

Index of Australian Fungi no. 19 (ISBN 978-0-6458841-8-0)

DOI: 10.5281/zenodo.1000557

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

Effectively published 20/10/2023 22:15:00

Cippumomyces romamitchelliae Y.P. Tan, *sp. nov.*

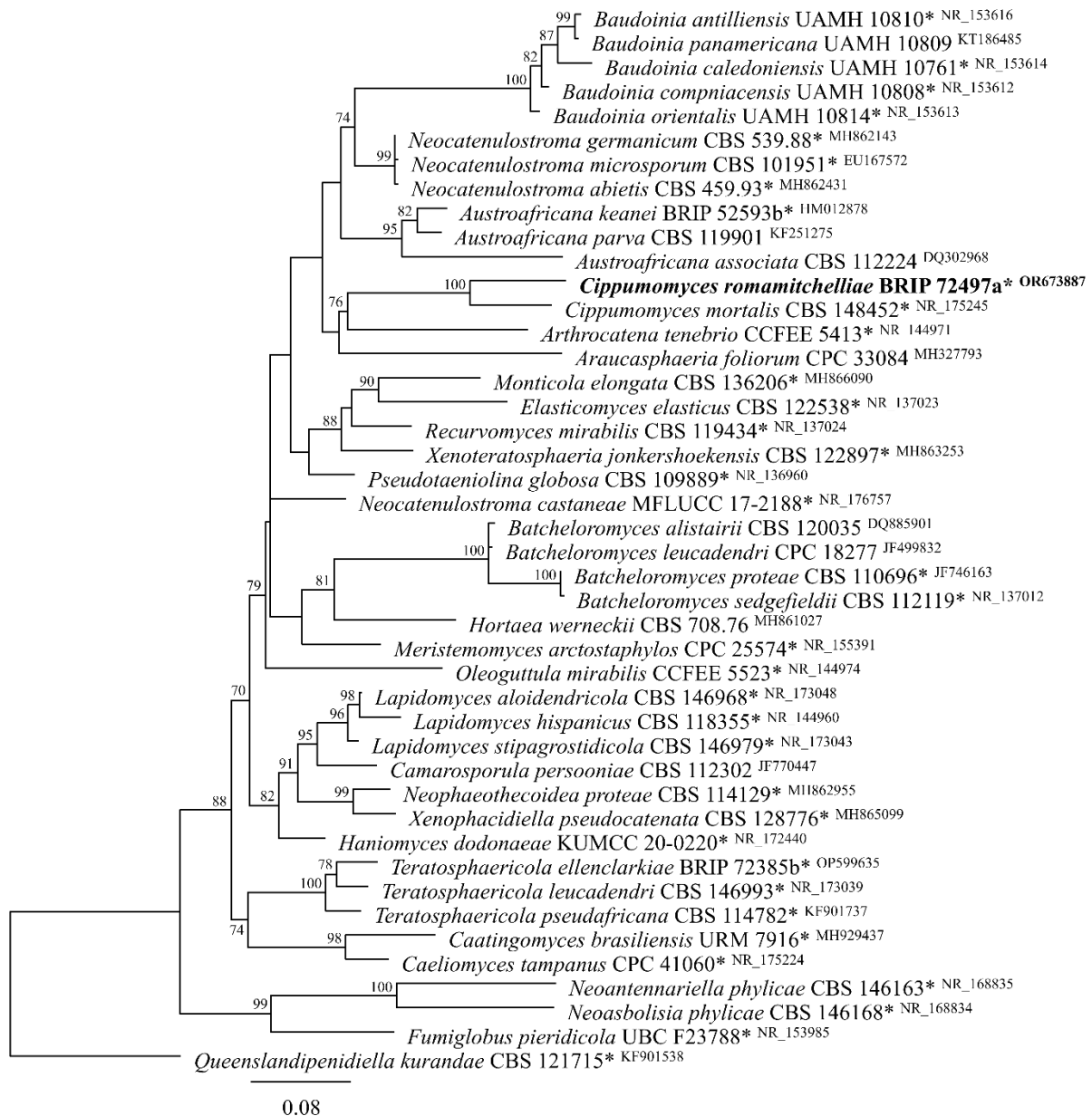
IF 901283

Classification — *Neoantennariellaceae*, *Capnodiales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA describe *Cippumomyces romamitchelliae* and are available under the accessions OR673887 (ITS) and OR673896 (LSU). *Cippumomyces romamitchelliae* differs from *C. mortalis* (ex-type strain CBS 148452) by sequence comparison of the ITS region (GenBank NR_175245; Identities 492/541 (91%), 13 gaps; unique nucleotide at positions 185(C), 186(C), 187(A), 188(A), 212(G), 215(T), 216(G), 235(T), 258(T), 260(T), 291(T), 296(T), 297(T), 448(T), 461(A), 501(A), 537(T), 538(A), 542(T), 543(C), 545(T), 555(C), 556(A), 557(T), 559(T), 578(T), 580(C), 581(A), 591(G), 592(T), 603(T), 604(G), 620(C), 621(T), 626(T), 628(A)), and LSU (GenBank NG_081351; Identities 702/726 (97%), four gaps; unique nucleotide at positions 86(G), 132(T), 181(T), 189(A), 193(G), 259(G), 400(A), 423(T), 428(T), 460(T), 461(C), 507(A), 510(G), 511(C), 515(A), 517(G), 518(A), 519(C), 525(T), 640(G)).

Specimen examined: Australia, Queensland, Petford, from soil, 19 Apr. 2021, *Y.P. Tan* (holotype BRIP 72497a permanently preserved in a metabolically inactive state).

