

Index of Australian Fungi no. 1 (ISBN 978-0-6455911-0-1)

DOI: [10.5281/zenodo.7250859](https://doi.org/10.5281/zenodo.7250859)

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

Effectively published 26/10/2022 10:15:00

Erythrobasidium primogenitum Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

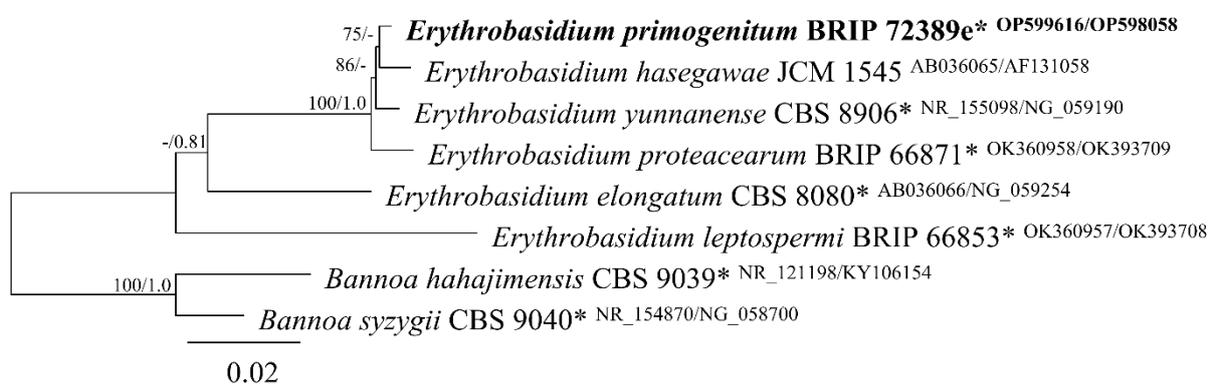
IF 900009

Classification — *Erythrobasidiaceae*, *Erythrobasidiales*, *Cystobasidiomycetes*

Diagnosis: Sequences from the rDNA describe *Erythrobasidium primogenitum* and are available in GenBank under the accessions OP599616 (ITS region) and OP598058 (LSU). *Erythrobasidium primogenitum* differs by sequence comparison of the ITS region from *E. hasegawae* (ex-type strain JCM 1545; GenBank NR_111008; Identities 587/596 (98%), Gap 1/596; unique nucleotides at positions 180(A), 226(C), 234(T), 284(A), 296(G), 299(T), 548(G) and 592(T), and *E. yunnanense* (ex-type strain CBS 8906; GenBank KY103394; Identities 683/689 (99%), Gaps 2/689; unique nucleotides at positions 180(A), 234(T), 296(G) and 501(C)).

Specimen examined: Australia, Queensland, Georgetown, from *Senna alata* (*Fabaceae*), 22 Apr. 2021, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72389e preserved in a metabolically inactive state).

Etymology: From Latin, *primogenitum*, meaning ‘first born’, in reference to the first species to be described in the Index of Australian Fungi.



Phylogenetic tree based on a maximum likelihood analysis of concatenated multilocus alignment (ITS and LSU) from species of *Erythrobasidium*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Bannoa hahajimensis* (ex-type strain CBS 114309) and *B. syzygii* (ex-type strain CBS 9040) were used as the outgroup. Ex-type strains are marked with asterisks (*).

Annulohypoxylon crowfoothodgkiniae Y.P. Tan, Bishop-Hurley, Bransgr. & R.G. Shivas, *sp. nov.*

IF 900010

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

Diagnosis: Sequences from the rDNA describe *Annulohypoxyton crowfoothodgkiniae* and are available in GenBank under the accessions OP599617 (ITS region) and OP598059 (LSU). *Annulohypoxyton crowfoothodgkiniae* differs by sequence comparison of the ITS region from *A. nitens* (strain CBS 119134; GenBank KC968927; Identities 830/839 (99%), two gaps; unique nucleotide at positions 213(T), 239(T), 278(T), 333(C)), *A. atroseum* (strain ATCC 76081; GenBank AF201712; Identities 457/464 (98%), one gap; unique nucleotide at positions 719(C), 768(A), 779(G), 783(T), 868(C)), and *A. stygium* (strain MUCL 54601; GenBank KY610409; Identities 515/528(98%), one gap; unique nucleotide at positions 357(C), 364(G), 381(T), 411(T), 429(T), 431(T), 438(T), 517(T), 736(T), 768(A), 779(G), 784(G)). *Annulohypoxyton crowfoothodgkiniae* differs by sequence comparison of the LSU from *A. atroseum* (strain ATCC 76081; GenBank KY610422; Identities 834/838 (99%); unique nucleotide at positions 184(A), 193(C), 407(A), 412(T)), and *A. stygium* (strain MUCL 54601; GenBank KY610475; Identities 800/805 (99%); unique nucleotide at positions 183(C), 405(T), 407(A), 410(T), 412(T)).

Specimen examined: Australia, Queensland, Mission Beach, from necrotic leaf spot of *Pandanus tectorius* (Pandanaeae), 30 Apr. 2021, K.L. Bransgrove, Y.P. Tan, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72527h preserved in a metabolically inactive state).

Etymology: Named after Dorothy Mary Crowfoot Hodgkin (1910–1994), a British chemist, whose research advanced the technique of X-ray crystallography to determine the 3-dimensional structure of biomolecules. Among her many discoveries were the confirmation of the structure of penicillin, and the structure of vitamin B₁₂, for which she was awarded the Nobel Prize in Chemistry.

Annulohypoxyton kwolekiae Y.P. Tan & R.G. Shivas, *sp. nov.*

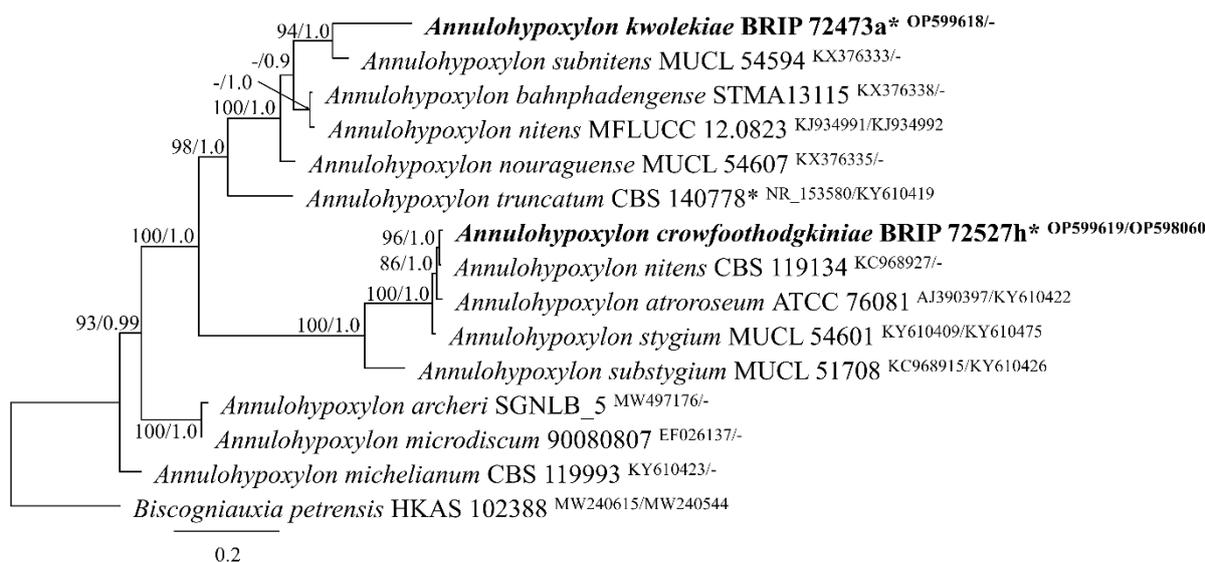
IF 900011

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

Diagnosis: Sequence from the rDNA describe *Annulohypoxyton kwolekiae* and is available in GenBank under the accession OP599618 (ITS region). *Annulohypoxyton kwolekiae* differs from *A. subnitens* (MUCL 54594) by sequence comparison of the ITS region (GenBank KX376333; Identities 486/518 (93%), nine gaps; unique nucleotide at positions 171(C), 195(A), 200(A), 338(T), 340(A), 346(T), 349(A), 544(C), 559(G), 566(C), 568(G), 571(C), 572(G), 578(C), 579(T), 588(C), 642(G), 644(A), 645(T), 649(G), 658(A), 667(A)).

