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

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Cladosporium harfordiae Y.P. Tan, Bishop-Hurley & Marney, *sp. nov.*

IF 901428

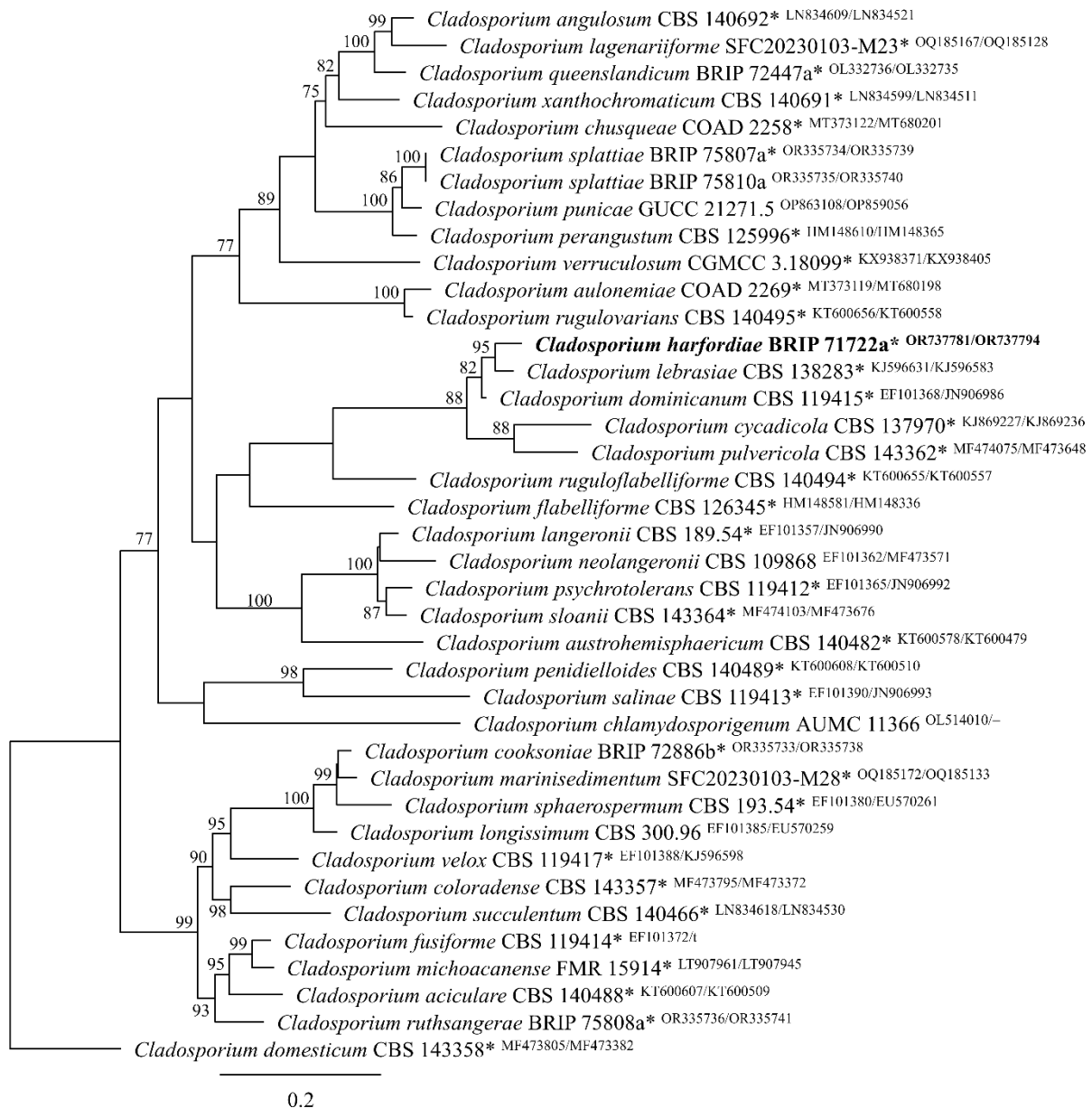
Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA describe *Cladosporium harfordiae* and are available under the accessions OR750692 (ITS), OR737781 (actin), and OR737794 (*tef1*).

Cladosporium harfordiae differs from *Cladosporium lebrasiae* (ex-type strain CBS 138283) by sequence comparison of actin (GenBank KJ596631; Identities 203/208 (98%); unique nucleotide at positions 67(C), 73(G), 134(C), 144(C), 145(C)), and *tef1* (GenBank KJ596583; Identities 202/220 (92%); unique nucleotide at positions 51(T), 56(C), 101(C), 109(G), 143(C), 156(T), 163(C), 167(G), 189(C), 207(A), 208(G), 210(C), 212(C), 214(G), 216(A), 229(G), 251(C), 258(T)).

Specimen examined: Australia, Queensland, from leaf spot on *Pennisetum* sp. (*Poaceae*), Feb. 2003, D.M. Persley & T.S. Marney (holotype BRIP 71722a permanently preserved in a metabolically inactive state).

Etymology: Named after Lesbia Harford (1891–1927), a poet, notable during her lifetime for her social and political activism in Australia. Most of Lesbia Harford's poetry, as well as her lost novel, *The Invaluable Mystery*, were published posthumously.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the actin and *tef1* sequences from related species of *Cladosporium*. 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. *Cladosporium domesticum* (ex-type strain CBS 143358) was used as the outgroup. GenBank accession numbers are indicated (superscript actin/ *tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Lecanicillium spenceae Y.P. Tan, Bishop-Hurley & Marney, *gen. et sp. nov.*

IF 901429

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

Diagnosis: Sequences from the rDNA and nrDNA describe *Lecanicillium spenceae* and are available under the accessions OR750698 (ITS), OR737787 (*rpb2*), and OR737798 (*tef1*).