Etymology: Named after Roma Flinders Mitchell (1913–2000), the first woman to hold a number of positions in Australia: the first woman to be a Queen’s Counsel, the first woman judge, the first woman chancellor of an Australian university, and the first woman Governor of an Australian state.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region sequences from related species of *Capnodiales*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Queenslandipenediella kurandae* (ex-type strain CBS 121715) 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 (*).

Hypoxylon judithwrightiae Y.P. Tan, Bishop-Hurley & Marney, *sp. nov.*

IF 901284

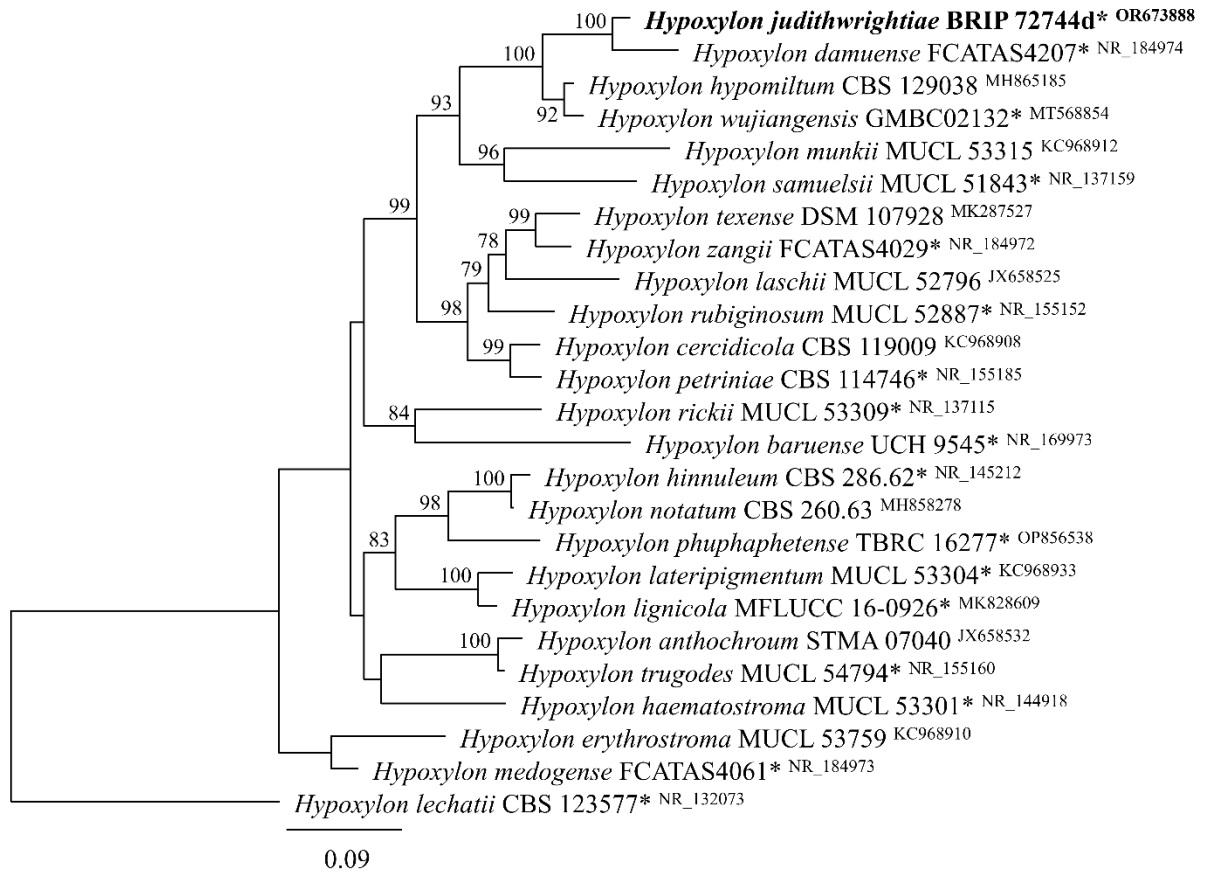
Classification — *Hypoxylaceae*, *Xylariales*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA describe *Hypoxylon judithwrightiae* and is available under the accessions OR673888 (ITS), and OR673897 (LSU). *Hypoxylon judithwrightiae* differs from *H. damuense* (ex-type strain FCATAS4207) by sequence comparison of the ITS region (GenBank NR_184974; Identities 560/592 (95%), five gaps; unique nucleotide at positions 227(T), 230(A), 233(C), 236(C), 242(G), 257(T), 258(T), 274(A), 288(T), 289(A), 300(C), 303(C), 305(C), 310(A), 311(T), 327(C), 328(A), 330(T), 331(G), 332(A), 569(T), 602(C), 645(C), 660(T), 661(G), 674(A), 679(T), 689(C), 695(T)), and LSU (GenBank NG_228942; Identities 833/835 (99%); unique nucleotide at positions 384(T), 478(G)).

