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Diversity and phylogeny of basidiomycetous yeasts from plant leaves and soil: Proposal of two new orders, three new families, eight new genera and one hundred and seven new species

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Abstract: Nearly 500 basidiomycetous yeast species were accepted in the latest edition of *The Yeasts: A Taxonomic Study* published in 2011. However, this number presents only the tip of the iceberg of yeast species diversity in nature. Possibly more than 99 % of yeast species, as is true for many groups of fungi, are yet unknown and await discovery. Over the past two decades nearly 200 unidentified isolates were obtained during a series of environmental surveys of yeasts in phyllosphere and soils, mainly from China. Among these isolates, 107 new species were identified based on the phylogenetic analyses of nuclear ribosomal DNA (rDNA) [D1/D2 domains of the large subunit (LSU), the small subunit (SSU), and the internal transcribed spacer region including the 5.8S rDNA (ITS)] and protein-coding genes [both subunits of DNA polymerase II (RPB1 and RPB2), the translation elongation factor 1-α (TEF1) and the mitochondrial gene cytochrome b (CYTB)], and physiological comparisons. Forty-six of these belong to 16 genera in the *Tremellomycetes* (*Agaricomycotina*). The other 61 are distributed in 26 genera in the *Pucciniomycotina*. Here we circumscribe eight new genera, three new families and two new orders based on the multi-locus phylogenetic analyses combined with the clustering optimisation analysis and the predicted similarity thresholds for yeasts and filamentous fungal delimitation at genus and higher ranks. Additionally, as a result of these analyses, three new combinations are proposed and 66 taxa are validated.

Key words: Basidiomycetous yeasts, Molecular phylogeny, Species diversity, Taxonomy.

Taxonomic novelties: New orders: *Heitmaniales* Q.M. Wang & F.Y. Bai, *Rosettozymales* Q.M. Wang & F.Y. Bai; **New families:** *Heitmaniaceae* Q.M. Wang & F.Y. Bai, *Jianyuniaceae* Q.M. Wang & F.Y. Bai, *Rosettozymaceae* Q.M. Wang & F.Y. Bai; **New genera:** *Begerowomyces* Q.M. Wang & F.Y. Bai, *Boekhoutia* Q.M. Wang & F.Y. Bai, *Meniscomyces* Q.M. Wang & F.Y. Bai, *Pseudosterigmatospora* Q.M. Wang & F.Y. Bai, *Robertozyma* Q.M. Wang & F.Y. Bai, *Rosettozyma* Q.M. Wang & F.Y. Bai, *Sterigmatospora* Q.M. Wang & F.Y. Bai, *Teunia* Q.M. Wang & F.Y. Bai; **New species:** *Begerowomyces foliicola* Q.M. Wang, F.Y. Bai & A.H. Li, *Bensingtonia pseudorectispora* Q.M. Wang, F.Y. Bai & A.H. Li, *Bensingtonia wuzhishanensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Boekhoutia sterigmata* Q.M. Wang, F.Y. Bai & A.H. Li, *Bulleribasidium cremeum* Q.M. Wang, F.Y. Bai & A.H. Li, *Bulleribasidium elongatum* Q.M. Wang, F.Y. Bai & A.H. Li, *Bulleribasidium phyllophilum* Q.M. Wang, F.Y. Bai & A.H. Li, *Bulleribasidium phyllostachydis* Q.M. Wang, F.Y. Bai & A.H. Li, *Bulleribasidium pseudopanici* Q.M. Wang, F.Y. Bai & A.H. Li, *Carlosrosaea foliicola* Q.M. Wang, F.Y. Bai & A.H. Li, *Carlosrosaea simaoensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma cylindrica* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma flava* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma fusiformis* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma iridis* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma pseudogriseoflava* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma rhododendri* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma sambuci* Q.M. Wang, F.Y. Bai & A.H. Li, *Chrysozyma sorbariae* Q.M. Wang, F.Y. Bai & A.H. Li, *Colacogloea aletridis* Q.M. Wang, F.Y. Bai & A.H. Li, *Colacogloea hydrangeae* Q.M. Wang, F.Y. Bai & A.H. Li, *Colacogloea rhododendri* Q.M. Wang, F.Y. Bai & A.H. Li, *Cystobasidium raffinophilum* Q.M. Wang, F.Y. Bai & A.H. Li, *Cystobasidium terricola* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces bifurcus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces elongatus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces longicylindricus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces longiovatus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces melastomatis* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces napiformis* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces ovatus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces polymorphus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces pseudoboekhoutii* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces pseudoyunnanensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces taiwanicus* Q.M. Wang, F.Y. Bai & A.H. Li, *Derxomyces xingshanicus* Q.M. Wang, F.Y. Bai & A.H. Li, *Dioszegia heilongjiangensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Dioszegia kandeliae* Q.M. Wang, F.Y. Bai, L.D. Guo & A.H. Li, *Dioszegia maotaiensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Dioszegia milinica* Q.M. Wang, F.Y. Bai & A.H. Li, *Dioszegia ovata* Q.M. Wang, F.Y. Bai & A.H. Li, *Filobasidium dingjieense* Q.M. Wang, F.Y. Bai & A.H. Li, *Filobasidium globosum* Q.M. Wang, F.Y. Bai & A.H. Li, *Filobasidium mali* Q.M. Wang, F.Y. Bai & A.H. Li, *Filobasidium mucilaginum* Q.M. Wang, F.Y. Bai & A.H. Li, *Genolevuria pseudoamylolytica* Q.M. Wang, F.Y. Bai & A.H. Li, *Heitmania cylindrica* Q.M. Wang, F.Y. Bai & A.H. Li, *Heitmania tridentata* Q.M. Wang, F.Y. Bai & A.H. Li, *Holtermannia saccardoi* Q.M. Wang, F.Y. Bai & A.H. Li, *Kockovaella haikouensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Kockovaella ischaemi* Q.M. Wang, F.Y. Bai & A.H. Li, *Kockovaella nitrophila* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa arboricola* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa chamaenerii* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa cylindrica* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa daliangziensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa foliicola* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa lulangica* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa myxariophila* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa rhododendri* Q.M. Wang, F.Y. Bai & A.H. Li, *Kondoa ribitophobia* Q.M. Wang, F.Y. Bai & A.H. Li, *Kwoniella ovata* Q.M. Wang, F.Y. Bai & A.H. Li, *Meniscomyces layueensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Microbotryozyma swertiae* Q.M. Wang, F.Y. Bai & A.H. Li, *Microsporomyces ellipsoideus* Q.M. Wang, F.Y. Bai & A.H. Li, *Microsporomyces pseudomagnisporus* Q.M. Wang, F.Y. Bai & A.H. Li, *Microsporomyces rubellus* Q.M. Wang, F.Y. Bai & A.H. Li, *Oberwinklerozyma dicranopteridis* Q.M. Wang, F.Y. Bai & A.H. Li, *Oberwinklerozyma nepetae* Q.M. Wang, F.Y. Bai & A.H. Li, *Phaeotremella lactea* Q.M. Wang, F.Y. Bai & A.H. Li, *Phaeotremella ovata* Q.M. Wang, F.Y. Bai & A.H. Li, *Phaffia aurantiaca* Q.M. Wang, F.Y. Bai & A.H. Li,

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Studies in Mycology

Phyllozyma aceris Q.M. Wang, F.Y. Bai & A.H. Li, *Phyllozyma jiayinensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Pseudobensingtonia fusiformis* Q.M. Wang, F.Y. Bai & A.H. Li, *Pseudohyphozyma hydrangeae* Q.M. Wang, F.Y. Bai & A.H. Li, *Pseudohyphozyma lulangensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Pseudosterigmatospora motuoensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Rhodosporidiobolus fuzhouensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Rhodosporidiobolus jianfalingensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Rhodosporidiobolus platycladi* Q.M. Wang, F.Y. Bai & A.H. Li, *Robertozyma ningxiaensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Rosettozyma cystopteridis* Q.M. Wang, F.Y. Bai & A.H. Li, *Rosettozyma motuoensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Rosettozyma petaloides* Q.M. Wang, F.Y. Bai & A.H. Li, *Ruinenia bangxiensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Ruinenia fanjingshanensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Ruinenia lunata* Q.M. Wang, F.Y. Bai & A.H. Li, *Saitozyma pseudoflava* Q.M. Wang, F.Y. Bai & A.H. Li, *Sakaguchia melibiophila* M. Groenew., Q.M. Wang & F.Y. Bai, *Slooffia globosa* Q.M. Wang, F.Y. Bai & A.H. Li, *Solicoccozyma gelidoterrea* Q.M. Wang, F.Y. Bai & A.H. Li, *Sporobolomyces cellobiolyticus* Q.M. Wang, F.Y. Bai & A.H. Li, *Sporobolomyces ellipsoideus* Q.M. Wang, F.Y. Bai & A.H. Li, *Sporobolomyces primogenomicus* Q.M. Wang & F.Y. Bai, *Sporobolomyces reniformis* Q.M. Wang, F.Y. Bai & A.H. Li, *Sterigmatospora layueensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Symmetrospora rhododendri* Q.M. Wang, F.Y. Bai & A.H. Li, *Teunia betulae* K. Sylvester, Q.M. Wang & Hittinger ex Q.M. Wang, F.Y. Bai & A.H. Li, *Teunia globosa* Q.M. Wang, F.Y. Bai & A.H. Li, *Teunia helanensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Teunia korlaensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Teunia tronadorensis* V. de Garcia, Zalar, Brizzio, Gunde-Cim. & van Brook ex Q.M. Wang, F.Y. Bai & A.H. Li, *Tremella shuangheensis* Q.M. Wang, F.Y. Bai & A.H. Li, *Vishniacozyma europaea* Q.M. Wang, F.Y. Bai & A.H. Li, *Vishniacozyma melezitolytica* Q.M. Wang, F.Y. Bai & A.H. Li, *Vishniacozyma pseudopenaeus* Q.M. Wang, F.Y. Bai & A.H. Li, *Yamadamyces terricola* Q.M. Wang, F.Y. Bai & A.H. Li, *Yurkovia longicylindrica* Q.M. Wang, F.Y. Bai & A.H. Li; **New combinations:** *Colacogloea subericola* (Belloch, Villa-Carv., Á;lv.-Rodríg. & Coque) Q.M. Wang, & F.Y. Bai, *Symmetrospora oryzicola* (Nakase & M. Suzuki) Q.M. Wang & F.Y. Bai, *Teunia cuniculi* (K.S. Shin & Y.H. Park) Q.M. Wang, F.Y. Bai & A.H. Li; **New validations:** *Apiotrichum xylopini* S.O. Suh, C.F. Lee, Gujjari & J.J. Zhou ex Kachalkin, Yurkov & Boekhout, *Bannozyma arctica* Vishniac & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Bulleribasidium panici* Fungsin, M. Takash. & Nakase ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Bulleribasidium siamense* Fungsin, M. Takash. & Nakase ex Q.M. Wang, F.Y. Bai, Boekhout & Nakase, *Carcinomyces arundinariae* Fungsin, M. Takash. & Nakase ex Yurkov, *Cystobasidium alpinum* Turchetti, Selbmann, Onofri & Buzzini, *Cystobasidium portillonense* Laich, Vaca & R. Chávez ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Derxomyces cylindricus* F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, *Derxomyces hubeiensis* F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, *Derxomyces nakasei* F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, *Dioszegia zsoltii* F.Y. Bai, M. Takash. & Nakase, *Genolevuria bromeliarum* Landell & P. Valente ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Glaciozyma* Turchetti, Connell, Thomas-Hall & Boekhout ex M. Groenew. & Q.M. Wang, *Glaciozyma antarctica* (Fell, Statzell, I.L. Hunter & Phaff) M. Groenew. & Q.M. Wang, *Glaciozyma martinii* Turchetti, Connell, Thomas-Hall & Boekhout, *Glaciozyma watsonii* Turchetti, Connell, Thomas-Hall & Boekhout, *Kockovaella mexicana* Lopandić, O. Molnár & Prillinger ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Kondoa thailandica* Fungsin, Hamam. & Nakase ex Q.M. Wang, M. Groenew., F.Y. Bai & Boekhout, *Kwoniella newhampshirensis* K. Sylvester, Q.M. Wang & C.T. Hittinger, *Kwoniella shandongensis* R. Chen, Y.M. Jiang & S.C. Wei ex M. Groenew. & Q.M. Wang, *Leucosporidium creatinivorum* (Golubev) M. Groenew. & Q.M. Wang, *Leucosporidium fragarium* (J.A. Barnett & Buhagiar) M. Groenew. & Q.M. Wang, *Leucosporidium intermedium* (Nakase & M. Suzuki) M. Groenew. & Q.M. Wang, *Leucosporidium muscorum* (Di Menna) M. Groenew. & Q.M. Wang, *Leucosporidium yakuticum* (Golubev) M. Groenew. & Q.M. Wang, *Naganishia onofrii* Turchetti, Selbmann & Zucconi ex Yurkov, *Naganishia vaughanmartiniae* Turchetti, Blanchette & Arenz ex Yurkov, *Nielozyma* Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Nielozyma formosana* Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Nielozyma melastomatis* Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Oberwinklerozyma silvestris* Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Oberwinklerozyma straminea* Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Papiliotrema aspenensis* (Ferreira-Paim, *et al.*) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Papiliotrema baii* Yurkov, M.A. Guerreiro & Á;. Fonseca ex Yurkov, *Papiliotrema frias* V. de García, Zalar, Brizzio, Gunde-Cim. & Van Broock ex Yurkov, *Papiliotrema hoabinhensis* D.T. Luong, M. Takash., Ty, Dung & Nakase ex Yurkov, *Papiliotrema japonica* J.P. Samp., Fonseca & Fell ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Papiliotrema terrestris* Crestani, Landell, Faganello, Vainstein, Vishniac & P. Valente ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Papiliotrema wisconsinensis* K. Sylvester, Q.M. Wang & Hittinger ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Piskurozyma fildesensis* T.T. Zhang & Li Y. Yu ex Yurkov, *Piskurozyma taiwanensis* Nakase, Tsuzuki & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Pseudoleucosporidium* V. de García, *et al.* ex M. Groenew. & Q.M. Wang, *Pseudoleucosporidium fasciculatum* (Babeva & Lisichk.) M. Groenew. & Q.M. Wang, *Pseudotremella lacticolour* Satoh & Makimura ex Yurkov, *Rhynchogastrema complexa* (Landell, *et al.*) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, *Rhynchogastrema fermentans* (C.F. Lee) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, *Rhynchogastrema glucofermentans* (S.O. Suh & M. Blackw.) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, *Rhynchogastrema nanyangensis* F.L. Hui & Q.H. Niu ex Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, *Rhynchogastrema tunnelae* (Boekhout, Fell, Scorzetti & Theelen) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, *Rhynchogastrema visegradensis* (G. Péter & Dlauchy) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout &Yurkov, *Ruinenia diospyri* Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Ruinenia pyrrosiae* Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Saitozyma ninhbinhensis* (D.T. Luong, M. Takash., Dung & Nakase)Yurkov, *Saitozyma paraflava* Golubev & J.P. Samp. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Tremella basidiomaticola* Xin Zhan Liu & F.Y. Bai, *Trimorphomyces sakaeraticus* Fungsin, M. Takash. & Nakase ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Vanrija meifongana* C.F. Lee ex Kachalkin Yurkov & Boekhout, *Vanrija nantouana* C.F. Lee ex Kachalkin Yurkov & Boekhout, *Vanrija thermophila* Vogelmann, S. Chaves & C. Hertel ex Kachalkin Yurkov & Boekhout, *Vishniacozyma foliicola* Q.M. Wang & F.Y. Bai ex Yurkov, *Vishniacozyma heimaeyensis* Vishniac ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Vishniacozyma psychrotolerans* V. de García, Zalar, Brizzio, Gunde-Cim. & Van Broock ex Yurkov, *Vishniacozyma taibaiensis* Q.M. Wang & F.Y. Bai ex Yurkov, *Vishniacozyma tephrensis* Vishniac ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Yamadamyces* Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Yamadamyces rosulatus* Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout.

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INTRODUCTION

Basidiomycetous yeasts are fungi that can be characterisedcharacterised by unicellular growth for all or the majority of their life cycles (Boekhout *et al.* 2011). These occur in all three subphyla of *Basidiomycota*, namely *Agaricomycotina*, *Pucciniomycotina* and *Ustilaginomycotina* (Bauer *et al.* 2006, Hibbett *et al.* 2007, Boekhout *et al.* 2011). Two hundred and twenty-four basidiomycetous yeast species belonging to 39 genera were included in the fourth edition of *The Yeasts*, *a Taxonomic Study* (Kurtzman & Fell 1998). That number more than doubled in the next twelve years to 463 species distributed in 62 genera in the fifth edition (Kurtzman *et al.* 2011). This increase in new species and genera has largely been driven by the adoption of ribosomal DNA (rDNA) gene sequence analyses to yeast identification (Nakase 2000, Fell *et al.* 2000, Scorzetti *et al.* 2002) and the availability of databases containing sequence data of the D1/D2 domains of the large subunit of rDNA (LSU rDNA) and the ITS (including 5.8S) region of rDNA of most of the known basidiomycetous yeast species (Fell *et al.* 2000, Scorzetti *et al.* 2002). These molecular taxonomic studies deeply improved our understanding of the phylogenetic relationships, systematics and ecology of basidiomycetous yeasts (Kurtzman & Fell 2006). However, these studies also demonstrated that many genera of basidiomycetous yeasts are polyphyletic (Aime *et al.* 2006, Boekhout *et al.* 2011). Recently, an updated taxonomic system of basidiomycetous yeasts was proposed and all polyphyletic genera were revised (Wang *et al.* 2014, 2015a,b,c, Liu *et al.*

2015a,b, Wang & Wang 2015). Vu *et al.* (2016) indicated that the above revision of basidiomycetous yeasts was a significant improvement in the generic taxonomy, although in a few cases the generic boundaries may still be too broadly defined.

It seems clear that there are still many gaps in our understanding of the yeast phylogeny and diversity. Mycologists have estimated that *ca.* 1 % fungal species have been described (Hawksworth 1991, 2001, Blackwell 2011, Hawksworth & Lücking 2017). Similar estimates exist for yeasts, indicating that *ca.* 12 000 undescribed yeast species await discovery (Lachance 2006), and there is ample evidence that many of these may reside in forests (Fonseca & Inácio 2006, Morais *et al.* 2006, Nakase *et al.* 2006). For example, more than 100 unknown yeast species in forests of Thailand have not yet been described (Nakase *et al.* 2006).

During a survey of the basidiomycetous yeast diversity in forests, mostly in China, more than 1 000 isolates including 180 strains representing potential novel species were isolated and examined over the past 20 years. In this study, 107 new basidiomycetous yeasts species in *Agaricomycotina* and *Pucciniomycotina* are described based on phylogenetic analyses of multiple loci: three nuclear rDNA genes–the small subunit rDNA (SSU), the D1/D2 domains of the large subunit rDNA (LSU), and the internal transcribed spacer including the 5.8S rDNA (ITS)–and four protein coding genes–the largest subunit of RNA polymerase II (RPB1), the second largest subunit of RNA polymerase II (RPB2), translation elongation factor 1-α (TEF1) and the mitochondrial gene cytochrome b (CYTB), and on phenotypic properties. Based on these results, eight new genera, three new families and two new orders are proposed.

MATERIALS AND METHODS

Strains and phenotypic characterisation

The strains studied are listed in Table 1. Strains were isolated from plant leaves by using the ballistoconidia-fall method as described by Nakase & Takashima (1993). Strains were isolated from soil by an enrichment method: one gram of each sample was placed into 10 ml Yeast Malt (YM, 0.3 % yeast extract, 0.3 % malt extract, 0.5 % peptone, 1 % glucose, Difco) broth containing 200ug/ml chloramphenicol in 15-ml conical tubes and cultured 3–7 d at 17 °C. Then enrichment samples were diluted to $1*10^{-3}$ or $1*10^{-4}$ and 200 µL of each dilution was plated on potato dextrose agar (PDA, 20 % potato infusion, 2 % glucose, 2 % agar, Difco) plates at 17 °C for 3–5 d to culture and isolate yeast strains. Morphological, physiological and biochemical characteristics were examined according to standard methods (Kurtzman *et al.* 2011). The potential sexual cycles of all new species were investigated using YM, PDA, V8 (10 % V8 juice, 2 % agar) and corn meal agar (CM, 5 % infusion corn meal, 1.5 % agar, Difco). A loopful of cells of each test strain is mixed on an agar plate incubated at 17 °C for one or two months. The cultures were examined with a microscope for the presence of filaments and sexual structures every two weeks. The ballistoconidium-forming activity of all new species was observed by the inverted-plate method (do Carmo-Sousa & Phaff 1962) using CM agar at 17 °C. After 3 to 14 d, the glass slide containing the discharged spores was removed for examination under the microscope.

DNA extraction and ribosomal DNA sequencing

Nuclear DNA was extracted using the method described previously by Wang & Bai (2008). The ITS (including 5.8S rDNA) region and LSU rDNA D1/D2 domains were sequenced using the methods described previously (Wang & Bai 2004). The small subunit (SSU) rDNA sequences were determined according to Wang *et al.* (2003). The CYTB sequences were performed as described by Wang & Bai (2008). The three nuclear protein-coding genes, RPB1, RPB2 and TEF1, were obtained using methods described previously (Wang *et al.* 2014). GenBank accession numbers for all sequences determined in this study are listed in Table 1.

Sequences were aligned with the MAFFT program (Standley 2013) using the G-INS-i algorithm and minor gaps in all alignments were manually deleted. The most appropriate model of DNA substitution was searched with Modeltest version 3.04 (Posada & Crandall 1998) using the Akaike information criterion (AIC). The model GTR + I + G was selected for Maximum likelihood (ML) and Bayesian inference (BI) analyses. ML analysis was conducted using RAxML-HPC 7.2.8 (Stamatakis 2006) with 1 000 bootstrap replicates. BI analysis was conducted using MrBayes 3.1.2 (Ronquist *et al.* 2012) with 10 000 000 generations using the parameter settings described previously (Wang *et al.* 2015a). A bootstrap percentage (BP) of $\geq$70 % or a Bayesian posterior probability (PP) of $\geq$0.9 was considered as significantly supported in all constructed trees in this study. The alignments and trees were deposited in TreeBASE (www.treebase.org, Nos. 24640–24646).

New species catalogised

Accurate identification of known yeast species and rapid detection of new species are currently possible because of the availability of ITS and D1/D2 sequence databases for most of the known yeasts (Kurtzman & Robnett 1998, Fell *et al.* 2000, Scorzetti *et al.* 2002, Boekhout *et al.* 2011, Kurtzman 2011, Liu *et al.* 2015a, Wang *et al.* 2015a, Vu *et al.* 2016). Recently *The Yeasts Trust* announced, a new yeasts database (Boekhout *et al.* 2016, http://theyeasts.org/) which provides the most up-to-date and accurate taxonomic information including DNA sequences and phenotypic characteristics on all published yeasts. Vu *et al.* (2016) recommended that the similarity thresholds to discriminate a yeast species were 1.59 % (or 0.79 % using ex-type strains only) and 0.49 % for ITS and D1/D2, respectively, based on the barcode data of *ca.* 9 000 yeast strains, which are in agreement with previous studies (Kurtzman & Robnett 1998, Fell *et al.* 2000, Scorzetti *et al.* 2002) that indicated sequence diversity among conspecific strains is less than 1 % in either the ITS or D1/D2 regions (Kurtzman & Fell 2006, Kurtzman 2014, 2015, Kurtzman *et al.* 2015). However, delineation of species using single region sequence is not always reliable for yeasts, especially for basidiomycetous yeasts, because different lineages may vary in their rates of nucleotide substitution for the diagnostic gene being used (Fell *et al.* 2000, Scorzetti *et al.* 2002). Thus, a combined sequence analysis of the D1/D2 domains and ITS region is recommended for species identification by Scorzetti *et al.* (2002) and Kurtzman & Fell (2006). Consequently, sequence analyses of both D1/D2 and ITS were used to differentiate the potentially new species and their closely related species in this study. In order to improve the species delimitation,

Table 1. List of yeasts employed and GenBank numbers determined in this study.

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
Kockovaella haikouensis sp. nov.	CGMCC 2.3443^T = HKX2 = CBS 15478	November 14, 2006	Haikou county, Hainan province, China	phylloplane	MK050274	MK849163	MK849301	MK849032	MK848902
	CGMCC 2.3444 = KX4	November 14, 2006	Haikou county, Hainan province, China	phylloplane	MK050275	–	–	–	–
K. ischaemi sp. nov.	CGMCC 2.3565^T = JH5.17 = CBS 15500	November 15, 2006	Jinghong, Yunnan province, China	leaf of *Ischaemum* sp.	MK050276	MK849185	MK849323	–	–
	CGMCC 2.3536 = JF5.5-2 = CBS 15496	November 15, 2006	Jianfaling, Hainan province, China	phylloplane	MK050277	MK849182	MK849320	–	–
K. nitrophila sp. nov.	CGMCC 2.3465^T = WZS12.1 = CBS 15487	November 16, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050278	MK849173	–	MK849043	MK848913
Genolevuria pseudoamylolytica sp. nov.	CGMCC 2.5809^T = HLJ1B6 = CBS 13955	August 23, 2014	Daliangzi river national forest park, Heilongjiang province, China	phylloplane	MK050279	MK849257	MK849394	MK849118	–
Vishniacozyma europaea sp. nov.	CGMCC 2.3099^T = G7.1-2 = CBS 15464	September 20, 2005	Germany	phylloplane	MK050335	MK849148	–	MK849018	MK848890
V. pseudopenaeus sp. nov.	CGMCC 2.3165^T = G7.20 = CBS 15472	September 20, 2005	Germany	phylloplane	MK050333	MK849155	–	MK849025	MK848897
	CGMCC 2.3182 = G7.14	September 20, 2005	Germany	phylloplane	MK050334	MK849158	–	MK849028	MK848898
	CBS 8412	1996	Netherlands	brine bath in cheese factory	AY250757/CBS Database	–	–	–	–
	CBS 9328	April 15, 1995	Carara, Costa Rica	soil	CBS Database	–	–	–	–
V. melezitolytica sp. nov.	CGMCC 2.3472^T = H5A3 = CBS 15490	April 16, 2007	Hebei province, China	phylloplane	MK050330	MK849177	MK849315	MK849046	–
	CGMCC 2.3105 = G18.1 = CBS 15467	September 20, 2005	Germany	phylloplane	MK050331	–	–	–	–
	CGMCC 2.3166 = G18.11	September 20, 2005	Germany	phylloplane	MK050332	MK849156	MK849295	MK849026	–
Saitozyma pseudoflava sp. nov.	CGMCC 2.5811^T = XZ200A1 = CBS 15576	September 22, 2014	Tibet, China	phylloplane	MK050284	MK849251	MK849387	MK849114	MK848987
Carlosrosaea foliicola sp. nov.	CGMCC 2.3447^T = WZS29.4 = CBS 15481	November 6, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050282	MK849166	MK849304	–	MK848905
C. simaoensis sp. nov.	CGMCC 2.3580^T = SM8.1 = CBS 15503	November 14, 2006	Simao county, Yunnan province, China	phylloplane	MK050283	MK849188	MK849326	MK849056	MK848924
Tremella shuangheensis sp. nov.	CGMCC 2.5615^T = SH58A1 = CBS 15561	August 20, 2015	Shuanghe county, Heilongjiang province, China	phylloplane	MK050285	MK849223	MK849362	MK849087	MK848956

Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
Kwoniella ovata sp. nov.	CGMCC 2.3439^T = H1C1 = CBS 15475	November 6, 2006	Hebei province, China	phylloplane	MK050289	MK849160	MK849298	MK849030	MK848899
Teunia korlaensis sp. nov.	CGMCC 2.3835^T = 141.19 = CBS 15653	February 21, 2008	Kuerlei county, Xinjiang province, China	soil	MK050286	MK849194	MK849332	–	MK848929
T. helanensis sp. nov.	CGMCC 2.4450^T = HLS02-1-5 = CBS 12498	August 21, 2009	Helanshan mountain, Ningxia province, China	soil	MK050287	MK849208	MK849347	MK849074	MK848942
T. globosa sp. nov.	CGMCC 2.5648^T = GPS23.2A6 = CBS 15566	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050288	MK849235	MK849374	MK849100	–
Dioszegia milinica sp. nov.	CGMCC 2.5628^T = GPS21.3B8 = CBS 15563	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050290	MK849231	MK849371	MK849097	MK848966
D. heilongjiangensis sp. nov.	CGMCC 2.5674^T = HLJ13.24 = CBS 13957	August 28, 2014	Chelu county, Heilongjiang province, China	phylloplane	MK050291	MK849245	MK849382	MK849109	MK848981
	CGMCC 2.5662 = HLJ41A9 = CBS 13966	August 26, 2014	Wuyiling natural reserve, Heilongjiang province, China	phylloplane	MK050292	MK849243	MK849380	MK849106	MK848978
	CGMCC 2.5672 = HLJ41A9B	August 26, 2014	Wuyiling natural reserve, Heilongjiang province, China	phylloplane	MK050293	–	–	–	–
D. ovata sp. nov.	CGMCC 2.3625^T = HBX1.27 = CBS 15657	November 24, 2006	Bangxi county, Hainan province, China	phylloplane	MK050294	MK849190	MK849328	–	MK848926
	TY-217	2003	Thailand	phylloplane	AY313036/AY313018	–	–	–	–
D. maotaiensis sp. nov.	CGMCC 2.4537^T = GZMT3A9 = CBS 15516	March 8, 2012	Maotai county, Guizhou province, China	phylloplane	MK050295	MK849210	MK849350	MK849076	MK848945
D. kandeliae sp. nov.	CGMCC 2.5658^T = 224191 = CBS 13951	April 15, 2014	Beilunhekou natural reserve, Guangxi province, China	leaf of *Kandelia candel*	MK050296	MK849241	MK849378	MK849104	MK848976
Bulleribasidium pseudopanici sp. nov.	CGMCC 2.4024^T = WZS17.20 = CBS 15510	November 22, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050323	MK849197	MK849336	MK849062	MK848932
	CGMCC 2.4022 = WZS29.3	November 16, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050324	MK849196	MK849335	MK849061	–
B. cremeum sp. nov.	CGMCC 2.4427^T = TW1.1F-025 = CBS 12487	August 18, 2009	Taiwan, China	phylloplane	MK050325	MK849198	MK849337	MK849064	MK848933

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Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
B. phyllostachydis sp. nov.	CGMCC 2.5812^T = XZ139E1 = CBS 15575	September 20, 2014	Motuo, Tibet, China	leaf of *Phyllostachys* sp.	MK050327	MK849261	MK849398	–	MK848993
B. elongatum sp. nov.	CGMCC 2.4428^T = TW1.1F-019 = CBS 12489	August 18, 2009	Taiwan, China	phylloplane	MK050326	MK849199	MK849338	MK849065	MK848934
B. phyllophilum sp. nov.	CGMCC 2.3320^T = HBX2.8 = CBS 15474	November 24, 2006	Bangxi county, Hainan province, China	phylloplane	MK050328	MK849159	MK849297	MK849029	–
	CGMCC 2.4018 = HBX1.23	November 24, 2006	Bangxi county, Hainan province, China	phylloplane	MK050329	MK849195	MK849334	MK849060	MK848931
	TY-199	2003	Thailand	phylloplane	AY313030	–	–	–	–
Derxomyces pseudoboekhoutii sp. nov.	CGMCC 2.4436^T = FJYZ12-8 = CBS 12493	August 18, 2011	Fuzhou county, Fujian province, China	phylloplane	MK050310	MK849202	MK849341	MK849068	MK848937
D. polymorphus sp. nov.	CGMCC 2.4437^T = FJYZ12-13 = CBS 15512	August 18, 2011	Fuzhou county, Fujian province, China	phylloplane	MK050309	MK849203	MK849342	MK849069	MK848938
D. xingshanicus sp. nov.	CGMCC 2.2459^T = HX16.1 = CBS 15445	July 7, 2003	Xingshan county, Hubei province, China	phylloplane	MK050308	MK849128	MK849269	MK849000	MK848873
D. pseudoyunnanensis sp. nov.	CGMCC 2.3563^T = SM37E2 = CBS 15499	November 10, 2006	Simao county, Yunnan province, China	phylloplane	MK050313	MK849184	MK849322	MK849052	MK848921
	CGMCC 2.3469 = WZS29.1B	November 16, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050316	MK849175	MK849313	MK849044	MK848914
	CGMCC 2.3568 = SM37.6 = CBS 15501	November 14, 2006	Simao county, Yunnan province, China	phylloplane	MK050314	MK849186	MK849324	MK849053	MK848922
	CGMCC 2.3449 = WZS29.18	November 16, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050317	–	–	–	–
	CGMCC 2.3458 = WZS29.1 = CBS 15484	November 16, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050315	MK849169	MK849307	MK849037	MK848907
	TW1.1F026	August 18, 2009	Taiwan, China	phylloplane	MK050318	–	–	–	–
D. longiovatus sp. nov.	CGMCC 2.3535^T = SM35.4 = CBS 15659	November 10, 2006	Simao county, Yunnan province, China	phylloplane	MK050312	MK849181	MK849319	MK849050	MK848919
D. napiformis sp. nov.	CGMCC 2.4446^T = TW1.1F028 = CBS 15748	August 18, 2009	Taiwan, China	phylloplane	MK050321	MK849207	MK849346	MK849073	MK848941
	TW1.1F05B	August 18, 2009	Taiwan, China	phylloplane	MK050322	–	–	–	–
D. bifurcus sp. nov.	CGMCC 2.3470^T = SM37.5 = CBS 15489	November 16, 2006	Simao county, Yunnan province, China	phylloplane	MK050319	MK849176	MK849314	MK849045	MK848915

Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
	CGMCC 2.3761 = SM37.15 = CBS 15508	October 16, 2007	Simao county, Yunnan province, China	phylloplane	MK050320	–	–	–	–
D. elongatus sp. nov.	CGMCC 2.3561^T = SM32.1 = CBS 15498	November 10, 2006	Simao county, Yunnan province, China	phylloplane	MK050311	MK849183	MK849321	MK849051	MK848920
D. melastomatis sp. nov.	CGMCC 2.3459^T = WZS19.7 = CBS 15485	November 16, 2006	Wuzhishan mountain, Hainan province, China	leaf of *Melastoma candidum*	MK050305	MK849170	MK849308	MK849038	MK848908
	CGMCC 2.2465 = HX7.3	October 13, 2002	Xingshan county, Hubei Province, China	leaf of *Stephanandra chinensis*	MK050306	–	–	–	–
	WZS10.7	November 15, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050307	–	–	–	–
D. taiwanicus sp. nov.	CGMCC 2.4429^T = TW3.1C-02 = CBS 12490	August 18, 2009	Taiwan, China	phylloplane	MK050303	MK849200	MK849339	MK849066	MK848935
	WZS36.3	November 17, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050304	–	–	–	–
D. ovatus sp. nov.	CGMCC 2.3572^T = SM32.2 = CBS 15654	November 10, 2006	Simao county, Yunnan province, China	phylloplane	MK050302	MK849187	MK849325	MK849055	MK848923
D. longicylindricus sp. nov.	CGMCC 2.5660^T = XZ132E37A = CBS 13979	September 21, 2014	Beibeng county, Motuo, Tibet, China	phylloplane	MK050300	MK849242	MK849379	MK849105	MK848977
	CGMCC 2.5813 = XZ129C6A	September 20, 2014	Motuo, Tibet, China	leaf of *Nepeta* sp.	MK050301	–	–	–	–
	5600	September 21, 2014	Beibeng county, Motuo, Tibet, China	phylloplane	MK088088	MK849216	MK849355	MK849082	MK848950
Phaeotremella lactea sp. nov.	CGMCC 2.5810^T = GPS20.4A1B = CBS 15574	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050280	MK849250	–	–	MK848986
P. ovata sp. nov.	CGMCC 2.5614^T = NW9D3 = CBS 15756	August 20, 2015	Nanwenghe, Heilongjiang province, China	phylloplane	MK050281	MK849222	MK849361	–	MK848949
Holtermannia saccardoi sp. nov.	CGMCC 2.3445^T = SM37.10 = CBS 15479	November 6, 2006	Simao county, Yunnan province, China	phylloplane	MK050336	MK849164	MK849302	MK849033	MK848903
	CGMCC 2.3460 = SM6.3	November 6, 2006	Simao county, Yunnan province, China	leaf of *Arisaema yunnanense*	MK050337	MK849171	MK849309	MK849039	MK848909
	CGMCC 2.3462 = SM32.11	November 6, 2006	Simao county, Yunnan province, China	phylloplane	MK050338	–	MK849310	MK849040	MK848910
	WZS12.12B	November 16, 2006		phylloplane	MK050339	–	–	–	–

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Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
			Wuzhishan mountain, Hainan province, China						
Solicoccozyma gelidoterrea sp. nov.	CGMCC 2.5814^T = HFB003-3 = CBS 15580	August 15, 2015	Daxinganling, China	soil	MK050340	MK849252	MK849388	–	–
	CGMCC 2.4893 = LZ3.17.4	October 12, 2012	China	soil	MK050341	MK849215	MK849354	MK849081	MK848948
	DBVPG10727	2017	Alps, Dolomites, Livigno, Italy	bark of spruce	MK070335/MK070317	–	–	–	–
	CBS 9627	November, 1981	Colorado, Longs Peak, Rocky Mountain National Park, USA	soil	KY105431/KY109663	–	–	–	–
	CBS 9287	n/a	Providenya, Russia	soil	MK397489	–	–	–	–
Filobasidium dingjieense sp. nov.	CGMCC 2.5649^T = GPS3.2A5 = CBS 15567	September 12, 2015	Dingjie county, Tibet, China	phylloplane	MK050342	MK849236	MK849375	–	MK848971
	GPS23.2A5	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050343	–	–	–	
F. globosum sp. nov.	CGMCC 2.5680^T = HLJ8A3 = CBS 15658	August 25, 2014	Yichun county, Heilongjiang province, China	phylloplane	MK050344	MN014083	MN014090	MN014092	MN014078
	CGMCC 2.5656 = HLJ8A3B	August 25, 2014	Yichun county, Heilongjiang province, China	phylloplane	MK050345	MK849240	MK849377	–	MK848975
F. mali sp. nov.	CGMCC 2.4012^T = KTAPG4-11.46 = CBS 15651	August 20, 2008	Qufu county, Shandong province, China	leaf of apple (*Malus pumila*)	MK050346	MK849333	–	–	MK848930
	CGMCC 2.4052 = KTAPG1-11.63	August 20, 2008	Tai'an county, Shandong province, China	leaf of apple (*Malus pumila*)	MK050347	–	–	–	–
	CGMCC 2.3464 = WZS19.13	November 16, 2006	Wuzhishan mountain, Hainan province, China	leaf of *Melastoma candidum*	MK050348	MK849172	MK849312	MK849042	MK848912
	KTAPG4-11.64	August 20, 2008	Qufu county, Shandong province, China	leaf of apple (*Malus pumila*)	GQ181171	–	–	–	–
	4QVF20 = CBS 10181	June, 1998	Arrabida Natural Park, Portugal	Leaf of *Quercus faginea*	EU002869/EU002805	–	–	–	–
F. mucilaginum sp. nov.	CGMCC 2.3463^T = SY2.1 = CBS 15486	November 16, 2006	Sanya county, Hainan province, China	phylloplane	MK050349	–	MK849311	MK849041	MK848911
Phaffia aurantiaca sp. nov.	CGMCC 2.5601^T = GPS23.2A4 = CBS 15548	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050350	MN014085	MN014089	MN014091	MN014077

Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
Kondoa cylindrica sp. nov.	CGMCC 2.3102^T = G6.1-1 = CBS 15466	September 20, 2005	Germany	phylloplane	MK050351	MK849150	MK849290	MK849020	MK848892
	CGMCC 2.3103 = G4.22A	September 20, 2005	Germany	phylloplane	MK050352	MK849151	MK849291	MK849021	MK848893
	CGMCC 2.3175 = G4.22B	September 20, 2005	Germany	phylloplane	MK050353	MK849157	MK849296	MK849027	–
	PYCC 5566	1998	Sesimbra, Portugal	basidiocarp of *Myxarium nucleatum*	AF444672/AF444766	–	–	–	–
K. chamaenerii sp. nov.	CGMCC 2.2652^T = XJ8A5 = CBS 15453	July 6, 2004	Bujin county, Xinjiang province, China	leaf of *Chamaenerion angustifolium*	MK050354	MK849135	MK849275	MK849005	MK848878
	CGMCC 2.2760 = XJ10A7	July 6, 2004	Bujin county, Xinjiang province, China	leaf of *Cotoneaster melanocarpus*	MK050355	–	MK849278	MK849007	MK848880
K. foliicola sp. nov.	CGMCC 2.3100^T = G9.1 = CBS 15465	September 20, 2005	Germany	phylloplane	MK050356	MK849262	MK849399	MK849120	MK848994
K. arboricola sp. nov.	CGMCC 2.2621^T = XZ12B5 = CBS 15452	September 21, 2004	Bomi county, Tibet, China	leaf of arbor	MK050357	MK849134	MK849274	–	–
	CGMCC 2.4886 = LWL4.17.24	October 12, 2012	China	soil	MK050358	MK849214	MK849353	–	–
K. lulangica sp. nov.	CGMCC 2.2762^T = XZ36D1 = CBS 15456	September 21, 2004	Lulang county, Tibet, China	phylloplane	MK050359	MK849138	MK849279	MK849008	MK848881
K. rhododendri sp. nov.	CGMCC 2.2763^T = XZ27E3 = CBS 15457	September 21, 2004	Bomi county, Tibet, China	leaf of *Rhododendron triflorum*	MK050360	MK849139	MK849280	MK849009	MK848882
K. daliangziensis sp. nov.	CGMCC 2.5610^T = HLJ22A8 = CBS 13974	August 28, 2014	Daliangzi river national forest park, Heilongjiang province, China	phylloplane	MK050361	MK849220	MK849359	MK849085	MK848954
	HLJ14.20B = CBS 15577	August 20, 2014	Chelu county, Heilongjiang province, China	phylloplane	MK050362	MK849256	MK849393	MK849117	MK848990
K. ribitophobia sp. nov.	CGMCC 2.4441^T = TW2.1E-016 = CBS 12496	August 17, 2009	Taiwan, China	phylloplane	MK050363	MK849204	MK849343	MK849070	MK848939
	CGMCC 2.4875 = HZZ9D.2	October 12, 2012	Houzhenzi, Shaaxi province, China	phylloplane	MK050364	MK849213	MK849352	MK849080	–
K. myxariophila sp. nov.	CGMCC 2.3106 = G18.2-2 = CBS 15468	September 20, 2005	Germany	phylloplane	MK050365	MK849152	MK849292	MK849022	MK848894
	AS483 = CBS 11525	November, 2008	Graubuenden Alp Flix, Switzerland	flower of *Dianthus superbus*	MN175324/FN428954	–	–	–	–
		1992	Portugal		AF444596/AF189904	–	–	–	–

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Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
	PYCC 5509^T = CBS 8379 = ZP 337			basidiocarps of *Myxarium nucleatum*					
	PYCC 8354 = ZP 338	1992	Portugal	basidiocarps of *Myxarium nucleatum*	MN175325	–	–	–	–
	PYCC 8305 = ZP 352	1996	Portugal	basidiocarps of *Myxarium nucleatum*	MN175326	–	–	–	–
Bensingtonia wuzhishanensis sp. nov.	CGMCC 2.3569^T = WZS33.18 = CBS 15661	November 14, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050366	–	–	MK849054	–
B. pseudorectispora sp. nov.	CGMCC 2.5677^T = XZ154D5 = CBS 15750	September 21, 2014	Bomi, Tibet, China	phylloplane	MK050367	MK849247	MK849384	MK849111	MK848983
Pseudobensingtonia fusiformis sp. nov.	CGMCC 2.5823^T = XZ152E3A = CBS 15647	September 21, 2014	Bomi, Tibet, China	phylloplane	MK050370	MK849123	MK849265	MK848997	MK848870
	CGMCC 2.5815 = XZ152E3 = CBS 15592	September 21, 2014	Bomi, Tibet, China	phylloplane	MK050368	MK849149	MK849289	MK849019	MK848891
	XZ152B1 = CBS 15663	September 21, 2014	Bomi, Tibet, China	phylloplane	MK050369	–	–	–	–
Boekhoutia sterigmata sp. nov.	CGMCC 2.4539^T = FJS3F22 = CBS 15553	October 29, 2011	Fanjingshan Mountain, Guizhou province, China	phylloplane	MK050371	MK849211	–	MK849078	MK848946
Ruinenia fanjingshanensis sp. nov.	CGMCC 2.4542^T = FJS6C7 = CBS 15745	October 29, 2011	Fanjingshan Mountain, Guizhou province, China	phylloplane	MK050372	MK849211	MK849267	MK849078	MK848946
R. bangxiensis sp. nov.	CGMCC 2.3454^T = HBX1.0 = CBS 10819	November 24, 2006	Bangxi county, Hainan province, China	phylloplane	MK050373	MK849167	MK849305	MK849035	–
	ST-153	February 3, 2001	Ban Paeng Distric, Nakhon Phanom Province, Thailand	phylloplane	MN194597/DQ404467	–	–	–	–
R. lunata sp. nov.	CGMCC 2.4426^T = TW 2.1E-028 = CBS 12525	August 17, 2009	Taiwan, China	phylloplane	KP020113	–	MN014088	MN014094	MN014079
	TW2.1E-05B	August 18, 2009	Taiwan, China	phylloplane	KP020110	–	–	MK849063	–
Sterigmatospora layueensis sp. nov.	CGMCC 2.5817^T = XZ100A2B = CBS 15649	September 18, 2014	Layue county, Tibet, China	phylloplane	MK050375	MK849259	MK849396	MK849119	–
Pseudosterigmatospora motuoensis sp. nov.	CGMCC 2.5816^T = XZ119B3 = CBS 15591	September 18, 2014	Motuo, Tibet, China	leaf of *Achyrospermum wallichianum*	MK050374	MK849253	MK849389	MK849115	MK848988

Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
Phyllozyma jiayinensis sp. nov.	CGMCC 2.5669^T = HLJ25.21 = CBS 13975	August 25, 2014	Qingshan county, Jiayin, Heilongjiang province, China	phylloplane	MK050376	–	–	MK849108	MK848980
P. aceris sp. nov.	CGMCC 2.2662^T = XZ17B1 = CBS 15773	September 21, 2004	Bomi county, Tibet, China	leaf of *Acer caudatum*	MK050377	MK849136	MK849276	MK849006	MK848879
	CGMCC 2.2617 = XZ14B2	September 21, 2004	Bomi county, Tibet, China	leaf of bamboo	MK050378	MK849132	–	MK849003	–
Meniscomyces layueensis sp. nov.	CGMCC 2.5818^T = XZ100 = CBS 15747	September 18, 2014	Layue county,Tibet, China	phylloplane	MK050379	MK849248	MK849385	MK849112	MK848984
	CGMCC 2.5681 = XZ100A2	September 18, 2014	Layue county,Tibet, China	phylloplane	MK050380	–	–	–	–
Sakaguchia melibiophila sp. nov.	CBS 5143^T = JCM 8162 = CGMCC 2.4235 = IGC 5612	n/a	The Netherlands	bronchial secretion	KJ778625/KJ708453/ KJ708356	KJ708079	KJ708268	KJ707858	KJ707732
Microsporomyces pseudomagnisporus sp. nov.	CGMCC 2.4538^T = FJS25C3 = CBS 15746	October 29, 2011	Fanjingshan Mountain, Guizhou province, China	phylloplane	MK050384	MK849125	MK849351	MK849077	–
M. rubellus sp. nov.	CGMCC 2.4444^T = TW1.3F-017 = CBS 15622	August 18, 2009	Taiwan, China	phylloplane	MK050385	MK849205	MK849344	MK849071	–
	CGMCC 2.4445 = TW1.3F-026 = CBS 12526	August 18, 2009	Taiwan, China	phylloplane	MK050386	MK849206	MK849345	MK849072	MK848940
M. ellipsoideus sp. nov.	CGMCC 2.5664^T = XZ137E4 = CBS 16020	September 20, 2014	Motuo county, Tibet, China	phylloplane	MK050387	MK849244	MK849381	MK849107	MK848979
Symmetrospora rhododendri sp. nov.	CGMCC 2.2613^T = XZ49DX = CBS 15447	September 21, 2004	Lulang county, Tibet, China	leaf of *Rhododendron* sp.	MK050388	MK849130	MK849271	MK849001	–
Cystobasidium raffinophilum sp. nov.	CGMCC 2.3822^T = 141.4 = CBS 15509	July 6, 2007	Yecheng county, Xinjiang province, China	soil	MK050389	MK849191	MK849329	MK849058	MK848927
C. terricola sp. nov.	CGMCC 2.3823^T = 140.23 = CBS 15650	July 6, 2007	Yecheng county, Xinjiang province, China	soil	MK050390	MK849192	MK849330	MK849059	MK848928
	CGMCC 2.3824 = 141.8	July 6, 2007	Yecheng county, Xinjiang province, China	soil	MK050391	MK849193	MK849331	–	–
Robertozyma ningxiaensis sp. nov.	CGMCC 2.4451^T = HLS10.23 = CBS 12499	August 21, 2009	Helanshan mountain, Ningxia province, China	soil	MK050392	–	MK849348	–	MK848943
	CGMCC 2.4452 = HLS14.23	August 21, 2009		soil	MK050393	MK849209	MK849349	MK849075	MK848944

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Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
			Helanshan mountain, Ningxia province, China						
Begerowomyces foliicola sp. nov.	CGMCC 2.3164^T = G7.4 = CBS 15655	September 20, 2005	Germany	phylloplane	MK050394	MK849154	MK849294	MK849024	MK848896
Rosettozyma petaloides sp. nov.	CGMCC 2.3446^T = WZS29.14 = CBS 15480	November 6, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050395	MK849165	MK849303	MK849034	MK848904
	CGMCC 2.3466 = WZS9.2 = CBS 15488	November 16, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050396	MK849174	–	–	–
	CGMCC 2.3461 = WZS29.15	November 6, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050397	–	–	–	–
R. cystopteridis sp. nov.	CGMCC 2.2615^T = XZ16E1 = CBS 15448	September 21, 2004	Bomi county, Tibet, China	leaf of *Cystopteris moupinensis*	MK050398	MK849131	MK849272	MK849002	MK848876
	CGMCC 2.2619 = XZ5B2 = CBS 15451	September 21, 2004	Bomi county, Tibet, China	leaf of *Rhododendron phaeochrysum*	MK050399	–	–	–	MK848877
R. motuoensis sp. nov.	CGMCC 2.5819^T = XZ118E6 = CBS 15588	September 19, 2014	Motuo, Tibet, China	phylloplane	MK050400	MK849260	MK849397	–	MK848991
Rhodosporidiobolus platycladi sp. nov.	CGMCC 2.3118^T = BJ6-3 = CBS 15469	March 27, 2006	Beijing, China	leaf of *Platycladus* sp.	MK050401	MK849153	MK849293	MK849023	MK848895
R. jianfalingensis sp. nov.	CGMCC 2.3532^T = JF25.7-1 = CBS 15494	May 10, 2007	Jianfaling, Hainan province, China	phylloplane	MK050402	MK849179	MK849317	MK849048	MK848917
	CGMCC 2.3531 = JF25.7-2	May 10, 2007	Jianfaling, Hainan province, China	phylloplane	MK050403	MK849178	MK849316	MK849047	MK848916
R. fuzhouensis sp. nov.	CGMCC 2.4435^T = FJYZ2-6 = CBS 12492	August 18, 2011	Fuzhou county, Fujian province, China	phylloplane	MK050404	MK849201	MK849340	MK849067	MK848936
	CGMCC 2.4442 = TW4.3F1	August 18, 2009	Taiwan, China	phylloplane	MK050405	–	–	–	–
	CGMCC 2.2286 = CBS 9205	January 1, 2001	Xishuang Banna, Yunnan province, China	leaf of *Ficus* sp.	KY105509/KY109744/MN180193	MN180194	MN180195	MN180197	MN180196
Sporobolomyces cellobiolyticus sp. nov.	CGMCC 2.5675^T = HLJ33B4 = CBS 13964	August 26, 2014	Wuyiling natural reserve, Heilongjiang province, China	phylloplane	MK050406	MK849246	MK849383	MK849110	MK848982
	CGMCC 2.5687 = HLJ32B2 = CBS 13963	August 25, 2014	Chelu county, Heilongjiang province, China	phylloplane	MK050407	MK849249	MK849386	MK849113	MK848985
	MCA 3774	n/a	Alaska, Siberia and Newfoundland, Canada	phylloplane	JN942193/JN940715	–	–	–	–

Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
	MCA 3785	n/a	Alaska, Siberia and Newfoundland, Canada	phylloplane	JN942199/JN940720	–	–	–	–
S. reniformis sp. nov.	CGMCC 2.5627^T = GPS21.2C2 = CBS 15562	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050408	MK849230	MK849370	MK849096	MK848965
S. ellipsoideus sp. nov.	CGMCC 2.5619^T = GPS21.5C1 = CBS 15590	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050409	MK849225	MK849364	MK849088	MK848957
	CGMCC 2.5620 = GPS23.3A5	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050410	–	–	–	–
	CGMCC 2.5621 = GPS20.1B3	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050411	MK849227	–	MK849090	MK848959
	CGMCC 2.5622 = GPS20.1A4	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050412	MK849228	MK849366	MK849091	MK848960
	CGMCC 2.5624 = GPS20.1H2	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050413	–	–	MK849093	MK848962
	CGMCC 2.5625 = GPS22.1B3	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050414	MK849229	MK849368	MK849094	MK848963
	CGMCC 2.5626 = GPS20.8C1	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050415	–	MK849369	MK849095	MK848964
	CGMCC 2.5631 = GPS20.8C10	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050416	MK849233	–	MK849099	MK848969
	CBS 2642	n/a	UK	milk	KY105474/KY109710	–	–	–	–
S. primogenomicus sp. nov.	JCM 8242^T = IAM13481 = CBS 15935	1983	Kanto region, Japan	a leaf of willow	MK050417/MK050418/ MK050419	MK849124	MK849266	MK848998	MK848872
Heitmania tridentata sp. nov.	CGMCC 2.5602^T = GPS20.16B3 = CBS 15549	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050420	MK849217	MK849356	MK849083	MK848951
H. cylindrica sp. nov.	CGMCC 2.5650^T = GPS20.2C8 = CBS 15568	September 20, 2015	Milin county, Tibet, China	phylloplane	MK050421	MK849237	MK849376	MK849101	MK848972
Heitmania sp.	CGMCC 2.3440 = SM35.2A	November 10, 2006	Simao county, Yunnan province, China	phylloplane	MK050422	MK849161	MK849299	MK849031	MK848900
Heitmania sp.	CGMCC 2.3624 = SM35.2B	November 10, 2006	Simao county, Yunnan province, China	phylloplane	MK050423	MK849189	MK849327	MK849057	MK848925
Microbotryozyma swertiae sp. nov.	CGMCC 2.3533^T = ZXS7.7 = CBS 15495	May 10, 2007	Chuxiong county, Yunnan province, China	leaf of *Swertia yunnanensis*	MK050424	MK849180	MK849318	MK849049	MK848918

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Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
Yamadamyces terricola sp. nov.	CGMCC 2.5820^T = 03-1 = CBS 15572	August 15, 2015	Daxinganling, China	soil	MK050425	MK849127	MK849268	MK848999	MK848874
Oberwinklerozyma dicranopteridis sp. nov.	CGMCC 2.3441^T = SM10.2 = CBS 15476	November 6, 2006	Simao county, Yunnan province, China	leaf of *Dicranopteris dichotoma*	MK050426	MK849162	MK849300	–	MK848901
O. nepetae sp. nov.	CGMCC 2.5824^T = XZ129C7 = CBS 15579	September 20, 2014	Motuo, Tibet, China	leaf of *Nepeta* sp.	MK050427	MK849254	MK849391	–	MK848992
Chrysozyma pseudogriseoflava sp. nov.	CGMCC 2.5629^T = GPS21.6B3 = CBS 15564	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050428	MK849232	MK849372	MK849098	MK848967
	CGMCC 2.5646 = GPS22.3A2	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050430	MK849234	MK849373	–	MK848970
	GPS20.6D2	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050429	–	–	–	–
C. sambuci sp. nov.	CGMCC 2.2618^T = XZ13C5 = CBS 15450	September 21, 2004	Bomi county, Tibet, China	leaf of *Sambucus williamsii*	MK050431	MK849133	MK849273	MK849004	–
	CGMCC 2.2755 = XZ13B7	September 21, 2004	Bomi county, Tibet, China	leaf of *Sambucus williamsii*	MK050432	MK849137	MK849277	–	–
C. rhododendri sp. nov.	CGMCC 2.5821^T = XZ160D3 = CBS 15583	September 21, 2014	Tibet, China	leaf of *Rhododendron* sp.	MK050433	MK849263	MK849400	MK849121	MK848995
C. iridis sp. nov.	CGMCC 2.2769^T = XZ8B3 = CBS 15461	September 21, 2004	Bomi county, Tibet, China	leaf of *Iris forrestii*	MK050434	MK849144	MK849285	MK849013	MK848886
C. sorbariae sp. nov.	CGMCC 2.2768^T = XZ9D1 = CBS 15460	September 21, 2004	Bomi county, Tibet, China	leaf of *Sorbaria arborea*	MK050435	MK849143	MK849284	MK849012	MK848885
	CGMCC 2.2767 = XZ11B4	September 21, 2004	Bomi county, Tibet, China	leaf of *Acer caudatum*	MK050436	MK849142	MK849283	–	MK848884
C. fusiformis sp. nov.	CGMCC 2.2765^T = XZ33C2 = CBS 15458	September 21, 2004	Lulang county, Tibet, China	phylloplane	MK050437	MK849140	MK849281	MK849010	MK848883
	CGMCC 2.2764 = XZ33Z1	September 21, 2004	Lulang county, Tibet, China	phylloplane	MK050438	–	–	–	–
C. cylindrica sp. nov.	CGMCC 2.3455^T = WZS29.2 = CBS 15482	November 6, 2006	Wuzhishan mountain, Hainan province, China	phylloplane	MK050439	MK849168	MK849306	MK849036	MK848906
C. flava sp. nov.		September 21, 2015	Milin county, Tibet, China	phylloplane	MK050440	MK849221	MK849360	MK849086	MK848955

Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
	CGMCC 2.5611^T = GPS20.4A1 = CBS 15552								
Yurkovia longicylindrica sp. nov.	CGMCC 2.5603^T = GPS20.2C3 = CBS 15550	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050441	MK849218	MK849357	MK849084	MK848952
Pseudohyphozyma lulangensis sp. nov.	CGMCC 2.2612^T = XZ50B2 = CBS 15446	September 21, 2004	Lulang county, Tibet, China	phylloplane	MK050442	MK849129	MK849270	–	MK848875
P. hydrangeae sp. nov.	CGMCC 2.2796^T = XZ46A1 = CBS 15462	September 21, 2004	Lulang county, Tibet, China	leaf of *Hydrangea heteromalla*	MK050443	MK849126	MK849287	MK849015	MK848888
	CGMCC 2.2797 = XZ46C5	September 21, 2004	Lulang county, Tibet, China	leaf of *Hydrangea heteromalla*	MK050444	MK849146	MK849288	MK849016	–
	CGMCC 2.5607 = GPS20.2D2	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050445	MK849219	MK849358	–	MK848953
	CGMCC 2.5618 = GPS23.3C2	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050446	MK849224	MK849363	–	–
	CGMCC 2.5623 = GPS23.3D3	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050447	–	MK849367	MK849092	MK848961
	GPS23.3D2	September 22, 2015	Lulang county, Tibet, China	phylloplane	MK050448	–	–	–	–
Slooffia globosa sp. nov.	CGMCC 2.5822^T = 4-6 = CBS 15573	August 15, 2015	Daxinganling, China	soil	MK050449	MK849255	MK849392	MK849116	MK848989
Colacogloea aletridis sp. nov.	CGMCC 2.2766^T = XZ31A1 = CBS 15459	April 4, 2005	Bomi county, Tibet, China	leaf of *Aletris pauciflora*	MK050450	MK849141	MK849282	MK849011	–
C. hydrangeae sp. nov.	CGMCC 2.2798^T = XZ46B3 = CBS 15463	April 11, 2005	Lulang county, Tibet, China	leaf of *Hydrangea heteromalla*	MK050451	MK849147	–	MK849017	MK848889
C. rhododendri sp. nov.	CGMCC 2.2770^T = XZ10F1 = CBS 15652	April 4, 2005	Bomi county, Tibet, China	leaf of *Rhododendron lulangense*	MK050452	MK849145	MK849286	MK849014	MK848887
	CGMCC 2.5651 = GPS20.5C1	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050457	MK849238	–	MK849102	MK848973
	CGMCC 2.5652 = GPS20.5D6	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050456	MK849239	–	MK849103	MK848974
	GPS20.5C5	September 21, 2015		phylloplane	MK050455	–	–	–	–

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Table 1. (Continued).