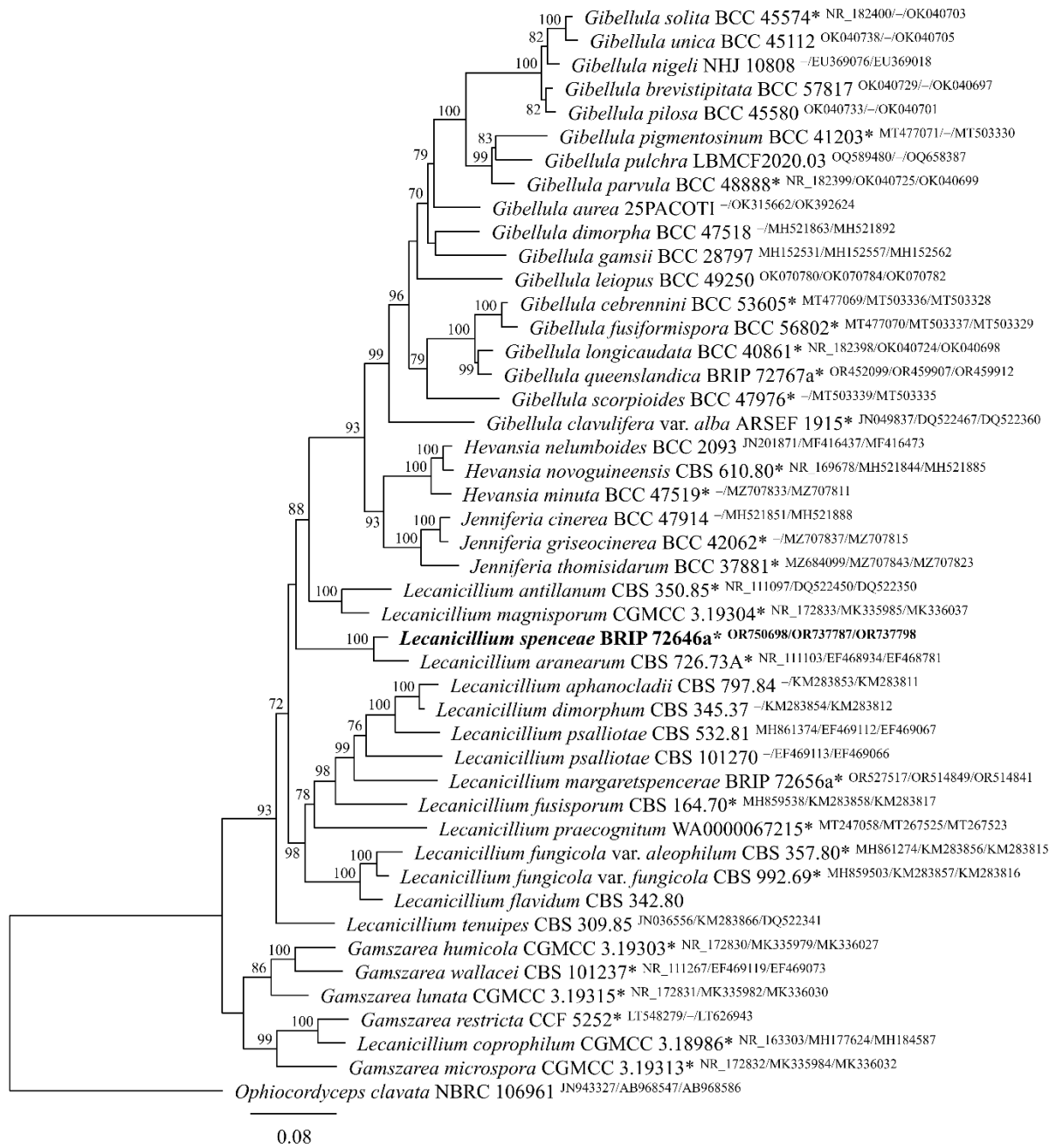
Lecanicillium spenceae differs from *Lecanicillium aranearum* (ex-type strain CBS 726.73A) by sequence comparison of the ITS region (GenBank NR_111103; Identities 513/541 (95%), three gaps; unique nucleotide at positions 145(A), 197(C), 211(T), 217(C), 220(A), 226(T), 247(G), 255(A), 257(A), 260(A), 265(A), 282(C), 284(G), 286(T), 311(A), 498(T), 527(T), 529(T), 579(T), 589(A), 590(C), 596(A), 598(C), 611(T), 632(C)), *rpb2* (GenBank EF468934; Identities 776/806 (96%); unique nucleotide at positions 16(C), 28(T), 62(T), 64(T), 70(A), 127(A), 136(C), 148(G), 154(C), 193(T), 202(A), 244(A), 271(T), 295(G), 328(C), 346(T), 397(C), 409(G), 424(T), 445(A), 484(T), 499(T), 577(A), 616(A), 622(T), 643(G), 697(T), 730(T), 748(G), 763(G)), and *tef1* (GenBank EF468781; Identities 957/992 (96%); unique nucleotide at positions 82(T), 109(T), 178(C), 179(A), 182, (A), 188(T), 190(T), 195(A), 271(C), 283(T), 311(C), 312(C), 317(A), 412(C), 416(A), 425(C), 472(T), 508(C), 512(A), 514(C), 541(C), 602(G), 613(C), 616(T), 670(T), 676(T), 679(C), 708(C), 712(C), 722(C), 862(T), 895(T), 896(T), 898(C), 943(T)).

