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Nomenclatural novelties: Y.P. Tan, S.L. Bishop-Hurley, J.R. Conroy & R.G. Shivas

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*Coniochaeta teitelbaumiae* Y.P. Tan & Conroy, *sp. nov.*

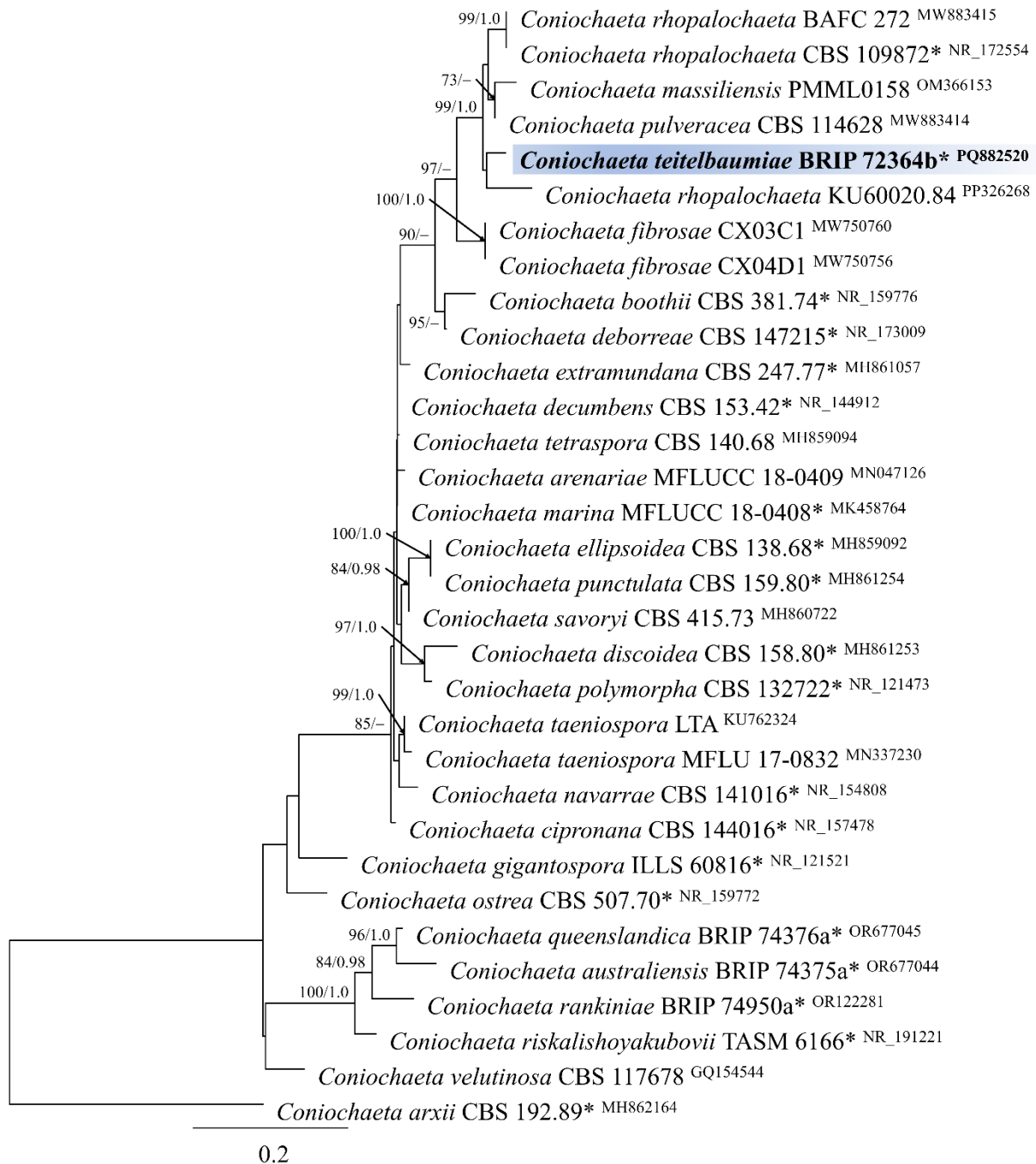
IF 901846

Classification — *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*

*Diagnosis*: Sequence from the rDNA describe *Coniochaeta teitelbaumiae*, and is available under the accession PQ882520 (ITS). *Coniochaeta teitelbaumiae* differs from *C. rhopalochaeta* (ex-type strain CBS 109872) by sequence comparison of the ITS region (GenBank NR\_172554; Identities 483/508 (95%), seven gaps (1%); unique nucleotide at positions 35(A), 70(C), 87(C), 88(A), 93(T), 108(C), 109(G), 113(A), 115(A), 128(G), 319(C), 343(C), 344(A), 347(C), 426(C), 436(T), 446(C), 488(G)). *Coniochaeta teitelbaumiae* differs from *C. pulveracea* (strain CBS 114628) by sequence comparison of the ITS region (GenBank MW883414; Identities 460/478 (96%), four gaps; unique nucleotide at positions 88(A), 93(T), 108(C), 109(G), 111(T), 113(A), 115(A), 128(G), 319(C), 343(C), 345(A), 426(C), 439(A), 449(T)). *Coniochaeta teitelbaumiae* differs from *C. fibrosae* (isolate CX03C1) by sequence comparison of the ITS region (GenBank MW750760; Identities 484/530 (91%), 24 gaps (4%); unique nucleotide at positions 30(T), 35(A), 44(A), 80(T), 87(C), 88(A), 99(A), 102(C), 108(C), 114(A), 115(A), 128(G), 273(T), 319(C), 328(T), 382(A), 