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

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*Aspergillus marneyi* Y.P. Tan, Bishop-Hurley, E. Lacey & R.G. Shivas, *sp. nov.*

IF 900143

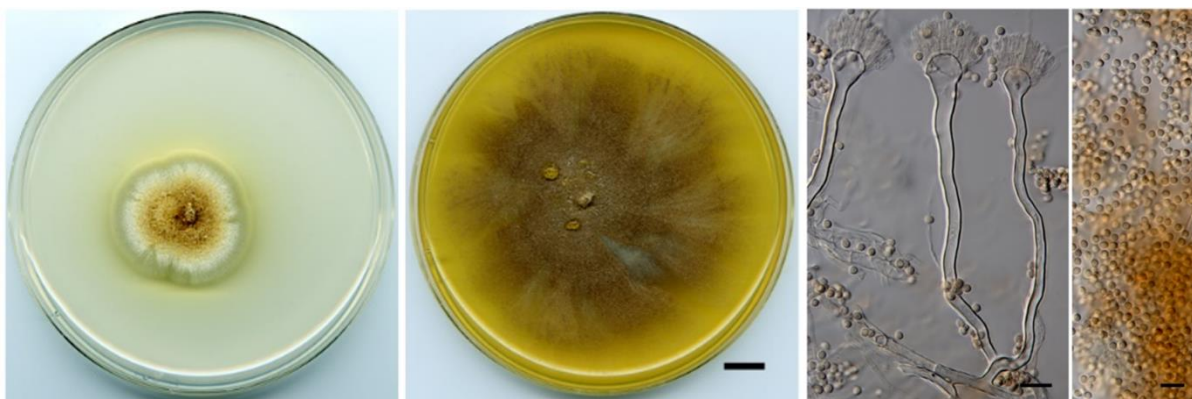
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

**Diagnosis:** Sequences from the rDNA and nrDNA describe *Aspergillus marneyi* and are available in GenBank under the accessions OL691080 (ITS region), OL741656 (DNA-directed RNA polymerase II second largest; *rpb2*) and OL741659 (beta-tubulin; *tub2*). *Aspergillus marneyi* differs from *A. alabamensis* (ex-type strain CBS 125693) by sequence comparison of the ITS region (GenBank FJ531193; Identities 478/481 (99%), one gap; unique nucleotide at positions 653(C), 657(G)), *rpb2* (GenBank KP987018; Identities 853/856 (99%); unique nucleotide at positions 44(G), 107(G), 152(C)), and *tub2* (GenBank FJ491731; Identities 492/499 (99%), one gap; unique nucleotide at positions 306(T), 335(T), 435(A), 587(G), 611(T), 633(G)).

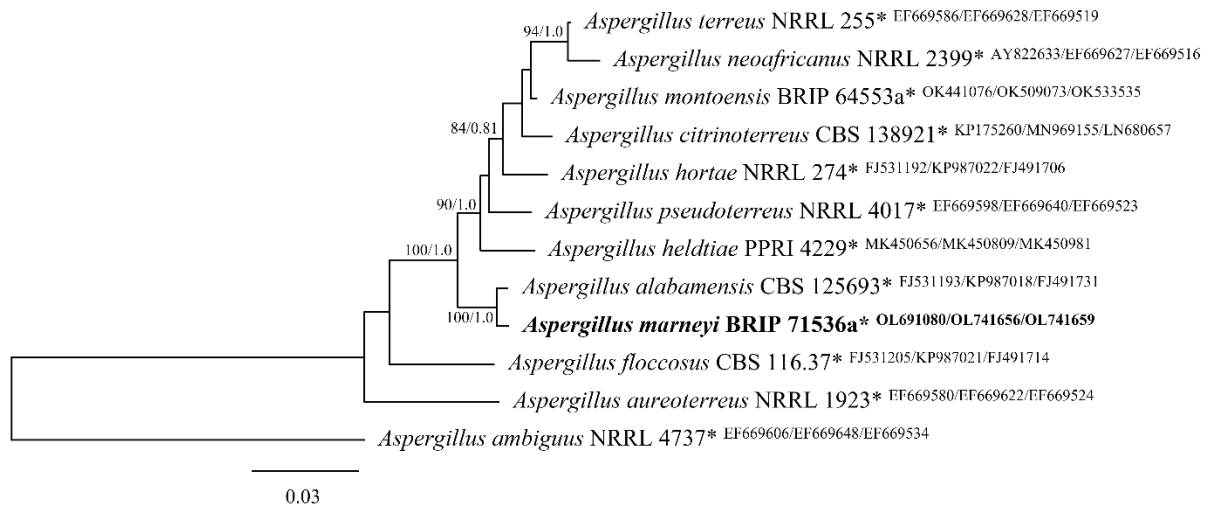
**Conidiophores** on aerial hyphae, erect to flexuous, unbranched, subcylindrical, 70–150 × 2.5–6 µm, hyaline, smooth, aseptate, widening towards the apex, biseriate with spathulate vesicles 8–12 µm diam; metulae on the upper half of the vesicle, cylindrical, 4–5.5 × 1.5–2 µm, hyaline. **Conidiogenous cells** phialides, cylindrical, 8–11 × 1.5–2 µm, 2 per metula, hyaline. **Conidial heads** columnar, 150–280 × 30–60 µm, cream to pale buff. **Conidia** subglobose, 2–3 µm diam, smooth, subhyaline, luteus en masse.

**Specimen examined:** Australia, New South Wales, Wantabadgery, from necrotic flecks in crowns of *Medicago sativa* (*Fabaceae*), Jul. 2002, T.S. Marney (holotype BRIP 71536a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Thomas Stephen Marney, an Australian microbiologist, who has collected and isolated many unusual fungi from plants, insects, and soil. Tom has diverse interests, and for more than 50 years has participated in chess, judo, and orienteering events in Australia.



*Aspergillus marneyi* strain BRIP 71536a. Colonies on potato dextrose agar after 1 wk (left) and 4 wk (right); conidial heads; conidiophores; and conidia. Scale bars = 1 cm (colony), 10 µm (conidiophores and conidia).



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (ITS, *rpb2* and *tub2*) from species of *Aspergillus* sect. *Terrei*. 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). *Aspergillus ambiguus* (ex-type strain NRRL 4737) was used as the outgroup. GenBank accessions are indicated (superscript ITS/*rpb2*/*tub2*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

*Beltraniella hesseae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

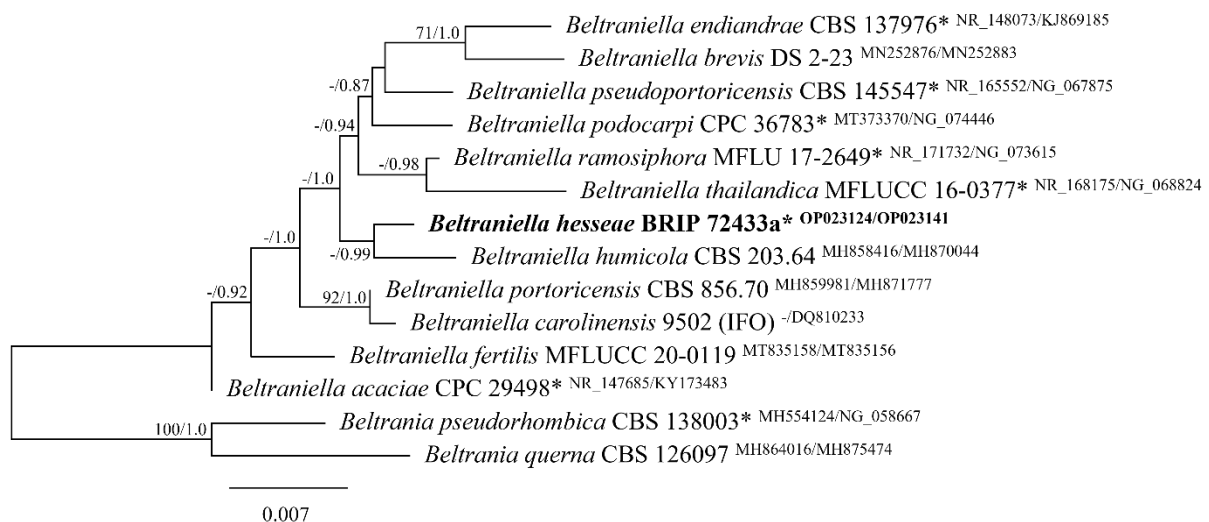
IF 900136

Classification — *Beltraniaceae*, *Xylariales*, *Sordariomycetes*

**Diagnosis:** Sequences from the rDNA describe *Beltraniella hesseae* and are available in GenBank under the accessions OP023124 (ITS region) and OP023141 (LSU). *Beltraniella hesseae* differs from *B. humicola* (CBS 203.64) by sequence comparison of the ITS region (GenBank MH858416; Identities 549/556 (99%); unique nucleotide at positions 210(G), 301(C), 514(T), 525(C), 527(T), 634(T), 635(T)), and LSU (GenBank MH870044; Identities 884/886 (99%); unique nucleotide at positions 88 (T), 526 (T)).