Specimen examined: Australia, Queensland, Wallaman, from an unidentified dead spider colonised by an unidentified gibellula-like fungus, 28 Apr. 2021, *T.S. Marney, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 72646a permanently preserved in a metabolically inactive state).

Etymology: Named after Catherine Helen Spence (1825–1910), an author, teacher, and suffragist in Australia.



Lecanicillium spenceae. Decayed spider colonised by both *L. spenceae* and an unidentified gibellula-like fungus.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the ITS, *rpb2*, and *tef1* sequences from related species of *Cordycipitaceae*. 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. *Ophiocordyceps clavata* (strain NBRC 106961) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/*rpb2*/*tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Neoceratosperma goldingiae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

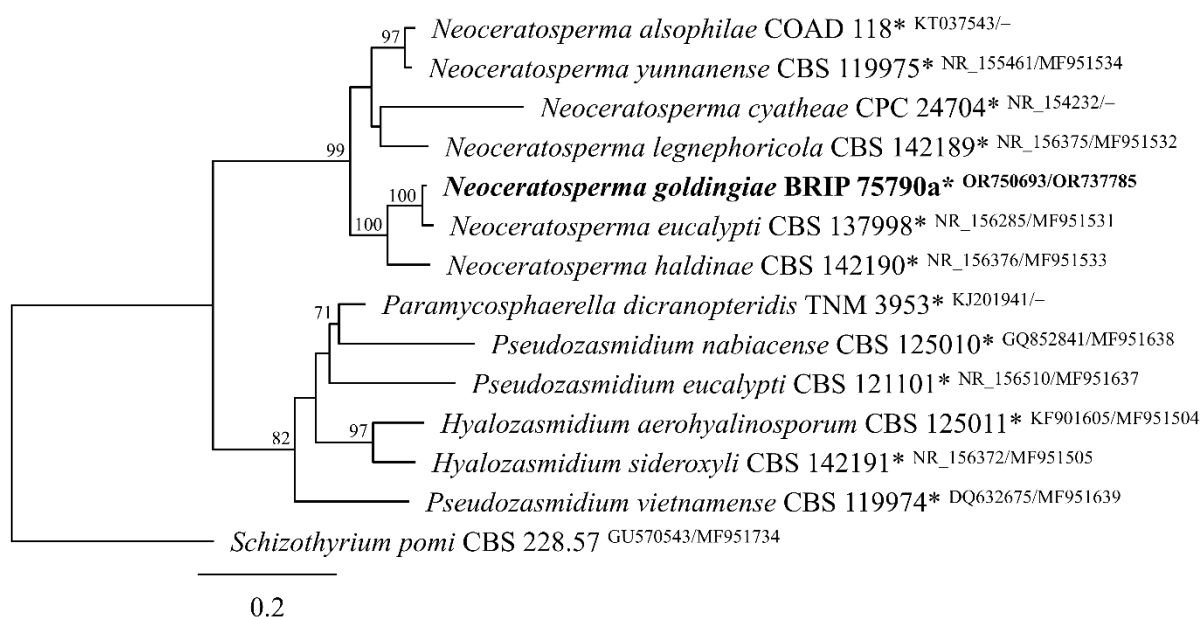
IF 901430

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

Diagnosis: Sequences from the rDNA describe *Neoceratosperma goldingiae* and are available under the accessions OR750693 (ITS), OR731500 (LSU), OR737782 (actin), (*rpb2*), and OR737795 (*tef1*). *Neoceratosperma goldingiae* differs from *Neoceratosperma eucalypti* (ex-type strain CBS 137998) by sequence comparison of the ITS region (GenBank NR_156285; Identities 615/617 (99%); unique nucleotide at positions 473(G), 536(C)), and *rpb2* (GenBank MF951531; Identities 884/908 (97%); unique nucleotide at positions 8(C), 48(C), 55(A), 87(G), 90(C), 105(C), 111(C), 495(C), 549(G), 555(T), 560(A), 573(C), 588(G), 592(C), 687(G), 714(C), 717(G), 753(C), 762(C), 774(G), 777(G), 783(G), 816(T), 819(G)).

Specimen examined: Australia, Queensland, Murray Upper, from leaf spot on *Chromolaena odorata* (*Asteraceae*), 27 Mar. 2023, K. Pukallus (holotype BRIP 75790a permanently preserved in a metabolically inactive state).

