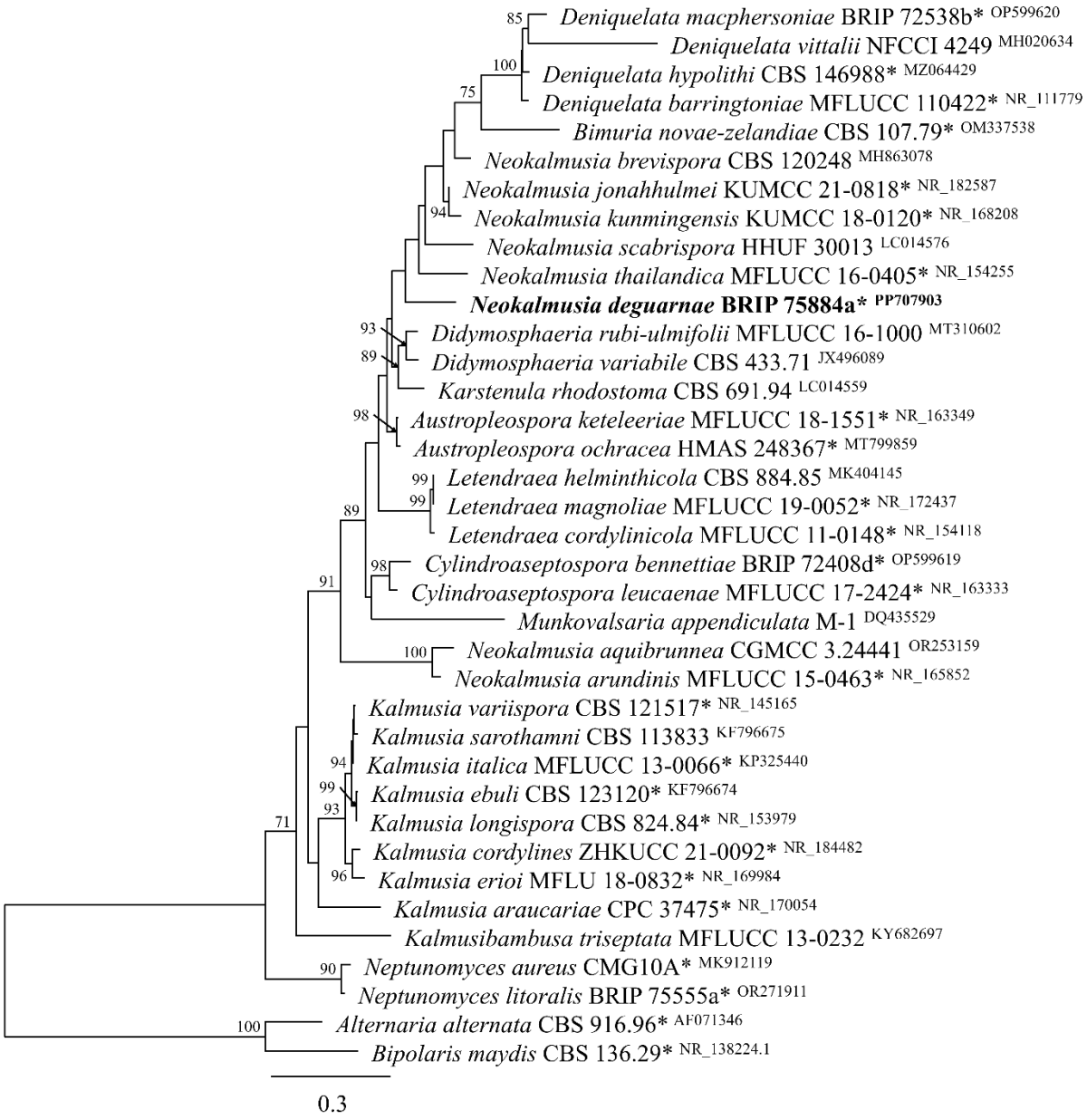
IF 902091

Classification — *Didymosphaeriaceae, Pleosporales, Dothideomycetes*

Diagnosis: Sequences from the rDNA *Neokalmusia deguarnae*, and are available in GenBank under the accessions PP707903 (ITS), and PP707922 (LSU). *Neokalmusia deguarnae* differs from *N. jonahhulmei* (ex-type strain KUMCC 21-0818) by sequence comparison of the ITS region (GenBank NR_182587; Identities 448/493 (91%), 15 gaps; (3%); unique nucleotide at positions 778(C), 780(T), 788(A), 801(T), 805(A), 810(A), 812(G), 817(A), 833(T), 838(A), 840(T), 846(T), 860(C), 888(T), 907(T), 1140(T), 1146(T), 1164(C), 1177(A), 1179(C), 1212(T), 1217(T), 1219(C), 1220(T), 1223(G), 1236(C), 1237(G), 1246(T), 1247(T), 1248(T)), and LSU (GenBank ON007039; Identities 837/868 (98%), three gaps; unique nucleotide at positions 21(C), 67(C), 69(T), 71(T), 72(T), 334(C), 388(G), 399(T), 406(T), 407(T), 428(T), 445(C), 465(T), 469(T), 473(T), 477(T), 478(T), 493(A), 494(C), 503(A), 507(A), 511(T), 515(A), 518(G), 542(T), 544(T), 673(T), 724(G)). *Neokalmusia deguarnae* differs from *N. brevispora* (ex-type strain HHUF 30016) by sequence comparison of the ITS region (GenBank NR_154262; Identities 429/467 (92%), 12 gaps (2%); unique nucleotide at positions 805(A), 810(A), 812(G), 817(A), 838(A), 840(T), 846(T), 847(C), 855(T), 860(C), 888(T), 926(A), 1146(T), 1148(C), 1164(C), 1177(A), 1212(T), 1217(T), 1219(C), 1220(T), 1223(G), 1236(C), 1237(G), 1246(T), 1247(T), 1248(T)). *Neokalmusia deguarnae* differs from *N. kunmingensis* (ex-type