**Specimen examined:** Australia, Queensland, Tully Falls, from leaf of *Digitaria ciliaris* (*Poaceae*), 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 72433a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Fanny Hesse (born Angelina Fanny Eilshemius, 1850–1934), a microbiologist and scientific illustrator, who first proposed the use of agar as a gelling agent for microbiological culture media. Agar overcame the problems with gelatin-based media that often broke down due to gelatin-liquefying organisms as well as temperature increases during incubation.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (ITS and LSU) from species of *Beltraniella*. 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). *Beltrania pseudorhombica* (ex-type strain CBS 138003) and *Beltrania querna* (strain CBS 126097) were used as the outgroup. GenBank accessions are indicated (superscript ITS/LSU). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

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

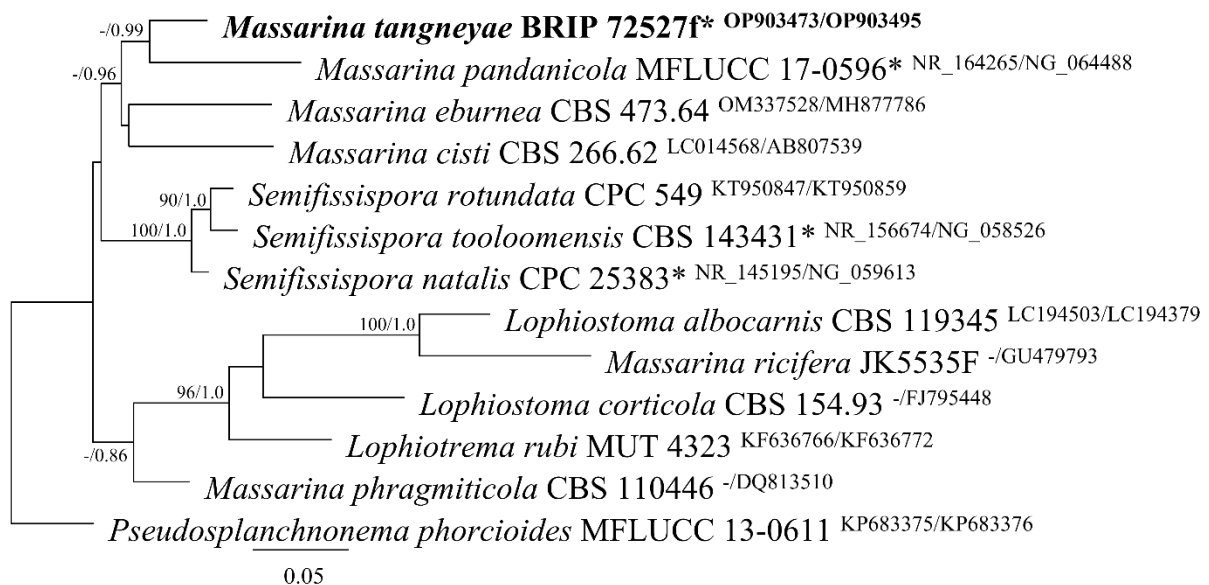
IF 900137

Classification — *Massarinaceae*, *Pleosporales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA describe *Massarina tangneyae* and are available in GenBank under the accessions OP903473 (ITS region) and OP903495 (LSU). *Massarina tangneyae* differs from *M. pandanicola* (ex-type strain MFLUCC 17-0596) by sequence comparison of the ITS region (GenBank NR\_164265; Identities 336/385 (87%), 13 gaps; unique nucleotide at positions 209(C), 236(G), 245(C), 246(C), 251(C), 259(C), 272(C), 275(C), 278(A), 281(C), 284(T), 285(C), 289(A), 298(T), 299(C), 300(T), 303(C), 308(T), 497(T), 502(C), 511(C), 515(C), 516(T), 519(G), 521(G), 522(C), 533(C), 538(C), 539(T), 553(G), 554(T), 555(T), 556(C)), and LSU (GenBank NG\_064488, Identities 819/841 (97%), two gaps; unique nucleotide at positions 82(T), 126(G), 153(A), 176(A), 177(C), 186(C), 187(C), 193(C), 392(C), 395(C), 426(C), 436(G), 455(T), 471(G), 481(C), 301(A), 515(C), 531(C), 532(G), 680(C)).

*Specimen examined*: Australia, Queensland, Mission Beach, from necrotic leaf spot on *Pandanus tectorius* (*Pandanaceae*), 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 72527f permanently preserved in a metabolically inactive state).

*Etymology*: Named after Dame Dorothy Margaret Tangney (1907–1985), who was the first woman elected to the Senate in Australia. In her maiden speech in 1943, Tangney expressed her belief in women as equal partners in Australian society and encouraged equal opportunities for all Australians. In her lifetime, Tangney championed the use of Federal powers to provide social security, housing, and education.



Phylogenetic tree based on maximum likelihood analysis of a concatenated alignment (ITS region and LSU) of selected species of *Massarinaceae*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Pseudoplanchnonema phorcioides* (strain MFLUCC 13-0611) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/LSU). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

*Paraphaeosphaeria traversiae* Y.P. Tan, Bishop-Hurley, Dhileepan & R.G. Shivas, *sp. nov.*

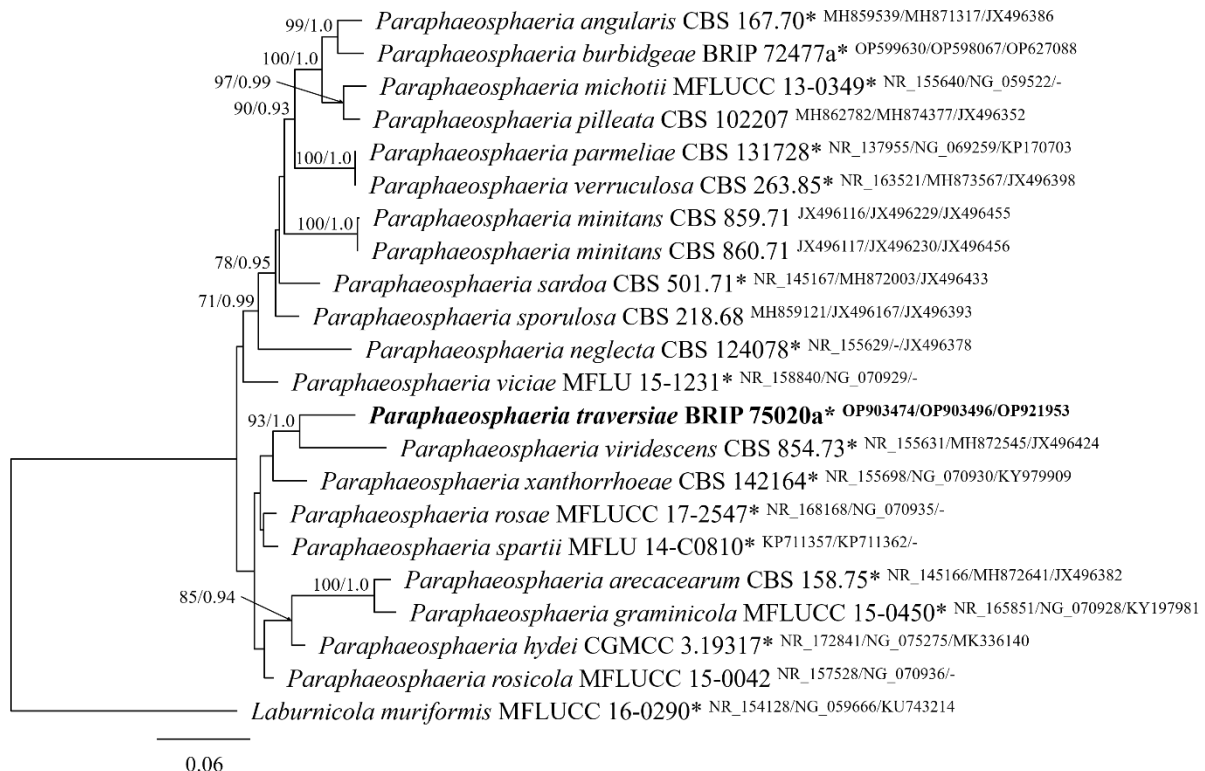
IF 900138

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

**Diagnosis:** Sequences from the rDNA and nrDNA describe *Paraphaeosphaeria traversiae* and are available in GenBank under the accessions OP903474 (ITS region), OP903496 (LSU) and OP921953 (beta-tubulin; *tub2*). *Paraphaeosphaeria traversiae* differs from *P. viridescense* (ex-type strain CBS 854.73) by sequence comparison of the ITS region (GenBank NR\_155631; Identities 495/540 (92%), 23 gaps; unique nucleotide at positions 172(A), 175(T), 176(G), 210(C), 215(G), 216(G), 218(G), 219(T), 222(C), 223(A), 225(C), 228(C), 238(G), 239(T), 240(T), 245(A), 247(T), 262(C), 304(T), 348(C), 642(T), 645(G)), LSU (GenBank MH872545; Identities 846/865 (98%), six gaps; 14(G), 20(A), 28(A), 108(T), 132(C), 188(G), 419(C), 492(C), 501(G), 502(T), 521(C), 682(C), 865(G)), and *tub2* (GenBank JX496424; Identities 354/392 (92%), nine gaps; unique nucleotide at positions 162(G), 228(T), 232(C), 233(T), 234(T), 254(T), 271(T), 274(T), 301(C), 315(C), 318(C), 322(A), 323(G), 327(T), 337(C), 343(A), 357(T), 388(A), 391(T), 422(A), 425(T), 426(T), 436(C), 455(C), 458(A), 460(C), 461(A), 523(C), 532(T)).

**Specimen examined:** Australia, Queensland, Mossman, leaf spot of *Cyperus aromaticus* (*Cyperaceae*), 11 May 2022, Y.P. Tan, M.D.E. Shivas & R.G. Shivas (holotype BRIP 75020a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Pamela Lyndon Travers (1899–1996), an Australian born British author, who was best known for her enduring book *Mary Poppins* (1934) and its sequels.



Phylogenetic tree based on maximum likelihood analysis of a concatenated alignment (ITS, LSU and *tub2*) of species of *Paraphaeosphaeria*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp).

