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

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

IF 901089

Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Akanthomyces australiensis* and are available in GenBank under the accessions OR527516 (ITS), OR527524 (LSU), OR512197 (SSU), OR514848 (*rpb2*), and OR514840 (*tef1*). *Akanthomyces australiensis* differs from *A. pyralidarum* (ex-type strain BCC28816) by sequence comparison of the ITS region (GenBank MT356080; Identities 478/518 (92%), 17 gaps; unique nucleotide at positions 183(C), 198(T), 199(A), 200(C), 239(T), 248(G), 288(T), 290(T), 296(T), 297(T), 300(T), 304(G), 306(A), 367(C), 487(C), 523(A), 539(G), 565(A), 591(T), 592(T), 622(C), 623(G), 625(G)), LSU (GenBank MT356091; 854/868 (98%), one gap; unique nucleotide at positions 86(T), 102(T), 154(T), 271(C), 272(C), 373(A), 461(T), 468(T), 485(C), 510(T), 518(T), 541(T), 716(A)), *rpb2* (GenBank MT478007; Identities 837/911 (92%), one gap; unique nucleotide at positions 21(T), 54(A), 62(A), 120(C), 141(A), 153(C), 165(T), 166(G), 192(T), 219(C), 242(G), 258(G), 327(T), 372(A), 374(G), 411(C), 414(T), 444(T), 450(A), 456(C), 460(T), 461(T), 462(G), 465(A), 467(C), 468(C), 471(A), 477(A), 493(T), 495(A), 498(C), 512(T), 516(G), 542(C), 556(T), 557(C), 573(A), 576(T), 594(G), 627(G), 628(T), 630(A), 645(G), 657(G), 669(A), 675(A), 685(A), 693(C), 696(T), 705(C), 720(C), 744(T), 765(T), 771(T), 786(T), 819(A), 822(C), 834(C), 841(A), 844(T), 845(A), 854(G), 856(C), 858(G), 864(T), 866(C), 872(A), 873(T), 881(C), 884(G), 886(G), 894(C), 901(T), *tef1* (GenBank MT477982; Identities 880/901 (98%); unique nucleotide at positions 45(T), 99(C), 204(C), 255(T), 310(A), 333(T), 354(T), 378(T), 387(T), 393(T), 462(T), 483(T), 495(C), 519(T), 657(C), 729(C), 774(C), 777(T), 885(T), 888(T), 897(T)).

*Specimen examined*: Australia, Queensland, Hervey Range, from an unidentified dead adult lepidopteran insect, 26 Apr. 2021, *T.S. Marney, M.D.E. Shivas & R.G. Shivas* (holotype BRIP 72630a permanently preserved in a metabolically inactive state).

*Etymology*: Named after the country from which it was collected.

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

IF 901090

Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Lecanicillium margaretspenceriae* and are available in GenBank under the accessions OR527517 (ITS), OR527525 (LSU), OR514849 (*rpb2*), and OR514841 (*tef1*). *Lecanicillium margaretspenceriae* differs from *L. aphanocladii* (strain CBS 797.84) by sequence comparison of LSU (GenBank KM283787; Identities 809/813 (99%); unique nucleotide at positions 85(G), 104(G), 194(C), 504(C)), and *tef1* (GenBank KM283811; Identities 847/895 (95%); unique nucleotide at positions 7(C),

178(C), 181(T), 182(T), 183(C), 202(C), 212(G), 213(C), 214(T), 272(A), 299(T), 300(C), 303(G), 314(A), 316(C), 324(A), 326(T), 340(C), 343(C), 352(C), 361(C), 372(C), 383(A), 406(T), 451(T), 463(C), 467(G), 478(T), 499(C), 508(T), 553(C), 554(G), 556(T), 616(C), 619(T), 673(T), 678(C), 706(C), 715(T), 736(C), 742(T), 773(G), 774(A), 776(A), 777(C), 824(G), 826(G), 851(G)). *Lecanicillium margaretspencerae* differs from *L. dimorphum* (strain CBS 345.37) by sequence comparison of LSU (GenBank KM283788; Identities 807/813 (99%); 85(G), 104(G), 194(C), 479(C), 480(T), 504(C)), and *tefl* (GenBank KM283812; Identities 851/895 (95%); unique nucleotide at positions 91(C), 178(C), 181(T), 182(T), 183(C), 212(G), 213(C), 514(T), 299(T), 300(C), 303(G), 314(A), 316(C), 324(A), 326(T), 340(C), 352(C), 361(C), 372(C), 383(A), 406(T), 451(T), 463(C), 467(G), 478(T), 499(C), 508(T), 553(C), 554(G), 556(T), 619(T), 673(T), 678(C), 706(C), 715(T), 736(C), 739(C), 773(G), 774(A), 776(A), 777(C), 824(G), 826(G), 851(G)). *Lecanicillium margaretspencerae* differs from *L. psalliotae* (strain CBS 101270) by sequence comparison of LSU (GenBank AF339558; Identities 621/623 (99%); unique nucleotide at positions 494(G), 536(T)), and *tefl* (GenBank EF469066; Identities 877/947 (93%), two gaps; unique nucleotide at positions 16(C), 61(C), 76(T), 79(T), 88(C), 109(T), 112(C), 151(T), 163(A), 166(C), 181(T), 182(T), 183(C), 212(G), 213(C), 214(T), 217(C), 220(C), 250(T), 272(A), 299(T), 300(C), 303(G), 314(A), 316(C), 340(C), 352(C), 361(C), 372(C), 383(A), 406(T), 424(C), 451(T), 463(C), 478(T), 481(T), 487(C), 499(C), 508(T), 532(C), 553(C), 554(G), 556(T), 563(G), 564(T), 565(T), 601(T), 613(A), 631(C), 641(A), 642(G), 659(A), 660(T), 673(T), 678(C), 705(C), 714(T), 773(G), 774(A), 776(A), 777(C), 805(C), 824(G), 826(G), 852(T), 861(G), 896(A), 907(G)).