Specimen examined: Australia, Queensland, Wallaman, from leaf of *Scleria* sp. (Cyperaceae), 28 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley & S.M. Thompson (holotype BRIP 72473a preserved in a metabolically inactive state).

Etymology: Named after Stephanie Louise Kwolek (1923–2014), a Polish-American polymer chemist, and the inventor of Kevlar, a strong and heat-resistant synthetic fibre.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region and LSU) from species of *Annulohypoxyton*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Biscogniauxia petrensis* (HKAS 102388) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Cylindroaseptospora bennettiae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 900012

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

Diagnosis: Sequences from the rDNA describe *Cylindroaseptospora bennettiae* and are available in GenBank under the accessions OP599619 (ITS region) and OP598060 (LSU). *Cylindroaseptospora bennettiae* differs from *C. leucaenae* (ex-type strain MFLUCC 17-2424) by sequence comparison of the ITS region (GenBank NR_163333; Identities 441/458 (96%), seven gaps; unique nucleotide at positions 252(C), 255(C), 289(G), 323(T), 336(C), 367(C), 371(T), 638(G), 658(C), 683(G)), and LSU (GenBank NG_066310; Identities 826/856 (96%), five gaps; unique nucleotide at positions 32(T), 38(C), 44(A), 47(C), 51(A), 56(C), 83(G), 85(G), 104(T), 111(T), 112(G), 114(C), 121(C), 123(A), 139(C), 148(A), 155(G) 160(G), 191(G), 195(C), 206(G), 405(C), 433(T), 497(A), 650(C)).

Specimen examined: Australia, Queensland, Petford, from leaf spot of *Themeda arguens* (*Poaceae*), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72408d preserved in a metabolically inactive state).

Etymology: Named after Isobel Ida Bennett (1909–2008), an Australian biologist and conservationist. Isobel Bennett co-authored and illustrated *Australian Seashores* (1952), which became a landmark textbook that was both influential in educating the general public about local seashores, and also inspired generations of marine scientists. Isobel Bennett’s research was often self-funded and spanned decades, covering the entire span of the Great Barrier Reef (2 000 km in length). Her subsequent publications, *The Great Barrier Reef* (1971) and *A Coral Reef Handbook* (1978), led to the recognition of the Great Barrier Reef as a UNESCO World Heritage Site in 1980. In 1984, Isobel Bennett was awarded the Order of Australia for services to marine biology. While reflecting on her life saying, she is quoted as saying “I never married. Although there were several opportunities, it

wasn't the right man. Had I married I probably wouldn't have been able to do many of the things I've done".

Deniquelata macphersoniae Y.P. Tan, Bishop-Hurley, Bransgr. & R.G. Shivas, *sp. nov.*

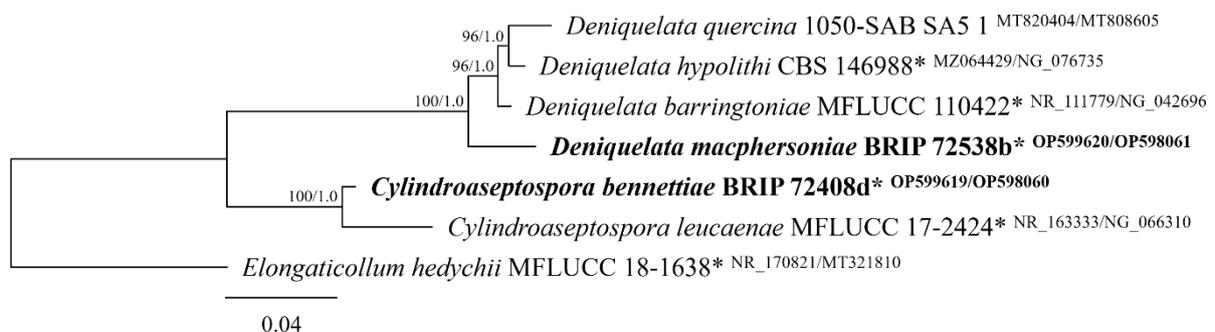
IF 900013

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

Diagnosis: Sequences from the rDNA describe *Deniquelata macphersoniae* and are available in GenBank under the accessions OP599620 (ITS region) and OP598061 (LSU). *Deniquelata macphersoniae* differs from *D. barringtoniae* (ex-type strain MFLUC 110422) by sequence comparison of the ITS region (GenBank NR_111779; Identities 680/735 (93%), 23 gaps; unique nucleotide at positions 163(C), 181(G), 193(C), 201(C), 207(T), 212(T), 231(G), 237(G), 252(C), 254(A), 261(G), 279(G), 288(G), 295(C), 316(C), 325(T), 327(C), 339(A), 341(C), 353(A), 354(G), 360(G), 362(G), 365(C), 421(C), 451(T), 460(C), 478(C), 619(C), 695(C), 797(A), 806(A)), and LSU (GenBank NG_042696; Identities 671/683 (98%), one gap; unique nucleotide at positions 83(C), 85(T), 89(G), 191(T), 419(C), 422(C), 423(C), 434(A), 437(C), 533(C), 562(C)). *Deniquelata macphersoniae* differs from *D. hypolithi* (ex-type strain CBS 146988) by sequence comparison of the ITS region (GenBank MZ064429; Identities 655/709 (92%), 20 gaps; unique nucleotide at positions 163(C), 176(G), 181(G), 193(C), 201(C), 211(G), 212(T), 231(G), 237(G), 252(C), 254(A), 261(G), 273(A), 279(G), 290(A), 295(C), 303(C), 316(C), 325(T), 327(C), 341(C), 343(G), 353(A), 354(G), 360(G), 362(G), 365(C), 450(T), 459(C), 477(C), 618(C), 694(C), 796(C), 805(A)), and LSU (GenBank NG_076735; Identities 797/814 (98%), one gap; unique nucleotide at positions 84(C), 183(A), 184(C), 185(G), 192(T), 420(C), 423(C), 424(C), 435(A), 438(C), 534(C), 563(C), 738(G), 747(G), 796(G), 805(C)).

Specimen examined: Australia, Queensland, Chillagoe, from *Polycarpaea spirostylis* (*Caryophyllaceae*), 19 Apr. 2021, K.L. Bransgrove, Y.P. Tan, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72538b preserved in a metabolically inactive state).

Etymology: Named after Hope Black (née Macpherson; 1919–2018), an Australian marine biologist, who made extensive biological surveys in the Snowy River Gorge and Port Phillip Bay. The results of her studies are still used today as baseline data from which to measure environmental changes in these regions. Hope Black was one of the first four women to conduct research in the sub-Antarctic at Macquarie Island. Hope Black was appointed the Curator of Molluscs at the National Museum of Victoria in 1946, the Museum's first woman in that role. When Hope Black married in 1965, she was forced to leave the Museum, and instead became a science teacher, who encouraged a passion for science in her students and promoted opportunities for women in science.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region and LSU) species from *Cyldroaseptospora* and *Deniquelata*. Analyses were performed on the

Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Elongaticollum hedychii* (ex-type strain MFLUCC 18-1638) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Dicephalospora sagerae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