Etymology: Named after Annie Mackenzie Golding (1855–1934), a suffragist, and political activist in Australia.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the ITS and *rpb2* sequences from related species of *Mycosphaerellaceae*. 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. *Schizothyrium pomi* (strain CBS 228.57) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/*rpb2*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Pseudocercospora raybouldiae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 901431

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

Diagnosis: Sequences from the rDNA describe *Pseudocercospora raybouldiae* and are available under the accessions OR750695 (ITS), OR731502 (LSU), OR737783 (actin), and OR737796 (*tef1*). *Pseudocercospora raybouldiae* differs from *P. hardenbergiae* (ex-type strain CPC 17177) by sequence comparison of the ITS region (GenBank LC599349; Identities 457/462 (99%); unique nucleotide at positions 124(T), 199(A), 200(C), 466(T), 547(C)), actin (GenBank LC599429; Identities 204/209 (98%); unique nucleotide at positions 57(C), 59(T), 99(A), 146(T), 191(C)), and *tef1* (GenBank LC599471; Identities 269/306 (88%), four gaps; unique nucleotide at positions 9(T), 11(C), 28(T), 30(C), 35(G), 36(A), 38(T), 40(A), 43(T), 79(T), 122(T), 123(C), 156(C), 157(C), 158(A), 189(G), 195(G), 197(A), 198(C), 200(A), 202(C), 208(T), 211(C), 224(T), 236(C), 239(T), 244(A), 249(C), 251(A), 259(C), 260(A), 262(G), 288(C)). *Pseudocercospora raybouldiae* differs from *P. stizobii* (strain CPC 25217) by sequence comparison of the ITS region (GenBank KT290143; Identities 463/464 (99%); unique nucleotide at positions 227(T)), actin (GenBank KT313498; Identities 197/205 (96%), four gaps; unique nucleotide at positions 25(T), 118(C), 147(C), 163(T)), and *tef1* (GenBank KT290197; Identities 436/501 (87%), 17 gaps; unique nucleotide at positions 10(G), 11(C), 13(G), 14(C), 21(C), 39(C), 40(A), 57(T), 58(T), 73(T), 150(A), 157(C), 171(A), 172(T), 176(T), 178(C), 185(C), 189(G), 197(A), 202(C), 208(T), 209(A), 211(C), 212(G), 220(C), 222(A), 224(T), 236(C), 239(T), 247(G), 249(C), 251(A), 259(C), 260(A), 267(A), 285(T), 381(G), 396(T), 408(T), 412(T), 413(G), 415(C), 419(A), 420(G), 422(C), 425(G), 430(A), 437(A)).

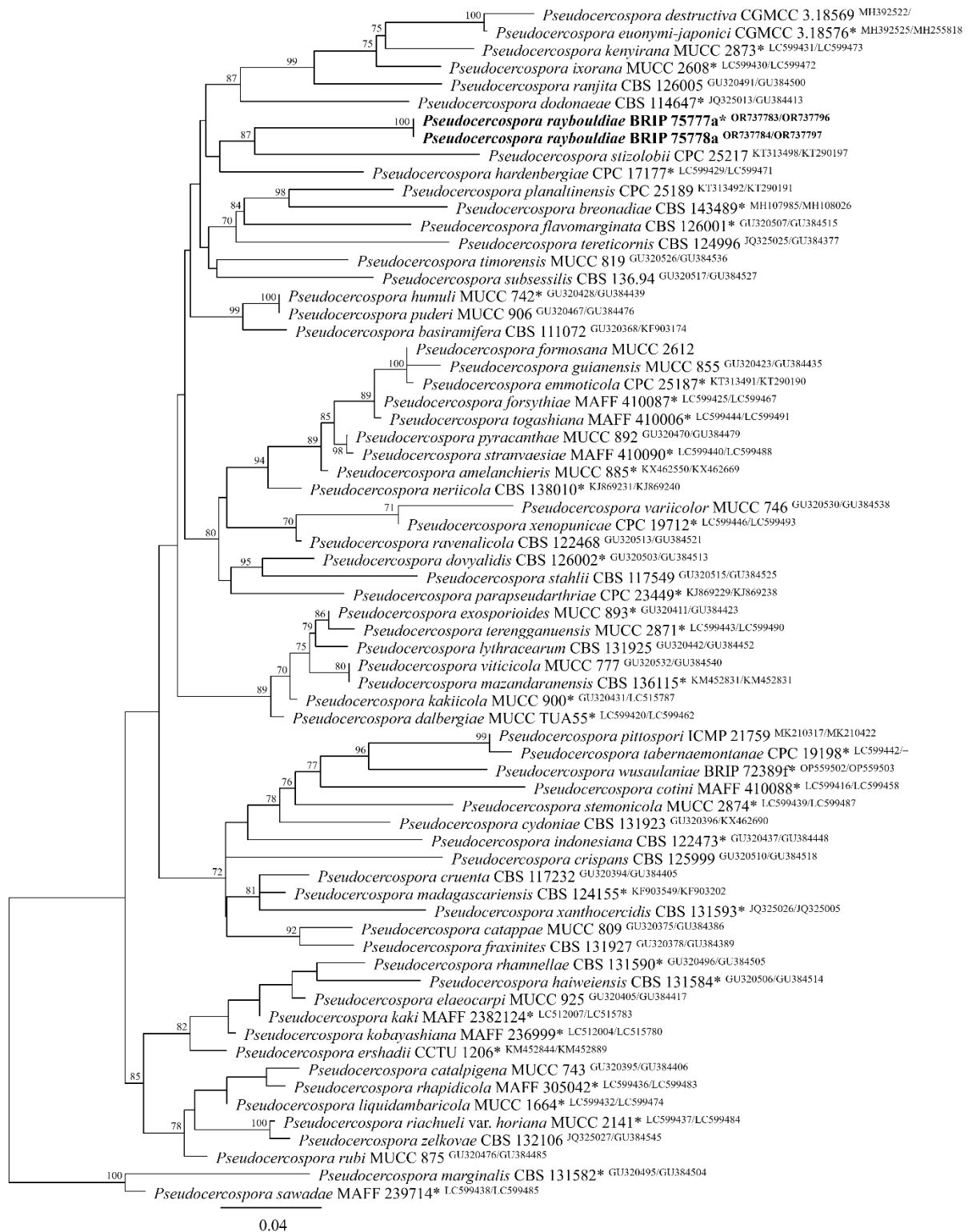
Leaf spots amphigenous although not easily observed on the lower surface due to the dense mass of white to silver stellate leaf scales, dark brown to blackish brown, irregular, 2–15 mm diam. *Mycelium* internal, external mycelium absent. *Stromata* erumpent, subglobose, 45–100 µm diam. *Conidiophores* sporodochial, on upper part of stromata, cylindrical, 15–30 × 2.5–4 µm, 0–1 septate, straight to sinuous, narrowed towards the apex, unbranched, subhyaline to pale brown, smooth. *Conidiogenous cells* terminal, or conidiophores reduced to conidiogenous cells, pale to medium brown, subcylindrical, smooth, proliferating sympodially, 10–30 × 2.5–3 µm. *Conidiogenous loci* inconspicuous or slightly refractive. *Conidia* solitary, pale brown, subcylindrical, straight to slightly curved, 25–80 × 3–5 µm, 0–10-septate, apex subobtuse, base obconically truncate; hila inconspicuous or slightly refractive, 1.5–2 µm diam.