398(G), 410(G), 411(A), 415(A), 420(G), 435(T)). *Coniochaeta teitelbaumiae* differs from *C. massiliensis* (isolate PMML0158) by sequence comparison of the ITS region (GenBank OM366153; Identities 324/345 (94%), four gaps (1%); unique nucleotide at positions 70(C), 88(A), 93(T), 108(C), 109(G), 111(T), 113(A), 115(A), 128(G), 129(A), 179(A), 238(A), 258(T), 285(T), 319(C), 343(C), 344(A)).

*Specimen examined*: Australia, Queensland, Branyan, from the leaf of *Solanum lycopersicum* (*Solanaceae*), 14 Apr. 2021, J.R. Conroy (holotype BRIP 72364b permanently preserved in a metabolically inactive state).

*Etymology*: Named after Ruth Teitelbaum (née Lichterman; 1924–1986), a mathematician and one of the first computer programmers in the world. Ruth Teitelbaum was in a special team with Marlyn Meltzer on the ENIAC (Electronic Numerical Integrator and Computer) project, using analogue technology to calculate ballistic trajectory equations.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of the ITS region from species of *Coniochaeta*. The ML analysis was performed on the IQ-TREE web server (1000 bootstrap replicates; Trifinopoulos et al. 2016) and Bayesian analysis was performed on the Geneious Prime 2025 platform with MrBayes v. 3.2.6 (Huselsenbeck & Ronquist, 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). *Coniochaeta arxii* (ex-type strain CBS 192.89) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in coloured bold. Ex-type strains are marked by an asterisk (\*).