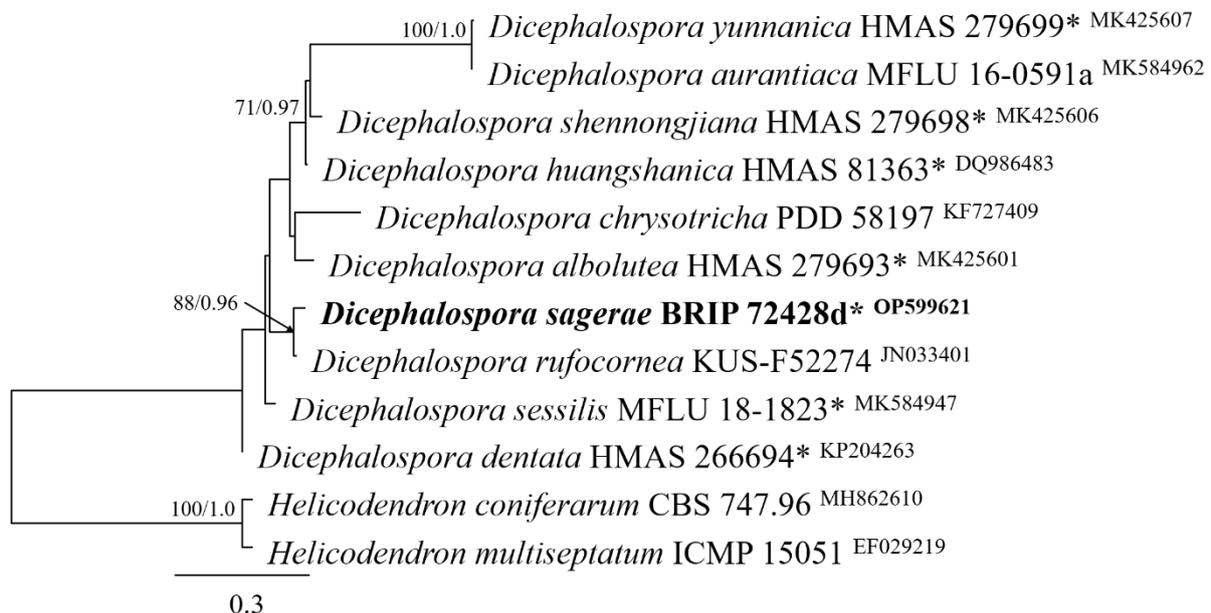
IF 900014

Classification — *Helotiaceae*, *Helotiales*, *Leotiomyces*

Diagnosis: Sequence from the rDNA describe *Dicephalospora sagerae* and is available in GenBank under the accession OP599621 (ITS region). *Dicephalospora sagerae* differs by sequence comparison of the ITS region from *D. rufocornea* (KUS-F52274; GenBank JN033401; Identities 448/457 (98%), one gap; unique nucleotide at positions 103(C), 123(C), 165(T), 172(T), 185(C), 226(C), 250(G), 440(T)).

Specimen examined: Australia, Queensland, Mission Beach, Lacey's Creek, from unidentified insect, 30 Apr. 2021, *M.D.E. Shivas & R.G. Shivas* (holotype BRIP 72428d preserved in a metabolically inactive state).

Etymology: Named after Ruth Sager (1918–1997), an American geneticist renowned for her research in the field of cytoplasmic genetics. Ruth Sager discovered the transmission of genetic traits through chloroplast DNA, the first known example of cellular genetics that did not involve the nucleus.



Phylogenetic tree based on a maximum likelihood analysis of the ITS region alignment from species of *Dicephalospora*. Analyses were performed on the Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS). *Helicodendron coniferarum* (strain CBS 747.96) and *H. multiseptatum* (strain ICMP 15051) were used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

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

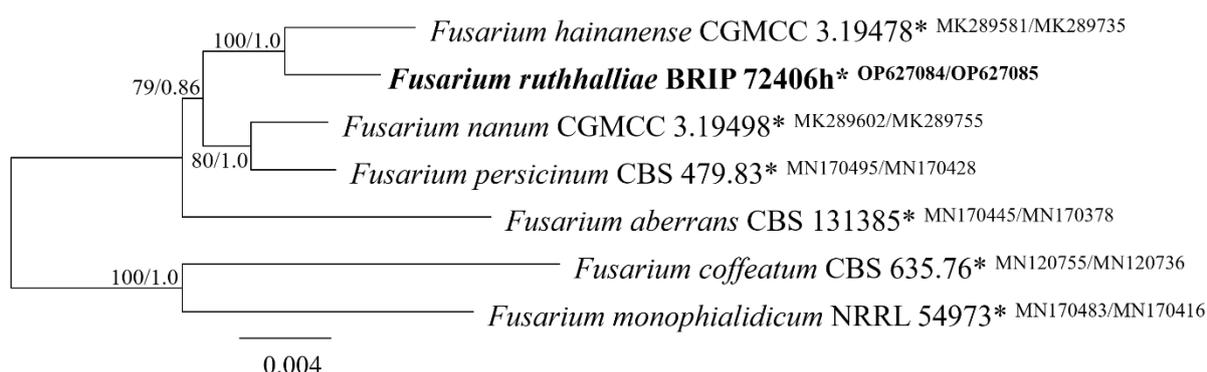
IF 900015

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

Diagnosis: Sequences from the rDNA and nrDNA describe *Fusarium ruthhalliae* and are available in GenBank under the accessions OP627084 (DNA-directed RNA polymerase II second largest, *rpb2*) and OP627085 (translation elongation factor 1-alpha, *tef1* α). *Fusarium ruthhalliae* differs from *F. hainanense* (ex-type strain CGMCC 3.19478) by sequence comparison of *tef1* α (GenBank MK289581; Identities 589/602 (98%), three gaps; unique nucleotide at positions 73(C), 99(G), 137(C), 233(T), 283(G), 303(T), 343(G), 441(C), 604(A), 623(T)).

Specimen examined: Australia, Queensland, Petford, from inflorescence of *Sorghum plumosum* (*Poaceae*), 19 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72406h preserved in a metabolically inactive state).

Etymology: Named after Ruth Milne Hall, an Australian microbiologist renowned for her research on mobile genetic elements in bacteria. Ruth Hall's research led to an understanding of how bacteria become resistant to many antibiotics simultaneously, as well as a recognition of the risks posed by the increased use of antibiotics in medicine and agriculture. In 2014, Ruth Hall was awarded the Medal of the Order of Australia for service to science in the field of microbiology.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (*rpb2* and *tef1* α) from species of *Fusarium incarnatum-equiseti* species complex. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript *tef1* α /*rpb2*). *Fusarium coffeatum* (ex-type strain CPC 16179) and *F. monophialidicum* (ex-type strain were used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Hypoxylon blackburniae Y.P. Tan & R.G. Shivas, *sp. nov.*

IF 900016

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

Diagnosis: Sequence from the rDNA describe *Hypoxylon blackburniae* and is available in GenBank under the accessions OP599622 (ITS region) and OP602214 (LSU). *Hypoxylon blackburniae* differs by sequence comparison of the ITS region from *H. begae* (GenBank JN660820; Identities 501/521 (96%); unique nucleotide at positions 149(T), 158(A), 181(A), 184(C), 211(C), 229(G), 230(C),

233(T), 234(A), 237(C), 245(C), 434(A), 435(G), 501(T), 502(G), 536(C), 537(A), 572(G), 584(G) 591(A)), and *H. vinosopulvinatum* (GenBank JQ009321; Identities 504/522 (97%), three gaps; unique nucleotide at positions 149(T), 158(A), 181(A), 197(A), 228(C), 231(T), 285(T), 494(A), 503(C), 515(C), 520(C), 521(G), 537(A), 572(G), 58-(G)).

Specimen examined: Australia, Queensland, Wallaman, from leaf of *Scleria* sp. (*Cyperaceae*), 28 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72467b preserved in a metabolically inactive state).

Etymology: Named after Elizabeth Helen Blackburn, a molecular biologist who was the first Australian woman to win a Nobel Prize. Elizabeth Blackburn was awarded the 2009 Nobel Prize in Physiology or Medicine, together with Carolyn W. Greider and Jack W. Szostak, for their discovery of how chromosomes are protected by telomeres and the enzyme telomerase.

Hypoxylon greiderae Y.P. Tan, Bishop-Hurley, Bransgr. & R.G. Shivas, *sp. nov.*

IF 900017

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

Diagnosis: Sequences from the rDNA describe *Hypoxylon greiderae* and are available in GenBank under the accessions OP599623 (ITS region) and OP598062 (LSU). *Hypoxylon blackburniae* differs by sequence comparison of the ITS region from *H. aveirense* (ex-type strain MUM 19.40; GenBank NR_173851; Identities 486/510 (95%), six gaps; unique nucleotide at positions 249(A), 252(C), 253(C), 254(C), 263(T), 288(A), 289(G), 472(A), 473(A), 479(C), 482(G), 485(T), 505(G), 507(G), 552(G), 581(G), 594(A), 603(A)).

Specimen examined: Australia, Queensland, Cardwell, from gills of *Phillipsia subpurpurea* (*Sarcoscyphaceae*), 27 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72533b preserved in a metabolically inactive state).

Etymology: Named after Carolyn Widney Greider, an American molecular biologist, who was awarded the 2009 Nobel Prize in Physiology or Medicine, together with Elizabeth Blackburn and Jack W. Szostak, for the discovery of how chromosomes are protected by telomeres and the enzyme telomerase.

