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

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Acremoniopsis crockfordiae Y.P. Tan, Marney & Bishop-Hurley, *sp. nov.*

IF 901724

Classification — *Acremoniopsidaceae*, *Hypocreales*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Acremoniopsis crockfordiae* and are available under the accessions PP420201 (ITS), PP415874 (LSU), PP438394 (*rpb2*), and PP438399 (*tefla*). *Acremoniopsis crockfordiae* differs from *A. suttoniae* (ex-type strain FMR 11780) by sequence comparison of the ITS region (GenBank NR_145059; Identities 484/525 (92%), 20 gaps; unique nucleotide at positions 147(T), 151(T), 181(T), 208(A), 211(A), 213(C), 217(T), 225(T), 247(A), 297(A), 298(T), 303(C), 426(C), 478(C), 516(T), 517(C), 518(C), 538(G), 550(C), 551(T), 578(T)), and LSU (GenBank NG_057045; Identities 784/798 (98%), two gaps; unique nucleotide at positions 89(C), 93(C), 130(C), 185(T), 190(G), 348(C), 381(C), 435(G), 456(A), 473(T), 491(C), 516(C)).

Specimen examined: Australia, Queensland, Hervey Range, on an unidentified dead insect (*Hemiptera*, *Sternorrhyncha*), 26 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 72602a permanently preserved in a metabolically inactive state).

Etymology: Named after Joan Marion Crockford (1919–2015), a geologist and invertebrate palaeontologist, who specialised in Palaeozoic bryozoan. Joan Crockford described two new families, seven new genera, and over 100 new species of bryozoans collected between 1940 and 1956 in Western Australia.



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

IF 901725

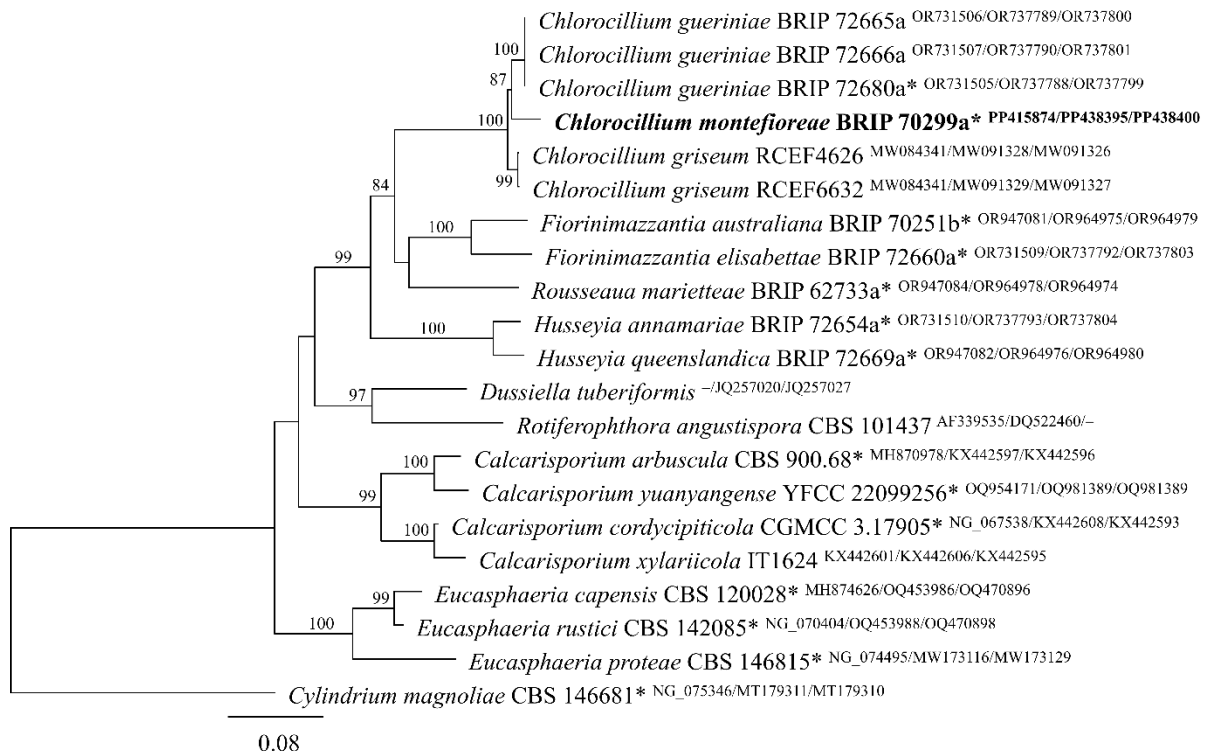
Classification — *Incertae sedis, Incertae sedis, Sordariomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Chlorocillium montefioreae* and are available under the accessions PP420202 (ITS), PP415874 (LSU), PP438395 (*rpb2*), and PP438400 (*tefla*). *Chlorocillium montefioreae* differs from *C. griseum* (ex-type strain CBS 387.73) by sequence comparison of the ITS region (GenBank NR_153915; Identities 532/543 (98%), seven gaps; unique nucleotide at positions 243(G), 255(C), 281(T), 539(A)).