*Laburnicola muriformis* (ex-type strain MFLUCC 16-0290) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/LSU/*tub2*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

*Penicillium allaniae* Y.P. Tan, Bishop-Hurley, Marney, R.G. Shivas, *sp. nov.*

IF 900139

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

**Diagnosis:** Sequences from the rDNA and nrDNA describe *Penicillium allaniae* and are available in GenBank under the accessions OP903475 (ITS region), OP925815 (LSU), OP921954 (camodulin; *cmdA*), OP921955 (*rpb2*) and OP921956 (*tub2*). *Penicillium allaniae* differs from *Pe. katangense* (ex-type strain CBS 247.67) by sequence comparison of the ITS region (GenBank AF033458; Identities 508/513 (99%), three gaps; unique nucleotide at positions 243(T), 272(C)), *cmdA* (GenBank KP016788; Identities 394/400 (99%); unique nucleotide at positions 74(G), 167(C), 171(C), 195(T), 354(C), 358(C)), *rpb2* (GenBank KP064646; Identities 849/855 (99%); unique nucleotide at positions 101(A), 416(C), 596(C), 602(T), 848(A)), and *tub2* (GenBank KP016757; Identities 392/404 (97%), six gaps; unique nucleotide at positions 252(A), 254(G), 270(T), 470(A), 482(T), 485(T)). *Penicillium allaniae* differs from *Pe. restrictum* (ex-type strain CBS 367.48) by sequence comparison of the ITS region (GenBank AF033457; Identities 506/513 (99%), three gaps; unique nucleotide at positions 190(C), 250(G), 524(G)), *cmdA* (GenBank KP016803; Identities 392/400 (98%), one gap; unique nucleotide at positions 21(C), 63(A), 118(C), 171(C), 195(T), 334(T), 352(A)), *rpb2* (GenBank JN121506; Identities 823/838 (98%); unique nucleotide at positions 52(T), 107(A), 170(G), 364(T), 416(C), 455(C), 501(G), 509(T), 512(T), 527(C), 575(G), 597(A), 701(T), 764(A), 800(T)), and *tub2* (GenBank KJ834486; Identities 409/423 (97%); unique nucleotide at positions 225(C), 245(A), 252(A), 255(G), 270(T), 274(C), 313(C), 346(T), 455(A), 468(C), 482(T), 485(T), 590(C), 596(C)).

**Specimens examined:** Australia, Queensland, Rossville, from soil, 8 May 2022, *M.D.E Shivas, R.G. Shivas & T.S. Marney* (holotype BRIP 74886a permanently preserved in a metabolically inactive state); Gillies Range, from soil, 13 May 2022, *M.D.E Shivas, R.G. Shivas & T.S. Marney*, culture BRIP 74899a (ITS, LSU, *cmdA*, *rpb2* and *tub2* sequences GenBank OP903476, OP925816, OP921957, OP921958 and OP921959).

**Etymology:** Named after Frances Elizabeth (Betty) Allan (1905–1952), who studied mathematics, statistics, applied biology and general agriculture at Cambridge University. Betty Allan became the first statistician at the Commonwealth Scientific and Industrial Research Organisation (CSIRO) and was the effective founder of the CSIRO Division of Mathematics and Statistics.

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

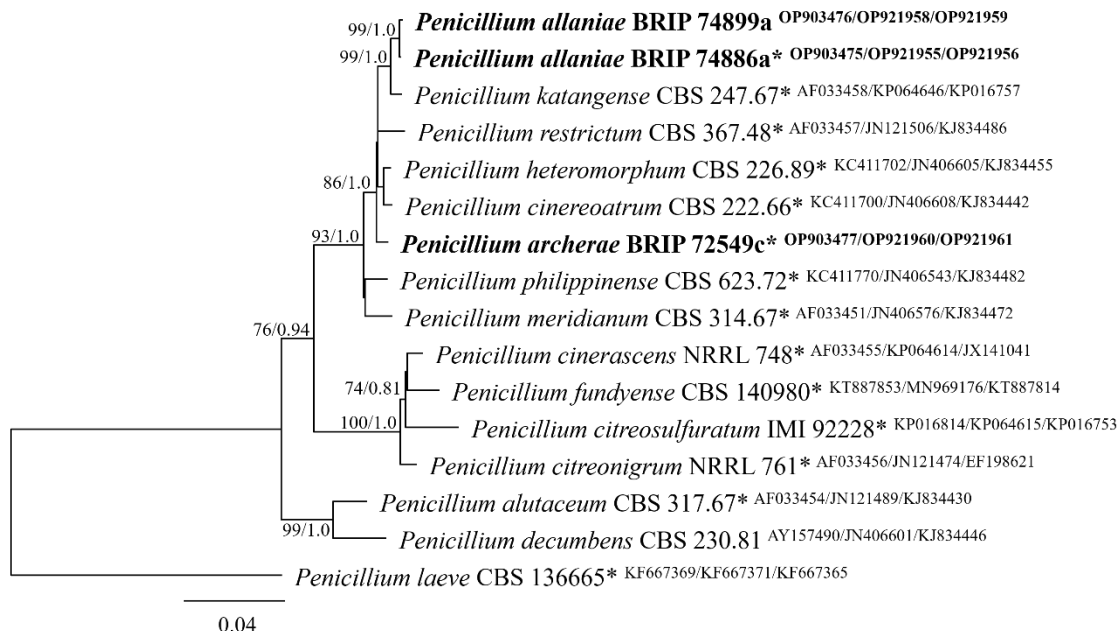
IF 900140

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

Diagnosis: Sequences from the rDNA and nrDNA describe *Penicillium archerae* and are available in GenBank under the accessions OP903477 (ITS region), OP921960 (*rpb2*) and OP921961 (*tub2*). *Penicillium archerae* differs from *Pe. cinereoatrum* (ex-type strain CBS 222.66) by sequence comparison of the ITS region (GenBank KC411700; Identities 503/506 (99%), one gap; unique nucleotide at positions 272(T), 274(G)), *rpb2* (GenBank JN406608; Identities 852/860 (99%); unique nucleotide at positions 116(T), 179(T), 236(C), 248(T), 530(T), 580(G), 755(A), 761(T)), and *tub2* (GenBank KJ834442; Identities 414/424 (98%), two gaps; unique nucleotide at positions 289(T), 343(T), 348(A), 386(A), 455(A), 505(A), 556(G), 586(T)). *Penicillium archerae* differs from *Pe. heteromorphum* (ex-type strain CBS 226.89) by sequence comparison of the ITS region (GenBank KC411702; Identities 504/506 (99%), one gap; unique nucleotide at position 609(T)), *rpb2* (GenBank JN406605; Identities 851/860 (99%); unique nucleotide at positions 1196(T), 146(T), 178(T), 236(C), 248(T), 530(T), 600(G), 755(A), 794(C)), and *tub2* (GenBank KJ834455; Identities 415/424 (98%), two gaps; unique nucleotide at positions 342(A), 333(T), 386(A), 397(T), 455(A), 505(A), 586(T)).

*Specimen examined*: Australia, Queensland, Mount Surprise, from soil, 21 Apr. 2021, Y.P. Tan (holotype BRIP 72549c permanently preserved in a metabolically inactive state).

*Etymology*: Named after Mary Ellinor Lucy Archer (1893–1979), who was the first female scientist at CSIRO, its chief librarian (1923–1954), and appointed a Member of the Order of the British Empire in 1956.



Phylogenetic tree based on maximum likelihood analysis of a concatenated alignment (ITS, *rpb2* and *tub2*) of selected species of *Penicillium* sect. *Exilicaulis*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Penicillium laeve* (ex-type strain CBS 136665) was used as the outgroup. GenBank accession

numbers are indicated (superscript ITS/*rpb2/tub2*). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (\*).

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

IF 900141

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

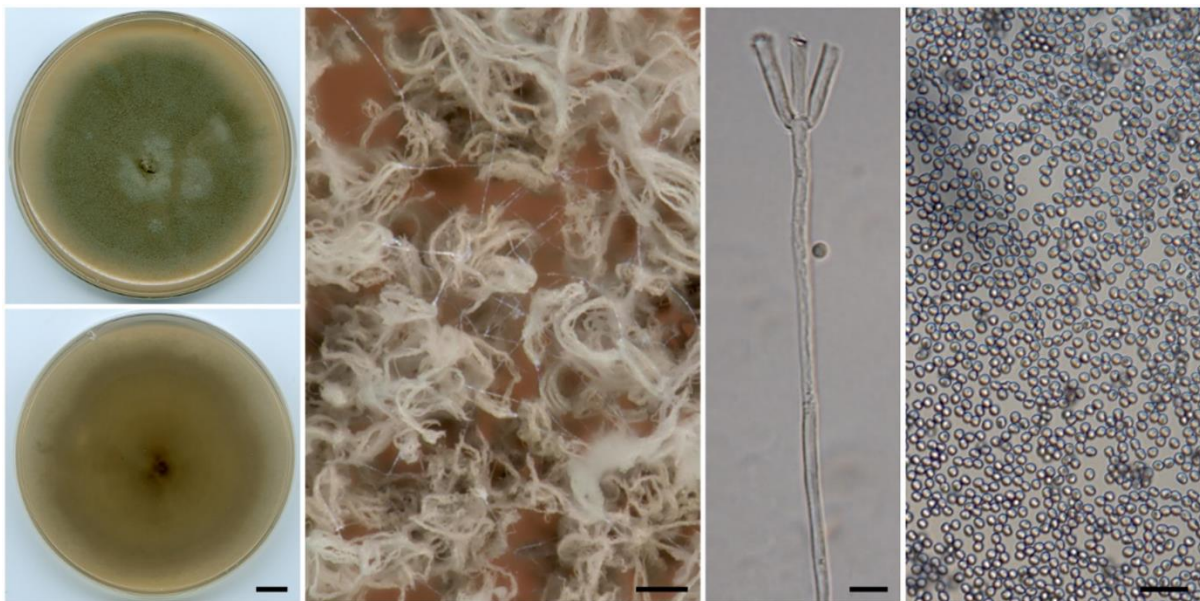
*Diagnosis*: Sequences from the nrDNA describe *Penicillium jenningsiae* and are available in GenBank under the accessions OL741660 (*rpb2*) and OL741657 (*tub2*). *Penicillium jenningsiae* differs from *Pe. sumatraense* (ex-type strain CBS 281.36) by sequence comparison of *rpb2* (GenBank KJ527395; Identities 783/788 (99%); unique nucleotide at positions 32(T), 44(C), 51(T), 173(C), 242(C)), and *tub2* (GenBank JN606639; Identities 420/443 (95%), seven gaps; 274(C), 279(A), 280(A), 294(A), 302(A), 376(G), 483(T), 498(T), 500(C), 509(C), 513(T), 522(G), 530(A), 548(A), 674(T), 686(T)).