*Specimen examined*: Australia, Queensland, Tully, from an unidentified dead insect, 29 Apr. 2021, T.S. Marney, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72656a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Dora Margaret Spencer (née Cumpston; 1916–2011), an entomologist renowned for her research in malaria entomology and mosquito-borne diseases.

*Pleurodesmospora entomophila* Y.P. Tan, Bishop-Hurley, R.G. Shivas & Marney, *sp. nov.*  
IF 901091

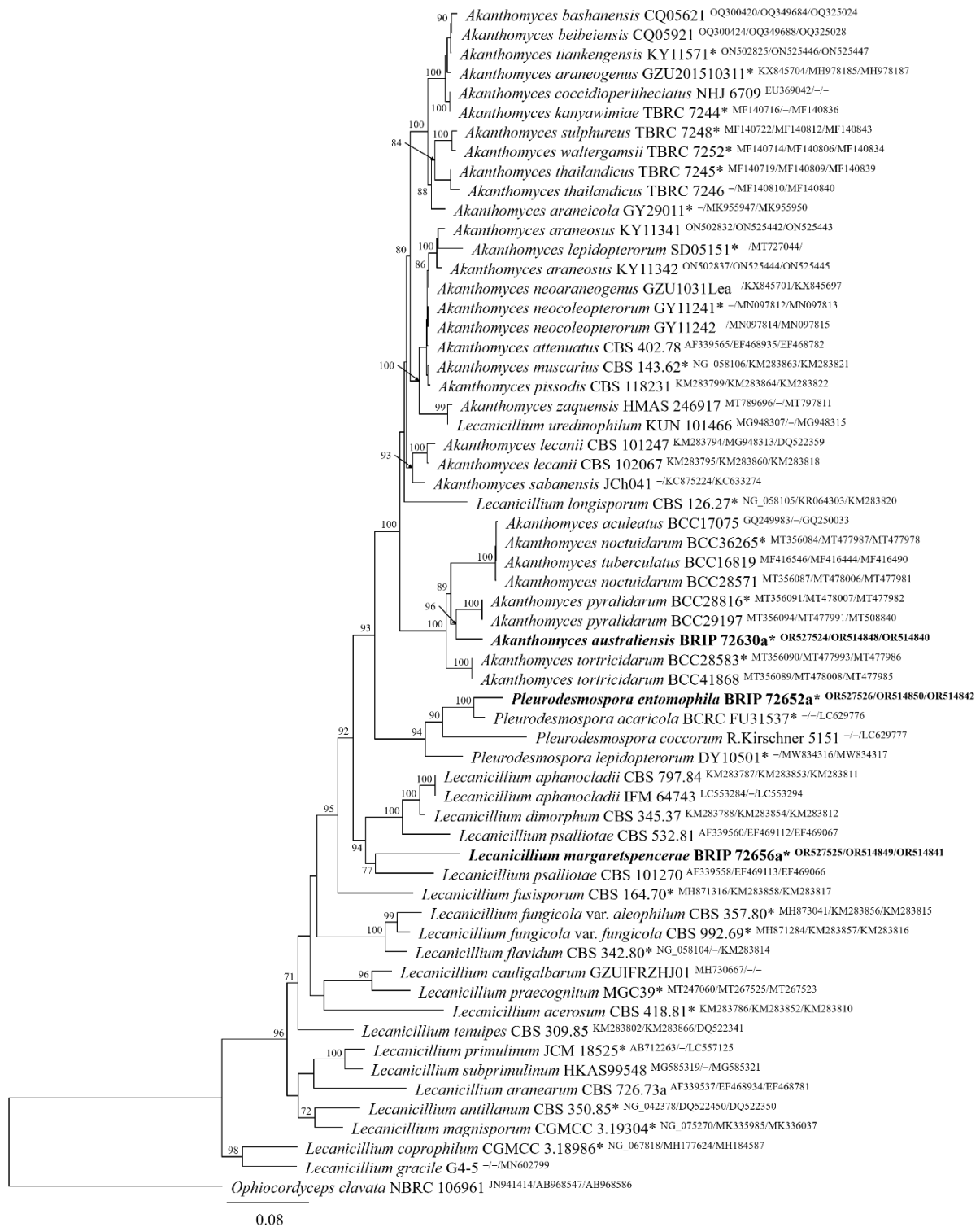
Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Pleurodesmospora entomophila* and are available in GenBank under the accessions OR527518 (ITS), OR527526 (LSU), OR514850 (*rpb2*), and OR514842 (*tefl*). *Pleurodesmospora entomophila* differs from *P. acaricola* (ex-type strain R. Kirschner 4968) by sequence comparison of the ITS region (GenBank MZ435417; Identities 560/572 (98%), two gaps; unique nucleotide at positions 155(A), 244(T), 259(C), 263(T), 490(C), 508(C), 526(A), 527(C), 563(C), 615(C)), and *tefl* (GenBank LC629776; Identities 906/922 (98%); unique nucleotide at positions 178(A), 190(A), 191(G), 279(C), 282(C), 286(A), 304(T), 421(A), 422(C), 465(T), 508(G), 519(T), 528(T), 666(T), 702(G), 900(C)). *Pleurodesmospora entomophila* differs from *P. coccorum* (strain R. Kirschner 5151) by sequence comparison of the ITS region (GenBank MZ435418; Identities 561/594 (94%), 11 gaps; unique nucleotide at positions 131(T), 179(C), 182(T), 190(T), 195(T), 221(A), 244(T), 255(T), 257(T), 259(C), 263(T), 266(T), 267(A), 283(G), 284(A), 491(G), 504(G), 505(A), 506(T), 511(T), 526(A), 527(C)), and *tefl* (GenBank LC629777; Identities 443/470 (94%); unique nucleotide at positions 24(G), 39(C), 42(T), 54(C), 102(C), 117(G), 120(T), 153(T), 190(A), 191(G), 192(C), 267(C), 304(T), 305(C), 306(C), 307(C), 312(C), 366(C), 369(T), 390(C), 393(C), 402(T), 417(T), 432(C), 441(T),