Chlorocillium montefioreae differs from *C. griseum* (strain RCEF4626) by sequence comparison of LSU (GenBank MW084341; Identities 762/767 (99%); unique nucleotide at positions 86(T), 178(T), 400(T), 424(T), 432(A)), *rpb2* (GenBank MW091328; Identities 832/876 (95%); unique nucleotide at positions 6(A), 18(G), 31(T), 39(C), 90(T), 96(G), 108(T), 111(C), 129(G), 189(T), 219(G), 225(A), 228(T), 252(T), 271(T), 274(A), 285(T), 318(C), 327(T), 330(G), 333(T), 417(G), 429(C), 474(C), 504(C), 525(T), 531(G), 585(A), 630(G), 636(C), 639(C), 694(C), 708(A), 723(G), 729(C), 741(A), 747(T), 756(A), 759(T), 768(T), 782(C), 789(C), 813(C)), and *tefla* (GenBank MW091326; Identities 850/872 (97%); unique nucleotide at positions 81(C), 90(C), 102(T), 135(G), 138(T), 240(A), 309(T), 302(T), 305(C), 387(G), 396(C), 453(T), 525(T), 528(C), 561(T), 636(T), 690(T), 693(C), 753(G), 795(A), 825(C), 831(T)).). *Chlorocillium montefioreae* differs from *C. gueriniae* (ex-type strain BRIP 72680a) by sequence comparison of the ITS region (GenBank OR750699; Identities 652/658 (99%), four gaps; unique nucleotide at positions 281(T), 539(A)), LSU (GenBank OR731505; Identities 818/524 (99%), one gap; unique nucleotide at positions 82(A), 86(T), 182(C), 424(T), 432(A)), *rpb2* (GenBank OR737788; Identities 844/893 (95%); unique nucleotide at positions 31(T), 39(C), 69(A), 90(T), 99(G), 108(T), 111(C), 120(G), 129(A), 159(T), 171(C), 186(C), 201(G), 219(G), 225(A), 227(T), 270(G), 271(T), 285(T), 300(C), 318(C), 327(T), 375(A), 382(C), 393(G), 417(G), 429(C), 505(A), 525(T), 531(G), 537(G), 558(G), 585(A), 630(G), 636(C), 639(C), 708(A), 723(G), 741(A), 756(A), 759(T), 768(T), 780(A), 786(A), 789(C), 795(C), 813(C), 878(C), 886(A)), and *tefla* (GenBank OR737799; Identities 854/873 (98%); unique nucleotide at positions 81(C), 102(T), 135(G), 138(T), 165(G), 240(A), 309(T), 312(T), 315(C), 396(C), 501(C), 525(T), 561(T), 562(A), 576(T), 636(T), 689(T), 692(T), 815(G), 831(T)).

Specimen examined: Australia, Queensland, Lake Eacham, on an unidentifiable dead arachnid on the underside of a leaf in the rainforest, 16 May 2019, *T.S. Marney, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 70299a permanently preserved in a metabolically inactive state).

Etymology: Named after Dorothy (Dora) Frances Montefiore (1851–1933), an advocate of women's rights.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the LSU, *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. *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 (*).