Hypoxylon szostakii Y.P. Tan, Bishop-Hurley, Bransgr. & R.G. Shivas, *sp. nov.*

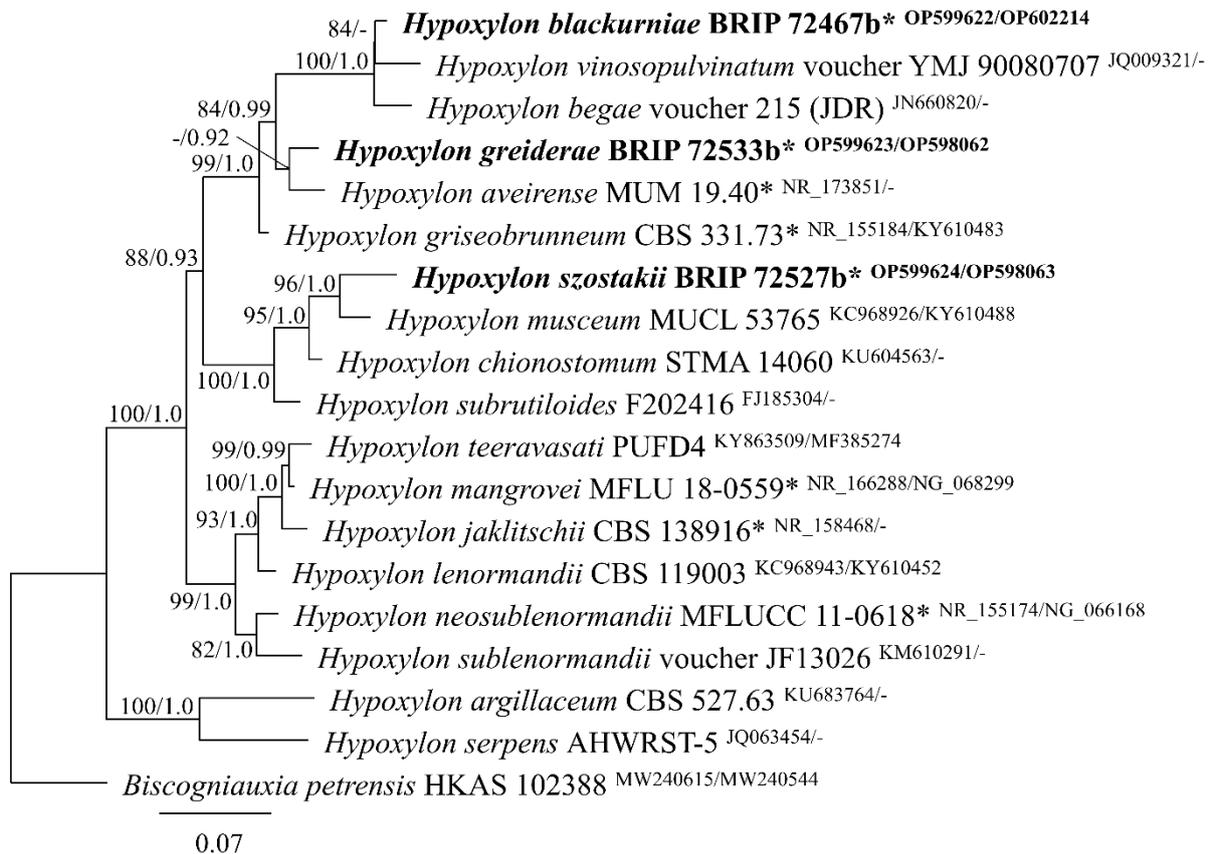
IF 900018

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

Diagnosis: Sequences from the rDNA describe *Hypoxylon greiderae* and are available in GenBank under the accessions OP599624 (ITS region) and OP598063 (LSU). *Hypoxylon blackburniae* differs from *H. musceum* (strain MUCL 53765) by sequence comparison of the ITS region (GenBank KC968926; Identities 590/634 (93%), 10 gaps; unique nucleotide at positions 208(A), 210(T), 211(C), 234(T), 282(T), 298(G), 303(A), 306(T), 326(C), 327(A), 342(C), 358(T), 372(A), 544(C), 555(G), 560(A), 592(A), 603(T), 604(C), 617(A), 633(G), 649(C), 650(T), 661(C), 604(C), 611(C), 616(T), 620(A), 629(C), 635(C), 637(T), 638(C), 642(A), 643(A)), and LSU (GenBank KY610488; Identities 790/815 (97%), two gaps; unique nucleotide at positions 175(A), 186(C), 187(A), 190(T), 192(C), 378(G), 411(A), 416(T), 455(T), 473(T), 481(C), 491(C), 511(C), 538(C), 540(T), 544(T), 547(A), 548(T), 549(T), 551(T), 552(A), 632(A), 676(T)).

Specimen examined: Australia, Queensland, Mission Beach, from necrotic leaf spot of *Pandanus tectorius* (Pandanaeae), 30 Apr. 2021, K.L. Bransgrove, Y.P. Tan, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72527b preserved in a metabolically inactive state).

Etymology: Named after Jack William Szostak, a Canadian American geneticist of Polish-British descent, who was awarded the 2009 Nobel Prize in Physiology or Medicine, together with Elizabeth Blackburn and Carolyn Greider, for the discovery of how chromosomes are protected by telomeres and the enzyme telomerase.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region and LSU) from species of *Hypoxylon*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Biscogniauxia petrensis* (HKAS 102388) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Neokirramyces connolei Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 900019

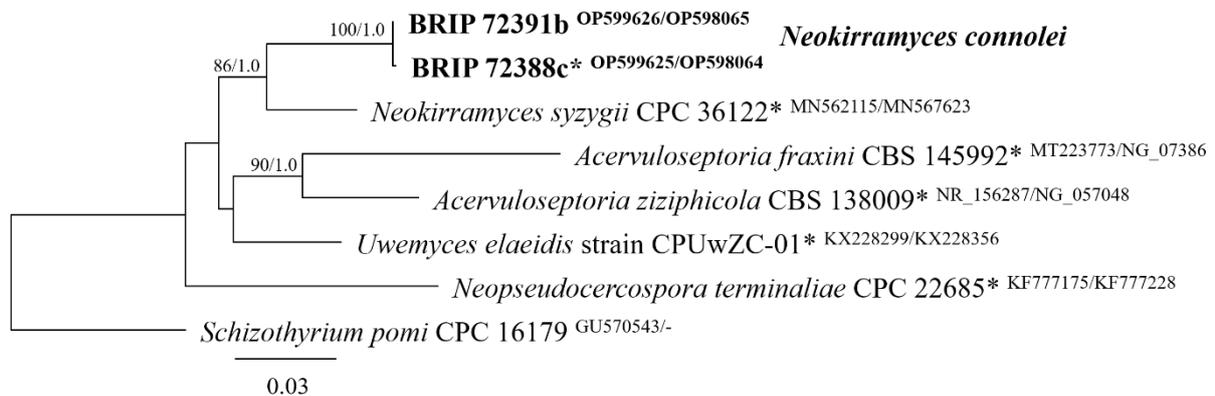
Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA describe *Neokirramyces connolei* ex-type strain BRIP 72388c and are available in GenBank under the accessions OP599625 (ITS region) and OP598064 (LSU). *Neokirramyces connolei* differs from *N. syzygii* (ex-type strain CPC 36122) by sequence comparison of the ITS region (GenBank NR_166317; Identities 438/478 (92%), 10 gaps; unique nucleotide at

positions 234(T), 239(C), 240(C), 241(C), 242(C), 243(G), 254(C), 268(T), 269(G), 280(T), 281(T), 294(A), 298(A), 300(C), 305(G), 306(C), 308(G), 473(G), 477(C), 483(C), 487(G), 507(T), 517(T), 518(C), 540(T), 562(T), 570(T), 576(C), 581(C)), and LSU (GenBank NG_068320; Identities 757/782 (97%); unique nucleotide at positions 72(G), 84(A), 102(T), 128(T), 155(T), 185(A), 393(G), 395(T), 409(T), 425(G), 427(C), 429(C), 432(C), 461(G), 467(G), 481(A), 492(T), 507(T), 519(T), 523(T), 540(C), 542(T), 669(T), 673(T), 718(G)).

Specimens examined: Australia, Queensland, Paluma Range, from leaf spot of *Smilax glycyphylla* (*Smilacaceae*), 26 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72388c preserved in a metabolically in active state); Cardwell, from leaf spot of *Smilax* sp. (*Smilacaceae*), 27 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas, culture BRIP 72391b, ITS and LSU sequences GenBank OP599626 and OP598065.