Hypoxylon judithwrightiae differs from *H. wujiangense* (ex-type strain GMBC02132) by sequence comparison of the ITS region (GenBank MT568854.1; Identities 485/529 (92%), 14 gaps; unique nucleotide at positions 202(A), 220(C), 233(C), 234(C), 272(G), 302(C), 306(G), 310(A), 311(T), 321(G), 329(T), 336(C), 351(A), 352(A), 353(C), 356(A), 366(A), 475(C), 557(A), 561(A), 562(A), 569(T), 584(T), 601(C), 602(C), 608(A), 615(A), 625(G), 645(C)), and LSU (GenBank MT568853; Identities 784/788 (99%); unique nucleotide at positions 384(T), 447(T), 448(C), 482(C)). *Hypoxylon judithwrightiae* differs from *H. hypomiltum* (strain CBS 129038) by sequence comparison of the ITS region (GenBank MH865185.1; Identities 569/628 (91%), 24 gaps; unique nucleotide at positions 202(A), 220(C), 233(C), 234(C), 257(T), 272(G), 301(C), 310(A), 311(T), 321(G), 329(T), 351(A), 352(A), 353(C), 356(A), 368(A), 475(C), 557(A), 561(A), 562(A), 569(T), 584(T), 602(C), 608(C), 625(G), 645(C), 646(T), 655(T), 661(G), 672(G), 674(A), 679(T), 696(T), 697(A), 702(A)), and LSU (GenBank MH876623; Identities 847/855 (99%), two gaps; unique nucleotide at positions 89(G), 118(C), 128(C), 186(C), 455(C), 482(C)).

Specimen examined: Australia, New South Wales, Rowlands Creek, from an unidentified dead insect, 15 Apr. 2021, *D. Teal* (holotype BRIP 72744d permanently preserved in a metabolically inactive state).

Etymology: Named after Judith Arundell Wright (1915–2000), a poet, author, and social and environmental activist.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region sequences from related species of *Hypoxylon*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Hypoxylon lechatii* (ex-type strain CBS 123577) 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 (*).