Speceis	Strain	Date	Location	Source	18S+ITS+D1/D2	RPB1	RPB2	TEF1	CYTB
			Milin county, Tibet, China						
	GPS20.5C3	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050453	–	–	–	–
	GPS20.5D1	September 21, 2015	Milin county, Tibet, China	phylloplane	MK050454	–	–	–	–

a case-by-case pairwise similarity approach was also provided here. We compared the sequence similarity and nucleotide variations in the ITS and D1/D2 regions among yeast genera containing more than two species in *Agaricomycotina* and *Pucciniomycotina* using the EMBOSS water alignment tool (http://www.ebi.ac.uk/Tools/psa/emboss_water/nucleotide.html; Madeira *et al.* 2019). The script, namely EMBOSS_water.py, was used to run the local alignment for the calculation of the sequence similarities and nucleotide variation including substitutions and deletions. All comparisons of sequence similarities were done with the type strains of the mentioned species in this study. It must be emphasised that diagnostic phenotypical features, especially physiological properties, were used to distinguish the new species from that previously described.

New generic and higher ranks circumscriptions

The circumscriptions of genera and higher ranks in the current study were performed mainly based on the multi-locus phylogenetic analyses used in previous studies (Wang *et al.* 2015a,b,c). The clustering optimisation analysis was done using the OPTSIL software (Göker *et al.* 2009) to yield non-hierarchical clusterings at generic levels by a given reference threshold, which had been employed in Liu *et al.* (2015b) and Wang *et al.* (2015b). The taxonomic thresholds predicted by Vu *et al.* (2016) to discriminate current yeast genera were 96.31 % for ITS and 97.11 % for D1/D2. Recently, the taxonomic thresholds predicted for filamentous fungal delimitation at the genus, family, order and class levels, recommended by Vu *et al.* (2019), were 94.3 %, 88.5 %, 81.2 % and 80.9 % for ITS, and 98.2 %, 96.2 %, 94.7 % and 92.7 % for D1/D2. The above taxonomic thresholds were considered, but not followed strictly, for circumscriptions of new genera and higher ranks in this study. Phenotypic differences were also discussed in the new generic circumscriptions.

RESULTS AND DISCUSSION

Diversity of phylloplane and soils yeasts

More than 1 000 plant leaves and 20 soil samples have been collected from 67 counties of 20 provinces in China (Tables 1 and 2, Fig. 1) during the past 20 years. About 1 440 strains isolated from those samples have been identified by ITS and D1/D2 sequences. Among them 180 strains belonging to *Ustilaginomycotina* were not considered in this study. The other 1 260 strains belonging to *Agaricomycotina* and *Pucciniomycotina* were distributed in 58 genera, e.i. *Ballistosporomyces*, *Bannoa*, *Bannozyma*, *Bensingtonia*, *Buckleyzyma*, *Bullera*, *Bulleribasidium*, *Chrysozyma*, *Colacogloea*, *Cryptococcus*, *Cryptotrichosporon*, *Curvibasidium*, *Cutaneotrichosporon*, *Cystobasidiopsis*, *Cystobasidium*, *Cystofilobasidium*, *Derxomyces*, *Dioszegia*, *Erythrobasidium*, *Fellozyma*, *Fibulobasidium*, *Filobasidium*, *Genolevuria*, *Hannaella*, *Holtermannia*, *Holtermanniella*, *Itersonilia*, *Kockovaella*, *Kondoa*, *Kwoniella*, *Leucosporidium*, *Microbotryum*, *Microsporomyces*, *Mrakia*, *Naganishia*, *Naohidea*, *Oberwinklerozyma*, *Papiliotrema*, *Phaeotremella*, *Phyllozyma*, *Piskurozyma*, *Pseudobensingtonia*, *Pseudohyphozyma*, *Rhodosporidiobolus*, *Rhodotorula*, *Ruinenia*, *Saitozyma*, *Slooffia*, *Solicoccozyma*, *Sporobolomyces*,

Table 2. List of known yeasts species in China.

Taxa	Present in number of samples	Resources	Location*
Tremellomycetes			
Tremellales			
Bulleraceae			
Bullera alba	54	Phylloplane	1; 3; 5; 13; 14; 15; 17; 19; 20; 21; 25; 26; 27; 29; 33; 34; 38; 39; 40; 41; 42; 43; 49; 50; 54; 66*
B. penniseticola	1	Phylloplane	52;
Genolevuria amylolytica	2	Phylloplane, 1 Soil, 1	2; 67;
G. tibetensis	7	Phylloplane, 6 Soil, 1	2; 44; 42; 44;
Bulleribasidiacea			
Bulleribasidium foliicola	10	Phylloplane	8; 12; 10;
B. hainanense	2	Phylloplane	10; 12;
B. oberjochense	3	Phylloplane	18; 44;
B. panici	3	Phylloplane	12;
B. pseudovariabilis	14	Phylloplane	9;12; 24; 25; 32;
B. sanyaense	3	Phylloplane	11; 10;
B. setariae	3	Phylloplane	12; 36; 44;
B. variabilis	31	Phylloplane	12; 25; 36; 44; 54;
B. wuzhishanense	1	Phylloplane	12;
Derxomyces anomalus	1	Phylloplane	40; 41;
D. boekhoutii	5	Phylloplane	4; 12;
D. boninensis	6	Phylloplane	10; 12; 24; 32;
D. cuulongensis	4	Phylloplane	44;
D. cylindricus	3	Phylloplane	44;
D. hainanensis	4	Phylloplane	12;
D. hubeiensis	4	Phylloplane	12; 24; 36;
D. komagatae	1	Phylloplane	25;
D. linzhiensis	5	Phylloplane	41; 44;
D. mrakii	55	Phylloplane	4;10;11;12; 24; 29; 32; 31; 36; 54; 55;
D. nakasei	10	Phylloplane	12; 24; 32;
D. pseudocylindrica	4	Phylloplane	12;
D. pseudohuiaensis	8	Phylloplane	24; 28; 31;
D. pseudoschimicola	29	Phylloplane	4; 10; 12; 24; 32; 36;
D. qinlingensis	2	Phylloplane	28; 30;
D. simaoensis	1	Phylloplane	54;
D. waltii	6	Phylloplane	12; 25;
D. wuzhishanensis	3	Phylloplane	12; 44;
D. yunnanensis	7	Phylloplane	36; 40,41; 44; 54;
Dioszegia athyrium	1	Phylloplane	25;
D. aurantiaca	50	Phylloplane	7; 12; 16; 24; 25; 27; 35; 38; 40; 41; 42; 44; 55; 67;
D. butyracea	1	Phylloplane	27;
D. changbaiensis	4	Phylloplane	25; 54;
D. cream	4	Phylloplane	25; 31; 45;
D. fristingensis	6	Phylloplane	35; 37; 42; 45;
D. hungarica	8	Phylloplane	3; 24; 25; 35;
D. statzelliae	1	Phylloplane	31;
D. takashimae	1	Phylloplane	8;
D. xingshanensis	2	Phylloplane	32;

(*continued on next page*)

Table 2. (Continued).

Taxa	Present in number of samples	Resources		Location*
D. zsoltii	21	Phylloplane		1; 3; 4; 13; 24; 25; 31;35; 51; 55;
Hannaella coprosmae	7	Phylloplane		25;
H. kunmingensis	2	Phylloplane		50;
H. luteola	18	Phylloplane		4; 8; 10; 12; 36; 44; 50; 51; 54;
H. oryzae	20	Phylloplane		1; 4; 10; 11; 25; 36; 45; 52;54; 55;
H. sinensis	25	Phylloplane		3;13; 8;10;11; 25; 31; 50; 51; 52; 54;
H. zeae	1	Phylloplane		51;
H. phyllophila	3	Phylloplane		67;
Vishniacozyma carnescens	5	Phylloplane, 3	Soil, 2	13; 26; 32; 35; 48;
V. dimennae	1	Phylloplane		13;
V. foliicola	3	Phylloplane	Soil	2;
V. globispora	1	Phylloplane		27;
V. heimaeyensis	1		Soil	48;
V. taibaiensis	2	Phylloplane		8;32;
V. tephrensis	2	Phylloplane		13; 26
V. victoriae	13	Phylloplane,11	Soil, 2	2; 23; 24;32; 42; 45; 48; 50; 52; 67;
Cryptococcaceae				
Kwoniella dendrophila	1	Phylloplane		13;
K. dejecticola	1	Phylloplane		26;
Cuniculitremaceae				
Kockovaella imperatae	1	Phylloplane		51;
K. mexicanus	3	Phylloplane		9; 51;
K. sacchari	2	Phylloplane		12; 51;
K. schimae	1	Phylloplane		51;
K. sichuanensis	1	Phylloplane		12;
Phaeotremellaceae				
Papiliotrema aureus	1	Phylloplane		4;
P. flavescens	3	Phylloplane		44; 52; 54;
P. fonsecae	2		Soil	48;
P. fuscus	1	Phylloplane		44;
P. laurentii	4	Phylloplane, 1	Soil, 3	31; 48;
Phaeotremella skinneri	2		Soil	2;
Sirobasidiaceae				
Fibulobasidium inconspicuum	2		Soil	2;
F. murrhardtense	1		Soil	2;
Naemateliaceae				
Tremella indecorata	1		Soil	2;
Trimorphmycetaceae				
Saitozyma ninhbinhensis	1	Phylloplane		54;
S. podzolica	5	Phylloplane		36; 54;
Trimorphomyces papilionaceus	2	Phylloplane		12;
Trichosporonales				
Tetragoniomycetaceae				
Cryptotrichosporon anacardii	1	Phylloplane		67;
C. tibetense	3	Phylloplane		38;
Takashimella formosensis	1	Phylloplane		44;
T. koratensis	1	Phylloplane		54;
Trichosporonaceae				

Table 2. (Continued).

Taxa	Present in number of samples	Resources		Location*
Cutaneotrichosporon arboriformis	1	Phylloplane		36;
C. moniliiforme	2	Phylloplane, 1	Soil, 1	2; 40,41;
Holtermanniales				
Holtermannia corniformis	2	Phylloplane		12; 54;
Holtermanniella festucosa	1		Soil	2;
H. nyarrowii	2	Phylloplane		54;
H. takashimae	1	Phylloplane		44;
H. wattica	7	Phylloplane, 6	Soil, 1	2; 67;
Filobasidiales				
Filobasidiaceae				
Filobasidium chernovii	7	Phylloplane, 6	Soil, 1	2; 11; 22; 67;
F. elegans	1	Phylloplane		12;
F. magnum	16	Phylloplane, 8	Soil, 8	2; 13; 22; 26; 32; 36; 48; 52; 67;
F. oeirense	1	Phylloplane		45;
F. wieringae	1	Phylloplane		52;
Naganishia adeliensis	4		Soil	48;
N. albida	10	Phylloplane, 3	Soil, 7	26; 48;
N. albidosimilis	1		Soil	48;
N. antarctica	1		Soil	48;
N. diffluens	2	Phylloplane		42;
N. liquefaciens	1	Phylloplane		32;
N. uzbekistanensis	3	Phylloplane	Soil	4; 48;
N. vishniacii	1		Soil	48;
Piskurozymaceae				
Piskurozyma cylindricus	2	Phylloplane		67;
P. filicatus	1		Soil	2;
Solicoccozyma terreus	3	Phylloplane, 1	Soil, 2	2; 44;
S. terricola	1		Soil	2;
Cystofilobasidiales				
Cystofilobasidiaceae				
Cystofilobasidium capitatum	4		Soil	2; 26
Itersonilia pannonica	11	Phylloplane		23; 24; 24; 35; 45 38; 53; 67;
I. perplexans	10	Phylloplane		25; 23; 32; 38; 40; 41; 54; 55;
Mrakiaceae				
Mrakia aquatica	1	Phylloplane		67;
M. blollopis	1	Phylloplane		2;
M. cryoconiti	1		Soil	42;
M. robertii	1		Soil	2;
Tausonia pullulans	1		Soil	2;
Udeniomyces kanasensis	5	Phylloplane		45; 46;
U. pseudopyricola	26	Phylloplane, 25	Soil, 1	4; 6; 25; 27; 32; 42; 48; 54; 55; 67;
U. puniceus	2	Phylloplane		27; 45;
U. pyricola	9	Phylloplane		4; 23; 24; 31; 54;
Agaricostibomycetes				
Agaricostibales				
Agaricostilbaceae				
Pseudobensingtonia musae	2	Phylloplane		12; 38;
Chionosphaeraceae				

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Table 2. (Continued).

Taxa	Present in number of samples	Resources	Location*
Ballistosporomyces bomiensis	2	Phylloplane	38;
B. changbaiensis	2	Phylloplane	25;
B. taupoensis	3	Phylloplane	25;
B. xanthus	6	Phylloplane	25;
Cystobasidiopsis lactophilus	1	Phylloplane	44;
C. lophatheri	1	Phylloplane	37;
Kondoaceae			
Kondoa changbaiensis	9	Phylloplane	25; 67;
K. phyllada	2	Phylloplane	1; 44;
K. sorbi	3	Phylloplane	25;
K. subrosea	2	Phylloplane	45;
K. thailandica	3	Phylloplane	36; 44; 38;
K. yuccicola	3	Phylloplane	45; 67;
Bensingtonia bomiensis	1	Phylloplane	38;
B. naganoensis	6	Phylloplane	25; 55;
B. pseudonaganoensis	21	Phylloplane	12; 24; 25; 32; 38; 67;
B. rectispora	4	Phylloplane	41;
Ruineniaceae			
Ruinenia clavata	1	Phylloplane	25;
R. diospyroris	5	Phylloplane	36;
Spiculogoeales			
Phyllozyma linderae	2	Phylloplane	25;
P. subbrunnea	1	Phylloplane	25;
P. coprosmicola	2	Phylloplane	25; 67;
P. dimmenae	1	Phylloplane	25;
Cystobasidiomycetes			
Cystobasidiales			
Cystobasidium calyptogenae	2	Phylloplane	44;
C. fimetarium	1	Soil	48;
C. lysinophilum	1	Soil	2;
C. minutum	3	Soil	48;
C. slooffiae	1	Soil	48;
C. pinicola	1	Phylloplane	26;
Erythrobasidiales			
Bannoa hahajimensis	4	Phylloplane	36; 44;
B. ogasawarensis	13	Phylloplane	4; 10; 12; 25; 36;
B. syzygii	2	Phylloplane	25; 42;
Bannozyma arctica	3	Phylloplane	32;
B. yamatoana	19	Phylloplane	12; 23; 24; 25; 44; 54; 55; 67;
Erythrobasidium hasegawianum	4	Phylloplane	25;
Naohidaeales			
Naohidea sebacea	1	Phylloplane	16; 32;
Buckeyzymaceae			
Buckleyzyma aurantiaca	1	Soil	2;
B. salicina	1	Phylloplane	45;
Symmetrosporaceae			
Symmetrospora coprosmae	9	Phylloplane	25; 27; 45; 50; 67;

Table 2. (Continued).

Taxa	Present in number of samples	Resources		Location*
S. oryzicola	6	Phylloplane		1; 25; 31; 32;
S. symmetrica	1	Phylloplane		1;
Microsporomycetaceae				
Microsporomyces magnisporus	6	Phylloplane		36;
Microbotryomycetes				
Microbotryales				
Microbotryum reticulatum	1	Phylloplane		54;
Sporidiobolales				
Rhodosporidium babjevae	1	Phylloplane		57;
Rhodosporidiobolus colostri	2	Phylloplane	Soil	2; 67;
R. fluviale	2	Phylloplane		12; 67;
R. lusitaniae	6	Phylloplane, 4	Soil, 2	4; 26; 36; 42;
R. microsporus	1	Phylloplane		10;
R. nylandii	1	Phylloplane		10;
R. odoratus	32	Phylloplane		1; 8; 10; 12; 25; 26; 31; 32; 38; 40; 41; 42; 44; 54; 66; 67;
R. poonsookiae	1	Phylloplane		51;
R. ruineniae	3	Phylloplane		25; 36; 66
Rhodotorula glutinis	1	Phylloplane		55;
R. graminis	1	Phylloplane		44;
R. kratochvilovae	1		Soil	48;
R. mucilaginosa	2	Phylloplane		26; 42;
R. paludigena	1	Phylloplane		44;
Sporobolomyces bannaensis	1	Phylloplane		12;
S. beijingensis	25	Phylloplane		1; 3; 18; 19; 22; 38; 56; 66
S. bischofiae	1	Phylloplane		44;
S. carnicolor	18	Phylloplane		4; 13; 8; 10; 11; 12; 36; 44; 54;
S. japonicus	3	Phylloplane		11; 12; 35;
S. jilinensis	20	Phylloplane		18; 19; 25; 56; 59; 60; 61; 63; 65
S. phaffii	7	Phylloplane		3; 25; 24; 27;
S. roseus	31	Phylloplane, 29	Soil, 2	1; 25; 26; 27; 34; 45; 48;
S. ruberrimus	10	Phylloplane		18; 19; 25; 56; 57; 58; 60
S. salmonicolor	6	Phylloplane		18; 19; 57; 67;
S. shibatanus	11	Phylloplane		3; 8; 25; 36; 51; 56; 66;
Kriegeriales				
Yamadamyces rosulatus	1		Soil	2; 67;
Leucosporidiales				
Leucosporidium fellii	1	Phylloplane		67;
L. scottii	1		Soil	2; 67;
Colacogloeaceae				
Colacogloea diffluens	1	Phylloplane		54;
C. falcata	3	Phylloplane		40; 41; 67;
C. foliorum	1	Phylloplane		67;
Chrysozymaceae				
Chrysozyma griseoflava	20	Phylloplane		12; 24; 25; 31; 44; 54; 67;
Fellozyma inositophila	4	Phylloplane		35; 32; 55; 67;
incertae sedis				
Curvibasidium cygneicollum	8	Phylloplane		25; 26; 38; 55;

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Table 2. (Continued).

Taxa	Present in number of samples	Resources	Location*
Slooffia tsugae	3	Phylloplane, 2 Soil, 1	2; 12;
Oberwinklerozyma yarrowii	2	Phylloplane	24; 54;
Pseudohyphozyma bogoriensis	1	Phylloplane	67;
P. buffonii	1	Phylloplane	40; 41;
P. pustula	1	Phylloplane	67;

Note: * 1: Baihua mountain, Beijing; 2: Mentougou, Beijing; 3: Songshan mountain, Beijing; 4: Fuzhou county, Fujian province; 5: Beilunhekou natural reserve, Guangxi province; 6: Fanjingshan Mountain, Guizhou province; 7: Maotai county, Guizhou province; 8: Bangxi county, Hainan province; 9: Haikou county, Hainan province; 10: Jianfaling, Hainan province; 11: Sanya county, Hainan province; 12: Wuzhishan mountain, Hainan province; 13: Yesanpo county, Hebei province; 14: Chelu county, Heilongjiang province; 15: Daliangzi river national forest park, Heilongjiang province; 16: Heihe county, Heilongjiang province; 17: Jiayin county, Heilongjiang province; 18: Nanwenghe, Heilongjiang province; 19: Shuanghe county, Heilongjiang province; 20: Wuyiling natural reserve, Heilongjiang province; 21: Yichun county, Heilongjiang province; 22: Hongqiqu county, Henan province; 23: Shennongjia, Hubei province; 24: Xingshan county, Hubei province; 25: Changbai Mountain, Jilin province; 26: Helanshan mountain, Ningxia province; 27: Liupan mountain, Ningxia province; 28: Fuping county, Shaaxi province; 29: Houzhenzi county, Shaaxi province; 30: Qinling Mountain, Shaaxi province; 31: Taibai County, Shaaxi province; 32: Taibai mountain, Shaaxi province; 33: Qufu county, Shandong province; 34: Tai'an county, Shandong province; 35: Taigu county, Shaxi province; 36: Taizhong county, Taiwan province; 37: Bayi county, Tibet; 38: Bomi county, Tibet; 39: Dingjie county, Tibet; 40: Layue county, Tibet; 41: Linzhi county, Tibet; 42: Lulang county, Tibet, 43: Milin county, Tibet; 44: Motuo county, Tibet; 45: unknown location, Xinjiang province; 46: Kanas Lake, Xinjiang province; 47: Kuerlei county, Xinjiang province; 48: Yecheng county, Xinjiang province; 49: Chuxiong county, Yunnan province; 50: Dali county, Yunnan province; 51: Jinghong county, Yunnan province; 52: Kunming county, Yunnan province; 53: Lijiang county, Yunnan province; 54: Simao county, Yunnan province; 55: Zixi montain, Yunnan province; 56: Tahe, Heilongjiang province; 57: Huzhong, Heilongjiang province; 58: Bailudao, Neimonggu province; 59: Dalinuoer, Neimonggu province; 60: Eerguna, Neimonggu province; 61: Hanma, Neimonggu province; 62: Honghuaerji, Neimonggu province; 63: Huihe, Neimonggu province; 64: Saihanwula, Neimonggu province; 65: Tumuji, Neimonggu province; 66: Yantai, Shandong province; 67: unknown location, Tibet.

Symmetrospora, *Takashimella*, *Tausonia*, *Tremella*, *Trimorphomyces*, *Udeniomyces*, *Vishniacozyma* and *Yamadamyces*, and represent 199 known species (Table 2) as well as 101 undescribed species (Table 1).

Among known species, 170 species belonging to 52 genera were isolated from surfaces of plant leaves commonly referred to as phylloplane (Fonseca & Inácio 2006, Morais *et al.* 2006, Nakase *et al.* 2006, Kemler *et al.* 2017, Limtong & Nasanit 2017). A total of 42 species belonging to 24 genera were isolated from soils (Table 2). The difference of species diversity between soils and leaves were not analysed in this study because soils and plants were not always collected simultaneously. Most species isolated from soils were previously reported among species occurring in soils by Botha (2006, 2011), Yurkov *et al.* (2016), Yurkov (2017) and Groenewald *et al.* (2018), such as *Vishniacozyma victoriae*, *Naganishia adeliensis*, *Tausonia pullulans*, *Holtermanniella wattica*, *Cystobasidium minutum* and *Cutaneotrichosporon moniliiforme* (Table 2). Among species isolated from soils in China, a few have been reported from habitats other than soils, for example, *Fibulobasidium inconspicuum* from leaves in a river (Sampaio *et al.* 2002), *Genolevuria tibetensis* from leaves (Wang *et al.* 2007) and *Yamadamyces rosulatus* from dead pine needle (Golubev & Scorzetti 2010).

Among the 101 undescribed species, some are represented by one or only a few isolates. It is difficult to determine if these are rare species or simply undersampled. We continuously collected samples from different locations in China over the past 20 years and some places were revisited many times, such as Milin, Lulang and Bomi counties in Tibet (Table 1). However, a number of single strain species isolated in 2004 were never isolated again despite resampling from the same locations in 2014 and 2015 (Table 1). Phenotypic for these seemingly rare species (Table S1) indicated that most of them grow at low temperature, which may result in slow-growing and competitive disadvantage to other dominating species in a microbial community. In contrast, some known species are frequently isolated from the same or different locations in China, such as *Bullera alba* isolated from 26 counties, *Dioszegia aurantiaca* from 14 locations and *Rhodosporidiobolus odoratus* from 16 locations (Table 2); these commonly isolated species all grow well at room temperature.

Species-by-species pairwise similarity comparison in basidiomycetous yeast genera

Over the past decades, the number of yeast species has increased from 700 (Kurtzman & Fell 1998) to 2 000 (Vu *et al.* 2016), which benefits from the application of DNA sequence analysis for identification of yeast species (Kurtzman *et al.* 2015). Relying on results from mating experiments and pairwise DNA-DNA hybridisation values for several ascomycetous genera and species, Kurtzman & Robnett (1998) suggested that different species are likely to show greater than 1 % substitutions in nucleotide sequences of the D1/D2 domains in pairwise comparisons and strains with less three nucleotides differences are likely to be either conspecific or sister species. Fell *et al.* (2000) observed that when a sufficient number of strains has been studied, different species of basidiomycetous yeasts differed in two or more nucleotides in the D1/D2 domains. In the same time, the authors pointed to several conflicts between taxonomic assignments and pairwise sequence comparisons. Specifically, strains of different species in both *Agaricomycotina* and *Pucciniomycotina* sometimes shared identical D1/D2 sequences but showed distinct sequences of the ITS region (Fell *et al.* 2000). The follow-up study performed by Scorzetti *et al.* (2002) did not find a common similarity threshold for basidiomycetous yeasts in both D1/D2 and ITS regions and suggested that both gene regions are necessary for a reliable species delimitation. Importantly, sequence variability patterns in these two gene regions dependent on a phylogenetic lineage. While ITS is often more

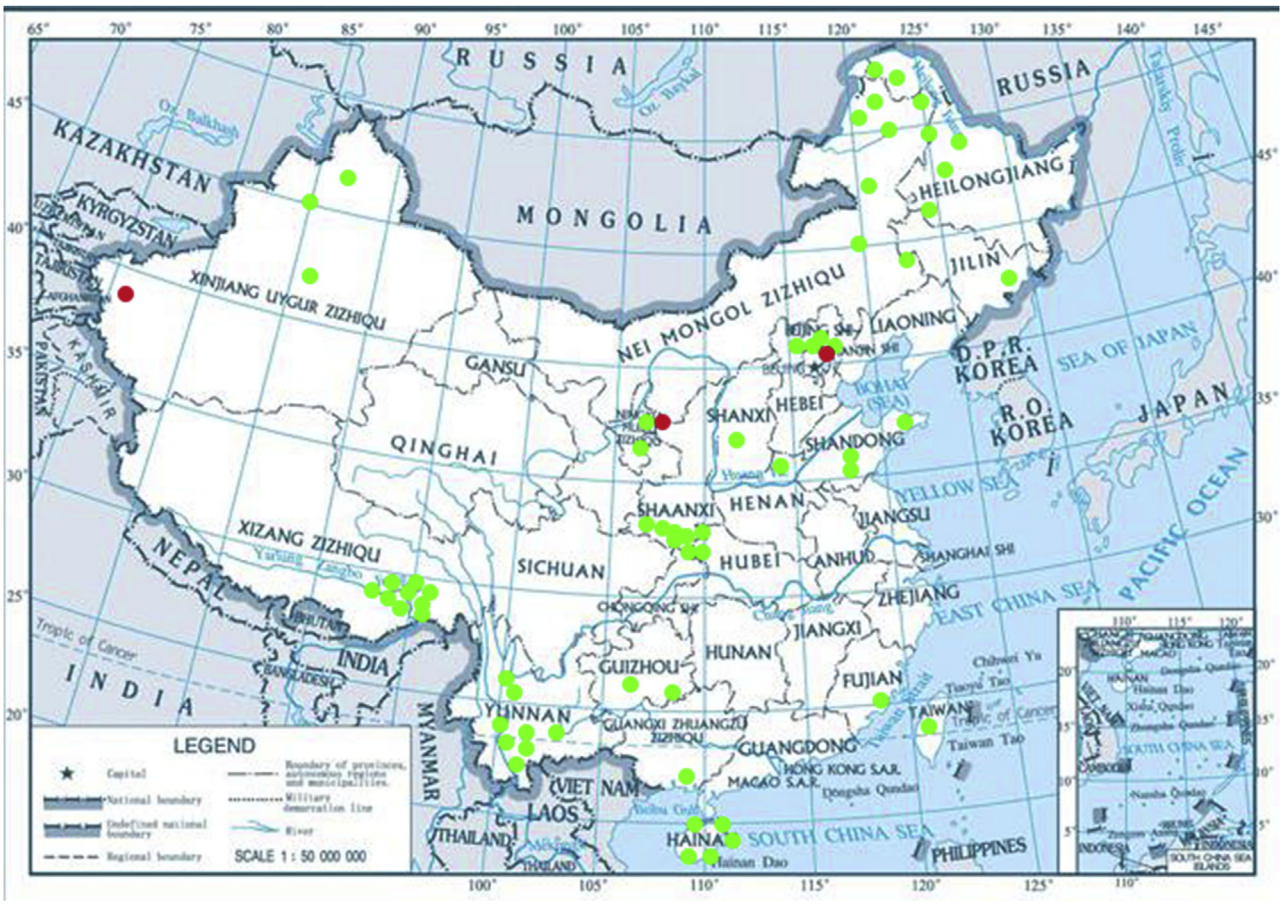


Fig. 1. Localisation of sampling sites in China. Red cycles represent soil origin, green cycles represent plant origin.

variable than D1/D2 domains of the LSU, the situation was opposite in *Trichosporonales* and among the members of the Aerius clade of *Filobasidiales* (Scorzetti et al. 2002). Sequence heterogeneity among sexually compatible strains of teleomorphic species exceeded 1 % in a few genera. Despite distant evolutionary relationships between ascomycetous and basidiomycetous yeasts, the "1 % threshold" was used as an argument to delimit species in the latter group. Even in ascomycetes, this cut-off value is not uniformly applied to all genera (e.g. *Clavispora*, *Metschnikowia*, *Ogataea*). Nevertheless, this threshold was repeatedly used in the taxonomic literature (e.g. Kurtzman & Fell 2006, Kurtzman 2014, 2015, Kurtzman *et al.* 2015). Results of studies performed by Kurtzman & Robnett (1998), Fell *et al.* (2000) and Scorzetti *et al.* (2002) were recently revised by Vu *et al.* (2016). The authors observed similar taxonomic threshold, 98.41 % (or 99.21 % using ex-type strains only) for ITS and 99.51 % for LSU, considering all species recognised as yeasts.

The above two threshold values have been calculated for all yeast species and strains. A case-by-case sequences similarity analysis for each genus should be more helpful than those general values to delimit yeast species. In the present work, the sequence similarities and nucleotide variation in the ITS region and D1/D2 domains among all yeast genera that contain more than two species were determined from local alignments for 40 genera of *Agaricomycotina* and 30 genera of *Pucciniomycotina* (Table 3 and Tables S2.1–S2.70). In agreement with previous observation, sequence variability in the ITS region was, in general, greater than in D1/D2 domains for most, but not all, studied yeast genera (Table 3). All species in *Holtermanniella* displayed larger variability in the D1/D2 domains (11–20 nt difference) than in the ITS region (3–7 nt difference). Sequence heterogeneity among species in the following four genera, *Solicoccozyma* and *Naganishia* in the *Filobasidiales*, *Trichosporon* and *Apiotrichum* in *Trichosporonales*, did not show a stable pattern. For example, type strain of *Solicoccozyma terrea* differed from *Solicoccozyma fuscescens* by 10 nt in D1/D2 domains, and three nt in ITS region, whereas the latter species differed from *Solicoccozyma aeria* at eight D1/D2 positions and 13 ITS positions. *Naganishia liquefaciens* and *Naganishia albidisimilis* had identical ITS sequences but showed eight D1/D2 nucleotide differences, whereas *Naganishia onofrii* and *Naganishia vaughanmartiniae* had identical D1/D2 sequences and 17 mismatches in ITS region. *Apiotrichum laibachii* and *Apiotrichum multisporum* shared identical ITS sequences and seven differences in the D1/D2 domains. In the same time sequences of *Apiotrichum scarabaeorum* and *Apiotrichum terrigenum* differed by five and 16 nucleotides in the D1/D2 domains and ITS region, respectively. Similarly, *Trichosporon asahii* differed from *Trichosporon coremiiforme* by two nucleotides in ITS region and eight nucleotide positions in D1/D2 domains, whereas the latter species differed from *Trichosporon dohaense* by only one nucleotide substitution in the D1/D2 domains and nine positions in ITS.

Our pairwise similarity comparison results indicated that a few well recognised species have less than 1 % nucleotide variation in both ITS region and D1/D2 domains, which in agreement with results by Scorzetti *et al.* (2002). However, these species can be separated by other taxonomic characters and multi-locus sequences analyses (MLS). For example, *Rhodotorula glutinis* and *Rhodotorula graminis* (D1/D2: 1, ITS: 2 Table S2.67) were

Table 3. Number of nucleotide variation and sequence similarities in the D1/D2 domain and ITS region among the type strains of species in the 70 genera.

Lineage/Genus	D1/D2	ITS
Agaricomycotina		
Tremellomycetes		
Trichosporonales		
Apiotrichum	2-66 (99.7-89.5 %)	1-62 (99.8-88.5 %)
Cryptotrichosporon	8-29 (98.5-95.7 %)	39-109 (92.7-78.6 %)
Cutaneotrichosporon	2-43 (99.7-93.1 %)	4-103 (99.2-78.4 %)
Takashimella	1-16 (99.8-96.9 %)	5-37 (98.9-91.9 %)
Trichosporon	1-49 (99.8-92.2 %)	0-82 (100.0-85.3 %)
Vanrija	11-123 (97.5-77.6 %)	11-122 (97.7-76.4 %)
Holtermanniales		
Holtermanniella	11-20 (98.3-96.7 %)	3-7 (99.3-98.4 %)
Cystofilobasidiales		
Cystofilobasidium	10-54 (98.3-90.7 %)	18-98 (97.1-84.0 %)
Mrakia	1-19 (99.8-97.0 %)	8-65 (98.7-90.2 %)
Itersonilia	7-30 (98.8-94.9 %)	18-30 (97.1-95.0 %)
Krasilnikovozyma	2-13 (99.6-97.5 %)	2-83 (97.7-87.7 %)
Tausonia	17-29 (97.3-95.3 %)	84-140 (86.5-80.1 %)
Udeniomyces	4-11 (99.4-98.3 %)	38-144 (94.4-78.6 %)
Filobasidiales		
Filobasidium	0-21 (100.0-96.7 %)	4-106 (99.3-84.2 %)
Goffeauzyma	3-51 (99.5-90.8 %)	3-195 (99.5-70.4 %)
Heterocephalacria	5-131 (99.1-77.1 %)	17-165 (96.2-73.8 %)
Naganishia	0-47 (100.0-92.4 %)	1-71 (99.8-89.1 %)
Piskurozyma	7-71 (98.8-88.3 %)	11-195 (98.2-73.0 %)
Solicoccozyma	3-48 (99.5-92.3 %)	3-144 (99.5-78.8 %)
Tremellales		
Bullera	8-45 (98.7-92.9 %)	15-183 (97.3-71.0 %)
Bulleribasidium	1-91 (99.8-84.2 %)	8-165 (98.1-70.8 %)
Carcinomyces	42-72 (91.9-86.6 %)	117-177 (75.1-66.2 %)
Carlosrosaea	14-16 (97.4-97.1 %)	63-84 (88.0-82.8 %)
Cryptococcus	0-31 (100-94.8 %)	1-33 (99.8-93.6 %)
Derxomyces	3-42 (99.5-93.5 %)	17-206 (96.4-66.6 %)
Dioszegia	3-29 (99.5-95.1 %)	6-87 (98.7-81.8 %)
Fellomyces	4-39 (99.4-93.8 %)	10-94 (98.1-83.3 %)
Fibulobasidium	2-6 (99.6-98.9 %)	44/11 (91.4 %)
Genolevuria	7-17 (98.8-96.7 %)	23-101 (95.4-80.8 %)
Hannaella	6-59 (99.0-89.6 %)	7-85 (98.4-83.4 %)
Kockovaella	2-39 (99.7-93.8 %)	4-85 (99.2-85.0 %)
Kwoniella	0-42 (100.0-93.3 %)	6-128 (98.9-77.3 %)
Naematelia	1-13 (99.8-97.9 %)	5-26 (99.0-94.3 %)
Papiliotrema	2-51 (99.6-91.7 %)	3-127 (99.5-78.1 %)
Phaeotremella	1-28 (99.8-95.3 %)	4-89 (99.2-83.5 %)
Pseudotremella	34-51 (94.4-91.9 %)	86-181 (84.6-70.6 %)
Rhynchogastrema	1-19 (99.8.0-97.0 %)	5-42 (99-91.5 %)
Saitozyma	18-64 (97.0-89.4 %)	29-92 (94.1-81.9 %)
Tremella	6-104 (99.0-88.6 %)	0-184 (100.0-66.9 %)
Vishniacozyma	7-64 (98.8-90.1 %)	6-162 (98.7-73.8 %)
Pucciniomycotina		
Agaricostilbomycetes		
Ballistosporomyces	2-34 (99.7 %-97.2 %)	17-53 (97.1-91.2 %)
Bensingtonia	8-52 (98.7-91.8 %)	52-235 (92.1-67.9 %)
Cystobasidiopsis	17-24 (97.2-96.1 %)	81-101 (86.9-82.0 %)
Kondoa	2-90 (99.7-83.8 %)	29-55 (95.5-67.7 %)
Kurtzmanomyces	10-61 (98.4-90.4 %)	83-179 (87.2-74.2 %)
Ruinenia	13-76 (97.8-88.3 %)	30-134 (94.7-78.6 %)
Sterigmatomyces	12-33 (97.9-94.7 %)	47-111 (92.2-81.8 %)
Spiculogloeomycetes		
Phyllozyma	3-91 (99.5-85.7 %)	8-143 (98.4-72.6 %)
Cystobasidiomycetes		
Bannoa	11-21 (98.3-96.8 %)	27-35 (95.5-94 %)
Buckleyzyma	4-21 (99.4-96.7 %)	28-76 (87.8-95.3 %)
Cystobasidium	3-44 (99.5-92.1 %)	6-134 (98.9-78.0 %)
Erythrobasidium	8-24 (98.7-96.0 %)	6-75 (99.0-88.3 %)
Microsporomyces	29-70 (94.3-86.1 %)	73-126 (86.1-77.7 %)
Occultifur	6-16 (99.0-97.3 %)	13-28 (97.4-94.9 %)
Sakaguchia	7-68 (98.7-87.7 %)	28-87 (95.2-85.3 %)
Symmetrospora	2-34 (99.7-94.6 %)	12-54 (97.9-91.1 %)
Microbotryomycetes		
Colacogloea	14-61 (97.7-90.2 %)	52-162 (92.2-74.0 %)
Curvibasidium	3-7 (99.5-98.9 %)	8-11 (98.7-98.2 %)
Glaciozyma	7-20 (98.9-96.4 %)	54-99 (91.3-84.2 %)
Hamamotoa	1-8 (99.8-98.7 %)	18-95 (97.2-85.5 %)
Heitmania	2 (97.7 %)	33-62 (94.6-89.9 %)
Leucosporidium	1-27 (99.8-95.3 %)	4-92 (99.3-84.7 %)
Oberwinklerozyma	3-10 (99.4-98.1 %)	42-49 (92.6-91.1 %)
Phenoliferia	5-14 (99.1-97.5 %)	3-28 (99.5-95.4 %)
Pseudohyphozyma	3-8 (99.5-98.6 %)	58-88 (90.8-86.6 %)
Rhodosporidiobolus	4-41 (99.2-93.1 %)	10-89 (98.1-85.2 %)
Rhodotorula	0-45 (100.0-92.6 %)	1-79 (99.8-85.9 %)
Slooffia	7-49 (98.9-92.1 %)	102-159 (85.1-76.9 %)
Spencerozyma	4-42 (99.3-93.0 %)	59-254 (91.7-67.5 %)
Sporobolomyces	5-49 (100.0-91.9 %)	3-94 (99.8–83.7 %)

distinguished by physiological properties (Sampaio 2011a) and on the basis of DNA-DNA hybridisation experiments (Kurtzman & Fell 1991). Recently, a MLS approach combining with the analysis of genes comprising mating locus was used to delimit species in the *Papiliotrema flavescens*/*Papiliotrema terrestris* species complex (Yurkov *et al.* 2015a), *Cryptococcus gattii*/*Cryptococcus neoformans* species complex (Hagen *et al.* 2015) and *Cryptococcus amylolentus* species complex (Passer *et al.* 2019), all of which showed less than 1 % ITS and D1/D2 sequences divergence (Tables S2. 24 and S2.34). Thus, it is important to keep in mind that delimitation of closely related species which have less than 1 % sequence heterogeneity in both D1/D2 and ITS regions requires additional analyses and more robust data such as detailed physiological characterisation, mating experiments, multi-locus analyses and even whole-genome comparisons. Delimitation of closely related species in

genera with a few known species is, thus, extremely difficult in spite of the lack of data for analyses.

New taxa delineation and phylogenetic placement

The sequences of the D1/D2 and ITS regions for the 199 strains (Table 1) including 11 isolates from Germany deposited in the China General Microbiological Culture Collection Center (CGMCC) and 16 strains from Japan, Thailand, Portugal, Italy, USA, DSMZ and CBS collections employed in this study were determined. The SSU region of 138 strains representing at least one strain of each potentially new species were sequenced. A total of 142 RPB1, 137 RPB2, 126 TEF1 and 126 CYTB new sequences were generated (Table 1). The D1/D2 and ITS sequences for each strain were blasted against the GenBank database using the BLASTn tool to search for their closely related described species. Sequences of their close relatives and other phylogenetic important taxa were retrieved from GenBank (Table S3). In order to show the phylogenetic positions of these undescribed strains, multi-loci phylogenetic trees were constructed from two datasets, the combined 5.8 S, D1/D2 and SSU dataset and the combined 5.8S, D1/D2, SSU, RPB1, RPB2, TEF1 and CYTB dataset. The phylogenetic trees (Figs 2, 4 and S1, S2) drawn from the seven-genes and three rDNA datasets were used to determine the phylogenetic positions for each new species. The trees (Figs 3, 5) constructed from the D1/D2 dataset were used to calculate the similarity between the new species and their closely related described species as the D1/D2 sequences are available for all known species employed here, which is not the case for the ITS and SSU sequences.

One hundred and seven new species were delimitated from the 199 strains using the species identification benchmarks suggested by Fell *et al.* (2000), Scorzetti *et al.* (2002), Kurtzman & Fell (2006), Kurtzman (2014, 2015) and Kurtzman *et al.* (2015) as well as the taxonomic thresholds of yeast species recommended by Vu *et al.* (2016) and phenotypical features (Kurtzman *et al.* 2011). Forty-three new species occur in 15 genera in the *Tremellomycetes* (*Agaricomycotina*) and 52 new species distribute in 20 genera in the *Pucciniomycotina* (Figs 2–6 and S1–S6, Table 1). However, none of these known genera appears as an obvious candidate to accommodate the other 12 new species. Therefore, eight new genera, named as *Begerowomyces*, *Boekhoutia*, *Meniscomyces*, *Pseudosterigmatospora*, *Robertozyma*, *Rosettozyma*, *Sterigmatospora* and *Teunia*, are proposed to accommodate these 12 species.

The novel genus *Teunia*, located in the *Cryptococcaceae* (*Tremellales*, *Tremellomycetes*, *Agaricomycotina*), was clustered with the genera *Cryptococcus* and *Kwoniella* with 96–100 % bootstrap and 1.0 posterior probability supports in seven-genes and rDNA phylogeny (Figs 2A and S1A). However, those three genera can be separated by the clustering optimisation analysis (Table S4). Three species, namely *Cryptococcus cuniculi*, *Fonsecazyma tronadorensis* and *Fonsecazyma betulae*, were classified in this new genus (Figs 2C, 3G and S1C). The phylogenetic position and composition of this clade have been changing during the last decade. The oldest known species *Cr. cuniculi* has affinity with the erroneously identified as *Cryptococcus heveanensis* strain CBS 8976 in the *Kwoniella* clade that was described by Shin *et al.* (2006). Later, Boekhout *et al.* (2011), de Garcia *et al.* (2012) and Weiss *et al.* (2014) also indicated that *Cr. cuniculi* belonged to the *Kwoniella* clade. de Garcia *et al.* (2012) described another species *Cryptococcus tronadorensis* in this clade resolved in a LSU-based phylogenetic analysis. However, a constrained with the seven-genes topology LSU phylogenetic analysis performed by Liu *et al.* (2015b) showed that *Cr. cuniculi* was placed in the *Tremella* clade I (Millanes *et al.* 2011) and not close to the *Kwoniella* clade, so that this species left unclassified as *Cr. cuniculi* pro tem. It is important to document that the phylogenetic analysis was inconsistant with the previous results obtained by Shin *et al.* (2006), Boekhout *et al.* (2011), de Garcia *et al.* (2012) and Weiss *et al.* (2014) indicating that *Cr. cuniculi* was most likely a member of *Cryptococcaceae*. Furthermore, the two closely related species *Cr. cuniculi* and *Cr. tronadorensis* were placed in two different clades (Liu *et al.* 2015b). The latter species was clustered with a good support with *Cryptococcus mujuensis* and *Kwoniella betulae*. It is important to note that *K. betulae* was described as a species of the genus *Kwoniella* based on its close phylogenetic relatedness to the erroneously identified as *Cr. heveanensis* strain CBS 8976. Because *K. betulae* was not related to other species of *Kwoniella* and *Cr. mujuensis* and *Cr. tronadorensis* were distantly related to the genus *Cryptococcus*, a new genus *Fonsecazyma* was proposed to accommodate *Fo. mujuensis*, the type species of *Fonsecazyma*, *Fo. tronadorensis* and *Fo. betulae* (Liu *et al.* 2015b). The type species of *Fonsecazyma* was included in the seven-genes phylogeny as a single-species lineage closely related to *Sirobasidium intermedium* (Liu *et al.* 2015a) which was also in agreement with the original paper (Shin *et al.* 2006). This was one of a few important conflicts between constrained LSU and seven-genes analyses. The decision to propose a new genus for this clade was supported by the results of the constrained LSU analysis which also demonstrated that the *Fonsecazyma* clade contained three potential new species isolated but not described in earlier studies performed by Inácio (2003). It was important to name this clade so that provisionally named as "*Cryptococcus*" new species would be properly placed and not mistaken with either *Kwoniella* or *Cryptococcus* (Liu *et al.* 2015b).

The phylogenetic analyses of the three datasets in this study also supported that *Fo. mujuensis* has affinity with *Si. intermedium* instead of the *Kwoniella* clade (Figs 2A, 3A and S1A). *Fo. tronadorensis* was originally described as *Cr. tronadorensis* and related to the *Kwoniella* clade (de Garcia *et al.* 2012). *Fo. betulae* was originally described as *K. betulae* (Sylvester *et al.* 2015). The analyses in this study showed that *Fo. tronadorensis*, *Fo. betulae*, *Cr. cuniculi* and three newly described species formed a well supported clade closely related to *Cryptococcus* and *Kwoniella,* but still separated from them (Figs 2C, 3G and S1C), which is in agreement with the results of de Garcia *et al.* (2012) and Sylvester *et al.* (2015). The question is why *Fo. tronadorensis* and *Fo. betulae* clustered with *Fo. mujuensis* instead of *Cr. cuniculi* in the D1/D2 tree from Liu *et al.* (2015b). After double-checking the D1/D2 alignment used in Liu *et al.* (2015b), we found out that the D1/D2 sequences of *Fo. mujuensis* and *Cr. cuniculi* were swapped with each other. We also checked the placement of other species in the D1/D2 tree from Liu *et al.* (2015b). We have not found other mistakes in that tree, which indicated that the D1/D2 dataset is reliable except for the sequence swap between *Fo. mujuensis* and *Cr. cuniculi*. Therefore, *Fo. tronadorensis*, *Fo. betulae* and *Cr. cuniculi* were combined or validated in the new genus *Teunia* in this study (see Taxonomy section).

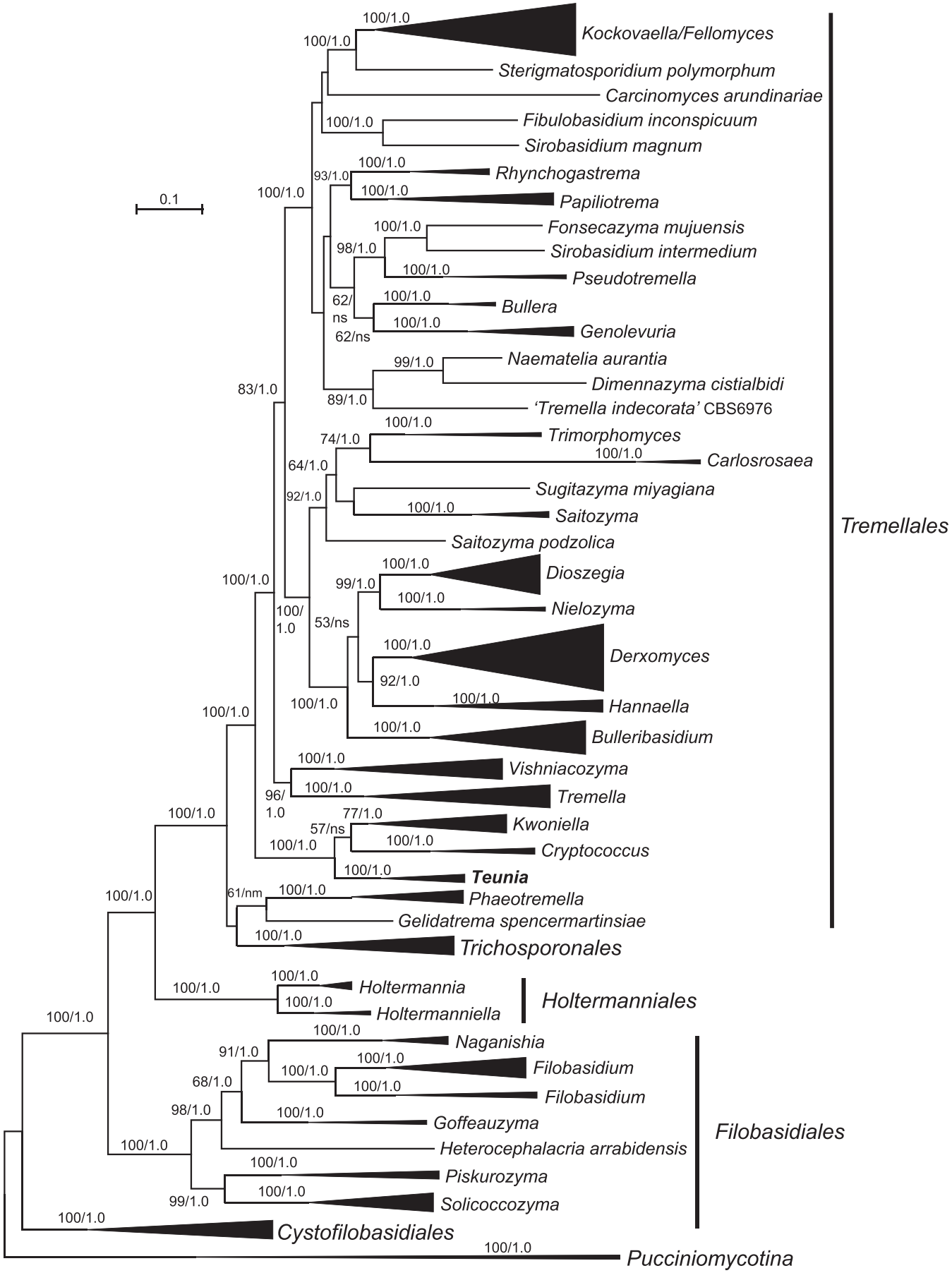
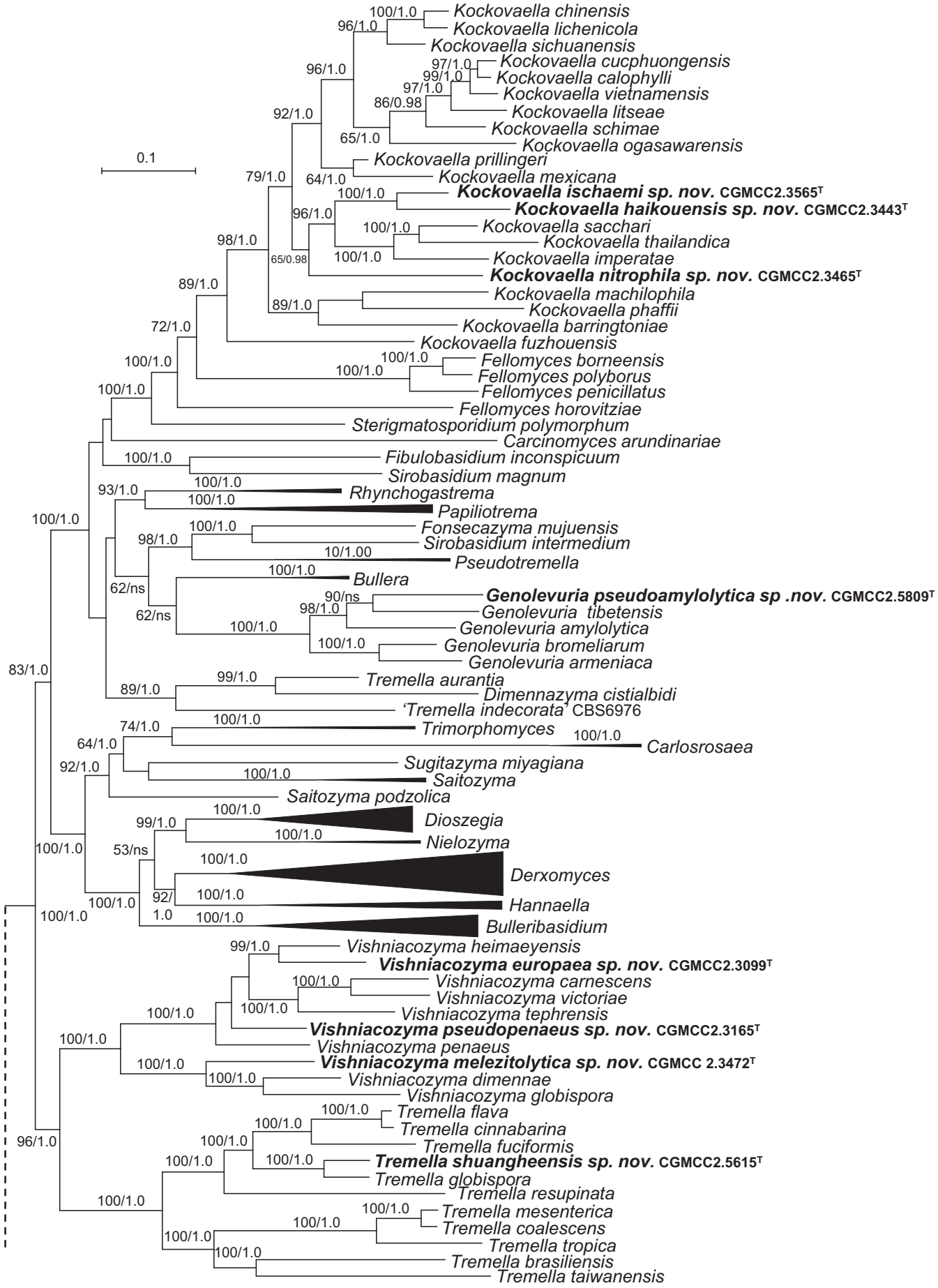


Fig. 2. Phylogenetic tree inferred using the combined sequences of RPB1, RPB2, TEF1, CYTB, SSU rDNA, LSU rDNA D1/D2 domains and 5.8S rDNA, depicting the phylogenetic positions of new taxa (in bold) within *Tremellomycetes* (*Agaricomycotina*). The tree backbone was constructed using maximum likelihood analysis. Bootstrap percentages of maximum likelihood analysis over 50 % from 1 000 bootstrap replicates and posterior probabilities of Bayesian inference above 0.9 are shown respectively from left to right on the deep and major branches. Bar = 0.05 substitutions per nucleotide position. Note: ns, not supported (BP < 50 % or PP < 0.9); nm, not monophyletic. The new taxa are in bold.



