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

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*Aschersonia isabelladesteeae* Y.P. Tan & Marney, *sp. nov.*

IF 901644

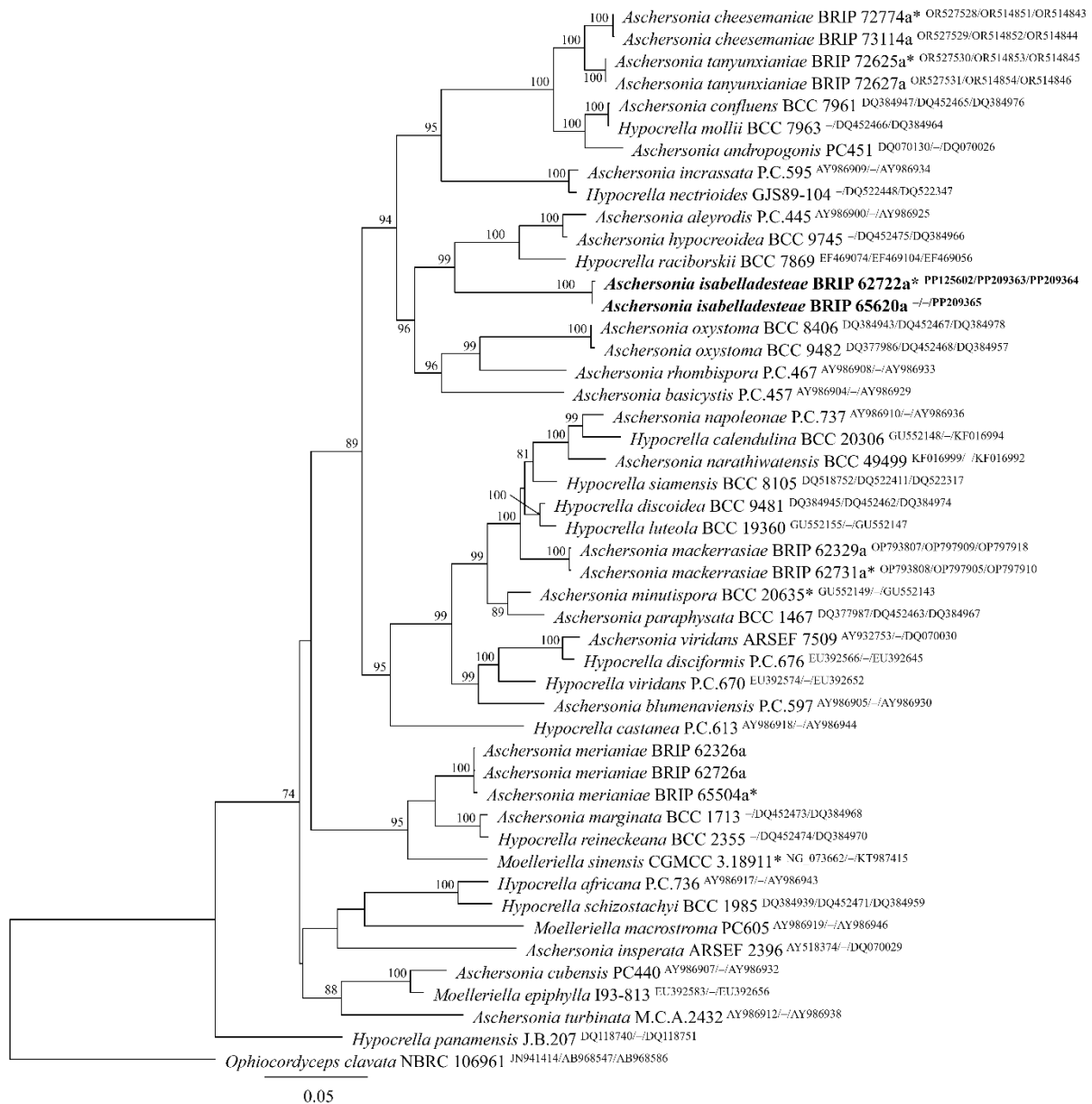
Classification — *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Aschersonia isabelladesteeae* and are available under the accession PP125602 (LSU), PP209363 (*rpb2*), and PP209364 (*tef1*). *Aschersonia isabelladesteeae* differs from *Aschersonia raciborskii* (strain BCC 7869) by sequence comparison of LSU (GenBank EF469074; Identities 498/513 (97%), four gaps; unique nucleotide at positions 40(T), 74(G), 139(T), 253(T), 388(T), 416(T), 433(T), 443(T), 446(C), 448(A), 501(C)), *rpb2* (GenBank EF469104; Identities 728/851 (886%); unique nucleotide at positions 4(A), 8(C), 13(C), 16(G), 22(A), 31(T), 34(C), 40(T), 46(G), 61(A), 70(G), 85(T), 88(A), 103(A), 109(C), 112(T), 121(A), 127(T), 136(C), 145(G), 148(G), 157(T), 172(G), 184(C), 199(T), 205(T), 208(G), 211(G), 220(T), 226(C), 229(A), 238(A), 241(T), 253(G), 256(A), 259(T), 274(A), 277(A), 286(T), 289(T), 292(C), 304(C), 313(T), 316(C), 322(C), 325(T), 328(A), 346(C), 349(C), 352(T), 353(G), 361(C), 379(G), 385(T), 386(T), 388(G), 406(T), 418(T), 439(A), 445(A), 