Thyridium crespinae Y.P. Tan, Marney & Bishop-Hurley, *sp. nov.*

IF 901726

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

Diagnosis: Sequences from the rDNA and nrDNA describe *Thyridium crespinae* and are available under the accessions PP420204 (ITS), PP415876 (LSU), PP438398 (*rpb2*), and PP438403 (*tef1a*). *Thyridium crespinae* differs from *T. curvatum* (ex-type strain CBS 490.82) by sequence comparison of the ITS region (GenBank AB278180; Identities 658/674 (98%), three gaps; unique nucleotide at positions 234(C), 237(C), 244(G), 254(T), 258(A), 274(G), 323(G), 521(G), 530(C), 582(C), 584(C), 586(T), 627(T)), and LSU (GenBank AB189156; Identities 572/576 (99%); unique nucleotide at positions 80(T), 371(C), 448(C), 523(G)).

Thyridium crespinae differs from *T. flavostromatum* (ex-type strain MAFF 247509) by sequence comparison of the ITS region (GenBank LC655959; Identities 502/522 (96%), four gaps; unique nucleotide at positions 236(C), 244(G), 254(T), 255(A), 256(T), 258(A), 274(G), 321(G), 521(G), 525(C), 530(C), 582(C), 584(C), 586(T), 627(T), 630(A)), and LSU (GenBank LC655963; Identities 814/819 (99%), one gap; unique nucleotide at positions 371(C), 450(C), 467(T), 716(A)). *Thyridium crespinae* differs from *T. hongkongense* (ex-type strain HKU39) by sequence comparison of the ITS region (GenBank NR_149339; Identities 500/514 (97%), two gaps; unique nucleotide at positions 250(C), 255(A), 256(T), 274(G), 321(G), 322(A), 521(G), 530(C), 545(A), 546(C), 627(T), 628(C)), and LSU (GenBank NG_056288; Identities 559/560 (99%); unique nucleotide at position 371(C)).

Thyridium crespinae differs from *T. limonesiae* (ex-type strain CBS 146752) by sequence comparison of the ITS region (GenBank NR_172355; Identities 461/477 (97%), two gaps; unique nucleotide at positions 234(C), 244(G), 255(A), 256(T), 274(G), 313(C), 314(T), 321(G), 521(G), 530(C), 582(C), 584(C), 586(T), 627(T)), and LSU (GenBank MW050976; Identities 452/454 (99%); unique nucleotide at positions 371(C), 485(C)).

Specimen examined: Australia, Queensland, Josephine Falls, from an unidentified dead insect, 23 May 2019, *T.S. Marney* (holotype BRIP 70260b permanently preserved in a metabolically inactive state).

Etymology: Named after Irene Crespin (1896–1980), a geologist and micropalaeontologist, notable for her research on *Foraminifera*.