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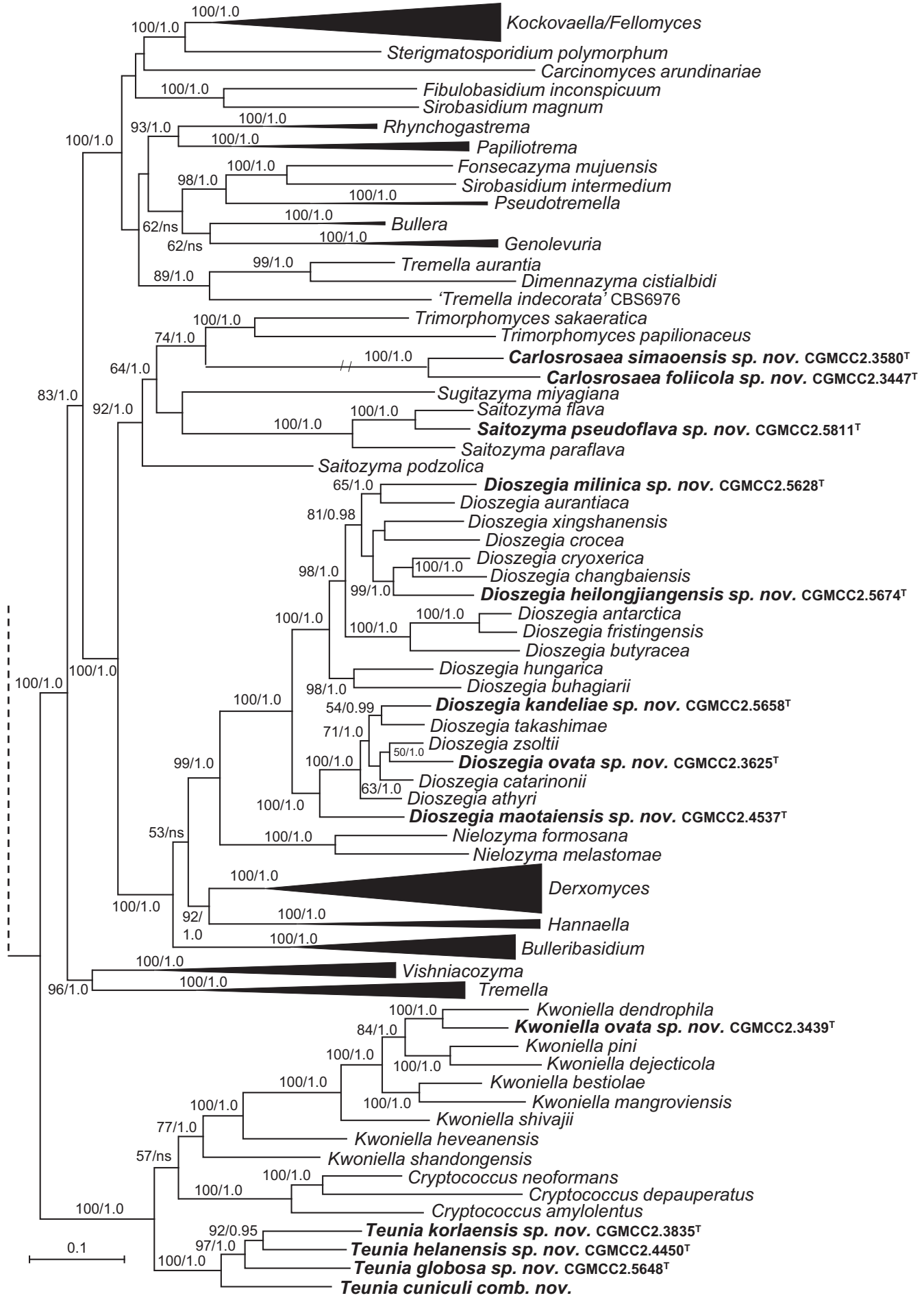

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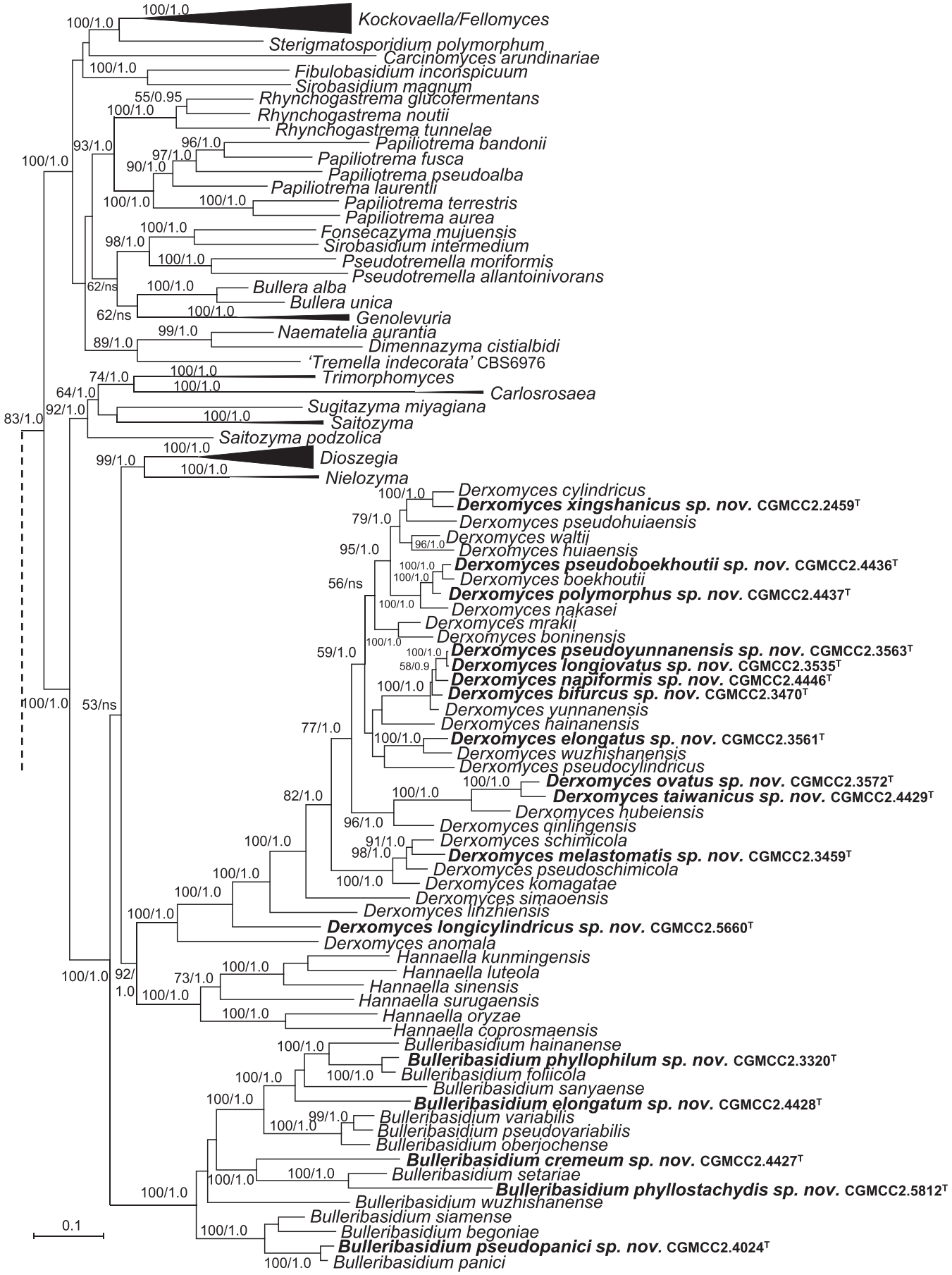

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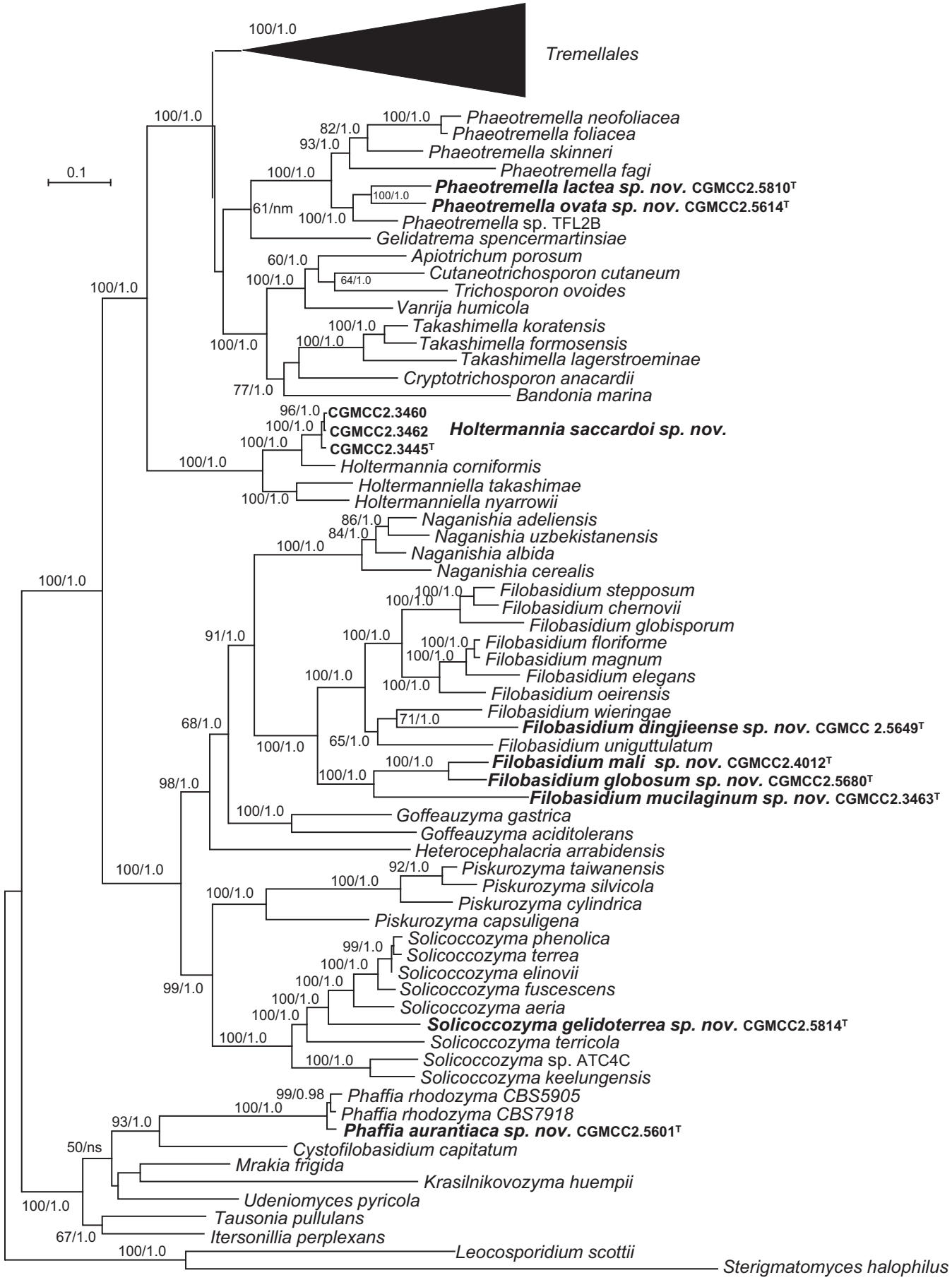

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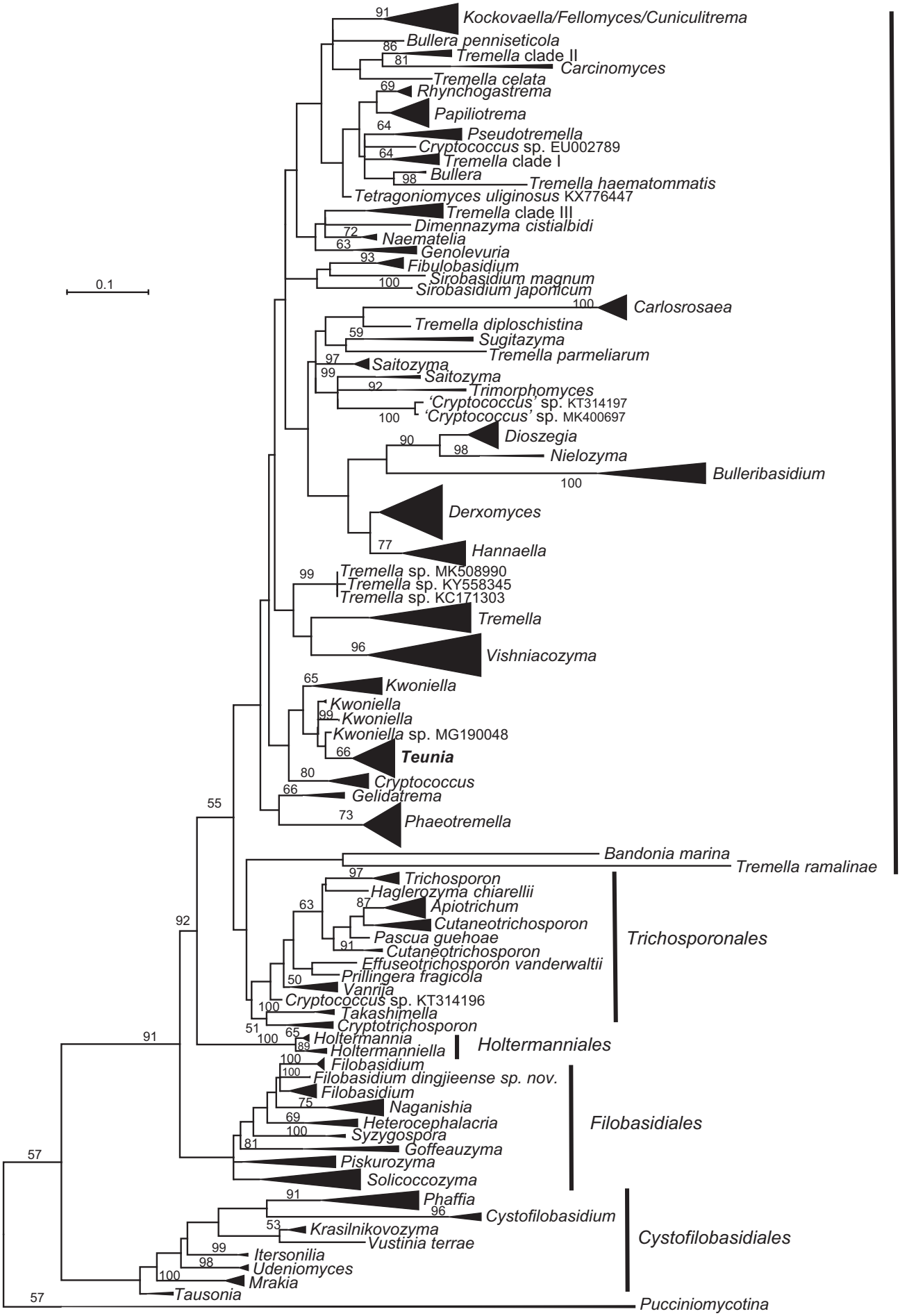
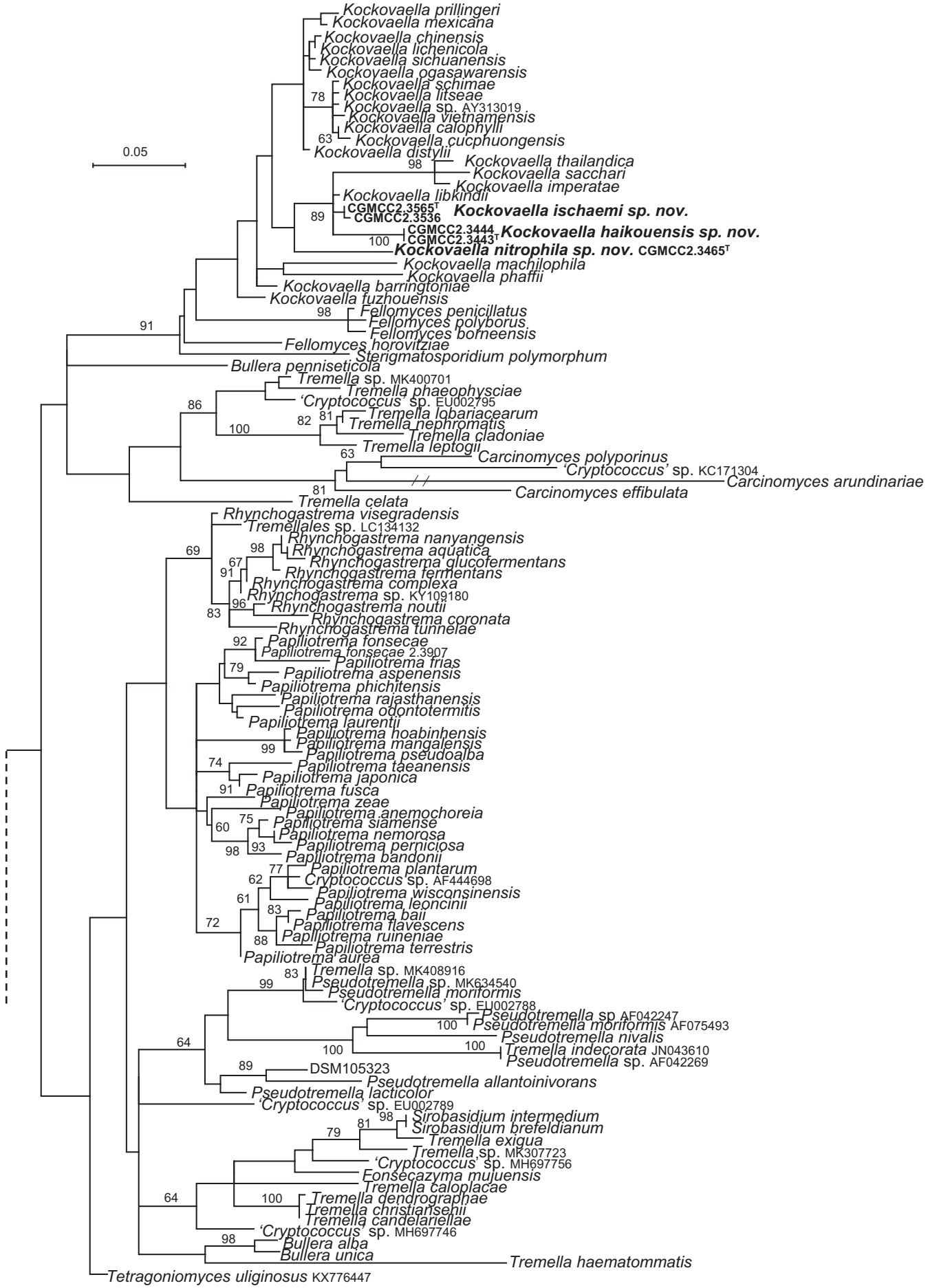


Fig. 3. Phylogeny of new yeast species in the *Tremellomycetes* (*Agaricomycotina*) inferred from the sequences of the LSU rDNA D1/D2 domains by maximum likelihood analysis and over 50 % from 1 000 bootstrap replicates is shown. Tree topology was backbone-constrained with the well-supported (>80 %) bipartitions of the topology of the seven-genes tree. Bar = 0.1 substitutions per nucleotide position.



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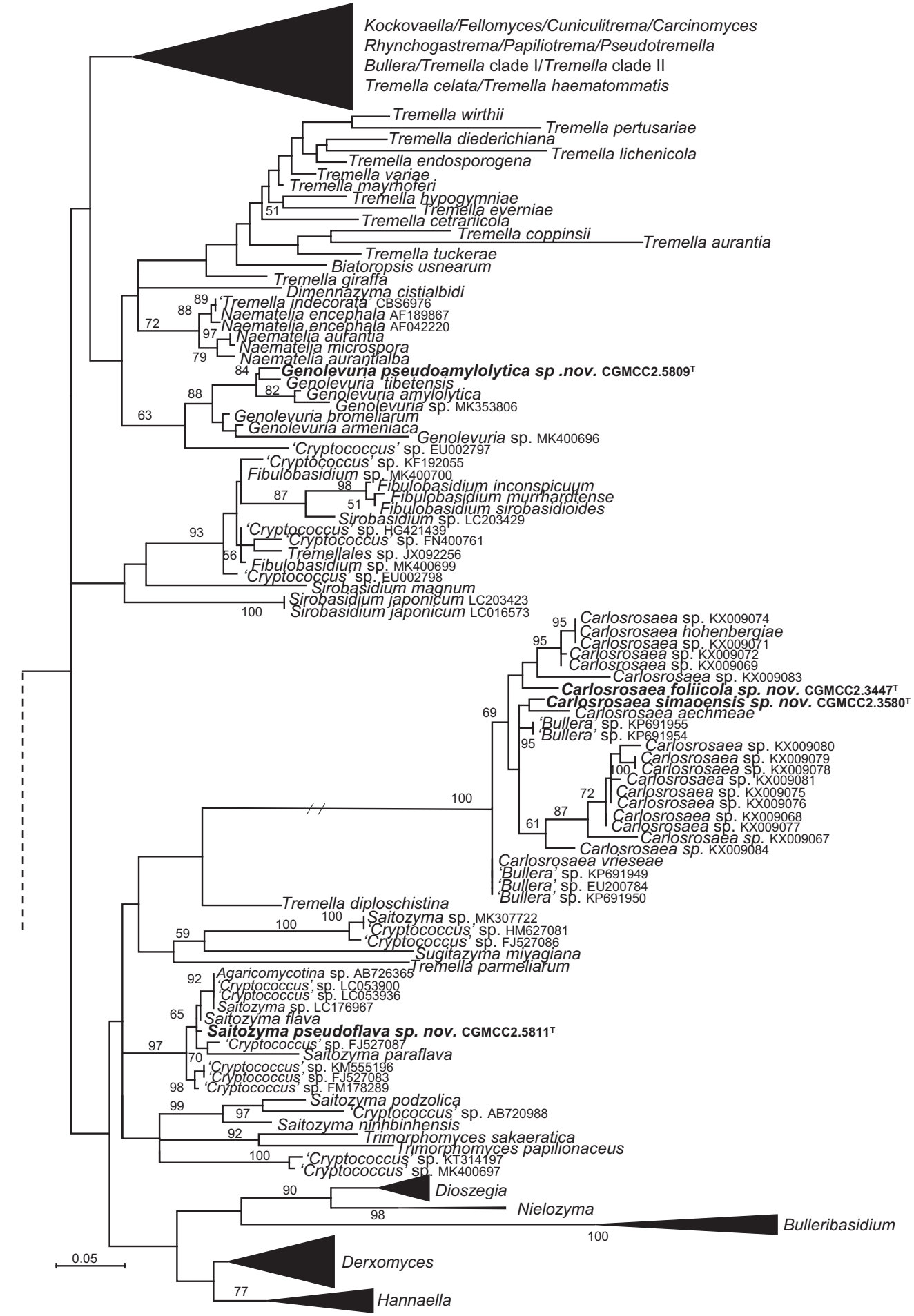

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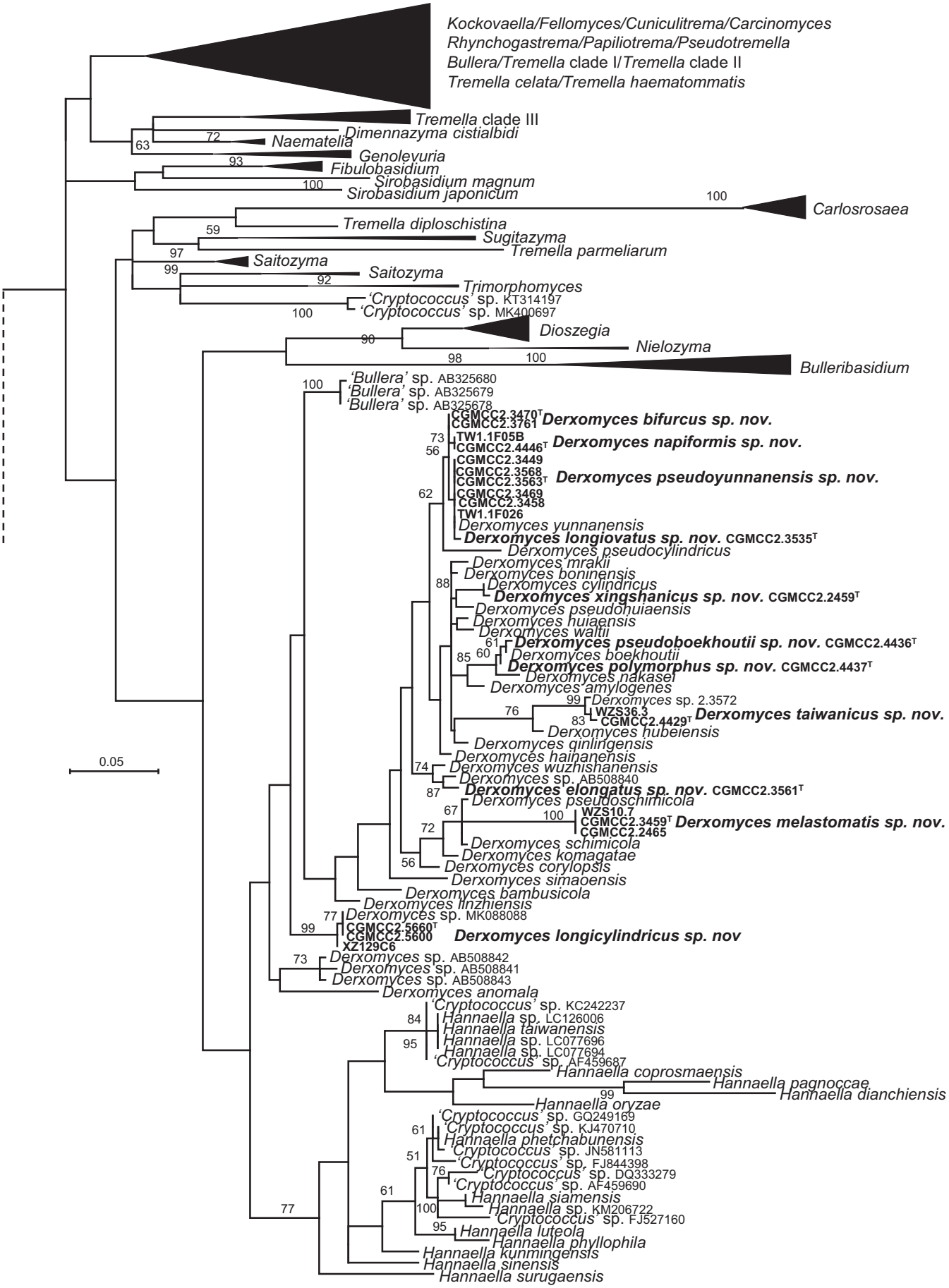

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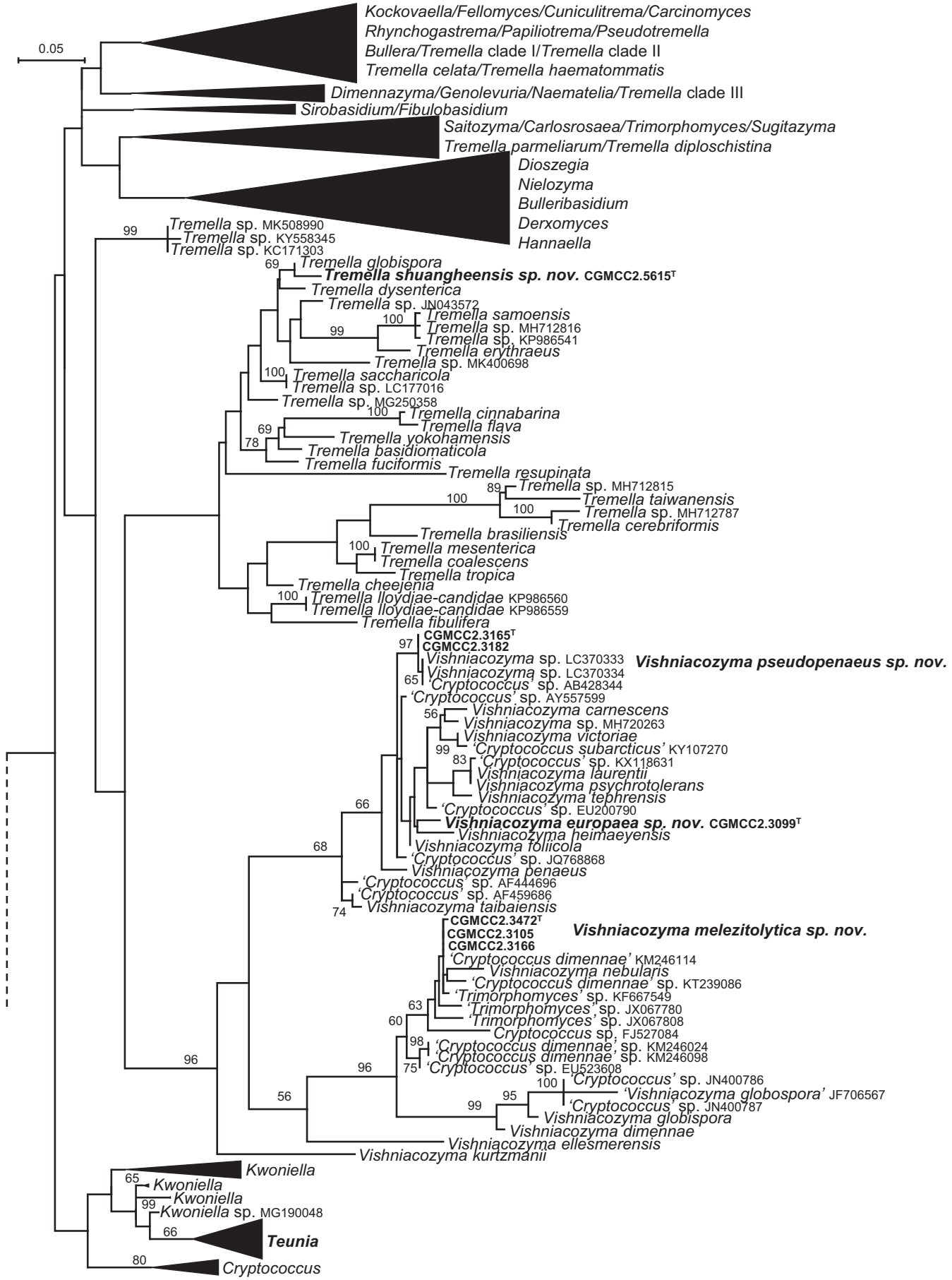

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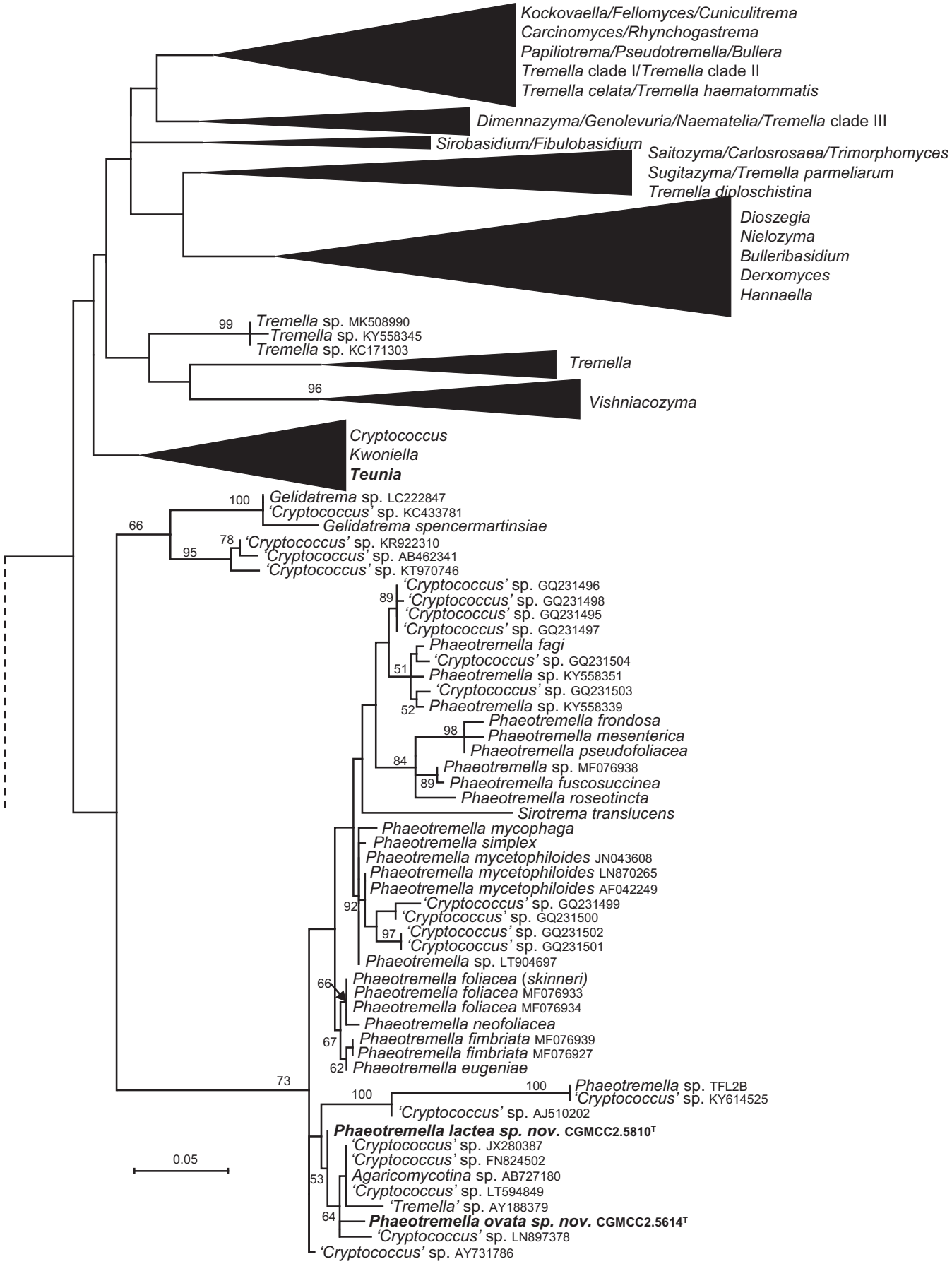

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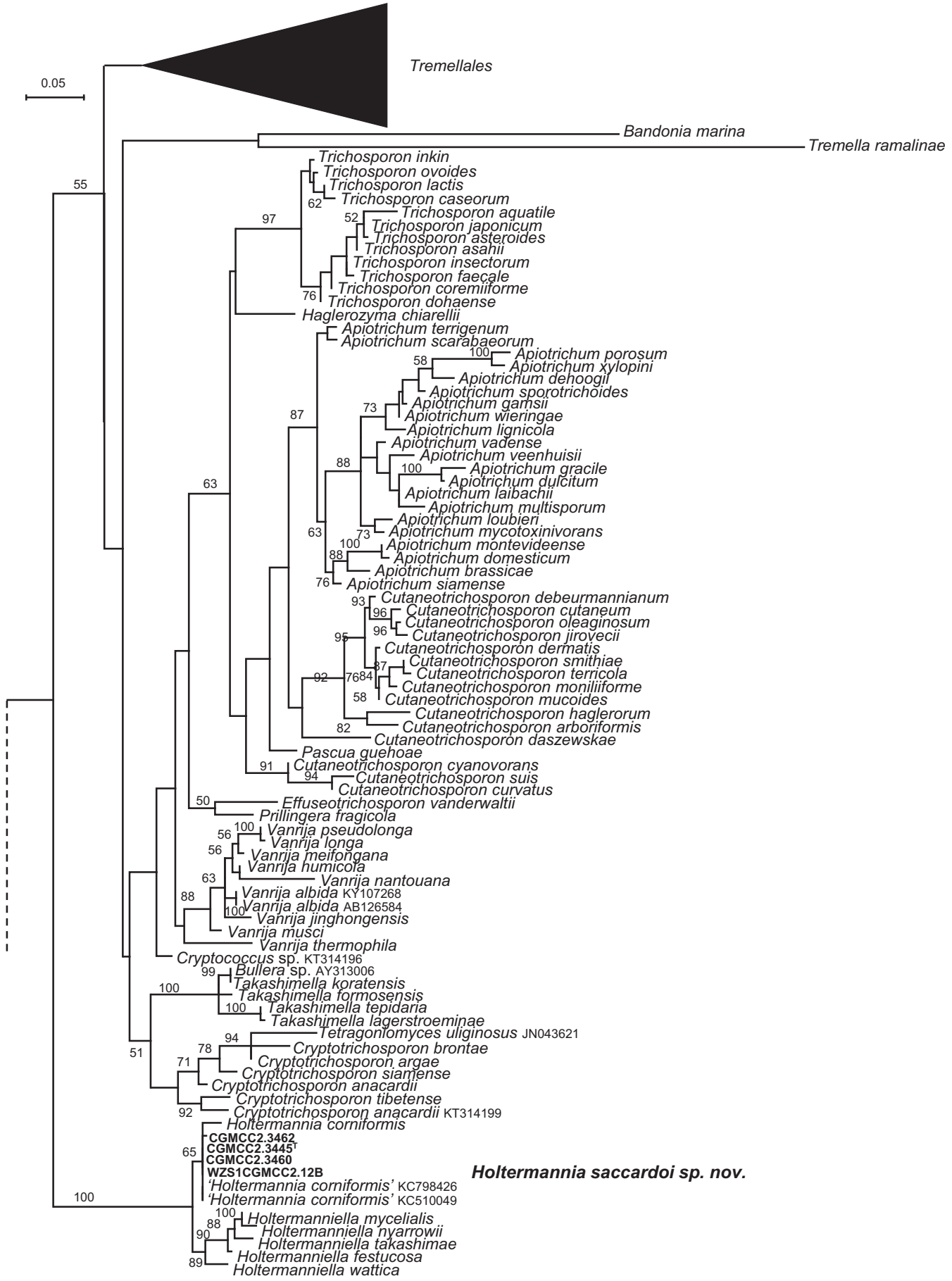

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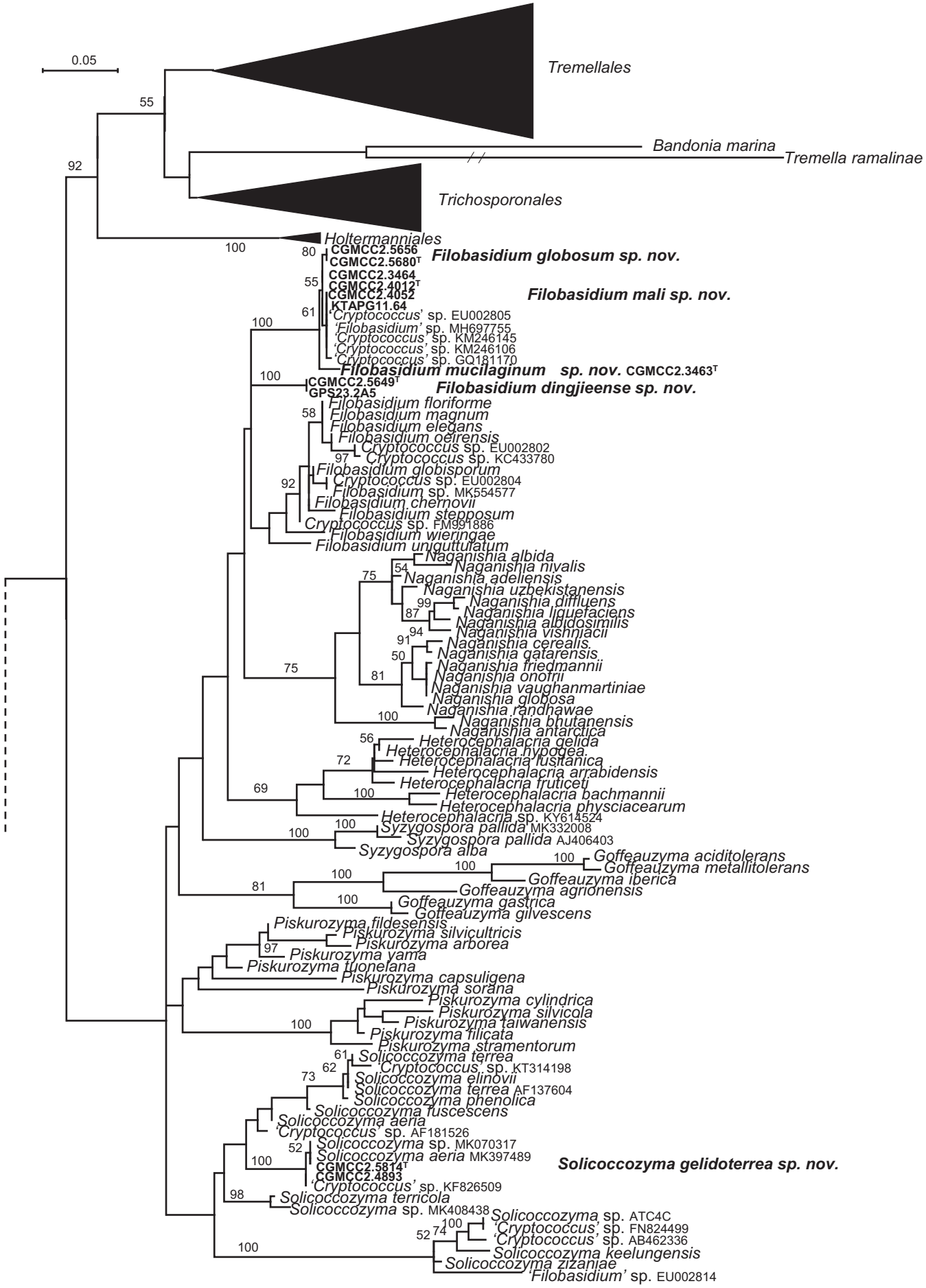

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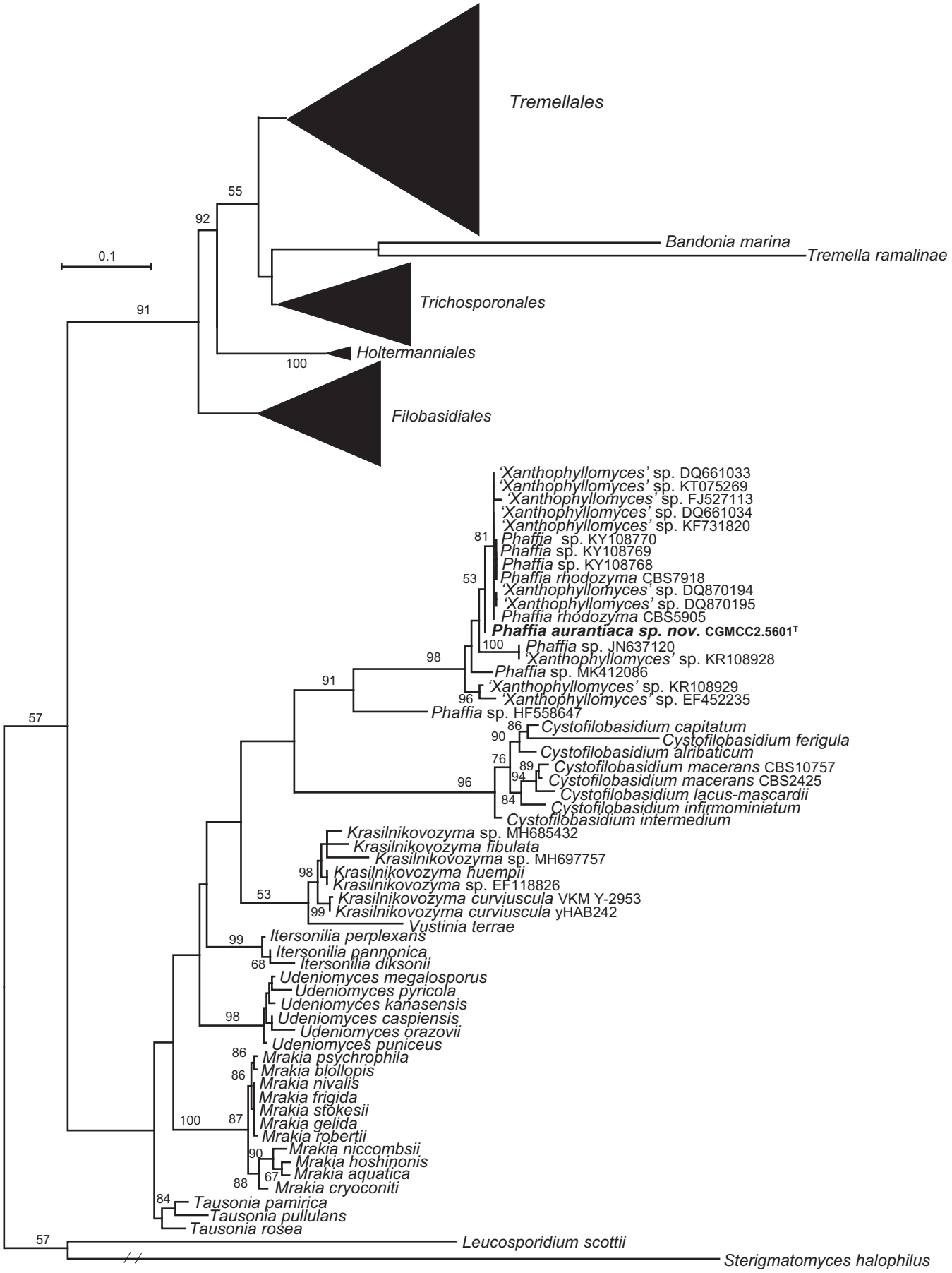


Fig. 3. (Continued).

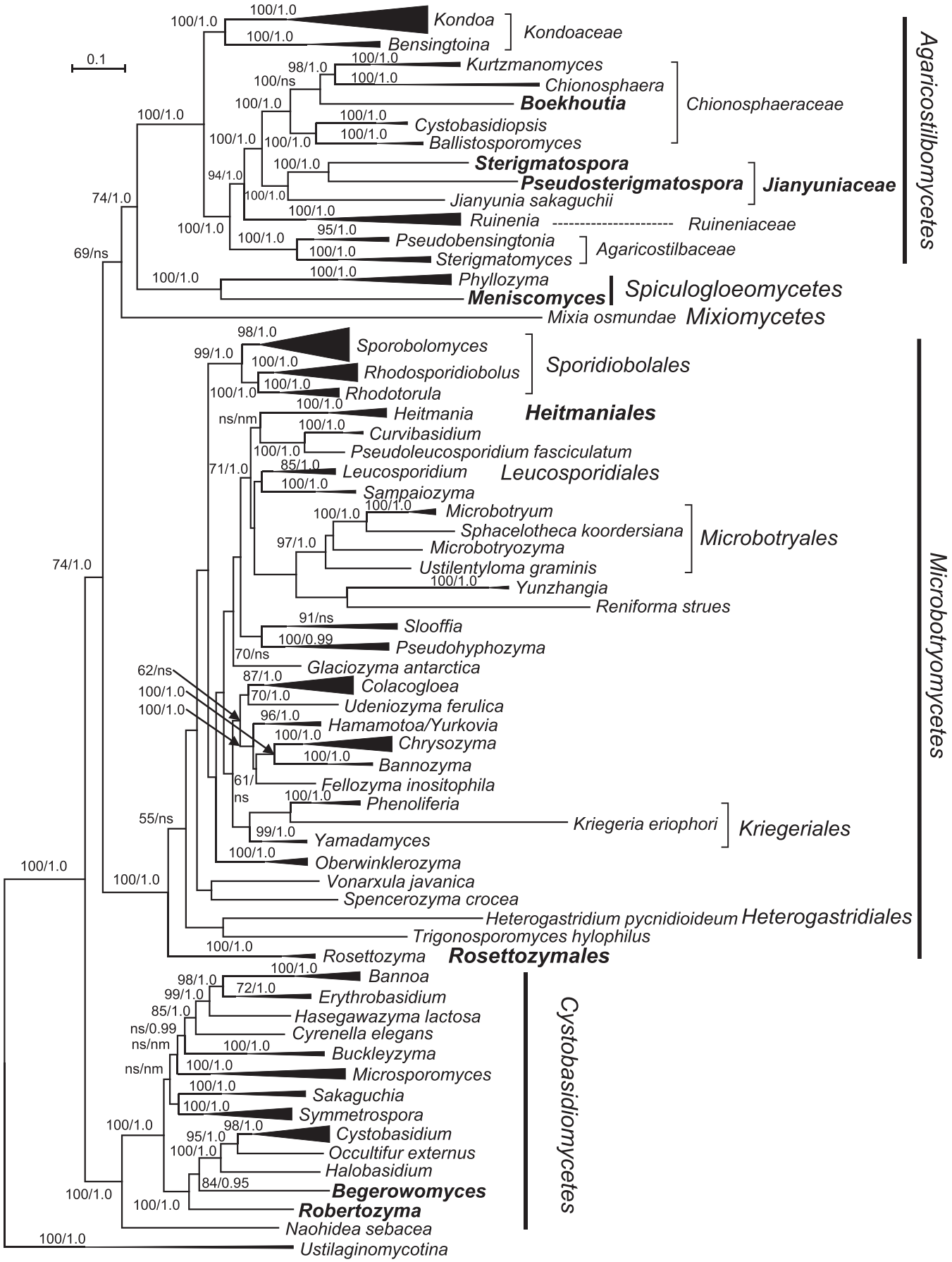


Fig. 4. Phylogenetic tree inferred using the combined sequences of RPB1, RPB2, TEF1, CYTB, SSU rDNA, LSU rDNA D1/D2 domains and 5.8S rDNA, depicting the phylogenetic positions of new taxa (in bold) within *Pucciniomycotina*. The tree backbone was constructed using maximum likelihood analysis. Bootstrap percentages of maximum likelihood analysis over 50 % from 1 000 bootstrap replicates and posterior probabilities of Bayesian inference above 0.9 are shown respectively from left to right on the deep and major branches. Bar = 0.2 substitutions per nucleotide position. Note: ns, not supported (BP < 50 % or PP < 0.9); nm, not monophyletic. The new taxa are in bold.

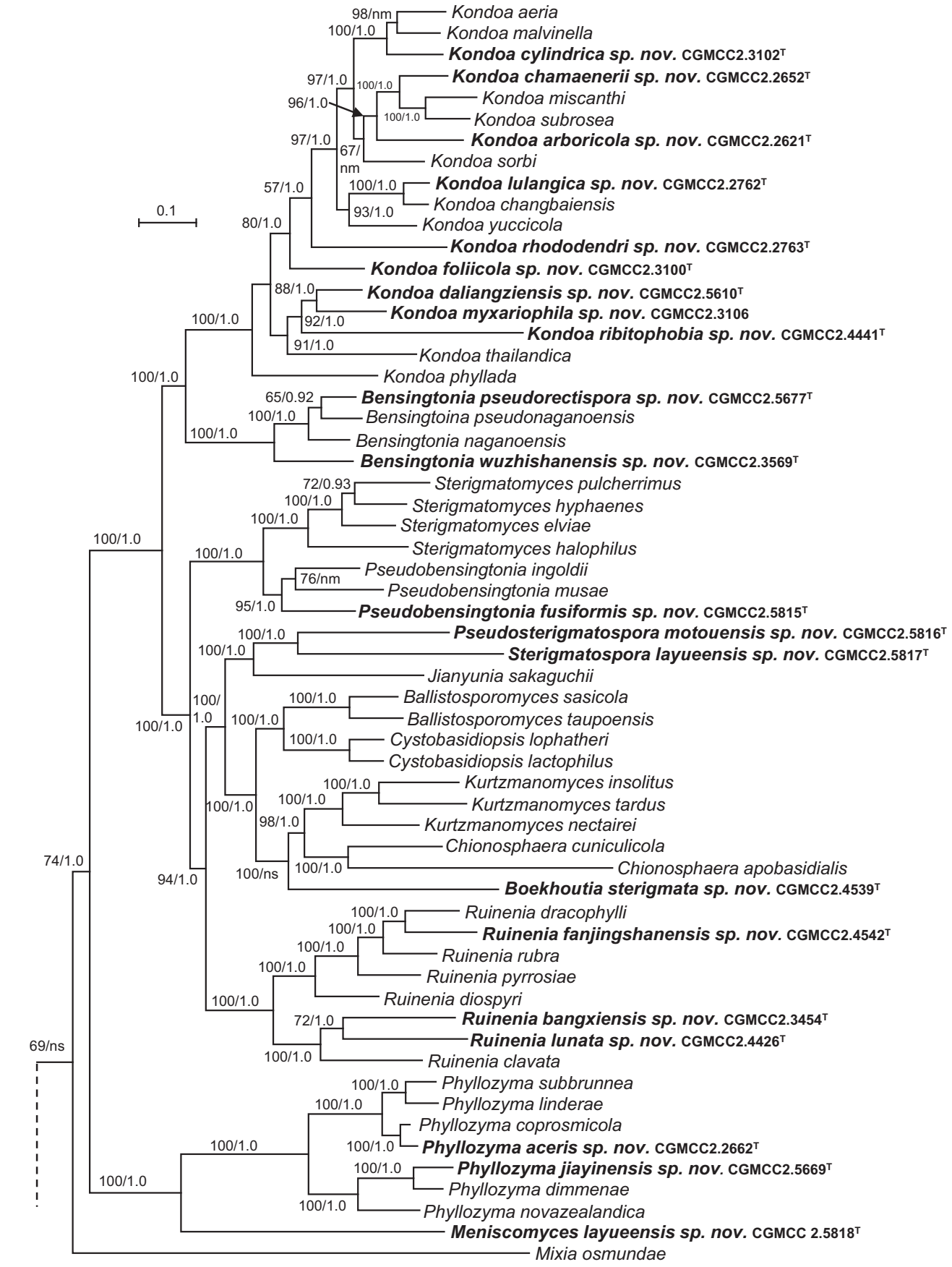


Fig. 4. (Continued).

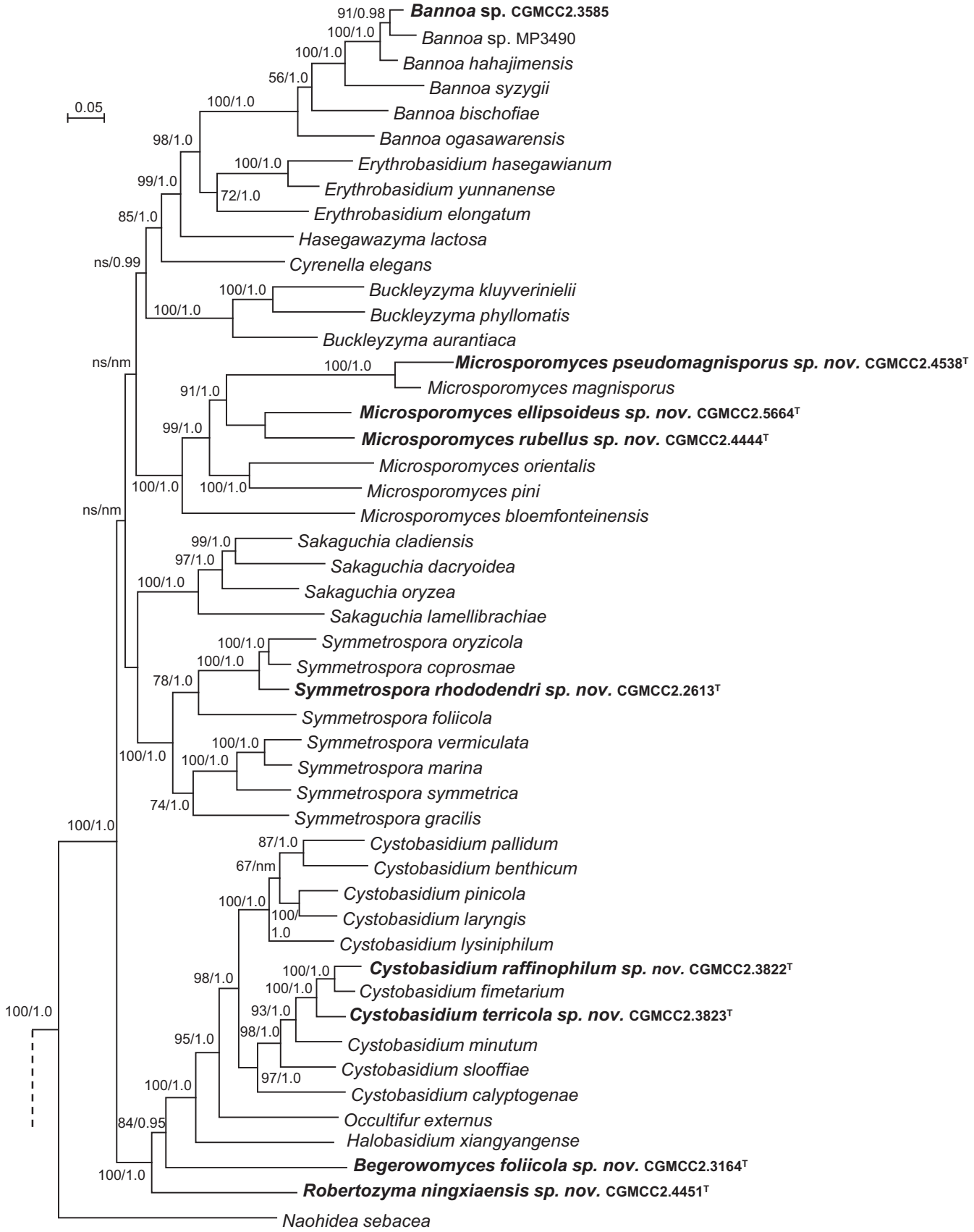


Fig. 4. (Continued).