*Exophiala holbertoniae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

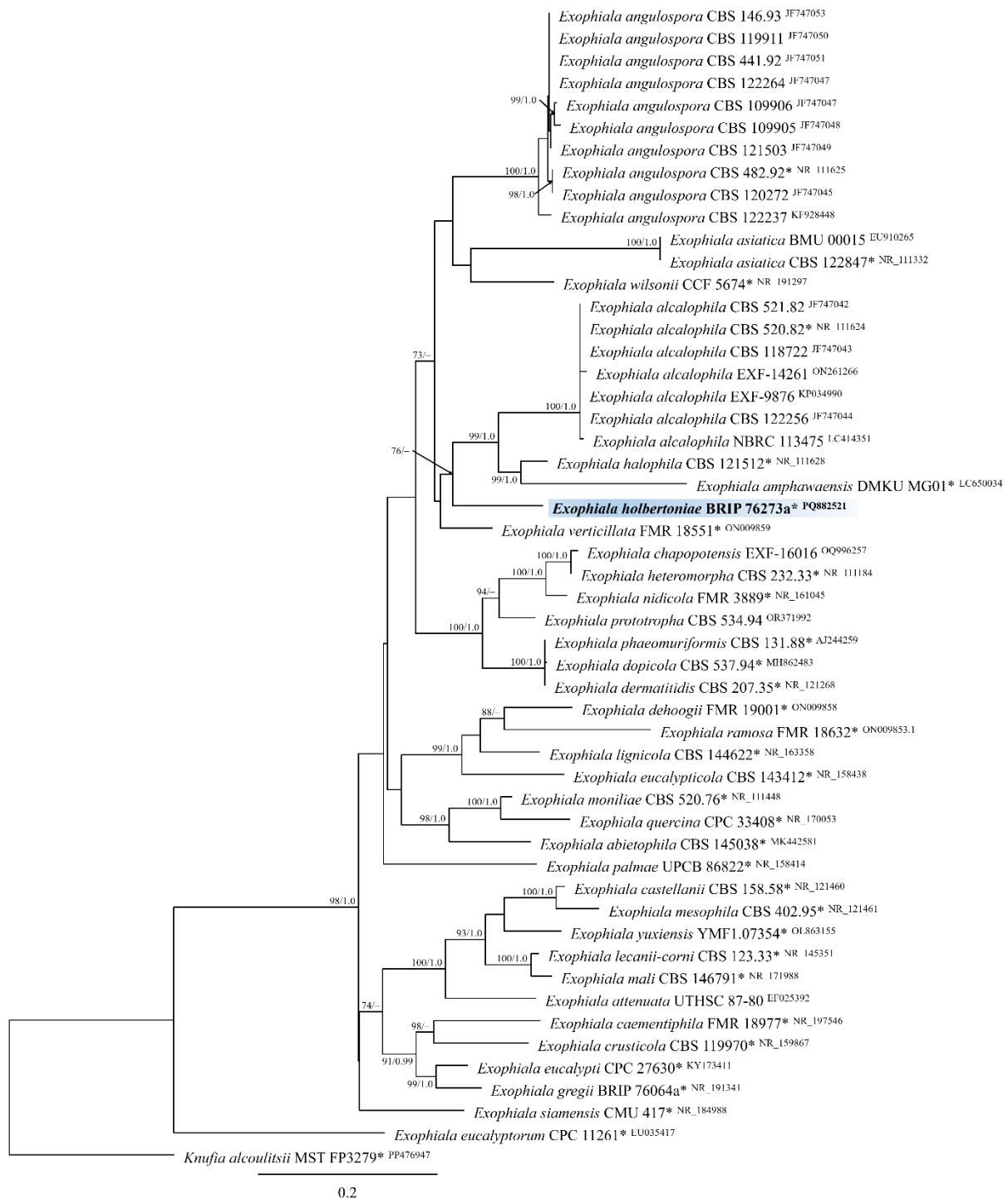
IF 901849

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Eurotiomycetes*

*Diagnosis*: Sequences from the rDNA describe *Exophiala holbertoniae*, and are available under the accessions PQ882521 (ITS), and PQ882517 (LSU). *Exophiala holbertoniae* differs from *E. verticillata* (ex-type strain FMR 18551) by sequence comparison of the ITS region (GenBank ON009859; Identities 366/398 (92%), nine gaps (2%); unique nucleotide at positions 141(C), 179(T), 217(G), 219(T), 220(T), 223(G), 224(C), 241(T), 246(A), 248(A), 272(G), 273(T), 282(A), 283(C), 284(T), 285(T), 289(T), 290(G), 297(G), 308(T), 309(G), 315(A), 485(G)), and LSU (GenBank ON009939; Identities 755/769 (98%), two gaps; unique nucleotide at positions 87(A), 128(C), 256(A), 398(A), 419(T), 432(T), 462(C), 493(C), 525(G), 653(A), 680(T), 686(T)). *Exophiala holbertoniae* differs from *E. wilsonii* (ex-type strain CCF 5674) by sequence comparison of the ITS region (GenBank NR\_191297.1; Identities 595/649 (92%), 19 gaps (2%); unique nucleotide at positions 126(T), 141(C), 142(A), 179(T), 182(T), 183(C), 217(G), 221(C), 238(C), 239(C), 245(G), 246(A), 281(C), 282(A), 284(T), 285(T), 288(A), 290(G), 291(C), 297(G), 309(G), 321(A), 334(G), 505(G), 528(C), 532(T), 540(T), 544(C), 546(C), 547(C), 575(C), 629(T), 630(G), 632(C), 648(T)), and LSU (GenBank OR555859; Identities 833/865 (96%), five gaps; unique nucleotide at positions 81(C), 82(T), 87(A), 128(C), 352(C), 378(T), 392(A), 398(A), 415(T), 424(T), 427(T), 432(T), 462(C), 475(C), 476(T), 496(T), 499(T), 503(C), 508(T), 522(A), 524(G), 535(G), 653(A), 707(T), 712(T), 848(C)).

*Specimen examined*: Australia, Queensland, Mount Glorious, from rotten wood, 11 Nov. 2023, *M.D.E. Shivas & R.G. Shivas* (holotype BRIP 76273a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Frances Elizabeth (Betty) Holberton (née Snyder; 1917–2001), a mathematician and computer programmer, who first worked on the ENIAC project that produced the general-purpose electronic digital computer in 1945. Betty Holberton also wrote the first statistical analysis package.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of the ITS region from species of *Exophiala*. The ML analysis was performed on the IQ-TREE web server (1000 bootstrap replicates; Trifinopoulos et al. 2016) and Bayesian analysis was performed on the Geneious Prime 2025 platform with MrBayes v. 3.2.6 (Huselsenbeck & Ronquist, 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). *Knufia alcoultsii* (ex-type strain MST FP3279) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in coloured bold. Ex-type strains are marked by an asterisk (\*).