465(T)). *Pleurodesmospora entomophila* differs from *P. lepidopterorum* (ex-type strain DY10501) by sequence comparison of the ITS region (GenBank MW826577; Identities 541/576 (94%), nine gaps; unique nucleotide at positions 131(T), 179(C), 182(T), 190(T), 195(T), 244(T), 249(C), 252(G), 253(T), 255(T), 257(T), 259(C), 263(T), 266(T), 267(A), 483(G), 484(A), 492(G), 505(G), 506(A), 507(T), 512(T), 527(A), 528(C), 565(C), 566(A)), and *tefl* (GenBank MW834317; Identities 929/969 (96%), two gaps; unique nucleotide at positions 21(C), 39(C), 54(C), 60(T), 102(C), 117(G), 120(T), 190(A), 191(G), 240(C), 258(C), 267(C), 270(T), 279(C), 282(C), 303(G), 304(T), 313(A), 397(G), 519(T), 528(T), 544(T), 546(T), 547(G), 548(C), 666(T), 699(C), 723(C), 756(T), 768(C), 777(T), 783(C), 804(C), 814(T), 894(C), 900(C), 939(T), 954(T)).

*Specimen examined*: Australia, Queensland, Wallaman, from an unidentified dead insect, 28 Apr. 2021, T.S. Marney, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72652a permanently preserved in a metabolically inactive state).

*Etymology*: In reference to the substrate from which the fungus was isolated.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the combined LSU, *rpb2* and *tef1* sequences from selected species of *Cordycipitaceae*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Ophiocordyceps clavata* (strain NBRC 106961) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU/*rpb2*/*tef1*). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (\*).

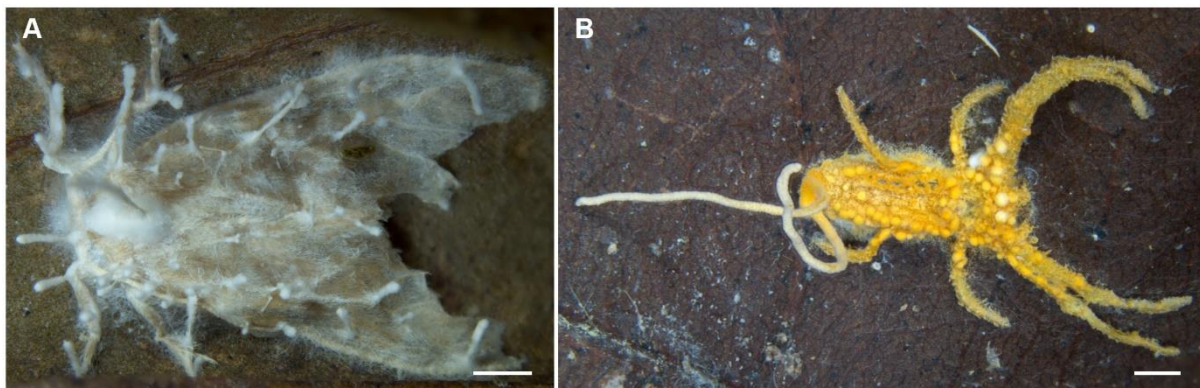
*Acremonium isabellae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*  
IF 901092