*Conidiophores* divaricate and biverticillate; stipes smooth, 100–250 × 2–3.5 µm; metulae cylindrical, 10–15 × 2–3.5 µm, swollen up to 5 µm diam at the apex, in verticils of 2–3 (–5). *Conidiogenous cells* phialides, cylindrical or lageniform, 8–12 × 2–4 µm, in verticils of 3–7 per metula, 7.5–10.5(–14) × 2.5–4 µm. *Conidia* globose to subglobose, 2–3 µm, smooth, borne in long chains.

*Specimen examined*: Australia, Queensland, Brisbane, from compost, 1 Sep. 2004, D.G. Holdom (holotype BRIP 45936a permanently preserved in a metabolically inactive state).

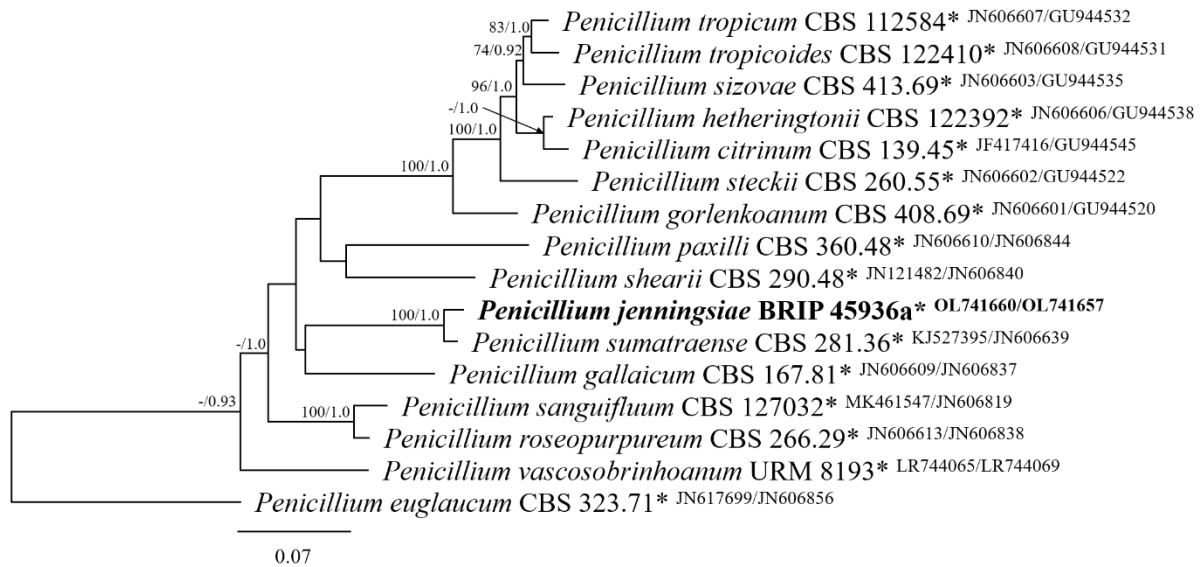
*Etymology*: Named after Margaret Augusta Jennings (1904–1994), a British scientist who was part of the team at the University of Oxford led by Howard Florey that worked on the production and clinical application of penicillin.

*Notes*: Metabolite analysis from incubated grains identified curvularin, dehydrocurvularin and related compounds as the dominant components.



*Penicillium jenningsiae*. Colonies on potato dextrose agar after 4wk (upper surface and reverse); colony surface; stipe with metulae; conidia. Scale bars = 1 cm (colony); 100 µm (colony surface); 10 µm (stipe and conidia).





Phylogenetic tree based on a maximum likelihood analysis of concatenated multilocus alignment (*rpb2* and *tub2*) from species of *Penicillium* sect. *Citrina*. 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). *Penicillium euglaucum* (ex-type strain CBS 323.71) was used as the outgroup. GenBank accessions are indicated (superscript *rpb2/tub2*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

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

IF 900142

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Penicillium newtonturnerae* and are available in GenBank under the accessions OP903478 (ITS region), OP925817 (LSU), OP921962 (*cmdA*), OP921963 (*rpb2*) and OP921964 (*tub2*). *Penicillium newtonturnerae* differs from *Pe. cataractarum* (ex-type strain CBS 140974) by sequence comparison of the *cmdA* (GenBank KT887769; Identities 364/373 (98%), one gap; unique nucleotide at positions 11(G), 49(A), 110(C), 167(A), 239(T), 319(T), 342(G)), *rpb2* (GenBank MN969180; Identities 807/820 (98%); unique nucleotide at positions 26(C), 40(C), 64(A), 106(T), 133(C), 142(C), 211(A), 319(G), 322(C), 346(C), 472(A), 553(T), 709(T)), and *tub2* (GenBank KT887808; Identities 468/482 (97%), one gap; unique nucleotide at positions 217(C), 241(A), 242(C), 288(G), 298(T), 304(G), 397(C), 400(C), 401(T), 461(T), 498(G), 548(T), 690(T)). *Penicillium newtonturnerae* differs from *Pe. globosum* (ex-type strain CGMCC 3.18800) by sequence comparison of the *cmdA* (GenBank MN969330; Identities 360/374 (96%), three gaps; unique nucleotide at positions 49(A), 75(T), 80(C), 110(C), 121(G), 147(C), 239(T), 313(G), 314(C), 319(T), 346(T)), *rpb2* (GenBank KY495067; Identities 735/741 (99%); unique nucleotide at positions 13(T), 68(C), 106(T), 280(A), 553(T), 569(C)), and *tub2* (GenBank KY495123; Identities 407/417 (98%), one gap; 288(G), 298(T), 304(G), 400(C), 401(T), 404(C), 461(T), 576(C), 600(T)).

*Specimen examined*: Australia, Queensland, Koah, from soil, 8 May 2022, *M.D.E. Shivas, R.G. Shivas & T.S. Marney* (holotype BRIP 74909a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Helen Alma Newton Turner (1908–1995), an Australian geneticist and statistician, who became Australia’s leading authority on sheep genetics having worked at CSIRO for over 40 years. Helen Newton Turner was internationally recognised as one of the pioneers of sheep breeding.

*Penicillium vickeryae* Y.P. Tan & R.G. Shivas, *sp. nov.*

IF 900144

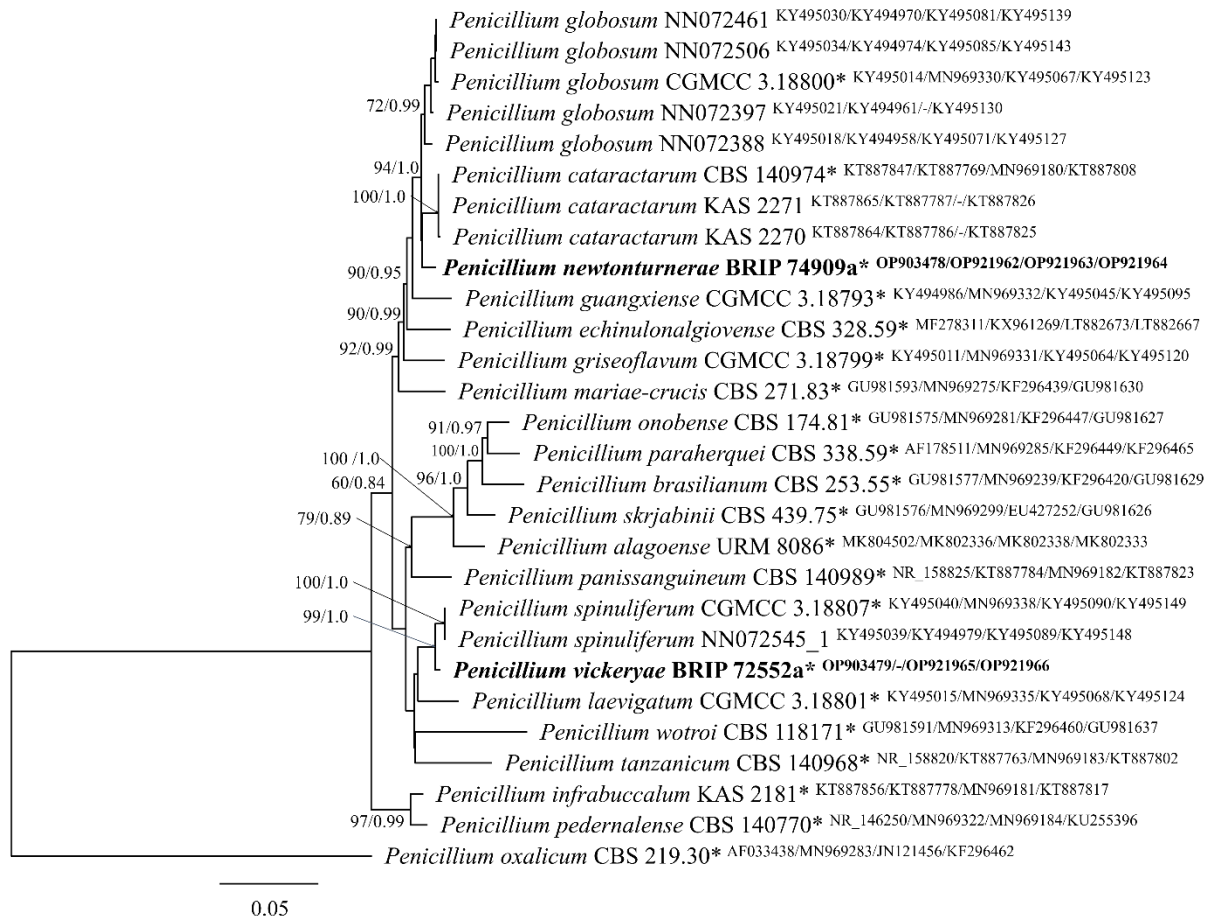
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Penicillium vickeryae* and are available in GenBank under the accessions OP903479 (ITS region), OP921965 (*rpb2*) and OP921966 (*tub2*). *Penicillium vickeryae* differs from *Pe. spinuliferum* (ex-type strain CGMCC 3.18807) by sequence comparison of *rpb2* (GenBank KY495090; Identities 744/750 (99%); unique nucleotide at positions 203(T), 289(A), 292(A), 367(T), 541(C), 556(G)), and *tub2* (GenBank KY495149; Identities 413/418 (99%), one gap; 278(T), 496(A), 530(T), 546(G)).