Specimens examined: Australia, Queensland, Monto, from leaf spot on *Croton phebaliioides* (*Euphorbiaceae*), 30 Dec. 2022, M.D.E. Shivas & R.G. Shivas (holotype BRIP 75777a permanently preserved in a metabolically inactive state); *ibid*, from leaf spot on *Croton phebaliioides* (*Euphorbiaceae*), 30 Dec. 2022, M.D.E. Shivas & R.G. Shivas, culture BRIP 75778a (ITS, LSU, actin and *tef1* sequences GenBank OR750696, OR731503, OR737784 and OR737797).

Etymology: Named after Ethel Harriet Raybould (1899–1987), a mathematics lecturer who taught at the University of Queensland from 1928 to 1955.



Pseudocercospora raybouldiae. Leaf spots on *Croton phebaloides*; conidia; sporodochial conidiophores; colonies on PDA after 4 wk; stromata on leaf surface (clockwise). Scale bars = 1 cm (leaf spots, colonies), 10 μm (conidia, sporodochial conidiophores and stromata on leaf).



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the actin and *tef1* sequences from related species of *Pseudocercospora*. 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. *Pseudocercospora marginalis* (ex-type strain CBS 131582) and *P. sawadae* (ex-type strain MAFF 239714) were used as the outgroup. GenBank accession numbers are indicated (superscript actin/ *tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

Thermothielavioides maryleeae Y.P. Tan, *sp. nov.*

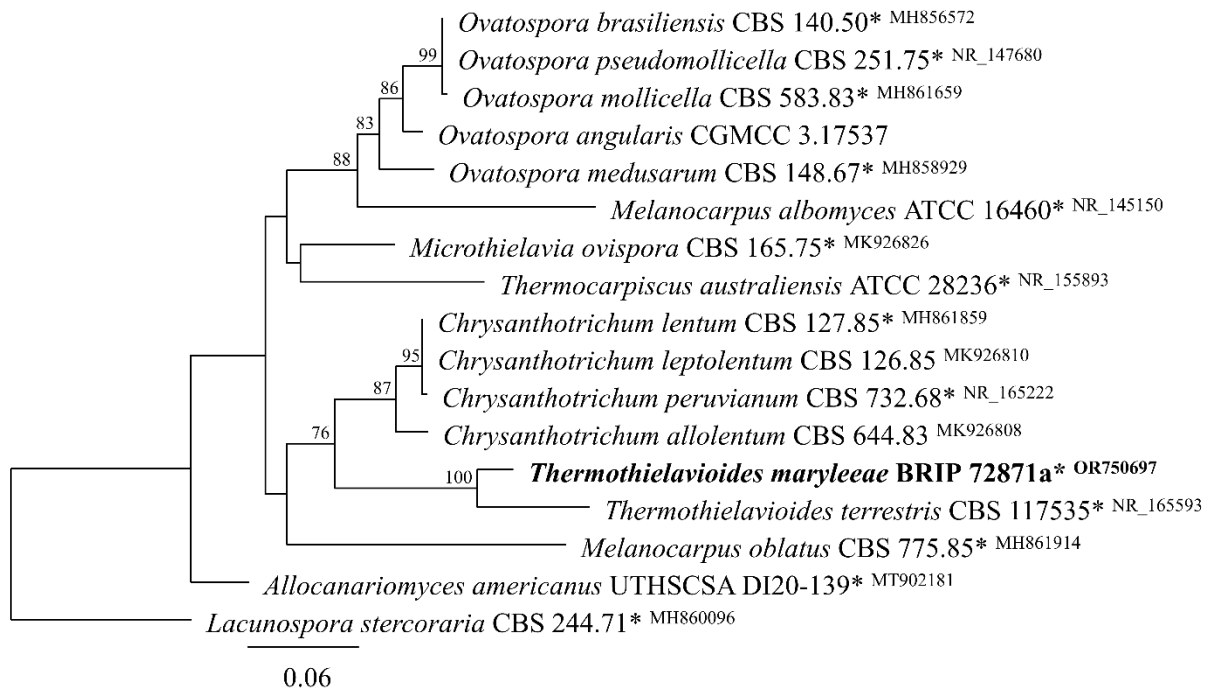
IF 901432

Classification — *Chaetomiaceae*, *Sordariales*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA describe *Thermothielavioides maryleeae* and are available under the accessions OR750697 (ITS) and OR731504 (LSU). *Thermothielavioides maryleeae* differs from *Thermothielavioides terrestris* (ex-type strain CBS 117535) by sequence comparison of the ITS region (GenBank NR_165593; Identities 523/554 (94%), 14 gaps; unique nucleotide at positions 55(A), 93(A), 119(C), 127(T), 181(C), 190(C), 193(A), 200(T), 202(T), 204(C), 232(A), 321(A), 360(A), 367(T), 410(A), 464(G), 493(T), 494(A), 522(G), 569(A)).