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

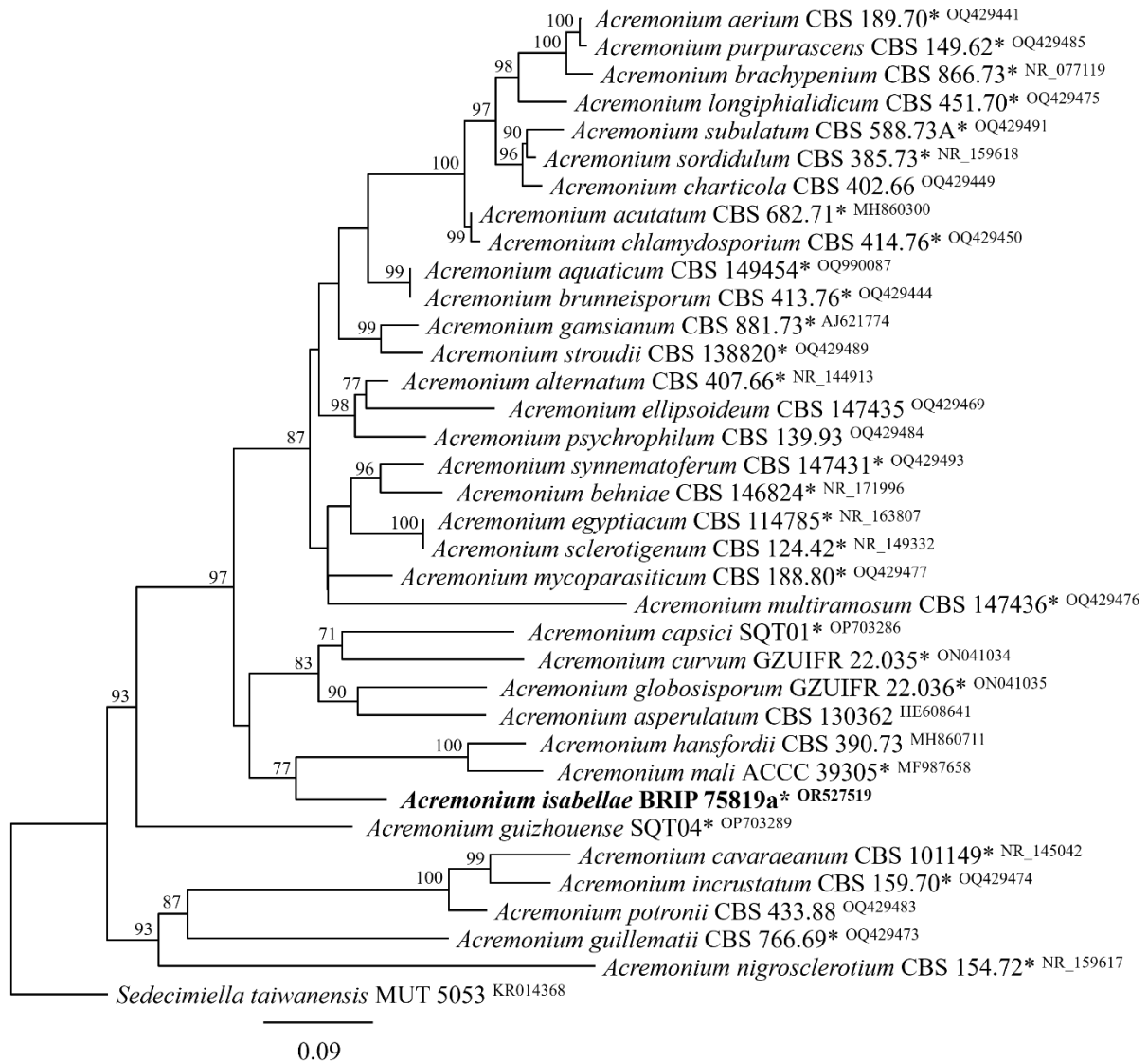
**Diagnosis:** Sequences from the rDNA describe *Acremonium isabellae* and are available in GenBank under the accessions OR527519 (ITS), and OR527527 (LSU). *Acremonium isabellae* differs from *Ac. handsfordii* (ex-type strain CBS 390.73) by sequence comparison of the ITS region (GenBank MH860711; Identities 387/434 (89%), 12 gaps; unique nucleotide at positions 268(C), 276(G), 279(T), 280(A), 282(C), 284(A), 286(C), 292(T), 293(T), 298(T), 303(G), 305(C), 318(T), 319(G), 321(G), 330(T), 451(G), 458(T), 464(C), 500(A), 501(A), 515(T), 539(C), 562(G), 573(T), 575(T), 576(A), 583(A), 592(T), 600(T), 601(G), 604(A), 627(T), 628(T), 648(A)), and LSU (GenBank MH872422; Identities 861/888 (97%), 10 gaps; unique nucleotide at positions 84(C), 91(T), 96(A), 159(A), 197(A), 242(T), 395(T), 433(T), 451(T), 453(T), 456(T), 483(G), 505(C), 512(T), 525(A), 530(A)). *Acremonium isabellae* differs from *Ac. mali* (ex-type strain ACCC 39305) by sequence comparison of the ITS region (GenBank MF987658; Identities 441/514 (86%), 20 gaps; unique nucleotide at positions 171(T), 176(T), 178(T), 181(A), 207(A), 208(T), 209(T), 229(C), 232(G), 235(C), 243(T), 244(A), 246(G), 254(T), 259(A), 281(T), 284(A), 286(C), 292(T), 293(T), 300(G), 301(T), 305(C), 315(T), 318(T), 319(G), 330(T), 451(G), 458(T), 464(C), 500(A), 501(A), 507(T), 515(T), 541(C), 562(G), 573(T), 575(T), 576(A), 583(A), 592(T), 600(T), 601(G), 604(A), 625(T), 627(T), 628(T), 648(A), 653(T), 654(T), 655(T), 656(C)), and LSU (GenBank NG\_088063; Identities 811/832 (97%), one gap; unique nucleotide at positions 84(C), 91(T), 96(A), 159(A), 197(A), 242(T), 395(T), 398(T), 430(G), 433(T), 451(T), 453(T), 456(T), 457(T), 483(G), 505(C), 512(T), 525(A), 527(C), 530(A)).