Thyridium ripperae Y.P. Tan, Marney & Bishop-Hurley, *sp. nov.*

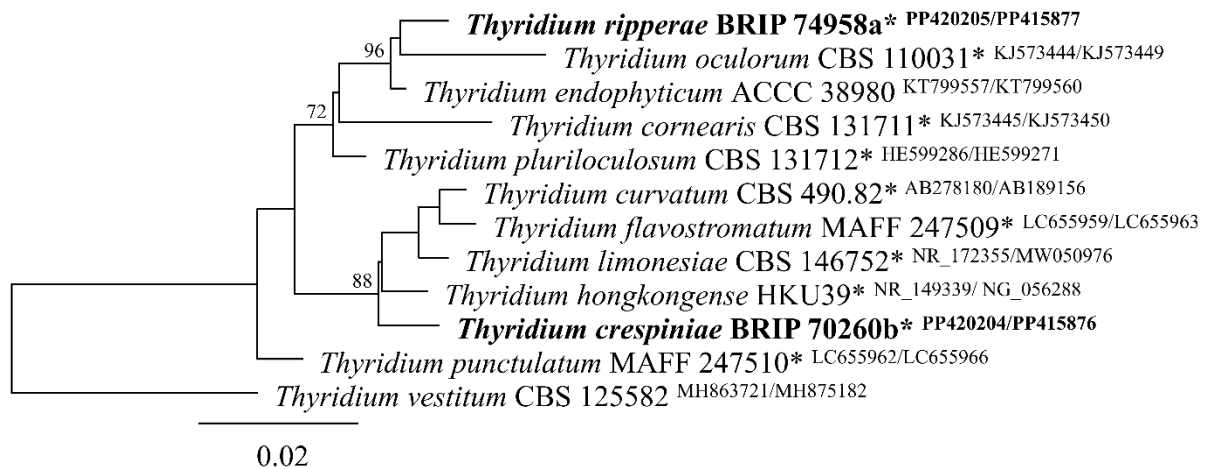
IF 901727

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

Diagnosis: Sequences from the rDNA and nrDNA describe *Thyridium ripperae* and are available under the accessions PP420205 (ITS), and PP415877 (LSU). *Thyridium ripperae* differs from *T. endophyticum* (ex-type strain ACCC 38980) by sequence comparison of the ITS region (GenBank KT799557; Identities 464/470 (99%), two gaps; unique nucleotide at positions 185(T), 235(A), 263(T), 271(T)), and LSU (GenBank KT799560; Identities 864/869 (99%), two gaps; unique nucleotide at positions 7(A), 388(A), 442(T)). *Thyridium ripperae* differs from *T. oculorum* (ex-type strain CBS 110031) by sequence comparison of the ITS region (GenBank KJ573444; Identities 470/483 (97%), three gaps; unique nucleotide at positions 235(A), 238(C), 240(T), 242(C), 245(G), 263(T), 280(A), 281(C), 305(A), 519(G)), and LSU (GenBank KJ573449; Identities 551/561 (98%), two gaps; unique nucleotide at positions 334(C), 388(A), 442(T), 445(T), 447(A), 478(T), 479(C), 513(C)).

Specimen examined: Australia, Tasmania, Collinsvale, from dung of *Trichosurus vulpecula* (*Phalangeridae*), 4 Aug. 2022, T.S. Marney & T. Scharaschkin (holotype BRIP 74958a permanently preserved in a metabolically inactive state).

Etymology: Named after Elizabeth (Betty) Arnold Ripper (1909–2004), a geologist, notable for her work on *Stromatoporoidea*.





Decaying bodies of dead arthropods on the underside of leaf surfaces in tropical Australian rainforests from which *Acremoniopsis crockfordiae* (BRIP 72602a) (left), *Chlorocillium montefioreae* (BRIP 70299a) (middle), and *Thyridium crespinae* (BRIP 70260b) (right) were isolated. Scale bars = 1 mm.

Fusarium idabrowneae Y.P. Tan, *sp. nov.*

IF 901728

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

Diagnosis: Sequences from the nrDNA describe *Fusarium idabrowneae* and are available under the accessions PP438396 (*rpb2*), and PP438401 (*tefla*). *Fusarium idabrowneae* differs from *F. coriorum* (ex-type strain BRIP 47195a) by sequence comparison of *tefla* (GenBank OQ626870; Identities 631/642 (98%), one gap; unique nucleotide at positions 75(T), 123(A), 187(T), 218(A), 275(G), 276(C), 303(G), 307(C), 612(C)). *Fusarium idabrowneae* differs from *F. curvatum* (ex-type strain CBS 238.94) by sequence comparison of *tefla* (GenBank MH484984; Identities 608/618 (98%), two gaps; unique nucleotide at positions 75(T), 197(T), 240(C), 275(G), 276(C), 303(G), 307(C), 321(G)). *Fusarium idabrowneae* differs from *F. nirenbergiae* (ex-type strain CBS 840.88) by sequence comparison of *tefla* (GenBank MH484978; Identities 609/617 (88%), three gaps; unique nucleotide at positions 76(T), 275(G), 303(G), 307(C), 320(C)).

Specimen examined: Australia, Queensland, from bulb rot of *Triteleia* sp. (*Asparagaceae*), 2001, V.M. Brake (holotype BRIP 74541a permanently preserved in a metabolically inactive state).

Etymology: Named after Ida Alison Browne (1990–1976), a geologist, and palaeontologist, who specialised in the systematic studies of brachiopods to assist her stratigraphical research. Ida Browne taught and mentored aspiring young women in palaeontology, and donated books to build geological libraries at the Australian Museum and the University of Wollongong.