strain HKAS 101765) by sequence comparison of the ITS region (GenBank NR_168208; 429/470 (91%), 13 gaps (2%); unique nucleotide at positions 780(T), 782(T), 788(A), 801(T), 805(A), 810(A), 812(G), 817(A), 833(T), 838(A), 846(T), 860(C), 888(T), 907(T), 922(T), 1140(T), 1146(T), 1148(C), 1164(C), 1177(A), 1179(C), 1212(T), 1217(T), 1219(C), 1220(T), 1223(G), 1236(C), 1237(G)), and LSU (GenBank NG_068857; Identities 813/842 (97%), three gaps; unique nucleotide at positions 67(C), 69(T), 72(T), 334(C), 388(G), 399(T), 406(T), 407(T), 418(T), 445(C), 446(T), 465(T), 469(T), 473(T), 477(T), 478(T), 493(A), 494(C), 503(A), 507(A), 511(T), 515(A), 518(G), 542(T), 544(T), 673(T), 680(T)).

Specimen examined: Australia, Queensland, Einasleigh Forsayth Road, from the roots of *Panicum* sp. (*Poaceae*), 24 Apr. 2023, *Y.P. Tan, M. Sudsanguan, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 75884a permanently preserved in a metabolically inactive state).

Etymology: Named after Rebecca de Guarna (fl. 13th century), a physician and surgeon, who wrote medical texts on fevers, urine, and embryos.



Phylogenetic tree based on the maximum likelihood analysis (ML) of the alignment of ITS sequences from related species of *Didymosphaeriaceae*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Alternaria alternata* (ex-type strain CBS 916.96) and *Bipolaris maydis* (ex-type strain CBS 136.29) were used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Nigrospora mercuriadeae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov*.