*Gongronella bartikiae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

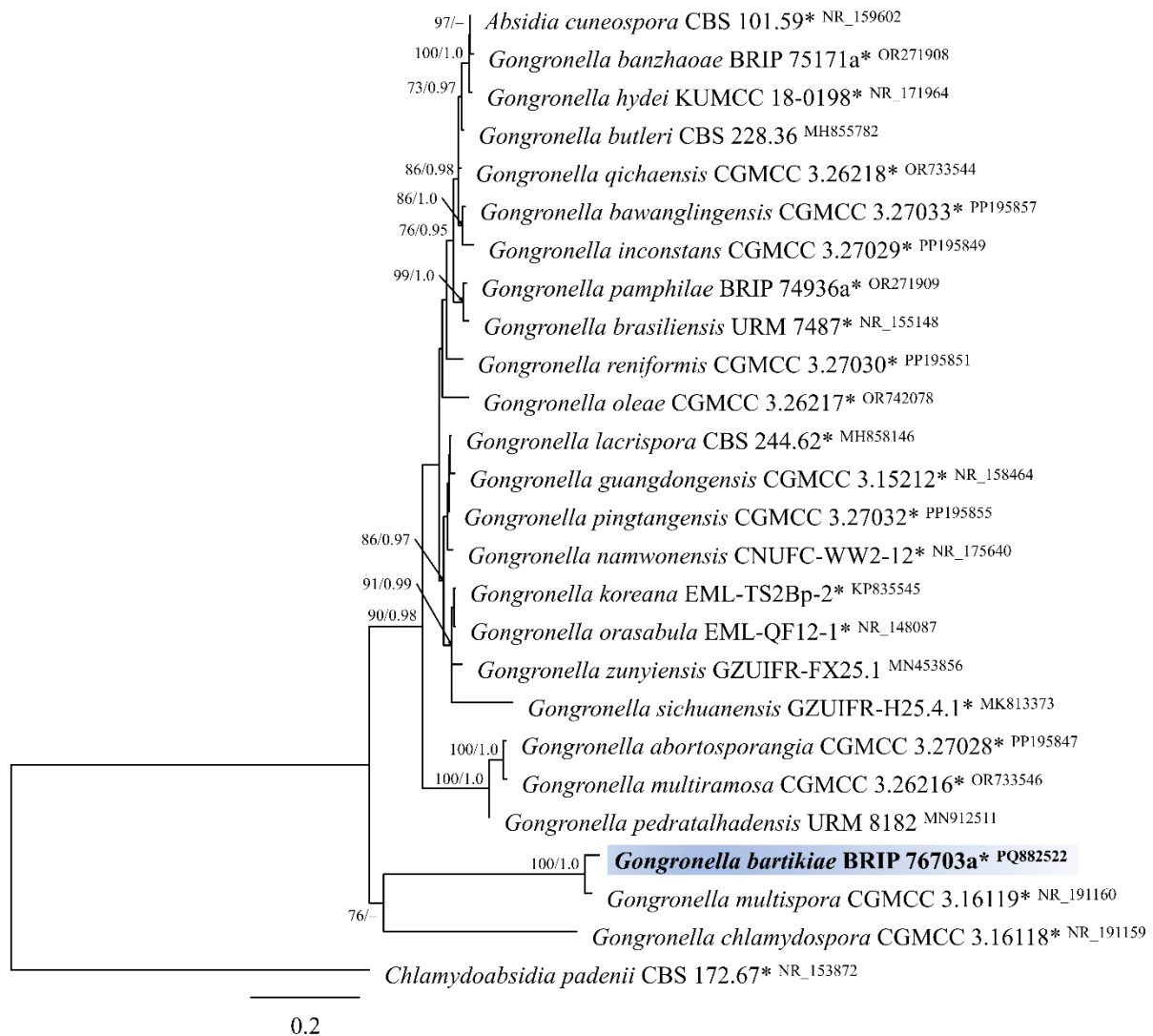
IF 902485

Classification — *Cunninghamellaceae*, *Mucorales*, *Mucoromycetes*

*Diagnosis*: Sequence from the rDNA describe *Gongronella bartikiae*, and is available under the accession PQ882522 (ITS). *Gongronella bartikiae* differs from *G. multispora* (ex-type strain CGMCC 3.16119) by sequence comparison of the ITS region (GenBank NR\_191160; Identities 524/541 (97%), five gaps; unique nucleotide at positions 224(C), 299(A), 301(T), 302(C), 604(T), 606(T), 612(A), 667(G), 703(T), 704(T), 707(A), 719(T)).