Paraphaeosphaeria jaguarinae Y.P. Tan & R.G. Shivas, *sp. nov.*

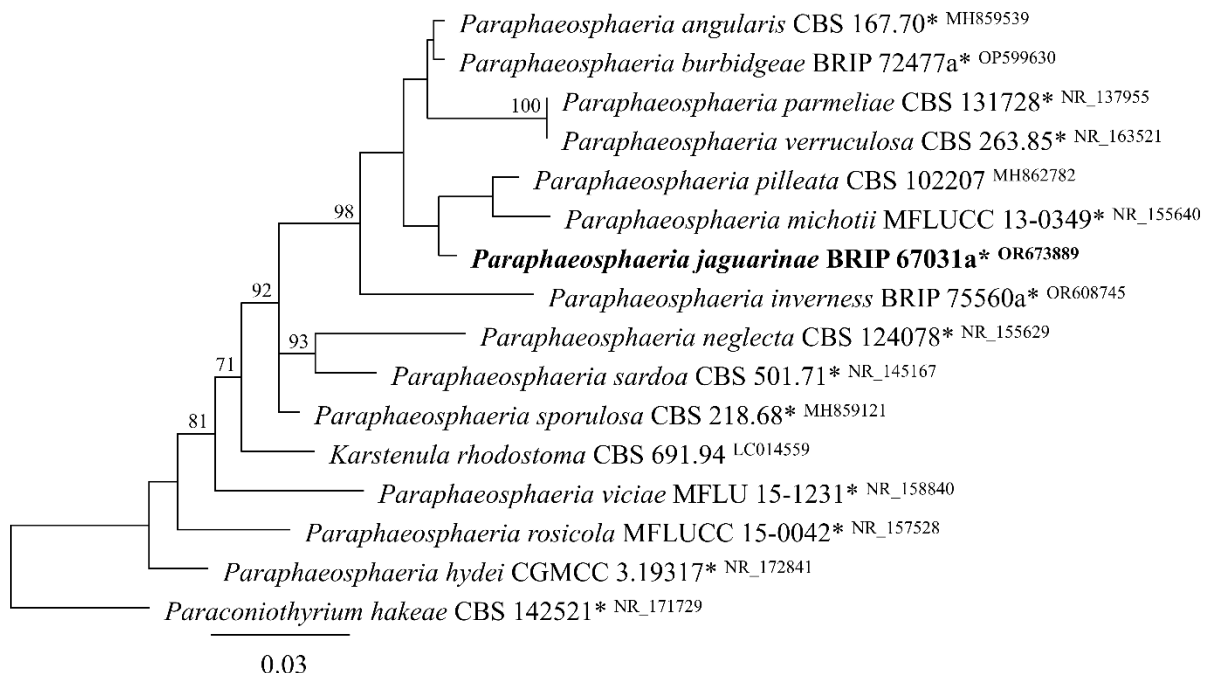
IF 901285

Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes*

Diagnosis: Sequence from the rDNA *Paraphaeosphaeria jaguarinae* and is available in GenBank under the accession OR673889 (ITS). *Paraphaeosphaeria jaguarinae* differs from *P. angularis* (ex-type strain CBS 167.70) by sequence comparison of the ITS region (GenBank MH859539; Identities 540/549 (98%), two gaps; unique nucleotide at positions 182(C), 183(A), 184(A), 208(G), 215(C), 242(C), 298(C)). *Paraphaeosphaeria jaguarinae* differs from *P. burbidgeae* (ex-type strain BRIP 72477a) by sequence comparison of the ITS region (GenBank OP599630; Identities 698/708 (99%), two gaps; unique nucleotide at positions 182(C), 183(A), 184(A), 208(G), 215(C), 298(C), 643(G)). *Paraphaeosphaeria jaguarinae* differs from *P. michotii* (ex-type strain MFLUCC 13-0349) by sequence comparison of the ITS region (GenBank NR_155640; Identities 547/562 (97%), six gaps; unique nucleotide at positions 182(C), 263(C), 298(C), 303(C), 345(C), 475(T), 485(A), 643(G)).

Specimen examined: Australia, Queensland, Mareeba Wetlands, from leaf spot on *Arundinella* sp. (*Poaceae*), 27 Apr. 2018, J. Kruse, M.D.E. Shivas & R.G. Shivas (holotype BRIP 67031a permanently preserved in a metabolically inactive state).