*Specimen examined*: Australia, Queensland, Wallaman, from soil, 2 Apr. 2021, *Y.P. Tan* (holotype BRIP 72552a permanently preserved in a metabolically inactive state).

*Eymology*: Named after Joyce Winifred Vickery (1908–1979), an Australian botanist and taxonomist, who worked mostly at the New South Wales Herbarium. Joyce Vickery’s major research interest centred on the taxonomic revision of Australian grass species. Joyce Vickery

has been commemorated by the names of several grasses, including *Amphibromus vickeryae*, *Aristida vickeryae*, *Austrostipa vickeryana* and *Rytidosperma vickeryae*.



Phylogenetic tree based on maximum likelihood analysis of concatenated alignment (ITS, *cmdA*, *rpb2* and *tub2*) of selected species of *Penicillium* sect. *Lanata-Divaricata*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Penicillium oxalicum* (ex-type strain CBS 219.30) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/*cmdA*/*rpb2*/*tub2*). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (\*).

*Penicillium tolerans* Y.P. Tan, Bishop-Hurley, E. Lacey, Grice & R.G. Shivas, *sp. nov.*

IF 900151

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*

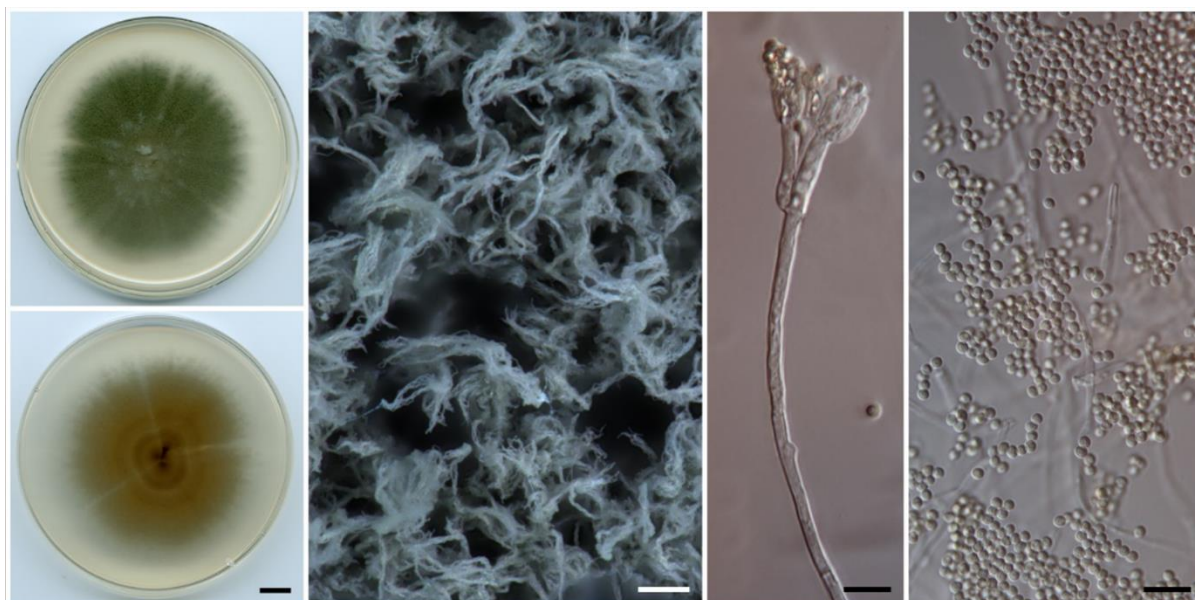
**Diagnosis:** Sequences from the rDNA and nrDNA describe *Penicillium tolerans* and are available in GenBank under the accessions OK639006 (ITS region) and OL741658 (*tub2*). *Penicillium tolerans* differs from *Pe. sclerotiorum* (ex-type strain CBS 287.36) by sequence comparison of the ITS region (GenBank JN626132; Identities 535/539 (99%), one gap; unique nucleotide at positions 174(A), 236(T), 500(T)), and *tub2* (GenBank JN626001; Identities 450/467 (96%), one gap; unique nucleotide at positions 192(C), 228(G), 236(C), 255(A), 258(G), 263(A), 273(C), 279(T), 300(A), 337(T), 373(T), 459(C), 461(A), 472(T), 497(C), 560(C)).

**Conidiophores** monoverticillate or biverticillate; stipes smooth to finely roughened, 100–300 × 2–3 µm; metulae cylindrical, 10–20 × 2–3 µm, in verticils of 2–4. **Conidiogenous cells** phialides, lageniform, 6–10 × 2.5–4 µm, in verticils of 2–5 per metula. **Conidia** globose to subglobose, 1.5–2.5 µm, smooth, borne in long chains.

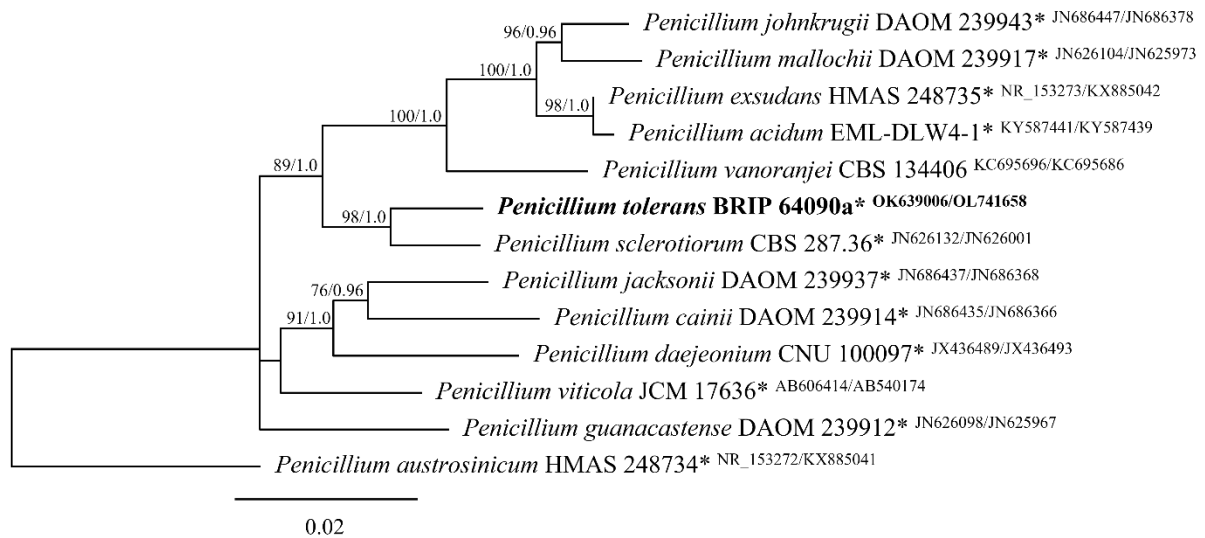
**Specimen examined:** Australia, Queensland, Walkamin, from soil, 27 Jan. 2016, K.R.E. Grice & P.R. Trevorrow (holotype BRIP 64090a permanently preserved in a metabolically inactive state).

**Etymology:** Named for its ability to survive in soil treated with disinfectants.

**Notes:** In 2015, the efficacy of disinfectants for use in footbaths and drive-through car dips was assessed following the detection of *Fusarium odoratissimum* on banana plantations in northern Queensland. Disinfectants that contained quaternary ammonium compounds, specifically didecyl dimethyl ammonium chloride or benzalkonium chloride, were tested at different concentrations for their ability to eliminate *F. odoratissimum* in soil. *Penicillium tolerans* was frequently isolated during these experiments, which indicated its ability to survive in soil treated with these disinfectants.



*Penicillium tolerans*. Colonies sporulating on potato dextrose agar after 4wk (upper surface and reverse); colony surface; conidiophore; conidia. Scale bars = 1 cm (colony), 100 µm (colony surface), 10 µm (conidiophore and conidia).