*Specimen examined*: Australia, Queensland, Bramston Beach, isolated from an unidentified basidiocarp, 14 Aug. 2024, *M.D.E. Shivas & R.G. Shivas* (holotype BRIP 76703a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Betty Jean Bartik (née Jennings; 1924–2011), a mathematician who became a computer programmer on the ENIAC project. Betty Bartik later, with Betty Snyder, became the sole programmers for the first commercial computer (UNIVAC).



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of the ITS region from species of *Gongronella*. The ML analysis was performed on the IQ-TREE web server (1000 bootstrap replicates; Trifinopoulos et al. 2016) and Bayesian analysis was performed on the Geneious Prime 2025 platform with MrBayes v. 3.2.6 (Huselsenbeck & Ronquist, 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). *Chlamydoabsidia padenii* (ex-type strain CBS 172.) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in coloured bold. Ex-type strains are marked by an asterisk (\*).

*Heterotruncatella bilasiae* Y.P. Tan & Conroy, *sp. nov.*

IF 902572

Classification — *Sporocadaceae*, *Amphisphaeriales*, *Sordariomycetes*

*Diagnosis*: Sequence from the rDNA describe *Heterotruncatella bilasiae*, and is available under the accession PQ882523 (ITS). *Heterotruncatella bilasiae* differs from *H. avellanea* (ex-type strain CBS 143896) by sequence comparison of the ITS region (GenBank NR\_161104; Identities 397/408 (97%), three gaps; unique nucleotide at positions 94(G), 119(G), 125(T), 127(C), 365(A), 376(C), 409(T), 452(T)). *Heterotruncatella bilasiae* differs from *H. longissima* (ex-type strain CPC 29114) by sequence comparison of the ITS region (GenBank NR\_161109; Identities 473/492 (96%), four gaps; unique nucleotide at positions 20(C), 36(C), 78(G), 97(A), 98(C), 110(C), 112(C), 119(G), 125(T), 127(C), 365(A), 376(C), 391(T), 409(T), 452(T)). *Heterotruncatella bilasiae* differs from *H. restionacearum* (ex-type strain CMW 18755) by sequence comparison of the ITS region (GenBank NR\_160986; Identities 441/458 (96%), three gaps; unique nucleotide at positions 78(G), 79(A), 83(C), 84(C), 94(G), 119(G), 125(T), 127(C), 365(A), 376(C), 391(T), 409(T), 452(T), 454(A)). *Heterotruncatella bilasiae* differs from *H. singularis* (ex-type strain CBS 144031) by sequence comparison of the ITS region (GenBank MH554161; Identities 475/492 (97%), three gaps; unique nucleotide at positions 20(C), 36(C), 78(G), 94(G), 97(A), 98(C), 119(G), 125(T), 127(C), 365(A), 376(C), 409(T), 429(C), 452(T)). *Heterotruncatella bilasiae* differs from *H. spadicea* (ex-type strain CBS 118145) by sequence comparison of the ITS region (GenBank DQ278912; Identities 441/458 (96%), four gaps; 78(G), 79(A), 83(C), 84(C), 94(G), 119(G), 125(T), 127(C), 365(A), 375(T), 376(C), 409(T), 452(T)). *Heterotruncatella bilasiae* differs from *H. youngii* (ex-type strain BRIP 74453a) by sequence comparison of the ITS region (GenBank OQ297075; Identities 528/549 (96%), nine gaps (1%); unique nucleotide at positions 20(C), 36(C), 78(G), 97(A), 98(C), 119(G), 125(T), 127(C), 375(T), 376(C), 409(T), 452(T)).

*Specimen examined*: Australia, Northern Territory, Douglas Daly, from phyllode of *Acacia* sp. (*Fabaceae*), 20 Sep. 2020, J.R. Conroy (holotype BRIP 71754c permanently preserved in a metabolically inactive state).

*Etymology*: Named after Frances V. Spence (née Bilas; 1922–2012), one of the six original programmers on the ENIAC project, the first general-purpose electronic digital computer.

*Heterotruncatella goldstineae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 903021