Fusarium nashariae Y.P. Tan, *sp. nov.*

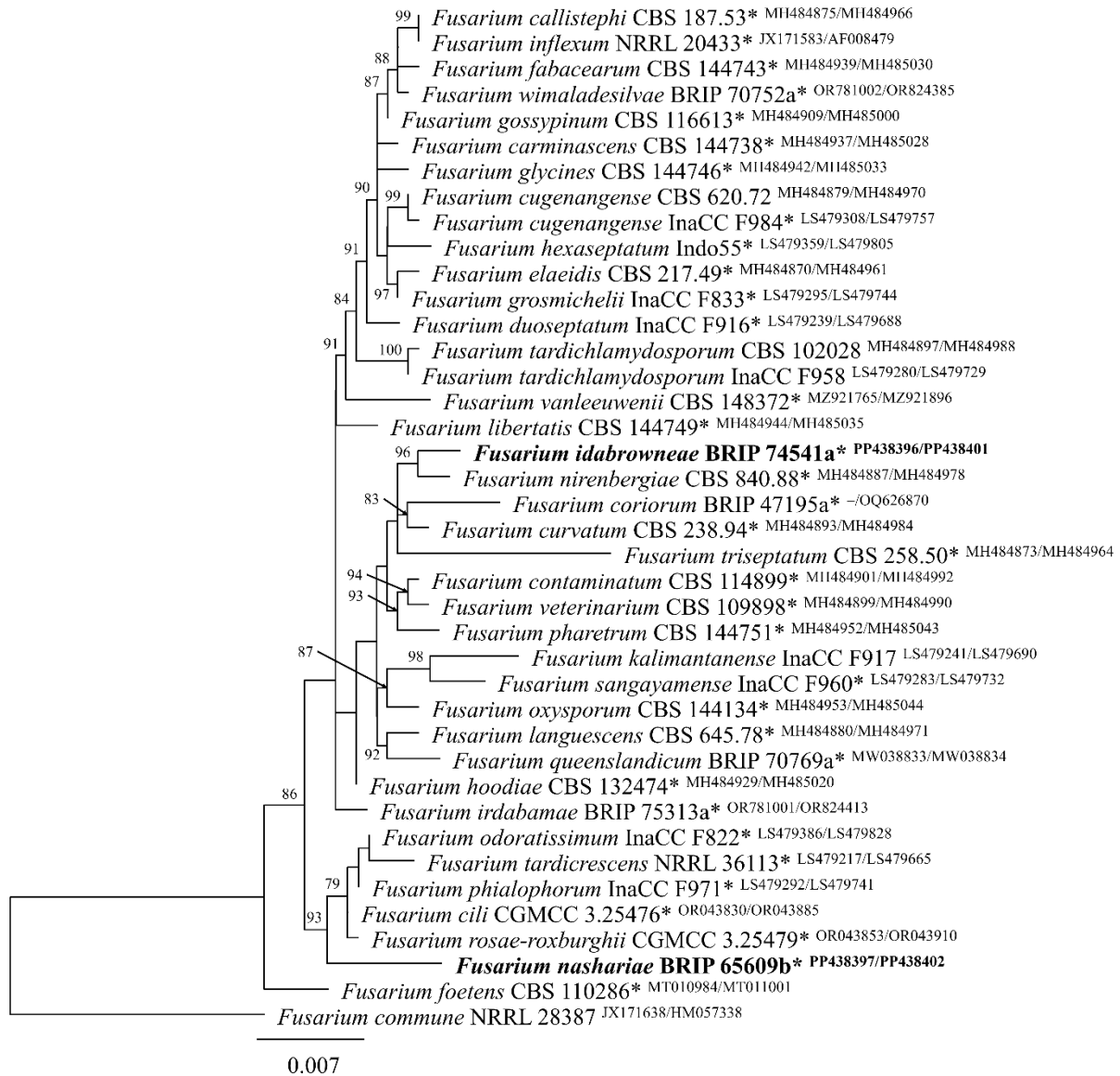
IF 901729

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

Diagnosis: Sequences from the nrDNA describe *Fusarium nashariae* and are available under the accessions PP438397 (*rpb2*), and PP438402 (*tefla*). *Fusarium nashariae* differs from *F. cili* (ex-type strain CGMCC 3.25476) by sequence comparison of *rpb2* (GenBank OR043830; Identities 880/888 (99%); unique nucleotide at positions 15(T), 120(T), 159(A), 186(A), 540(A), 612(G), 750(A), 879(C)), and *tefla* (GenBank OR043885; Identities 628/645 (97%), five gaps; unique nucleotide at positions 75(T), 110(T), 117(T), 127(T), 187(T), 257(T), 275(G), 303(G), 307(C), 341(C), 366(A), 630(C)). *Fusarium nashariae* differs from *F. odoratissimum* (ex-type strain InaCC F822) by sequence comparison of *rpb2* (GenBank LS479386; Identities 847/855 (99%); unique nucleotide at positions 120(T), 159(A), 186(A), 459(T), 540(A), 612(G), 750(A), 879(C)), and *tefla* (GenBank LS479828; Identities 558/576 (97%), five gaps; unique nucleotide at positions 75(T), 110(T), 117(T), 127(T), 187(T), 257(T), 275(G), 303(G), 307(C), 341(C), 366(A), 434(C), 630(C)). *Fusarium nashariae* differs from *F. phialophorum* (ex-type strain InaCC F971) by sequence comparison of *rpb2* (GenBank LS479292; Identities 847/855 (99%); unique nucleotide 120(T), 159(A), 186(A), 459(T), 540(A), 612(G), 879(C)), and *tefla* (GenBank LS479741; Identities 559/576 (97%), five gaps; unique nucleotide at positions 75(T), 110(T), 117(T), 127(T), 187(T), 257(T), 275(G), 303(G), 307(C), 341(C), 366(A), 630(C)). *Fusarium nashariae* differs from *F. rosae-roxburghii* (ex-type strain CGMCC 3.25479) by sequence comparison of *rpb2* (GenBank OR043853; Identities 