Etymology: Named after Ella Hattan, better known by her nom-de-guerre *La Jaguarina*, who was one of the most skilled sword fighters of the nineteenth century.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region sequences from species of *Paraphaeosphaeria*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Paraconiothyrium hakeae* (ex-type strain CBS 142521) 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 (*).

Penicillium carolineherscheliae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

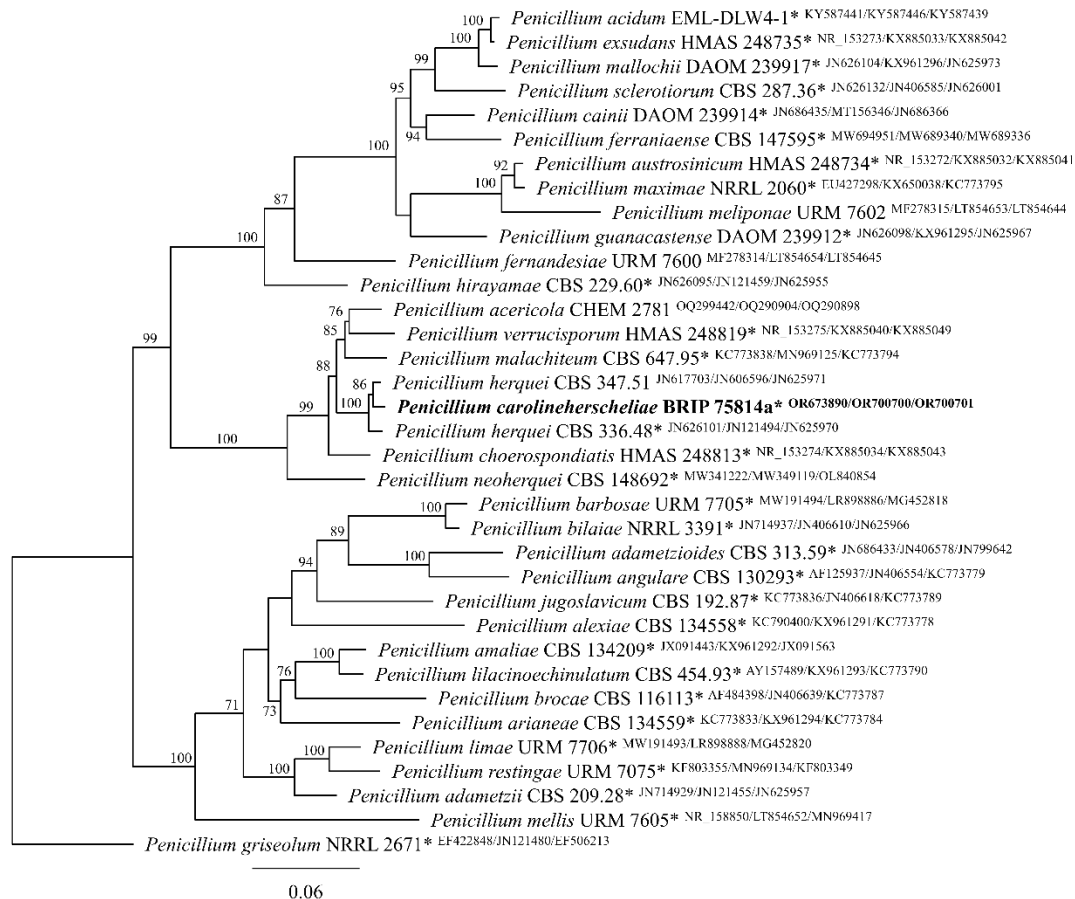
IF 901286

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Penicillium carolineherscheliae* and are available under the accessions OR673890 (ITS), OR673898 (LSU), OR700700 (*rpb2*), and OR700701 (*tub2*). *Penicillium carolineherscheliae* differs from *Pe. herquei* (ex-type strain CBS 336.48) by sequence comparison of *rpb2* (GenBank JN121494; Identities 819/829 (99%); unique nucleotide at positions 220(A), 250(C), 304(C), 361(T), 394(C), 416(T), 463(T), 487(C), 526(G), 727(G)), and *tub2* (GenBank JN625970; Identities 454/471 (96%), two gaps; unique nucleotide at positions 221(C), 266(T), 281(T), 285(A), 290(T), 303(C), 305(C), 331(C), 367(G), 483(A), 505(C), 507(G), 515(T), 631(C), 643(C)).