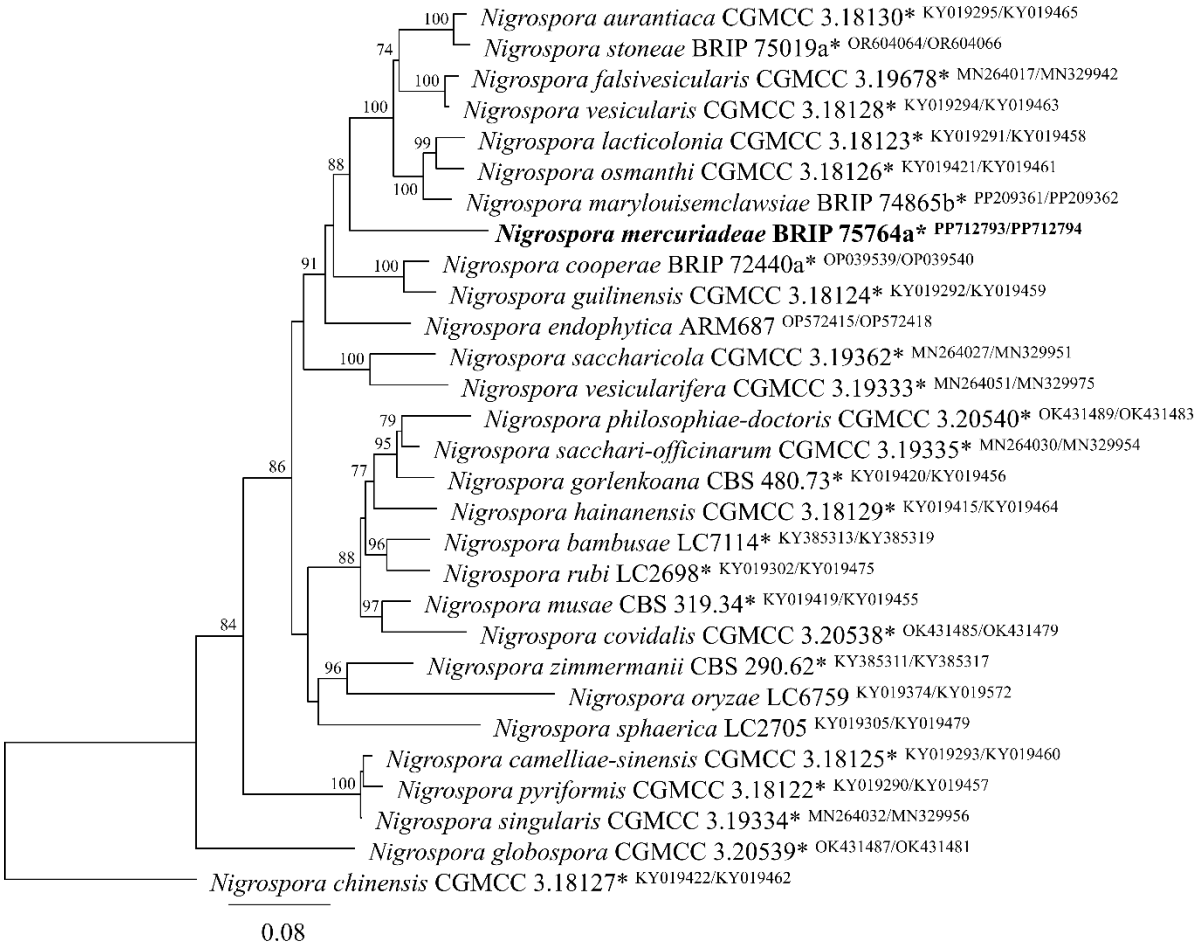
IF 902092

Classification — *Incertae sedis, Incertae sedis, Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Nigrospora mercuriadeae*, and are available in GenBank under the accessions PP707904 (ITS), PP712793 (*tef1a*), and PP712794 (*tub2*). *Nigrospora mercuriadeae* differs from *N. lacticolonia* (ex-type strain CGMCC 3.18123) by sequence comparison of the ITS region (GenBank NR_153471; Identities 492/508 (97%), eight gaps; unique nucleotide at positions 258(C), 497(A), 498(A), 513(T), 561(C), 562(T), 610(C), 611(C)), *tef1a* (GenBank KY019291; Identities 231/256 (90%), nine gaps; unique nucleotide at positions 84(C), 185(C), 190(G), 191(C), 194(T), 195(A), 196(C), 203(T), 206(T), 212(G), 213(G), 218(T), 221(A), 234(A), 238(A), 261(C)), and *tub2* (GenBank KY019458; Identities 361/395 (91%), 13 gaps; (3%); unique nucleotide at positions 420(G), 431(G), 441(T), 442(T), 465(G), 485(G), 486(C), 509(G), 512(C), 518(G), 519(G), 526(G), 532(C), 589(C), 598(G), 616(T), 649(T), 682(C), 721(T)). *Nigrospora mercuriadeae* differs from *N. osmanthi* (ex-type strain CGMCC 3.18126) by sequence comparison of the ITS region (GenBank NR_153474; Identities 500/516 (97%); eight gaps (1%); unique nucleotide at positions 258(C), 497(A), 498(A), 513(T), 561(C), 562(T), 610(C), 611(C)), *tef1a* (GenBank KY019421; Identities 235/261 (90%), six gaps (2%); unique nucleotide at positions 29(G), 30(G), 31(T), 35(A), 84(C), 186(G), 188(C), 191(C), 192(T), 195(A), 