448(T), 466(A), 469(A), 478(C), 493(T), 499(T), 502(G), 508(G), 511(T), 535(C), 541(G), 547(T), 550(T), 554(T), 559(C), 565(G), 571(G), 574(A), 577(G), 580(T), 583(G), 592(C), 598(A), 601(C), 604(T), 610(G), 613(A), 614(T), 622(G), 625(C), 628(T), 634(T), 641(C), 643(A), 646(C), 655(A), 658(G), 665(G), 667(A), 673(C), 676(T), 682(A), 688(G), 692(T), 694(G), 700(A), 712(G), 715(A), 721(C), 725(G), 726(C), 727(T), 728(C), 733(T), 736(T), 739(T), 740(A), 745(C), 766(G), 772(C), 775(G), 784(T), 820(A)), and *tef1* (GenBank EF469056; Identities 894/978 (91%); unique nucleotide at positions 14(C), 44(G), 47(T), 95(T), 104(T), 114(T), 128(C), 137(C), 149(T), 174(A), 200(A), 206(T), 215(G), 218(C), 227(T), 236(G), 239(C), 257(C), 260(T), 263(C), 281(T), 285(C), 287(T), 300(T), 303(C), 304(A), 305(G), 308(T), 313(G), 323(C), 335(T), 356(C), 363(A), 371(C), 380(C), 383(T), 389(C), 401(C), 431(C), 443(T), 455(C), 507(A), 530(T), 533(T), 539(T), 551(C), 572(C), 587(A), 596(C), 603(G), 604(T), 605(C), 623(T), 641(C), 644(T), 695(T), 699(A), 700(T), 710(C), 713(G), 746(C), 752(G), 758(T), 761(C), 767(C), 770(T), 773(C), 794(C), 800(T), 813(G), 822(C), 823(G), 824(C), 833(T), 836(T), 854(C), 866(C), 869(T), 872(G), 905(T), 914(C), 932(G), 859(G), 974(C)).