Specimen examined: Australia, New South Wales, Rowlands Creek, from an unidentified dead insect, 26 Feb. 2023, *D. Teal* (holotype BRIP 75814a permanently preserved in a metabolically inactive state).

Etymology: Named after Caroline Herschel (1750–1858), an astronomer.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the combined ITS, *rpb2*, and *tub2* sequences from selected species of *Penicillium* sect. *Sclerotiorum*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Penicillium griseolum* (ex-type strain NRRL 2671) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/*rpb2*/*tub2*). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (*).

Phaeoseptoriella emmelinepankhurstiae Y.P. Tan, *sp. nov.*

IF 901287

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

Diagnosis: Sequence from the rDNA describe *Phaeoseptoriella emmelinepankhurstiae* and is available in GenBank under the accession OR673891 (ITS). *Phaeoseptoriella emmelinepankhurstiae* differs from *Ph. zae* (ex-type strain CBS 144614) by sequence comparison of the ITS region (GenBank MK442611; Identities 523/558 (94%), 11 gaps; unique nucleotide at positions 127(A), 136(C), 138(T), 143(A), 146(C), 147(T), 161(C), 187(A), 203(C), 205(T), 207(C), 209(A), 214(C), 224(A), 260(T), 264(G), 479(T), 480(G), 481(G), 482(T), 495(T), 547(A), 566(C), 587(C)).

Specimen: Australia, Queensland, Taunton, from leaf lesion of *Sporobolus natalensis* (*Poaceae*), 8 Feb. 2017, *J.S. Vitelli* (holotype BRIP 65639a permanently preserved in a metabolically inactive state).

Etymology: Named after Emmeline Pankhurst (1858–1928), who organised the British suffragette movement and helped women win the right to vote.