**Specimen examined:** Australia, New South Wales, Rowlands Creek, from an unidentified dead spider, 26 Feb. 2023, *I. Teal & D. Teal* (holotype BRIP 75819a permanently preserved in a metabolically inactive state).

**Etymology:** Named after Isabella Teal, who has collected many fungi on dead insects and spiders in northern New South Wales.



A. Dead adult lepidopteran insect on leaf surface from which *Akanthomyces australiensis* (ex-type strain BRIP 72630a) was isolated. B. Dead spider on leaf surface from which *Acremonium isabellae* (ex-type strain BRIP 75803a) was isolated. Scale bars = 1 mm.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the combined ITS and LSU sequences from species of *Acremonium*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Sedecimiella taiwanensis* (strain MUT 5053) 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 (\*).

*Aschersonia cheesemaniae* Y.P. Tan, Bishop-Hurley & Marney, *sp. nov.*

IF 901093

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

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Aschersonia cheesemaniae* and are available in GenBank under the accessions OR527520 (ITS), OR527528 (LSU), OR514851 (*rpb2*), and OR514843 (*tef1*). *Aschersonia cheesemaniae* differs from *As. confluens* (strain BCC 7961) by sequence comparison of the ITS region (GenBank JN049841; Identities 492/534 (92%), nine gaps; unique nucleotide at positions 142(T), 157(C), 171(C), 189(T), 199(A), 200(T), 203(T), 204(G), 209(C), 221(C), 231(C), 232(T), 245(G), 248(T), 252(T), 282(G), 284(A), 285(T), 286(C), 302(C), 314(G), 323(C), 329(G), 332(C), 403(G), 544(A), 558(C), 574(T), 575(A), 576(T), 590(T), 622(T), 633(G), 635(T), LSU (GenBank DQ384947; Identities 863/878 (98%), three gaps; unique nucleotide at positions 31(C), 128(G), 276(T), 277(T), 457(T), 514(T), 516(T), 540(T), 542(A), 549(T), 550(A), 576(T)), *rpb2* (GenBank DQ452465; Identities 780/843 (93%); unique nucleotide at positions 64(C), 71(C), 91(C), 97(C), 127(G), 133(T), 136(C), 149(C), 151(A), 154(C), 175(G), 184(T), 193(C), 205(A), 220(T), 232(C), 250(G), 268(C), 271(C), 325(G), 352(T), 355(A), 376(T), 389(G), 430(G), 439(G), 448(C), 460(C), 481(C), 520(C), 526(A), 529(C), 538(C), 556(G), 562(C), 583(A), 584(T), 614(G), 615(G), 619(C), 624(A), 626(T), 628(A), 637(A), 655(C), 658(A), 668(C), 670(G), 688(A), 694(G), 718(C), 719(C), 733(T), 745(T), 760(A), 763(A), 766(T), 769(A), 790(T), 805(T), 820(C), 829(A), 838(G)), and *tef1* (GenBank DQ384976; Identities 882/926 (95%); unique nucleotide at positions 20(T), 62(C), 93(C), 131(C), 152(C), 179(G), 191(G), 197(A), 218(T), 257(C), 263(C), 279(C), 284(T), 371(C), 377(C), 395(T), 419(T), 422(C), 434(G), 488(C), 512(T), 518(G), 521(T), 530(C), 533(T), 542(C), 548(G), 632(T), 635(C), 692(T), 698(C), 725(T), 743(T), 746(T), 755(C), 758(T), 800(C), 803(G), 845(T), 878(T), 881(C), 893(C), 902(C), 911(T)).

*Specimen examined*: Australia, Queensland, Paluma, from an unidentified dead insect, 26 Apr. 2021, *T.S. Marney* (holotype BRIP 72774a permanently preserved in a metabolically inactive state); *ibid.*, from an unidentified dead insect, 26. Apr. 2021, *T.S. Marney*, culture BRIP 73114a (LSU, SSU, *rpb2*, and *tef1* sequences GenBank OR527529, OR514852, OR512198, and OR514844).