Colonies on PDA after 4 wk at 25 °C circular, 17–25 mm diam., pale yellow, flat, with narrow mycelial margin 4–5 mm, surface butyrous from abundant conidial production; reverse yellow to pale orange.

*Specimens examined*: Australia, Queensland, Kuranda, on unidentified dead insect (*Hemiptera*, *Sternorrhyncha*), 5 Jun. 2015, T.S. Marney, K.L. Bransgrove, M.D.E. Shivas & R.G. Shivas (holotype BRIP 62722a permanently preserved in a metabolically inactive state); Queensland, Kuranda, on unidentified dead insect (*Hemiptera*, *Sternorrhyncha*), 5 Apr. 2017, T.S. Marney, culture BRIP 65620a (*tef1* sequence GenBank PP209365).

*Etymology*: Named after Isabella d'Este (1474–1539), patron of the arts during the Italian Renaissance.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of LSU, *rpb2* and *tef1* from related species of *Clavicipitaceae*. 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 LSU/*rpb2*/*tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

*Chlamydocillium margaretcollinsiae* Y.P. Tan, Marney & R.G. Shivas, *sp. nov.*

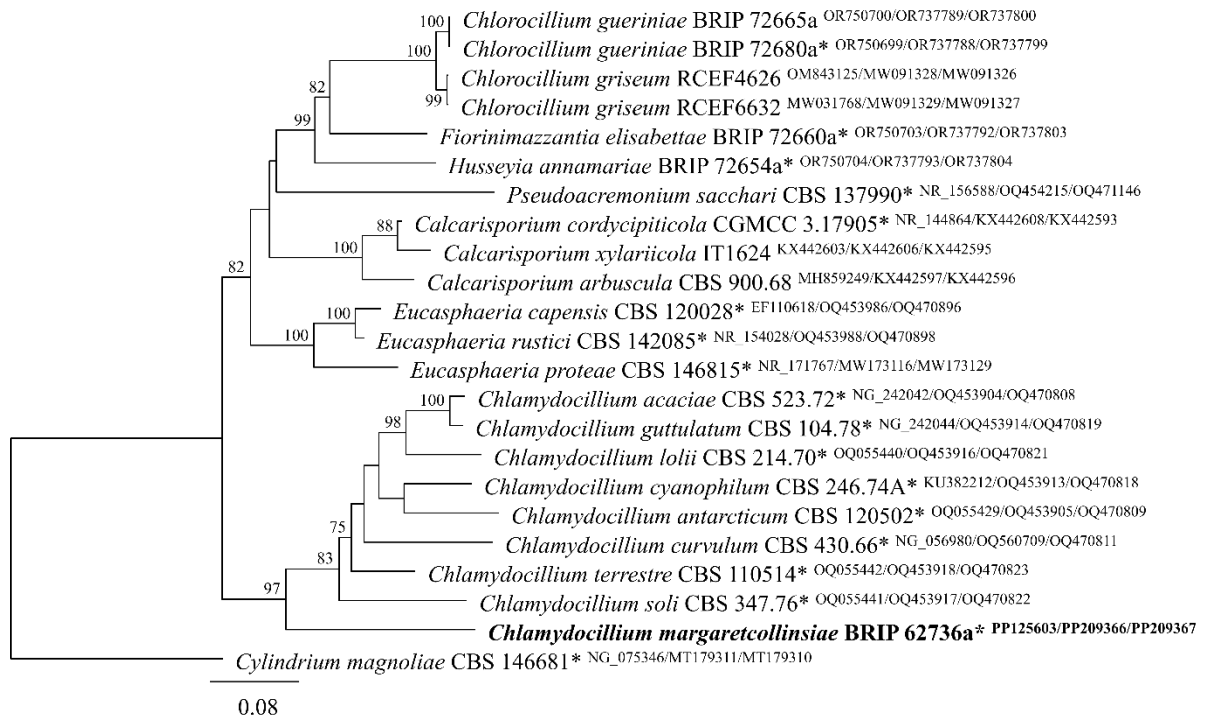
IF 901645

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

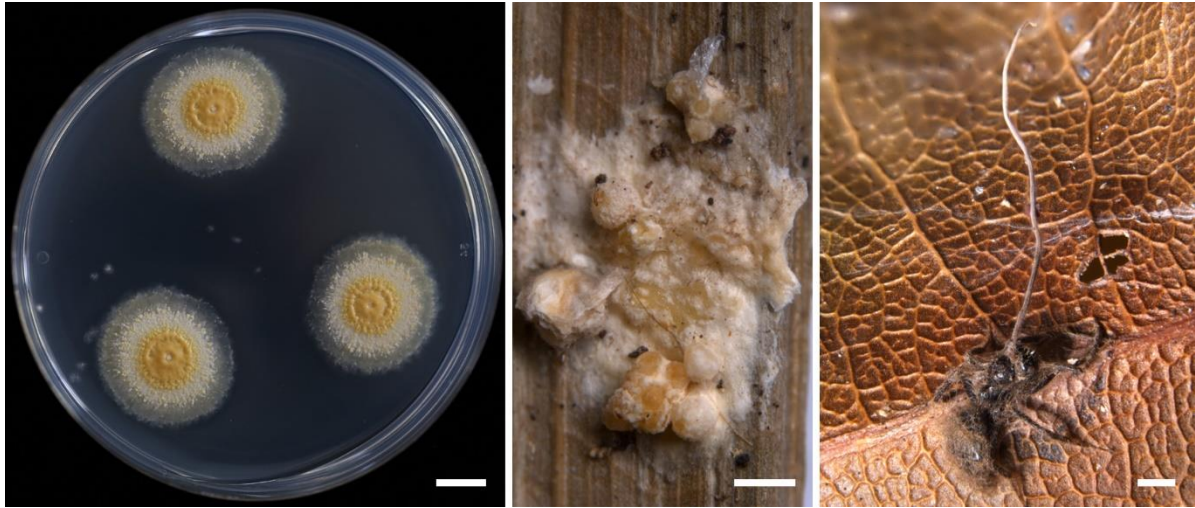
*Diagnosis*: Sequences from the rDNA and nrDNA describe *Chlamydocillium margaretcollinsiae* and are available under the accession PP125603 (LSU), PP125604 (SSU), PP209366 (*rpb2*), and PP209367 (*tef1*). *Chlamydocillium margaretcollinsiae* differs from *Chlamydocillium acaciae* (ex-type strain CBS 523.72) by sequence comparison of LSU (GenBank NG\_242042; Identities 730/781 (93%), three gaps; unique nucleotide at positions 89(T), 91(A), 92(C), 126(A), 130(A), 147(T), 154(A), 173(C), 191(C), 195(T), 196(G), 199(T), 330(C), 334(T), 339(A), 344(G), 354(T), 371(A), 393(G), 397(A), 398(C), 399(C), 400(T), 404(G), 