Classification — *Sporocadaceae*, *Amphisphaeriales*, *Sordariomycetes*

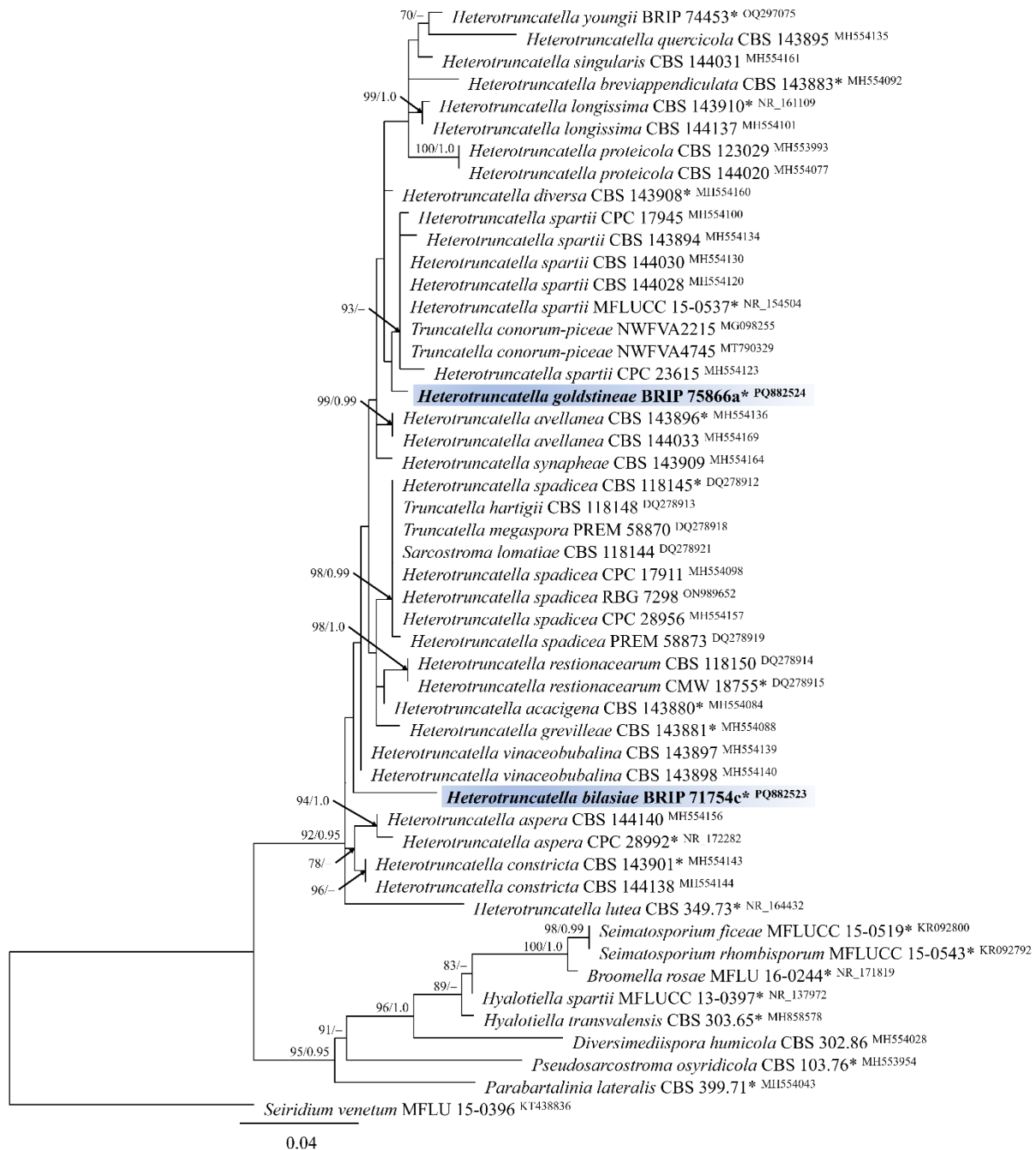
**Diagnosis:** Sequences from the rDNA describe *Heterotruncatella goldstineae*, and are available under the accessions PQ882524 (ITS), and PQ882518 (LSU). *Heterotruncatella goldstineae* differs from *H. acacigena* (ex-type strain CBS 143880) by sequence comparison of the ITS region (GenBank NR\_161094; Identities 484/489 (99%), one gap; unique nucleotide at positions 475(A), 485(T), 501(T), 585(T)), and LSU (GenBank NG\_069585; Identities 826/828 (99%); unique nucleotide at positions 489(T), 490(C)). *Heterotruncatella goldstineae* differs from *H. grevilleae* (ex-type strain CBS 143881) by sequence comparison of the ITS region (GenBank NR\_161095; Identities 482/489 (99%), one gap; unique nucleotide at positions 173(T), 182(T), 201(A), 475(A), 485(T), 585(T)), and LSU (GenBank NG\_069586; Identities 827/829 (99%), unique nucleotide at position 489(T)).