*Etymology*: Named after Lucy Evelyn Cheeseman (1881–1969), an entomologist renowned for her biological specimens collected from expeditions in the South Pacific.

*Aschersonia tanyunxianiae* Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

IF 901094

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

*Diagnosis*: Sequences from the rDNA and nrDNA describe *Aschersonia tanyunxianiae* and are available in GenBank under the accessions OR527530 (LSU), OR512199 (SSU), OR514853 (*rpb2*), and OR514845 (*tef1*). *Aschersonia tanyunxianiae* differs from *As. cheesemaniae* (ex-type strain BRIP 72774a) by sequence comparison of LSU (GenBank OR527528; Identities 865/874 (99%), two gaps; unique nucleotide at positions 154(T), 272(C), 536(T), 537(C), 544(C), 545(T), 571(C)), *rpb2* (GenBank OR514851; Identities 911/946 (96%), three gaps, unique nucleotide at positions 136(T), 138(G), 159(G), 162(A), 171(C), 195(A), 207(C), 219(T), 258(T), 376(C), 384(C), 407(T), 417(A), 511(T), 513(C), 516(G), 519(G), 566(G), 605(T), 613(C), 633(T), 756(G), 777(C), 792(C), 825(A), 882(C),

903(C), 927(G)), and *tefl* (GenBank OR514843; Identities 921/942 (98%); unique nucleotide at positions 18(C), 132(C), 183(T), 255(T), 258(G), 300(T), 309(A), 510(C), 528(T), 531(C), 546(C), 549(T), 600(A), 696(T), 750(C), 792(T), 849(A), 876(C), 891(T), 909(C), 933(C)). *Aschersonia tanyunxianiae* differs from *As. confluens* (strain BCC 7961) by sequence comparison of the LSU region (GenBank DQ384947; Identities 866/878 (99%), three gaps; unique nucleotide at positions 26(C), 123(G), 154(T), 271(T), 452(T), 509(T), 511(T), 535(T), 536(T)), *rpb2* (GenBank DQ452465; Identities 787/843 (93%); unique nucleotide at positions 51(C), 58(C), 78(C), 84(C), 114(G), 120(T), 123(C), 141(C), 159(G), 180(C), 192(A), 195(A), 237(G), 255(C), 312(G), 339(T), 342(A), 363(T), 384(C), 407(T), 426(G), 462(T), 468(G), 507(C), 511(T), 519(G), 525(C), 543(G), 549(C), 567(G), 570(A), 571(T), 601(G), 602(G), 605(T), 606(C), 611(A), 613(C), 615(A), 624(A), 633(T), 642(C), 645(A), 655(C), 657(G), 675(A), 681(G), 705(C), 706(C), 720(T), 732(T), 747(A), 750(A), 753(T), 807(C), 816(A)), and *tefl* (GenBank DQ384976; Identities 879/823 (95%); unique nucleotide at positions 60(C), 91(C), 129(C), 132(C), 150(C), 177(G), 183(T), 189(G), 195(A), 216(T), 258(G), 261(C), 277(C), 282(T), 300(T), 309(A), 369(C), 375(C), 393(T), 417(T), 420(C), 432(G), 486(C), 516(G), 519(T), 540(C), 549(T), 600(A), 630(T), 633(C), 690(T), 723(T), 741(T), 744(T), 750(C), 753(C), 756(T), 792(T), 798(C), 801(G), 843(T), 849(A), 879(C), 900(C)).

*Specimen examined:* Australia, Queensland, Tully, from unidentified dead insect, 29 Apr. 2021, T.S. Marney, M.D.E. Shivas & R.G. Shivas (holotype BRIP 72625a permanently preserved in a metabolically inactive state); Wallaman, from unidentified dead insect, 28. Apr. 2021, T.S. Marney, M.D.E. Shivas & R.G. Shivas, culture BRIP 72627a (LSU, SSU, *rpb2*, and *tefl* sequences GenBank OR527531, OR512200, OR514854, and OR514846).

*Etymology:* Named after Tan Yunxian (1461–1554), a physician during the Ming dynasty in China, who documented the symptoms and treatment of medical conditions in ‘Miscellaneous Records of a Female Doctor.’