413(G), 424(C), 434(C), 442(C), 458(C), 459(A), 462(T), 477(G), 478(G), 485(T), 488(G), 494(C), 495(T), 514(C), 515(C), 530(G), 531(C), 542(T), 543(A), 552(T), 556(A), 615(T), 652(T), 770(A)). *Chlamydocillium margaretcollinsiae* differs from *Chlamydocillium guttulatum* (ex-type strain CBS 104.78) by sequence comparison of LSU (GenBank NG\_242044; Identities 731/781 (94%), three gaps; unique nucleotide at positions 89(T), 91(A), 92(C), 126(A), 130(A), 147(T), 154(A), 173(C), 191(C), 195(T), 196(G), 199(T), 330(C), 334(T), 339(A), 344(G), 354(T), 371(A), 393(G), 397(A), 398(C), 400(T), 404(G), 413(G), 424(C), 434(C), 442(C), 458(C), 459(A), 462(T), 477(G), 478(G), 485(T), 488(G), 494(C), 514(C), 515(C), 517(T), 530(G), 531(C), 542(T), 543(A), 552(T), 556(A), 515(T), 652(T), 770(A)).

*Specimen examined*: Australia, Queensland, Mission Beach, isolated from an ant (*Polyrhachis brevinoda*) infected with *Ophiocordyceps* sp., 7 Jun. 2015, T.S. Marney, M.D.E. Shivas & R.G. Shivas (holotype BRIP 62736a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Margaret James Strickland Collins (1922–1996), an entomologist and civil rights advocate.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of LSU, *rpb2* and *tub2* 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. *Cylandrium magnoliae* (ex-type strain CBS 146681) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU/*rpb2*/*tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).



*Aschersonia isabelladesteeae* (BRIP 65620a) and *Chlamydocillium margaretcollinsiae* (BRIP 62736a). Colonies of *A. isabelladesteeae* on PDA after 4 wk (left), stromata on leaf (middle). An ant (*Polyrhachis brevinoda*) infected with *Ophiocordyceps* sp. from which *C. margaretcollinsiae* was isolated (right). Scale bars = 1 cm (left), 1 mm (middle), 1 mm (right).