Etymology: Named after Michael Desmond (Des) Connole (1927–2020), an Australian veterinary mycologist, who was actively engaged in research, training, diagnosis, and control of veterinary mycoses in Australia for nearly 50 years. Des Connole established the first Australian veterinary mycology unit while based in Brisbane, Queensland. He was a founding member of the Australian Society of Microbiology.



Phylogenetic tree based on a maximum likelihood analysis the concatenated alignment (ITS region and LSU) from *Neokirramyces* and phylogenetically related taxa. Analyses were performed on the Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Schizothyrium pomi* (strain CPC 16179) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Neottiosporina ashworthiae Y.P. Tan & R.G. Shivas, *sp. nov.*

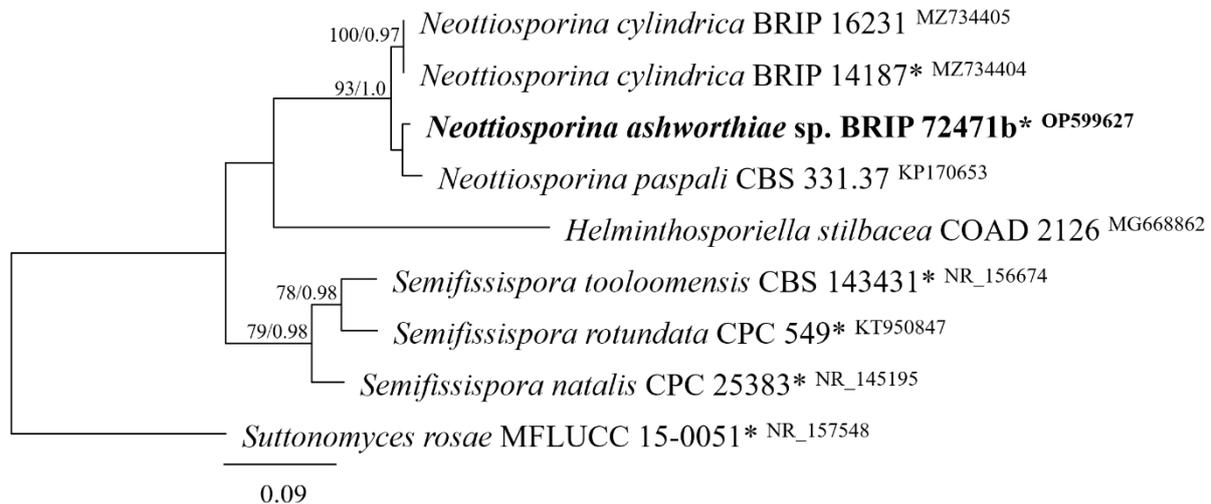
IF 900020

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

Diagnosis: Sequence from the rDNA describe *Neottiosporina ashworthiae* and is available in GenBank under the accession OP599627 (ITS region). *Neottiosporina ashworthiae* differs by sequence comparison of the ITS region from *N. paspali* (CBS 331.371 GenBank KP170653; Identities 484/494 (98%); unique nucleotides at positions 194(C), 274(T), 275(C), 282(T), 291(T), 294(C), 493(C), 532(C), 534(T), 601(T)).

Specimen examined: Australia, Queensland, Wallaman, from *Scleria* sp. (Cyperaceae), 28 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson (holotype BRIP 72471b preserved in a metabolically inactive state).

Etymology: Named after Phyllis Ashworth (1902–1996), who was one of Australia’s first medical scientists, specialising in bacteriology (Hammersmith Hospital, London) and biochemistry (St. Vincent’s Hospital, Melbourne). Phyllis Ashworth was a foundation member of the Baker Institute, an internationally renowned medical research facility based in the Melbourne.



Phylogenetic tree based on a maximum likelihood analysis of the ITS region alignment from species of *Neottiosporina*. Analyses were performed on the Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS). *Suttonomyces rosae* (ex-type strain MFLUCC 15-0051) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Nothophoma taboriae Y.P. Tan, *sp. nov.*

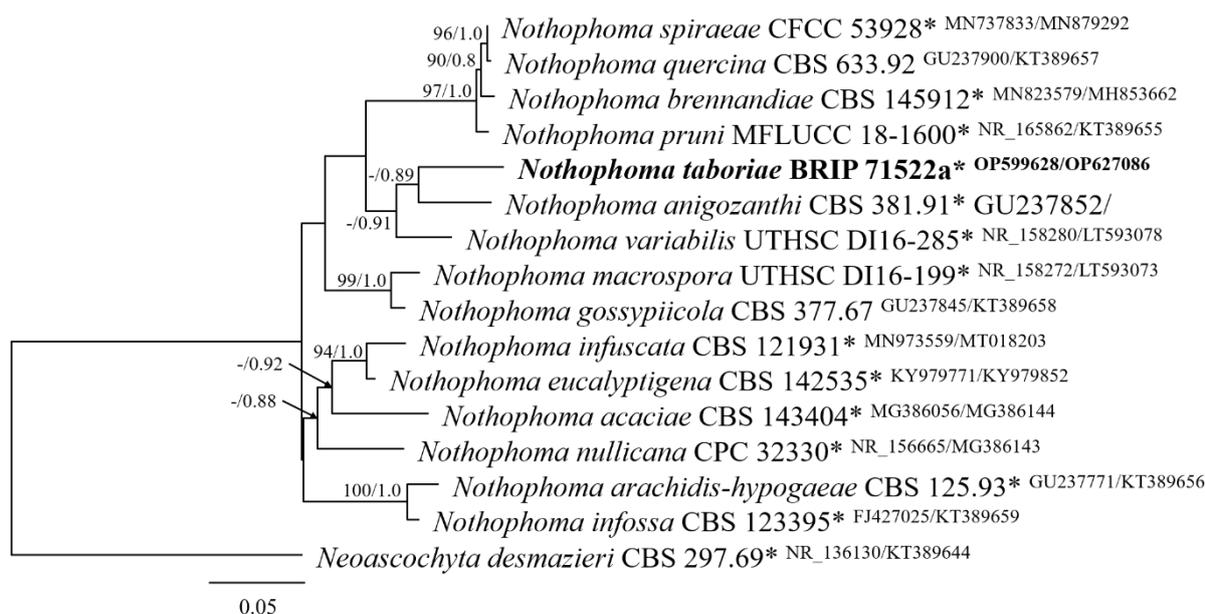
IF900021

Classification — *Didymellaceae*, *Pleosporales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Nothophoma taboriae* and are available in GenBank under the accessions OP599628 (ITS region) and OP627086 (*rpb2*). *Nothophoma taboriae* differs from by sequence comparison of the ITS region *N. anigozanthi* (ex-type strain CBS 381.91; GenBank GU237852; Identities 420/423 (99%); unique nucleotides at positions 299(A), 479(C), 510(C)), and *rpb2* gene (GenBank KT389655; Identities 557/596 (93%); unique nucleotides at positions 145(T), 148(C), 151(T), 175(C), 194(T), 229(T), 235(C), 265(T), 274(T), 289(C), 301(T), 352(C), 370(G), 373(C), 400(C), 427(C), 488(C), 499(T), 511(T), 620(C), 550(C), 559(C), 568(C), 574(G), 577(G), 586(A), 592(T), 594(G), 625(A), 631(T), 640(G), 646(G), 661(G), 664(T), 676(C), 691(A), 694(T), 712(C), 721(T)).

Specimen examined: Australia, Queensland, Mount Mee, from leaf spot of undet. *Myrtaceae*, 02 Aug. 2020, Y.P. Tan (holotype BRIP 71522a preserved in a metabolically inactive state).

Etymology: Named after Alicjar (Ala) E. Tabor, an Australian molecular microbiology professor, in recognition of her research on bovine reproductive and parasitic diseases, and as well as mentorship of Australian microbiologists, including the author.