Phaeoseptoriella vidagoldsteiniae Y.P. Tan, *sp. nov.*

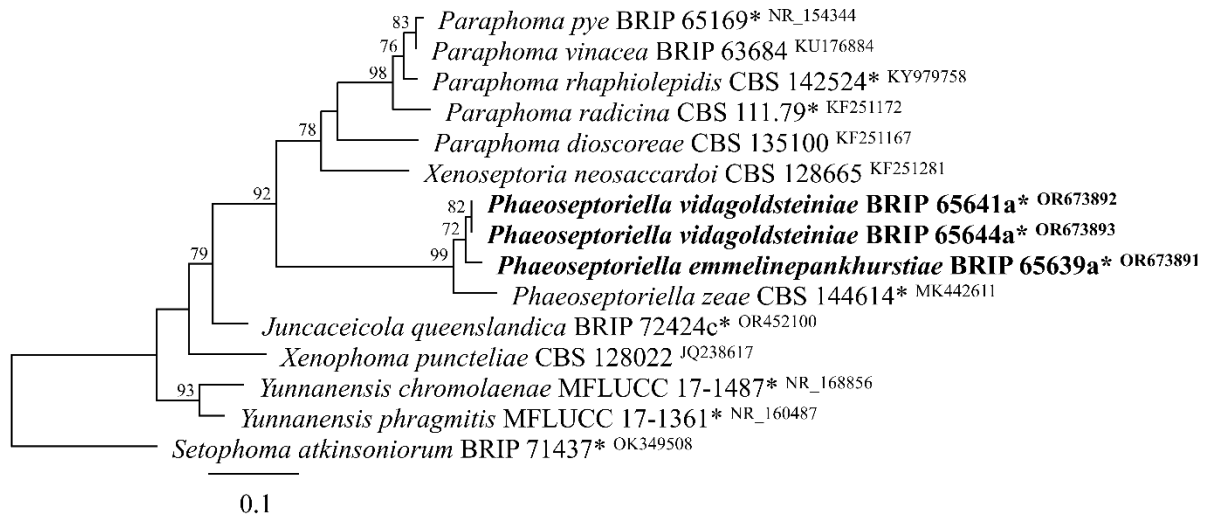
IF 901288

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

Diagnosis: Sequence from the rDNA describe *Phaeoseptoriella vidagoldsteiniae* and is available in GenBank under the accession OR673892 (ITS). *Phaeoseptoriella vidagoldsteiniae* differs from *Ph. zae* (ex-type strain CBS 144614) by sequence comparison of the ITS region (GenBank MK442611; Identities 526/556 (95%), 11 gaps; unique nucleotide at positions 147(G), 156(C), 157(C), 158(T), 163(A), 166(C), 167(T), 173(C), 207(A), 223(C), 225(T), 227(C), 229(A), 234(C), 266(C), 501(T), 502(G), 503(G), 609(C)). *Phaeoseptoriella vidagoldsteiniae* differs from *Ph. emmelinepankhurstiae* (ex-type strain 65639a) by sequence comparison of the ITS region (GenBank OR673891; Identities 615/629 (98%), two gaps; unique nucleotide at positions 147(G), 157(C), 173(C), 181(T), 245(G), 266(C), 282(A), 286(T), 504(C), 517(C), 569(G), 588(T)).

Specimen: Australia, Queensland, Taunton, from leaf lesion of *Sporobolus natalensis* (*Poaceae*), 8 Feb. 2017, *J.S. Vitelli* (holotype BRIP 65641a permanently preserved in a metabolically inactive state); *ibid*, from leaf lesions on *Sporobolus natalensis* (*Poaceae*), 8 Feb. 2017, *J.S. Vitelli*, culture BRIP 65644a (ITS sequence GenBank OR673893).

Etymology: Named after Vida Jane Mary Goldstein (1869–1949), a suffragist and social reformer in Australia.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region sequences from related species of *Phaeosphaeriaceae*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Setophoma atkinsoniorum* (ex-type strain BRIP 71437) 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 (*).