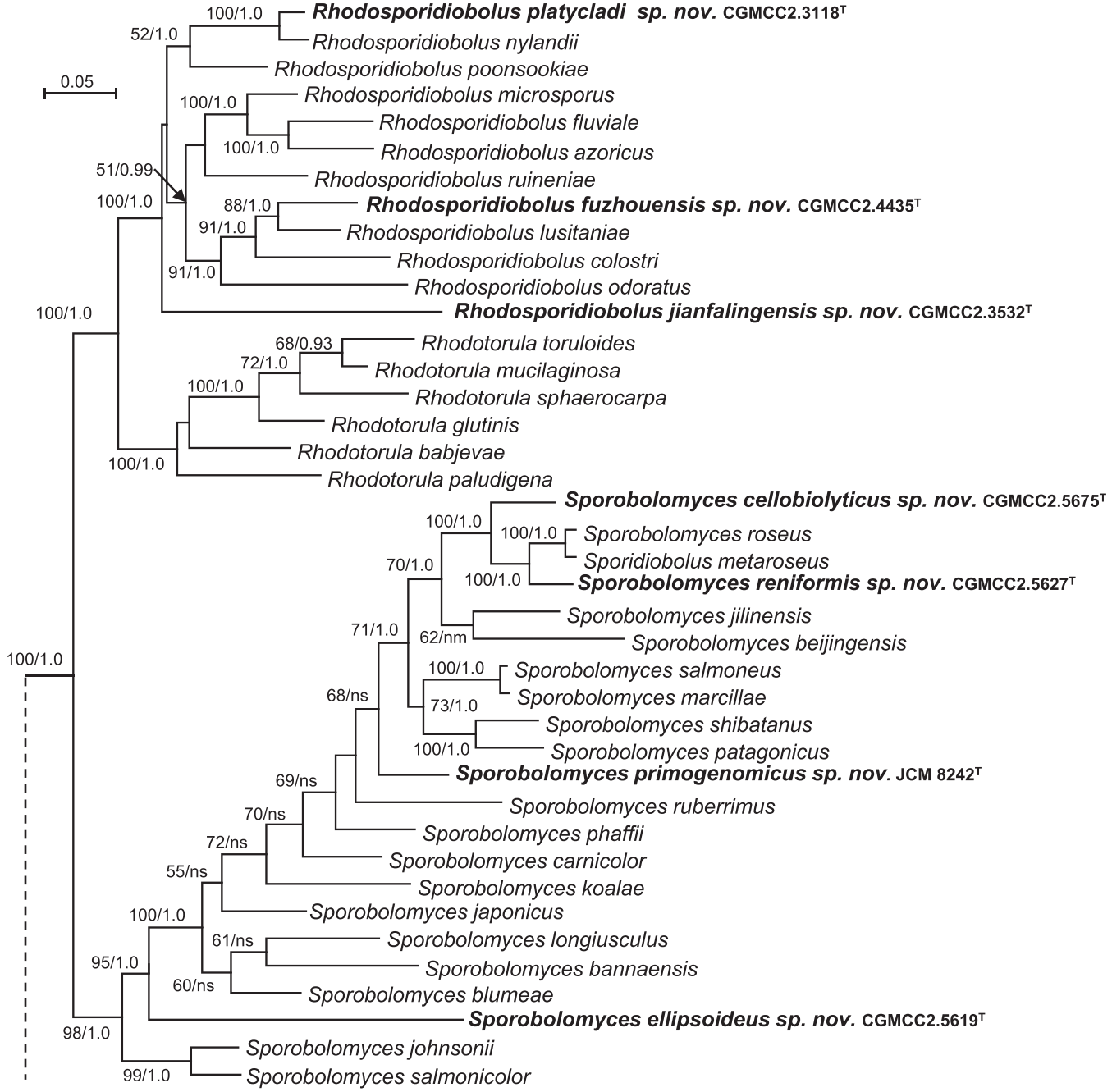


Fig. 4. (Continued).

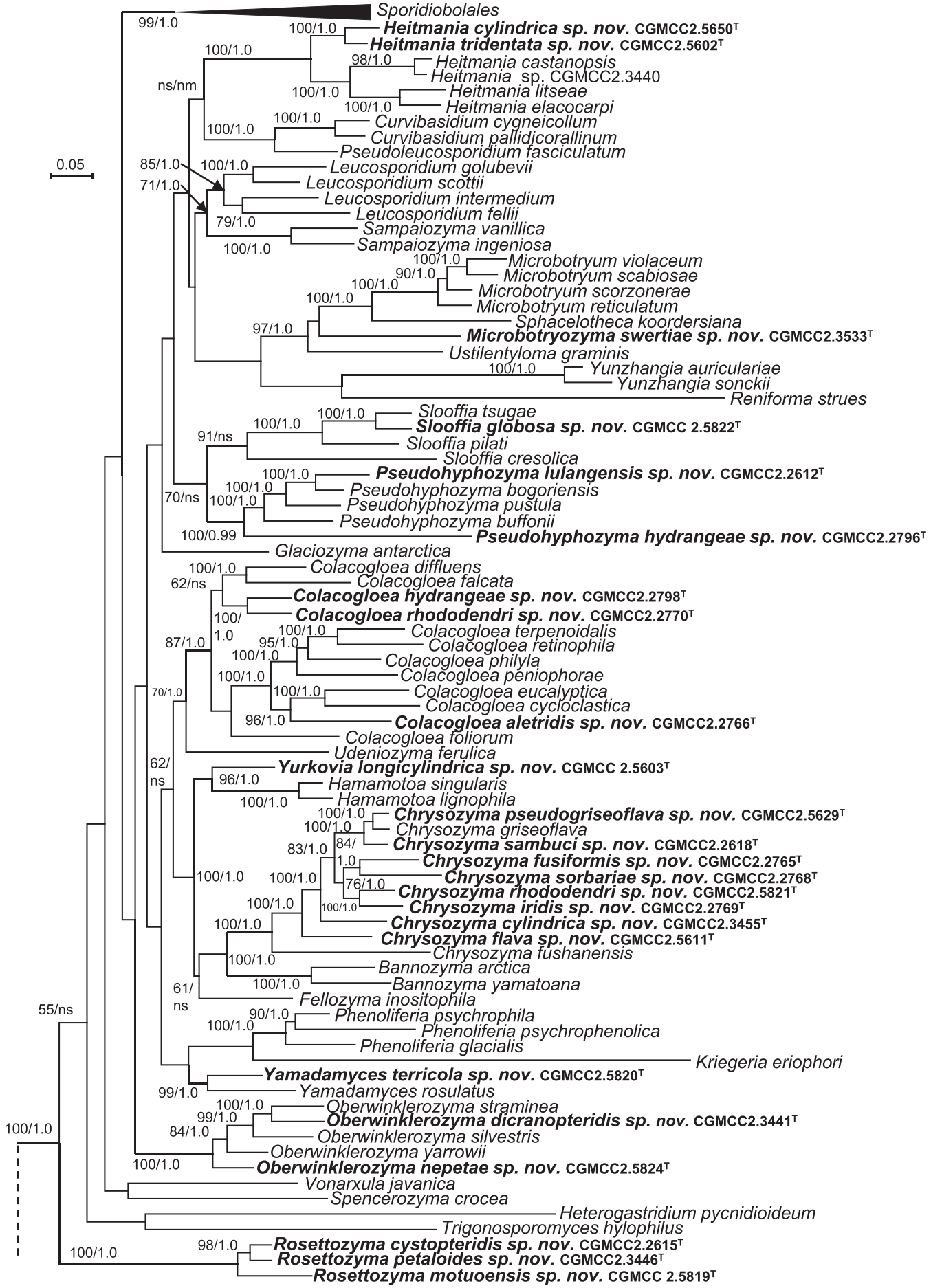


Fig. 4. (Continued).

Fig. 5. Phylogeny of new yeast species in the *Pucciniomycotina* inferred from the sequences of the LSU rDNA D1/D2 domains by maximum likelihood analysis and over 50 % from 1 000 bootstrap replicates is shown. Tree topology was backbone-constrained with the well-supported (>80 %) bipartitions of the topology of the seven-genes tree. Bar = 0.1 substitutions per nucleotide position.

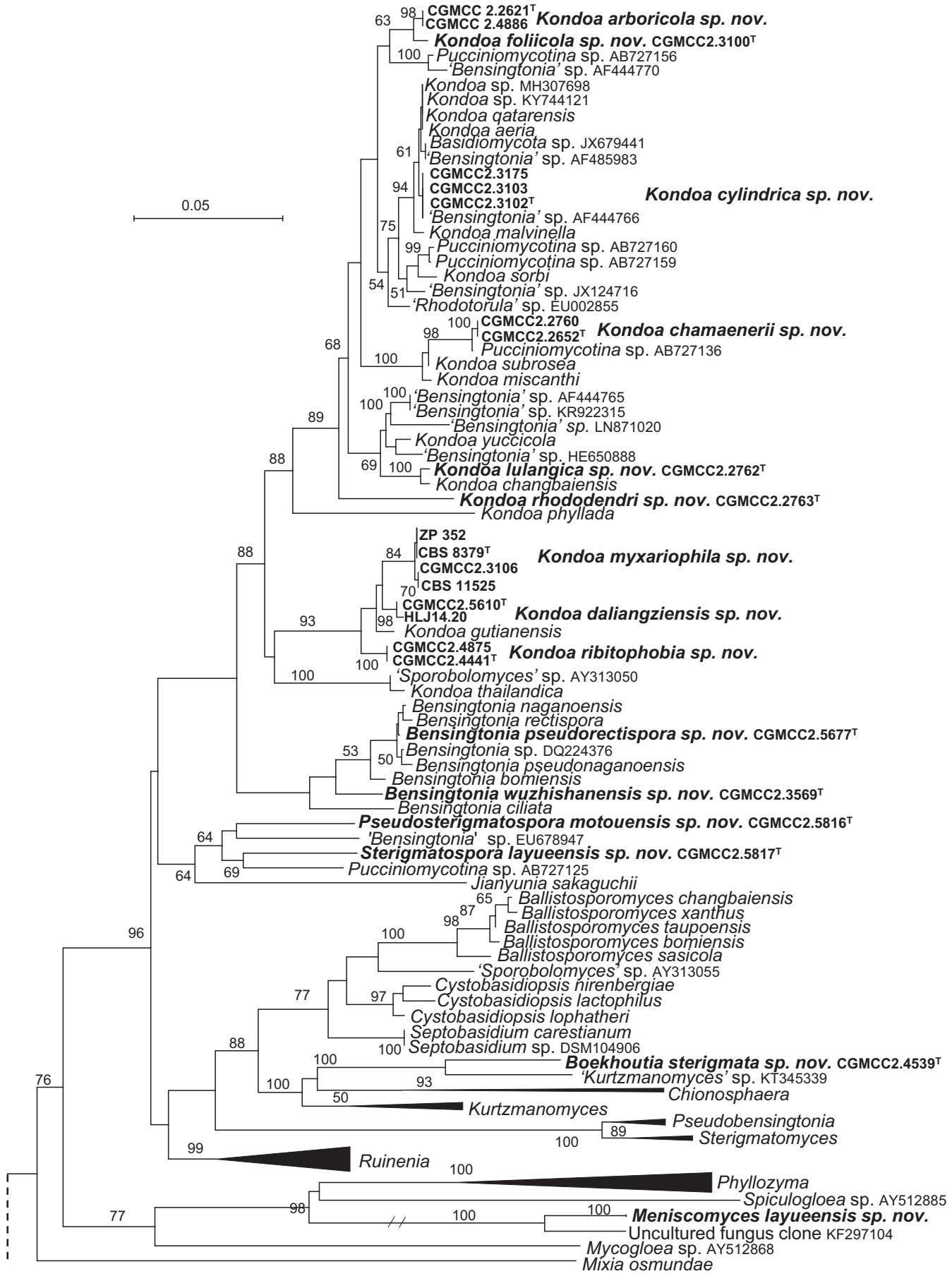


Fig. 5. (Continued).

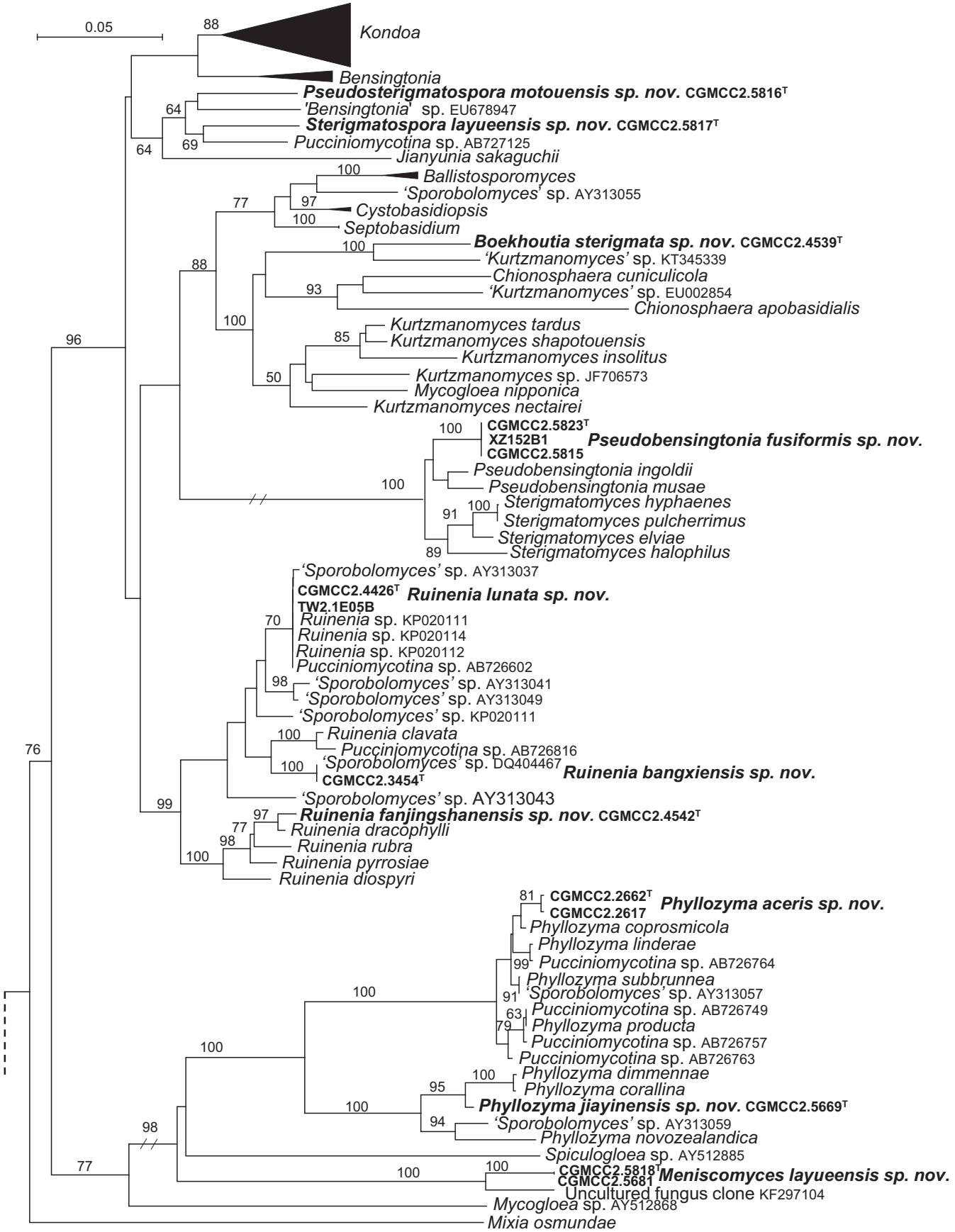


Fig. 5. (Continued).

Fig. 5. (Continued).

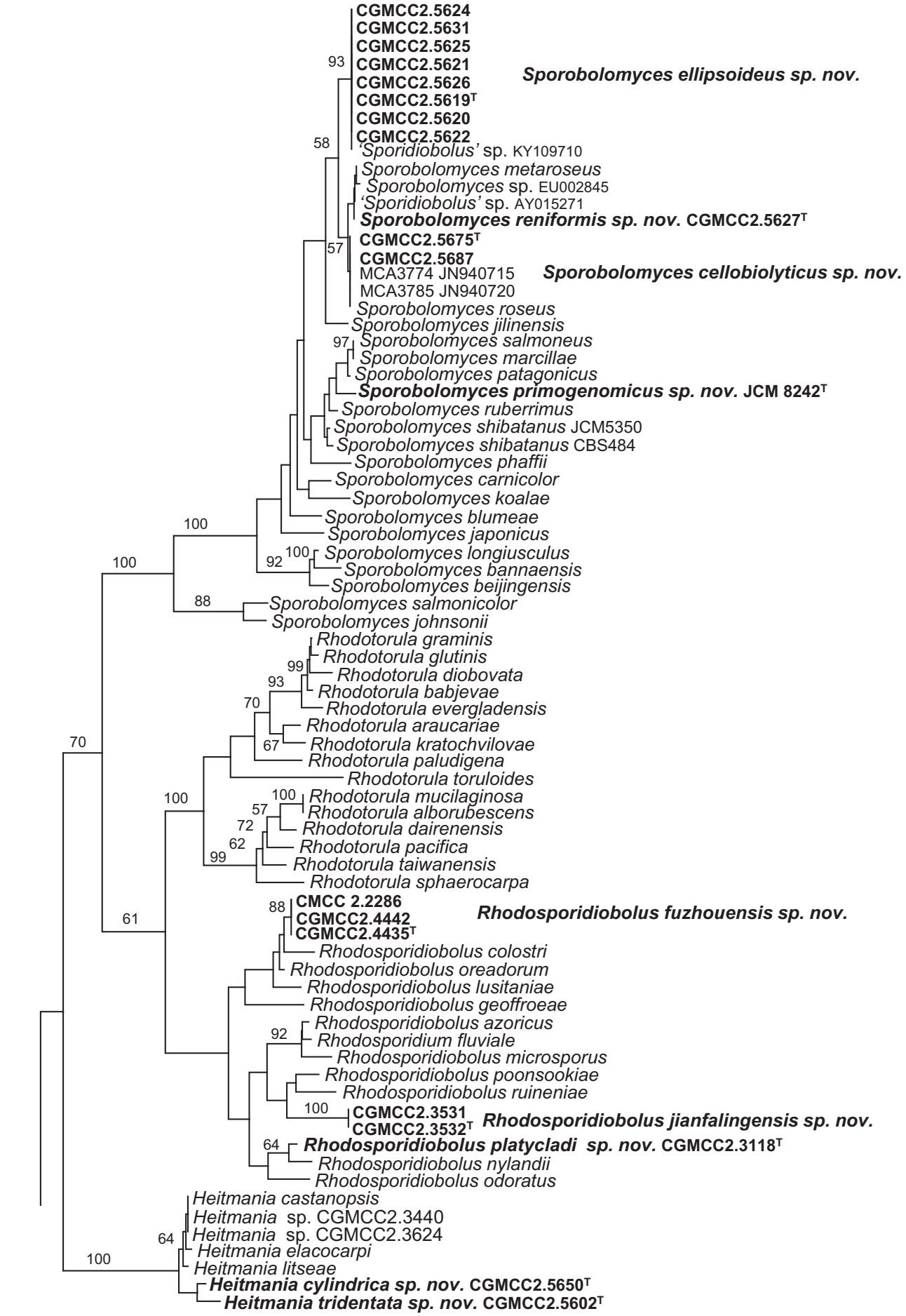


Fig. 5. (Continued).

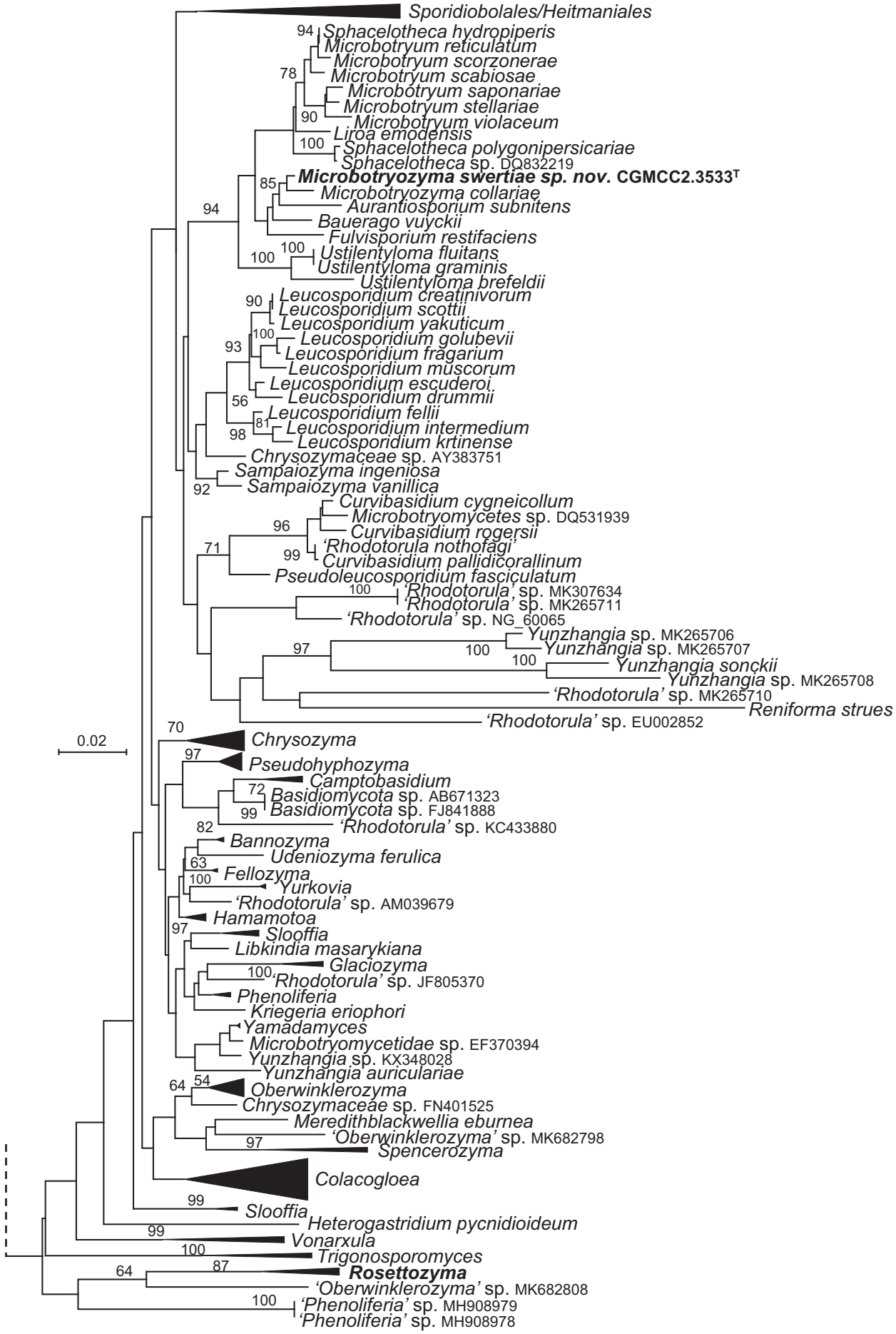


Fig. 5. (Continued).

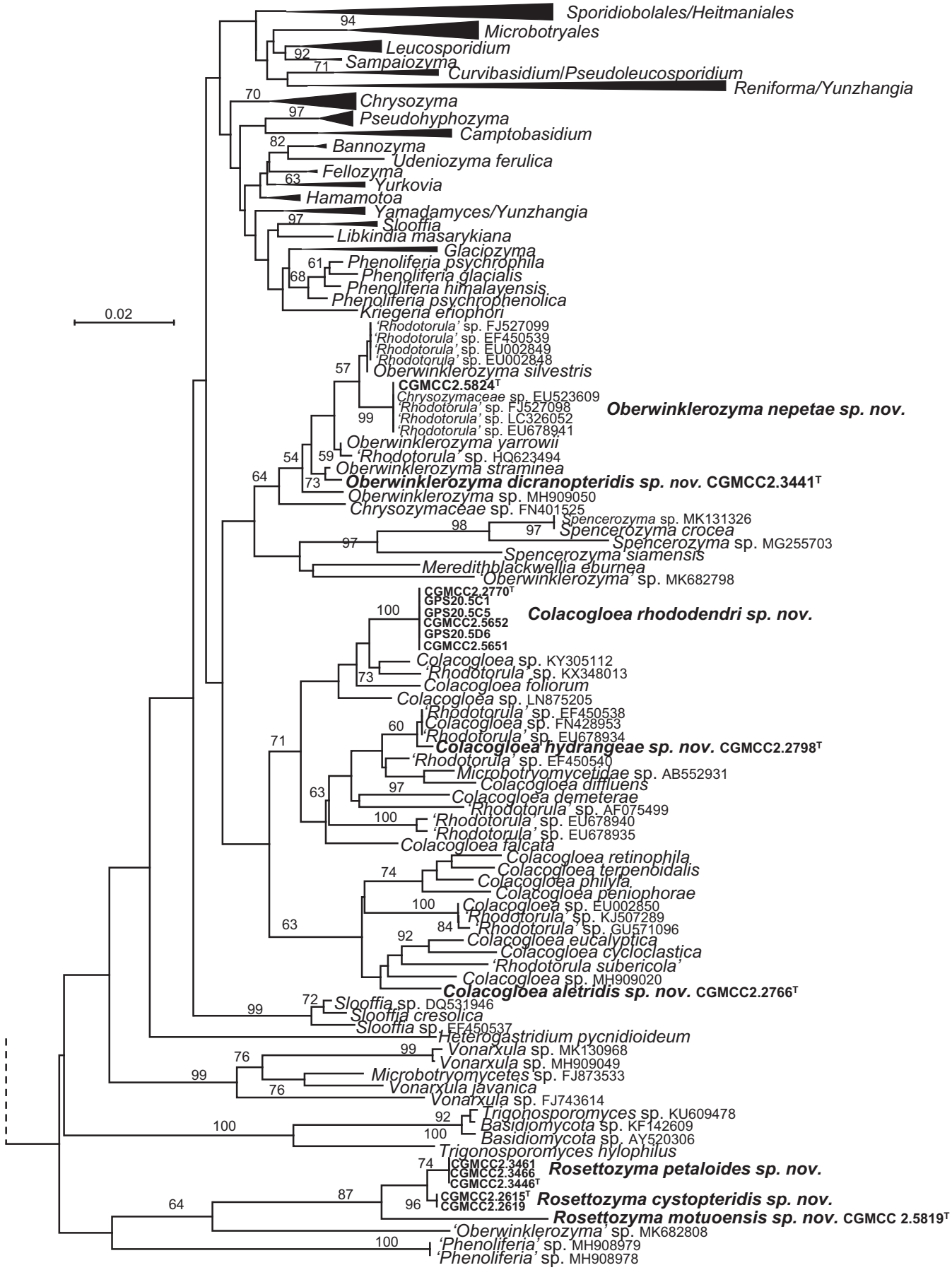


Fig. 5. (Continued).

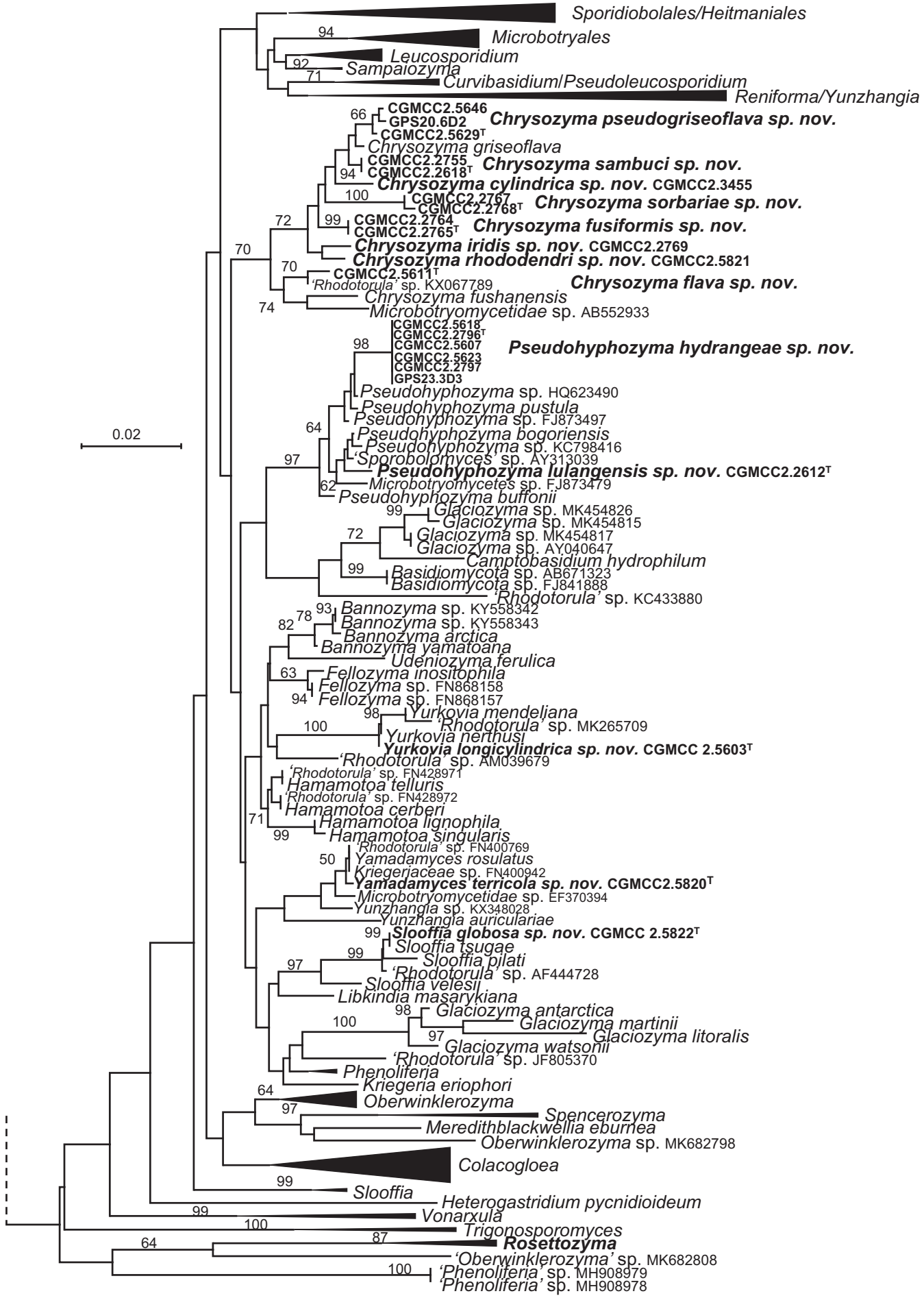


Fig. 5. (Continued).

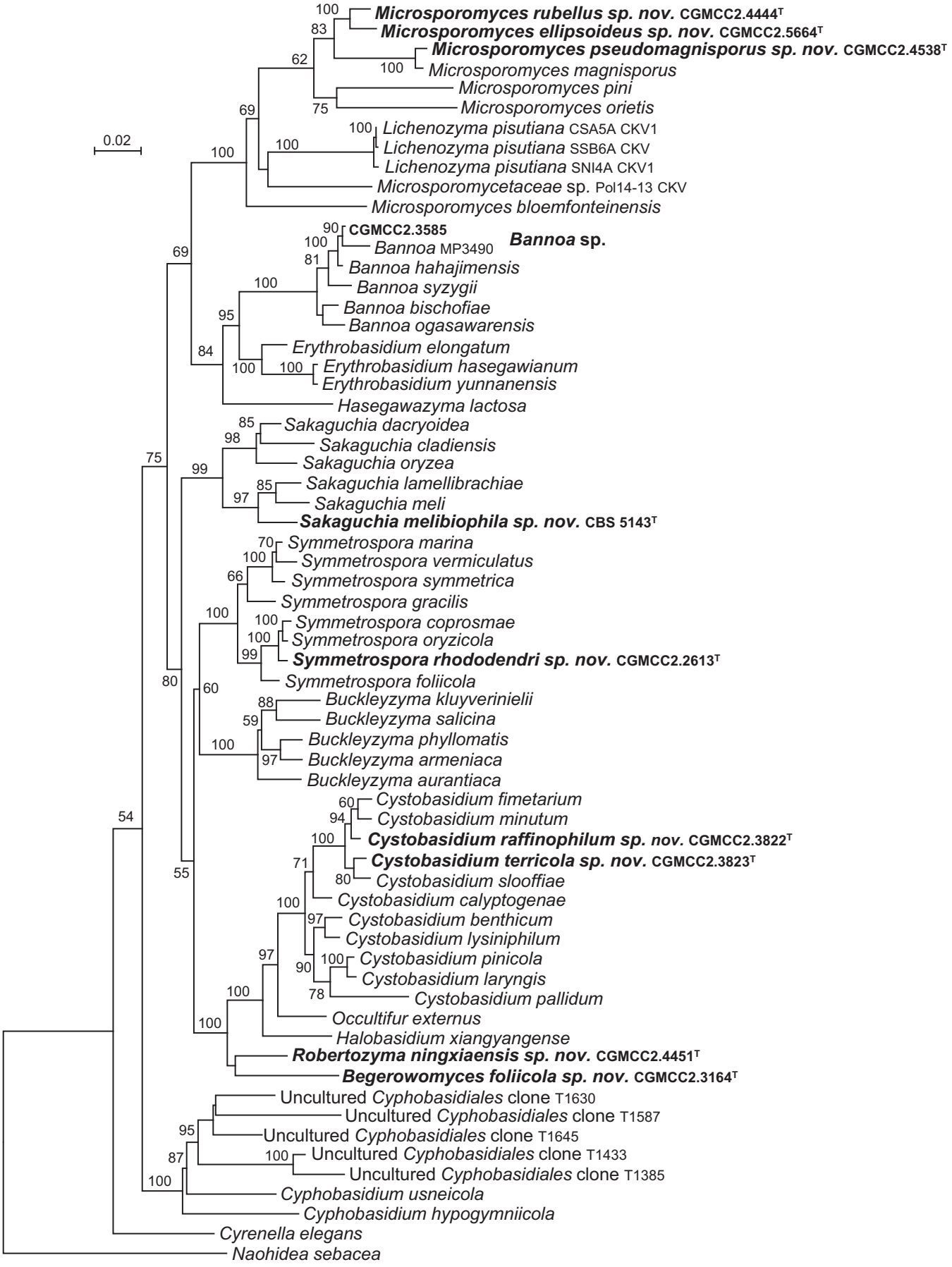


Fig. 6. Phylogenetic tree inferred using the combined sequences of SSU rDNA, LSU rDNA D1/D2 domains and ITS region (including 5.8S rDNA), depicting the phylogenetic positions of *Lichenozyma* and new taxa (in bold) within *Cystobasidiomycetes* (*Pucciniomycotina*). The tree was constructed using maximum likelihood analysis and over 50 % from 1 000 bootstrap replicates is shown. Bar = 0.02 substitutions per nucleotide position.

The novel genera *Begerowomyces* and *Robertozyma*, represented by CGMCC 2.4451 and CGMCC 2.3164, respectively, were closely related to *Occultifur*, *Cystobasidium* and two monophyletic genera, *Queiroziella* and *Halobasidium,* described by Crous *et al.* (2018) and Guo *et al.* (2019), respectively, as two separated branches in the *Cystobasidiomycetes* (Figs 4A and S2A), which indicated that they did not belong to the genera *Occultifur*, *Cystobasidium*, *Queiroziella* or *Halobasidium*. The BLASTn results showed that CGMCC 2.3164 and CGMCC 2.4451 had less than 90–93 % and 87–91 % (with 91 % coverage) similarities with other genera in *Cystobasidiomycetes*, such as *Occultifur*, *Cystobasidium* and *Symmetrospora*, in the D1/D2 and ITS regions, respectively. The sequence similarities between CGMCC 2.4451 and CGMCC 2.3164 were 93.6 % and 88.2 % in the D1/D2 and ITS regions, respectively. The comparison of the sequence similarities between CGMCC 2.4451, CGMCC 2.3164 and other genera in the *Cystobasidiomycetes* indicated that CGMCC 2.4451 and CGMCC 2.3164 should represent two novel genera according to the yeast genera thresholds predicted by Vu *et al.* (2016).

The novel genera *Pseudosterigmatospora* and *Sterigmatospora*, represented by CGMCC 2.5817 and CGMCC 2.5816, respectively, were located in the *Agaricostilbomycetes* and closely related to *Jianyunia sakaguchii* (Figs 4A and S2A). BLASTn searches of the D1/D2 sequences showed that CGMCC 2.5817 and CGMCC 2.5816 had the highest match with *Bensingtonia rectispora* with less than 90 % coverage and 90 % similarity. CGMCC 2.5817 had the highest match with species of *Ballistosporomyces* with 50 % coverage and less than 91 % similarity when using ITS sequences as query. However, CGMCC 2.5816 was more related to species of *Ruinenia* with less than 50 % coverage and 90 % similarity. CGMCC 2.5817 and CGMCC 2.5816 have 91.8 % and 65.5 % similarities in the D1/D2 and ITS regions, respectively. The low similarities in the above analyses indicated that CGMCC 2.5817 and CGMCC 2.5816 were separated and did not belong to any existing genus in the *Agaricostilbomycetes*. The phylogenetic analysis based on the combined three rDNA loci and seven-genes datasets showed that CGMCC 2.5817, CGMCC 2.5816 and *J. sakaguchii* formed a clade separated from other families in the *Agaricostilbales*. Because only *J. sakaguchii* occured in the new "*Agaricostilbales* family 2", recognised by the nested analyses of the GMYC approach, this new family was not proposed by Wang *et al.* (2015b). It is now appropriate to proposed the "*Agaricostilbales* family 2" as a new family, named as *Jianyuniaceae*, in this study with two novel genera *Pseudosterigmatospora* and *Sterigmatospora* included in this clade.

The novel genus *Boekhoutia*, represented by CGMCC 2.4539, was closely related to *Kurtzmanomyces* and *Chionosphaera*. A BLASTn search of the D1/D2 sequence of CGMCC 2.4539 revealed that the closest match was *Kurtzmanomyces shapotouensis* with 99 % coverage and 87 % similarity. However, the closest matches using the ITS sequence were the species of *Cystobasidiopsis* wih 71 % coverage and less than 82 % similarity. The results of the BLASTn searches indicated that the phylogenetic position of CGMCC 2.4539 is unclear. In order to clarify its position, the phylogenetic analyses were performed based on different datasets using different algorithms (Figs 4A, 5A and S2A). CGMCC 2.4539 was located in the family *Chionosphaeraceae* as an isolated branch and loosely related to the genera *Chionosphaera* and *Kurtzmanomyces* without support in the tree from the single D1/D2 dataset (Fig. 5A). However, CGMCC 2.4539 formed a clade with *Cystobasidiopsis* in the ITS tree with 86 % bootstrap support (data not shown). CGMCC 2.4539 clustered with *Kurtzmanomyces* without support as a separated long branch in the tree of the combined three rDNA dataset (Fig. S2A), and located in a separated bottom branch from *Kurtzmanomyces* and *Chionosphaera* in the tree of the seven-genes dataset (Fig. 4A). The above analyses indicated that placing CGMCC 2.4539 into *Chionosphaera* and *Kurtzmanomyces* is arbitrary. Therefore, a new genus, *Boekhoutia* is proposed to accommodate this strain.

The novel genus *Meniscomyces*, represented by CGMCC 2.5818, was located in the *Spiculogloeomycetes* (Figs 4A and S2A). The ITS and D1/D2 sequences of CGMCC 2.5818 are very divergent from other yeast species. A BLASTn search of the D1/D2 sequences revealed that CGMCC 2.5818 matched with *Phyllozyma* with less than 70 % coverage and 82–83 % similarity, and genera, such as *Tremella*, in the *Tremellomycetes* (*Agaricomycotina*) with 79–81 % similarity. Only the 5.8S region of the ITS sequence of CGMCC 2.5818 matched with some taxa in the *Pucciniomycotina* and *Agaricomycotina*, such as *Crustoderma* and *Tygervalleyomyces*, using ITS sequences as the query. A BLASTn search of the SSU sequences showed that CGMCC 2.5818 matched to the taxa in *Pucciniomycotina*, with *Phyllozyma* as the best match with 89 % similarity. The phylogenetic analyses based on different datasets (Figs 4, 5 and S2) showed that CGMCC 2.5818 is related to *Phyllozyma*, *Mycogloea sp.* TUB FO40962 and *Spiculogloea sp.* TUB RB1040 in the *Spiculogloeomycetes*, with *Spiculogloea sp.* TUB RB1040 as its closes relative (Fig. 5). Because sequences of only a few *Spiculogloea* and *Mycogloea* species are available at present, it is difficult to elucidate the higher taxonomic position of CGMCC 2.5818. Consequently, CGMCC 2.5818 was placed in a new genus *Meniscomyces* (see Taxonomy section), which is temporarily treated as '*incertae sedis*' in the *Spiculogloeomycetes*.

The novel genus *Rosettozyma*, represented by the groups of CGMCC 2.2615, CGMCC 2.3466 and CGMCC 2.5819, located in a separated clade at the bottom of the tree, is separated from all known orders and other taxa in the *Microbotryomycetes* (Figs 4A and S2A). A BLASTn search of the D1/D2 and ITS sequences revealed that these three groups matched to the genera in the *Microbotryomycetes*, such as *Rhodotorula*, *Chrysozyma*, *Oberwinklerozyma*, *Phenoliferia*, *Vonarxula* and *Yunzhangia*, with 86–89 % and 84–94 % similarities (42–59 % coverage), respectively, which are below the fungal order thresholds of 94.7 % for D1/D2 and 81.2 % for ITS, recommended by Vu *et al.* (2016). The phylogenetic analysis and the comparison of predicted taxonomic thresholds indicated that the CGMCC 2.2615, CGMCC 2.3466 and CGMCC 2.5819 groups could represent a new order. Therefore, *Rosettozyma*, *Rosettozymaceae* and *Rosettozymales* are proposed (see Taxonomy section).

The genus *Heitmania* belongs to the *Microbotryomycetes*, but no higher categories were assigned to place this genus in although it represents an isolated clade in the *Microbotryomycetes* (Liu *et al.* 2017). Two new species of *Heitmania* are proposed in this study that represented a subclade that was separated from the already described species in the trees constructed from the different datasets (Figs 4A and S2A). The phylogenetic analysis based on the increased number of sampled species showed that this genus was more related to the order *Sporidiobolales* than the other taxa in the *Microbotryomycetes* in the tree of the three rDNA loci dataset

(Fig. S2), but located in a separated branch from other existing orders in the *Microbotryomycetes* in the tree of the seven-genes dataset (Fig. 4) agreeing with the result from Liu *et al.* (2017). The genus *Heitmania* had a less than 93 % similarity with other taxa in the *Microbotryomycetes* in the D1/D2 domains and 82–88 % (60–78 % coverage) in the ITS region. The above data indicated that a new order could be circumscribed to accommodate the genus *Heitmania*. Therefore, *Heitmaniaceae* and *Heitmaniales* are proposed in the Taxonomy section.

Some novel species described latter were represented by a single strain or a few of isolates. In order to find potentially conspecific strains of different origin for those new species, we used the ITS and D1/D2 sequences of those species to blast the similar sequences against GenBank, *The Yeasts Trust* database or MycoBank (Robert *et al*. 2005, http://www.mycobank.org/). Sixty identical or similar sequences, which are from 46 unpublished strains and 14 uncultured fungus clones, were added in the new species delimitation below.

New species identification in the *Tremellomycetes* (*Agaricomycotina*)

Kockovaella (Cuniculitremaceae, Tremellales)

Five strains, isolated from Yunnan and Hainan provinces, South China, were located in the *Kockovaella* clade as three separate groups that were also separated from other species of *Kockovaella* (Figs 2B, 3B and S1B). Groups CGMCC 2.3443 and CGMCC 2.3536, both containing two strains, clustered together in the tree constructed by the seven-genes and three rDNA loci datasets (Figs 2B and S1B) and were most closely related to *Kockovaella libkindii* in the tree drawn by the D1/D2 dataset (Fig. 3B). Strains in the CGMCC 2.3443 group have identical ITS and D1/D2 sequences, which indicated that they are conspecific. Strains in the CGMCC 2.3536 group, also with identical ITS and D1/D2 sequences, differed from the CGMCC 2.3443 group by 12 nucleotides (nt) (~2 %) substitutions in the D1/D2 domains and 16 nt (~3.2 %) mismatches (including substitutions and deletions) in the ITS regions. These two groups differed from *Koc. libkindii* by three nt (~0.5 %) and 11–17 nt (~2.2–3.4 %) mismatches in the D1/D2 and ITS regions, respectively. Strain CGMCC 2.3465 was placed in the *Kockovaella* clade (Fig. 2B) as a separated branch at the bottom of the clade. It differed from other *Kockovaella* species by more than 3 % and 7 % mismatches in the D1/D2 and ITS regions, respectively.

The above sequence comparisons indicated that the five novel strains represent three novel species in the genus *Kockovaella*.

Genolevuria (Bulleraceae, Tremellales)

CGMCC 2.5809 has a close relationship with *Genolevuria amylolytica* and *Genolevuria tibetensis* (Figs 2B, 3C and S1B). They differed from each other by 10–15 nt (~2–3 %) substitutions and ~10 % mismatches in the D1/D2 and ITS regions, respectively. Therefore, CGMCC 2.5809 is proposed as a new species in the genus *Genolevuria*.

Vishniacozyma (Bulleraceae, Tremellales)

Six strains formed three groups, represented by CGMCC 2.3099, CGMCC 2.3472 and CGMCC 2.3165, in the *Vishniacozyma* clade (Figs 2B and S1B). Group CGMCC 2.3472, consisting of three strains, possessed similar sequences with one nt and five nt difference in the D1/D2 and ITS regions, respectively, which indicated they were conspecific. An isolate IA19 (KM246197/KM246114) named as '*Cryptococcus dimennae*' in the GenBank database had identical or similar D1/D2 sequences (zero to one nt difference) with the CGMCC 2.3472 group, however, there were nine to ten nt (~1.9–2.0 %) differences in the ITS regions, which indicated that the isolate IA19 may represent a different taxon and is not conspecific to the strains of the CGMCC 2.3472 group. The CGMCC 2.3472 group was closely related to *Vishniacozyma nebularis*, *Vishniacozyma dimennae* and *Vishniacozyma globispora* (Figs 2B, 3F and S1F), which differed from the three known species by 9–28 nt (~1.5–4 %) substitutions in the D1/D2 domains and by more than 9 % mismatches in ITS regions. More than seven nt (~1.1 %) D1/D2 sequence difference were observed between group CGMCC 2.3472 and other eight undescribed or erroneously identified strains (Fig. S1F), which indicated that those strains represent different species from group CGMCC 2.3472. Group CGMCC 2.3099 was more closely related to *Vishniacozyma foliicola* and *Vishniacozyma heimaeyensis* (Figs 2B and S1F). They differed from *V. foliicola* and *V. heimaeyensis* by seven to ten nt (~1.1–1.6 %) substitutions in the D1/D2 domains and by 15–18 nt (~3 %) mismatches in the ITS region. The two strains in the CGMCC 2.3165 group had identical sequences in the ITS and D1/D2 regions. They also had the same ITS sequences as '*Cryptococcus*' *sp.* SJ8L03 (FJ153171) and SJ8L02 (FJ153172), and a similar ITS (four nt difference) and D1/D2 sequences (one nt difference) as '*Cryptococcus*' *sp.* KY763 (AB428345/AB428344). A Blast search against *The Yeasts Trust* database (or MycoBank) showed that CBS 8412 isolated from food in the Netherlands and CBS 9328 isolated from soil in Costa Rica have similar D1/D2 sequences (99.68–99.84 %) and ITS sequences (99.45 %) with CGMCC 2.3165 group. The above analysis indicated that they should be conspecific. The CGMCC 2.3165 group differed from CGMCC 2.3099, *V. foliicola* and *V. heimaeyensis* by 8–11 nt (~1.3–1.8 %) mismatches in the D1/D2 domains, and by more than 5 % nucleotide divergence in the ITS region.

Based on the above sequence comparisons, those six strains should represent three novel species in the genus of *Vishniacozyma*.

Carlosrosaea (Trimorphomycetaceae, Tremellales)

The genus *Carlosrosaea* was circumscribed with a single species *Carlosrosaea vrieseae* (Liu *et al.* 2015b). Recently, Felix *et al.* (2017) described two novel species, namely *Carlosrosaea hohenbergiae* and *Carlosrosaea aechmeae*. Strains from all three species were isolated from bromeliads in Brazil (Landell *et al.* 2015, Felix *et al.* 2017). Two Chinese isolates, CGMCC 2.3580 isolated from Yunnan province and CGMCC 2.3447 isolated from Hainan province, were placed in the genus *Carlosrosaea* with an affinity to *Ca. vrieseae* based on phylogenetic analysis of the sequences of the ITS and D1/D2 regions (Fig. 3C). They differed from *Ca. vrieseae* by 11–13 nt (~1.8–2.2 %) substitutions in the D1/D2 domains, and by more than 9 % mismatches in the ITS regions. CGMCC 2.3580 and CGMCC 2.3447 differed from each other by 12 nt (~2 %) substitutions and more than 12 % mismatches in the D1/D2 and ITS regions, respectively.

The above analyses indicated that the two novel strains represent two undescribed *Carlosrosaea* species.

Note: An uncultured fungal clone 2170_736 (KP891580) from *Scolytus multistriatus*, Sweden, has an identical ITS sequence with CGMCC 2.3447, which indicates that the species represented by CGMCC 2.3447 is also distributed outside of China.

Saitozyma (Trimorphomycetaceae, Tremellales)

CGMCC 2.5811, located in the genus *Saitozyma* was closely related to *Saitozyma flava* in the tree obtained from the combined seven-genes dataset (Fig. 2C). Although they differed from each other by only two nt in the D1/D2 domains, there were 14 nt (~3 %) differences in the ITS region, which indicated that CGMCC 2.5811 was not conspecific to *Sa. flava*. More than seven nt D1/D2 heterogeneity (~1.1 %) were observed between CGMCC 2.5811, *Saitozyma paraflava* and the potential new species from Thailand and Japan (Fig. 3C). The above analyses indicated that CGMCC 2.5811 represented a novel *Saitozyma* species.

Note: The monophyly of *Saitozyma* was not supported by this study (Fig. 2C), which need more robust data and species to confirm.

Tremella (Tremellaceae, Tremellales)

CGMCC 2.5615 had the closest relationship with *Tremella globispora* (Figs 2B and 3F). They differed from each other by seven nt (~1.1 %) substitutions in the D1/D2 domains and 17 nt (~3 %) mismatches in the ITS region. Thus, it should be proposed as a new species in *Tremella*.

Kwoniella (Cryptococcaceae, Tremellales)

CGMCC 2.3439 was placed in the *Kwoniella* clade with an affinity to *Kwoniella endophytica*, *Kwoniella botswanensis*, *Kwoniella mangrovensis*, *Kwoniella pini*, *Kwoniella dejecticola*, *Kwoniella dendrophila* and *Kwoniella shivajii* in the trees from the D1/D2 as well as the three rDNA and seven-genes datasets (Figs 2C, 3G and S1C). It differed from those six species by 11–18 nt (~2–3 %) substitutions in the D1/D2 domains and 7 % mismatches in the ITS region. The analysis of the ITS and D1/D2 sequences indicated that CGMCC 2.3439 belongs to a novel species within *Kwoniella*.

Teunia (Cryptococcaceae, Tremellales)

CGMCC 2.3835, CGMCC 2.4450 and CGMCC 2.5648 formed a separate branch in the tree of the three rDNA and seven-genes datasets, and were located in the genus *Teunia*, a clade newly named in this study (Figs 2C and S1C). CGMCC 2.5648 was closely related to the misidentified strain '*Piskurozyma taiwanensis*' CBS 9926 (KY102949/KY107271) and '*Cryptococcus*' *sp.* F6 (AY518273/AY508880) with two nt differences in the D1/D2 domains and 12–17 nt (~2.1–3 %) mismatches in the ITS regions, which indicated that they probably belong to different species. CGMCC 2.3835 and CGMCC 2.4450 differed from their closest undescribed or erroneously identified strains, '*Fonsecazyma*' *sp.* 21S4 (MK400702),'*Kwoniella*' *sp.* PY016 (KY399877), '*Kwoniella*' *sp.* HB31-3 (KJ507251), '*Cryptococcus*' *sp.* BI226 (EU678944), '*Cryptococcus*' *sp.* SAP963.4 (JX067803), '*Cryptococcus*' *sp.* RT 1.5.17 (AY731785) and '*Cryptococcus heveanensis*' YM25139 (JQ964208) (Fig. 3G), by 8–13 nt (~1.3–2 %) substitutions in the D1/D2 domains.

The above sequence comparisons proved that the three new strains belong to three novel species in the genus *Teunia*.

Note: Based on the D1/D2 sequences comparisons, more than 30 undescribed or erroneously identified strains may represent more than 20 species in *Teunia* clade (Fig. 3G), which need to be clarified in the future because the ITS sequences are not available at present.

Dioszegia (Bulleribasidiaceae, Tremellales)

Seven strains with orange-coloured colonies distributed in five groups loctated in the *Dioszegia* clade (Figs 2C, 3D and S1C). Group CGMCC 2.5628 was closely related to *Dioszegia crocea* and *Dioszegia aurantiaca* and differed from them by 12–13 nt (~1.9–2.1 %) in the D1/D2 domains and 8–11 nt (~1.7–2.3 %) mismatches in the ITS region. Three strains in group CGMCC 2.5674 had identical sequence in the ITS and D1/D2 regions. They differed from *Dioszegia cryoxerica* and *Dioszegia changbaiensis* by 13–16 nt (~2.1–2.6 %) in the D1/D2 domains and about 5 % mismatches in the ITS region. Groups CGMCC 2.3625, CGMCC 2.5658 and CGMCC 2.4537 formed three separate branches, clustering with *Dioszegia athyrii*, *Dioszegia catarinoi*, *Dioszegia takashimae* and *Di. zsoltii.* Group CGMCC 2.3625 and an unpublished strain, TY-217 (AY313036/AY313018) possessed similar sequences with only one and three nt differences in the D1/D2 and ITS regions, respectively, which indicated that they are conspecific. Group CGMCC 2.3625 differed from these four known species (Fig. 3D) by zero to five nt and more than 21 nt (~4 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.5658 differed from these four known species by one to five nt in D1/D2 domains and 11–15 nt (~2.1–3 %) mismatches in the ITS regions. Group CGMCC 2.4537 differed from them by five to ten nt (~0.8–1.6 %) and more than 33 nt (~6 %) mismatches in the ITS and D1/D2 regions, respectively. An uncultured fungal clone CMH458 (KF800549) from indoor air in Kansas City, Missouri, USA had an identical ITS sequence as CGMCC 2.4537, which indicated that this species may be common in different locations.

According to the above sequence analyses five novel species in the genus *Dioszegia* are proposed in the Taxonomy section.

Bulleribasidium (Bulleribasidiaceae, Tremellales)

Seven strains formed five groups in the genus *Bulleribasidium*, represented by CGMCC 2.4024, CGMCC 2.4427, CGMCC 2.5812, CGMCC 2.4428 and CGMCC 2.3320 (Figs 2D, 3D and S1D). One nt difference was found in the D1/D2 domains between two strains in the CGMCC 2.4024 group. This group differed from its closest relative *Bulleribasidium panici* by three to four nt (~0.6 %) substitutions in the D1/D2 domains and nine nt (~1.8 %) mismatches in the ITS regions. Groups CGMCC 2.4427 and CGMCC 2.5812 were most closely related to *Bulleribasidium setariae*. CGMCC 2.5812 differed from *Bu. setariae* by nine nt (~1.5 %) and 16 nt (~2.6 %) mismatches in the D1/D2 and ITS regions, respectively. CGMCC 2.4427 had 45 nt (~7.4 %) differences in the D1/D2 domains and ~19 % in the ITS regions from *Bu. setariae*. Groups CGMCC 2.3320 and CGMCC 2.4428 had an affinity to *Bulleribasidium foliicola*. Group CGMCC 2.3320 consisted of two strains with similar D1/D2 (one nt difference) and ITS sequences (three nt differences). A Blast search against *The Yeasts Trust* database showed that two strains, BSB09 (KY305125) isolated from bromeliad, Brazil and TY-199

(AY313030) found in the phyllosphere of Thailand have 99.5–99.8 % sequences similarity with the CGMCC 2.3320 group in the ITS region, which indicated that they are conspecific. They differed from *Bu. foliicola* by three to four nt (~0.6 %) in the D1/D2 domains and nine to ten (~1.7–1.9 %) mismatches in the ITS regions. Group CGMCC 2.4428 had a greater sequence disparity with *Bu. foliicola* with 19 nt (~3.1 %) difference in the D1/D2 domains and more than 11 % in the ITS region.

The above sequence comparisons indicated that these seven novel strains represent five undescribed species of *Bulleribasidium*.