*Heterotruncatella goldstineae* differs from *H. spadicea* (ex-type strain CBS 118145) by sequence comparison of the ITS region (GenBank DQ278912; Identities 515/522 (99%), three gaps; unique nucleotide at positions 170(C), 475(A), 485(T), 585(T)). *Heterotruncatella goldstineae* differs from *H. spartii* (ex-type strain MFLUCC 15-0537) by sequence comparison of the ITS region (GenBank NR\_154504; Identities 545/553 (99%), three gaps; unique nucleotide at positions 188(G), 205(C), 585(T)), and LSU (GenBank NG\_059567; Identities 868/874 (99%), two gaps; unique nucleotide at positions 454(T), 455(C), 474(C), 510(G)). *Heterotruncatella goldstineae* differs from *H. synapheae* (ex-type strain CBS 143909) by sequence comparison of the ITS region (GenBank MH554164; Identities 483/489 (99%), one gap; unique nucleotide at positions 188(G), 255(T), 256(A), 475(A), 585(T)), and LSU (GenBank MH554360; Identities 825/828 (99%); unique nucleotide at positions 196(C), 489(T), 491(T)). *Heterotruncatella goldstineae* differs from *H. vinaceobubalina* (ex-type strain CBS 143897) by sequence comparison of the ITS region (GenBank MH554139; Identities 485/489 (99%), one gap; unique nucleotide at positions 229(A), 475(A), 585(T)), and LSU (GenBank MH554341; Identities 825/828 (99%); unique nucleotide at positions 465(T), 489(T), 490(C)).

**Specimen examined:** Australia, Queensland, Einasleigh, from the leaf spot of *Erythrophleum chlorostachys* (*Fabaceae*), 24 Apr. 2023, Y.P. Tan, M. Sudsanguan, M.D.E. Shivas & R.G. Shivas (holotype BRIP 75866a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Adele Goldstine (née Katz; 1920–1964), a mathematician who wrote the manual for ENIAC. Adele Goldstine also trained some of the six women, Frances Spence, Ruth Teitelbaum, Betty Holberton, Marlyn Meltzer, Kathleen McNulty and Jean Jennings Bartik, who were the original programmers for ENIAC.





Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of the ITS region from species of *Heterotruncatella*. The ML analysis was performed on the IQ-TREE web server (1000 bootstrap replicates; Trifinopoulos et al. 2016) and Bayesian analysis was performed on the Geneious Prime 2025 platform with MrBayes v. 3.2.6 (Huselsenbeck & Ronquist, 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). *Seiridium venetum* (MFLU 15-0396) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is shown in coloured bold. Ex-type strains are marked by an asterisk (\*).

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

IF 903215

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

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Hypoxylon mcnultyae*, and are available under the accessions PQ882526 (ITS), and PQ877434 (*tub2*). *Hypoxylon mcnultyae* differs from *Hy. lateripigmentum* (ex-type strain MUCL 53304) by sequence comparison of the ITS region (GenBank KC968933; Identities 423/432 (98%), two gaps; unique nucleotide at positions 213(C), 215(T), 303(T), 341(T), 351(C), 558(T), 597(T)). *Hypoxylon mcnultyae* differs from *Hy. lignicola* (ex-type strain MFLUCC 16-0926) by sequence comparison of the ITS region (GenBank MK828609; Identities 491/511 (96%), three gaps; unique nucleotide at positions 262(T), 281(T), 283(C), 303(T), 339(G), 340(T), 351(C), 527(A), 528(A), 531(C), 539(T), 558(T), 560(G), 580(T), 632(A), 641(A), 657(A)).

*Specimen examined*: Australia, New South Wales, Rowlands Creek, from an unidentified lichen, 19 Feb. 2024, *J. Blacker & D.D. Teal* (holotype BRIP 76563a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Kathleen (Kay) Rita Mauchly Antonelli (née McNulty; 1921–2006), a mathematician and one of the original programmers of the ENIAC project, who helped create and define the work of software programming.