204(T), 207(A), 208(G), 213(G), 218(T), 219(G), 221(A), 234(A), 238(A), 261(C)), and *tub2* (GenBank KY019461; Identities 281/416 (92%), nine gaps (2%); unique nucleotide at positions 413(C), 416(G), 420(G), 431(G), 441(T), 442(T), 452(C), 465(G), 469(G), 485(G), 486(C), 489(G), 491(A), 500(C), 504(A), 518(G), 519(G), 526(G), 532(C), 550(C), 589(C), 598(G), 616(T), 661(C), 721(T)). *Nigrospora mercuriadeae* differs from *N. marylouisemclawsiae* (ex-type strain BRIP 74865b) by sequence comparison of the ITS region (GenBank PP125567; Identities 587/602 (98%), eight gaps; unique nucleotide at positions 258(C), 497(A), 498(A), 493(T), 561(C), 562(T), 575(C)).

Specimen: Australia, Queensland, Ingham, from necrotic leaf spot of *Chromolaena odorata* (*Asteraceae*), 20 Feb. 2023, *K. Pukallus* (holotype BRIP 75764a permanently preserved in a metabolically inactive state).

Etymology: Named after Mercuriade of Salerno (fl. 14th century), a physician and surgeon, who helped usher in a medical renaissance in Europe.



Phylogenetic tree based on a maximum likelihood analysis (ML) of the concatenated alignment of *tef1a*, and *tub2* sequences from species of *Nigrospora*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Nigrospora chinensis* (ex-type strain CGMCC 3.18127) was used as the outgroup. GenBank accession numbers are indicated (superscript *tef1a*/*tub2*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Phaeoseptoriella edithcowaniae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