Derxomyces (Bulleribasidiaceae, Tremellales)

Twenty three strains separated in twelve groups located in the *Derxomyces* clade (Figs 2D, 3E and S1D). Three strains in group CGMCC 2.5660 differed from each other by one nt in both the D1/D2 and ITS regions. This group differed from its closest relative *Derxomyces linzhiensis* by 23 nt (~4 %) in the D1/D2 domains and more than 9 % mismatches in the ITS regions. Groups CGMCC 2.3572 and CGMCC 2.4429 were closely related to *Derxomyces hubeiensis* (Figs 2D and S1D). Strains in the CGMCC 2.4429 group had similar sequences with three nt differences in the ITS region, which indicated that they are conspecific. They differed from group CGMCC 2.3572 by two to four nt in the D1/D2 domains and 14–17 nt (~2.7–3.3 %) mismatches in the ITS regions. These two groups differed from *De. hubeiensis* by 13–15 nt (~2.1–2.4 %) in the D1/D2 domains and more than 6 % mismatches in the ITS regions. Group CGMCC 2.3459 contained three strains with identical ITS and D1/D2 sequences and were closely related to *Derxomyces schimicola* and *Derxomyces pseudoschimicola*. The former differed from the known two species by six to seven nt (~1.0 %) in the D1/D2 domains and 8–18 nt (~1.4–3.0 %) mismatches in the ITS regions. Group CGMCC 2.2459 was closely related to *Derxomyces cylindricus*, and differed from it by four nt (~0.6 %) and 11 nt (~2.2 %) mismatches in the D1/D2 and ITS regions, respectively. Groups CGMCC 2.4436 and CGMCC 2.4437 were most closely related to *Derxomyces boekhoutii* (Fig. S1D). These two groups differed from each other by three nt (~0.5 %) and 18 nt (~3.5 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.4436 differed from *De. boekhoutii* by three nt (~0.5 %) and 12 nt (~2.4 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.4437 and *De. boekhoutii* had two nt and 16 nt (~3.1 %) differences in the D1/D2 and ITS regions, respectively. Group CGMCC 2.3561 differed from *Derxomyces wuzhishanensis* by seven nt (~1.1 %) and 18 nt (~3.5 %) mismatches in the D1/D2 and ITS regions, respectively.

Four groups represented by CGMCC 2.3535, CGMCC 2.3563, CGMCC 2.3470 and CGMCC 2.4446 were closely related to *Derxomyces yunnanensis*. Group CGMCC 2.3535 and *De. yunnanensis* had identical D1/D2 sequences, and 10 nt (~1.9 %) differences in the ITS region, which indicated that they represent different taxa. Group CGMCC 2.3563 contained six strains that do not have more than three nt differences in both the ITS and D1/D2 regions, which indicated that they are conspecific. Group CGMCC 2.3470 comprised two strains with two nt differences in the ITS regions. The two strains in group CGMCC 2.4446 possessed identical sequences. Groups CGMCC 2.4446 and CGMCC 2.3470 differed by one nt and 13 nt (~2.5 %) mismatches in the D1/D2 and ITS regions, respectively. These four groups and *De. yunnanensis* differed from one another by zero to four nt in the D1/D2 domains and 9–23 nt (~1.8–4.5 %) mismatches in the ITS region.

Based on the above sequence comparisons twelve novel species of *Derxomyces* are proposed in the Taxonomy section.

Note: An uncultured fungal isolate, OTU 265 (KT328670) from coffee leaf infected by an rust fungus (*Hemileia vastatrix*), Finca Don Julio, USA, has one nt difference with CGMCC 2.4446 in the ITS region, which indicated that this species may be also found in the USA.

Phaeotremella (Phaeotremellaceae, Tremellales)

The BLASTn searches of the D1/D2 and ITS regions revealed that the strains CGMCC 2.5810 and CGMCC 2.5614 belonged to *Phaeotremella*, with the best matches *Phaeotremella foliacea* CBS 5029 (previously named as *Phaeotremella skinneri*, Spirin *et al.* 2018) and five '*Cryptococcus*' *spp.* with 98.6–98.2 % similarity in the D1/D2 domains and 94 % similarity in the ITS regions. CGMCC 2.5810 and CGMCC 2.5614 formed a subclade with the unpublished strains TFL2B (MG909557/KY614525), '*Tremella*' *sp.* H-080.13 (AY188379) and '*Cryptococcus*' *sp.* CBS11775 (LT904718/FN824502) in the tree of the D1/D2 dataset (Fig. 3H). CGMCC 2.5614 differed from these unpublished strains by five to ten nt substitutions in the D1/D2 domains and by 15–17 nt (~3–3.4 %) mismatches in the ITS regions, which indicated that they belong to different species. CGMCC 2.5810 and CGMCC 2.5614 differed from TFL2B by 11–12 nt in the D1/D2 domains and more than 6 % mismatches in the ITS regions. CGMCC 2.5614 differed from *Pha. foliacea* (*Pha. skinneri*) and *Pha. foliacea* (voucher Miettinen 14610) by 33–37 nt (~6.6–7.4 %) mismatches in the ITS regions and 15–16 nt substitutions (~2.4–2.6 %) in the D1/D2 domains. CGMCC 2.5810 differed from *Pha. foliacea* (*Pha. skinneri*), *Pha. foliacea* (voucher Miettinen 14610) and '*Cryptococcus*' *sp.* GT-388 (HQ890369) by 8–10 nt (~1.3–1.6 %) in the D1/D2 domains, and more than 5 % mismatches in the ITS regions.

The above data indicated that CGMCC 2.5810 and CGMCC 2.5614 represent two novel species of *Phaeotremella*.

Note: An uncultured *Tremellales* clone, 5_D20 (HQ211529) from Arctic soil, Canada has 99.4 % ITS sequence similarity with CGMCC 2.5810 by blast search against the MycoBank database, which indicated that this species may be also found in other locations than China.

Holtermannia (Holtermanniaceae, Holtermanniales)

Four isolates, CGMCC 2.3445, CGMCC 2.3460, CGMCC 2.3462 and WZS12.12B, isolated from plant leaves collected in Yunnan province clustered in the genus *Holtermannia* (Wuczkowski *et al.* 2011) in the tree obtained from the three rDNA and seven-genes datasets (Figs 2E and S1E). Similar sequences were found between these four strains with no more than 3 nt differences in the ITS and D1/D2 regions. They differed from *Holtermannia corniformis* by five to six nt (~1 %) substitutions in the D1/D2 domains and 23–25 nt (~4 %) mismatches in the ITS region, which indicated that they represent a new species of *Holtermannia*.

Note: An uncultured endophytic fungal clone, WFc36 (KF709568) isolated from *Warburgia ugandensis* in Austria has two nt difference with group CGMCC 2.3445 in the ITS region, which indicated that this new species should be found outside of China. Two strains '*Holtermannia corniformis*' MB128 (KC798426) and JM11 (KC510049), have identical or very

similar D1/D2 sequences, which indicated that they may be conspecific.

Solicoccozyma (Piskurozymaceae, Filobasidiales)

CGMCC 2.5814 and CGMCC 2.4893 had ten nt constituting indels in the ITS regions and identical sequence in the D1/D2 domains. Similar sequences with zero to one nt difference in the D1/D2 and ITS regions were found between CGMCC 2.5814 and '*Solicoccozyma aeria*' CBS 9627 (KY105431/KY109663) and RUB096 (MK397489), *Solicoccozyma sp.* DBVPG10727 (MK070335/MK070317) and '*Cryptococcus*' *sp.* CRUB 2005 (KF826509). So these six strains were considered to be conspecific. They differed from the type strain of *Solicoccozyma aeria* by 19 nt (~3 %) in the D1/D2 domains, and more than 4 % mismatches in the ITS regions. Therefore, a novle species of *Solicoccozyma* is proposed to accommodate them (Figs 2E and 3J).

Note: The uncultured eukaryote clone LTSP_EUKA_P5P23 (FJ554237) collected from the long-term soil productivity (LTSP) in Skulow Lake in Canada, had the same ITS sequence as CGMCC 2.4893. CGMCC 2.5814 and seven uncultured clones, clone 81a17 (EU554946) and clone 54a11(EU554878) collected from soil of nptII transformed poplar plantation in Canada, clone LTSP_EUKA_P4M17 (FJ553878) from LTSP from Skulow Lake in Canada, clone BF-OTU106(AM901762) from house dust in Finland, clone C4 6B (GU366710) from temperate forest soil in USA, clone 3200K2 (KF617524) from *Picea mariana* forest soil mineral horizon in Bonanza Creek LTER, Alaska, USA, and clone N131(JF300706) from boreal forest soil in Sweden, contain identical or only one nt difference in the ITS regions. Based on the comparison of environmental DNA sequences, the novel species (see Taxonomy section) is commonly and abundantly found in diverse locations.

Filobasidium (Filobasidiaceae, Filobasidiales)

CGMCC 2.5649 and GPS23.2A5 have identical sequences and formed a separate branch in the *Filobasidium* (Figs 2E, 3J and S1E). They differed from other *Filobasidium* species by 19 nt (~3 %) in the D1/D2 domains and more than 11 % mismatches in the ITS region, which indicated that they represent a novel species in *Filobasidium*.

Seven isolates, CGMCC 2.3463, CGMCC 2.3464, CGMCC 2.4012, CGMCC 2.4052, CGMCC 2.5680, CGMCC 2.5656 and KTAPG1-11.64, formed a separate subclade distingushied from the other *Filobasidium* species (Figs 2E and 3J). CGMCC 2.3464 differed from CGMCC 2.4012, CGMCC 2.4052 and KTAPG1-11.64 by two nt in the D1/D2 domains and five nt in the ITS regions. CGMCC 2.5656 and CGMCC 2.5680 with identical ITS and D1/D2 sequences differed from the above three strains by one to two nt in the D1/D2 domains, and by 29–33 nt (~5 %) mismatches in the ITS regions. CGMCC 2.3463 differed from the above two groups, represented by CGMCC 2.4012 and CGMCC 2.5680, by five to six nt substitutions in the D1/D2 domains and more than 16 % mismatches in the ITS regions. The ITS and D1/D2 sequence comparisons indicated that these seven strains could be classified into three distinct species. Therefore, three novel species are proposed to accommodate the groups CGMCC 2.5680, CGMCC 2.4012 and CGMCC 2.3463.

Note: Three strains, '*Cryptococcus*' *sp.* SC15d50p10-8 (HQ631032) isolated from *Saccharum officinarum* in USA, O382A (JX394019) isolated from tree hollows in Brazil and CBS 10181 (EU002869/EU002805) isolated in Portugal, differ from group CGMCC 2.4012 by one to three nt in ITS region or two nt in D1/D2 domains, which indicated that they are conspecific. Seven strains, *Filobasidium sp.* KBP Y-5548 (MH697755/MH697755) isolated from *Plumeria obtusa* in Vietnam, '*Cryptococcus*' *sp.* MG34 (KM246229/KM246145), IA06 (KM246189/KM246106) isolated from coffee in Brazil, 11-1115 (KM986117/KM206723) isolated from Hungary, *Filobasidium sp.* HB22-2 (KJ507269) isolated from flower of *Caragana sinica* in South Korea, '*Cryptococcus*' *sp.* LB17_3 (KJ159043) isolated from the leaf-cutting ant in Brazil and GY2L20 (FJ527080) from Taiwan, China, have one to two nt difference with group CGMCC 2.4012 in the D1/D2 domain. However, the former four strains differ from group CGMCC 2.4012 by 19–37 nt (~3–5 %) mismatches in the ITS region, which indicated that they belong to different species. The taxonomic position of the latter three strains will be fixed in future because their ITS sequences are not available at present.

Phaffia (Mrakiaceae, Cystofilobasidiales)

Strain CGMCC 2.5601 was placed in the genus *Phaffia* (Figs 2E, 3K and S1E). It differed from *Phaffia rhodozyma* by three nt substitutions in the D1/D2 domains and 7 % mismatches in the ITS regions. Although more than four potentially new species in this genus should be described (David-Palma *et al.* 2014, Fig. S3), only one species, *P. rhodozyma*, is accepted in this genus (Liu *et al*. 2015b). Therefore, the second *Phaffia* species is proposed to accommodate CGMCC 2.5601 as a novel species to improve the species diversity in *Phaffia*.

New species identification in the *Agaricostilbomycetes* (*Pucciniomycotina*)

Kondoa (Kondoaceae, Agaricostilbales)

Fifteen strains, representing ten candidate novel species, were placed in the *Kondoa* clade (Figs 4B, 5B and S2B). Group CGMCC 2.3102, containing three strains with one nt substitution in the D1/D2 domains, had identical ITS sequences with strain PYCC 5566 (AF444672) and one nt D1/D2 sequences difference (AF444766), which indicated that they were conspecific. This group differed from its closest relative *Kondoa aeria* by two nt and 41 nt (~6 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.2652, consisting of two strains with identical sequences, was closely related to *Kondoa subrosea* and differed from it by ten nt (~1.6 %) and 50 nt (~8 %) mismatches in the D1/D2 and ITS regions, respectively. Groups CGMCC 2.2621, including two strains with identical sequences, and CGMCC 2.3100 were closely related to *Kondoa sorbi* (Figs 4B and S2B). These two groups differed from *Kon. sorbi* by 25 nt (~4 %) in the D1/D2 domains and greater than 122 nt (~18 %) mismatches in the ITS region. Groups CGMCC 2.3100 and CGMCC 2.2621 showed five nt differences in the D1/D2 domains and more than 12 % differences in the ITS region. Group CGMCC 2.2762 showed high affinity to *Kondoa changbaiensis* and differed from it by three nt substitutions and 32 nt (~5 %) mismatches in the D1/D2 and ITS region, respectively.

Groups CGMCC 2.4441, including two strains with two nt differences in the ITS regions, CGMCC 2.5610, containing two strains with one nt substitution in the D1/D2 domains, and

CGMCC 2.3106 were closely related to *Kondoa gutianensis*. These three groups differed from *Kon. gutianensis* by 9–15 nt (~1.4–2.4 %) in the D1/D2 domains and more than 75 nt (~12 %) mismatches in the ITS region. CGMCC 2.3106 and the unpublished strain *Kondoa sp.* AS483 (FN428954) isolated from flower of *Dianthus superbus* had identical D1/D2 sequences and three nt differences in the ITS region, which indicated that they are conspecific. An uncultured corn field bulk soil clone 09D70C34 (HG937064) collected from Göttingen, Lower Saxony, Germany, and CGMCC 2.3106 had three nt differences in the ITS regions, which indicated that this candidate novel species occurs in the soil environment. Similar sequences were found between CGMCC 2.3106, CBS 8379 and the unnamed strain, *Kondoa sp.* ZP 352 (AY512854) with one nt substitutions in the D1/D2 domains. CGMCC 2.3106 differed from CBS 8379 (AF444596), ZP 352 (MN175326) and ZP 338 (MN175325) by two nt substitutions and five indels in the ITS region, which indicated that they may be conspecific.

Group CGMCC 2.2763 was placed in a separate branch in the trees obtained from the rDNA and seven-genes datasets (Figs 4B and S2B). This group differed from other species of *Kondoa* by ~20 % mismatches in the D1/D2 domains and with even greater diversity in the ITS regions.

The above phylogenetic analysis indicated that these fifteen strains represent nine novel species in *Kondoa*.

Bensingtonia (Kondoaceae, Agaricostilbales)

Strains CGMCC 2.5677 and CGMCC 2.3569 were placed in two separate branches in the genus *Bensingtonia* (Figs 4B and S2B). CGMCC 2.5677 was closely related to *Bensingtonia naganoensis* and *Bensingtonia pseudonaganoensis*, and differed from them by four to seven nt substitutions in the D1/D2 domains and 52–60 nt (~8–9 %) mismatches in the ITS regions. CGMCC 2.3569 had affinity to *Bensingtonia bomiensis* and *Bensingtonia pseudonaganoensis* (Fig. 5B). 20 nt (~3.2 %) differences in the D1/D2 domains and 93–101 nt (~14–15 %) differences in the ITS regions were observed between them.

Based on the analysis of the ITS and D1/D2 sequences two novel species of *Bensingtonia*, are proposed to accommodate CGMCC 2.3569 and CGMCC 2.5677.

Pseudobensingtonia (Agaricostilbaceae, Agaricostilbales)

CGMCC 2.5815, CGMCC 2.5823 and XZ152B1 have identical sequences and were placed in the *Pseudobensingtonia* clade (Figs 4B, 5C and S2B). They differed from *Pseudobensingtonia ingoldii* and *Pseudobensingtonia musae* by 23–24 nt (~4 %) in the D1/D2 domains and 87–94 nt (~14–15 %) mismatches in the ITS regions. Therefore, a new species of *Pseudobensingtonia* is proposed to accommodate these three strains.

Ruinenia (Ruineniaceae, Agaricostilbales)

Four strains were placed in three separate branches in the *Ruinenia* clade (Figs 4B, 5C and S2B). Group CGMCC 2.4426 contained two strains with identical D1/D2 and ITS sequences. This group differed from the undescribed strains, '*Sporobolomyces*' *sp.* TY-139 (AY313063/AY313037), '*Ruinenia*' *sp.* TW 1.1F038 (KP020109), '*Ruinenia*' *sp.* TW2.1E-026 (KP020111), '*Ruinenia*' *sp.* TW2.1E-041 (KP020112) and '*Ruinenia*' *sp.* TW 2.1E012 (KP020114), by 6–9 (~1–1.4 %) mismatches in the ITS regions, which indicated that these unpublished strains may represent different species. Group CGMCC 2.4426 was closely related to *Ruinenia clavata* (Figs 4B and S2B) and differed from *Ru. clavata* by more than 34 nt (~5.5 %) and 90 nt (~14.5 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.3454 and *Ruinenia clavata* formed a subclade (Fig. 5C). They differed from each other by 31 nt (~5 %) in the D1/D2 domains and 111 nt (~17 %) in the ITS regions. Group CGMCC 2.4542 differed from its closest relative *Ruinenia dracophylli* by 13nt (~2 %) and 27 nt (~4 %) mismatches in the D1/D2 and ITS regions, respectively.

Based on the above phylogenetic analysis three novel *Ruinenia* species are proposed.

Boekhoutia (Chionosphaeraceae, Agaricostilbales)

The circumscription of new genera in the above section showed that strain CGMCC 2.4539 represents a novel genus, *Boekhoutia*. Consequently, a new species name for CGMCC 2.4539 is proposed in the Taxonomy section.

Note: The unpublished strain *Kurtzmanomyces sp.* YM25263 (KT345339) isolated from Yunnan province, China, was closely related to CGMCC 2.4539 in the tree of the D1/D2 dataset (Fig. 5A), which indicated that this strain represents a new member of *Boekhoutia*.

Sterigmatospora (Jianyuniaceae, Agaricostilbales)

Strain CGMCC 2.5817 has been proposed in the above circumscription of new genera to represent the new genus *Sterigmatospora*. Therefore, a novel species name is proposed to accommodate this strain.

Note: Strain RP146, namely *Pucciniomycotina sp.* (AB727125), isolated from Japan (Takashima *et al.* 2012) clustered with CGMCC 2.5817 in the tree of the D1/D2 dataset (Fig. 5A), which indicated that this strain represents a member of *Sterigmatospora*.

Pseudosterigmatospora (Jianyuniaceae, Agaricostilbales)

CGMCC 2.5816 represented the new monotypic genus *Pseudosterigmatospora*, that was closely related to *Sterigmatospora* in the new circumscribed family *Jianyuniaceae* (Figs 4B and S2B). A new species name is proposed for CGMCC 2.5816.

Note: '*Bensingtonia*' *sp.* BI183 (EU678947), an unpublished species isolated from Brazil, was closely related to CGMCC 2.5816 in the tree drawn from the D1/D2 dataset (Fig. 5A).

New species identification in the *Spiculogloeomycetes* (*Pucciniomycotina*)

Phyllozyma (Spiculogloeaceae, Spiculogloeales)

CGMCC 2.5669 was closely related to *Phyllozyma corallina* and *Phyllozyma dimennae* (Figs 4B, 5C and S2B), and differed from them by 17–18 nt (~3 %) substitutions in the D1/D2 domains, and 41–47 nt (~6.2–7.2 %) mismatches in the ITS region. Strains CGMCC 2.2662 and CGMCC 2.2617 had two nt differences in the ITS region and differed from their closest relative *Phyllozyma coprosmicola* by seven (~1.1 %) and eight nt (~1.5 %) substitutions in the D1/D2 and ITS regions, respectively.

The above data indicated that these three strains represented two new species in *Phyllozyma*.

Meniscomyces (incertae sedis, Spiculogloeomycetes)

CGMCC 2.5818 and CGMCC 2.5681 have identical D1/D2 and ITS sequences. They belong to the new genus *Meniscomyces* (Figs 4B and S2B). A new species name is proposed to accommodate these two strains.

Note: An uncultured fungal clone, 103 NA2 P31 C4 (KF297104) from a soil sample in Ellef Ringnes Island, Canada, was closely related to CGMCC 2.5681 and CGMCC 2.5818 in the tree drawn from the D1/D2 dataset (Fig. 5A), which indicated that other *Meniscomyces* species may occur in nature.

New species identification in the *Cystobasidiomycetes* (*Pucciniomycotina*)

Sakaguchia (Sakaguchiaceae, incertae sedis)

CGMCC 2.4235 (= JCM 8162 = CBS 5143) was named as *Rhodotorula araucariae* in the chemotaxonomic studies of basidiomycetous yeasts (Sugiyama *et al.* 1985, Hamamoto *et al.* 1986a,b). The result from Gadanho & Sampaio (2002) indicated that IGC 5612 (= CBS 5143) was closely related to *Sakaguchia dacryoides* rather than *Rhodotorula* and *Rhodosporidium*. Our analysis also supported CGMCC 2.4235 was located in the *Sakaguchia* clade (Figs 5D, 6 and S4), which differed from its closest relatives, *Sakaguchia lamellibrachii* and *Sakaguchia meli*, by 12–20 nt (~2.2–4 %) and 27–33 nt (~4–6 %) mismatches in the D1/D2 and ITS regions, respectively. Thus, a new species of *Sakaguchia* is proposed to accommodate it in the Taxonomy section.

Note: Two strains, '*Sakaguchia lamellibrachiae*' MTW10.1 (LC435582) isolated from water in Thailand and '*Rhodotorula*' *sp.* GY28L06 (FJ527100) isolated from plant in Taiwan, China, have one to two nt D1/D2 sequences differences from CGMCC 2.4235, which indicated they may be conspecific.

Symmetrospora (Symmetrosporaceae, incertae sedis)

CGMCC 2.2613 was found to be closely related to *Symmetrospora coprosmae* and *Symmetrospora oryzicola* (Figs 4C and S2C), and differed from them by two to three nt substitutions in the D1/D2 domains and eight to nine nt (~1.3–1.5 %) mismatches in the ITS regions, which indicated that CGMCC 2.2613 represent a different species.

Microsporomyces (Mycrosporomycetaceae, incertae sedis)

Strain CGMCC 2.4538 and its closest relative *Microsporomyces magnisporus* differed from each other by one nt in their D1/D2 domains. However, 11 nt (~2 %) mismatches were found in the ITS region, which indicated that they belong to different species. Strains CGMCC 2.4444, CGMCC 2.4445 and CGMCC 2.5664 were closely related to *Microsporomyces orientalis* (Fig. 5D). The former two strains with identical sequences differed from *Mi. orientalis* by 18 nt (~3.2 %) and 92 nt (~15 %) mismatches in the D1/D2 and ITS regions, respectively. The latter strain differed from *Mi. orientalis* by 17 nt (~3 %) in the D1/D2 domains and 81 nt (~14 %) mismatches in the ITS region. CGMCC 2.4444 and CGMCC CGMCC 2.5664 differed from each other by 6 nt (~1 %) substitutions and 41 nt (~6.8 %) mismatches in the D1/D2 and ITS regions, respectively.

Based on the above sequence comparisons three novel species are proposed to accommodate groups CGMCC 2. 4538, CGMCC 2. 5664 and CGMCC 2. 4444.

Note: Group CGMCC 2.4444 and the published strain NIP038 (AB726620) contained the same sequences in the D1/D2 domains, which indicated that they may be conspecific.

Cystobasidium (Cystobasidiaceae, Cystobasidiales)

CGMCC 2.3822, CGMCC 2.3823 and CGMCC 2.3824 were placed in the *Cystobasidium* clade (Figs 4C, 5D and S2C) and were closely related to *Cystobasidium fimetarium* and *Cystobasidium minutum*. CGMCC 2.3822 differed from *Cy. fimetarium* and *Cy. minutum* by 8–11 nt (~1.3–1.8 %) and 9–12 nt (~1.5–2 %) mismatches in the D1/D2 and ITS regions, respectively. CGMCC 2.3823 and CGMCC 2.3824, having two nt differences in the ITS regions, differed from *Cy. fimetarium* and *Cy. minutum* by 9–14 nt (~1.5–2.4 %) and 16 nt (~2.6 %) mismatches in the D1/D2 and ITS regions, respectivley. CGMCC 2.3823 and CGMCC 2.3824 were closely related to *Cystobasidium halotolerans* in the D1/D tree (Fig. 5D); they differed from *Cy. halotolerans* by three to four nt in the ITS region, however, by 19–26 nt mismatches in the D1/D2 domain.

The above data indicated that these strains represented two novel species of *Cystobasidium*.

Note: CGMCC 2.3822 and the published strain TP-Snow-Y153 (JQ768912) had three nt differences in the D1/D2 domains, which indicated that they may be conspecific.

Robertozyma (incertae sedis, Cystobasidiales)

CGMCC 2.4451 and CGMCC 2.4452 had identical D1/D2 and ITS sequences. They belong to the newly described genus *Robertozyma* (Figs 4C, 5D and S2C). A new species is proposed to accommodate these two strains.

Begerowomyces (incertae sedis, Cystobasidiales)

The genus *Begerowomyces*, represented by CGMCC 2.3164, is proposed in this study (Figs 4C, 5D and S2C). Consequently, a new species name is proposed later.

Note: '*Cystobasidium*' *sp.* BSB307 (KY305128) isolated from Brazil clustered with CGMCC 2.3164, which indicated that this strain should represent a new taxon in *Begerowomyces*.

Lichenozyma and Halobasidium (incertae sedis)

The genus *Lichenozyma* has been proposed to accommodate yeasts isolated from and detected in the lichen *Cladonia* samples (Černajová & Škaloud, 2019). Interestingly, these yeasts have been reported as common inhabitants of lichens in Europe and USA (Spribille *et al.* 2016, Černajová & Škaloud, 2019). Some yeasts detected as a part of symbiotic three-partner system in the cortex of ascomycete macrolichens by Spribille *et al.* (2016). Although Spribille *et al.* (2016) suggested in their highly cited paper that these yeasts are possibly unculturable lichen associates, seven living axenic cultures have been obtained from air-dried *Cladonia* thali by Černajová & Škaloud (2019).

Phylogenetically *Lichenozyma* has been placed inside the genus *Microsporomyces* (Černajová & Škaloud, 2019). It is important to note that although, the dataset used by Černajová & Škaloud (2019) was largely based on the seven-genes (Wang *et al.* 2015a,b), all yeasts from lichens in the analysis contained predominantly ITS sequences. Only four isolates contained all three rDNA loci, ITS, LSU and SSU. No sequence of

protein-coding genes has been obtained for the genus *Lichenozyma* or other lichenicolous fungi, including yeasts from ascomycete macrolichens (Spribille *et al.* 2016) and *Cyphobasidium* (Millanes *et al.* 2016). As the result, phylogenetic analyses inferred with Bayesian Inference and Maximum Likelihood algorithms gave different topologies and several lineages identified previously identified by Wang *et al.* (2015a,b) has not been resolved by Černajová & Škaloud (2019). The subsequent analysis of the three rDNA loci (consisting mainly of ITS sequences) suggested that the genus *Microsporomyces* is polyphyletic and supported the erection of the *Lichenozyma*. The fact that monophyly of the *Microsporomyces* clade received no statistical support (both BI and ML) can be explained with very poor taxon sampling in both genus *Microsporomyces* and outgroups.

We included available LSU, SSU and ITS sequences of *Lichenozyma pisutiana* in our combined three rDNA loci, combined ITS and LSU and LSU datasets. Our analyses demonstrated that *Lichenozyma pisutiana* was placed inside the genus *Microsporomyces* with high statistical support. The genus *Microsporomyces* was resolved with high statistical support in the combined three rDNA loci and combined ITS (ML: 100 %) and LSU (ML: 99 %) trees (Figs 6 and S5, S6). Our analyses do not support a separate phylogenetic position of the genus *Lichenozyma.* Therefore, the *Lichenozyma* species should be transferred into *Microsporomyces* as synonym.

The genus *Halobasidium* has been proposed to accommodate a single yeast isolate from pickling sauce for a traditional high-salt fermented food in China (Guo *et al.* 2019). Although the presented phylogenetic tree clearly showed a separated phylogenetic position of the *Halobasidium xiangyangense*, the tree is very poor in terms of taxon sampling. The analysis did not include 9 out of 18 *Cystobasidium* species (*C. alpinum*, *C. fimetarium*, *C. halotolerans*, *C. iriomotense*, *C. keelungensis*, *C. oligophagum*, *C. ongulense*, *C. portillonense*, and *C. tubaki*), including the type species of the genus *C. fimetarium*, *Occultifur mephitis*, and numerous sequences representing yet undescribed yeast species in *Cystobasidiales*. Among sequences representing potential new taxa in *Cystobasidiaceae*, *Cystobasidiomycetes sp.* DSM 28479 (NCBI Taxonomy ID 1524830) and JS-40 (NCBI Taxonomy ID 1082630) showed 99 and 97 % (LSU) and 97 and 95 % (ITS) similarity to *Halobasidium xiangyangense*, respectively. These yeasts are likely to represent closely related species (DSM 28479) or conspecific isolates (JS-40). It is important to note that *Cystobasidiomycetes sp.* DSM 28479 (cited as *Rhodotorula sp.* MB27) has been found to be the closest outgroup to the *Cystobasidium* - *Occultifur* clade by Yurkov *et al.* (2015b). Phylogenetic placement presented by Guo *et al.* (2019) contradicts larger phylogenetic analyses published by Yurkov *et al.* (2015b), who showed that LSU and combined rDNA phylogenies are able to resolve genera *Cystobasidium*, *Occultifur* and "*Rhodotorula*" *sp.* MB27.

Phylogenetic analysis performed in the present study showed that LSU alone is not sufficient to resolve genera in Cystobasidiaceae, including *Cystobasidium*, *Halobasidium*, *Occultifur*, *Queiroziella* and newly proposed *Begerowomyces* and *Robertozyma* (Fig. S5). Combined phylogenetic analyses of the rDNA cistron and the seven-genes analysis resolved this genus with good statistical support (Fig. 4A). The constrained LSU analysis confirmed that the two aforementioned *Cystobasidiomycetes* belong to the genus *Halobasidium* (Figs 5D and S5).

With these examples we would like to show that good taxon sampling is essential for phylogenetic studies and taxonomy of basidiomycetous yeasts. A particular attention should be given to newly erected monotypic yeast genera, which should be preferably circumscribed using multi-gene phylogenies, as in the case of recent descriptions of genera *Heitmania*, *Libkindia* and *Yurkovia* (Liu *et al.* 2017, Mašínová *et al.* 2017).

New species identification in the *Microbotryomycetes* (*Pucciniomycotina*)

Rhodosporidiobolus (Sporidiobolaceae, Sporidiobolales)

Three groups, represented by CGMCC 2.3532, CGMCC 2.4435 and CGMCC 2.3118, were located in the *Rhodosporidiobolus* clade (Figs 4D, 5E and S2D). Group CGMCC 2.3532, containing two strains with identical sequences, clustered with *Rhodosporidiobolus poonsookiae* and *Rhodosporidiobolus ruineniae* without support in the tree obtained from the D1/D2 dataset (Fig. 5E), but it was located in a different place in the trees of the three rDNA loci and seven-genes datasets (Figs 4D and S2D). The BLASTn searches of the ITS and D1/D2 indicated that CGMCC 2.3532 are more related to *Rh. ruineniae* than other species. This group differed from *Rh. ruineniae* by 16 nt (~3 %) in the D1/D2 domains and 32 nt (~5 %) mismatches in the ITS region. Group CGMCC 2.4435, consisting of three strains with one nt difference in the D1/D2 domains, differed from its closest relative, *Rhodosporidiobolus lusitaniae* by eight nt (~1.3 %) and 22 nt (~4 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.3118 was most closely related to *Rhodosporidiobolus nylandii* and differed from it by five nt and 14 nt (~3 %) mismatches in the D1/D2 and ITS regions, respectively.

The sequence comparisons showed that these three groups represent three distinct novel species in *Rhodosporidiobolus*.

Note: Three unpublished strains '*Sporobolomyces' sp.* Vega180 (EU002899), '*Sporobolomyces' sp.* Vega122 (EU009966) and *Rhodosporidiobolus sp.* Vega175 (MG471376) isolated from Coffea in Puerto Rico, USA, and '*Rhodosporidiobolus odoratus*' AUMC 10780 (KY495748) isolated from fresh guava juice collected from shops in Assiut city, Egypt, had one to two nt difference from CGMCC 2.3118 in the ITS region, which indicated that they are conspecific. '*Sporidiobolus' sp.* ST-88 (DQ404450) and '*Sporidiobolus' sp*. ST-90 (DQ404451) differed from CGMCC 2.3532 group by three to five nt in the D1/D2 domains, however, the ITS sequences of those two strains are not available. Therefore, the taxonomic positions of those two strains were not delineated.

Sporobolomyces (Sporidiobolaceae, Sporidiobolales)

Twelve strains forming four groups clustered in the genus *Sporobolomyces* based on the sequence analysis of the seven genes and rDNA loci datasets (Figs 4D, 5E and S2D). CGMCC 2.5675, CGMCC 2.5687 and two published strains, '*Sporobolomyces aff. jilinensis*' MCA 3774 (JN942193/JN940715) and MCA 3785 (JN942199/JN940720) had identical D1/D2 and ITS sequences. They differed from *Sporobolomyces jilinensis* by 12 nt (~2 %) and 10 nt (~1.7 %) mismatches in the D1/D2 and ITS regions, respectively. Groups CGMCC 2.5627 represented

by a single strain. Group CGMCC 2.5619 contained eight Chinese strains and one strain from UK (CBS 2642) with identical D1/D2 sequences and three nt ITS sequences difference, which indicated that they are conspecific. Groups CGMCC 2.5619 and CGMCC 2.5627 were most closely related to *Sporidiobolus metaroseus* and *Sporobolomyces roseus* (Fig. 5E). Group CGMCC 2.5627 differed from these two species by two to three nt in the D1/D2 domains and nine nt (~1.5 %) in the ITS regions. Group CGMCC 2.5619 differed from them by five to six nt (~1 %) in the D1/D2 domains and 19 nt (~3 %) in the ITS regions. The two new groups differed from each other by four nt and 18 nt (~3 %) in the D1/D2 and ITS regions, respectively. Based on the above sequence analyses three novel species of *Sporobolomyces*, are proposed to accommodate the groups CGMCC 2. 5675, CGMCC 2. 5627 and CGMCC 2. 5619.

The placement of IAM 13481 was not stable in the trees from the three datasets (Figs 4D, 5E and S2D). The BLASTn searches of the ITS and D1/D2 sequences showed that IAM 13481 had the highest match with *Sporobolomyces ruberrimus* and differed from it by 12 nt (~2 %) in both the D1/D2 and ITS regions. Originally IAM 13481 (= YK 419) was designated as *Sporobolomyces roseus* (Yamazaki & Komagata, 1983). Valério *et al.* (2008) indicated that this strain was incorrectly named and did not belong to S*p. roseus.* Since then this strain was treated as an unnamed taxon of *Sporobolomyces* (Valério *et al.* 2008). However, the genome of this strain (http://genome.jgi.doe.gov/pages/search-for-genes.jsf?organism=Sporo1b) had been sequenced by the Joint Genome Institute (http://www.jgi.doe.gov) ten years ago, which was the first *Pucciniomycotina* species with a genome sequence. After the genome was released, the genetic and genomic studies of degrading mycotoxin and mating type genes in the basidiomycetous yeasts based on this strain have been reported (Coelho *et al.* 2008, 2011, Ianiri *et al.* 2013, 2016). Unfortunately, a formal name has been unavailable for this strain until now, therefore, a new species name of *Sporobolomyces* is proposed to accommodate it.

Heitmania (Heitmaniaceae, Heitmaniales)

Two isolates, CGMCC 2.5602 and CGMCC 2.5650, formed a subclade in *Heitmania* (Figs 4D and S2D). These two strains differed from each other by four nt substitutions and 40 nt (~6 %) mismatches in the D1/D2 and ITS regions, respectively. CGMCC 2.5602 differed from the other *Heitmania* species, *Heitmania litseae*, *Heitmania elacocarpi* and *Heitmania castanopsis*, by six to eight nt (~1.0–1.4 %) substitutions and 86 nt (~14 %) mismatches in the D1/D2 and ITS regions, respectively. The differences between CGMCC 2.5650 and the other three known *Heitmania* species ranged between four to six nt in the D1/D2 domains and were greater than 15 % in the ITS regions. Two novel species are suggested to accommodate these two strains.

Microbotryozyma (Ustilentylomataceae, Microbotryales)

The genus *Microbotryozyma* contains a single species, namely *Microbotryozyma collariae*, and was located in the family *Ustilentylomataceae* (Figs 4A, 5F and S2E). Strain CGMCC 2.3533 differed from *Mi. collariae* by six nt (~1 %) and 57nt (~11 %) in the D1/D2 and ITS regions, respectively. Therefore, a novel species is suggested to accommodate this strain.

Yamadamyces (Kriegeriaceae, Kriegeriales)

CGMCC 2.5820 clustered with the monotypic genus *Yamadamyces* in the trees obtained from the seven-genes as well as three rDNA loci datsets (Figs 4E and S2E). One nt difference in the D1/D2 domains and 56 nt (~10 %) mismatches in the ITS regions were found between CGMCC 2.5820 and *Yamadamyces rosulatus*, which indicated that CGMCC 2.5820 could represent a novel *Yamadamyces* species .

Oberwinklerozyma (incertae sedis)

Groups CGMCC 2.3441 and CGMCC 2.5824 were located in the *Oberwinklerozyma* clade (Figs 4E, 5G and S2E). CGMCC 2.5824 and four unpublished strains labeled as '*Rhodotorula' sp.* n-w29 (LC326052) and '*Rhodotorula' sp.* BI157 (EU678941), *Chrysozymaceae sp.* SJ13L05 (EU523609/FJ153202) and '*Rhodotorula' sp.* GY23L16 (HQ623608/FJ527098) contained identical sequences in the D1/D2 domains, and the latter two strains had two to three nt substitutions with CGMCC 2.5824 in the ITS regions, which indicated that they are conspecific. They differed from *Oberwinklerozyma yarrowii* by seven nt (~1.2 %) and more than 40 nt (~6 %) mismatches in the D1/D2 and ITS regions, respectively. CGMCC 2.3441 occupied a separated bottom branch in the *Oberwinklerozyma* clade. It differed from the other *Oberwinklerozyma* species by more than six nt (~1 %) in the D1/D2 domains and 68 nt (~11 %) mismatches in the ITS regions, respectively.

The phylogenetic analysis showed that these strains represented two novel species in *Oberwinklerozyma*.

Chrysozyma (Chrysozymaceae, incertae sedis)

The genus *Chrysozyma*, containing the two species *Chrysozyma griseoflava* and *Chrysozyma fushanensis*, was recently proposed (Wang *et al.* 2015b) based on the phylogenetic analysis of seven genes. Thirteen strains formed eight groups and were all closely related to *Ch. griseoflava* (Figs 4E, 5H and S2E). Group CGMCC 2.5629 consisted of three strains that had one nt difference in the D1/D2 domains. They differed from *Ch. griseoflava* by seven nt (~1.1 %) and nine nt (~1.3 %) substitutions in the D1/D2 and ITS regions, respectively. Groups CGMCC 2.2618 and CGMCC 2.2765, both containing two strains with identical sequences, differed from *Ch. griseoflava* by three to nine nt (~0.5–1.5 %) and 20–54 nt (~3–8 %) mismatches in the D1/D2 and ITS regions, respectively. Two strains in the CGMCC 2.2768 group had similar sequences with two nt and four nt in the D1/D2 and ITS regions, respectively. Six nt differences in the D1/D2 domains and 64 nt (~9 %) in the ITS regions were found between the CGMCC 2.2768 group and *Ch. griseoflava.* Groups CGMCC 2.5821, CGMCC 2.2769 and CGMCC 2.3455, all represented by only a single strain, differed from *Ch. griseoflava* by two to four nt in the D1/D2 domains and 71–75 nt (~10–11 %) mismatches in the ITS regions. Group CGMCC 2.5611 and '*Rhodotorula*' *sp.* DSM 101778 (KX067789) published by Prior *et al.* (2017), had three nt differences in the ITS regions, which indicated that they are conspecific. This group differed from *Ch. griseoflava* by 11 nt (~1.8 %) and 84 nt (~14 %) mismatches in the D1/D2 and ITS regions, respectively.

The above sequence comparisons indicated that these eight groups represent eight novel taxa in *Chrysozyma*.

Yurkovia (Chrysozymaceae, incertae sedis)

Analysis of the sequences of the ITS region and D1/D2 domains suggested that CGMCC 2.5603 has affinity to the genus *Yurkovia* (Mašínová *et al.* 2017) (Figs 4E, 5H and S2E). Four nt and 40 nt (~7 %) differences in the D1/D2 and ITS regions, respectively, were observed between CGMCC 2.5603 and *Yurkovia mendeliana*. CGMCC 2.5603 had identical sequences as *Yurkovia nerthusi* in the D1/D2 domains, however, they differed from each other by 39 (~6 %) mismatches in the ITS region, which indicated that CGMCC 2.5603 represents a novel species in *Yurkovia*.

Pseudohyphozyma (incertae sedis)

The seven strains CGMCC 2.2612, CGMCC 2.2796, CGMCC 2.2797, CGMCC 2.5607, CGMCC 2.5618, CGMCC 2.5623 and GPS23.3D2 were located in the *Pseudohyphozyma* clade, forming two groups (Figs 4E, 5H and S2E). Group CGMCC 2.2612 and *Pseudohyphozyma bogoriensis* differed from each other by four nt and 22 nt (~4 %) mismatches in the D1/D2 and ITS regions, respectively. Group CGMCC 2.2796 contained six strains with one nt difference in the ITS regions and differed from its closest relative *Pseudohyphozyma pustula* by five nt and 22nt (~4 %) mismatches in the D1/D2 and ITS regions, respectively.

The above sequence comparisons indicated that these seven strains represent two novel species in *Pseudohyphozyma*.

Slooffia (incertae sedis)

Strain CGMCC 2.5822 was placed in the genus *Sloofia* with 100 % bootstrap support (Figs 4E, 5H and S2E). It had identical D1/D2 sequences with *Slooffia tsugae* and 37 nt (~5 %) differences in the ITS region, which indicated that CGMCC 2.5822 represents a different species.

Colacogloea (Colacogloeaceae, incertae sedis)

Eight strains formed three groups in the *Colacogloea* clade (Figs 4E, 5G and S2E). Group CGMCC 2.2766 differed from its closest relative *Colacogloea cycloclastica* by 32 nt (~5 %) in the D1/D2 domains and more than 13 % mismatches in the ITS region. Groups CGMCC 2.2798 and CGMCC 2.2770, consisting of six strains with one nt and two nt difference in the D1/D2 and ITS regions, respectively, were closely related to *Colacogloea diffluens*. The two groups differed from *Co. diffluens* by 22–26 nt (~3.6–4.3 %) in the D1/D2 domains, and more than 14 % mismatches in the ITS regions. Groups CGMCC 2.2798 and CGMCC 2.2770 differed from each other by 26 nt (~4.3 %) substitutions and 8.8 % mismatches in the D1/D2 and ITS regions, respectively.

The sequence comparisons indicated that these eight strains represent three novel species in *Colacogloea*.

Rosettozyma (Rosettozymaceae, Rosettozymales)

Six strains, separated in three groups were located in the newly circumscribed genus *Rosettozyma* (Figs 4E, 5G and S2E). CGMCC 2.3446, CGMCC 2.3461 and CGMCC 2.3466 had one nt difference in the D1/D2 domains and shared the same ITS sequences, which indicated that they are conspecific. CGMCC 2.2615 and CGMCC 2.2619 had one and three nt differences in the D1/D2 and ITS regions, respectively, which indicated that they belong to the same species. Group CGMCC 2.2615 differed from the CGMCC 2.3446 group by four to six nt and 12–14 nt (~2–2.3 %) mismatches in the D1/D2 and ITS regions, respectively. CGMCC 2.5819 differed from groups CGMCC 2.2615 and CGMCC 2.3446 by 28–30 nt (~4.7–5 %) in the D1/D2 domains and 30–43 nt (~5–7.2 %) mismatches in the ITS regions.

The above data indicated that these six strains represent three novel *Rosettozyma* species.

Taxonomy

New taxa in *Tremellomycetes* (*Agaricomycotina*)

Kockovaella haikouensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828736. Fig. 7A, B.

Etymology: the specific epithet *haikouensis* refers to the geographic origin of the type strain, Haikou county, Hainan.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal or ovoid, 1.8–3.5 × 2.5–5.0 µm and single, budding is polar (Fig. 7A), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on CM, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal or some what kidney-shaped, 3.3–5.0 × 5.0–8.3 µm (Fig. 7B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, soluble starch (variable), D-xylose (variable), L-arabinose (variable), D-ribose, D-glucosamine, N-Acetyl-D-glucosmine, ethanol (variable), glycerol (variable), erythritol (variable), ribitol (variable), galactitol, D-mannitol, methyl α-D-glucoside, salicin, DL-lactate(variable), succinate (variable) are assimilated as sole carbon sources. L-sorbose, inulin, D-arabinose, L-rhamnose, methanol, D-glucitol, citrate, myo-inositol and hexdecane are not assimilated. Ammonium sulfate, L-lysine (variable), ethylamine hydrochloride (delayed) and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive. The major ubiquinone is Q-10.

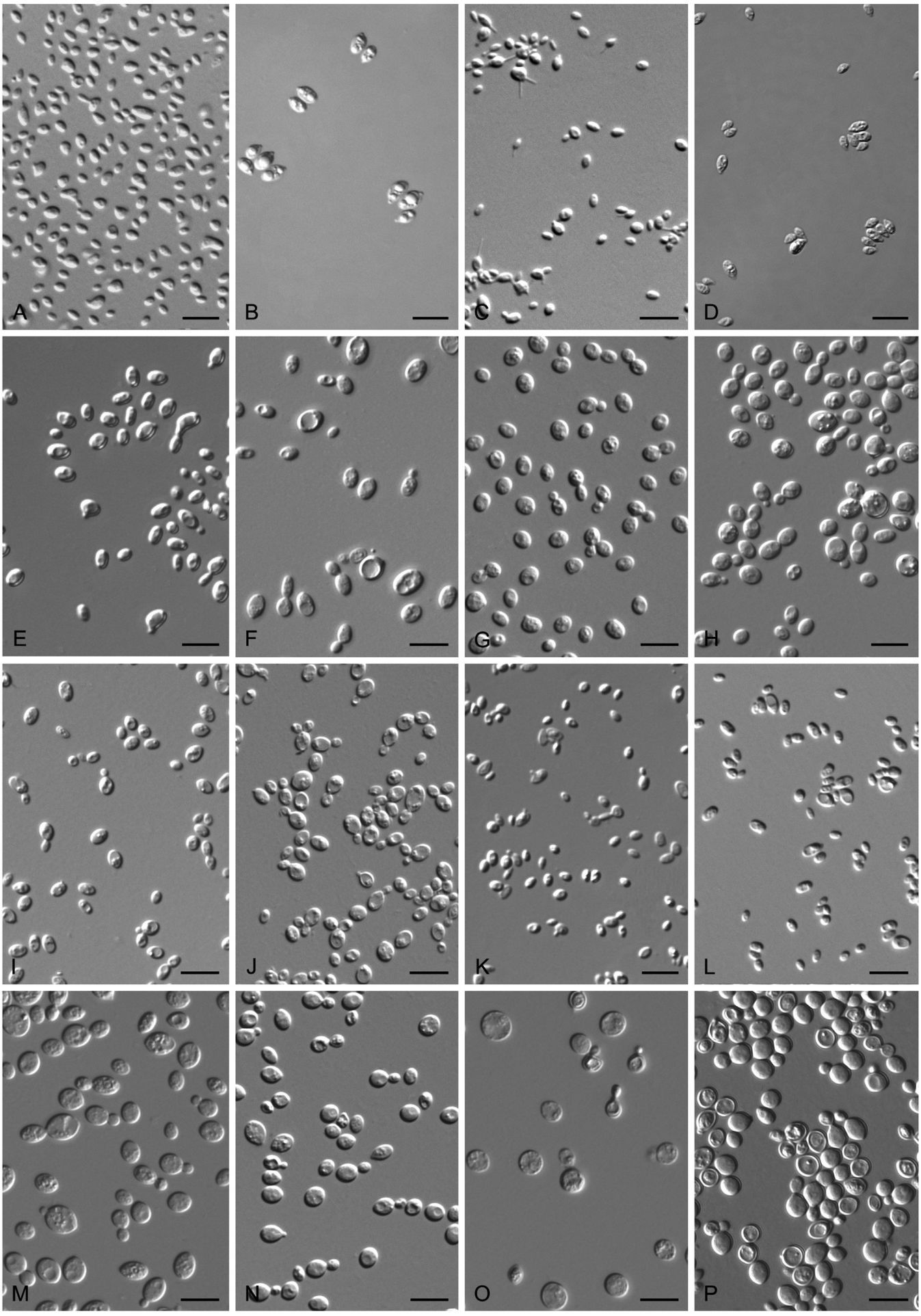
Physiologically, *Koc. haikouensis* differs from the closely related species *Koc. ischaemi* in its inability to assimilate inulin, D-arabinose, L-rhamnose and sodium nitrite and its ability to assimilate ethylamine (Table S1.1).

Typus: **China**, Haikou county, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3443^{T} preserved in a metabolically inactive state, ex-type CBS 15478 = HKX2).

Kockovaella ischaemi Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828738. Fig. 7C, D.

Etymology: the specific epithet *ischaemi* refers to *Ischaemum*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal or ovoid, 2.0–3.8 × 2.3–6.2 µm and single or pairs, budding is polar (Fig. 7C), blastoconidia are produced on short stalk-like conidiophores, a sediment is formed. After 1 mo at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17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal or some what kidney-shaped, 2.0–3.7 × 4.2–6.7 µm (Fig. 7D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose (weak), D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, glycerol (variable), ribitol (variable), galactitol, D-mannitol, Methyl-α-D-glucoside (variable), salicin (weak), succinate (weak), citrate (variable) and myo-Inositol (variable) are assimilated as sole carbon sources. L-sorbose, methanol, ethanol, erythritol, D-glucitol, DL-lactate and hexadecane are not assimilated. Ammonium sulfate, sodium nitrite and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate, L-lysine and ethylamine hydrochloride are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive. The major ubiquinone is Q-10.

Physiologically, *Koc. ischaemi* differs from the closely related species *Koc. haikouensis* in its inability to assimilate ethylamine and its ability to assimilate inulin, D-arabinose, L-rhamnose and sodium nitrite (Table S1.1).

Typus: **China**, Jinghong, Yunnan province, obtained from a leaf of *Ischaemum sp.*, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3565^{T} preserved in a metabolically inactive state, ex-type CBS 15500 = JH5.17)

Kockovaella nitrophila Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828739. Fig. 7E.

Etymology: the specific epithet *nitrophila* refers to the physiological character of assimilating nitrate.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ellipsoidal, 2.4–4.4 × 3.7–4.5 µm and single, budding is polar (Fig. 7E), a sediment is formed. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is creamish white, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (weak), sucrose, maltose, trehalose, melibiose (weak), raffinose, melezitose, inulin, D-xylose (weak), L-arabinose (weak), D-arabinose (weak), D-ribose (weak) and DL-lactate (weak) are assimilated as sole carbon sources. L-sorbose, cellobiose, lactose, soluble starch, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine (weak), ethylamine hydrochloride (weak) and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 37 °C. Growth in vitamin-free medium is positive (weak). Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive. The major ubiquinone is Q-10.

Physiologically, *Koc. nitrophila* differs from its five closely related species, *Koc. ischaemi*, *Koc. haikouensis*, *Koc. sacchari*, *Koc. thailandica* and *Koc. imperatae*, in its inability to assimilate cellobiose, melibiose, D-glucosamine, N-Acetyl-D-glucosamine and D-mannitol and its ability to assimilate potassium nitrate (Table S1.1).

Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3465^{T} preserved in a metabolically inactive state, ex-type CBS 15487 = WZS12.1).

Genolevuria pseudoamylolytica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828740. Fig. 7F.

Etymology: the specific epithet *pseudoamylolytica* refers to the similar colony morphology to that of *Genolevuria amylolytica*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and subglobosal, 2.9–5.2 × 3.3–7.7 µm and single, budding is polar (Fig. 7F), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, mucoid, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, inulin (weak), soluble starch, D-xylose (weak), L-arabinose, D-arabinose, D-ribose, L-rhamnose (weak), D-glucosamine, N-Acetyl-D-glucosamine, D-mannitol (weak), D-glucitol (weak), Methyl-α-D-glucoside and salicin are assimilated as sole carbon sources. Methanol, ethanol, glycerol, erythritol, ribitol, galactitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *G. pseudoamylolytica* differs from the two closely related species, *G. amylolytica* and *G. tibetensis*, in its inability to assimilate ribitol and succinate and the ability to assimilate L-sorbose and potassium nitrate (Table S1.2).

Fig. 7. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *Koc. haikouensis* CGMCC 2.3443^{T}; (C, D) *Koc. ischaemi* CGMCC 2.3565^{T}; (E) *Koc. nitrophila* CGMCC 2.3465^{T}; (F) *G. pseudoamylolytica* CGMCC 2.5809^{T}; (G) *Tr. shuangheensis* CGMCC 2.5615^{T}; (H) *V. melezitolyticum* CGMCC 2.3472^{T}; (I) *V. pseudopenaeus* CGMCC 2.3165^{T}; (J) *V. europaea* CGMCC 2.3099^{T}; (K) *Ca. follicola* CGMCC 2.3447^{T}; (L) *Ca. simaoensis* CGMCC 2.3580^{T}; (M) *Kwoni. ovata* CGMCC 2.3439^{T}; (N) *Te. helanensis* CGMCC 2.4450^{T}; (O) *Te. globosa* CGMCC 2.5648^{T}; (P) *Te. korlaensis* CGMCC 2.3835^{T}. Bars = 10 µm.

Typus: **China**, Daliangzi river national forest park, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2014, Q.-M. Wang (**holotype** CGMCC 2.5809^T preserved in a metabolically inactive state, ex-type CBS 13955 = HLJ1B6).

Tremella shuangheensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828741. Fig. 7G.

Etymology: the specific epithet *shuangheensis* refers to the geographic origin of the type strain, Shuanghe county, Heilongjiang.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ellipsoidal, 3.2–4.6 × 4.0–5.5 µm and single, budding is polar (Fig. 7G), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, mucoid, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed and weak), L-sorbose (weak), sucrose, maltose, cellobiose, trehalose, lactose (delayed), melibiose (delayed), melezitose (delayed and weak), inulin (delayed), soluble starch (delayed and weak), D-xylose, L-arabinose (weak), D-arabinose (delayed and weak), D-ribose (delayed and weak), L-rhamnose (delayed and weak), D-glucosamine (delayed and weak), N-Acetyl-D-glucosamine (delayed and weak), ethanol (delayed and weak), glycerol, erythritol, ribitol, galactitol, D-mannitol (delayed and weak), D-glucitol (delayed and weak), Methyl-α-D-glucoside (delayed and weak), salicin (delayed and weak), D-gluconate (delayed and weak), DL-lactate (delayed and weak), succinate (delayed and weak) and myo-inositol (delayed and weak) are assimilated as sole carbon sources. Raffinose, methanol, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is delayed. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *T. shuangheensis* differs from the closely related species *T. globispora* in its ability to assimilate lactose, melibiose, inulin and the inability to assimilate citrate (Table S1.3).

Typus: **China**, Shuanghe county, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2015, Q.-M. Wang (**holotype** CGMCC 2.5615^T preserved in a metabolically inactive state, ex-type CBS 15561 = SH58A1).

Vishniacozyma melezitolytica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828742. Fig. 7H.

Etymology: the specific epithet *melezitolytica* refers to the physiological character of assimilating melezitose.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 2.6–5.0 × 3.9–6.1 µm and single, budding is polar (Fig. 7H), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is brownish-cream, butyrous, glistening and smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (variable), sucrose, maltose, cellobiose, trehalose, lactose, raffinose, melezitose, inulin (variable), D-xylose, L-arabinose, D-arabinose (variable), D-ribose (variable), L-rhamnose, N-Acetyl-D-glucosamine (variable), D-glucosamine (variable), ethanol, glycerol, ribitol (variable), galactitol (variable), D-mannitol, D-glucitol (variable), Methyl-α-D-glucoside (variable), salicin (weak), succinate (variable) and myo-inositol (variable) are assimilated as sole carbon sources. Melibiose, soluble starch, methanol, erythritol, D-gluconate, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), L-lysine, ethylamine hydrochloride (variable) and cadaverine dihydrochloride (variable) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is variable. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *V. melezitolytica* differs from the closely related species *V. dimennae* and *V. globispora* in its inability to assimilate DL-lactate and citrate and its ability to assimilate melezitose (Table S1.4).

Typus: **China**, Hebei province, obtained from a leaf of an unidentified plant, Apr. 2007, Q.-M. Wang (**holotype** CGMCC 2.3472^T preserved in a metabolically inactive state, ex-type CBS 15490 = H5A3).

Vishniacozyma pseudopenaeus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828743. Fig. 7I.