*Orbiocrella zlotorzycycae* Y.P. Tan, Bishop-Hurley & Marney, *sp. nov.*

IF 901095

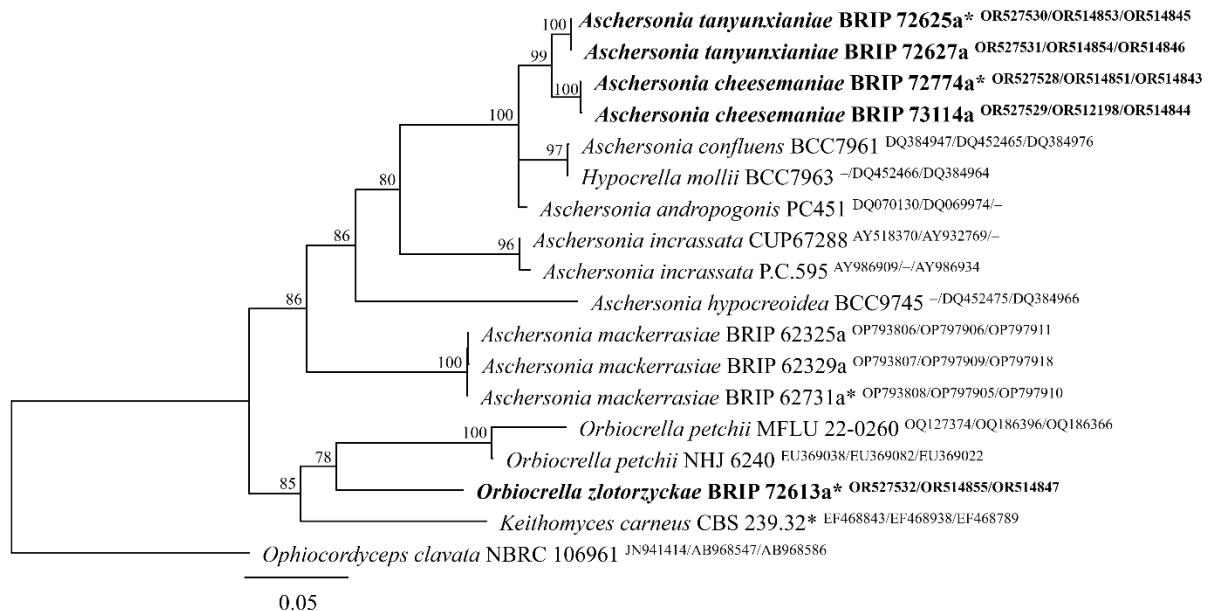
Classification — *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis:* Sequences from the rDNA and nrDNA describe *Orbiocrella zlotorzycycae* and are available in GenBank under the accessions OR527522 (ITS), OR527532 (LSU), OR514855 (*rpb2*), and OR514847 (*tefl*). *Orbiocrella zlotorzycycae* differs from *O. petchii* (strain NHJ 6209) by sequence comparison of the ITS region (GenBank JN049861; Identities 176/184 (96%); unique nucleotide at positions 343(A), 344(T), 376(T), 419(T), 475(T), 477(T), 511(A), 517(A)), LSU (GenBank EU369038; Identities 855/860 (99%); unique nucleotide at positions 83(C), 472(C), 487(C), 488(T), 506(G)), and *tefl* (GenBank EU369022; Identities 881/981 (90%), six gaps; unique nucleotide at positions 28(T), 34(T), 43(T), 49(C), 55(C), 58(G), 61(T), 64(C), 67(T), 127(C), 133(T), 145(G), 160(C), 163(T), 166(T), 187(T), 188(G), 197(G), 199(T), 220(T), 236(A), 237(A), 271(T), 274(T), 304(T), 317(G), 337(T), 349(T), 362(A), 363(C), 368(G), 377(T), 378(C), 382(T), 391(T), 397(T), 403(T), 412(T), 434(A), 435(C), 469(G), 481(T), 493(A), 499(T), 517(T), 521(G), 522(T), 544(T), 550(T), 553(T), 556(C), 568(T), 583(C), 586(T), 609(A), 611(T), 616(T), 618(A), 619(G), 637(A), 643(T), 655(T), 667(T), 679(T), 712(T), 713(C), 717(C), 719(T), 733(T), 748(T), 751(A), 760(T), 763(C), 787(C), 793(T), 805(C), 817(T), 827(T), 829(T), 859(T), 868(T), 890(A), 905(T), 907(T), 913(T), 928(T), 943(T), 946(T), 950(G), 952(T), 958(T), 973(G), 976(T), 982(C)).



*Specimen examined:* Australia, Queensland, Paluma, from an unidentified dead insect, 26 Apr. 2021, T.S. Marney (holotype BRIP 72613a permanently preserved in a metabolically inactive state).

*Etymology:* Named after Jadwiga Złotorzycka (1926–2002), an entomologist who specialised in the taxonomy of Mallophaga.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the combined LSU, *rpb2* and *tef1* sequences from selected species of *Clavicipitaceae*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Ophiocordyceps clavata* (strain NBRC 106961) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU/*rpb2*/*tef1*). Novel taxa are shown in bold. Ex-type strains are marked by an asterisk (\*).