Phylogenetic tree based on a maximum likelihood analysis of concatenated multilocus alignment (ITS and *tub2*) from species of *Penicillium* sect. *Scleroriotum*. 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). *Penicillium austrosinicum* (ex-type strain HMAS 248734) was used as the outgroup. GenBank accessions are indicated (superscript ITS/*tub2*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

*Podospora bizantiorum* Y.P. Tan, *sp. nov.*

IF 900135

Classification — *Podosporaceae*, *Sordariales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA and nrDNA described *Podospora bizantiorum* and are available in GenBank under the accessions OP903480 (ITS region), OP903497 (LSU), OP921967 (*rpb2*) and OP921968 (*tub2*). *Podospora bizantiorum* differs from *Po. intestinacea* (strain CBS 113106) by sequence comparison of the ITS region (GenBank AY999121; Identities 496/562 (88%), 29 gaps; unique nucleotide at positions 190(A), 193(A), 199(G), 206(T), 208(G), 240(C), 241(C), 243(G), 265(T), 268(C), 273(T), 276(C), 287(G), 288(A), 290(T), 297(G), 299(T), 308(G), 318(T), 326(C), 449(C), 508(T), 513(A), 514(G), 524(T), 534(G), 536(C), 539(T), 544(G), 583(T), 586(T), 620(G), 631(C), 634(A), 635(C)), and LSU (GenBank AY999104; Identities 806/836 (96%), four gaps; unique nucleotide at positions 80(T), 116(C), 118(C), 119(G), 120(G), 121(C), 122(G), 124(T), 128(C), 129(G), 152(T), 155(A), 176(T), 182(C), 183(C), 184(T), 186(G), 371(A), 464(G), 466(G), 468(C), 474(C), 504(C), 512(G), 520(C), 539(C), 540(T), 715(A)).

*Specimen examined*: Australia, Queensland, Barwidgi, from soil, 20 Apr. 2021, Y.P. Tan (holotype BRIP 72548b permanently preserved in a metabolically inactive state).

*Etymology*: Named after David John Bizant and Julie Bizant, for their unconditional love and support for the author.

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

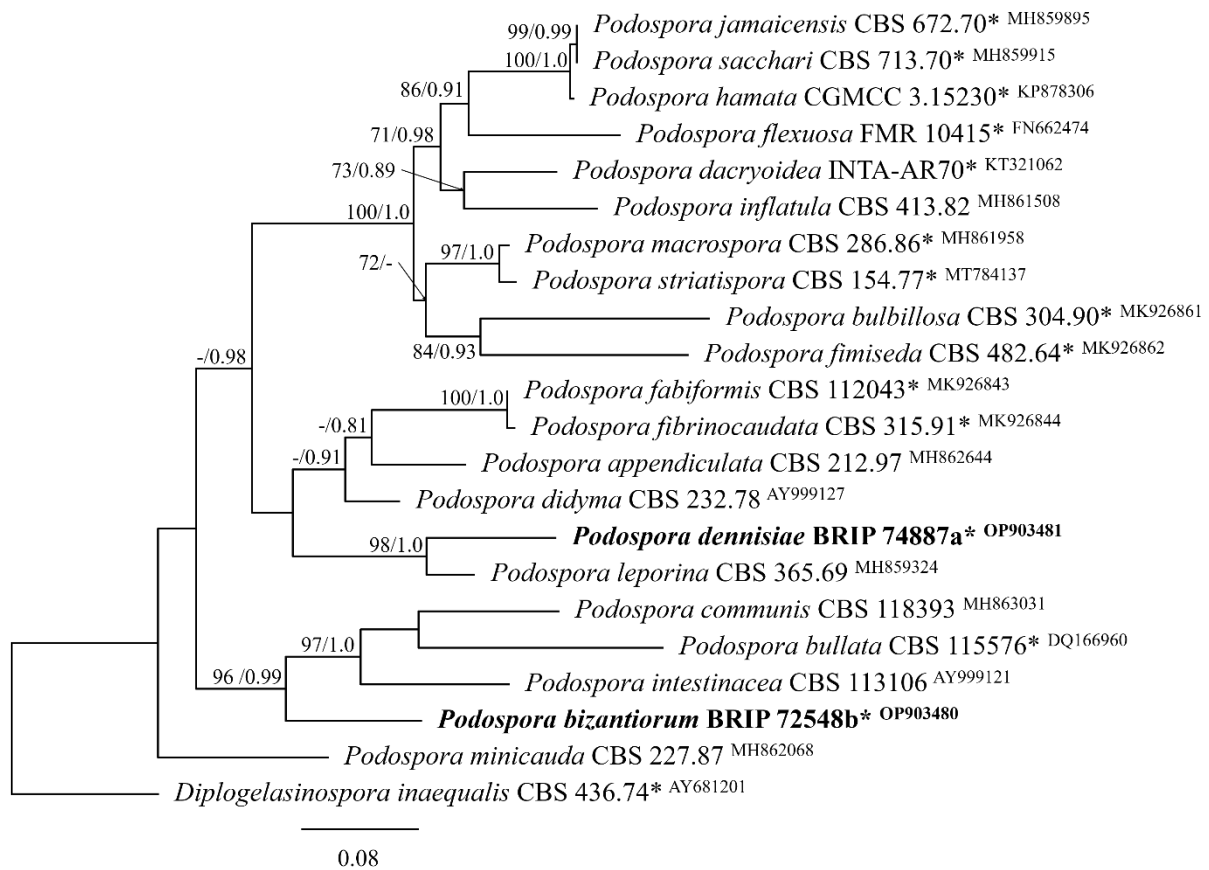
IF 900146

Classification — *Podosporaceae*, *Sordariales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA and nrDNA described *Podospora dennisiae* and are available in GenBank under the accessions OP903481 (ITS region) and OP903498 (LSU). *Podospora dennisiae* differs from *Po. leporina* (strain CBS 365.69) by sequence comparison of the ITS region (GenBank MH859324; Identities 405/432 (94%), two gaps; unique nucleotide at positions 235(C), 236(T), 240(C), 247(G), 249(G), 251(A), 253(G), 255(T), 269(G), 270(C), 272(G), 274(C), 292(C), 431(T), 455(C), 560(G), 561(C), 572(C), 573(A), 576(G), 588(C), 598(T), 610(C), 612(T), 613(C)), and LSU (GenBank MH871063; Identities 854/873 (98%); unique nucleotide at positions 157(G), 181(G), 185(T), 189(T), 195(G), 274(C), 379(G), 393(C), 431(G), 469(G), 472(C), 473(A), 487(T), 511(C), 516(T), 568(C), 571(C), 701(A)).

*Specimen examined*: Australia, Queensland, Rossville, from soil, 13 May 2022, M.D.E. Shivas, R.G. Shivas & T.S. Marney (holotype BRIP 74887a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Elizabeth (Liz) Salisbury Dennis (1943–), a pioneering Australian plant molecular biologist who specialised in gene expression, the molecular bases of plant development, plant gene regulation, and mapping plant genomes. Liz Dennis was elected a Fellow of the Australian Academy of Technological Sciences and Engineering in 1987, and the Australian Academy of Science in 1995.



Phylogenetic tree based on maximum likelihood analysis of the ITS region of species of *Podospora*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Diplogelasinospora inaequalis* (ex-type strain CBS 436.74) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (\*).

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

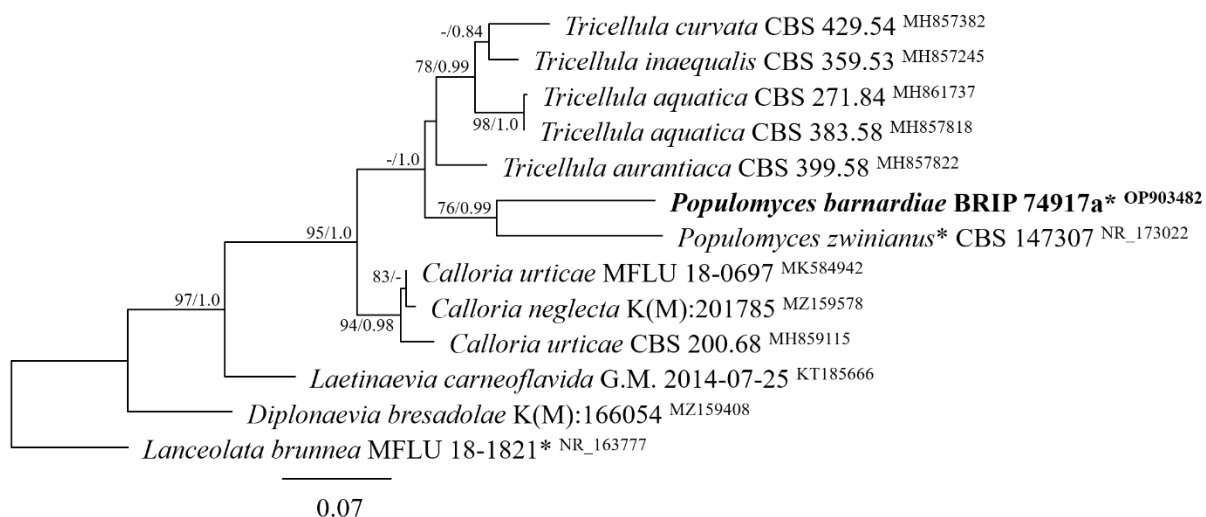
IF 900147

Classification — *Incertae sedis*, *Helotiales*, *Leotiomyces*

**Diagnosis:** Sequences from the rDNA describe *Populomyces barnardiae* and are available in GenBank under the accessions OP903482 (ITS region) and OP903499 (LSU). *Populomyces barnardiae* differs from *Pu. zwinianus* (ex-type strain CBS 147307) by sequence comparison of the ITS region (GenBank NR\_173022; Identities 442/507 (87%), 13 gaps; unique nucleotide at positions 174(C), 176(T), 177(T), 178(C), 179(G), 181(G), 182(T), 207(T), 226(G), 228(C), 235(C), 259(A), 261(C), 264(C), 280(T), 284(C), 296(G), 297(A), 298(C), 309(G), 310(A), 313(A), 314(A), 315(C), 322(G), 330(T), 339(C), 387(A), 394(C), 405(T), 406(T), 414(G), 497(T), 516(T), 522(C), 523(A), 542(G), 552(T), 556(C), 559(C), 578(T), 580(A), 581(C), 589(C), 593(C), 594(A), 597(G), 600(A), 603(C), 607(A), 612(G), 619(C)), and LSU (GenBank MW883835; Identities 624/669 (93%), four gaps; unique nucleotide at positions 132(C), 179(C), 268(T), 309(A), 317(C), 324(G), 334(G), 358(A), 384(G), 386(G), 387(C), 388(C), 397(A), 399(T), 412(A), 421(G), 424(G), 425(G), 426(C), 446(C), 463(G), 465(G), 466(T), 481(C), 503(T), 504(C), 516(G), 524(G), 574(T), 628(C), 629(C), 643(T), 658(T), 678(C), 696(G), 699(C), 706(T), 709(T), 733(T), 759(G), 780(G)).