Etymology: the specific epithet *pseudopenaeus* refers to the similar colony morphology and physiological characteristics to that of *Vishniacozyma penaeus*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subsphaeroidal and ellipsoidal, 2.6–3.5 × 2.8–5.0 µm and single, budding is polar (Fig. 7I), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale grayish-cream, mucoid, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, soluble starch (varialbe), D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, D-gluconate, ethanol (varialbe), glycerol, erythritol (varialbe), ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, , DL-lactate (varialbe), succinate (weak), citrate and myo-inositol are assimilated as sole carbon sources. Inulin, methanol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), L-lysine, ethylamine hydrochloride (weak) and cadaverine dihydrochloride (variable) are assimilated as sole nitrogen sources. Sodium nitrite are not assimilated as sole nitrogen sources. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is positive. Starch-like substances are

produced or not. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *V. pseudopenaeus* differs from the closely related species *V. penaeus* in its ability to grow in vitamin-free medium, however, the latter does not grow in vitamin-free medium (Table S1.4).

Typus: **Germany**, obtained from a leaf of an unidentified plant, Sep. 2005 (**holotype** CGMCC 2.3165^T preserved in a metabolically inactive state, ex-type CBS 15472 = G7.20).

Vishniacozyma europaea Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828744. Fig. 7J.

Etymology: the specific epithet *europaea* refers to the geographic origin of the type strain, Europe.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ellipsoidal, 2.4–4.8 × 3.0–9.6 µm and single, budding is polar (Fig. 7J), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish cream, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, ethanol (delayed and weak), glycerol (delayed and weak), erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, succinate, citrate (weak) and myo-inositol are assimilated as sole carbon sources. L-sorbose, inulin, methanol, DL-lactate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *V. europaea* differs from the closely related species *V. foliicola* in its inability to produce starch-like substances and its ability to assimilate soluble starch and potassium nitrate (Table S1.4).

Typus: **Germany**, obtained from a leaf of an unidentified plant, Sep. 2005 (**holotype** CGMCC 2.3099^T preserved in a metabolically inactive state, ex-type CBS 15464 = G7.1-2).

Carlosrosaea foliicola Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828745. Fig. 7K.

Etymology: the specific epithet *foliicola* refers to the substrate origin of the type strain, leaves.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 1.7–4.0 × 2.5–5.8 µm and single, budding is polar (Fig. 7K), a sediment is formed. After 1 mo at 17 °C, a part ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is white-cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose (delayed and weak), D-ribose, L-rhamnose (delayed and weak), D-glucosamine, ethanol, glycerol, erythritol, ribitol (delayed and weak), galactitol (delayed and weak), D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate (delayed and weak), citrate (delayed and weak) and myo-inositol (weak) are assimilated as sole carbon sources. L-sorbose, inulin, methanol and hexadecane are not assimilated. Ammonium sulfate is assimilated as sole nitrogen sources. Potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ca. foliicola* differs from the closely related species *Ca. simaoensis* in its ability to assimilate erythritol (Table S1.5).

Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3447^T preserved in a metabolically inactive state, ex-type CBS 15481 = WZS29.4).

Carlosrosaea simaoensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828746. Fig. 7L.

Etymology: the specific epithet *simaoensis* refers to the geographic origin of the type strain, Simao county, Yunnan.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 2.0–2.6 × 3.3–4.2 µm and single, budding is polar (Fig. 7L), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is white-cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose (delayed and weak), D-ribose, L-rhamnose (delayed and weak), D-glucosamine, ethanol, glycerol, ribitol, galactitol (delayed and weak), D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate (delayed and weak), succinate (weak), citrate and myo-inositol (delayed and weak) are assimilated as sole carbon sources. L-sorbose, inulin, methanol, erythritol and hexadecane are not assimilated. Ammonium sulfate is assimilated as sole nitrogen sources. Potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ca. foliicola* and *Ca. simaoensis*, and their three closely related species, *Ca. vrieseae*, *Ca. hohenbergiae*

and *Ca. aechmeae*, can be distinguished from each other by the ability to assimilate inulin, erythritol, L-lysine and cadaverine and form starch like compounds (Table S1.5).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3580^T preserved in a metabolically inactive state, ex-type CBS 15503 = SM8.1).

Kwoniella ovata Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828747. Fig. 7M.

Etymology: the specific epithet *ovata* refers to the ovoid cell morphology of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 4.2–6.8 × 5.2–7.9 µm and single, budding is polar (Fig. 7M), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is tannish-white, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, ethanol, glycerol, ribitol (delayed and weak), galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside (weak), succinate and myo-inositol (weak) are assimilated as sole carbon sources. L-sorbose, melibiose, inulin, D-glucosamine, methanol, erythritol, salicin, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, sodium nitrite and L-lysine (weak) are assimilated as sole nitrogen sources. Potassium nitrate, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 37 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kwon. ovata* differs from its closely related species *Kwon. pini* and *Kwon. dejecticola* in its ability to grow at 37 °C (Table S1.6).

Typus: **China**, Hebei province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3439^T preserved in a metabolically inactive state, ex-type CBS 15475 = H1C1).

Teunia Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828751.

Etymology: the genus is named in honour of Dr. Teun Boekhout for his contributions to yeast taxonomy.

This genus is proposed for the clade represented by *Cryptococcus cuniculi*, which clustered with *Fonsecazyma tronadorensis* (*Cryptococcus tronadorensis*), *Fonsecazyma betulae* (*Kwoniella betulae*) and three new species represented by CGMCC 2.4450, CGMCC 2.5648 and CGMCC 2.3835, respectively. Member of the *Cryptococcaceae* (*Tremellales*). The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a well supported clade within *Cryptococcaceae* (Fig. 2).

Sexual reproduction not known. Colonies cream to yellow, butyrous to mucoid. Budding cells present. Pseudohyphae and hyphae are not produced. Ballistoconidia are not formed.

Type species: *Teunia korlaensis* Q.M. Wang, F.Y. Bai & A.H. Li.

New species and combinations for *Teunia*

Teunia betulae K. Sylvester, Q.M. Wang & Hittinger ex Q.M. Wang, F.Y. Bai & A.H. Li, ***sp. nov.*** MycoBank MB828752.
For description see FEMS Yeast Res. 15: 7 (2015).
Holotype: NRRL Y-63732 (preserved in a metabolically inactive state).
Synonym: *Kwoniella betulae* K. Sylvester *et al.*, FEMS Yeast Res. 15: 7 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Fonsecazyma betulae* K. Sylvester, Q.M. Wang & Hittinger ex Yurkov, Kachalkin & Boekhout, Stud. Mycol. 81: 129 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Teunia cuniculi (K.S. Shin & Y.H. Park) Q.M. Wang, F.Y. Bai & A.H. Li, ***comb. nov.*** MycoBank MB828753.
Basionym: *Cryptococcus cuniculi* K.S. Shin & Y.H. Park, Int. J. Syst. Evol. Microbiol. 56: 2243 (2006).

Teunia tronadorensis V. de García, Zalar, Brizzio, Gunde-Cim. & van Brook ex Q.M. Wang, F.Y. Bai & A.H. Li, ***sp. nov.*** MycoBank MB828754.
For description see FEMS Microbiol. Ecol. 82(2): 536 (2012).
Holotype: CRUB 1299 (preserved in a metabolically inactive state).
Synonym: *Cryptococcus tronadorensis* V. de García *et al.*, FEMS Microbiol. Ecol. 82(2): 536 (2012), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Fonsecazyma tronadorensis* V. de García, Zalar, Brizzio, Gunde-Cim. & van Brook ex Yurkov, Stud. Mycol. 81: 129 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Teunia helanensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828755. Fig. 7N.

Etymology: the specific epithet *helanensis* refers to the geographic origin of the type strain, Helanshan mountain, Ningxia.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid, subglobosal and ellipsoidal, 3.0–4.7 × 4.1–6.6 µm and single, budding is polar (Fig. 7N), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, mucoid, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed), maltose, cellobiose, trehalose, lactose, soluble starch (delayed), D-xylose, L-arabinose (delayed), D-arabinose (delayed), D-ribose (delayed and weak), L-rhamnose, D-glucosamine (delayed), ethanol (delayed), glycerol (delayed), galactitol, D-mannitol, D-glucitol, salicin and succinate are assimilated as sole carbon sources. L-sorbose, sucrose, melibiose, raffinose, melezitose, inulin, methanol, erythritol, ribitol, Methyl-α-D-glucoside, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and L-lysine are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated.

Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Te. helanensis* differs from the closely related species *Te. korlaensis* in its inability to assimilate sucrose and its ability to assimilate soluble starch, D-arabinose, L-rhamnose, ethanol, erythritol, D-glucitol, succinate and L-lysine (Table S1.7).

Typus: **China**, Helanshan mountain, Ningxia province, obtained from soil, Aug. 2009, P.J. Han (**holotype** CGMCC 2.4450^T preserved in a metabolically inactive state, ex-type CBS 12498 = HLS02-1-5).

Teunia globosa Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828756. Fig. 7O.

Etymology: the specific epithet *globosa* refers to the globosal vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are globosal, 4.5–8.0 × 5.1–8.0 µm and single, budding is polar (Fig. 7O), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish cream, butyrous, smooth and partly wrinkled, semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose (weak), melezitose, inulin (delayed and weak), soluble starch, D-xylose (delayed and weak), D-ribose (delayed and weak), L-rhamnose (delayed and weak), D-glucosamine (delayed and weak), N-Acetyl-D-glucosamine (weak), ethanol, D-mannitol, salicin, succinate (delayed and weak) and myo-inositol are assimilated as sole carbon sources. L-sorbose, melibiose, raffinose, L-arabinose, D-arabinose, methanol, glycerol, erythritol, ribitol, galactitol, D-glucitol, Methyl-α-D-glucoside, D-gluconate, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 22 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Te. globosa* differs from the closely related species *Te. betulae* in its inability to assimilate L-arabinose and its ability to assimilate ethanol (Table S1.7).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5648^T preserved in a metabolically inactive state, ex-type CBS 15566 = GPS23.2A6).

Teunia korlaensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828757. Fig. 7P.

Etymology: the specific epithet *korlaensis* refers to the geographic origin of the type strain, Korla county, Xinjiang.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal to globosal, 3.8–5.1 × 4.3–5.9 µm and single, budding is polar (Fig. 7P), a sediment is formed. After 1 mo at 17 °C, a part ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose (weak), melezitose (weak), inulin (weak), D-xylose (weak), L-arabinose (weak), D-ribose (delayed and weak), L-rhamnose (weak), galactitol, D-mannitol and salicin (weak) are assimilated as sole carbon sources. L-sorbose, melibiose, raffinose, soluble starch, D-arabinose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, ribitol, erythritol, D-glucitol, Methyl-α-D-glucoside, D-gluconate, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, ethylamine hydrochloride (weak) and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite and L-lysine are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Te. korlaensis* differs from the closely related species *Te. helanensis* in its inability to assimilate soluble starch, D-arabinose, L-rhamnose, ethanol, erythritol, D-glucitol, succinate and L-lysine and its ability to assimilate sucrose (Table S1.7).

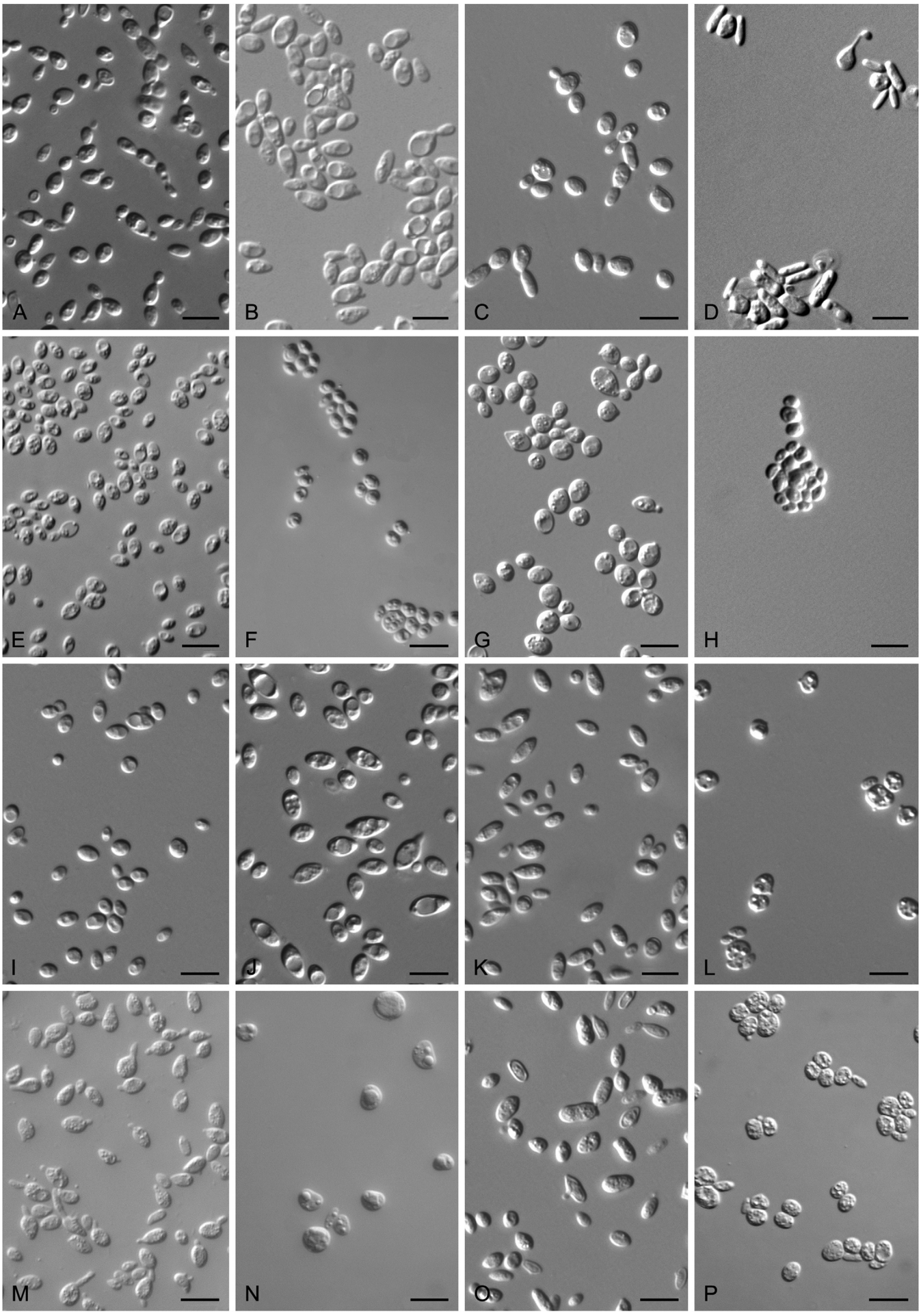
Typus: **China**, Korla county, Xinjiang province, obtained from soil, Feb. 2008, Q.-M. Wang (**holotype** CGMCC 2.3835^T preserved in a metabolically inactive state, ex-type CBS 15653 = 141.19).

Saitozyma pseudoflava Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828758. Fig. 8A.

Etymology: the specific epithet *pseudoflava* refers to the similar colony morphology to that of *Saitozyma flava*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ovoid, 3.2–4.3 × 5.2–6.8 µm and single, budding is polar (Fig. 8A), a sediment is formed. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, melibiose (weak), raffinose, melezitose, inulin (weak), D-xylose, L-arabinose, D-arabinose (weak), D-ribose, L-rhamnose (delayed and weak), D-glucosamine (delayed and weak), N-Acetyl-D-glucosamine (delayed and weak), ribitol (delayed and weak), galactitol (delayed and weak), D-mannitol (delayed and weak), D-glucitol, Methyl-α-D-glucoside, salicin (delayed and weak), D-gluconate (delayed and weak) and myo-inositol are assimilated as sole carbon sources. L-sorbose, trehalose, lactose, soluble starch, methanol, ethanol, glycerol, erythritol, DL-lactate, succinate, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine and ethylamine hydrochloride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(delayed and weak) are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sa. pseudoflava* differs from its closely related species *Sa. paraflava* and *Sa. flava* in its inability to assimilate cellobiose, trehalose, soluble starch, DL-lactate, succinate and citrate (Table S1.8).

Typus: **China**, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5811^T preserved in a metabolically inactive state, ex-type CBS 15576 = XZ200A1).

Dioszegia milinica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828759. Fig. 8B.

Etymology: the specific epithet *milinica* refers to the geographic origin of the type strain, Milin county, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.9–6.4 × 5.0–10.3 µm and single, budding is polar (Fig. 8B), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin, soluble starch (delayed and weak), D-xylose, L-arabinose, D-arabinose, L-rhamnose (delayed and weak), D-glucosamine (delayed and weak), galactitol, D-glucitol, succinate and citrate are assimilated as sole carbon sources. L-sorbose, lactose, D-ribose, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, D-mannitol, Methyl-α-D-glucoside, salicin, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), L-lysine (weak) and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is positive. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Di. milinica* differs from the closely related species *Di. aurantiaca* in its inability to assimilate D-ribose, N-Acetyl-D-glucosamine, glycerol, erythritol, ribitol, D-mannitol, Methyl-α-D-glucoside, salicin, DL-lactate and sodium nitrite and its ability to assimilate inulin and ethylamine (Table S1.9).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5628^T preserved in a metabolically inactive state, ex-type CBS 15563 = GPS21.3B8).

Dioszegia heilongjiangensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828760. Fig. 8C, D.

Etymology: the specific epithet *heilongjiangensis* refers to the geographic origin of the type strain, Heilongjiang province.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ellipsoidal, 3.2–5.0 × 4.5–7.3 µm and single, budding is polar (Fig. 8C), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish to light orange, butyrous, smooth and partly wrinkled. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are subglobosal to napiform, 4.0–5.0 × 5.0–6.0 µm (Fig. 8D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose (weak), maltose (weak), cellobiose (weak), trehalose (weak), melibiose, raffinose, melezitose, inulin (weak), D-xylose (delayed), L-arabinose, D-arabinose (delayed and weak), galactitol (weak), D-glucitol, salicin (weak) and succinate are assimilated as sole carbon sources. L-sorbose, lactose, soluble starch, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, D-mannitol, Methyl-α-D-glucoside, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite and ethylamine hydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Di. heilongjiangensis* differs from the closely related species *Di. changbaiensis* and *Di. cryoxerica* in its inability to assimilate D-ribose, L-rhamnose and D-mannitol and its ability to grow in vitamin-free medium (Table S1.9).

Typus: **China**, Chelu county, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2014, Q.-M. Wang (**holotype** CGMCC 2.5674^T preserved in a metabolically inactive state, ex-type CBS 13957 = HLJ13.24).

Dioszegia ovata Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828761. Fig. 8E, F.

Etymology: the specific epithet *ovata* refers to the ovoid cell morphology of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.3–4.6 × 3.8–7.7 µm and single, budding is polar (Fig. 8E), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pink to orange, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are globosal and subglobosal to napiform, 3.1–6.2 × 3.8–6.9 µm (Fig. 8F).

Fig. 8. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A) *Sa. pseudoflava* CGMCC 2.5811^T; (B) *Di. milinica* CGMCC 2.5628^T; (C, D) *Di. heilongjiangensis* CGMCC 2.5674^T; (E, F) *Di. ovata* CGMCC 2.3625^T; (G, H) *Di. maotaiensis* CGMCC 2.4537^T; (I) *Di. kandeliae* CGMCC 2.5658^T; (J) *Bu. phyllostachydis* CGMCC 2.5812^T; (K, L) *Bu. cremeum* CGMCC 2.4427^T; (M, N) *Bu. pseudopanici* CGMCC 2.4024^T; (O, P) *Bu. phyllophilum* CGMCC 2.3320^T. Bars = 10 µm.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (delayed), sucrose, maltose, cellobiose, trehalose, lactose (delayed), melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine (delayed and weak), galactitol, D-mannitol, Methyl-α-D-glucoside, salicin (weak) and succinate (delayed and weak) are assimilated as sole carbon sources. Inulin, methanol, ethanol, glycerol, erythritol, ribitol, D-glucitol, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and potassium nitrate (delayed and weak) are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is positive. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Di. ovata* and the closely related species *Di. maotaiensis*, *Di. kandeliae*, *Di. zsoltii*, *Di. catarinoi*, *Di. takashimae* and *Di. athyrii* can be distinguished from one another. *Di. ovata* differs from the other six species in its ability to grow at 32 °C (Table S1.9).

Typus: **China**, Bangxi county, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3625^T preserved in a metabolically inactive state, ex-type CBS 15657 = HBX1.27).

Dioszegia maotaiensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828762. Fig. 8G, H.

Etymology: the specific epithet *maotaiensis* refers to the geographic origin of the type strain, Maotai county, Guizhou.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 3.6–5.2 × 4.5–6.2 µm and single, budding is polar (Fig. 8G), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are are subglobosal to ellipsoidal, 2.4–3.5 × 3.5–5.3 µm (Fig. 8H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin, soluble starch (delayed and weak), D-xylose, L-arabinose, D-arabinose, L-rhamnose, succinate (delayed and weak) and citrate (delayed and weak) are assimilated as sole carbon sources. L-sorbose, lactose, D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and ethylamine hydrochloride are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, L-lysine and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Di. maotaiensis* and the closely related species *Di. ovata*, *Di. kandeliae*, *Di. zsoltii*, *Di. catarinoi*, *Di. takashimae* and *Di. athyrii* can be distinguished from one another. *Di. maotaiensis* and *Di. ovata* differ from the other five species in their ability to grow in vitamin-free medium (Table S1.9).

Typus: **China**, Maotai county, Guizhou province, obtained from a leaf of an unidentified plant, Mar. 2012, Q.-M. Wang (**holotype** CGMCC 2.4537^T preserved in a metabolically inactive state, ex-type CBS 15516 = GZMT3A9).

Dioszegia kandeliae Q.M. Wang, F.Y. Bai, L.D. Guo & A.H. Li ***sp. nov.*** MycoBank MB828763. Fig. 8I.

Etymology: the specific epithet *kandeliae* refers to *Kandelia*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal to subglobosal, 2.5–4.2 × 3.2–5.5 µm and single, budding is polar (Fig. 8I), a ring and a sediment are formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange-red, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, melezitose, inulin (weak), soluble starch (delayed and weak), D-xylose (delayed and weak), L-arabinose (delayed and weak), D-glucosamine (delayed and weak), N-Acetyl-D-glucosamine (delayed and weak), ethanol (delayed and weak), glycerol (delayed and weak), ribitol (delayed and weak) and D-glucitol are assimilated as sole carbon sources. Raffinose, D-arabinose, D-ribose, L-rhamnose, methanol, erythritol, galactitol, D-mannitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and L-lysine are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is negative. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Di. kandeliae* and the closely related species *Di. ovata*, *Di. maotaiensis*, *Di. zsoltii*, *Di. catarinoi*, *Di. takashimae* and *Di. athyrii* can be distinguished from one another. *Di. kandeliae* differs from the other six species in its inability to assimilate raffinose and L-rhamnose (Table S1.9).

Typus: **China**, Beilunhekou natural reserve, Guangxi province, obtained from a leaf of *Kandelia candel*, Apr. 2014, L.-D. Guo (**holotype** CGMCC 2.5658^T preserved in a metabolically inactive state, ex-type CBS 13951 = 224191).

Bulleribasidium phyllostachydis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828765. Fig. 8J.

Etymology: the specific epithet *phyllostachydis* refers to *Phyllostachys*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal, ovoid and ellipsoidal, 2.6–4.8 × 3.7–11.3 µm and single, budding is polar (Fig. 8J), a sediment is formed. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellow, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on

corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, cellobiose, trehalose, melibiose, raffinose, melezitose, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine (weak), N-Acetyl-D-glucosamine (weak), galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside (weak), salicin (weak) and D-gluconate are assimilated as sole carbon sources. L-sorbose, maltose, lactose, inulin, soluble starch, methanol, ethanol, glycerol, erythritol, ribitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and L-lysine (delayed and weak) are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Bu. phyllostachydis* differs from its closely related species *Bu. setariae* in its inability to assimilate maltose, inulin, DL-lactate, succinate and citrate (Table S1.10).

Typus: **China**, Motuo county, Tibet, obtained from a leaf of *Phyllostachys sp.*, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5812^T preserved in a metabolically inactive state, ex-type CBS 15575 = XZ139E1).

Bulleribasidium cremeum Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828766. Fig. 8K, L.

Etymology: the specific epithet *cremeum* refers to the pale-cream colony morphology.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 1.7–4.8 × 4.5–8.7 µm and single, budding is polar (Fig. 8K), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale-cream, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal to napiform, 3.3–6.7 × 4.0–6.7 µm (Fig. 8L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose (delayed and weak), trehalose, melibiose, raffinose, melezitose, D-xylose (delayed and weak), L-arabinose (delayed and weak), D-arabinose, salicin (weak) and succinate are assimilated as sole carbon sources. L-sorbose, lactose, inulin, soluble starch, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and L-lysine are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Bu. cremeum* differs from its closely related species, *Bu. phyllostachydis*, *Bu. wuzhishanense* and *Bu. setariae*, in its inability to assimilate galactitol, D-mannitol and Methyl-α-D-glucoside (Table S1.10).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4427^T preserved in a metabolically inactive state, ex-type CBS 12487 = TW1.1F-025).

Bulleribasidium pseudopanici Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828767. Fig. 8M, N.

Etymology: the specific epithet *pseudopanici* refers to the similar colony morphology to that of *Bulleribasidium panici*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid, 2.3–5.0 × 3.8–7.6 µm and single, budding is polar (Fig. 8M), a sediment is formed. After 1 mo at 17 °C, a part ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, slightly wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are subglobosal or ellipsoidal, 4.4–7.4 × 5.9–7.4 µm (Fig. 8N).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, galactitol, D-mannitol, D-glucitol (variable), Methyl-α-D-glucoside, salicin and myo-inositol are assimilated as sole carbon sources. L-sorbose, lactose, inulin, soluble starch, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, D-gluconate, DL-lactate, succinate, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride, cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

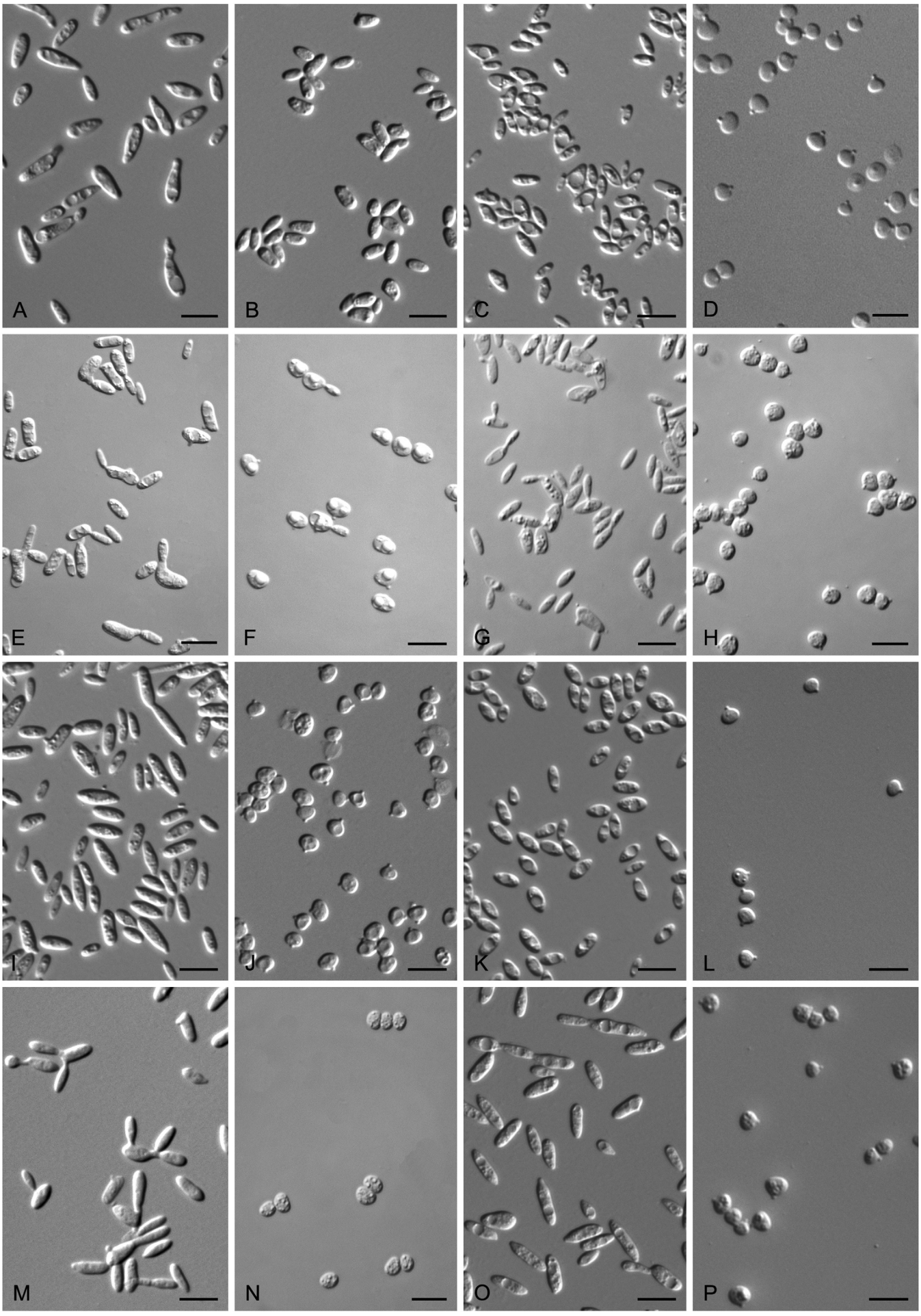
Physiologically, *Bu. pseudopanici* differs from its closely related species *Bu. panici* in its inability to assimilate L-sorbose, soluble starch, D-glucosamine, erythritol, ribitol, D-gluconate, DL-lactate and succinate and its ability to form starch like compounds (Table S1.10).

Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.4024^T preserved in a metabolically inactive state, ex-type CBS 15510 = WZS17.20).

Bulleribasidium phyllophilum Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828768. Fig. 8O, P.

Etymology: the specific epithet *phyllophilum* refers to leaves, the substrate origin of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.0–4.0 × 4.0–9.3 µm and single, budding is polar (Fig. 8O), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is prey-cream, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not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observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal, subglobosal to napiform, 3.8–6.2 × 4.6–6.2 µm (Fig. 8P).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin (variable), soluble starch (variable), D-xylose, L-arabinose, D-arabinose, L-rhamnose, D-glucosamine (weak), N-Acetyl-D-glucosamine (variable), galactitol, D-mannitol, D-glucitol (variable), Methyl-α-D-glucoside (delayed and weak) and myo-inositol (variable) are assimilated as sole carbon sources. L-sorbose, lactose, D-ribose, methanol, ethanol, glycerol, erythritol, ribitol, salicin, DL-lactate, succinate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), L-lysine (variable) and ethylamine hydrochloride (variable) are assimilatedas sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Bu. phyllophilum* and its closely related species *Bu. foliicola* cannot be distinguished from each other. The former did not grow at 30 °C, but the latter grew weak (Table S1.10).

Typus: **China**, Bangxi county, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3320^{T} preserved in a metabolically inactive state, ex-type CBS 15474 = HBX2.8).

Bulleribasidium elongatum Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828769. Fig. 9A.

Etymology: the specific epithet *elongatum* refers to the elongate vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.7–4.1 × 6.8–12.5 µm and single, budding is polar (Fig. 9A), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, D-xylose, L-arabinose (delayed and weak), D-arabinose (delayed and weak), D-ribose (delayed and weak), L-rhamnose (delayed and weak), D-glucosamine (delayed and weak), ribitol (delayed and weak) and galactitol are assimilated as sole carbon sources. L-sorbose, lactose, inulin, soluble starch, methanol, ethanol, glycerol, erythritol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, sodium nitrite (delayed and weak), L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Bu. elongatum* differs from its closely related species, *Bu. phyllophilum*, *Bu. foliicola* and *Bu. hainanense*, in its inability to assimilate D-mannitol and its ability to assimilate cadaverine (Table S1.10).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4428^{T} preserved in a metabolically inactive state, ex-type CBS 12489 = TW1.1F-019).

Derxomyces pseudoboekhoutii Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828770. Fig. 9B.

Etymology: the specific epithet *pseudoboekhoutii* refers to the similar colony morphology to that of *Derxomyces boekhoutii*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal or ovoid, 2.5–3.8 × 5.0–7.5 µm and single, budding is polar (Fig. 9B), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin, D-xylose, L-arabinose, D-arabinose, D-ribose (delayed), galactitol (weak), D-mannitol (delayed and weak) and Methyl-α-D-glucoside are assimilated as sole carbon sources. L-sorbose, lactose, soluble starch, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, D-glucitol, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride (delayed and weak), cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 25 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. pseudoboekhoutii* differs from the closely related species *De. boekhoutii* in its inability to assimilate soluble starch and grow in vitamin-free medium and its ability to assimilate D-arabinose and D-ribose (Table S1.11).

Typus: **China**, Fuzhou county, Fujian province, obtained from a leaf of an unidentified plant, Aug. 2011, Q.-M. Wang (**holotype** CGMCC 2.4436^{T} preserved in a metabolically inactive state, ex-type CBS 12493 = FJYZ12-8).

Derxomyces polymorphus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828771. Fig. 9C, D.

Etymology: the specific epithet *polymorphus* refers to the variable vegetative cell morphology of the type strain.

Fig. 9. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A) *Bu. elongatum* CGMCC 2.4428^{T}; (B) *De. pseudoboekhoutii* CGMCC 2.4436^{T}; (C, D) *De. polymorphus* CGMCC 2.4437^{T}; (E, F) *De. xingshaicus* CGMCC 2.2459^{T}; (G, H) *De. pseudoyunnanensis* CGMCC 2.3563^{T}; (I, J) *De. longiovatus* CGMCC 2.3535^{T}; (K, L) *De. napiformis* CGMCC 2.4446^{T}; (M, N) *De. bifurcus* CGMCC 2.3470^{T}; (O, P) *De. elongatus* CGMCC 2.3561^{T}. Bars = 10 µm.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid to fusiform, 2.0–4.8 × 4.7–8.0 µm and single, budding is polar (Fig. 9C), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, smooth and dull. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are subglobosal to napiform, 3.0–4.3 × 4.3–5.7 µm (Fig. 9D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin (weak), soluble starch, D-xylose, L-rhamnose (weak), galactitol, D-glucitol, salicin (weak) and succinate are assimilated as sole carbon sources. L-sorbose, lactose, L-arabinose, D-arabinose, D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, D-mannitol, Methyl-α-D-glucoside, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), L-lysine, ethylamine hydrochloride, cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 27–28 °C. Growth in vitamin-free medium is weak. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. polymorphus* differs from the closely related species *De. nakasei* in its inability to assimilate L-sorbose, L-arabinose, D-arabinose, D-ribose, D-glucosamine, erythritol, D-mannitol, Methyl-α-D-glucoside, DL-lactate and myo-inositol (Table S1.11).

Typus: **China**, Fuzhou county, Fujian province, obtained from a leaf of an unidentified plant, Aug. 2011, Q.-M. Wang (**holotype** CGMCC 2.4437^T preserved in a metabolically inactive state, ex-type CBS 15512 = FJYZ12-13).

Derxomyces xingshanicus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828772. Fig. 9E, F.

Etymology: the specific epithet *xingshanicus* refers to the geographic origin of the type strain, Xingshan county, Hubei.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.0–5.0 × 5.5–11.2 µm and single, budding is polar (Fig. 9E), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellow, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae and hyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are are ellipsoidal to napiform, 3.0–6.2 × 5.5–8.0 µm (Fig. 9F).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin (weak), soluble starch (weak), D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine (weak), erythritol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate (weak) and myo-inositol are assimilated as sole carbon sources. L-sorbose, lactose, methanol, ethanol, glycerol, ribitol, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. xingshanicus* differs from the closely related species *De. cylindricus* in its inability to assimilate L-sorbose, ribitol and sodium nitrite and its ability to assimilate erythritol (Table S1.11).

Typus: **China**, Xingshan county, Hubei province, obtained from a leaf of an unidentified plant, Jul. 2003, Q.-M. Wang (**holotype** CGMCC 2.2459^T preserved in a metabolically inactive state, ex-type CBS 15445 = HX16.1).

Derxomyces pseudoyunnanensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828773. Fig. 9G, H.

Etymology: the specific epithet *pseudoyunnanensis* refers to the similar colony morphology to that of *Derxomyces yunnanensis*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 1.5–4.3 × 5.7–10.0 µm and single, budding is polar (Fig. 9G), a sediment is formed. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are globose and subglobosal to napiform, 3.6–4.4 × 3.6–5.1 µm (Fig. 9H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (variable), sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin, soluble starch (variable), D-xylose, L-arabinose (variable), D-arabinose, D-ribose (variable), L-rhamnose, galactitol (variable), D-mannitol (variable), D-glucitol (variable), Methyl-α-D-glucoside (variable), salicin (variable) and myo-inositol (weak) are assimilated as sole carbon sources. Lactose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, DL-lactate, succinate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), L-lysine, ethylamine hydrochloride, cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is variable. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. pseudoyunnanensis* can not be distinguished from its close relative *De. longiovatus* (Table S1.11).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3563^T preserved in a metabolically inactive state, ex-type CBS 15499 = SM37E2).

Derxomyces longiovatus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828774. Fig. 9I, J.

Etymology: the specific epithet *longiovatus* refers to the long ovoid vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are long ovoid, cylindrical and ellipsoidal, 1.8–3.7 × 3.9–13.8 µm and single, budding is polar (Fig. 9I), a sediment is formed. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar,

after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, dull. The margin is entire or eroded. In Dalmau plate culture on corn meal agar, pseudohyphae and hyphaeare formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are subglobosal to napiform, 3.2–4.5 × 4.8–6.5 µm (Fig. 9J).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose (delayed and weak), trehalose, melibiose, raffinose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, L-rhamnose (delayed and weak), salicin (delayed and weak) and myo-inositol (weak) are assimilated as sole carbon sources. L-sorbose, lactose, D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, DL-lactate, succinate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride, cadaverine dihydrochloride are assimilatedas sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. longiovatus* and its closely related species *De. pseudoyunnanensis* as well as *De. yunnanensis* are very similar. The two new species are not distinguishable, they differ from *De. yunnanensis* in its ability to assimilate inulin (Table S1.11).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3535^T preserved in a metabolically inactive state, ex-type CBS 15659 = SM35.4).

Derxomyces napiformis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828775. Fig. 9K, L.

Etymology: the specific epithet *napiformis* refers to the napiform ballistoconidia of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal to ovoid, 1.5–4.3 × 5.0–8.6 µm and single, budding is polar (Fig. 9K), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, slightly wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal to napiform, 2.9–3.6 × 4.2–4.6 µm (Fig. 9L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, D-xylose, L-arabinose, D-arabinose, L-rhamnose, Methyl-α-D-glucoside, succinate and myo-inositol are assimilated as sole carbon sources. L-sorbose, lactose, inulin, soluble starch, D-ribose, D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, salicin, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. napiformis* differs from its closely related species *De. bifurcus* in its inability to assimilate inulin, D-ribose and potassium nitrate and its ability to assimilate Methyl-α-D-glucoside, succinate and myo-inositol (Table S1.11).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4446^T preserved in a metabolically inactive state, ex-type CBS 15748 = TW1.1F028).

Derxomyces bifurcus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828776. Fig. 9M, N.

Etymology: the specific epithet *bifurcus* refers to the vegetative cells producing bifurcate budding of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 1.5–2.8 × 5.0–8.3 µm and single, budding is bifurcate or multi-polar (Fig. 9M), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, wrinkled and dull. The margin is entire or eroded. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are are ellipsoidal to napiform, 3.0–4.0 × 5.0–6.6 µm (Fig. 9N).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin, soluble starch (weak), D-xylose, L-arabinose, D-arabinose, D-ribose and L-rhamnose are assimilated as sole carbon sources. L-sorbose, lactose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

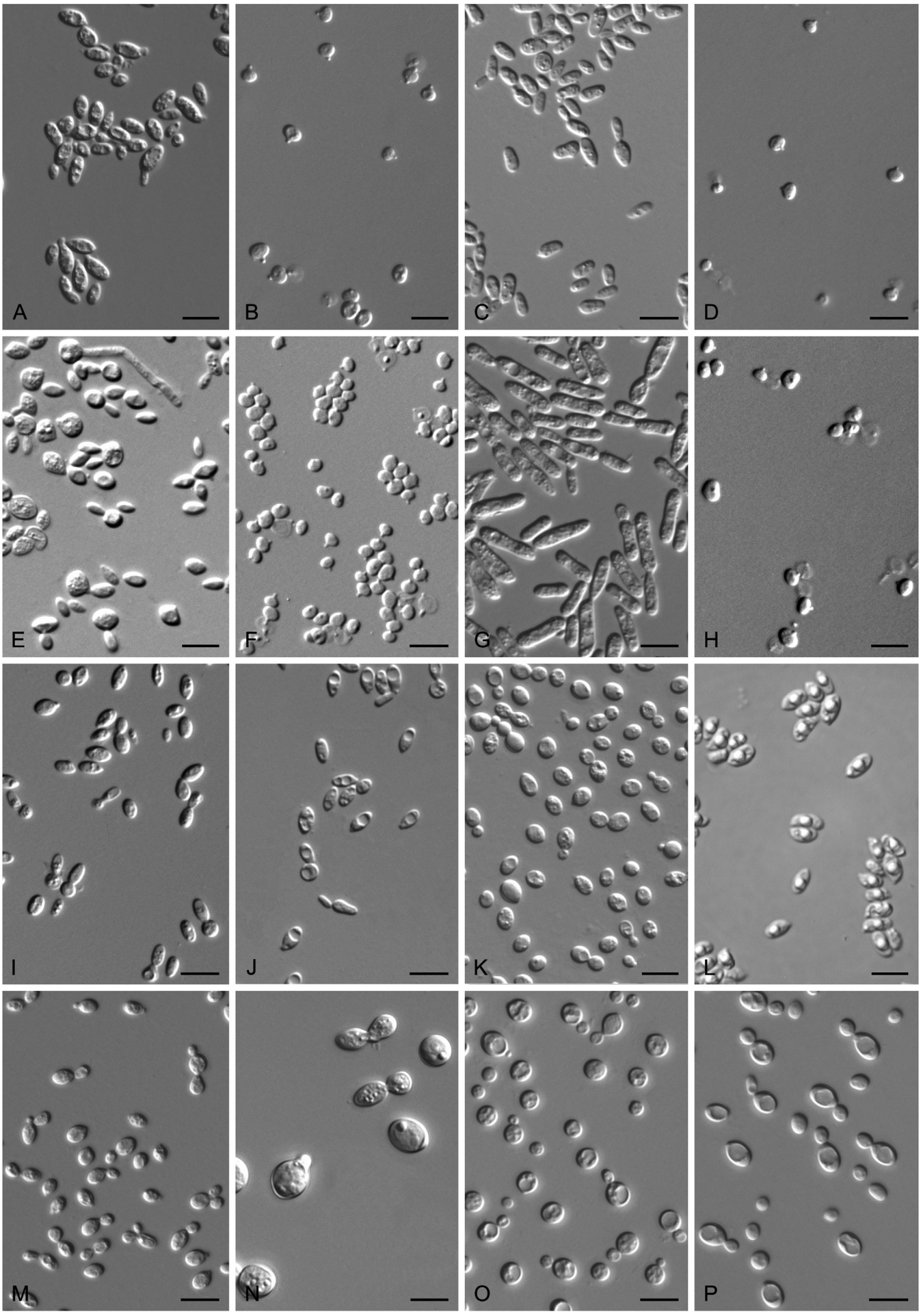
Physiologically, *De. bifurcus* differs from its closely related species *De. napiformis* in its inability to assimilate Methyl-α-D-glucoside, succinate and myo-inositol and its ability to assimilate inulin, D-ribose and potassium nitrate (Table S1.11).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3470^T preserved in a metabolically inactive state, ex-type CBS 15489 = SM37.5).

Derxomyces elongatus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828777. Fig. 9O, P.

Etymology: the specific epithet *elongatus* refers to the elongate vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and long ellipsoidal, 3.1–6.0 × 6.1–16.7 µm and single, budding is polar (Fig. 9O), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, slight wrinkled and dull. The margin is entire. In Dalmau plate culture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on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are globosal and subglobosal to napiform, 3.3–4.0 × 3.3–5.1 µm (Fig. 9P).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin, soluble starch (delayed), D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, ethanol, glycerol (delayed and weak), galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, succinate and citrate are assimilated as sole carbon sources. L-sorbose, lactose, methanol, erythritol, ribitol, salicin, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. elongatus* differs from the closely related species *De. wuzhishanensis* in its inability to grow in vitamin-free medium and its ability to assimilate D-glucosamine, D-mannitol, citrate, potassium nitrate, ethylamine and cadaverine (Table S1.11).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3561^{T} preserved in a metabolically inactive state, ex-type CBS 15498 = SM32.1).

Derxomyces melastomatis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828778. Fig. 10A, B.

Etymology: the specific epithet *melastomatis* refers to *Melastoma*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.3–4.0 × 4.7–8.2 µm and single, budding is polar (Fig. 10A), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are are ellipsoidal to napiform, 2.7–4.0 × 2.9–5.3 µm (Fig. 10B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose (weak), melezitose, inulin, soluble starch (weak), D-xylose, L-arabinose, D-arabinose (weak), D-ribose (weak), L-rhamnose, galactitol, D-mannitol (weak), D-glucitol, Methyl-α-D-glucoside, salicin (weak), succinate and myo-inositol are assimilated as sole carbon sources. L-sorbose, lactose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, L-lysine (weak), ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. melastomatis* differs from the closely related species *De. komagatae*, *De. schimicola* and *De. pseudoschimicola* in its ability to assimilate inulin (Table S1.11).

Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf *Melastoma candidum*, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3459^{T} preserved in a metabolically inactive state, ex-type CBS 15485 = WZS19.7).

Derxomyces taiwanicus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828779. Fig. 10C, D.

Etymology: the specific epithet *taiwanicus* refers to the geographic origin of the type strain, Taiwan.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 3.0–3.7 × 4.4–8.2 µm and single, budding is polar (Fig. 10C), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale-yellow, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are are ellipsoidal to napiform, 2.9–4.3 × 3.0–4.3 µm (Fig. 10D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (delayed and weak), sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, D-xylose, L-arabinose, D-arabinose (delayed and weak), D-ribose (delayed and weak), L-rhamnose, ribitol (delayed and weak), galactitol (delayed and weak), D-mannitol, D-glucitol (delayed and weak), Methyl-α-D-glucoside, salicin (delayed and weak) and succinate are assimilated as sole carbon sources. Lactose, inulin, soluble starch, D-glucosamine, methanol, ethanol, glycerol, erythritol, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and L-lysine are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. taiwanicus* differs from the closely related species *De. ovatus* in its inability to assimilate myo-inositol (Table S1.11).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4429^{T} preserved in a metabolically inactive state, ex-type CBS 12490 = TW3.1C-02).

Fig. 10. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *De. melastomatis* CGMCC 2.3459^{T}; (C, D) *De. taiwanicus* CGMCC 2.4429^{T}; (E, F) *De. ovatus* CGMCC 2.3572^{T}; (G, H) *De. longicylindricus* CGMCC 2.5660^{T}; ; (I) *Pha. lactea* CGMCC 2.5810^{T}; (J) *Pha. ovata* CGMCC 2.5614^{T}; (K, L) *Ho. saccardoi* CGMCC 2.3445^{T}; (M) *So. gelidoterrea* CGMCC 2.5814^{T}; (N) *Fi. dingjieense* CGMCC 2.5649^{T}, (O) *Fi. globosum* CGMCC 2.5680^{T}; (P) *Fi. mali* CGMCC 2.4012^{T}. Bars = 10 µm.

Derxomyces ovatus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828780. Fig. 10E, F.

Etymology: the specific epithet *ovatus* refers to the ovoid vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid or ellipsoidal, 2.0–5.4 × 3.8–7.7 µm and single, budding is polar (Fig. 10E), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellow, butyrous, smooth and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal to napiform, 1.8–3.6 × 3.0–4.5 µm (Fig. 10F).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (delayed and weak), sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin (delayed and weak), soluble starch (weak), D-xylose, L-arabinose, L-rhamnose, ethanol (delayed and weak), galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin (delayed and weak), succinate and myo-inositol are assimilated as sole carbon sources. Lactose, D-arabinose, D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (delayed and weak) and L-lysine are assimilated as sole nitrogen sources. Sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is netative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. ovatus* differs from the closely related species *De. taiwanicus*. in its ability to assimilate myo-inositol (Table S1.11).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3572^T preserved in a metabolically inactive state, ex-type CBS 15654 = SM32.2).

Derxomyces longicylindricus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828781. Fig. 10G, H.

Etymology: the specific epithet *longicylindricus* refers to the long cylindrical vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are long cylindrical, 2.9–5.0 × 7.1–22 µm and single, budding is polar (Fig. 10G), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal to napiform, 2.4–-4.2 × 3.6–6.0 µm (Fig. 10H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (weak), sucrose, maltose, cellobiose (weak), trehalose, melibiose, raffinose, melezitose, inulin, soluble starch (weak), D-xylose, L-arabinose, L-rhamnose, D-glucitol (delayed and weak), Methyl-α-D-glucoside and succinate (delayed and weak) are assimilated as sole carbon sources. Lactose, D-ribose, D-arabinose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *De. longicylindricus* differs from the closely related species *De. linzhiensis* in its inability to assimilate D-arabinose, galactitol, D-mannitol and cadaverine and its ability to assimilate L-rhamnose, L-lysine and ethylamine (Table S1.11).

Typus: **China**, Beibeng county, Motuo, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5660^T preserved in a metabolically inactive state, ex-type CBS 13979 = XZ132E37A).

Phaeotremella lactea Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828782. Fig. 10I.

Etymology: the specific epithet *lactea* refers to the colony colour of this species.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 2.7–4.0 × 4.4–6.6 µm and single, budding is polar (Fig. 10I), a sediment is present. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, inulin, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, ribitol, D-mannitol, D-glucitol, salicin, D-gluconate, succinate and myo-inositol are assimilated as sole carbon sources. L-sorbose, soluble starch, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), sodium nitrite (weak), L-lysine (weak) and ethylamine hydrochloride (weak) are assimilated as sole nitrogen sources. Cadaverine dihydrochloride is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive (weak). Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Pha. lactea* differs from the closely related species *Pha. ovata* in its inability to assimilate soluble starch, N-Acetyl-D-glucosamine, galactitol, Methyl-α-D-glucoside and cadaverine and its ability to assimilate raffinose, succinate and myo-inositol (Table S1.12).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5810^T preserved in a metabolically inactive state, ex-type CBS 15574 = GPS20.4A1B).

Phaeotremella ovata Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828783. Fig. 10J.

Etymology: the specific epithet *ovata* refers to the ovoid vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and fusiform, 2.0–3.4 × 4.8–8.2 µm and single, budding is polar (Fig. 10J), a sediment is formed. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellow, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin and D-gluconate are assimilated as sole carbon sources. L-sorbose, raffinose, methanol, ethanol, glycerol, erythritol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Pha. ovata* differs from its closely related species *Pha. lactea* in its inability to assimilate raffinose, succinate and myo-inositol and its ability to assimilate soluble starch, N-Acetyl-D-glucosamine, Methyl-α-D-glucoside and cadaverine (Table S1.12).

Typus: **China**, Nanwenghe, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2015, Q.-M. Wang (**holotype** CGMCC 2.5614^T preserved in a metabolically inactive state, ex-type CBS 15756 = NW9D3).

Holtermannia Sacc. & Traverso, Syll. Fung. 19: 871. 1910. ***emend.*** Q.M. Wang, F.Y. Bai & A.H. Li.
Type species: *Holtermannia pinguis* (Holterm.) Sacc. & Traverso.

This genus is emended to include *Holtermannia corniformis* and six other sexual species (Kobayasi 1937), and one newly described anamorphic species *Holtermannia saccardoi* (Figs 2E and S1E).

Sexual reproduction observed in most species. For teleomorphic taxa, the corniform basidiocarps are narrowly clavate and often slightly compressed. The basidiocarps are simple or infrequently branched. The tertiary hyphae have clamp connections (Bandoni *et al.* 2011). Colonies whitish to cream, mucoid. Budding cells present. Ballistoconidia formed or not.

Holtermannia saccardoi Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828784. Fig. 10K, L.

Etymology: the specific epithet *saccardoi* named in honour of P.A. Saccardo for his proposal of the genus *Holtermannia*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are globosal, ovoid and ellipsoidal, 3.1–5.8 × 3.6–6.4 µm and single, budding is polar (Fig. 10K), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, mucoid, smooth and shiny. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal, 4.1–5.9 × 7.4–9.1 µm (Fig. 10L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), sucrose, maltose, cellobiose, trehalose, lactose (variable), melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate (variable), succinate (weak), citrate (variable) and myo-inositol are assimilated as sole carbon sources. L-sorbose, inulin, D-glucosamine, methanol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine and cadaverine dihydrochloride (variable) are assimilated as sole nitrogen sources. Sodium nitrite and ethylamine hydrochloride are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ho. saccardoi* differs from its closely related species *Ho. corniformis* in its inability to assimilate L-sorbose and its ability to assimilate melibiose, raffinose, erythritol and potassium nitrate (Table S1.13).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3445^T preserved in a metabolically inactive state, ex-type CBS 15479 = SM37.10).

Solicoccozyma gelidoterrea Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828785. Fig. 10M.

Etymology: the specific epithet *gelidoterrea* refers to the cold environments origin of all strains used in this study.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and ovoid, 3.3–4.8 × 4.1–5.5 µm and single, budding is polar (Fig. 10M), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose (variable), lactose, melibiose (variable), raffinose, melezitose, inulin, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, ethanol, ribitol, galactitol, glycerol (variable), D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, D-gluconate and myo-inositol are assimilated as sole carbon sources. Soluble starch, methanol, erythritol, DL-lactate, succinate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *So. gelidoterrea* differs from its four closely related species, *So. aeria*, *So. terrea*, *So. phenolica* and *So. fuscescens*, in its inability to assimilate succinate and its ability to assimilate inulin (Table S1.14).

Typus: **China**, Daxinganling, obtained from soil, Aug. 2015, Q.-M. Wang (**holotype** CGMCC 2.5814^T preserved in a metabolically inactive state, ex-type CBS 15580 = HFB003-3).

Filobasidium dingjieense Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828786. Fig. 10N.

Etymology: the specific epithet *dingjieense* refers to the geographic origin of the type strain, Dingjie county, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are globosal and ellipsoidal, 6.8–10.6 × 6.9–10.6 µm and single, budding is polar (Fig. 10N), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is gray-cream, mucoid, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed and weak), sucrose, maltose, cellobiose, trehalose, melezitose, D-xylose, L-arabinose, ethanol (delayed and weak), glycerol (delayed and weak), Methyl-α-D-glucoside (weak), succinate, citrate and myo-inositol are assimilated as sole carbon sources. L-sorbose, lactose, melibiose, raffinose, inulin, soluble starch, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, salicin, DL-lactate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. L-lysine is not assimilated. Maximum growth temperature is 19 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Fi. dingjieense* differs from its closely related species *Fi. uniguttulatum* in its inability to assimilate raffinose, L-rhamnose, N-Acetyl-D-glucosamine, ribitol, D-mannitol, D-glucitol, salicin, hexadecane and L-lysine and its ability to assimilate cellobiose, potassium nitrate and sodium nitrite (Table S1.15).

Typus: **China**, Dingjie county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5649^T preserved in a metabolically inactive state, ex-type CBS 15567 = GPS3.2A5).

Filobasidium globosum Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828788. Fig. 10O.

Etymology: the specific epithet *globosum* refers to the globosal vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are globosal, 2.7–6.7 × 2.7–6.7 µm and single, budding is polar (Fig. 10O), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is gray-cream, mucoid, smooth and shiny. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, inulin, D-xylose (delayed and weak), L-arabinose, L-rhamnose (delayed and weak), D-mannitol, Methyl-α-D-glucoside (weak), succinate (weak) and myo-inositol (weak) are assimilated as sole carbon sources. L-sorbose, soluble starch, D-arabinose, D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-glucitol, salicin, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Fi. globosum* differs from its closely related species *Fi. mali* in its inability to assimilate ribitol, galactitol, salicin and ethylamine and its ability to assimilate lactose and grow in vitamin-free medium (Table S1.15).

Typus: **China**, Yichun county, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2014, Q.-M. Wang (**holotype** CGMCC 2.5680^T preserved in a metabolically inactive state, ex-type CBS 15658 = HLJ8A3).

Filobasidium mali Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828789. Figs 10P and 11A.

Etymology: the specific epithet *mali* refers to the substrate origin of the type strain, *Malus*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ellipsoidal, 3.0–4.6 × 3.0–7.7 µm and single, budding is polar (Fig. 10P), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is gray-cream, mucoid, smooth and shiny. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, Galactose, L-sorbose, sucrose, maltose, cellobiose (or weak), trehalose, melibiose (or weak), raffinose (or weak), melezitose (or weak), D-xylose (or delayed and weak), L-arabinose (or weak), L-rhamnose (or delayed and weak), ethanol (or weak), D-mannitol, ribitol, galactitol, Methyl-α-D-glucoside (or weak), salicin (or weak), D-Gluconate (weak), succinate (delayed and weak) and myo-inositol (delayed and weak) are assimilated as sole carbon sources. Lactose (variable), inulin, soluble starch, D-arabinose (variable), D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, D-glucitol (variable), erythritol, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), L-lysine, and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and ethylamine hydrochloride (variable) are not assimilated. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is negative.