*Eutiarospora mintziae* Y.P. Tan, Ryley & Bishop-Hurley, *sp. nov.*

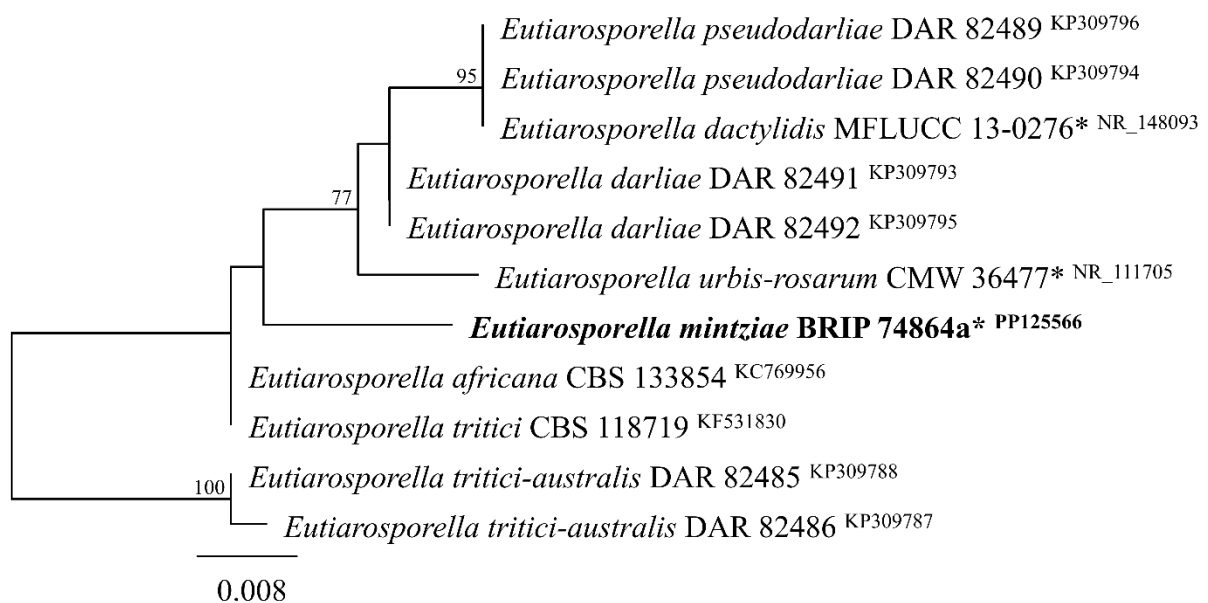
IF 901646

Classification — *Botryosphaeriaceae*, *Botryosphaeriales*, *Dothideomycetes*

**Diagnosis:** Sequence from the rDNA describe *Eutiarospora mintziae* and is available under the accession PP125566 (ITS). *Eutiarospora mintziae* differs from *Eutiarospora dactylidis* (ex-type strain MFLUCC 15-0915) by sequence comparison of the ITS region (GenBank NR\_148093; Identities 425/441 (96%), seven gaps; unique nucleotide at positions 208(C), 265(G), 272(C), 298(G), 306(T), 312(G), 517(C), 573(T), 574(G)). *Eutiarospora mintziae* differs from *Eutiarospora urbis-rosarum* (ex-type strain CMW 36477) by sequence comparison of the ITS region (GenBank NR\_111705; Identities 430/449 (96%), eight gaps; unique nucleotide at positions 208(C), 234(C), 241(G), 265(G), 272(C), 292(G), 298(G), 312(G), 490(C), 573(T), 574(G)).

**Specimen examined:** Australia, Queensland, Peregian Beach, from necrotic sheath of *Spinifex sericeus* (*Poaceae*), 27 Apr. 2022, M.J. Ryley (holotype BRIP 74864a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Beatrice Mintz (1921–2022), an embryologist in the USA, who was a pioneer of genetic engineering that paved the way for progress in cancer research.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region species of *Eutiarospora*. 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. *Eutiarospora tritici-australis* (strains DAR 82485 and DAR 82486) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/actin/*tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

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

IF 901647

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the nrDNA describe *Fusarium bryceae* and are available under the accessions PP209368 (*rpb2*), and PP209369 (*tef1*). *Fusarium bryceae* differs from *Fusarium incarnatum* (ex-type strain CBS 132.73) by sequence comparison of *rpb2* (GenBank MN170409; Identities 833/839 (99%); unique nucleotide at positions 143(A), 341(G), 458(A), 584(G), 710(C), 904(C)), and *tef1* (GenBank MN170476; Identities 528/569 (93%), seven gaps; unique nucleotide at positions 97(G), 109(T), 124(C), 125(C), 134(T), 147(A), 148(G), 228(T), 255(C), 259(A), 260(T), 299(C), 304(A), 305(T), 333(C), 336(A), 338(A), 347(T), 372(G), 379(C), 406(C), 407(T), 412(T), 415(T), 418(A), 449(T), 450(T), 452(C), 618(T), 621(C), 625(A), 629(), 632(T), 637(T)). *Fusarium bryceae* differs from *Fusarium monophialidicum* (ex-type strain NRRL 54973) by sequence comparison of *rpb2* (GenBank MN170416; Identities 832/839 (99%); unique nucleotide at positions 95(C), 143(A), 236(T), 509(A), 620(T), 689(T), 904(C)), and *tef1* (GenBank MN170483; Identities 534/568 (94%), four gaps; unique nucleotide at positions 94(A), 97(G), 112(G), 114(C), 122(T), 124(C), 137(C), 147(A), 148(G), 238(T), 255(C), 260(T), 304(A), 327(T), 331(C), 333(C), 336(A), 372(G), 379(C), 416(G), 418(A), 432(C), 449(T), 450(T), 452(C), 609(A), 618(T), 625(A), 629(T), 637(T)).