**Specimen examined:** Australia, Queensland, Lake Eacham, from soil, 8 May 2022, *M.D.E. Shivas, R.G. Shivas & T.S. Marney* (holotype BRIP 74917a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Mildred Macfarlan Barnard (1908–2000), an Australian mathematician, and statistician. Mildred Barnard became a biometrician with the Division of Forest Products, Council for Scientific and Industrial Research (1936–1941), and later, a lecturer in mathematical statistics at the University of Queensland (1970–1978).



Phylogenetic tree based on a maximum likelihood analysis of the ITS region from selected species of *Helotiales*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Lanceolata brunnea* (type specimen MFLU 18-1821) 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 (\*).



*Pseudopeyronellaea aitkeniae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

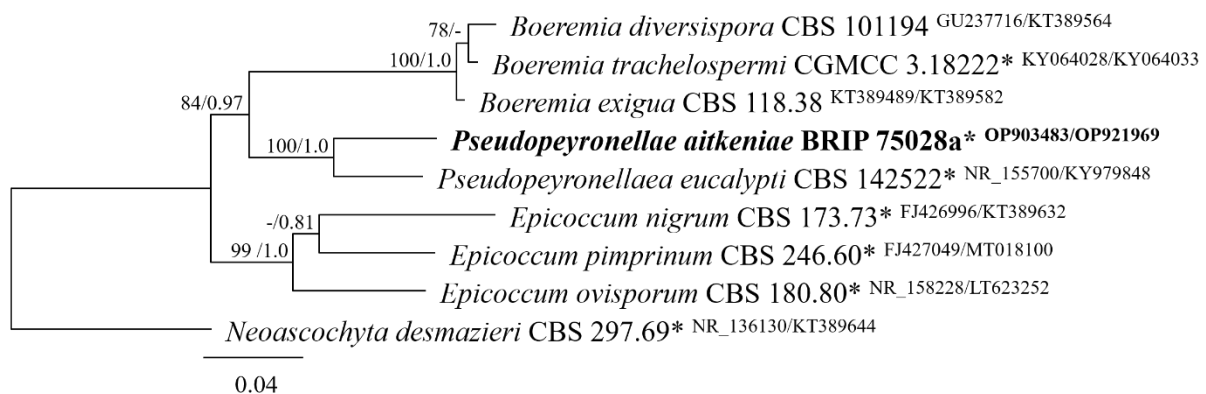
IF 900150

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

**Diagnosis:** Sequences from the rDNA and nrDNA describe *Pseudopeyronellaea aitkeniae* and are available under the accessions OP903483 (ITS region), OP925818 (LSU) and OP921969 (*rpb2*). *Pseudopeyronellaea aitkeniae* differs from *Ps. eucalypti* (ex-type strain CBS 142522) by sequence comparison of the ITS region (GenBank NR\_155700; Identities 476/487 (98%); unique nucleotide at positions 183(C), 248(C), 256(C), 271(T), 293(C), 297(G), 507(C), 531(G), 579(T), 592(A), 602(C)), and *rpb2* (GenBank KY979848; Identities 722/798 (90%), one gap; unique nucleotide at positions 12(G), 19(T), 30(T), 36(C), 39(T), 45(A), 66(G), 75(G), 81(C), 99(C), 105(C), 111(G), 126(T), 138(G), 147(C), 156(T), 174(C), 175), 177(G), 180(G), 192(A), 195(C), 207(C), 216(C), 219(T), 225(T), 231(C), 240(G), 264(G), 267(C), 288(T), 300(T), 315(T), 324(C), 339(T), 369(T), 384(C), 405(C), 426(T), 432(T), 444(T), 447(G), 465(G), 471(C), 477(A), 480(G), 511(G), 522(T), 541G), 555(G), 576(A), 583(G), 588(A), 592(G), 594(A), 597(A), 612(C), 616(C), 618(A), 621(G), 627(C), 636(T), 645(A), 654(C), 660(G), 663(T), 669(C), 708(T), 739(T), 740(C), 756(C), 762(C), 768(A), 774(C)).

**Specimen examined:** Australia, Queensland, Mossman, leaf spot of *Sphaegneticola trilobata* (*Asteraceae*), 11 May 2022, Y.P. Tan, M.D.E. Shivas & R.G. Shivas (holotype BRIP 75028a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Yvonne Aitken (1911–2004), an Australian agricultural scientist who studied genetic factors that controlled reproductive development in plants grown in different seasons and climates. Yvonne Aitken became a world authority on predicting geographic and climatic limits for plant varieties, which led to improved pasture species and more consumable crops for people and animals. Yvonne Aitken was appointed a Member of the Order of Australia in 1989.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated alignment (ITS and *rpb2*) from selected species of *Didymellaceae*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Neoscochyta desmazieri* (type specimen CBS 297.69) 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 (\*).

*Remotididymella villepreuxpowerae* Y.P. Tan, Bishop-Hurley, Pukallus & R.G. Shivas, *sp. nov.*

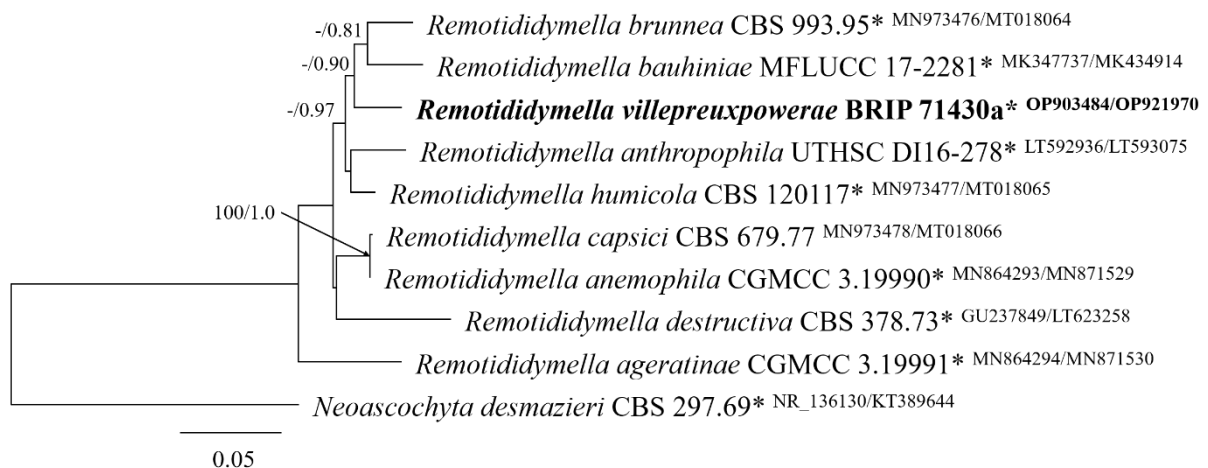
IF 900148

Classification — *Incertae sedis*, *Pleosporales*, *Dothideomycetes*

Diagnosis: Sequences from the rDNA and nrDNA describe *Remotididymella villepreuxpowerae* and are available under the accessions OP903484 (ITS region), OP903500 (LSU) and OP921970 (*rpb2*). *Remotididymella villepreuxpowerae* differs from *R. brunnea* (ex-type strain CBS 993.95) by sequence comparison of the ITS region MN973476; Identities 405/408 (99%); unique nucleotide at positions 139(C), 193(T), 194(T), 202(T), 214(C), 235(G), 247(G), 274(G), 280(A), 295(C), 304(C), 319(C), 334(C), 340(G), 355(C), 370(G), 376(C), 427(C), 448(G), 472(C), 520(A), 526(C), 553(C), 568(C), 580(G), 583(A), 592(A), 598(C), 604(T), 622(A), 646(C), 715(C), 727(C)).

*Specimen examined*: Australia, Queensland, Cardwell, *Chromolaena odorata* (*Asteraceae*), 1 Jul. 2020, K. Pukallus (holotype BRIP 71430a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Jeanne Villepreux-Power (1794–1871), a French marine biologist. Jeanne Villepreux-Power invented the aquarium and used it to study marine life.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated alignment (ITS and *rpb2*) from species of *Remotididymella*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Neoscochyta desmazieri* (type strain CBS 297.69) 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 (\*).