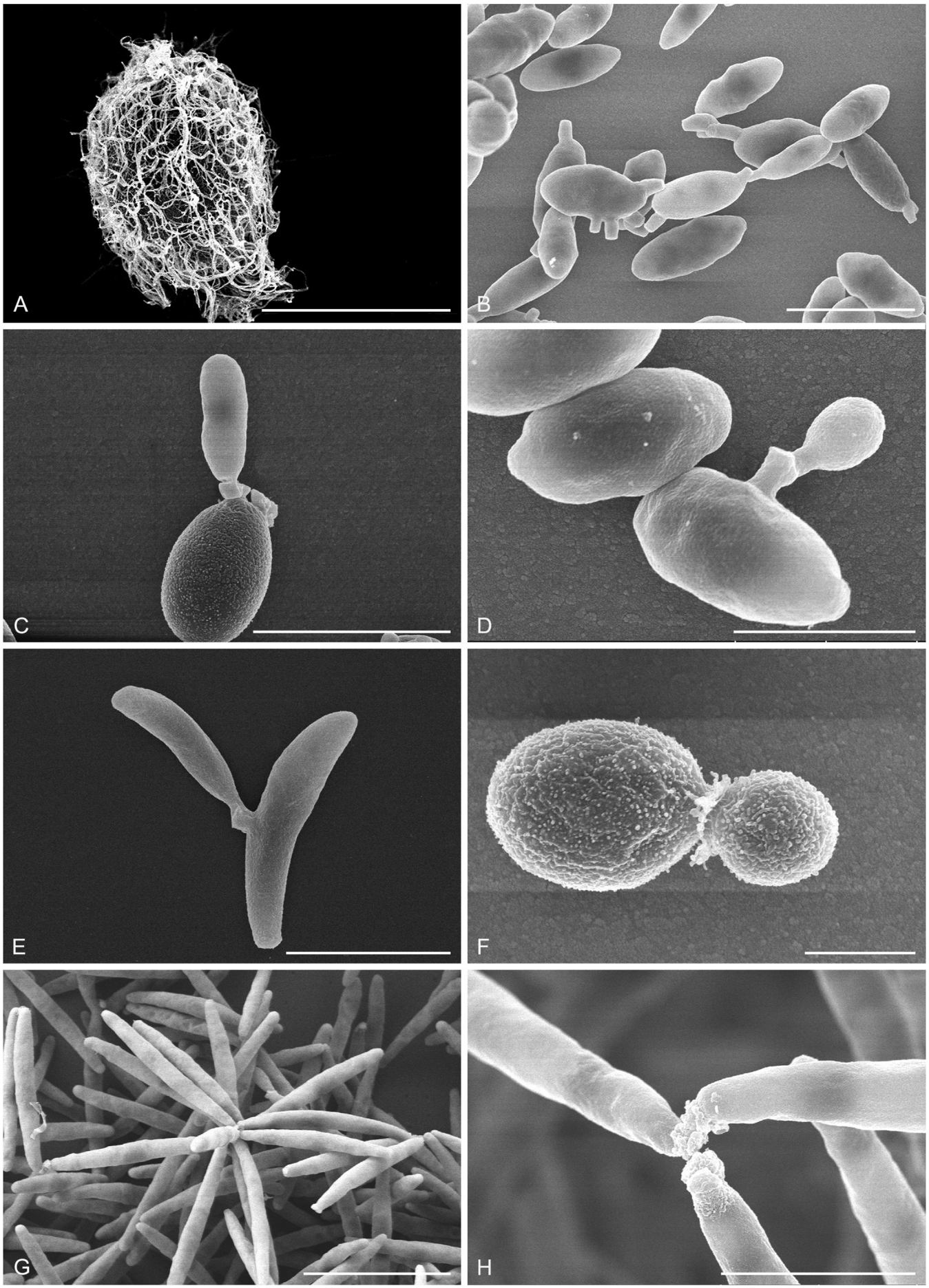
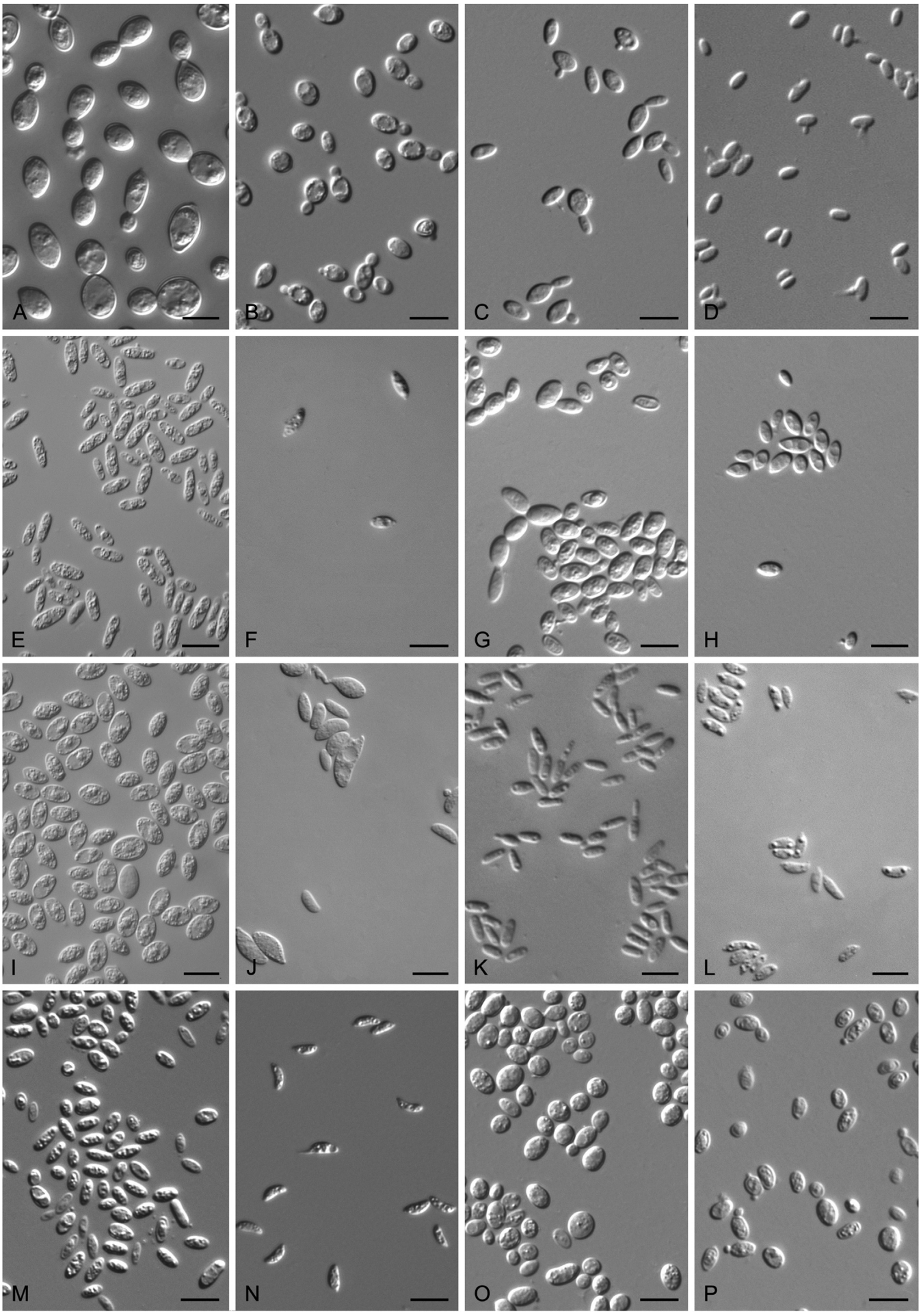


Fig. 11. SEM image of vegetative cells grown in YM broth for 5 d at 17 °C. (A) *Fi. mali* CGMCC 2.4012^{T}, Bars = 4 µm; (B) *Boe. sterigmata* CGMCC 2.4539^{T}, Bars = 5 µm; (C) *St. layueensis* CGMCC 2.5817^{T}, Bars = 5 µm; (D) *Pse. motuoensis* CGMCC 2.5816^{T}, Bars = 2 µm; (E) *Me. layueensis* CGMCC 2.5818^{T}, Bars = 5 µm; (F) *Beg. foliicola* CGMCC 2.3164^{T}, Bars = 1 µm; (G, H) *Ros. petaloides* CGMCC 2.3446^{T}, G Bars = 10 µm, H Bars = 3 µm.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Starch-like substances are produced or not. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Fi. mali* differs from its closely related species *Fi. globosum* in its inability to grow in vitamin-free medium and its ability to assimilate ribitol, galactitol and salicin (Table S1.15).

Typus: **China**, Tai'an county, Shandong province, obtained from isolated from apple, Aug. 2008, Q.-M. Wang (**holotype** CGMCC 2.4012^T preserved in a metabolically inactive state, ex-type CBS 15651 = KTAPG4-11.64).

Filobasidium mucilaginum Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828790. Fig. 12A.

Etymology: the specific epithet *mucilaginum* refers to the mucoid colony morphology of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are subglobosal and ellipsoidal, 3.8–8.1 × 3.8–8.8 µm and single, budding is polar (Fig. 12A), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is gray-cream, mucoid, smooth and shiny. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose (delayed and weak), melibiose (delayed and weak), raffinose, melezitose, soluble starch (weak), D-xylose, L-arabinose (delayed and weak), D-arabinose (delayed and weak), ethanol (delayed and weak), glycerol (delayed and weak), erythritol (delayed and weak), ribitol (delayed and weak), galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, succinate (delayed and weak) and myo-inositol (delayed and weak) are assimilated as sole carbon sources. L-sorbose, inulin, D-ribose, L-rhamnose, D-glucosamine, methanol, DL-lactate, citrate and hexadecane are not assimilated. Ammonium sulfate and potassium nitrate (delayed and weak) are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Fi. mucilaginum* differs from its closely related species *Fi. globosum* and *Fi. mali* in its inability to assimilate Methyl-α-D-glucoside and its ability to assimilate L-sorbose and D-glucitol (Table S1.15).

Typus: **China**, Sanya county, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3463^T preserved in a metabolically inactive state, ex-type CBS 15486 = SY2.1).

Phaffia aurantiaca Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828791. Fig. 12B.

Etymology: the specific epithet *aurantiaca* refers to the orange colony colour of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 3.4–6.4 × 5.2–8.9 µm and single, budding is polar (Fig. 12B), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is orange, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, D-xylose (delayed and weak), L-arabinose, D-ribose, ethanol, glycerol, erythritol, ribitol (delayed and weak), galactitol (delayed and weak), D-mannitol, D-glucitol, Methyl-α-D-glucoside (delayed and weak), salicin (delayed and weak), DL-lactate and succinate are assimilated as sole carbon sources. L-sorbose, inulin, soluble starch, D-arabinose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is negative. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Pha. aurantiaca* differs from its closely related species *Pha. rhodozyma* in its inability to assimilate soluble starch and its ability to assimilate galactose, lactose, melibiose, erythritol and ethylamine (Table S1.16).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5601^T preserved in a metabolically inactive state, ex-type CBS 15548 = GPS23.2A4).

New taxa in *Agaricostilbomycetes* (*Pucciniomycotina*)

Kondoa cylindrica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828792. Fig. 12C, D.

Etymology: the specific epithet *cylindrica* refers to the cylindrical ballistoconidia of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.4–4.8 × 4.8–8.5 µm and single, budding is polar (Fig. 12C), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale orange, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are cylindrical, 2.1–2.9 × 4.3–5.7 µm (Fig. 12D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose (variable), trehalose, raffinose (variable), melezitose (variable), soluble starch, D-xylose (variable), L-arabinose (variable), D-

Fig. 12. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A) *Fi. mucilaginum* CGMCC 2.3463^T; (B) *Pha. aurantiaca* CGMCC 2.5601^T; (C, D) *Kon. cylindrica* CGMCC 2.3102^T; (E, F) *Kon. chamaenerii* CGMCC 2.2652^T; (G, H) *Kon. foliicola* CGMCC 2.3100^T; (I, J) *Kon. arboricola* CGMCC 2.2621^T; (K, L) *Kon. lulangica* CGMCC 2.2762^T; (M, N) *Kon. daliangziensis* CGMCC 2.5610^T, (O) *Kon. ribitophobia* CGMCC 2.4441^T; (P) *Kon. myxariophila* CBS 8379^T. Bars = 10 µm.

ribose (variable), L-rhamnose, ethanol (variable), glycerol, erythritol (variable), ribitol (variable), galactitol (variable), D-mannitol, D-glucitol, Methyl-α-D-glucoside (variable), salicin (variable), succinate (delayed and weak) and citrate (variable) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, inulin, D-arabinose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, D-gluconate, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable) and cadaverine dihydrochloride (variable) are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine and ethylamine hydrochloride are not assimilated. Maximum growth temperature is 22–25 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. cylindrica* differs from its closely related species *Kon. aeria* and *Kon. malvinella* in its inability to assimilate DL-lactate and its ability to grow in vitamin-free medium (Table S1.17).

Typus: **Germany**, obtained from a leaf of an unidentified plant, Sep. 2005 (**holotype** CGMCC 2.3102^T preserved in a metabolically inactive state, ex-type CBS 15466 = G6.1-1).

Kondoa chamaenerii Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828793. Fig. 12E, F.

Etymology: the specific epithet *chamaenerii* refers to *Chamaenerion*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 2.6–4.3 × 5.7–10.0 µm and single, budding is polar (Fig. 12E), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is pinkish-cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are long ellipsoidal, 2.9–4.3 × 7.1–10.0 µm (Fig. 12F).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), L-sorbose (variable), sucrose, maltose, cellobiose (variable), trehalose, lactose (variable), raffinose (variable), inulin (weak), soluble starch (variable), glycerol, ribitol (delayed and weak), mannitol (delayed and weak) and D-glucitol (variable) are assimilated as sole carbon sources. Melibiose, melezitose, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, erythritol, galactitol, D-Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and potassium nitrate are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. chamaenerii*. differs from its closely related species *Kon. subrosea* and *Kon. miscanthi* in its inability to assimilate succinate (Table S1.17).

Typus: **China**, Bujin county, Xinjiang province, obtained from a leaf of *Chamaenerion angustifolium*, Jul. 2004, F.-Y. Bai (**holotype** CGMCC 2.2652^T preserved in a metabolically inactive state, ex-type CBS 15453 = XJ8A5).

Kondoa foliicola Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828794. Fig. 12G, H.

Etymology: the specific epithet *foliicola* refers to the substrate origin of the type strain, leaves.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and somewhat ovoid, 3.1–5.4 × 5.1–7.8 µm and single, budding is polar (Fig. 12G), a sediment is formed. After 1 mo at 17 °C, an incomplete ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale-yellow, butyrous, dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal or ovoid, 2.5–4.0 × 3.8–8.8 µm (Fig. 12H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, cellobiose, trehalose, lactose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, glucosamine, glycerol, ribitol and D-mannitol are assimilated as sole carbon sources. Galactose, L-sorbose, maltose, melibiose, inulin, D-ribose, L-rhamnose, D-N-methanol, ethanol, erythritol, galactitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), L-lysine and ethylamine hydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. foliicola* differs from its closely related species *Kon. arboricola* in its inability to assimilate maltose, grow in vitamin-free medium and produce starch like compounds and its ability to assimilate melezitose, D-arabinose and D-glucosamine (Table S1.17).

Typus: **Germany**, obtained from a leaf of an unidentified plant, Sep. 2005 (**holotype** CGMCC 2.3100^T preserved in a metabolically inactive state, ex-type CBS 15465 = G9.1).

Kondoa arboricola Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828795. Fig. 12I, J.

Etymology: the specific epithet *arboricola* refers to the substrate origin of the type strain, tree.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 2.9–5.0 × 7.1–10.0 µm and single, budding is polar (Fig. 12I), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish cream, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 3.0–5.7 × 7.0–15.7 µm (Fig. 12J).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose (variable), sucrose (variable), maltose, cellobiose, trehalose, lactose (delayed and weak), raffinose, inulin (variable), soluble starch (variable), D-xylose (variable), L-arabinose (variable), ethanol (variable), glycerol, ribitol (variable), D-mannitol (variable), D-glucitol (variable), DL-lactate (variable) and succinate (variable) are assimilated as sole carbon sources. Galactose, melibiose, melezitose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol,

erythritol, galactitol, Methyl-α-D-glucoside, salicin, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), L-lysine (weak) and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. arboricola* differs from its closely related species *Kon. foliicola* in its inability to assimilate melezitose, D-arabinose and D-glucosamine and its ability to assimilate maltose, grow in vitamin-free medium and produce starch like compounds (Table S1.17).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of tree, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2621^T preserved in a metabolically inactive state, ex-type CBS 15452 = XZ12B5).

Kondoa lulangica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828796. Fig. 12K, L.

Etymology: the specific epithet *lulangica* refers to the geographic origin of the type strain, Lulang county, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.4–3.8 × 5.0–7.6 µm and single, budding is polar (Fig. 12K), a sediment is formed. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is pale pink, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.6–2.9 × 5.7–8.6 µm (Fig. 12L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose (delayed), maltose, trehalose (delayed and weak), melezitose (delayed and weak), soluble starch (weak), glycerol, erythritol (delayed), D-mannitol, D-glucitol and Methyl-α-D-glucoside are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, inulin, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, ribitol, galactitol, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 24 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. lulangica* differs from its closely related species *Kon. changbaiensis* in its inability to assimilate cellobiose, raffinose and ribitol and its ability to assimilate erythritol, Methyl-α-D-glucoside and grow in vitamin-free medium (Table S1.17).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2762^T preserved in a metabolically inactive state, ex-type CBS 15456 = XZ36D1).

Kondoa daliangziensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB832014. Fig. 12M, N.

Etymology: the specific epithet *daliangziensis* refers to the geographic origin of the type strain, Daliangzi River National Forest Park, Heilongjiang.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 2.7–4.4 × 4.3–8.4 µm and single, budding is polar (Fig. 12M), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale orange, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.6–3.1 × 7.1–8.6 µm (Fig. 12N).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose (variable), maltose, cellobiose, trehalose, melezitose, L-arabinose (variable), ethanol (variable), glycerol, ribitol (variable), D-mannitol (variable), D-glucitol (variable), salicin (variable) and DL-lactate (variable) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, galactitol, Methyl-α-D-glucoside, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride (weak) and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is variable. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. daliangziensis* and *Kon. ribitophobia* are difficult to distinguish from each other. The latter can grow at 25 °C, but the former does not. *Kon. daliangziensis* differs from *Kon. gutianensis* in its inability to assimilate galactose and inulin and its ability to assimilate L-lysine (Table S1.17).

Typus: **China**, Daliangzi river national forest park, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2014, Q.-M. Wang (**holotype** CGMCC 2.5610^T preserved in a metabolically inactive state, ex-type CBS 13974 = HLJ22A8).

Kondoa ribitophobia Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828798. Fig. 12O.

Etymology: the specific epithet *ribitophobia* refers to the physiological character of not assimilating ribitol.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are globosal, oval and ellipsoidal, 3.3–4.9 × 4.5–8.3 µm and single, budding is polar (Fig. 12O), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale yellow, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), L-sorbose (variable), sucrose, maltose, cellobiose (variable), trehalose, melezitose, inulin (variable), L-arabinose (variable), L-rhamnose (variable), ethanol (variable), glycerol, D-mannitol (delayed and weak), D-glucitol (variable), Methyl-α-D-glucoside (variable), salicin (weak) and succinate (variable) are assimilated as sole carbon sources. Lactose, melibiose, raffinose, soluble starch, D-

xylose, D-arabinose, D-ribose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, ribitol, galactitol, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), L-lysine (variable), ethylamine hydrochloride (variable) and cadaverine dihydrochloride (variable) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is variable. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. ribitophobia* differs from its closely related species *Kon. gutianensis* in its inability to assimilate ribitol (Table S1.17).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4441^{T} preserved in a metabolically inactive state, ex-type CBS 12496 = TW2.1E-016).

Kondoa myxariophila J.P. Sampaio, Q.M. Wang & F.Y. Bai ***sp. nov.*** MycoBank MB828799. Figs 12P and 13.

Etymology: the specific epithet *myxariophila* refers to the association of the novel taxon with the fruiting bodies of *Myxarium nucleatum* (*Auriculariales*).

Sexual characteristics: The sexual stage is observed PDA and MYP plates incubated at 20 °C for 8–12 wk and occurs in individual strains in the absence of mating. Hyphae are 3–5 µm in diameter and have clamp connections. Basidia are cylindrical, transversely-septate, usually four-celled and measure 40–60 × 7.5–5 µm (Fig. 13A, C). Basidiospores are formed at the end of basidial sterigmata, measuring 10–5 µm in length. Basidiospores are oval, measure 11–9 × 7–5 µm (Fig. 13B), are forcefully ejected (ballistospores) and germinate by budding. Haustorial branches are conspicuously formed and occur laterally on hyphae (Fig. 13C, D).

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal to ovoid, measure 3–4 × 4–6 µm and occur single or in pairs and budding is polar (Fig. 12P). A sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale yellow, butyrous, semi-glossy and smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Ballistoconidia can be produced in solid medium (CMA) but are rare and measure 4–5 × 5–8 µm (Fig. 13E).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, trehalose, melibiose (variable), cellobiose (variable), raffinose (variable), melezitose, soluble starch, D-xylose, L-arabinose (delayed and weak), D-arabinose (delayed and weak), D-ribose (variable), L-rhamnose (delayed and weak), D-glucosamine (variable), glycerol (delayed and weak), ribitol (variable), salicin (variable), D-mannitol (delayed and weak), D-glucitol (delayed and weak), succinate (delayed and weak) and citrate (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, inulin, methanol, ethanol, erythritol, galactitol, Methyl-α-D-glucoside, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), sodium nitrite (variable), ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. L-lysine is not assimilated. Maximum growth temperature is 22–25 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. myxariophila* differs from its closest relatives, *Kon. daliangziensis*, *Kon. ribitolophobia* and *Kon. gutianensis*, in its inability to assimilate L-lysine and its ability to assimilate soluble starch and D-xylose (Table S1.17).

Typus: **Portugal**, Sesimbra, obtained from the fruiting body of *Myxarium nucleatum* (*Auriculariales*), Nov. 1992, J.P. Sampaio

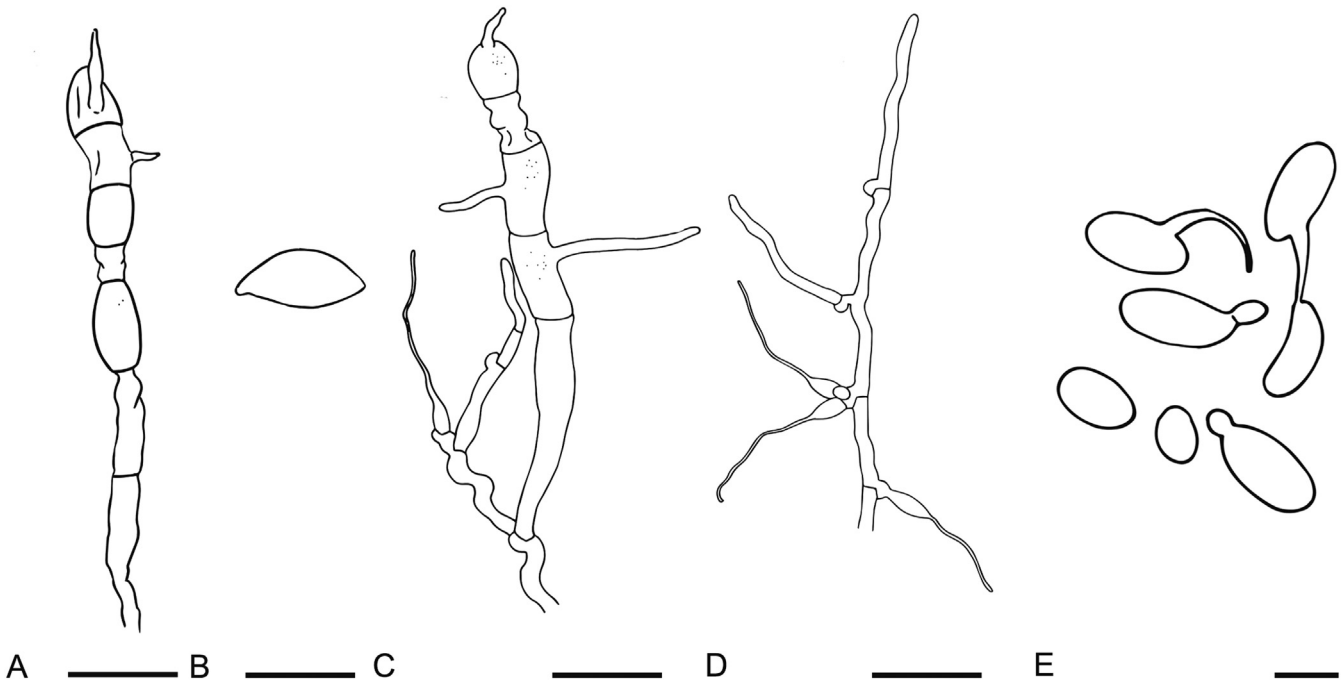


Fig. 13. Vegetative cells, ballistoconidia and the sexual stage of *Kon. myxariophila* CBS 8379^{T}. (A) Basidia; (B) Basidiospores; (C, D) Haustorial branches; (E) Ballistoconidia. Bars = 10 µm.

(**holotype** PYCC 5509^{T} preserved in a metabolically inactive state, ex-type CBS 8379 = ZP 337).

Note: Besides several sexual strains isolated with the ballitoconidium-fall method from basidiocarps of *Myxarium nucleatum* in Portugal (PYCC 5509 = ZP 337; PYCC 8354 = ZP 338; and PYCC 8305 = ZP 352) in 1992 and 1996, another strain was isolated from the leaf of an unidentified plant, collected in Germany in September 2005 (CGMCC 2.3106 = CBS 15468). Although a sexual stage has not been reported for the culture isolated in Germany, these four strains have similar ITS sequences. Therefore, *Kon. myxariophila* appears to be capable to engage in mycoparasitism because it produces haustorial branches and is ecologically associated with other fungi. Nevertheless, the mycoparasitic strategy might be combined with a saprobe lifestyle in the phylloplane since *Kon. myxariophila* is also able to produce ballistoconidia and is also found in association with plant leafs. Similarly to the other two sexual species in the genus, *Kon. aeria* and *Kon. malvinella*, *Kon. myxariophila* does not produce teliospores, produces transversely-septate basidia and its basidiospores are forcefully discharged (ballistospores).

Kondoa rhododendri Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828800. Fig. 14A, B.

Etymology: the specific epithet *rhododendri* refers to *Rhododendron*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid, ellipsoidal and cylindrical, 2.7–4.8 × 4.5–9.5 µm and single, budding is polar (Fig. 14A), a sediment is formed. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is pinkish cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are long ellipsoidal or ovoid, 3.0–4.3 × 7.9–10.0 µm (Fig. 14B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed), L-sorbose (delayed), sucrose, maltose, cellobiose (delayed and weak), trehalose, melezitose (delayed), inulin (weak), D-xylose (delayed), L-arabinose (delayed and weak), D-ribose (delayed and weak), ethanol (weak), glycerol (delayed), ribitol, galactitol (delayed and weak), D-mannitol and D-glucitol are assimilated as sole carbon sources. Lactose, melibiose, raffinose, soluble starch, D-arabinose, L-rhamnose, D-glucosamine, methanol, erythritol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 25 ΄IC. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Kon. rhododendri* differs well from other *Kondoa* species in its assimilation of carbon and nitrogen sources (Table S1.17).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Rhododendron triflorum*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2763^{T} preserved in a metabolically inactive state, ex-type CBS 15457 = XZ27E3).

Bensingtonia wuzhishanensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828801. Fig. 14C, D.

Etymology: the specific epithet *wuzhishanensis* refers to the geographic origin of the type strain, Wuzhishan mountain, Hainan.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical or fusiform, 3.4–4.0 × 7.6–10.0 µm and single, budding is polar (Fig. 14C), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is ivory to cream, mucoid, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are cylindrical, 2.9–3.7 × 7.4–10.0 µm (Fig. 14D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose (delayed and weak), melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose (delayed and weak), D-arabinose, D-ribose, L-rhamnose (weak), D-glucosamine (delayed and weak) , ethanol, glycerol (weak), erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate (delayed and weak) and citrate (weak) are assimilated as sole carbon sources. L-sorbose, inulin, methanol, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite (delayed and weak), L-lysine, ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Be. wuzhishanensis* differs from its closely related species, *Be. pseudorectispora*, *Be. bomiensis*, *Be. naganoensis*, *Be. pseudonaganoensis* and *Be. rectispora*, in its ability to assimilate D-ribose, ethanol and erythritol (Table S1.18).

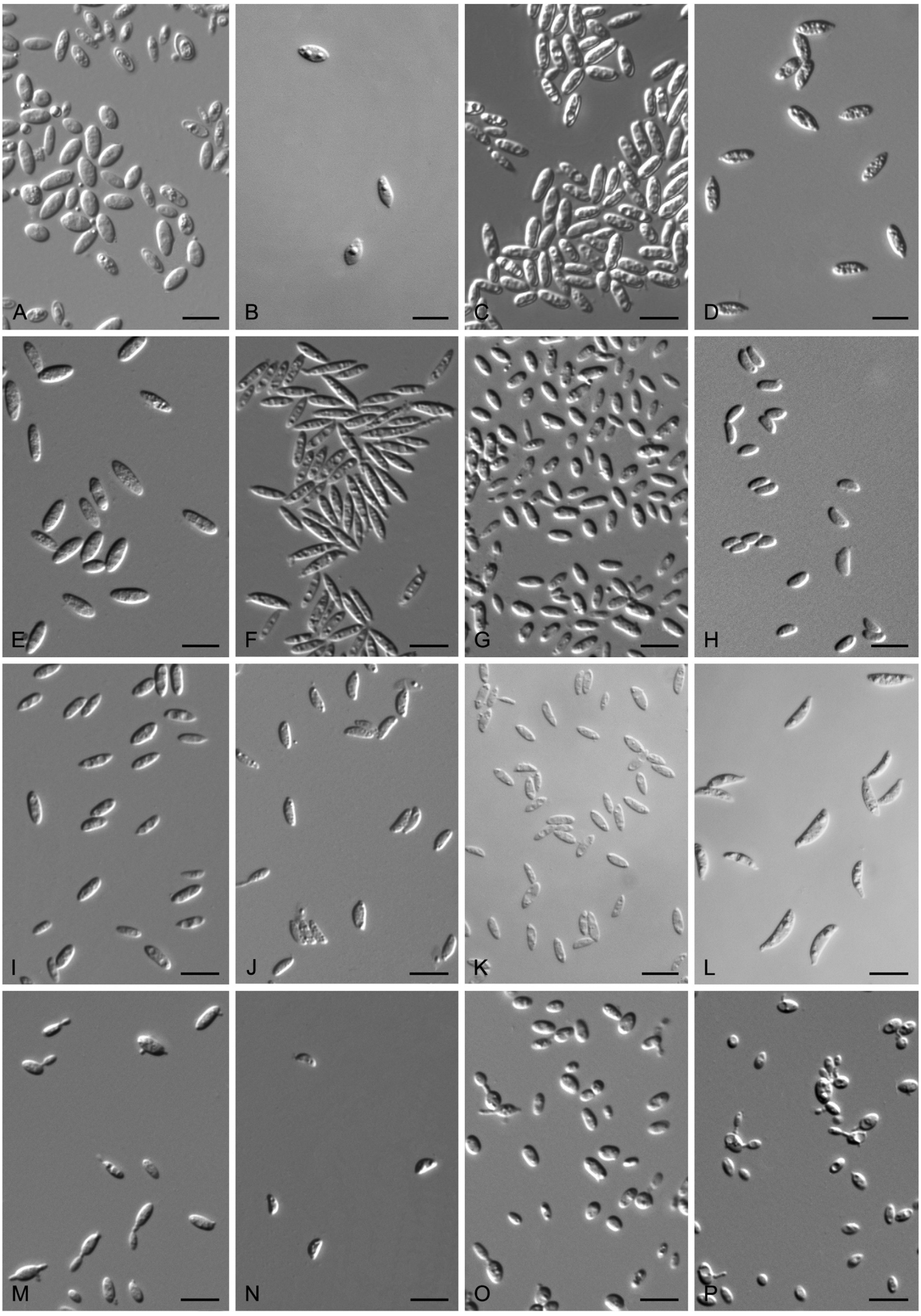
Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3569^{T} preserved in a metabolically inactive state, ex-type CBS 15661 = WZS33.18).

Bensingtonia pseudorectispora Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828802. Fig. 14E.

Etymology: the specific epithet *pseudorectispora* refers to the similar colony morphology to that of *Bensingtonia rectispora*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.8–3.2 × 7.2–10.3 µm and single, budding is polar (Fig. 14E), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pink red, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, maltose, melezitose, D-mannitol and salicin are assimilated as sole carbon sources. Galactose, L-sorbose, sucrose, cellobiose, trehalose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-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glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-glucitol, Methyl-α-D-glucoside, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Be. pseudorectispora* differs from its closely related species *Be. rectispora* in its inability to assimilate sucrose, trehalose and glycerol and its ability to assimilate salicin and ethylamine (Table S1.18).

Typus: **China**, Bomi, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5677^T preserved in a metabolically inactive state, ex-type CBS 15750 = XZ154D5).

Pseudobensingtonia fusiformis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828803. Fig. 14F.

Etymology: the specific epithet *fusiformis* refers to the fusiform vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, ellipsoidal and fusiform, 7.6–13.3 × 2.2–3.6 µm and single, budding is polar (Fig. 14F), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is yellow, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose, sucrose, cellobiose, trehalose, lactose, raffinose, inulin, D-xylose, L-arabinose (variable), D-ribose (weak), ethanol (variable), glycerol, erythritol, ribitol, D-mannitol, D-glucitol, D-gluconate and succinate are assimilated as sole carbon sources. Galactose, maltose, melibiose, melezitose, soluble starch, D-arabinose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ps. fusiformis* differs from its closely related species *Ps. ingoldii* and *Ps. musae* in its inability to assimilate citrate and its ability to assimilate inulin (Table S1.19).

Typus: **China**, Bomi, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5823^T preserved in a metabolically inactive state, ex-type CBS 15647 = XZ152EA3).

Ruinenia fanjingshanensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828804. Fig. 14G, H.

Etymology: the specific epithet *fanjingshanensis* refers to the geographic origin of the type strain, Fanjingshan Mountain, Guizhou.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.1–3.6 × 5.0–7.9 µm and single, budding is polar (Fig. 14G), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pink-red, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.1–3.6 × 5.0–7.9 µm (Fig. 14H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, maltose, trehalose, melibiose, raffinose, inulin, soluble starch (weak), ribitol and D-mannitol are assimilated as sole carbon sources. Galactose, L-sorbose, sucrose, cellobiose, lactose, melezitose, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, galactitol, D-glucitol, Methyl-α-D-glucoside, salicin, D-gluconate, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite and L-lysine are not assimilated. Maximum growth temperature is 21 °C. Growth in vitamin-free medium is negative Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ru. fanjingshanensis* differs from its closely related species *Ru. dracophylli* in its inability to assimilate L-sorbose, sucrose, maltose, cellobiose, melezitose, glycerol, ribitol, galactitol, D-mannitol, D-glucitol, salicin and succinate and its ability to assimilate trehalose, inulin, ethylamine and cadaverine (Table S1.20).

Typus: **China**, Fanjingshan Mountain, Guizhou province, obtained from a leaf of an unidentified plant, Oct. 2011, Q.-M. Wang (**holotype** CGMCC 2.4542^T preserved in a metabolically inactive state, ex-type CBS 15745 = FJS6C7).

Ruinenia bangxiensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828805. Fig. 14I, J.

Etymology: the specific epithet *bangxiensis* refers to the geographic origin of the type strain, Bangxi county, Hainan.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.2–3.7 × 6.4–10.5 µm and single, budding is polar (Fig. 14I), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pinkish-orange, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar.

Fig. 14. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *Kon. rhododendri* CGMCC 2.3463^T; (C, D) *Ben. wuzhishanensis* CGMCC 2.3569^T; (E) *Ben. pseudorectispora* CGMCC 2.5677^T; (F) *Ps. fusiformis* CGMCC 2.5823^T; (G, H) *Ru. fanjingshanensis* CGMCC 2.4542^T; (I, J) *Ru. bangxiensis* CGMCC 2.3454^T; (K, L) *Ru. lunata* CGMCC 2.4426^T; (M, N) *Boe. sterigmata* CGMCC 2.4539^T, (O) *St. layueensis* CGMCC 2.5817^T; (P) *Pse. motuoensis* CGMCC 2.5816^T. Bars = 10 µm.

Ballistoconidia are allantoid or reniform, 2.4–2.9 × 5.3–7.3 µm (Fig. 14J).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, inulin (variable), soluble starch (weak), D-xylose (weak), L-arabinose (delayed and weak), ethanol (variable), ribitol (variable), D-glucitol (variable), succinate (variable), and D-mannitol are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate and L-lysine (variable) are assimilated as sole nitrogen sources. Sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 25 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ru. bangxiensis* differs from its closely related species *Ru. clavata* in its inability to assimilate D-ribose and cadaverine and its ability to assimilate potassium nitrate (Table S1.20).

Typus: **China**, Bangxi county, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3454^T preserved in a metabolically inactive state, ex-type CBS 10819 = HBX1.0).

Ruinenia lunata Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828806. Fig. 14K, L.

Etymology: the specific epithet *lunata* refers to the falcate ballistoconidia of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal to falcate, 1.8–3.5 × 5.0–9.0 µm and single, budding is polar (Fig. 14K), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange-red, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are reniform to falcate, 3.0–6.5 × 6.0–13.0 µm (Fig. 14L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose (variable), trehalose, melibiose, raffinose, melezitose, ribitol (delayed), D-mannitol (delayed) and D-glucitol (delayedand weak) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, inulin, soluble starch, L-rhamnose, D-xylose, L-arabinose, D-arabinose, D-ribose, D-glucosamine, methyl α-D-glucoside, methanol, ethanol, erythritol, galactitol, glycerol, DL-lactic acid, critic acid, salicin, succinic acid, inositol and hexdecane are not assimilated. Ammonium sulfate and ethylamine hydrochloride (variable) are assimilated as sole nitrogen sources. L-lysine, sodium nitrite, potassium nitrate and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 22 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ru. lunata* differs from its closely related species *Ru. bangxiensis* and *Ru. clavata* in its inability to assimilate soluble starch and D-xylose and grow at 25 °C (Table S1.20).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4426^T preserved in a metabolically inactive state, ex-type CBS 12525 = TW 2.1E-028).

Boekhoutia Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828807.

Etymology: the genus is named in honour of Dr. Teun Boekhout for his research contributions to yeast taxonomy.

This genus is proposed for the branch represented by strain CGMCC 2.4539, which formed a separate clade from *Kurtzmanomyces*. Member of the *Chionosphaeraceae* (*Agaricostilbales*). The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate branch within *Chionosphaeraceae* (Fig. 4A).

Sexual reproduction not known. Colonies orange red, butyrous. Budding cells present and blastoconidia produced at the end of a stalk-like conidiophore. Conidiophore single or multiple, usually multifurcate. Pseudohyphae and hyphae not produced. Ballistoconidia formed.

Type species: *Boekhoutia sterigmata* Q.M. Wang, F.Y. Bai & A.H. Li.

Note: *Boekhoutia* and its close relative *Kurtzmanomyces* can produce stalk-like conidiophores, the former usually produces multifurcate conidiophores; each conidiophore of the latter can produce sequential multiple blastoconidia (Sampaio 2011b). *Boekhoutia* does not assimilate ethanol and D-mannitol, whereas all species of *Kurtzmanomyces* assimilate these two carbon sources.

Boekhoutia sterigmata Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828808. Figs 11B and 14M, N.

Etymology: the specific epithet *sterigmata* refers to the vegetative cells producing conidia on stalk-like conidiophores in the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.8–3.2 × 7.2–10.3 µm and single, budding is polar (Fig. 14M), a sediment is present. One or more conidia are produced on each stalk-like conidiophore. Conidiophore is single or multiple, usually multifurcate. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is deep pink red, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.6–3.2 × 3.8–5.8 µm (Fig. 14N).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose (delayed and weak), cellobiose, trehalose, melezitose and inulin are assimilated as sole carbon sources. L-sorbose, lactose, melibiose, raffinose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine

hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Typus: **China**, Fanjingshan Mountain, Guizhou province, obtained from a leaf of an unidentified plant, Oct. 2011, Q.-M. Wang (**holotype** CGMCC 2.4539^T preserved in a metabolically inactive state, ex-type CBS 15553 = FJS3F22).

Jianyuniaceae Q.M. Wang & F.Y. Bai ***fam. nov.*** MycoBank MB828809.
Member of the *Agaricostilbales* (*Agaricostilbomycetes*). The diagnosis of the family *Jianyuniaceae* is based on the the genus *Jianyunia*. The nomenclature of the family is based on the genus *Jianyunia*.

Type genus: *Jianyunia* Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout.

Genera accepted: *Jianyunia* Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, *Sterigmatospora* Q.M. Wang & F.Y. Bai, *Pseudosterigmatospora* Q.M. Wang & F.Y. Bai.

Sterigmatospora Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828810.

Etymology: the genus is named based on the morphology of the vegetative cells, which produce conidia on stalk-like conidiophores.

This genus is proposed for the branch represented by strain CGMCC 2.5817, which formed a separate clade. Member of the *Jianyuniaceae* (*Agaricostilbales*). The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate branch within *Jianyuniaceae* (Fig. 4A).

Sexual reproduction not known. Colonies cream, butyrous. Budding cells present and blastoconidia produced on stalk-like conidiophores. Conidiophore single or multiple, usually cluster on cells. Pseudohyphae and hyphae not produced. Ballistoconidia not formed.

Type species: *Sterigmatospora layueensis* Q.M. Wang, F.Y. Bai & A.H. Li.

Note: *Sterigmatospora* and *Pseudosterigmatospora* can produce stalk-like conidiophores, the former usually produces cluster of conidiophores from one site on cells, the latter can form bifurcate or trifurcate conidophores. They are also distinguished by some physiological characteristics (Table S1.21), such as assimilation of raffinose and growth in vitamin-free medium.

Sterigmatospora layueensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828811. Figs 11C and 14O.

Etymology: the specific epithet *layueensis* refers to the geographic origin of the type strain, Layue county, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.8–3.5 × 3.8–5.9 µm and single, budding is polar (Fig. 14O), a sediment is present. One or more conidia are produced on each stalk-like conidiophore. Conidiophore is single or multiple, usually cluster on cells. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is pale yellow, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose, sucrose, maltose, cellobiose, trehalose, raffinose, melezitose, D-xylose (variable), L-arabinose (variable), ribitol (variable), D-mannitol, D-glucitol, Methyl-α-D-glucoside and salicin (variable) are assimilated as sole carbon sources. Galactose, lactose, melibiose, inulin, soluble starch, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, galactitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 20 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Typus: **China**, Layue county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5817^T preserved in a metabolically inactive state, ex-type CBS 15649 = XZ100A2B).

Pseudosterigmatospora Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828812.

Etymology: the genus is named because of a similar morphology as present in the genus *Sterigmatospora*.

This genus is proposed for the branch represented by strain CGMCC 2.5816, which formed a separate clade. Member of the *Jianyuniaceae* (*Agaricostilbales*). The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate branch within *Jianyuniaceae* (Fig. 4A).

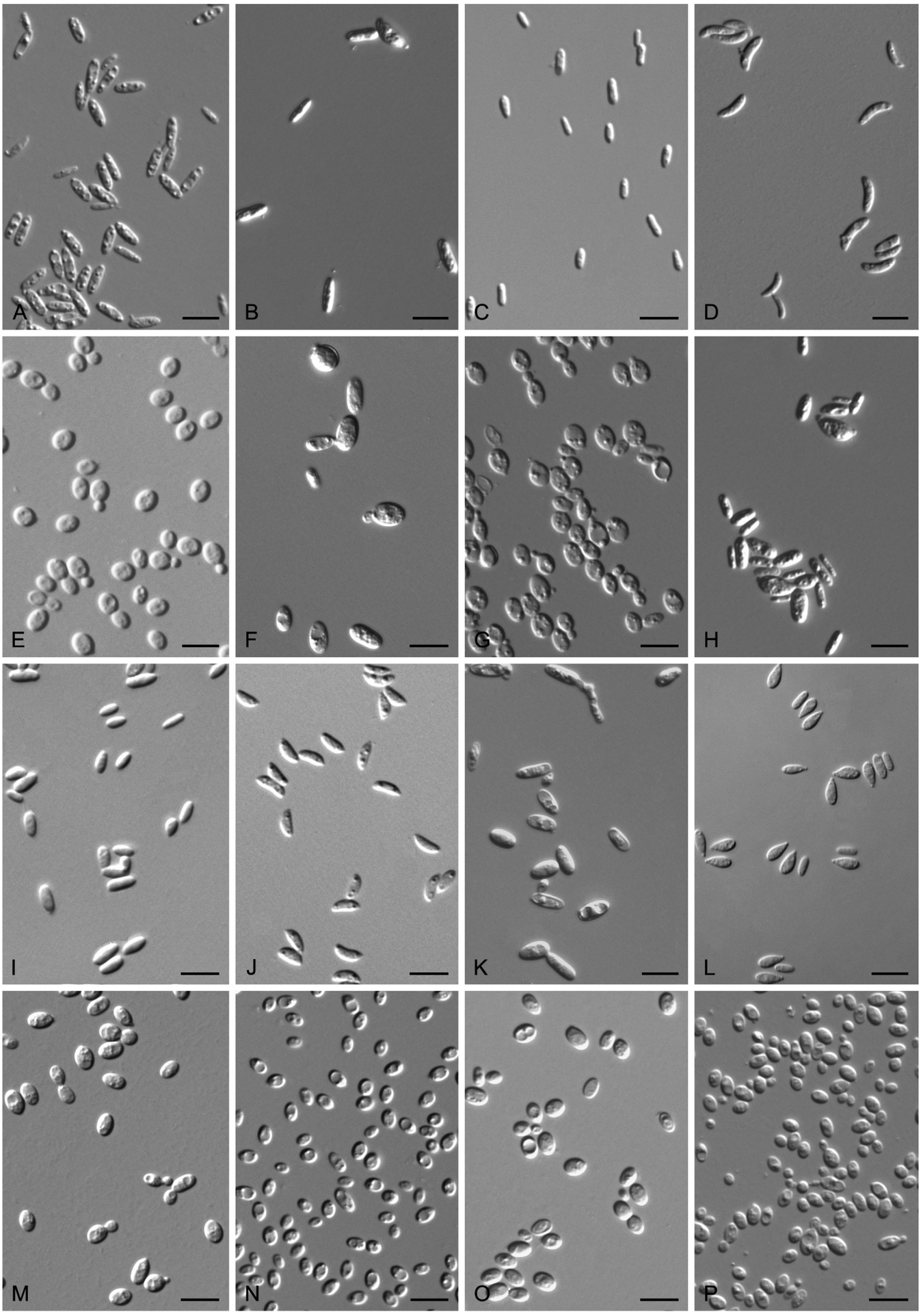
Sexual reproduction not known. Colonies white to cream, butyrous. Budding cells present and blastoconidia produced on stalk-like conidiophores. Conidiophores single or multiple, usually bifurcate, somewhat trifurcate. Pseudohyphae and hyphae not produced. Ballistoconidia not formed.

Type species: *Pseudosterigmatospora motuoensis* Q.M. Wang, F.Y. Bai & A.H. Li.

Pseudosterigmatospora motuoensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB832545. Figs 11D and 14P.

Etymology: the specific epithet *motuoensis* refers to the geographic origin of the type strain, Motuo, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.2–3.0 × 3.7–5.3 µm and single, budding is polar (Fig. 14P), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. One or more conidia are produced on each stalk-like conidiophore. Conidiophore is single or multiple, usually bifurcate, somewhat trifurcate. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed.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Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed and weak), L-sorbose (delayed and weak), sucrose, maltose (delayed and weak), trehalose, melezitose, ethanol, D-mannitol, D-glucitol and salicin (delayed and weak) are assimilated as sole carbon sources. Cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, Methyl-α-D-glucoside, D-gluconate, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite (delayed and weak), L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Typus: **China**, Motuo, Tibet, obtained from a leaf of *Achyrospermum wallichianum*, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5816^{T} preserved in a metabolically inactive state, ex-type CBS 15591 = XZ119B3).

New taxa in *Spiculogloeomycetes* (*Pucciniomycotina*)

Phyllozyma aceris Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828813. Fig. 15A, B.

Etymology: the specific epithet *aceris* refers to *Acer*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 2.6–3.5 × 5.5–8.9 µm and single, budding is polar (Fig. 15A), a sediment is present. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pink-orange, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid, falcate or cylindrical, 2.5–3.7 × 10.0–13.3 µm (Fig. 15B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, trehalose, raffinose, inulin (delayed and weak), ribitol (delayed and weak), D-mannitol, D-glucitol (weak) and succinate (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, maltose, cellobiose, lactose, melibiose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and potassium nitrate are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 20 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Phy. aceris* differs from its closely related species *Phy. coprosmicola* in its inability to assimilate glycerol, D-gluconate, DL-lactate and sodium nitrite (Table S1.22).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Acer caudatum*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2. 2662^{T} preserved in a metabolically inactive state, ex-type CBS 15773 = XZ17B1).

Phyllozyma jiayinensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828814. Fig. 15C.

Etymology: the specific epithet *jiayinensis* refers to the geographic origin of the type strain, Jiayin, Heilongjiang.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 1.4–2.0 × 3.2–7.3 µm and single, budding is polar (Fig. 15C), a sediment is present. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and somewhat wrinkled and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, trehalose, D-mannitol, D-glucitol (delayed), D-gluconate (weak) and DL-lactate (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, sucrose, maltose, cellobiose, lactose, melibiose, raffinose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, salicin, citrate, succinate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and potassium nitrate (delayed and weak) are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Phy. jiayinensis* and its closely related species *Phy. dimennae* and *Phy. corallina* are distinguishable from one another by assimilation of sucrose, D-xylose, glycerol, ribitol, D-glucitol, Methyl-α-D-glucoside, DL-lactate, succinate and sodium nitrite (Table S1.22).

Typus: **China**, Qingshan county, Jiayin, Heilongjiang province, obtained from a leaf of an unidentified plant, Aug. 2014, Q.-M. Wang (**holotype** CGMCC 2.5669^{T} preserved in a metabolically inactive state, ex-type CBS 13975 = HLJ25.21).

Meniscomyces Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828815.

Etymology: the genus is named after the lunately shaped vegetative cells.

Fig. 15. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *Phy. aceris* CGMCC 2.2662^{T}; (C) *Phy. jiayinensis* CGMCC 2.5669^{T}; (D) *Me. layueensis* CGMCC 2.5818^{T}; (E) *Sa. melibiophila* CBS 5143^{T}; (F) *Mi. ellipsoideus* CGMCC 2.5664^{T}; (G, H) *Mi. rubellus* CGMCC 2.4444^{T}; (I, J) *Mi. pseudomagnisporus* CGMCC 2.4538^{T}; (K, L) *Sy. rhododendri* CGMCC 2.2613^{T}; (M) *Cy. raffinophilum* CGMCC 2.3822^{T}; (N) *Cy. terricola* CGMCC 2.3823^{T}, (O) *Do. ningxiaensis* CGMCC 2.4451^{T}; (P) *Beg. foliicola* CGMCC 2.3164^{T}. Bars = 10 µm.

This genus is proposed for the branch represented by strain CGMCC 2.5818^T, which formed a separate clade. Member of the *Spiculogloeomycetes*. The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate branch within the *Spiculogloeomycetes* (Fig. 4A).

Sexual reproduction not known. Colonies cream, butyrous. Budding cells present. Cells special, lunate, allantoid and falcate, which differs from the cell morphology of other taxa in *Spiculogloeomycetes* (*Pucciniomycotina*). Pseudohyphae and hyphae not produced. Ballistoconidia not formed.

Type species: *Meniscomyces layueensis* Q.M. Wang, F.Y. Bai & A.H. Li.

Meniscomyces layueensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828816. Figs 11E and 15D.

Etymology: the specific epithet *layueensis* refers to the geographic origin of the type strain, Layue county, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are lunate, allantoids and falcate, 1.4–2.6 × 7.1–10.0 µm and single, budding is polar (Fig. 15D), a sediment is present. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose (variable), trehalose, melezitose and succinate are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, D-gluconate, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine and ethylamine hydrochloride (weak) are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Typus: **China**, Layue county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5818^T preserved in a metabolically inactive state, ex-type CBS 15747 = XZ100).

New taxa in *Cystobasidiomycetes* (*Pucciniomycotina*)

Sakaguchia melibiophila M. Groenew., Q.M. Wang, & F.Y. Bai ***sp. nov.*** MycoBank MB828817. Fig. 15E

Etymology: the specific epithet *melibiophila* refers to the physiological character of assimilating melibiose.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 2.5–4.4 × 3.8–5.6 µm and single, budding is polar (Fig. 15E), a sediment is formed. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is orange-red, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, cellobiose, trehalose, melibiose (delayed), D-xylose, L-arabinose, D-arabinose (delayed), D-ribose (delayed), ethanol, glycerol, ribitol, D-mannitol, salicin, D-glucitol, D-gluconate DL-lactate, succinate, citrate, myo-Inositol are assimilated as sole carbon sources. Sucrose, maltose, lactose, raffinose, melezitose, inulin, soluble starch, L-rhamnose, D-glucosamine, methanol, erythritol, galactitol and Methyl-α-D-glucoside are not assimilated. Potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochlorideare assimilated as sole nitrogen sources. Maximum growth temperature is 35 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sa. melibiophila* differs from its closely related species *Sa. lamellibrachiae* and *Sa. meli* in its ability to assimilate cellobiose, melibiose, ribitol, and nitrate (Table S1.23).

Typus: **Netherlands**, obtained from bronchial secretion, J. Swieringa (**holotype** CBS 5143^T preserved in a metabolically inactive state, ex-type JCM 8162 = CGMCC 2.4235).

Microsporomyces ellipsoideus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828818. Fig. 15F.

Etymology: the specific epithet *ellipsoideus* refers to the ellipsoidal vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal or cylindrical, 6.0–7.5 × 9.0–14.5 µm and single, budding is polar (Fig. 15F), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is brownish-orange, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, trehalose, melibiose (weak), raffinose, soluble starch, glycerol, D-glucitol, Methyl-α-D-glucoside, salicin and succinate (delayed and weak) are assimilated as sole carbon sources. L-sorbose, cellobiose, lactose, melezitose, inulin, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, erythritol, ribitol, galactitol, D-mannitol, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate and L-lysine (weak) are assimilated as sole nitrogen sources. Sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Mi. ellipsoideus* differs from its closely related species *Mi. rubellus* in its inability to assimilate melezitose, ribitol and galactitol and its ability to soluble starch and Methyl-α-D-glucoside (Table S1.24).

Typus: **China**, Motuo county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC

2.5664^T preserved in a metabolically inactive state, ex-type CBS 16020 = XZ137E4).

Microsporomyces rubellus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828819. Fig. 15G, H.

Etymology: the specific epithet *rubellus* refers to the pale red colony colour of this species.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 3.8–6.2 × 5.1–8.1 µm and single, budding is polar (Fig. 15G), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale-red, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid, reniform or cylindrical, 2.1–5.7 × 5.0–11.4 µm (Fig. 15H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, trehalose, melibiose, raffinose, melezitose, glycerol (delayed and weak), ribitol, galactitol, D-mannitol (delayed and weak), D-glucitol (weak), salicin (variable) and DL-lactate (variable) are assimilated as sole carbon sources. L-sorbose, cellobiose, lactose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, erythritol, Methyl-α-D-glucoside, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable) and L-lysine (variable) are assimilated as sole nitrogen sources. Sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Mi. rubellus* differs from its three closely related species *Mi. ellipsoideus* in its inability to assimilate soluble starch and Methyl-α-D-glucoside and its ability to assimilate melezitose, ribitol and galactitol (Table S1.24).

Typus: **China**, Taiwan province, obtained from a leaf of an unidentified plant, Aug. 2009, Q.-M. Wang (**holotype** CGMCC 2.4444^T preserved in a metabolically inactive state, ex-type CBS 15622 = TW1.3F-017).

Microsporomyces pseudomagnisporus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828820. Fig. 15I, J.

Etymology: the specific epithet *pseudomagnisporus* refers to the similar colony morphology to that of *Microsporomyces magnisporus*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 2.0–3.0 × 4.0–8.0 µm and single, budding is polar (Fig. 15I), a sediment is formed. After 1 mo at 17 °C, a part ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange, butyrous, wrinkled and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.5–3.3 × 5.8–8.3 µm (Fig. 15J).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, sucrose, trehalose (weak), melibiose (weak), raffinose (weak), melezitose (weak), inulin (delayed), D-arabinose (weak), ethanol, ribitol (weak), D-mannitol (weak), D-glucitol (weak), Methyl-α-D-glucoside (weak) and succinate (weak) are assimilated as sole carbon sources. Maltose, cellobiose, lactose, soluble starch, D-xylose, L-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, galactitol, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 19 °C. Growth in vitamin-free medium is postive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Mi. pseudomagnisporus* differs from its closely related species *Mi. magnisporus* in its inability to assimilate maltose, soluble starch, N-Acetyl-D-glucosamine, DL-lactate, citrate and sodium nitrite and its ability to assimilate inulin, ethanol, L-lysine, ethylamine and cadaverine (Table S1.24).

Typus: **China**, Fanjingshan Mountain, Guizhou province, obtained from a leaf of an unidentified plant, Oct. 2011, Q.-M. Wang (**holotype** CGMCC 2.4538^T preserved in a metabolically inactive state, ex-type CBS 15746 = FJS25C3).

Symmetrospora rhododendri Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828821. Fig. 15K, L.