Phylogenetic tree based on a maximum likelihood analysis of the *rpb2* gene from species of *Nothophoma*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/*rpb2*). *Neoscochyta desmazieri* (ex-type strain CBS 297.69) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Paraconiothyrium bishopiae Y.P. Tan & R.G. Shivas, *sp. nov.*

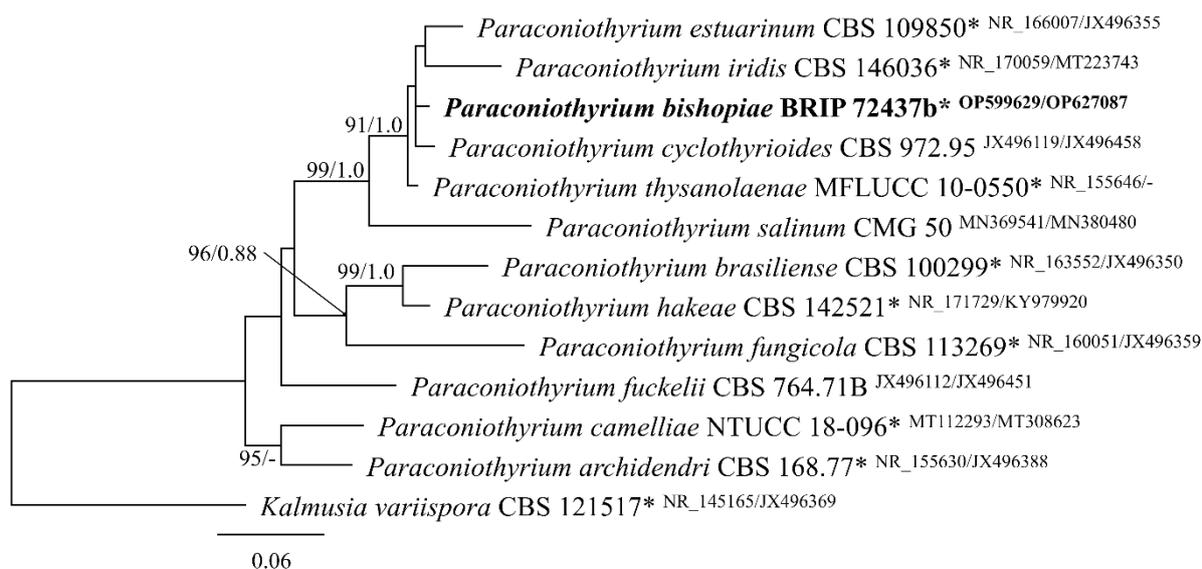
IF 900022

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

Diagnosis: Sequences from the rDNA and nrDNA describe *Paraconiothyrium bishopiae* and are available in GenBank under the accession OP599629 (ITS region), OP598066 (LSU) and OP627087 (beta-tubulin, *tub2*). *Paraconiothyrium bishopiae* differs from *P. cyclothyrioides* (CBS 972.95) by sequence comparison of the ITS region (GenBank JX496119; Identities 500/509 (99%), one gap; unique nucleotides at positions 236(T), 313(C), 636(C), 644(C), 672(C)), and *tub2* (GenBank JX496458; Identities 443/454 (98%), one gap; unique nucleotides at positions 141(G), 162(C), 324(T), 342(T), 434(C), 444(G), 445(T), 456(G), 466(G), 489(T)).

Specimen examined: Australia, Queensland, Wallaman, from leaf of undet. *Poaceae*, 28 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley & S.M. Thompson (holotype BRIP 72437b preserved in a metabolically inactive state).

Etymology: Named after Ruth Frances Bishop (1933–), an Australian virologist who devoted her career to improving child health. Ruth Bishop led the team that discovered the human rotavirus, which was later shown to be the major cause of gastroenteritis in children worldwide.



Phylogenetic tree based on a maximum likelihood analysis the concatenated alignment (ITS region and *tub2*) from species of *Paraconiothyrium*. Analyses were performed on the Geneious Prime® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/*tub2*). *Kalmusia variispora* (ex-type strain CBS 121517) was used as the outgroup. Ex-type strains are marked with asterisks (*).

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

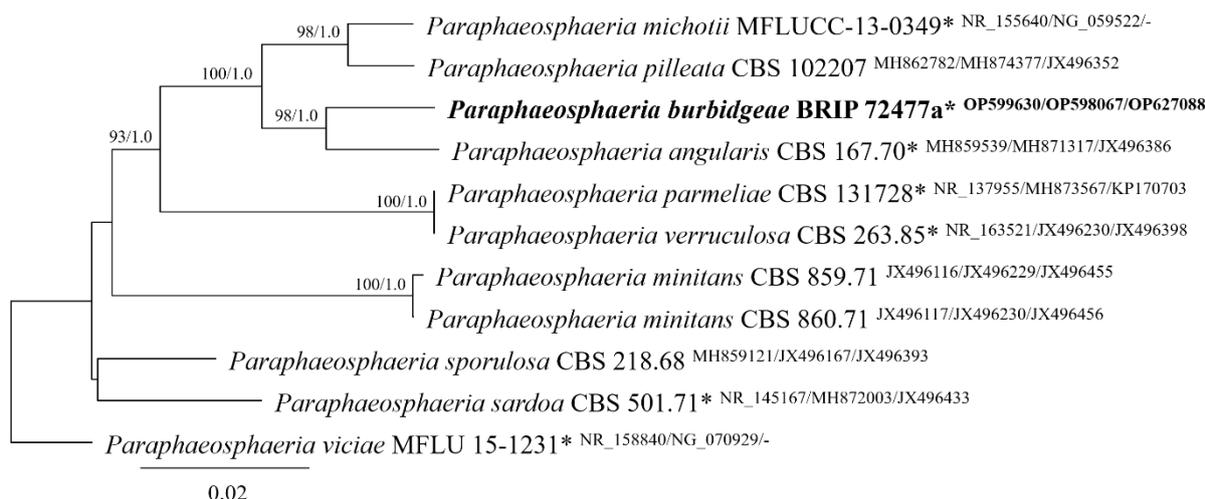
IF 900023

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

Diagnosis: Sequences from the rDNA and nrDNA describe *Paraphaeosphaeria burbidgeae* and are available in GenBank under the accession OP599630 (ITS region), OP598067 (LSU) and OP627088 (*tub2*). *Paraphaeosphaeria burbidgeae* differs from *P. angularis* (ex-type strain CBS 167.70) by sequence comparison of the LSU (GenBank NG_057963; Identities 843/848 (99%), one gap; unique nucleotide at positions 424(C), 435(C), 499(C), 507(T)), and *tub2* (GenBank JX496386; Identities 414/453 (91%), two gaps; unique nucleotide at positions 139(G), 142(C), 145(G), 150(A), 153(T), 161(A), 163(G), 172(C), 175(C), 176(G), 191(T), 231(T), 310(T), 312(C), 323(A), 324(A), 325(C), 330(T), 332(T), 341(C), 345(G), 347(C), 384(C), 423(C), 443(T), 445(G), 450(G), 452(G), 457(C), 474(C), 495(C), 504(G), 514(C), 534(T), 546(T), 558(T), 570(T)).

Specimen examined: Australia, Queensland, Barwidgi, from leaf of *Sorghum plumosum* (*Poaceae*), 20 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72477a preserved in a metabolically inactive state).

Etymology: Named after Nancy Tyson Burbidge (1912–1977), an Australian systemic botanist and the first female curator of the National Australian Herbarium. Nancy Burbidge published the *Dictionary of Australian Plant Genera* (1963), the first comprehensive paper on the phytogeography of the Australian region. Nancy Burbidge was awarded an Order of Australia in 1976 for services to botany.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region, LSU and *tub2*) from selected species of *Paraphaeosphaeria*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAXML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAXML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU/*tub2*). *Paraphaeosphaeria viciae* (ex-type strain MFLU 15-1231) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Phyllosticta westeae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