*Scolecobasidium millerae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 900149

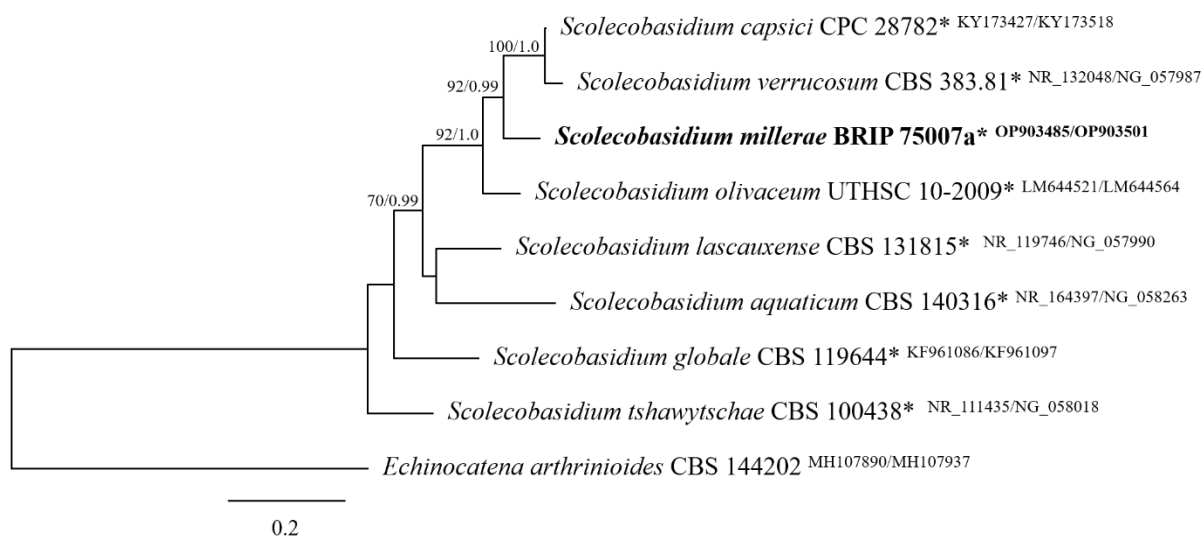
Classification — *Incertae sedis*, *Incertae sedis*, *Incertae sedis*

*Diagnosis*: Sequences from the rDNA describe *Scolecobasidium millerae* and are available in GenBank under the accessions OP903485 (ITS region) and OP903501 (LSU).

*Scolecobasidium millerae* differs from *S. verrucosum* (ex-type strain CBS 383.81) by sequence comparison of the ITS region (GenBank NR\_132048; Identities 501/600 (83%), 33 gaps; unique nucleotide at positions 177(C), 183(T), 218(T), 228(G), 230(C), 233(C), 236(C), 237(G), 245(T), 247(T), 250(T), 256(A), 257(A), 264(G), 265(C), 269(G), 272(G), 283(T), 285(G), 298(G), 309(T), 444(C), 450(G), 454(G), 457(G), 460(G), 463(C), 464(G), 467(G), 482(T), 511(C), 568(C), 611(C), 615(T), 616(C), 620(G), 622(G), 623(G), 624(A), 679(C), 680(G), 681(G), 682(A), 683(A), 685(C), 686(A), 687(A), 688(C), 692(C), 712(C)), and LSU (GenBank NG\_057987; Identities 791/799 (99%), one gap; unique nucleotide at positions 62(T), 107(A), 170(T), 171(C), 380(T), 443(C), 662(T)).

*Specimen examined*: Australia, Queensland, Cairns, leaf spot of *Epipremnum pinnatum* (*Araceae*), 12 May 2022, Y.P. Tan, M.D.E. Shivas & R.G. Shivas (holotype BRIP 75007a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Emma Miller (1839–1917) an English-born Australian women’s rights and labour activist, who became a seamstress to support her family after the death of her husband. Emma Miller championed equal pay and equal opportunity for women; supported the 1891 Australian shearers’ strike, which led to the formation of the Australian Labor Party; and actively opposed conscription.



Phylogenetic tree based on a maximum likelihood analysis of a concatenated alignment (ITS and LSU) from selected species of *Scolecobasidium*. The maximum likelihood analysis and Bayesian inference were both done on the IQ-TREE web server based on GTR substitution model with gamma-distribution rate variation. Bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp).

*Echinocatena arthrinioides* (strain CBS 144202) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS/LSU). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).

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

IF 900145

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

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Zasmidium johnsoniae* and are available in GenBank under the accessions OP256852 (ITS region), OP289000 (actin), OP289001 (*rpb2*) and OP288999 (translation elongation factor 1-alpha; *tef1a*). *Zasmidium johnsoniae* differs from *Z. grevilleae* (ex-type strain CBS 124107) by sequence comparison of the ITS region (GenBank FJ839634; Identities 592/594 (99%), one gap; unique nucleotide at position 629(A)), and *rpb2* (GenBank MF951705; Identities 694/699 (99%), one gap; unique nucleotide at positions 229(T), 490(T), 505(A), 658(C)). *Zasmidium johnsoniae* differs from *Z. hakeicola* (ex-type strain CBS 144590) by sequence comparison of the ITS region (GenBank NR\_163384; Identities 535/538 (99%); unique nucleotide at positions 208(C), 311(T), 528(C)), actin (GenBank MK442647; Identities 88/91 (97%); unique nucleotide at positions 61(A), 87(C), 123(T)), and *rpb2* (GenBank MK442687; Identities 852/858 (99%); unique nucleotide at positions 322(C), 430(C), 490(T), 505(A), 631(T), 737(T)). *Zasmidium johnsoniae* differs from *Z. proteacearum* (ex-type strain CBS 116003) by sequence comparison of the ITS region (GenBank FJ839635; Identities 561/584 (96 %), 23 gaps), actin (GenBank KF903478; Identities 126/136 (93%), four gaps; unique nucleotide at positions 35(T), 46(C), 48(T), 54(T), 60(C), 61(A)), and *rpb2* (GenBank KF902504; Identities 712/714, one gap; unique nucleotide at position 418(C)).

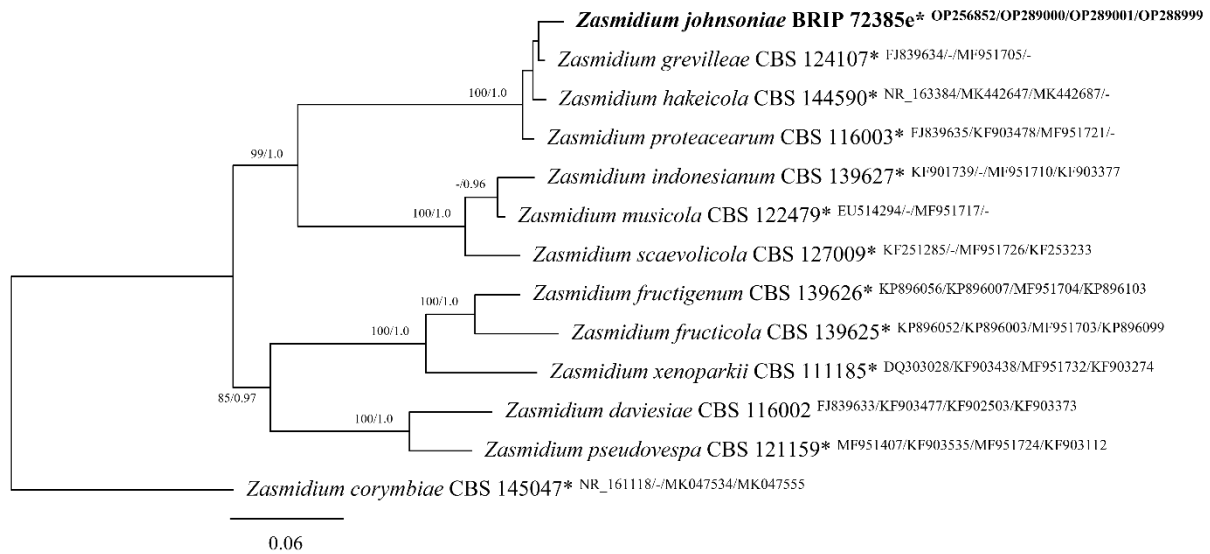
*Leaf spots* on *Grevillea decora* subsp. *decora*; on upper leaf surface discrete, trapezoid to irregular, bordered by veins, grey to blackish brown, 2–9 × 1–3 mm, with diffuse pale yellow haloes up to 2 mm wide; on the corresponding lower leaf surface dark grey to black. *Mycelium* internal. Stromata absent or formed from a few swollen hyphal cells up to 20 µm diam, intraepidermal, reddish brown. *Conidiophores* solitary or in loose fascicles of up to 15, arising from stromata, unbranched, erect, straight or curved, often geniculate at the apex, subcylindrical, 55–100 × 4–6 µm, 1–4 septate, brown, smooth. *Conidiogenous cells* integrated, terminal, proliferation sympodial, cylindrical and often geniculate, 30–40 × 4–5 µm, with thickened darkened loci, 2–3 µm diam. *Conidia* solitary, cylindrical to slightly obclavate, 35–45 × 5–6 µm, pale to brown to brown, verruculose, (1–) 3 (–4) -septate; *hila* thickened and darkened, 2–3 µm diam.

*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 72385e permanently preserved in a metabolically inactive state).

*Etymology*: Named after Katherine Johnson (1918–2020), a brilliant mathematician, who for more than 30 years worked for National Aeronautics and Space Administration (NASA, USA), where she helped put an astronaut into orbit and men on the moon. Katherine Johnson started high school when she was 10 years old; graduated from high school at 14; and obtained university degrees in mathematics and French at 18. In 2015, President Barack Obama awarded Katherine Johnson the Presidential Medal of Freedom, which is America's highest civilian honour. One of Katherine's biographers wrote that as an African American woman working in the sciences, she pushed boundaries, overcame adversity, and continues to inspire generations of young people to reach for the stars.



*Zasmidium johnsoniae*. Host plant (*Grevillea decora* subsp. *decora*); on leaf spots; colonies on potato dextrose agar (upper surface and reverse); conidiophores; conidia. Scale bars = 1 cm (leaves and colonies), 10 µm (conidiophores and conidia).



Phylogenetic tree based on a maximum likelihood analysis of a concatenated multilocus alignment (ITS, actin, *rpb2* and *tef1a*) from species of *Zasmidium*. 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). *Zasmidium corymbiae* (ex-type strain CBS 145047) was used as the outgroup. GenBank accessions are indicated (superscript ITS/actin/*rpb2*/*tef1a*). Novel taxon is shown in bold. Ex-type strains are marked by an asterisk (\*).