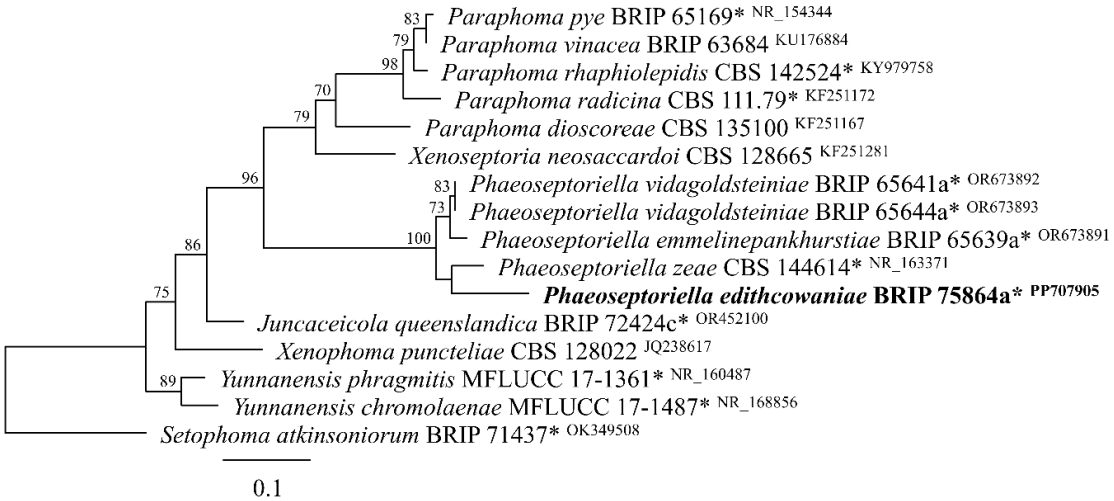
IF 902093

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA describe *Phaeoseptoriella edithcowaniae*, and are available in GenBank under the accessions PP707905 (ITS), and PP708933 (LSU). *Phaeoseptoriella edithcowaniae* differs from *P. emmelinepankhurstiae* (ex-type strain BRIP 65639a) by sequence comparison of the ITS region (GenBank OR673891; Identities 560/623 (90%), 31 gaps (4%); unique nucleotide at positions 172(G), 173(C), 175(A), 176(A), 183(A), 190(G), 198(A), 228(A), 229(T), 230(A), 264(T), 265(G), 266(T), 286(T), 287(G), 303(A), 304(C), 308(A), 505(T), 521(A), 522(C), 524(G), 526(C), 538(G), 539(G), 544(G), 571(T), 583(T), 589(G), 594(C), 595(A), 608(T)). *Phaeoseptoriella edithcowaniae* differs from *P. vidagoldsteiniae* (ex-type strain BRIP 65641a) by sequence comparison of the ITS region (GenBank OR673892; Identities 583/643 (91%), 29 gaps (4%); unique nucleotide at positions 172(G), 173(C), 175(A), 176(A), 195(A), 198(A), 199(T), 228(T), 229(T), 230(A), 265(G), 266(T), 286(T), 287(G), 302(A), 304(C), 305(A), 307(G), 308(A), 505(T), 521(A), 525(G), 526(C), 527(C), 538(G), 539(G), 544(G), 571(T), 583(T), 594(C), 595(A)). *Phaeoseptoriella edithcowaniae* differs from *P. zeae* (ex-type strain CBS 144614) by sequence comparison of the ITS region (GenBank NR_163371; Identities 429/464 (92%), seven gaps; unique nucleotide at positions 228(T), 229(T), 230(A), 245(C), 247(T), 249(C), 251(A), 256(C), 264(T), 265(G), 286(T), 287(G), 305(A), 307(G), 308(A), 505(T), 517(A), 523(G), 526(C), 527(C), 538(G), 539(G), 544(G), 571(T), 583(T), 594(C), 595(A), 628(C)).

Specimen: Australia, Queensland, Herberton, from leaf spot on *Heteropogon triticeus* (*Poaceae*), 23 Apr. 2023, *Y.P. Tan, M. Sudsanguan, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 75864a permanently preserved in a metabolically inactive state).

Etymology: Named after Edith Dircksey Cowan (née Brown; 1861–1932), a social worker, who fought for reforms that enhanced the rights and welfare of women and children. Edith Cowan was the first woman to serve as a member of parliament of an Australian parliament.



Phylogenetic tree based on the maximum likelihood analysis (ML) of the alignment of ITS sequences from related species of *Phaeosphaeriaceae*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Setophoma atkinsoniorum* (ex-type strain BRIP 71437a) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Poaceascoma calendae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