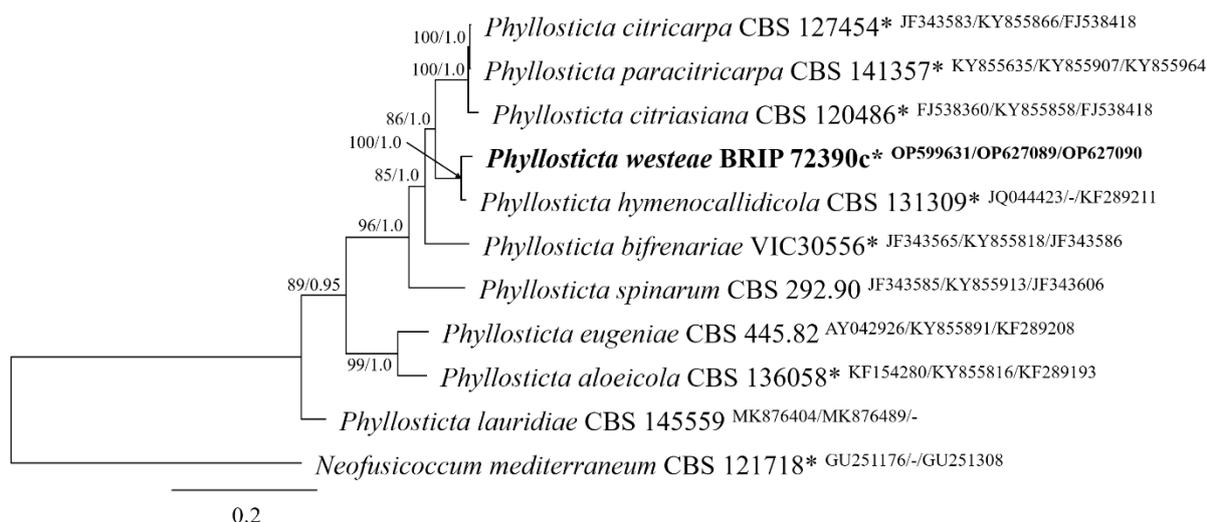
IF 900024

Classification — *Phyllostictaceae*, *Botryosphaeriales*, *Dothideomycetes*,

Diagnosis: Sequences from the rDNA and nrDNA describe *Phyllosticta westeae* and are available in GenBank under the accession OP599631 (ITS region), OP627089 (*rpb2*) and OP627090 (*tef1* α). *Phyllosticta westeae* differs from *P. hymenocallidicola* (ex-type strain CBS 131309) by sequence comparison of the ITS region (GenBank NR_137083; Identities 642/649 (99%); unique nucleotide at positions 222(C), 329(C), 371(A), 377(C), 394(G), 677(C), 725(C)), and *tef1* α (GenBank KF289211; Identities 195/199 (98%); unique nucleotide at positions 104(G), 141(G), 161(C), 178(A)).

Specimen examined: Australia, Queensland, Cardwell, from leaf of *Clerodendrum inerme* (*Lamiaceae*), 27 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72390c preserved in a metabolically inactive state).

Etymology: Named after Gretna Margaret Weste (1917–2006), in recognition of her contributions to plant pathology and mycology in Australia. Gretna Weste was Australia's foremost expert on the plant pathogen *Phytophthora cinnamomi* how it killed native plants. Her investigations revealed the cyclic nature of infestation, namely that once *P. cinnamomi* had killed all susceptible plants, it too died out, thereby allowing vegetation regeneration. In 1989, Gretna Weste was awarded a Member in the Order of Australia (AM) for service to science.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region, *rpb2* and *tef1* α) from selected species of *Phyllosticta*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/*rpb2*/*tef1* α). *Neofusicoccum mediterraneum* (ex-type strain CBS 121718) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Pseudochaetosphaeronema sklodowskacurieae Y.P. Tan & R.G. Shivas, *sp. nov.*

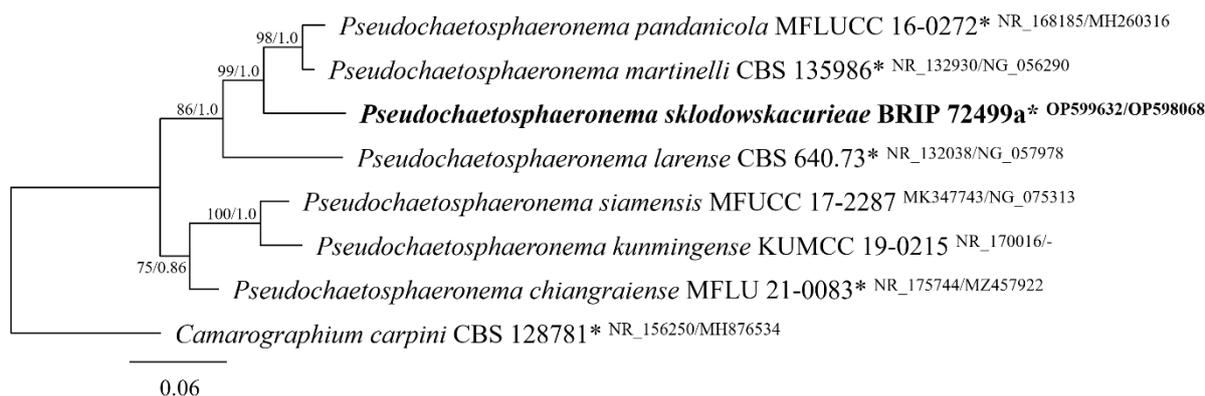
IF 900025

Classification — *Incertae sedis*, Pleosporales, Dothideomycetes

Diagnosis:

Specimen examined: Australia, Queensland, Mount Surprise, from soil, 21 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72499a preserved in a metabolically inactive state).

Etymology: Named after Marie Salomea Skłodowska–Curie (1867–1934), one of the most famous scientists in the modern industrial world. Marie Curie conducted pioneering research on radioactivity (a term which she coined). Marie Curie was the first woman to win a Nobel Prize, the first person and the only woman to win the Nobel Prize twice, and the only person to win the Nobel Prize in two scientific fields (Physics and Chemistry).



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region and LSU) from species of *Pseudochaetosphaeronema*. Analyses were performed on the Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Camarographium carpini* (ex-type strain CBS 128781) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Saitozyma carsoniae Y.P. Tan & R.G. Shivas, *sp. nov.*

IF 900026

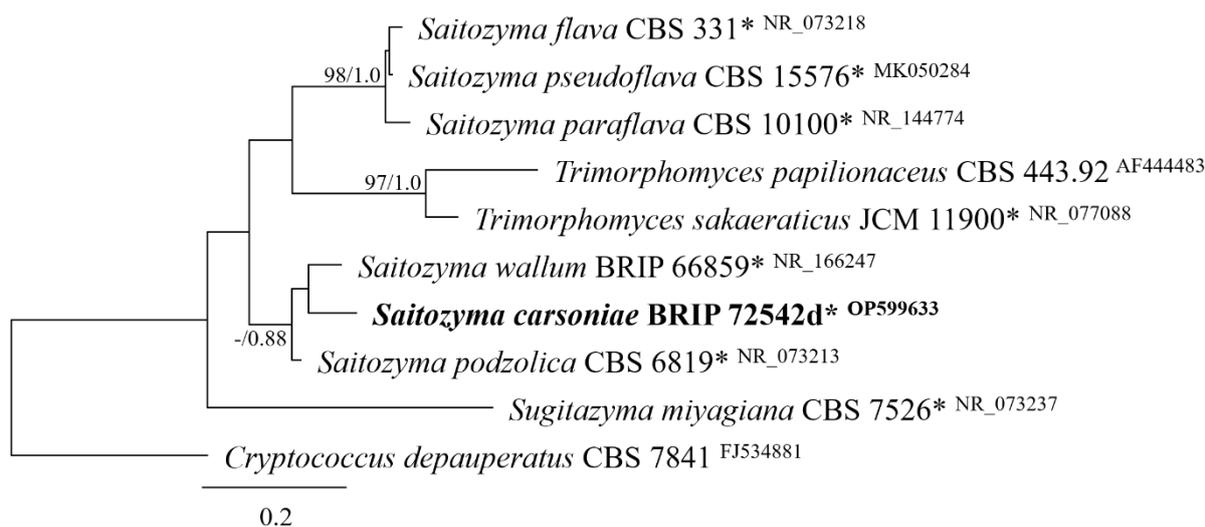
Classification — *Trimorphomycetaceae*, *Tremellales*, *Tremellomycetes*

Diagnosis: Sequence from the rDNA describe *Saitozyma carsoniae* and is available in GenBank under the accession OP599633 (ITS region). *Saitozyma carsoniae* differs by sequence comparison of the ITS region from *S. podzolica* (ex-type strain CBS 6819; GenBank NR_073213; Identities 464/501 (93%), five gaps; unique nucleotide at positions 176(T), 185(T), 219(T), 228(A), 230(A), 244(T), 258(A), 259(G), 264(C), 265(T), 266(T), 386(A), 469(T), 477(C), 482(A), 483(G), 485(A), 487(T), 493(A), 501(G), 502(A), 526(T), 545(A), 547(C), 548(A), 561(C), 569(T), 577(T), 579(T), 580(T), 587(C)), and *S. wallum* (ex-type strain BRIP 66859; GenBank NR_166247; Identities 441/481 (92%), nine gaps; unique nucleotide at positions 215(C), 219(T), 229(C), 230(A), 233(T), 259(G), 264(C), 265(T), 266(T), 386(A), 397(C), 408(G), 460(G), 475(T), 477(C), 482(A), 483(G), 484(T), 486(T), 493(A), 501(G), 502(A), 503(A), 546(G), 547(C), 548(A), 561(C), 568(A), 580(T), 585(A), 615(A)).