*Pottera beatricis* Y.P. Tan & Bishop-Hurley, *gen. et sp. nov.*

*Pottera* Y.P. Tan & Bishop-Hurley IF 901096

*Pottera beatricis* Y.P. Tan & Bishop-Hurley IF 901097

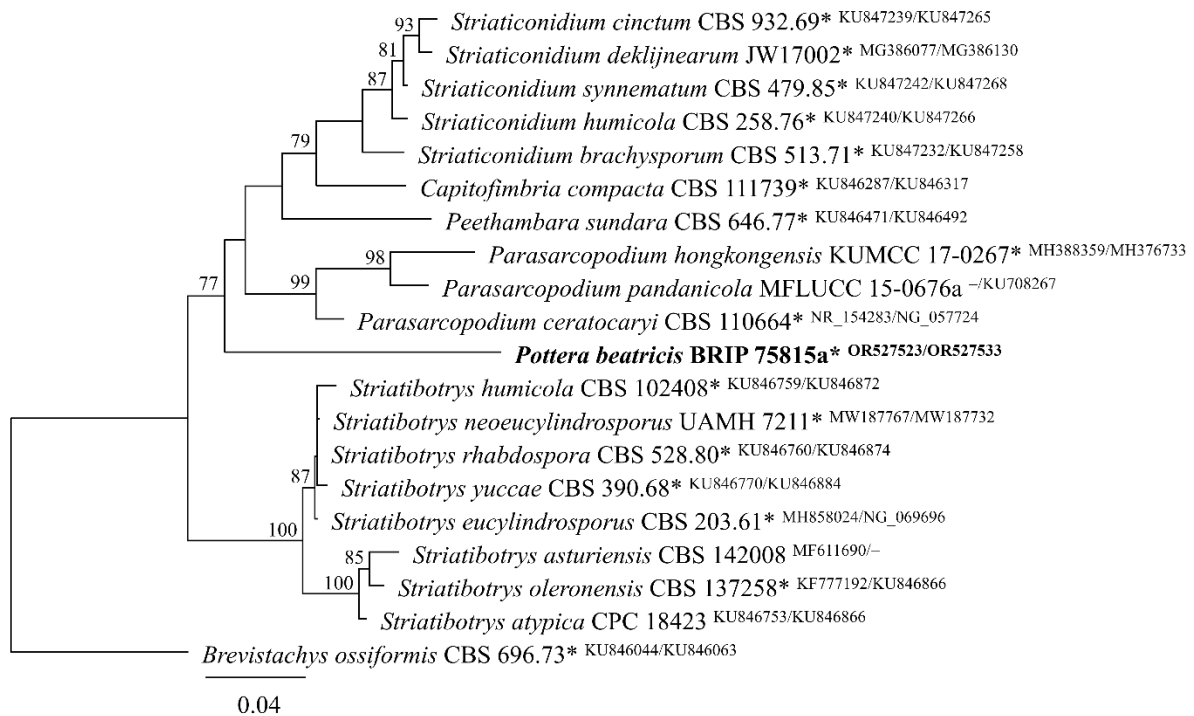
Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes*

*Diagnosis*: Sequences from the rDNA describe *Pottera beatricis* and are available in GenBank under the accessions OR527523 (ITS), and OR527533 (LSU). *Pottera beatricis* differs from *Parasarcopodium ceratocaryi* (ex-type strain CBS 110664) by sequence comparison of the ITS region (GenBank NR\_154283; Identities 471/579 (81%), 60 gaps; unique nucleotide at positions 161(A), 215(A), 219(C), 225(C), 234(A), 253(T), 257(C), 264(A), 271(C), 278(A), 284(C), 286(C), 301(A), 304(C), 306(G), 308(T), 309(C), 312(T), 321(T), 323(T), 386(C), 482(C), 506(C), 528(G), 535(C), 552(C), 567(A), 570(G), 571(G), 572(T), 573(A), 576(A), 577(A), 578(A), 587(T), 593(G), 603(T), 605(A), 609(T), 611(C), 620(A), 630(A), 649(G), 652(T), 654(T), 683(T), 688(T), 705(G)), and LSU (GenBank NG\_057724; Identities 818/870 (94%), six gaps; 40(C), 41(T), 91(G), 94(T), 125(A), 128(A), 182(C), 185(C), 194(G), 197(T), 245(T), 342(G), 352(T), 377(A), 378(C), 397(T), 402(C), 403(G), 408(C), 410(T), 411(G), 422(C), 423(A), 431(C), 432(G), 438(C), 458(A), 459(G), 468(C), 475(G), 476(G), 486(G), 491(C), 492(C), 512(C), 513(C), 515(T), 517(C), 521(G), 528(C), 529(C), 578(G), 579(T), 764(C), 841(G)).

*Specimen examined*: Australia, New South Wales, Rowlands Creek, from an unidentified dead spider, 26 Feb. 2023, *D. Teal* (holotype BRIP 75815a permanently preserved in a metabolically inactive state).

*Etymology*: Named after Helen Beatrix Potter (1866–1943), a writer, illustrator, naturalist, environmentalist, and amateur mycologist. Beatrix Potter was best known for her children's books, such as 'The Tale of Peter Rabbit', which featured animals.

Notes — *Pottera* is described as the smallest phylogenetic clade that contains the type species, *Pottera beatricis*, but excludes *Capitofimbria compacta*, *Parasarcopodium ceratocaryi*, *Peethambara sundara*, *Striatibotrys eucylindrosporus*, and *Striaticonidium cinctum*.



Phylogenetic tree based on the maximum likelihood analysis of the alignment of the combined ITS and LSU sequences from selected species of *Stachybotryaceae*. The phylogenetic analysis was performed with the IQ-TREE web server (<http://iqtree.cibiv.univie.ac.at/>) based on the substitution model with gamma-distribution rate variation. *Brevistachys ossiformis* (ex-type strain CBS 696.73) 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 (\*).