880/888 (99%); unique nucleotide at positions 15(T), 120(T), 159(T), 186(A), 540(A), 750(A), 879(C)), and *tefla* (GenBank OR043910; Identities 627/645 (97%), five gaps; unique nucleotide at positions 75(T), 110(T), 117(T), 127(T), 187(T), 257(T), 275(G), 303(G), 307(C), 319(C), 341(C), 366(A), 630(C)). *Fusarium nashariae* differs from *F. tardicrescens* (ex-type strain NRRL 36113) by sequence comparison of *rpb2* (GenBank LS479217; Identities 828/835 (99%); unique nucleotide at positions 110(T), 159(A), 177(C), 186(A), 348(A), 530(A), 750(A)), and *tefla* (GenBank LS479665; Identities 557/576 (97%), six gaps; unique nucleotide at positions 75(T), 110(T), 117(T), 127(T), 187(T), 257(T), 275(G), 303(G), 307(C), 341(C), 366(A), 434(C), 630(C)).

Specimen examined: Australia, Queensland, Elimbah, from root rot of *Cordyline* sp. (*Asparagaceae*), 28 Mar. 2017, *M. Hardy* (holotype BRIP 65609b permanently preserved in a metabolically inactive state).

Etymology: Named after Beryl Nashar (née Scott; 1923–2012), a geologist, and academic. In 1952, Beryl Nashar was the first woman to earn a PhD in geology from an Australian university, and in 1969 became the first woman appointed as Dean at an Australian university. Throughout her life, Beryl Nashar advocated for women to receive adequate education and training to allow them to fully participate in the workforce.



Phylogenetic tree based on the maximum likelihood analysis of the concatenated alignment of the *rpb2* and *tef1a* from related species of *Fusarium oxysporum* 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 commune* (strain NRRL 28387) was used as the outgroup. GenBank accession numbers are indicated (superscript *rpb2/tef1a*). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (*).