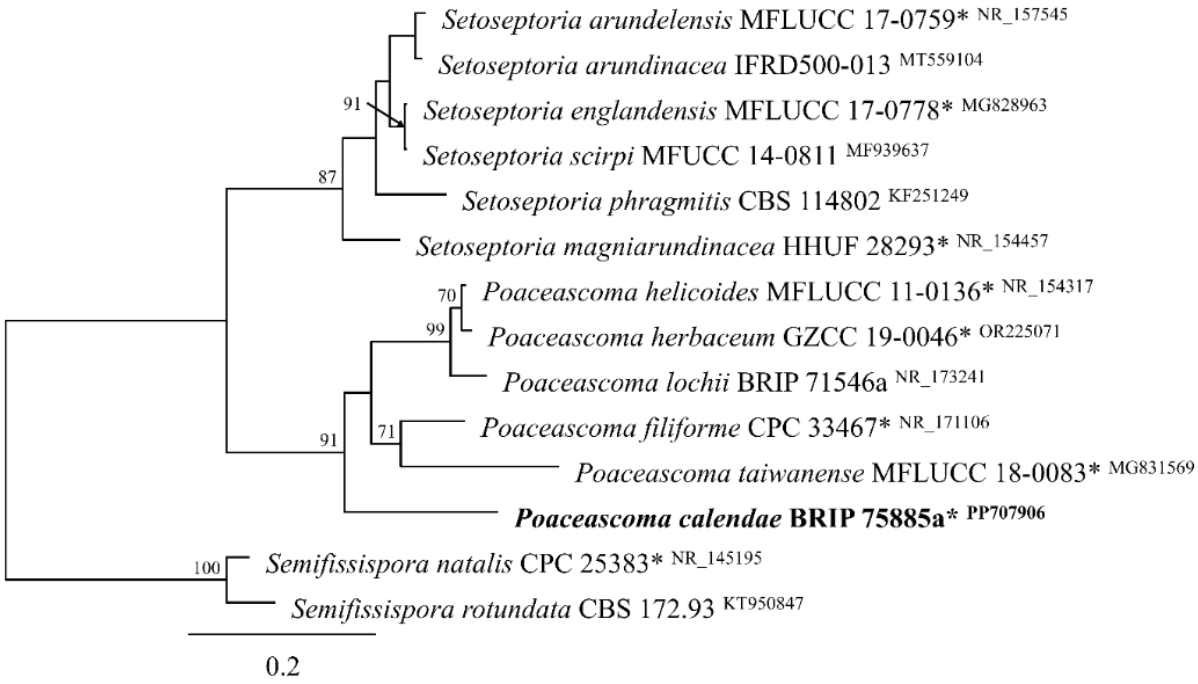
IF 902094

Classification — *Lentitheciaceae, Pleosporales, Dothideomycetes*

Diagnosis: Sequences from the rDNA *Poaceascoma salpeae*, and are available in GenBank under the accessions PP707906 (ITS), and PP707923 (LSU). *Poaceascoma salpeae* differs from *Po. filiforme* (ex-type strain CPC 33467) by sequence comparison of the ITS region (GenBank NR_171106; Identities 505/594 (85%), 34 gaps (5%); unique nucleotide at positions 152(G), 165(T), 168(T), 182(G), 199(C), 205(C), 206(G), 222(C), 228(C), 232(T), 235(C), 237(G), 243(A), 249(A), 255(T), 260(T), 266(C), 272(G), 274(A), 281(C), 282(A), 287(C), 417(C), 426(G), 453(C), 469(C), 470(C), 478(C), 481(T), 483(G), 491(C), 492(G), 495(G), 498(G), 501(C), 503(A), 518(C), 520(T), 532(G), 534(G), 555(G), 565(G), 591(G), 592(C), 596(C), 599(A), 602(G), 606(A), 609(G), 610(T), 611(C), 615(G), 616(C), 634(A), 639(C)), and LSU (GenBank MT373345; Identities 828/863 (96%), five gaps; unique nucleotide at positions 186(A), 262(C), 277(C), 388(G), 395(C), 413(C), 414(C), 415(G), 416(C), 418(T), 470(G), 486(C), 492(T), 501(G), 518(A), 520(G), 526(T), 532(C), 652(T), 682(C), 687(C)). *Poaceascoma salpeae* differs from *Po. helicoides* (ex-type strain MFLUCC 11-0136; Identities 331/371 (89%), 16 gaps (4%); unique nucleotide at positions 147(G), 148(G), 150(G), 151(T), 171(G), 230(T), 232(T), 233(T), 235(C), 244(A), 247(C), 248(A), 249(A), 251(C), 255(T), 258(T), 272(G), 274(A), 275(A), 284(A), 287(C), 417(C), 426(G), 453(C)), and LSU (GenBank NG_059565; Identities 765/796 (96%), two gaps; unique nucleotide at positions 80(C), 82(C), 85(G), 119(C), 122(G), 126(G), 141(C), 153(A), 191(C), 194(G), 276(C), 277(C), 388(G), 395(C), 413(C), 414(C), 415(G), 416(C), 418(T), 470(G), 486(C), 501(G), 518(A), 520(G), 526(T), 532(C), 682(C), 683(G), 687(C)).

Specimen examined: Australia, Queensland, Einasleigh Forsayth Road, from the roots of *Panicum* sp. (*Poaceae*), 24 Apr. 2023, *Y.P. Tan, M. Sudsanguan, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 75885a permanently preserved in a metabolically inactive state).

Etymology: Named after Constance Calenda (fl. 15th century), a surgeon who specialised in the diseases of the eye.