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

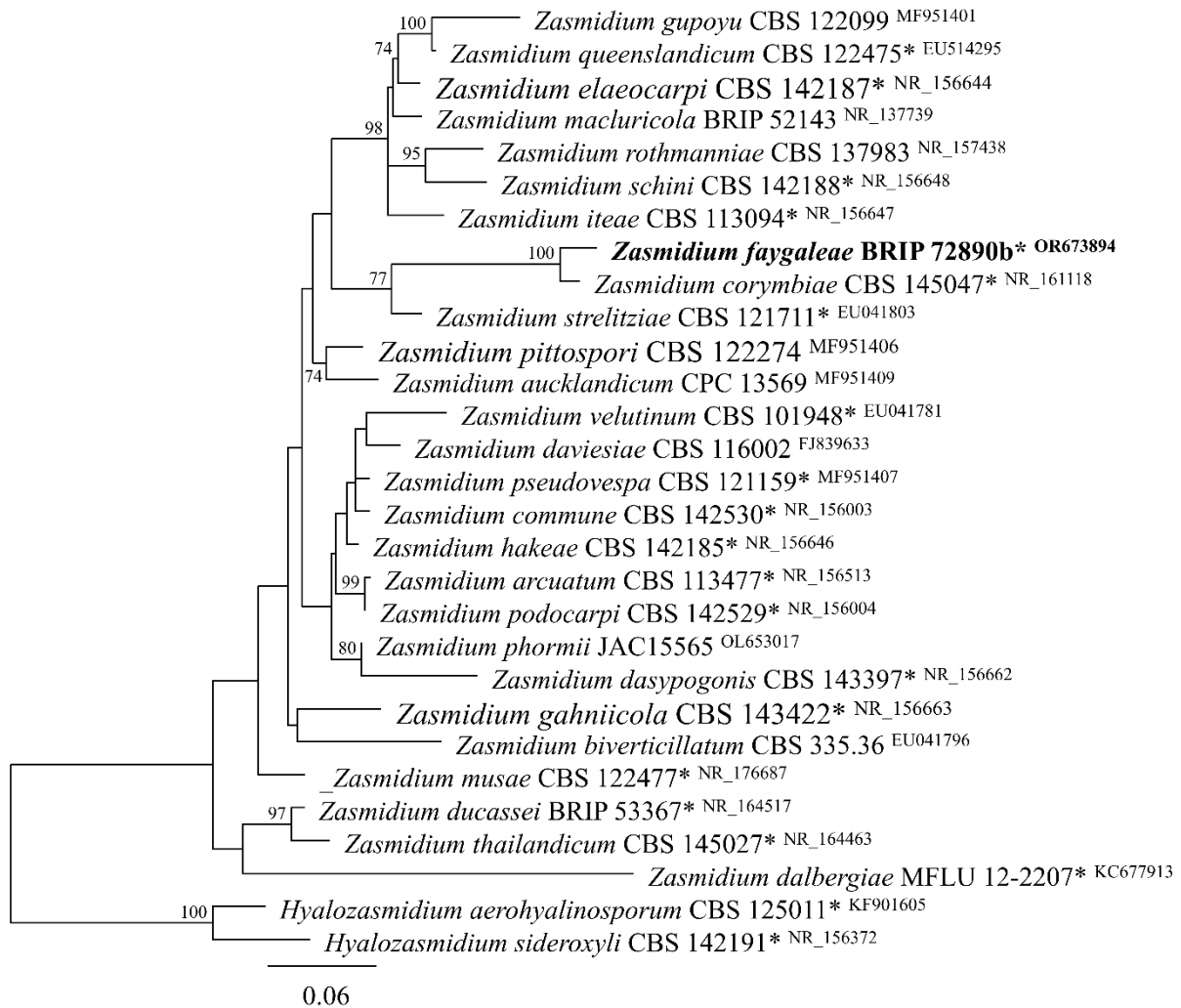
IF 901289

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes*,

Diagnosis: Sequences from the rDNA describe *Zasmidium faygaleae* and are available in GenBank under the accessions OR673894 (ITS) and OR673899 (LSU), OR680058 (*rpb2*), and OR680059 (*tef1*). *Zasmidium faygaleae* differs from *Z. corymbiae* (ex-type strain CBS 145047) by sequence comparison of the ITS region (GenBank NR_161118; Identities 526/538 (98%), three gaps; unique nucleotide at positions 260(A), 262(A), 292(T), 515(T), 522(T), 579(T), 622(A), 624(C), 625(A)), *rpb2* (GenBank MK047534; Identities 853/927 (92%), unique nucleotide at positions 14(A), 20(T), 44(C), 47(A), 59(C), 92(C), 95(G), 119(G), 134(T), 149(T), 158(T), 164(A), 167(G), 206(G), 221(G), 266(A), 299(A), 318(T), 331(C), 348(T), 351(A), 357(T), 368(T), 377(G), 380(C), 386(G), 407(G), 425(C), 455(G), 470(G), 479(T), 491(C), 500(T), 520(A), 524(A), 527(A), 539(T), 545(C), 566(T), 581(C), 590(T), 593(C), 596(T), 602(T), 605(A), 608(T), 623(C), 630(G), 632(G), 641(T), 644(C), 653(T), 668(C), 677(G), 701(A), 713(T), 722(A), 734(T), 737(A), 740(A), 743(C), 761(C), 762(T), 770(T), 773(G), 815(G), 827(A), 845(C), 854(C), 866(C), 875(T), 890(C), 899(A), 905(T)), and *tef1* (GenBank MK047555; Identities 383/455 (84%), 14 gaps; unique nucleotide at positions 9(C), 11(G), 15(A), 16(C), 17(T), 23(A), 32(G), 33(A), 34(C), 35(A), 39(T), 42(G), 45(G), 51(C), 56(C), 87(T), 89(G), 91(T), 92(G), 134(G), 143(C), 163(C), 169(A), 170(T), 172(T), 185(G), 189(G), 198(C), 211(A), 215(A), 243(T), 246(C), 252(A), 267(T), 276(C), 294(T), 309(T), 312(C), 333(G), 345(C), 348(C), 349(A), 353(A), 354(C), 357(C), 358(C), 362(T), 365(T), 366(C), 371(T), 372(A), 373(T), 375(C), 378(C), 383(A), 386(T), 391(G), 393(G)).

Specimen examined: Australia, New South Wales, Rowlands Creek, from an unidentified dead insect, 19 Jun. 2021, *D. Teal* (holotype BRIP 72890b permanently preserved in a metabolically inactive state).

Etymology: Named after Gwendoline Fay Gale (née Gilding; 1932–2008), a cultural geographer and academic in Australia, who shed light on the inequalities and injustices suffered by Indigenous women, and pioneered reforms to assist women to achieve their full academic potential.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region sequences from species of *Zasmidium*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Hyalozasmidium arohyalinosporum* (ex-type strain CBS 125011) and *Hy. sideroxyli* (ex-type strain CBS 142191) were used as the outgroup. GenBank accession numbers are indicated (superscripted ITS). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).