Specimen examined: Australia, Queensland, Barwidgi, from soil, 20 Apr. 2021, Y.P. Tan (holotype BRIP 72871a permanently preserved in a metabolically inactive state).

Etymology: Named after Mary Lee (née Walsh; 1821–1909), a suffragist, social reformer, and women's rights activist in South Australia in the late nineteenth century.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region sequences from related species of *Chaetomiaceae*. 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. *Lacunospora stercoraria* (ex-type strain CBS 244.71) 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 (*).

Chlorocillium gueriniae Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney, *sp. nov.*

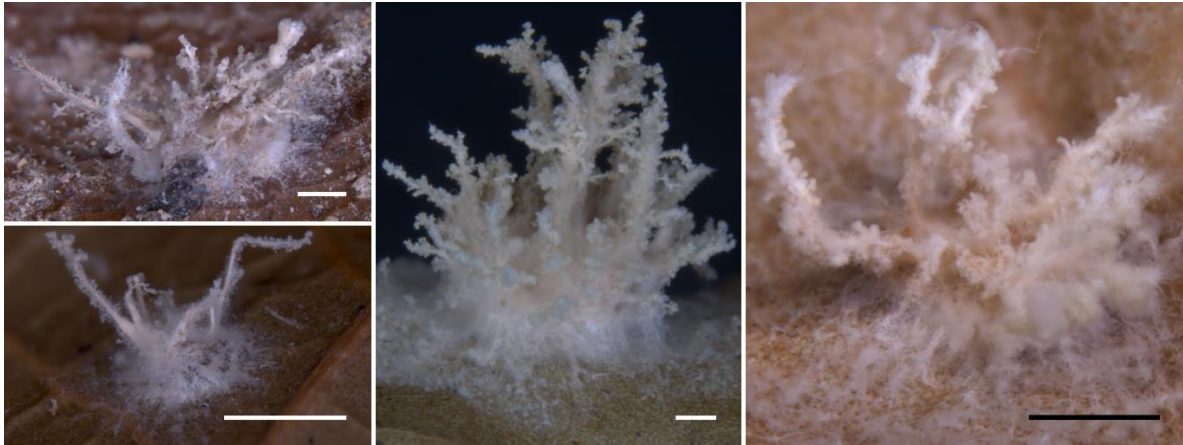
IF 901433

Classification — *Incertae sedis*, *Incertae sedis*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Chlorocillium gueriniae* and are available under the accessions OR750699 (ITS), OR731505 (LSU), OR737788 (*rpb2*), and OR737799 (*tefl*). *Chlorocillium gueriniae* differs from *Chlorocillium griseum* (ex-type strain CBS 387.73) by sequence comparison of the ITS region (GenBank NR_153915; Identities 535/543 (98%), five gaps; unique nucleotide at positions 176(T), 291(G), 303(C)), and LSU (GenBank NG_058935; Identities 665/669 (99%), one gap; unique nucleotide at positions 56(G), 156(T), 374(T)). *Chlorocillium gueriniae* differs from *Chlorocillium griseum* (strain RCEF4626) by sequence comparison of the ITS region (GenBank OM843125; Identities 555/563 (98%), four gaps; unique nucleotide at positions 153(A), 176(T), 291(G), 303(C)), LSU (GenBank MW084341; Identities 763/768 (99%), one gap; unique nucleotide at positions 56(G), 142(T), 146(T), 374(T)), *rpb2* (GenBank MW091328; Identities 872/904 (96%); unique nucleotide at positions 34(A), 46(G), 97(G), 124(G), 127(T), 136(C), 148(A), 187(C), 199(T), 214(T), 217(T), 229(A), 280(T), 298(A), 302(A), 328(T), 358(G), 361(T), 403(G), 410(T), 502(C), 532(C), 533(G), 722(C), 757(C), 775(T), 808(G), 811(T), 814(G), 823(T)), and *tefl* (GenBank MW091326; Identities 909/921 (99%); unique nucleotide at positions 149(C), 224(A), 446(G), 512(T), 560(T), 587(C), 635(C), 812(G), 854(A), 875(A), 884(C), 932(C)).

Specimens examined: Australia, Queensland, Mission Beach, from an unidentified dead *Arthropoda* on a leaf, 30 Apr. 2021, T.S. Marney, Y.P. Tan, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72680a permanently preserved in a metabolically inactive state); Tully, from an unidentified dead *Arthropoda* on a leaf, 29 Apr. 2021, T.S. Marney, Y.P. Tan, M.D.E. Shivas & R.G. Shivas, culture BRIP 72665a (ITS, LSU, *rpb2* and *tefl* sequences GenBank OR750700, OR731506, OR737789 and OR737800); *ibid*, from an unidentified dead *Arthropoda* on a leaf, 29 Apr. 2021, T.S. Marney, Y.P. Tan, M.D.E. Shivas & R.G. Shivas, culture BRIP 72666a (ITS, LSU, *rpb2* and *tefl* sequences GenBank OR750701, OR731507, OR737790 and OR737801); *ibid*, from an unidentified dead *Arthropoda* on a leaf, 29 Apr. 2021, T.S. Marney, Y.P. Tan, M.D.E. Shivas & R.G. Shivas, culture BRIP 72668a (ITS, LSU, *rpb2* and *tefl* sequences GenBank OR750702, OR731508, OR737791 and OR737802);

Etymology: Named after Julia Margaret “Bella” Guerin (1858–1923), a suffragist, and school teacher in Australia.