*Specimen examined*: Australia, Queensland, Peregian Beach, on *Spinifex sericeus* (*Poaceae*), 9 May 2022, M.J. Ryley (holotype BRIP 74865c permanently preserved in a metabolically inactive state).

*Etymology*: Named after Lucy Meredith Bryce (1897–1968), a haematologist, and medical researcher, who worked with the Australian Red Cross Society to establish the first blood transfusion service in Australia.

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

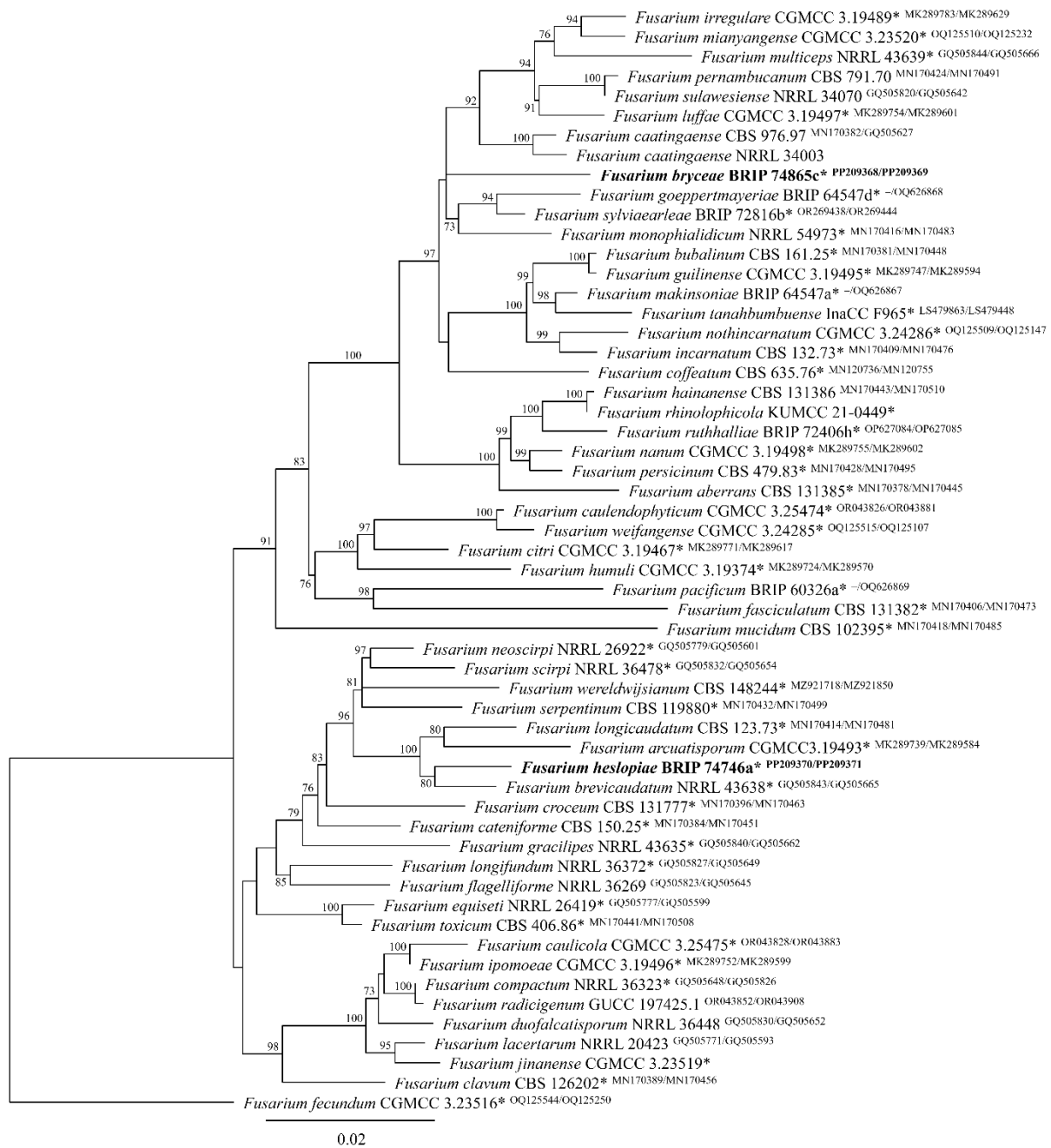
IF 901648

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the nrDNA describe *Fusarium heslopiae* and are available under the accessions PP209370 (*rpb2*), and PP209371 (*tef1*). *Fusarium heslopiae* differs from *Fusarium brevicaudatum* (ex-type strain NRRL 43638) by sequence comparison of *rpb2* (GenBank GQ505843; Identities 883/892 (99%); unique nucleotide at positions 139(T), 235(A), 310(C), 370(C), 386(T), 439(T), 538(T), 944(G), 947(A)), and *tef1* (GenBank GQ505665; Identities 614/630 (97%), two gaps; unique nucleotide at positions 33(A), 47(G), 65(A), 90(C), 92(C), 113(C), 199(T), 253(C), 292(C), 558(C), 561(T), 580(T), 585(T), 595(T)).

*Specimen examined*: Australia, Queensland, Goomeri, on *Sporobolus creber* (*Poaceae*), 24 Mar. 2022, J.S. Vitelli, D. Officer, M.D.E. Shivas & R.G. Shivas (holotype BRIP 74746a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Barbara Farnsworth Heslop (née Cupit; 1925–2013), an immunologist who specialised in transplantation immunology and immunogenetics.



Phylogenetic tree based on the maximum likelihood analysis of the combined alignment of the *rpb2* and *tef1* sequences from species of *Fusarium incarnatum-equiseti* species complex. 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. *Fusarium fecundum* (ex-type strain CGMCC 3.23516) was used as the outgroup. GenBank accession numbers are indicated (superscript *rpb2/tef1*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).