Neoeriomycopsis wadeae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

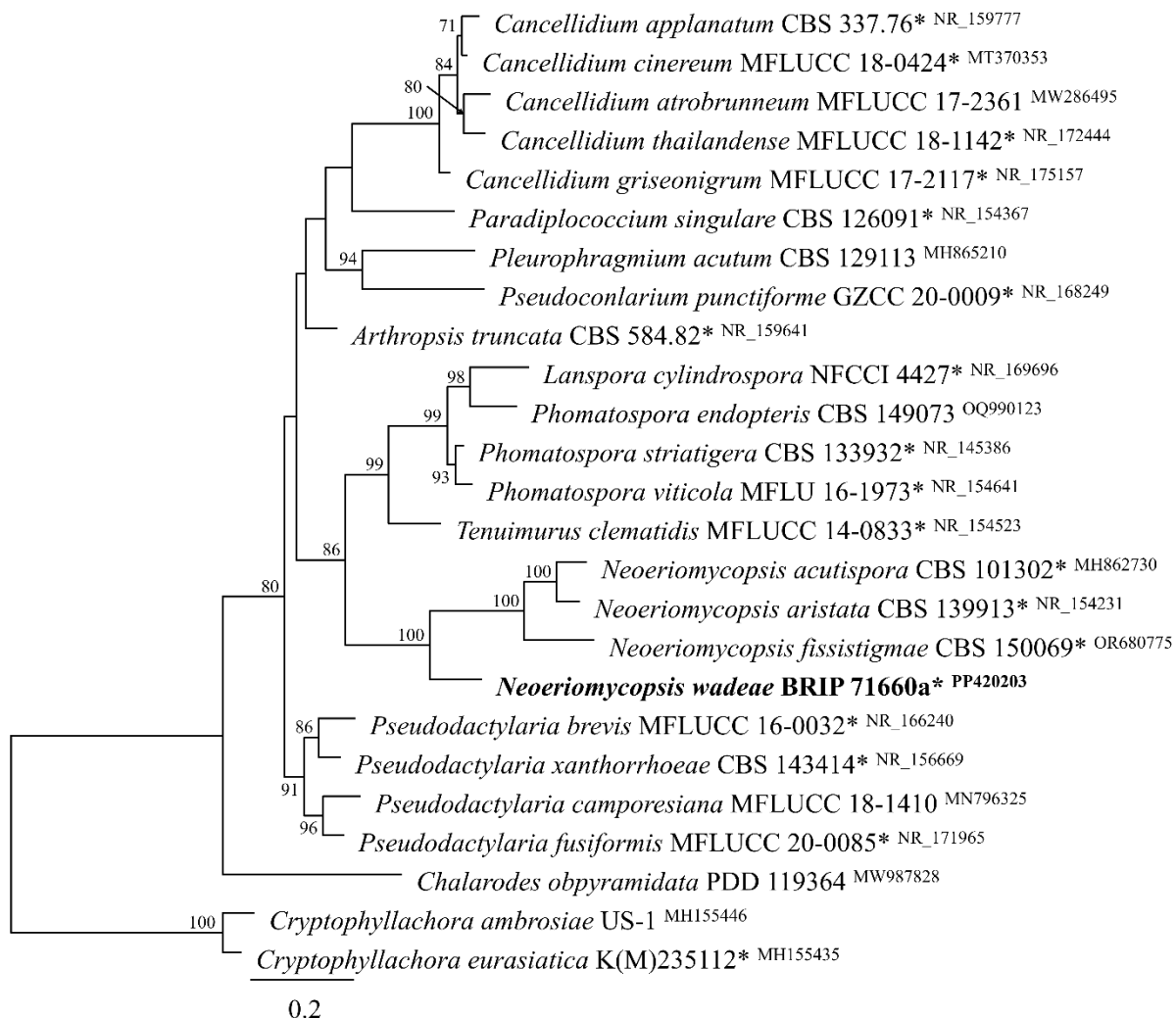
IF 901730

Classification — *Incertae sedis, Incertae sedis, Sordariomycetes*

Diagnosis: Sequence from the rDNA describe *Neoeriomycopsis wadeae* and is available under the accession PP420203 (ITS). *Neoeriomycopsis wadeae* differs from *N. aristata* (ex-type strain CBS 139913) by sequence comparison of the ITS region (GenBank NR_154231; Identities 318/371 (86%), gaps 22/371 (5%); unique nucleotide at positions 15(A), 16(C), 28(C), 32(G), 24(C), 43(C), 44(C), 52(A), 59(A), 60(A), 64(C), 80(G), 99(A), 100(G), 103(C), 104(T), 112(A), 114(A), 116(A), 122(C), 145(C), 146(T), 147(A), 154(T), 156(C), 173(C), 182(A), 203(C), 215(T), 258(T), 335(T)).

Specimen examined: Australia, Queensland, Cape Tribulation, from leaf of *Scipodendron ghaeri* (Cyperaceae), 28 Aug. 2020, A.R. McTaggart, M.D.E. Shivas & R.G. Shivas (holotype BRIP 71660a permanently preserved in a metabolically inactive state).

Etymology: Named after Mary Julia Wade (1928–2005), a palaeontologist, and world-renowned authority on Ordovician nautiloids, dinosaur trackways, Precambrian fossils, and Cretaceous marine reptiles. Mary Wade became the Deputy Director of the Queensland Museum in 1980.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the ITS region of related species of *Sordariomycetes Incertae sedis*. 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. *Cryptophyllachora ambrosiae* (strain US-1) and *C. eurasiatica* (type specimen K(M)235112) 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 (*).