Decayed *Arthropoda* on leaves from which isolates of *Chlorocillium gueriniae* were obtained. BRIP 72666a (top left), BRIP 72680a (bottom left), BRIP 72668a (middle), BRIP 72665a (right). Scale bars = 1 mm.

Fiorinimazzantia elisabettae Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney, *gen. et. sp. nov.*

Fiorinimazzantia Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney IF 901434

Fiorinimazzantia elisabettae Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney IF 901435

Classification — *Incertae sedis*, *Incertae sedis*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Fiorinimazzantia elisabettae* and are available under the accessions OR750703 (ITS), OR731509 (LSU), OR737792 (*rpb2*), and OR737803 (*tef1*). *Fiorinimazzantia elisabettae* differs from *Chlorocillium gueriniae* (ex-type strain BRIP 72680a) by sequence comparison of the ITS region (GenBank OR750699; Identities 630/694 (91%); 26 gaps; unique nucleotide at positions 195(C), 213(T), 214(G), 215(T), 216(T), 223(C), 232(C), 233(C), 234(T), 235(C), 250(A), 252(C), 261(A), 286(A), 295(A), 309(G), 318(T), 321(C), 322(A), 323(A), 483(T), 511(C), 526(C), 534(G), 538(C), 539(C), 540(C), 543(G), 547(A), 551(A), 554(G), 574(G), 575(A), 616(G), 650(A), 657(C), 660(T)), and LSU (GenBank OR731505; Identities 833/849 (98%), two gaps; unique nucleotide at positions 54(T), 55(T), 59(T), 244(T), 245(T), 345(T), 347(T), 359(G), 442(C), 449(T), 478(G), 540(A)). *Fiorinimazzantia elisabettae* differs from *Chlorocillium griseum* (ex-type strain CBS 387.73) by sequence comparison of the ITS region (GenBank NR_153915; Identities 465/530 (88%), 27 gaps; unique nucleotide at positions 182(T), 213(T), 214(G), 215(T), 216(T), 223(C), 232(C), 233(C), 234(T), 235(C), 250(A), 255(C), 261(A), 295(T), 309(G), 318(T), 321(C), 322(A), 323(A), 483(T), 511(C), 522(T), 526(C), 534(G), 538(C), 539(C), 540(C), 543(G), 547(A), 551(G), 554(G), 574(G), 575(A), 616(G), 650(A), 657(C), 660(T)), and LSU (GenBank NG_058935; Identities 651/668 (97%), one gap; unique nucleotide at positions 54(T), 55(T), 59(T), 155(T), 244(T), 245(T), 345(T), 347(T), 359(G), 373(T), 404(T), 405(T), 442(C), 449(T), 478(G), 540(A)).

Specimen examined: Australia, Queensland, Tully, from an unidentified dead insect colonised by an unidentified hirsutella-like fungus, 29 Apr. 2021, *T.S. Marney, Y.P. Tan, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 72660a permanently preserved in a metabolically inactive state).

Etymology: Named after Elisabetta Fiorini Mazzanti (1799–1879), a botanist, mycologist, and writer.

Notes — *Fiorinimazzantia* is described as the smallest phylogenetic clade that contains the type species, *Fiorinimazzantia elisabettae*, but excludes *Chlorocillium gueriniae*, *C. griseum*, *Dussiella tuberiformis*, *Rotiferophthora angustispora*, and *R. minutispora*.

Husseyia annamariae Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney, *gen. et. sp. nov.*

Husseyia Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney IF 901436

Husseyia annamariae Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney IF 901437