*Nigrospora marylouisemclawsiae* Y.P. Tan, Ryley & Bishop-Hurley, *sp. nov.*

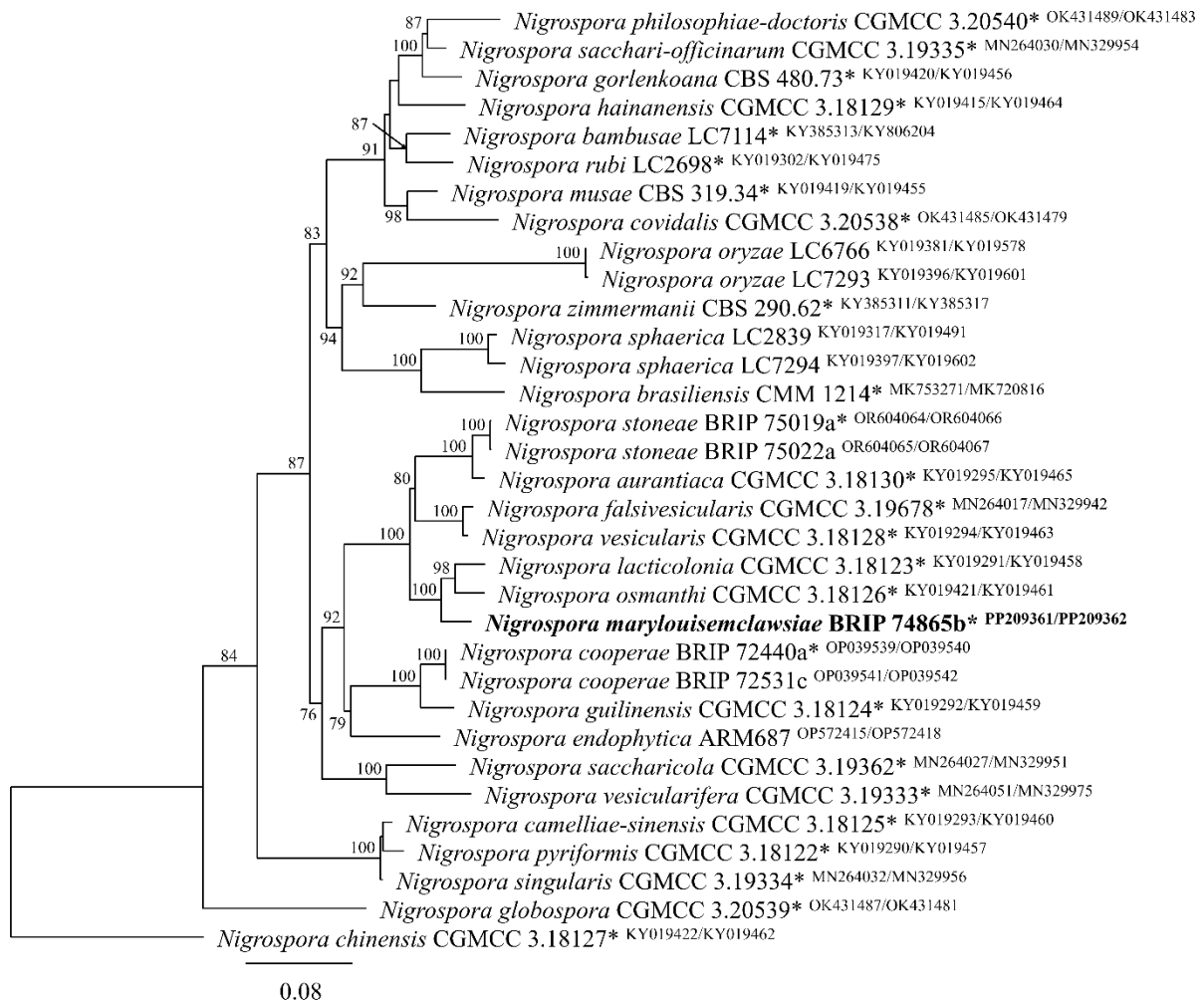
IF 901649

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

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Nigrospora marylouisemclawsiae* and are available under the accessions PP125567 (ITS), PP209361 (*tef1*), and PP209362 (*tub2*). *Nigrospora marylouisemclawsiae* differs from *Nigrospora lacticolonina* (ex-type strain CGMCC 3.18123) by sequence comparison of the ITS region (GenBank NR\_153471; Identities 447/448 (99%); unique nucleotide at position 577(T)), *tef1* (GenBank KY019291; Identities 429/469 (91%), 10 gaps; unique nucleotide at positions 19(T), 22(T), 43(C), 46(G), 49(T), 53(A), 55(C), 67(C), 79(C), 83(C), 84(C), 186(T), 188(T), 207(T), 209(T), 210(G), 216(A), 226(G), 228(G), 382(A), 384(C), 392(G), 394(C), 403(C), 404(G), 405(G), 411(C), 420(T), 423(C), 427(T)), and *tub2* (GenBank KY019458; Identities 379/390 (97%); unique nucleotide at positions 406(T), 479(A), 500(G), 510(C), 526(T), 533(G), 537(G), 610(C), 670(T), 682(T), 703(C)). *Nigrospora marylouisemclawsiae* differs from *Nigrospora osmanthi* (ex-type strain CGMCC3.18126) by sequence comparison of the ITS region (GenBank KX986010; Identities 447/448 (99%); unique nucleotide at