Phylogenetic tree based on the maximum likelihood analysis (ML) of the alignment of ITS sequences from related species of *Lentitheciaceae*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Semifissispora natalis* (ex-type strain CPC 25383) and *S. rotundata* (strain CBS 172.93) were used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Zasmidium morrisoniae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 902095

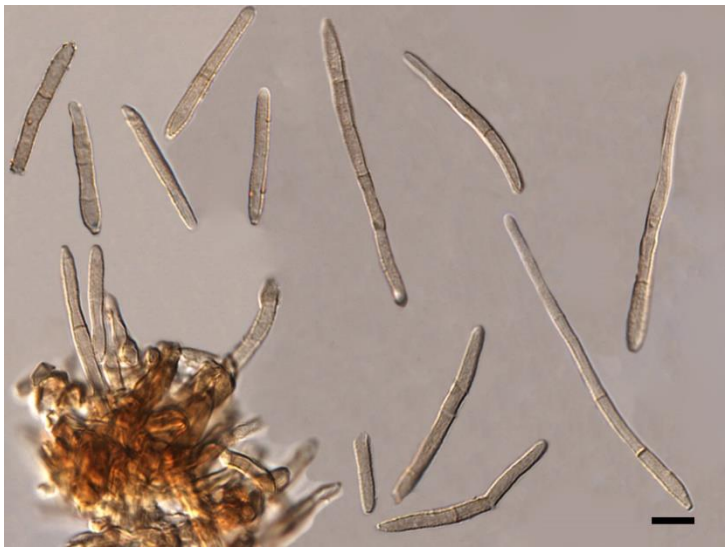
Classification — *Mycosphaerellaceae, Mycosphaerellales, Dothideomycetes*

Diagnosis: Sequences from the rDNA and nrDNA *Zasmidium morrisoniae*, and are available in GenBank under the accessions PP707907 (ITS), PP707924 (LSU), PP712795 (actin), PP712796 (*rpb2*), and PP712797 (*tef1a*). *Zasmidium morrisoniae* differs from *Z. musae* (ex-type strain CBS 122477) by sequence comparison of the ITS region (GenBank NR_176687; Identities 503/513 (98%), one gap; unique nucleotide at positions 142(C), 184(T), 278(C), 279(G), 420(G), 487(G), 524(C), 526(C), 588(T)), and actin (GenBank EU514346; Identities 185/195 (95%); unique nucleotide at positions 53(A), 63(C), 64(T), 75(C), 95(G), 139(T), 142(T), 150(C), 151(T), 158(T)).