*Hypoxylon meltzeriae* Y.P. Tan & Bishop-Hurley, *sp. nov.*

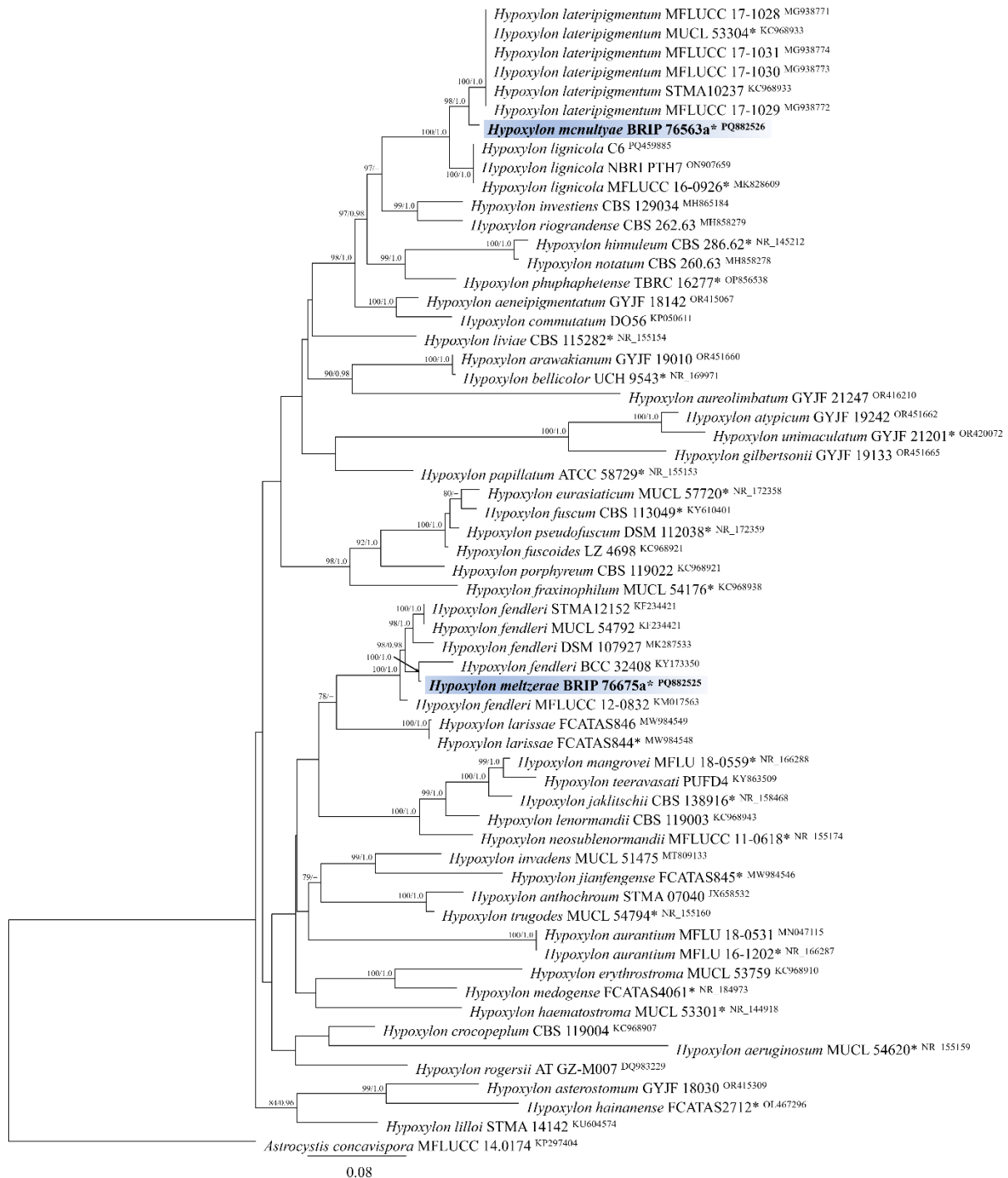
IF 901833

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

*Diagnosis*: Sequences from the rDNA describe *Hypoxylon meltzeriae*, and are available under the accessions PQ882525 (ITS), and PQ882519 (LSU). *Hypoxylon meltzeriae* differs from *Hy. fendleri* (strain BCC 32408) by sequence comparison of the ITS region (GenBank KY173350; Identities 565/576 (98%), three gaps; unique nucleotide at positions 204(G), 217(C), 244(A), 249(C), 251(C), 260(A), 267(C), 528(G)), and LSU (GenBank KY173349; Identities 829/830 (99%); unique nucleotide at position 181(G)).

*Specimen examined*: Australia, Queensland, Samford Valley, from an unidentified lichen on the trunk of *Diploglottis australis* (*Sapindaceae*), 18 Jun. 2024, *S.L. Bishop-Hurley & G.J. Bishop-Hurley* (holotype BRIP 76675a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Marlyn Meltzer (née Wescoff; 1922–2008), a mathematician, who with Ruth Teitelbaum was in a special team on the ENIAC project, using analogue technology to calculate ballistic trajectory equations.



Phylogenetic tree based on the maximum likelihood (ML) analysis of the alignment of the ITS region from related species of *Hypoxylon*. The ML analysis was performed on the IQ-TREE web server (1000 bootstrap replicates; Trifinopoulos et al. 2016) and Bayesian analysis was performed on the Geneious Prime 2025 platform with MrBayes v. 3.2.6 (Huselsenbeck & Ronquist, 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). *Astrocystis concavisporea* (strain MFLUCC 14.0174) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxa are shown in coloured bold. Ex-type strains are marked by an asterisk (\*).

*References*

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Trifinopoulos J, Nguyen LT, Von Haeseler A, et al. (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research* 44: W232–W235.