position 577(T)), *tef1* (GenBank KY019421; Identities 434/474 (92%), 10 gaps; unique nucleotide at positions 19(T), 22(T), 24(C), 46(G), 48(A), 53(A), 79(C), 150(G), 171(C), 173(A), 186(T), 188(T), 190(G), 196(C), 204(T), 205(T), 207(T), 209(T), 226(G), 228(G), 378(T), 381(C), 392(G), 395(C), 396(A), 403(C), 405(G), 420(T), 423(C), 427(T)), and *tub2* (GenBank KY019461; Identities 394/405 (97%); unique nucleotide at positions 406(T), 470(C), 479(A), 487(G), 500(G), 509(G), 526(T), 533(G), 537(G), 610(C)).

*Specimen examined*: Australia, Queensland, Peregian Beach, *Spinifex sericeus* (*Poaceae*), 9 May 2022, M.J. Ryley (holotype BRIP 74865b permanently preserved in a metabolically inactive state).

*Etymology*: Named after Mary-Louise McLaws (1953–2023), an epidemiologist, who specialised in infectious diseases.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of *tef1* and *tub2* from species of *Nigrospora*. 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. *Nigrospora chinensis* (ex-type strain CGMCC 3.18127) was used as the outgroup. GenBank accession numbers are indicated (superscript actin). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

*Acknowledgement* — J.S. Bartlett is thanked for the identification of insect hosts from which some of these fungi were isolated.