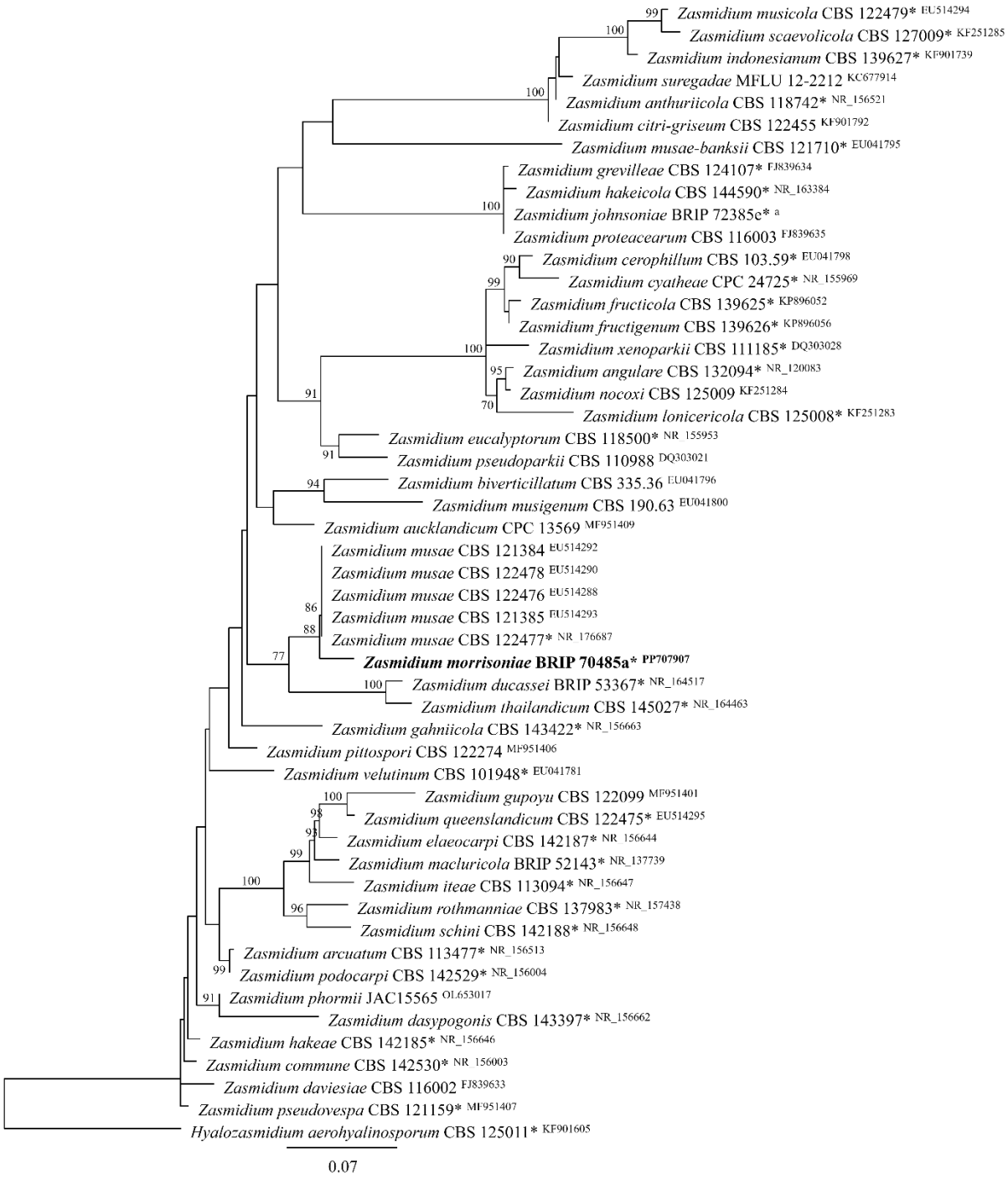
Leaf spots on *Freycinetia scandens*; amphigenous and extending through to the opposite side of the leaf, circular to subcircular or semicircular at leaf edge, 1–4 cm diam, grey in the central necrotic part and pale brown towards the margins, with diffuse water-soaked pale green to pale yellow haloes up to 1 cm wide. *Mycelium* internal. *Stromata* amphigenous, abundant, emergent from stomata, 40–80 µm diam, subglobose, dark reddish brown. *Conidiophores* in loose fascicles, arising from stromata, unbranched, erect, straight or curved, often geniculate, subcylindrical, 15–40 × 3–4 µm, 1–4 septate, brown, smooth. *Conidiogenous cells* integrated, terminal, proliferation sympodial, cylindrical, often geniculate, 15–25 × 2.5–3.5 µm, with thickened darkened loci. *Conidia* solitary, cylindrical, straight or curved, 12–90 × 2–3 µm, pale brown, finely verruculose, 0–4 septate; hila thickened and darkened, 1–1.5 µm diam.

Specimens examined: Australia, Queensland, Lake Eacham, on leaves of *Freycinetia scandens* (*Pandanaceae*), 16 May 2019, *J.M. Morrison* (holotype BRIP 70485a permanently preserved in a metabolically inactive state), herbarium specimen BRIP 74671a; Mossman, on leaves of *F. scandens* (*Pandanaceae*), 27 Jul. 1993, *R.G. Shivas*, herbarium specimen BRIP 21780a.

Etymology: Named after the collector, Jennifer Morrison, a plant pathologist who noticed the leaf spots, and isolated the fungus during a field trip in far northern Queensland.



Zasmidium morrisoniae (BRIP 74671a). Stroma and conidiophores. Scale bar = 10 µm.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of ITS sequences from related species of *Zasmidium*. The ML analysis was executed on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/) based on the GTR substitution model with gamma-distribution rate variation. *Hyalozasmidium aerohyalinosporum* (ex-type strain CBS 125011) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).