Specimen examined: Australia, Queensland, Petford, from soil, 19 Apr. 2021, Y.P. Tan, K.L.

Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72542d preserved in a metabolically inactive state).

Etymology: Named after Rachel Louise Carson (1907–1964), an American marine biologist, writer, and conservationist. Her book most influential book, *Silent Spring* (1962), described the harmful effect of pesticides on the environment. Rachel Caron’s scientific knowledge and poetic writing is widely credited with helping the global environmental movement reach a broad audience.



Phylogenetic tree based on a maximum likelihood analysis of the ITS region from species of *Tremellomycetes*. Analyses were performed on the Geneious Prime © 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS). *Cryptococcus depauperatus* (strain CBS 7841) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

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

IF 900027

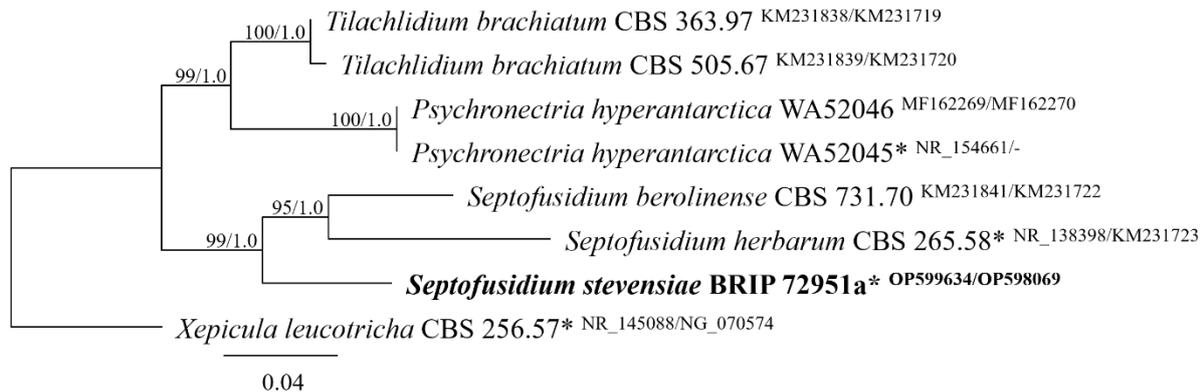
Classification — *Tilachlidiaceae*, *Hypocreales*, *Sordariomycetes*

Diagnosis: Sequences from the rDNA describe *Septofusidium stevensiae* and are available in GenBank under the accessions OP599634 (ITS region) and OP598069 (LSU). *Septofusidium stevensiae* differs from *S. berolinense* (strain CBS 731.70) by sequence comparison of the ITS region (GenBank KM231841; Identities 479/554 (86%), 24 gaps; unique nucleotide at positions 172(A), 182(A), 210(T), 223(A), 226(T), 246(T), 258(T), 264(G), 267(T), 275(G), 276(A), 278(T), 279(T), 281(A), 294(A), 295(C), 301(G), 304(A), 315(A), 318(C), 321(G), 322(A), 490(T), 503(A), 504(A), 512(T), 517(T), 522(T), 543(A), 544(G), 548(C), 550(T), 556(T), 557(C), 564(G), 569(G), 574(A), 575(T), 586(A), 603(A), 611(A), 612(C), 613(T), 614(T), 615(T), 617(A), 631(T), 659(C), 663(A)), and LSU (GenBank KM231722; Identities 783/810 (97%), two gaps; unique nucleotide at positions 82(T), 84(G), 174(C), 193(C), 371(T), 373(T), 378(C), 448(T), 450(G), 452(T), 453(T), 456(A), 466(T), 481(C), 484(C), 485(T), 490(G), 505(T), 515(T), 519(T), 521(C), 523(A), 541(T), 755(T), 832(A)). *Septofusidium stevensiae* differs from *S. herbarum* (ex-type strain CBS 265.58) by sequence comparison of the ITS region (GenBank NR_138398; Identities 453/546 (83%), 21 gaps; unique nucleotide at positions 172(A), 173(T), 210(T), 226(T), 227(T), 234(G), 241(T), 244(T), 246(T), 253(C), 258(T), 267(T), 275(G), 276(A), 278(T), 279(T), 280(T), 284(T), 285(C), 286(T), 294(A), 297(A), 299(T), 300(G), 301(T), 303(T), 315(A), 317(A), 318(C), 321(G), 323(T), 325(A), 329(A), 389(T), 396(A), 459(T), 461(T), 503(A), 504(A), 510(T), 511(T), 512(T), 515(T), 516(G), 517(T), 521(A), 522(T), 527(T), 541(C), 543(A), 544(G), 547(G), 553(C), 556(T), 564(G), 569(G), 574(A), 575(T), 586(A), 590(C), 593(A), 600(T), 602(T), 603(A), 611(A), 612(C), 613(T), 628(A), 631(T), 635(G), 641(T), 646(T)), and LSU (GenBank KM231723; Identities 765/811 (94%), two gaps; unique nucleotide at positions 80(T), 82(T), 112(T), 120(G), 124(T), 154(A), 174(C), 179(T), 182(T), 186(T), 187(A), 200(A), 250(A), 371(T), 373(T), 374(A), 387(C), 393(T), 403(A), 414(T), 448(T),

452(T), 453(T), 456(A), 460(T), 466(T), 481(C), 484(C), 485(T), 490(G), 504(T), 515(T), 519(T), 523(A), 565(A), 566(T), 570(C), 630(A), 641(T), 656(T), 657(A), 715(A), 755(T), 832(A)).

Specimen examined: Australia, Queensland, Tully, from unidentified insect, 29 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72951a preserved in a metabolically inactive state).

Etymology: Named after Nettie Maria Stevens (1861–1912), an American geneticist who discovered sex chromosomes (in male mealworms), which later became known as the X and Y chromosomes.



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region and LSU) from species of *Tilachlidiaceae*. Analyses were performed on the Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp).

GenBank accessions are indicated (superscript ITS/LSU). *Xepicula leucotricha* (ex-type strain CBS 256.57) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).

Teratosphaericola ellenclarkiae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

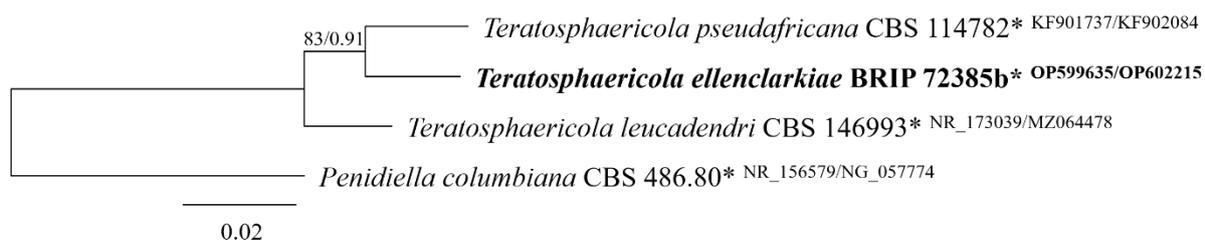
IF 900028

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*

Diagnosis: Sequence from the rDNA describe *Teratosphaericola ellenclarkiae* and is available in GenBank under the accessions OP599635 (ITS region) and OP602215 (LSU). *Teratosphaericola ellenclarkiae* differs by sequence comparison of the ITS region from *T. pseudoafricana* (ex-type strain CBS 114782; GenBank NR_154468; Identities 469/491 (96%), four gaps; unique nucleotide at positions 176(C), 185(C), 186(C), 210(A), 215(T), 287(A), 312(A), 507(C), 526(T), 546(T), 548(C), 554(A), 585(T), 589(C), 604(G), 611(T), 621(A), 623(G)).

Specimen examined: Australia, Queensland, White Mountains, from *Grevillea decora* subsp. *decora* (*Proteaceae*), 24 Apr. 2021, Y.P. Tan, K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72385b preserved in a metabolically inactive state).

Etymology: Named after Ellen Clark (1915–1988), an Australian naturalist, who without formal qualifications made many scientific contributions. Ellen Clark is best known for having described and named many of Australia's freshwater crayfish (yabbies).



Phylogenetic tree based on a maximum likelihood analysis of the concatenated alignment (ITS region and LSU) from species of *Teratopshaericola*. Analyses were performed on the Geneious Prime[®] 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accessions are indicated (superscript ITS/LSU). *Penidiella columbiana* (ex-type strain CBS 121517) was used as the outgroup. Novel taxon is in bold. Ex-type strains are marked with asterisks (*).