Classification — *Incertae sedis*, *Incertae sedis*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Husseyia annamariae* and are available under the accessions OR750704 (ITS), OR731510 (LSU), OR737793 (*rpb2*), and OR737804 (*tef1*). *Husseyia annamariae* differs from *Chlorocillium gueriniae* (ex-type BRIP 72680a) by sequence comparison of the ITS region (GenBank OR750699; Identities 563/652 (86%), 46 gaps; unique nucleotide at positions 77(C), 177(A), 178(T), 178(T), 179(T), 188(C), 196(T), 197(T), 199(G), 200(T), 220(T), 235(C), 244(T), 245(A), 254(T), 258(A), 267(G), 270(G), 275(A), 291(T), 293(T), 365(A), 449(T), 476(T), 477(C), 482(T), 489(T), 501(G), 536(C), 537(T), 539(A), 543(G), 549(T), 566(T), 567(T), 568(T), 569(T), 571(G), 573(A), 574(C), 581(T), 592(T), 595(T)), and LSU (GenBank OR731505; Identities 791/814 (97%), four gaps; unique nucleotide at positions 17(G), 19(T), 22(C), 116(C), 175(A), 311(G), 312(T), 324(G), 327(T), 331(C), 333(G), 370(A), 390(G), 391(C), 425(G), 507(A), 508(C), 512(T), 569(T)). *Husseyia annamariae* differs from *Chlorocillium griseum* (ex-type strain CBS 387.73) by sequence comparison of the ITS region (GenBank NR_153915; Identities 320/361 (88%), 16 gaps; unique nucleotide at positions 275(A), 291(T), 293(T), 365(A), 449(T), 476(T), 477(C), 482(T), 489(T), 501(G), 536(C), 537(T), 539(A), 543(G), 549(T), 566(T), 567(T), 568(T), 569(T), 571(G), 573(A), 574(C), 581(T), 592(T)), and LSU (GenBank NG_058935; Identities 617/641 (96%), three gaps; unique nucleotide at positions 17(G), 19(T), 22(C), 116(C), 120(T), 175(A), 311(G), 312(T), 324(G), 327(T), 331(C), 334(A), 338(T), 370(A), 390(G), 391(C), 424(C), 507(A), 508(C), 512(T), 559(T)). *Husseyia annamariae* differs from *Fiorinimazzantia elisabettae* (ex-type BRIP 72660a) by sequence comparison of the ITS region (GenBank OR750703; Identities 553/637 (87%), 34 gaps; unique nucleotide at positions 77(C), 160(A), 177(A), 178(T), 196(T), 200(T), 204(C), 206(T), 212(C), 217(G), 220(T), 221(C), 223(G), 224(G), 235(C), 241(C), 243(C), 244(T), 253(T), 268(G), 272(T), 275(A), 276(T), 285(G), 288(T), 289(C), 291(T), 293(T), 365(A), 477(T), 482(T), 493(G), 503(G), 505(A), 507(G), 509(T), 536(C), 537(T), 539(A), 543(G), 549(T), 563(T), 565(G), 566(T), 573(A), 574(C), 581(T), 592(T), 595(T), 615(C)), and LSU (GenBank OR731509; Identities 786/812 (97%), two gaps; unique nucleotide at positions 17(G), 20(C), 22(C), 24(C), 116(C), 175(A), 209(C), 210(C), 310(C), 311(G), 327(T), 331(C), 333(G), 369(C), 370(A), 390(G), 391(C), 407(T), 414(C), 445(G), 465(T), 569(T)).

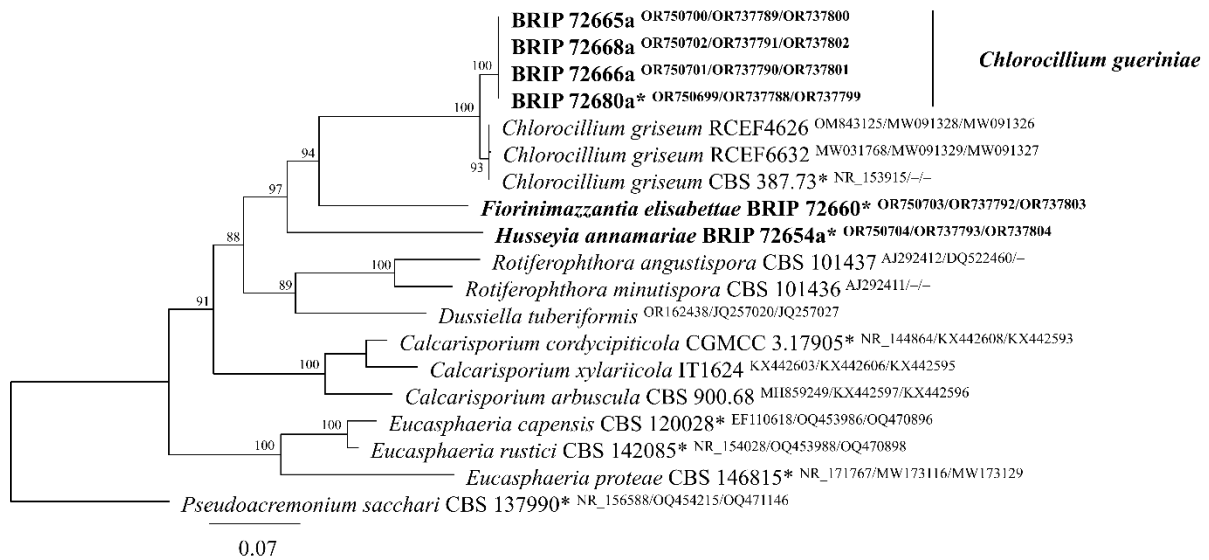
Specimen examined: Australia, Queensland, Wallaman, from an unidentified dead spider colonised by an unidentified hevansia-like fungus, 28 Apr. 2021, *T.S. Marney, Y.P. Tan, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 72654a permanently preserved in a metabolically inactive state).

Etymology: Named after Anna Marie Hussey (née Reed; 1805–1853), a mycologist, illustrator, and writer.

Notes — *Husseyia* is described as the smallest phylogenetic clade that contains the type species, *Husseyia annamariae*, but excludes *Chlorocillium gueriniae*, *C. griseum*, *Dussiella tuberiformis*, *Fiorinimazzantia elisabettae*, *Rotiferophthora angustispora*, and *R. minutispora*.



Decayed insect colonised by an unidentified hirsutella-like fungus from which *Fiorinimazzantia elisabettae* was isolated (left). Decayed spider colonised by an unidentified hevansia-like fungus from which *Husseyia annamariae* was isolated (right). Scale bars = 1 mm.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the ITS, *rpb2*, and *tef1* sequences from related species of *Sordariomycetes*. 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. *Pseudoacremonium sacchari* (ex-type strain CBS 137990) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/*rpb2*/*tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (*).

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