Etymology: the specific epithet *rhododendri* refers to *Rhododendron*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 3.4–4.7 × 6.6–9.4 µm and single, budding is polar (Fig. 15K), a sediment is formed. After 1 mo at 17 °C, a part ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pinkish orange, butyrous, slight wrinkled and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal to long ovoid, 1.7–3.6 × 5.0–7.1 µm (Fig. 15L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose (delayed), sucrose, trehalose, melibiose, L-arabinose, glycerol, ribitol (weak), D-mannitol, D-glucitol and succinate (weak) are assimilated as sole carbon sources. Maltose, cellobiose, lactose, melezitose, raffinose, inulin, soluble starch, D-xylose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate and L-lysine are assimilated as sole nitrogen sources. Sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 25 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sy. rhododendri* differs from its closely related species *Sy. coprosmae* and *Sy. oryzicola* in its inability to assimilate L-sorbose, cellobiose, melezitose, D-arabinose, D-

ribose, Methyl-α-D-glucoside, salicin and DL-lactate and its ability to assimilate lactose, inulin, nitrate and cadaverine (Table S1.25).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of *Rhododendron sp.*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2613^T preserved in a metabolically inactive state, ex-type CBS 15447 = XZ49DX).

New combinations for *Symmetrospora*

Symmetrospora oryzicola (Nakase & M. Suzuki) Q.M. Wang & F.Y. Bai, ***com. nov.*** MycoBank MB832091.
Basionym: *Sporobolomyces oryzicola* Nakase & M. Suzuki, J. Gen. Appl. Microbiol., 32(2): 152 (1986).

Cystobasidium raffinophilum Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828822. Fig. 15M.

Etymology: the specific epithet *raffinophilum* refers to the ability to assimilate raffinose.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 3.1–5.0 × 4.5–6.8 µm and single, budding is polar (Fig. 15M), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange-pink, mucoid, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed), sucrose, cellobiose, trehalose, raffinose, melezitose, inulin (weak), D-xylose, L-arabinose, D-arabinose, D-ribose (delayed and weak), ethanol, glycerol, ribitol (delayed and weak), galactitol, D-mannitol, succinate (weak) and citrate (weak) are assimilated as sole carbon sources. L-sorbose, maltose, lactose, melibiose, soluble starch, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and potassium nitrate are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Cy. raffinophilum* differs from its closely related species *Cy. fimetarium* in its inability to assimilate lactose, salicin, DL-lactate and its ability to assimilate galactose, raffinose, melezitose, galactitol and potassium nitrate (Table S1.26).

Typus: **China**, Yecheng county, Xinjiang province, obtained from soil, Jul. 2007, Q.-M. Wang (**holotype** CGMCC 2.3822^T preserved in a metabolically inactive state, ex-type CBS 15509 = 141.4).

Cystobasidium terricola Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828823. Fig. 15N.

Etymology: the specific epithet *terricola* refers to the origin of the substrate of the type strain, soil.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.1–4.2 × 2.8–5.7 µm and single, budding is polar (Fig. 15N), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pink-red, mucoid, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), L-sorbose (variable), sucrose, cellobiose, trehalose, lactose, raffinose (variable), melezitose, D-xylose, L-arabinose, D-arabinose (delayed and weak), D-ribose, ethanol, glycerol, ribitol, D-mannitol, D-glucitol, salicin, DL-lactate (delayed and weak), succinate and citrate (variable) are assimilated as sole carbon sources. Maltose, melibiose, inulin, soluble starch, L-rhamnose, D-glucosamine, methanol, erythritol, galactitol, Methyl-α-D-glucoside, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (delayed and weak), sodium nitrite (delayed and weak), L-lysine (delayed and weak), ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 35 °C. Growth in vitamin-free medium is weak. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Cy. terricola* and its three closely related species, *Cy. raffinophilum*, *Cy. minutum* and *Cy. fimetarium*, are distinguishable by the assimilation of L-sorbose, galactose, lactose, raffinose, melezitose, galactitol, D-glucitol, salicin, DL-lactate and potassium nitrate (Table S1.26).

Typus: **China**, Yecheng county, Xinjiang province, obtained from soil, Jul. 2007, Q.-M. Wang (**holotype** CGMCC 2.3823^T preserved in a metabolically inactive state, ex-type CBS 15650 = 140.23).

Robertozyma Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828824.

Etymology: the genus is named in honour of Dr. V. Robert for his contributions to the yeast taxonomy.

This genus is proposed for the branch represented by strain CGMCC 2.4451 which formed a separate clade. Member of the *Cystobasidiales* (*Cystobasidiomycetes*). The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate branch within the *Cystobasidiales* (Fig. 4).

Sexual reproduction not known. Colonies orange, butyrous. Budding cells present. Pseudohyphae and hyphae not produced. Ballistoconidia not formed.

Type species: *Robertozyma ningxiaensis* Q.M. Wang, F.Y. Bai & A.H. Li.

Note: *Robertozyma* and its closely related genera, *Begerowomyces* and *Halobasidium,* have a similar colony morphology, however, they can be distinguished by some physiological characters (Table S1.27). *Robertozyma* does not assimilate sucrose, melezitose, D-xylose and ethanol, whereas species of *Begerowomyces* and *Halobasidium* can use them. *Begerowomyces* species assimilate erythritol and galactitol, whereas species of *Robertozyma* and *Halobasidium* do not assimilate these two carbon resources.

Robertozyma ningxiaensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828826. Fig. 15O.

Etymology: the specific epithet *ningxiaensis* refers to the geographic origin of the type strain, Ningxia province, China.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are oval and ellipsoidal, 3.2–4.5 × 3.9–6.8 µm and single, budding is polar (Fig. 15O), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange red, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed and weak), trehalose, glycerol, D-mannitol, salicin (delayed and weak) and succinate are assimilated as sole carbon sources. L-sorbose, sucrose, maltose, cellobiose, lactose, melibiose, raffinose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, erythritol, ribitol, galactitol, D-glucitol, Methyl-α-D-glucoside, D-gluconate, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine and ethylamine hydrochloride are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Typus: **China**, Helanshan mountain, Ningxia province, obtained from soil, Aug. 2009, P.J. Han (**holotype** CGMCC 2.4451^T preserved in a metabolically inactive state, ex-type CBS 12499 = HLS10.23).

Begerowomyces Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828827.

Etymology: the genus is named in honour of Dr. Dominik Begerow for his contributions to yeast taxonomy and his proposal of the order *Cystobasidiales*.

This genus is proposed for the branch represented by strain CGMCC 2.3164, which formed a separate clade. Member of the *Cystobasidiales* (*Cystobasidiomycetes*). The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate branch within the *Cystobasidiales* (Fig. 4).

Sexual reproduction not known. Colonies yellow, butyrous. Budding cells present. Pseudohyphae and hyphae not produced. Ballistoconidia not formed.

Type species: *Begerowomyces foliicola* Q.M. Wang, F.Y. Bai & A.H. Li.

Begerowomyces foliicola Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828828. Figs 11F and 15P.

Etymology: the specific epithet *foliicola* refers to the type strain isolated from a leaf.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid and ellipsoidal, 2.6–3.9 × 2.7–6.0 µm and single, budding is polar (Fig. 15P), a sediment is formed. After 1 mo at 17 °C, a pellicle and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish cream, butyrous, wrinkled and smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed and weak), sucrose (delayed), maltose (delayed and weak), cellobiose (delayed and weak), trehalose (delayed and weak), melezitose, inulin (delayed and weak), D-xylose, L-arabinose (delayed and weak), ethanol, erythritol (delayed), ribitol, galactitol, D-mannitol (delayed), D-glucitol (delayed) and succinate (delayed) are assimilated as sole carbon sources. L-sorbose, lactose, melibiose, raffinose, soluble starch, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (delayed and weak), L-lysine and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Typus: **Germany**, obtained from a leaf of an unidentified plant, Sep. 2005 (**holotype** CGMCC 2.3164^T preserved in a metabolically inactive state, ex-type CBS 15655 = G7.4).

New taxa in *Microbotryomycetes* (*Pucciniomycotina*)

Rosettozymales Q.M. Wang & F.Y. Bai ***ord. nov.*** MycoBank MB828829.
Member of the *Microbotryomycetes*. The diagnosis of the order *Rosettozymales* is based on the the genus *Rosettozyma*. The nomenclature of the order is based on the genus *Rosettozyma*.

Type family: *Rosettozymaceae* Q.M. Wang & F.Y. Bai.

Rosettozymaceae Q.M. Wang & F.Y. Bai ***fam. nov.*** MycoBank MB828830.
Member of the *Rosettozymales* (*Microbotryomycetes*). The diagnosis of the family *Rosettozymaceae* is based on the the genus *Rosettozyma*. The nomenclature of the family is based on the genus *Rosettozyma*.

Type genus: *Rosettozyma* Q.M. Wang & F.Y. Bai.

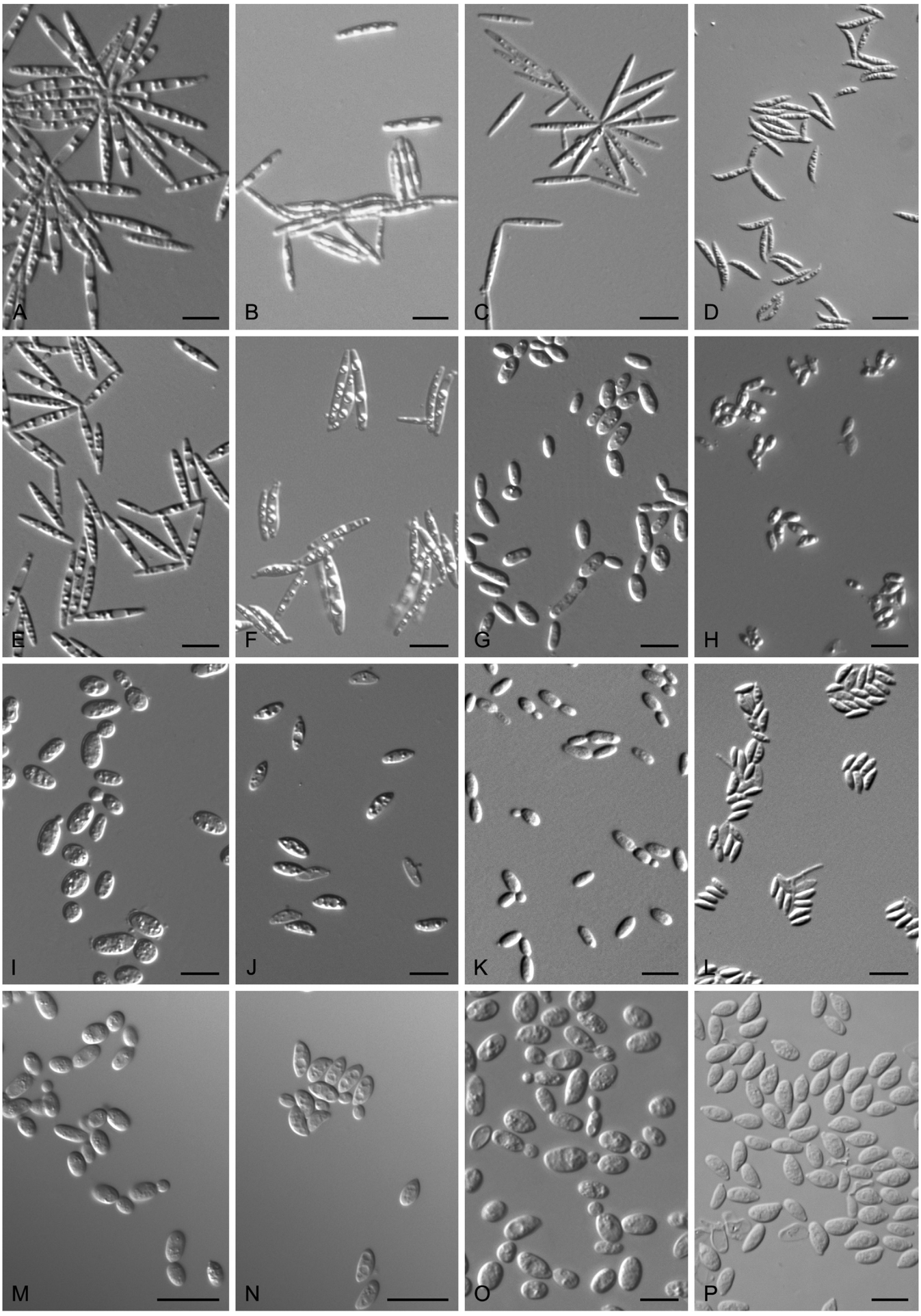
Genus accepted: *Rosettozyma* Q.M. Wang & F.Y. Bai.

Rosettozyma Q.M. Wang & F.Y. Bai ***gen. nov.*** MycoBank MB828831.

Etymology: the genus is named based on the morphology of the vegetative cells forming a rosette.

This genus is proposed for the clade represented by CGMCC 2.3446, which formed a separate clade from other orders and taxa in the *Microbotryomycetes*. Member of *Microbotryomycetes*. The genus is mainly circumscribed by the phylogenetic analysis of the seven genes dataset, in which it occurred as a separate clade within the *Microbotryomycetes* (Fig. 4).

Sexual reproduction not known. Colonies white, butyrous. Budding cells present and always form rosette-like clusters. Pseudohyphae and hyphae not produced. Ballistoconidia formed.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Type species: *Rosettozyma petaloides* Q.M. Wang, F.Y. Bai & A.H. Li.

Note: Except the genus *Rosettozyma*, species in *Yamadamyces* and *Meredithblackwellia* also form rosette-like cell clusters (Golubev & Scorzetti 2010, Toome *et al.* 2013).

Rosettozyma petaloides Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828832. Figs 11G, H and 16A, B.

Etymology: the specific epithet *petaloides* refers to the vegetative cells forming a petale morphology of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are elongate fusiform, either singly or in rosettes, 2.2–3.2 × 9.8–18.7 µm, budding is polar (Fig. 16A), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is whitish to cream, butyrous, slightly wrinkled and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are cylindrical or falcate, 1.3–1.6 × 9.3–12.0 µm (Fig. 16B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose (variable), trehalose, lactose (variable), raffinose (variable), melezitose, D-xylose, L-arabinose, D-arabinose (variable), D-ribose (variable), ethanol (variable), glycerol, ribitol (variable), D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin (delayed and weak), DL-lactate (variable), succinate (delayed and weak) and citrate (delayed and weak) are assimilated as sole carbon sources. Galactose, L-sorbose, melibiose, inulin, soluble starch, L-rhamnose, D-glucosamine, methanol, erythritol, galactitol, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), sodium nitrite (variable), L-lysine (variable), ethylamine hydrochloride (delayed and weak) and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is delayed and weak. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ro. petaloides* and its two closely related species, *Ro. cystopteridis* and *Ro. motuoensis*, can be distinguished from one another by the assimilation of D-xylose, L-arabinose, D-arabinose, glycerol and succinate. *Ro. petaloides* differs from the other species in its ability to assimilate D-xylose and glycerol (Table S1.28).

Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3446^T preserved in a metabolically inactive state, ex-type CBS 15480 = WZS29.14).

Rosettozyma cystopteridis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828833. Figs 16C, D and 17A, B.

Etymology: the specific epithet *cystopteridis* refers to *Cystopteris*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, either singly or in rosettes, 2.2–2.8 × 11.4–20.3 µm, budding is polar (Fig. 16C), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is whitish to cream, butyrous, slightly wrinkle, semi-glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or falcate, 1.7–2.8 × 7.7–15.4 µm (Fig. 16D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, trehalose, melezitose, L-arabinose (variable), D-arabinose, ethanol, erythritol (variable), D-mannitol, D-glucitol, Methyl-α-D-glucoside (variable) and salicin are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, D-ribose, L-rhamnose, D-glucosamine, methanol, glycerol, ribitol, galactitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ro. cystopteridis* and its two closely related species, *Ro. petaloides* and *Ro. motuoensis*, can be distinguished from one another by the assimilation of D-xylose, L-arabinose, D-arabinose, glycerol and succinate. *Ro. cystopteridis* differs from *Ro. petaloides* in its inability to assimilate D-xylose and glycerol. *Ro. cystopteridis* differs from *Ro. motuoensis* in its inability to assimilate succinate and its ability to assimilate D-arabinose (Table S1.28).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Cystopteris moupinensis*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2615^T preserved in a metabolically inactive state, ex-type CBS 15448 = XZ16E1).

Rosettozyma motuoensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828834. Figs 16E, F and 17C.

Etymology: the specific epithet *motuoensis* refers to the geographic origin of the type strain, Motuo, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, either singly or in rosettes, 1.5–2.5 × 12.5–20.0 µm, budding is polar (Fig. 16E), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is white, butyrous, smooth, semi-glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or falcate, 1.4–2.3 × 11.7–21.0 µm (Fig. 16F).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, trehalose, melezitose, ethanol, D-mannitol, D-glucitol, Methyl-α-D-glucoside and succinate are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-

Fig. 16. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *Ros. petaloides* CGMCC 2.3446^T; (C, D) *Ros. cystopteridis* CGMCC 2.2615^T; (E, F) *Ros. motuoensis* CGMCC 2.5819^T; (G, H) *Sp. cellobiolyticus* CGMCC 2.5675^T; (I, J) *Sp. reniformis* CGMCC 2.5627^T; (K, L) *Sp. ellipsoideus* CGMCC 2.5619^T; (M, N) *Sp. primogenomicus* IAM13481^T; (O, P) *Rh. platycladi* CGMCC 2.3118^T. Bars = 10 µm.

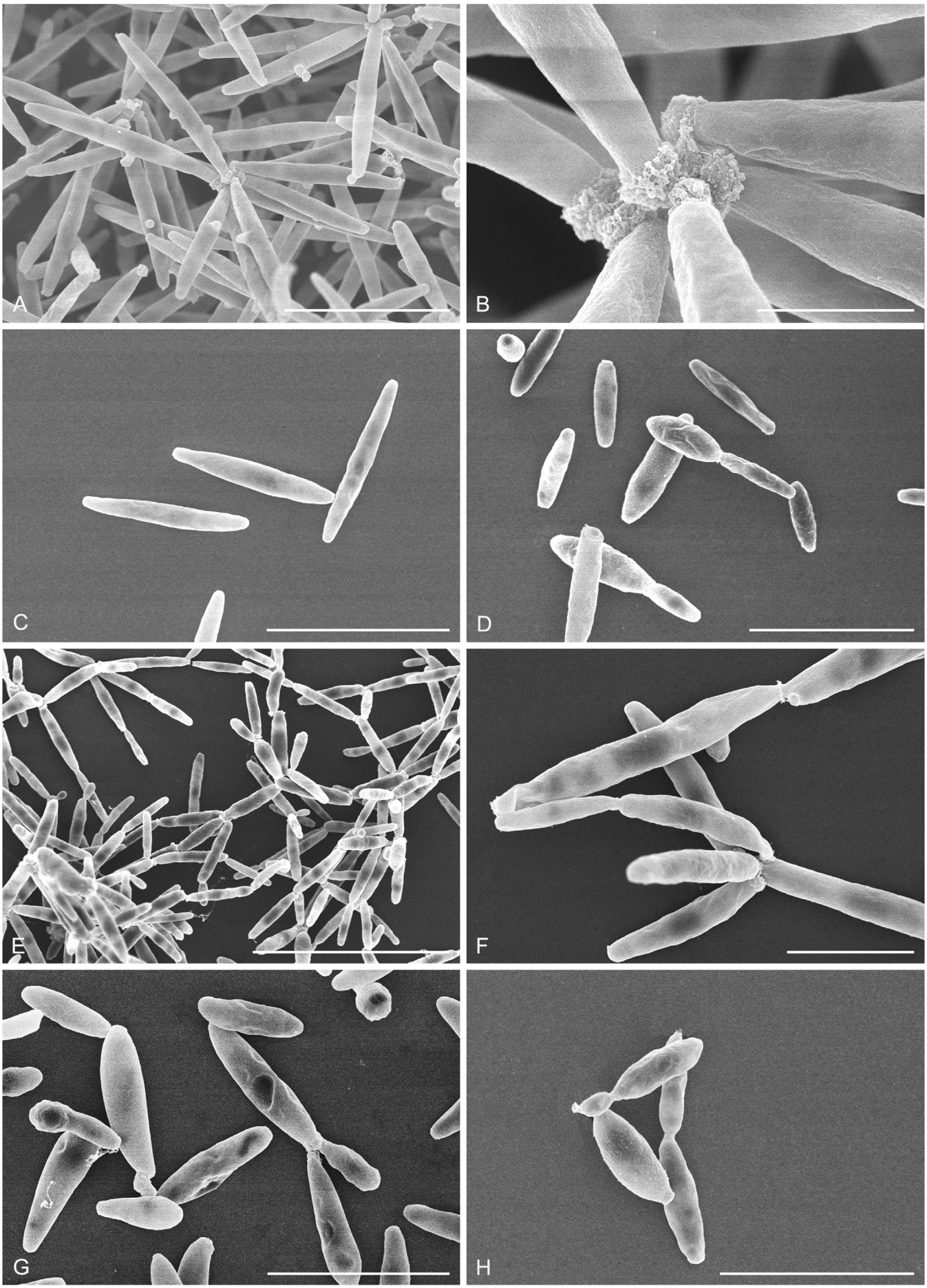


Fig. 17. SEM image of vegetative cells grown in YM broth for 5 d at 17 °C. (A, B) *Ros. cystopteridis* CGMCC 2.2615^T, A Bars = 10 μm, B Bars = 2 μm; (C) *Ros. motuoensis* CGMCC 2.5819^T, Bars = 10 μm; (D) *He. tridentata* CGMCC 2.5602^T, Bars = 10 μm; (E, F) *He. cylindrica* CGMCC 2.5650^T, E Bars = 20 μm, F Bars = 5 μm; (G) *Ya. terricola* CGMCC 2.5820^T, Bars = 10 μm; (H) *Ch. rhododendri* CGMCC 2.5821^T, Bars = 5 μm.

rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, salicin, D-gluconate, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ro. motuoensis* and their two closely related species, *Ro. petaloides* and *Ro. cystopteridis*, can be distinguished from one another by the assimilation of D-xylose, L-arabinose, D-arabinose, glycerol and succinate. *Ro. motuoensis* differs from *Ro. petaloides* in its inability to assimilate D-xylose, L-arabinose and glycerol and its ability to assimilate succinate. *Ro. motuoensis* differs from *Ro. cystopteridis* in its inability to assimilate D-arabinose and its ability to assimilate succinate (Table S1.28).

Typus: **China**, Motuo, Tibet, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5819^T preserved in a metabolically inactive state, ex-type CBS 15588 = XZ118E6).

Sporobolomyces cellobiolyticus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828835. Fig. 16G, H.

Etymology: the specific epithet *cellobiolyticus* refers to the physiological character of assimilating cellobiose.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ovoid, ellipsoidal and cylindrical, 2.6–4.8 × 5.6–12.0 µm and single, budding is polar (Fig. 16G), a sediment is formed. On YM agar, after 1 mo at 17 °C, the streak culture is orange, butyrous, smooth. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal or reniform, 1.9–3.2 × 5.1–7.1 µm (Fig. 16H).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), L-sorbose (variable), sucrose, maltose, cellobiose (delayed), trehalose, raffinose (delayed), melezitose, inulin, D-ribose (variable), ethanol (variable), glycerol (variable), ribitol (variable), D-mannitol (variable), D-glucitol, Methyl-α-D-glucoside, salicin (variable), DL-lactate (variable) and succinate (variable) are assimilated as sole carbon sources. Lactose, melibiose, soluble starch, D-xylose, L-arabinose, D-arabinose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, galactitol, D-gluconate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (variable), sodium nitrite (variable), L-lysine, ethylamine hydrochloride (variable) and cadaverine dihydrochloride (variable) are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sp. cellobiolyticus* differs from its closely related species *Sp. jilinensis* in its inability to assimilate soluble starch and D-xylose and its ability to assimilate cellobiose and inulin (Table S1.29).

Typus: **China**, Wuyiling natural reserve, Heilongjiang province, obtained from a leaf of an unidentified plant, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5675^T preserved in a metabolically inactive state, ex-type CBS 13964 = HLJ33B4).

Sporobolomyces reniformis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828836. Fig. 16I, J.

Etymology: the specific epithet *reniformis* refers to the reniform ballistoconidia.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal to ovoid, 3.8–5.7 × 5.8–10.7 µm and single, budding is polar (Fig. 16I), a sediment is formed. On YM agar, after 1 mo at 17 °C, the streak culture is orange red, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal or reniform, 2.8–3.8 × 7.5–10.0 µm (Fig. 16J).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose, sucrose, maltose, trehalose, raffinose, ethanol (delayed and weak) and DL-lactate are assimilated as sole carbon sources. Galactose, cellobiose, lactose, melibiose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, D-gluconate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, and cadaverine dihydrochloride (delayed and weak) are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, L-lysine and ethylamine hydrochloride are not assimilated. Maximum growth temperature is 30 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sp. reniformis* differs from its closely related species *Sp. ellipsoideus* in its inability to assimilate melezitose, D-mannitol and D-glucitol (Table S1.29).

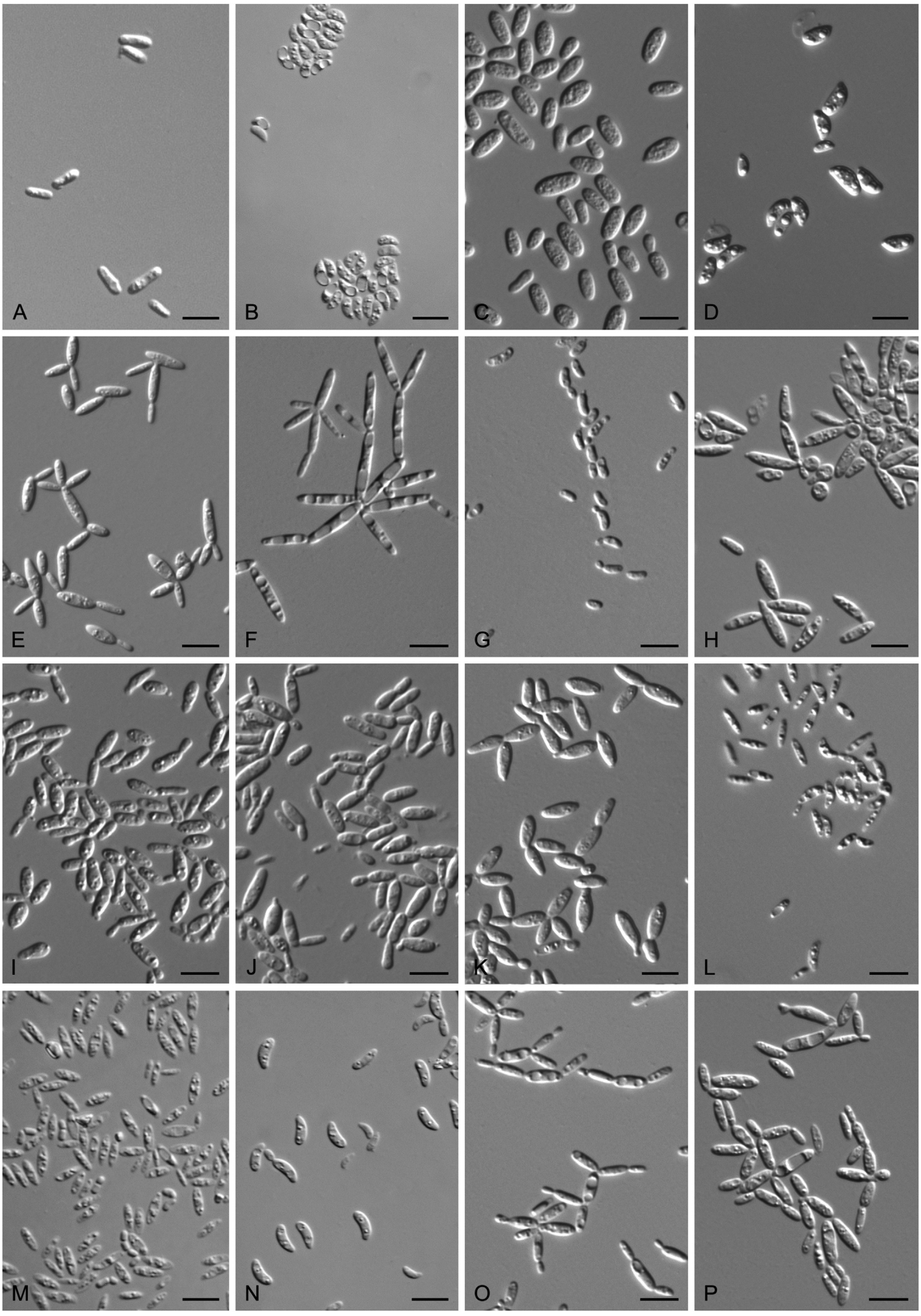
Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5627^T preserved in a metabolically inactive state, ex-type CBS 15562 = GPS21.2C2).

Sporobolomyces ellipsoideus Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828837. Fig. 16K, L.

Etymology: the specific epithet *ellipsoideus* refers to the ellipsoidal cell morphology.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 2.1–2.9 × 3.6–8.8 µm and single, budding is polar (Fig. 16K), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is orange, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal, allantoid or reniform, 1.2–2.5 × 5.0–7.1 µm (Fig. 16L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), L-sorbose (variable), sucrose, maltose, cellobiose (variable), trehalose, lactose (variable), raffinose (weak), melezitose, inulin (variable), soluble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starch (variable), D-ribose (variable), L-arabinose (variable), D-arabinose (variable), L-rhamnose (variable), D-glucosamine (variable), ethanol (variable), glycerol (variable), ribitol (variable), D-mannitol, D-glucitol, Methyl-α-D-glucoside (variable), DL-lactate (variable), succinate (variable), citrate (variable) and salicin (variable) are assimilated as sole carbon sources. Melibiose, D-xylose, N-Acetyl-D-glucosamine, D-gluconate, methanol, erythritol, galactitol, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, Sodium nitrite (variable), L-lysine, ethylamine hydrochloride (variable) and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sp. ellipsoideus* differs from its closely related species *Sp. reniformis* in its ability to assimilate melezitose, D-mannitol and D-glucitol (Table S1.29).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5619^T preserved in a metabolically inactive state, ex-type CBS 15590 = GPS21.5C1).

Sporobolomyces primogenomicus Q.M. Wang & F.Y. Bai ***sp. nov.*** MycoBank MB828838. Fig. 16M, N.

Etymology: the specific epithet *primogenomicus* refers to the fact that the type strain was the first sequenced genome in the *Pucciniomycotina*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal, 2.0–3.8 × 3.0–5.6 µm and single, budding is polar (Fig. 16M), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is red, butyrous, shiny. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.0–2.7 × 3.3–5.8 µm (Fig. 16N).

Physiological and biochemical characteristics: Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, glycerol, ribitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate and citrate (delayed) are assimilated as sole carbon sources. Lactose, melibiose, inulin, L-rhamnose, erythritol, galactitol and myo-inositol are not assimilated. Potassium nitrate (weak) is assimilated as sole nitrogen sources.

Physiologically, *Sp. primogenomicus* differs from its closely related species *Sp. ruberrimus* in its ability to assimilate L-sorbose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, ribitol, D-glucitol, Methyl-α-D-glucoside and DL-lactate (Table S1.29). The data of carbon assimilation were collected from Yamazaki & Komagata (1983).

Typus: **Japan**, Kanto region, obtained from a willow leaf, 1983, M. Yoshizawa (**holotype** JCM 8242^T preserved in a metabolically inactive state, ex-type CBS 15935 = IAM13481).

Acception of *Sporobolomyces shibatanus* in the genus *Sporobolomyces*

Sporobolomyces shibatanus (Okun.) Verona & Cif., Atti Ist. Bot. R. Univ. Pavia, 3. Ser. 10: 246. 1939.

Synonym: Sporidiobolus pararoseus Fell & Tallman, Curr. Microbiol. 5: 80. 1981.

Note: *Sporobolomyces shibatanus* was omitted from the list of accepted species of *Sporobolomyces* in our previous study (Wang *et al.* 2015b), deleted by accident in the final version. *Sporobolomyces shibatanus* is the anamorph of *Sporidiobolus pararoseus* (Sampaio 2011c), but the former was published earlier than the latter. Thus, *Sporidiobolus pararoseus* should be considered as a synonym of *Sporobolomyces shibatanus* at present.

Rhodosporidiobolus platycladi Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828839. Fig. 16O, P.

Etymology: the specific epithet *platycladi* refers to *Platycladus*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and ovoid, 4.0–6.2 × 5.5–9.7 µm and single, budding is polar (Fig. 16O), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pale cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal or reniform, 3.1–5.0 × 7.0–10.0 µm (Fig. 16P).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose (weak), sucrose, maltose, cellobiose, trehalose, raffinose, melezitose, D-xylose, L-arabinose, glycerol, ribitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside (weak) and salicin (weak) are assimilated as sole carbon sources. Galactose, lactose, melibiose, inulin, soluble starch, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, erythritol, galactitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite (weak), L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 32 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Rh. platycladi* differs from its closely related species *Rh. nylandii* in its inability to assimilate soluble starch, D-arabinose, D-ribose, ethanol and succinate and its ability to assimilate D-xylose, L-arabinose and L-lysine (Table S1.30).

Typus: **China**, Beijing, obtained from a leaf of *Platycladus orientalis*, Mar. 2006, S.-A. Wang (**holotype** CGMCC 2.3118^T preserved in a metabolically inactive state, ex-type CBS 15469 = BJ6-3).

Rhodosporidiobolus jianfalingensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828840. Fig. 18A, B.

Fig. 18. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *Rh. jianfalingensis* CGMCC 2.3532^T; (C, D) *Rh. fuzhouensis* CGMCC 2.4435^T; (E) *He. tridentata* CGMCC 2.5602^T; (F) *He. cylindrica* CGMCC 2.5650^T; (G) *Mic. swertiae* CGMCC 2.3533^T; (H) *Ya. terricola* CGMCC 2.5820^T; (I) *O. nepetae* CGMCC 2.5824^T; (J) *O. dicranopteridis* CGMCC 2.3441^T; (K, L) *Ch. pseudogriseoflava* CGMCC 2.5629^T; (M, N) *Ch. sambuci* CGMCC 2.2618^T; (O) *Ch. iridis* CGMCC 2.2769^T; (P) *Ch. rhododendri* CGMCC 2.5821^T. Bars = 10 µm.

Etymology: the specific epithet *jianfalingensis* refers to the geographic origin of the type strain, Jianfaling, Hainan.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 1.4–2.9 × 4.3–10.0 µm and single, budding is polar (Fig. 18A), a sediment is present. After 1 mo at 17 °C, a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is pale cream, butyrous, slightly wrinkled and glossy. The margin is entire or eroded. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.1–2.9 × 5.0–7.1 µm (Fig. 18B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose (weak), melibiose (weak), raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose (weak), D-ribose (weak), L-rhamnose, D-glucosamine (weak), Methyl-α-D-glucoside, salicin, succinate (weak) and citrate (weak) are assimilated as sole carbon sources. L-sorbose, inulin, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, DL-lactate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite and L-lysine are assimilated as sole nitrogen sources. Ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 25 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Rh. jianfalingensis* differs from its closely related four species, *Rh. platycladi*, *Rh. nylandii*, *Rh. odoratus* and *Rh. ruineniae*, in its inability to assimilate L-sorbose, glycerol, ribitol, D-mannitol and D-glucitol (Table S1.30).

Typus: **China**, Jianfaling, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3532^{T} preserved in a metabolically inactive state, ex-type CBS 15494 = JF25.7-1).

Rhodosporidiobolus fuzhouensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828841. Fig. 18C, D.

Etymology: the specific epithet *fuzhouensis* refers to the geographic origin of the type strain, Fuzhou county, Fujian.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 3.2–5.0 × 6.1–11.0 µm and single, budding is polar (Fig. 18C), a sediment is formed. After 1 mo at 17 °C, a pellicle and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is pink orange, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.8–4.9 × 6.0–9.2 µm (Fig. 18D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delayed), L-sorbose, trehalose, D-xylose (variable), D-ribose (variable), ethanol, ribitol (variable), D-mannitol (variable), D-glucitol, salicin (variable) and succinate (variable) are assimilated as sole carbon sources. Sucrose, maltose, cellobiose, lactose, melibiose, raffinose, melezitose, inulin, soluble starch, L-arabinose, D-arabinose, L-rhamnose, D-glucosamine, methanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, gluconate, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate and L-lysine (delayed and weak) are assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Rh. fuzhouensis* differs from its closely related species *Rh. lusitaniae* in its inability to assimilate galactitol, citrate, potassium nitrate and sodium nitrite (Table S1.30).

Typus: **China**, Jinghong, Yunnan province, obtained from a leaf of an unidentified plant, Aug. 2011, Q.-M. Wang (**holotype** CGMCC 2.4435^{T} preserved in a metabolically inactive state, ex-type CBS 12492 = FJYZ2-6).

Heitmaniales Q.M. Wang & F.Y. Bai ***ord. nov.*** MycoBank MB828842.
Member of the *Microbotryomycetes*. The diagnosis of the order *Heitmaniales* is based on the the genus *Heitmania*. The nomenclature of the order is based on the genus *Heitmania*.
Type family: *Heitmaniaceae* Q.M. Wang & F.Y. Bai.

Heitmaniaceae Q.M. Wang & F.Y. Bai ***fam. nov.*** MycoBank MB828843.
Member of the *Microbotryomycetes*. The diagnosis of the family *Heitmaniaceae* is based on the the genus *Heitmania*. The nomenclature of the family is based on the genus *Heitmania*.

Type genus: *Heitmania* X.Z. Liu, F.Y. Bai, M. Groenew. & Boekhout, Index Fungorum 381: 1 (2018).

Genus accepted: *Heitmania* X.Z. Liu, F.Y. Bai, M. Groenew. & Boekhout, Index Fungorum 381: 1 (2018).
Synonyms: *Heitmania* X.Z. Liu, F.Y. Bai, M. Groenew. & Boekhout, Int. J. Syst. Evol. Microbiol. 67: 4538 (2017), *nom. inval.*, Art. 40.1 (Shenzhen).

Heitmania tridentata Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828844. Figs 17D and 18E.

Etymology: the specific epithet *tridentata* refers to the vegetative cell morphology of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 2.6–3.4 × 5.9–12.0 µm and single, budding is polar, usually tridentate (Fig. 18E), a sediment is formed. After 1 mo at 17 °C, a part ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, maltose, trehalose, ethanol and D-mannitol (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, sucrose, cellobiose, lactose, melibiose, raffinose, melezitose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Sodium nitrite and ethylamine hydrochloride are

not assimilated. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *He. tridentata* differs from its closely related species *He. cylindrica* in its inability to assimilate melezitose, glycerol, D-glucitol, succinate and ethylamine (Table S1.31).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5602^T preserved in a metabolically inactive state, ex-type CBS 15549 = GPS20.16B3).

Heitmania cylindrica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828845. Figs 17E, F and 18F.

Etymology: the specific epithet *cylindrica* refers to the vegetative cell morphology of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are elongate cylindrical, 2.5–3.4 × 9.9–16.3 µm and single, budding is polar (Fig. 18F), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose (delayed and weak), maltose (delayed), trehalose (delayed), melezitose (delayed), ethanol, glycerol, D-mannitol, D-glucitol and succinate are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, ribitol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (delayed and weak), L-lysine and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *He. cylindrica* differs from its closely related species *He. tridentata* in its ability to assimilate melezitose, glycerol, D-glucitol, succinate and ethylamine (Table S1.31).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5650^T preserved in a metabolically inactive state, ex-type CBS 15568 = GPS20.2C8).

Microbotryozyma swertiae Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828846. Fig. 18G.

Etymology: the specific epithet *swertiae* refers to *Swertia*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and lunate, 1.7–2.5 × 3.9–5.6 µm and single, budding is polar (Fig. 18G), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose (delayed), sucrose, maltose, cellobiose, trehalose, lactose, melezitose, D-xylose, D-ribose (delayed and weak), glycerol, ribitol (delayed and weak), D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin and succinate (delayed and weak) are assimilated as sole carbon sources. Galactose, melibiose, raffinose, inulin, soluble starch, L-arabinose, D-arabinose, L-rhamnose, D-glucosamine, methanol, ethanol, erythritol, galactitol, D-gluconate, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate and ethylamine hydrochloride are assimilatedas sole nitrogen sources. Sodium nitrite, L-lysine and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Mic. swertiae* differs from its closely related species *Mic. collariae* in its inability to assimilate D-gluconate, DL-lactate and sodium nitrite (Table S1.32).

Typus: **China**, Chuxiong county, Yunnan province, obtained from a leaf of *Swertia yunnanensis*, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3533^T preserved in a metabolically inactive state, ex-type CBS 15495 = ZXS7.7).

Yamadamyces terricola Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828847. Figs 17G and 18H.

Etymology: the specific epithet *terricola* refers to the substrate from which the type strain was isolated, soil.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are fusiform, 2.5–3.4 × 6.0–11.8 µm and single, budding is polar (Fig. 18H), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, trehalose, melezitose, D-glucosamine (delayed and weak), ethanol, glycerol (weak), ribitol, D-mannitol, D-glucitol and succinate (delayed and weak) are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, N-Acetyl-D-glucosamine, methanol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine (weak), ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is postive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ya. terricola* differs from its closely related species *Ya. rosulatus* in its inability to assimilate cellobiose, L-rhamnose, N-Acetyl-D-glucosamine, salicin, D-gluconate, DL-lactate, citrate, myo-inositol, potassium nitrate and sodium nitrite and its ability to growin vitamin-free medium (Table S1.32).

Typus: **China**, Daxinganling, obtained from soil, Aug. 2015, Q.-M. Wang (**holotype** CGMCC 2.5820^T preserved in a metabolically inactive state, ex-type CBS 15572 = 03-1).

Note: The genus *Yamadamyces* was invalidly published because its type species was based on an invalid name (Art. 40.1, ICN Shenzhen Code), thus it was validated in the Validated Taxa section.

Oberwinklerozyma nepetae Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828848. Fig. 18I.

Etymology: the specific epithet *nepetae* refers to *Nepeta*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, ellipsoidal and ovoid, 2.7–3.2 × 6.4–8.9 µm and single, budding is polar (Fig. 18I), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is white cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, L-sorbose, sucrose, maltose, cellobiose, trehalose, melibiose, raffinose, melezitose, D-mannitol, D-glucitol, Methyl-α-D-glucoside and salicin are assimilated as sole carbon sources. Galactose, lactose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *O. nepetae* differs from its closely related species *O. yarrowii* and *O. silvestris* in its inability to assimilate galactose, D-glucosamine, ethanol, glycerol, DL-lactate, succinate, citrate and myo-inositol (Table S1.33).

Typus: **China**, Motuo, Tibet, obtained from a leaf of *Nepeta sp.*, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5824^T preserved in a metabolically inactive state, ex-type CBS 15579 = XZ129C7).

Oberwinklerozyma dicranopteridis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828849. Fig. 18J.

Etymology: the specific epithet *dicranopteridis* refers to *Dicranopteris*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and cylindrical, 2.2–3.7 × 6.4–10.5 µm and single, budding is polar (Fig. 18J), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose, lactose, raffinose, melezitose, D-xylose, L-arabinose (delayed and weak), D-arabinose, D-glucosamine, ethanol, glycerol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate (delayed and weak), succinate, citrate (delayed and weak) and myo-inositol are assimilated as sole carbon sources. Melibiose, inulin, soluble starch, D-ribose, L-rhamnose, methanol, erythritol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochlorideare assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *O. dicranopteridis* differs from its closely related species *O. straminea* in its ability to assimilate cellobiose, lactose, D-arabinose, galactitol, Methyl-α-D-glucoside and salicin (Table S1.33).

Typus: **China**, Simao county, Yunnan province, obtained from a leaf of *Dicranopteris dichotoma*, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3441^T preserved in a metabolically inactive state, ex-type CBS 15476 = SM10.2).

Chrysozyma pseudogriseoflava Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828850. Fig. 18K, L.

Etymology: the specific epithet *pseudogriseoflava* refers to the similar colony morphology to that of *Chrysozyma griseoflava*.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, ellipsoidal to fusiform, 3.3–4.7 × 6.9–9.7 µm and single, budding is polar (Fig. 18K), a sediment is formed. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth, dull and partly wrinkled. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or cylindrical, 2.3–3.1 × 4.6–7.7 µm (Fig. 18L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, raffinose, melezitose, ethanol and DL-lactate are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, Methyl-α-D-glucoside, salicin, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. pseudogriseoflava* differs from its closely related species *Ch. griseoflava* in its inability to assimilate galactose, soluble starch, D-xylose, D-arabinose, glycerol, ribitol, D-glucitol, salicin and citrate and its ability to assimilate raffinose, DL-lactate and L-lysine (Table S1.34).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5629^T preserved in a metabolically inactive state, ex-type CBS 15564 = GPS21.6B3).

Chrysozyma sambuci Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828851. Fig. 18M, N.

Etymology: the specific epithet *sambuci* refers to *Sambucus*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are long ellipsoidal and cylindrical, 2.4–4.0 × 7.2–13.5 µm and single, budding is polar (Fig. 18M), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 2.2–2.9 × 5.9–8.8 µm (Fig. 18N).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, melezitose, inulin (variable), soluble starch (variable), D-arabinose (variable), ethanol (delayed and weak), D-mannitol (variable), D-glucitol (variable) and salicin (variable) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, raffinose, D-xylose, L-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, Methyl-α-D-glucoside, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride (weak) and cadaverine dihydrochloride (weak) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 23–24 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. sambuci* and its closely related species *Ch. milinensis* and *Ch. griseoflava* can be distinguished from one another by the assimilation of galactose, raffinose, D-xylose, glycerol, DL-lactate, citrate, sodium nitrite and L-lysine (Table S1.34).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Sambucus williamsii*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2618^T preserved in a metabolically inactive state, ex-type CBS 15450 = XZ13C5).

Chrysozyma iridis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828852. Fig. 18O.

Etymology: the specific epithet *iridis* refers to *Iris*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 2.8–3.2 × 7.2–10.3 µm and single, budding is polar (Fig. 18O), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (weak), sucrose, maltose, cellobiose, trehalose, melezitose, inulin (weak), D-glucitol (delayed and weak), D-mannitol and salicin (delayed) are assimilated as sole carbon sources. L-sorbose, lactose, melibiose, raffinose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, Methyl-α-D-glucoside, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate and ethylamine hydrochloride are assimilated as sole nitrogen sources. Sodium nitrite, L-lysine and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. iridis* differs from its closely related species *Ch. rhododendri* in its inability to assimilate raffinose, D-xylose, L-arabinose, ethanol and Methyl-α-D-glucoside (Table S1.34).

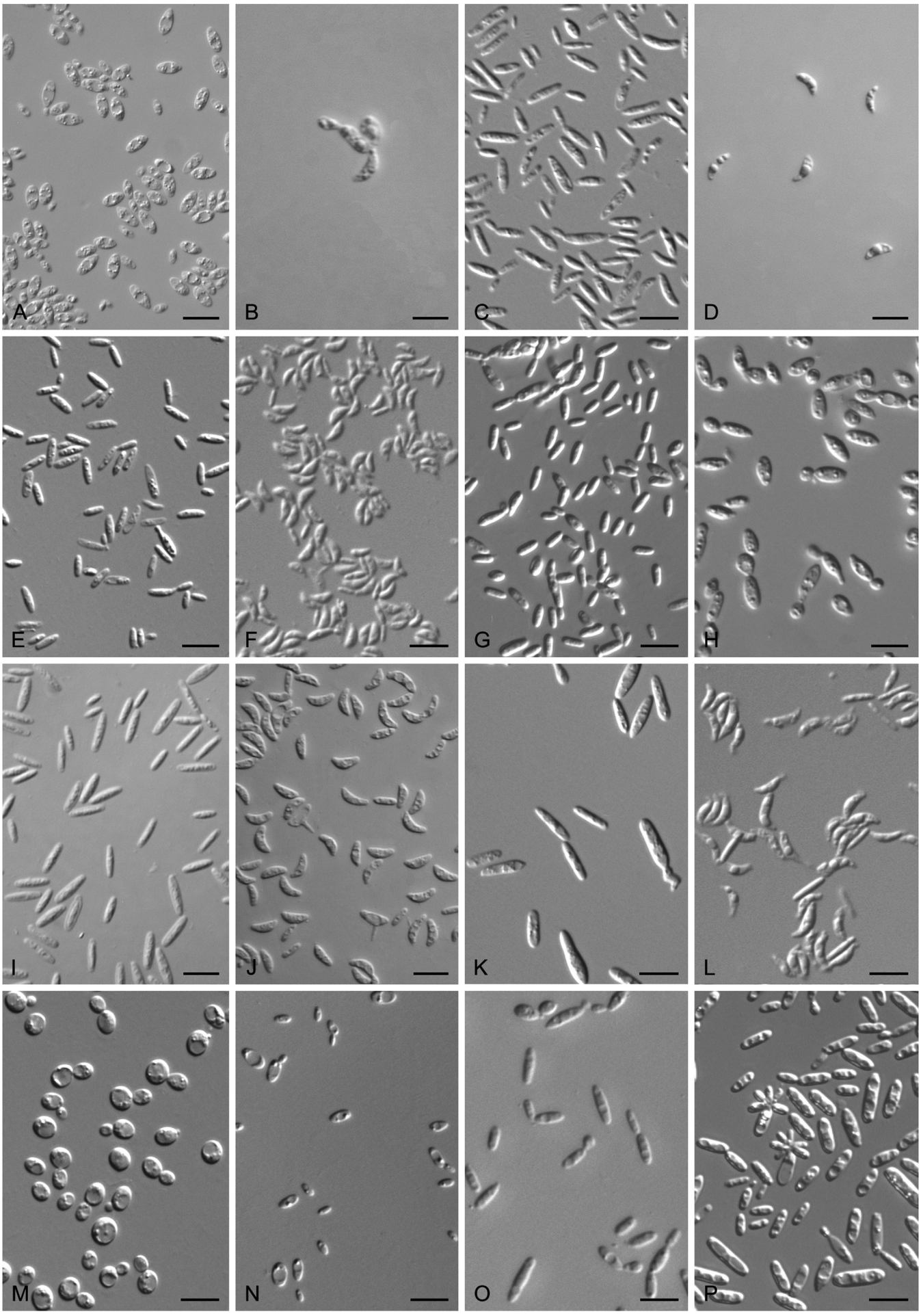
Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Iris forrestii*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2769^T preserved in a metabolically inactive state, ex-type CBS 15461 = XZ8B3).

Chrysozyma rhododendri Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828853. Figs 17H and 18P.

Etymology: the specific epithet *rhododendri* refers to *Rhododendron*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical to long ellipsoidal, 1.9–3.7 × 7.5–12.5 µm and single, budding is polar (Fig. 18P), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, mucoid, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, raffinose, melezitose, D-xylose, L-arabinose, ethanol, D-mannitol, D-glucitol, Methyl-α-D-glucoside and salicin are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, inulin, soluble starch, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.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Physiologically, *Ch. rhododendri* differs from its closely related species *Ch. iridis* in its ability to assimilate raffinose, D-xylose, L-arabinose, ethanol and Methyl-α-D-glucoside (Table S1.34).

Typus: **China**, Tibet, obtained from a leaf of *Rhododendron sp.*, Sep. 2014, Q.-M. Wang (**holotype** CGMCC 2.5821^T preserved in a metabolically inactive state, ex-type CBS 15583 = XZ160D3).

Chrysozyma fusiformis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828854. Fig. 19A, B.

Etymology: the specific epithet *fusiformis* refers to the fusiform vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal to fusiform, 3.0–4.6 × 4.7–8.2 µm and single, budding is polar (Fig. 19A), a sediment is present. After 1 mo at 17 °C, a ring and sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and dull surface. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are ellipsoidal orallantoid, 2.9–4.3 × 7.1–11.4 µm (Fig. 19B).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, melibiose, melezitose, ethanol, D-mannitol and succinate (delayed and weak) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, glycerol, erythritol, ribitol, galactitol, D-glucitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 24 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. fusiformis* differs well from other *Chrysozyma* species in its assimilation of carbon and nitrogen sources (Table S1.34).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2765^T preserved in a metabolically inactive state, ex-type CBS 15458 = XZ33C2).

Chrysozyma sorbariae Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828855. Fig. 19C, D.

Etymology: the specific epithet *sorbariae* refers to *Sorbaria*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are elongate ellipsoidal and cylindrical, 1.7–2.7 × 5.8–10.4 µm and single, budding is polar (Fig. 19C), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and semi-gloosy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or falcate, 2.1–2.9 × 6.4–7.9 µm (Fig. 19D).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, trehalose, melezitose, inulin (delayed and weak), D-mannitol and D-glucitol are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak) and sodium nitrite are assimilated as sole nitrogen sources. L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 ΄IC. Growth in vitamin-free medium is variable. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. sorbariae* differs well from other *Chrysozyma* species in its assimilation of carbon and nitrogen sources (Table S1.34).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Sorbaria arboricola*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2768^T preserved in a metabolically inactive state, ex-type CBS 15460 = XZ9D1).

Chrysozyma cylindrica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828856. Fig. 19E, F.

Etymology: the specific epithet *cylindrica* refers to the cylindrical vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 2.2–3.2 × 3.9–10.0 µm and single, budding is polar (Fig. 19E), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish-cream, butyrous, smooth and semi-glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 1.5–2.5 × 3.8–6.3 µm (Fig. 19F).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (delay and weak), sucrose, trehalose (delay), melezitose, D-mannitol and D-glucitol are assimilated as sole carbon sources. L-sorbose, maltose, cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite and L-lysine are not assimilated. Maximum growth temperature is

Fig. 19. Vegetative cells grown in YM broth for 5 d at 17 °C and ballistoconidia produced on corn meal agar after 7 d at 17 °C. (A, B) *Ch. fusiformis* CGMCC 2.2765^T; (C, D) *Ch. sorbariae* CGMCC 2.2768^T; (E, F) *Ch. cylindrica* CGMCC 2.3455^T; (G) *Ch. flava* CGMCC 2.5611^T; (H) *Pseu. hydrangea* CGMCC 2.2796^T; (I, J) *Pseu. lulangensis* CGMCC 2.2612^T; (K, L) *Yu. longicylindrica* CGMCC 2.5603^T; (M) *Sl. globosa* CGMCC 2.5822^T; (n) *Co. aletridis* CGMCC 2.2766^T; (O) *Co. hydrangeae* CGMCC 2.2798^T; (P) *Co. rhododendri* CGMCC 2.2770^T. Bars = 10 µm.

22–23 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. cylindrica* differs well from other *Chrysozyma* species in its assimilation of carbon and nitrogen sources (Table S1.34).

Typus: **China**, Wuzhishan mountain, Hainan province, obtained from a leaf of an unidentified plant, Nov. 2006, Q.-M. Wang (**holotype** CGMCC 2.3455^T preserved in a metabolically inactive state, ex-type CBS 15482 = WZS29.2).

Chrysozyma flava Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828857. Fig. 19G.

Etymology: the specific epithet *flava* refers to the yellow colony colour of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal or to cylindrical, 2.1–3.1 × 4.0–10.8 µm and single, budding is polar (Fig. 19G), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellow, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, melezitose, ethanol, D-mannitol and D-gluconate (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, D-glucitol, Methyl-α-D-glucoside methanol, glycerol, erythritol, ribitol, galactitol, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate is assimilated as sole nitrogen sources. Potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ch. flava* differs well from other *Chrysozyma* species in its assimilation of carbon and nitrogen sources (Table S1.34).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5611^T preserved in a metabolically inactive state, ex-type CBS 15552 = GPS20.4A1).

Pseudohyphozyma hydrangeae Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828858. Fig. 19H.

Etymology: the specific epithet *hydrangeae* refers to *Hydrangea*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 3.0–4.3 × 5.8–9.1 µm and single, budding is polar (Fig. 19H), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, maltose, cellobiose, trehalose, melezitose, inulin (variable), soluble starch (variable), D-xylose (variable), L-arabinose (variable), D-arabinose (variable), ethanol, ribitol, D-mannitol, D-glucitol and succinate (variable) are assimilated as sole carbon sources. Galactose, L-sorbose, sucrose, lactose, melibiose, raffinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 29 °C. Growth in vitamin-free medium is variable. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ps. hydrangeae* and its four closely related species, *Ps. lulangensis*, *Ps. bogoriensis*, *Ps. pustula* and *Ps. buffonii*, can be distinguished from one another by the assimilation of galactose, L-sorbose, melezitose, glycerol, salicin, citrate, potassium nitrate and sodium nitrite (Table S1.35).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of *Hydrangea heteromalla*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2796^T preserved in a metabolically inactive state, ex-type CBS 15462 = XZ46A1).

Pseudohyphozyma lulangensis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828859. Fig. 19I, J.

Etymology: the specific epithet *lulangensis* refers to the geographic origin of the type strain, Lulang county, Tibet.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 3.0–4.0 × 8.4–11.1 µm and single, budding is polar (Fig. 19I), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is white cream, butyrous, smooth and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid or reniform, 1.9–2.7 × 5.1–8.3 µm (Fig. 19J).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, maltose (weak), cellobiose, trehalose, D-xylose (delayed), L-arabinose, D-arabinose (delayed and weak), D-ribose (delayed), D-glucosamine, ethanol, ribitol (delayed), D-mannitol, D-glucitol (delayed) and salicin are assimilated as sole carbon sources. Galactose, L-sorbose, sucrose, lactose, melibiose, raffinose, melezitose, inulin, soluble starch, L-rhamnose, methanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Potassium nitrate and sodium nitrite are not assimilated. Maximum growth temperature is 23 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Ps. lulangensis* differs from its closely related species *Ps. bogoriensis* in its inability to assimilate galactose, L-sorbose, soluble starch, glycerol and succinate and its ability to grow in vitamin-free medium (Table S1.35).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2612^T preserved in a metabolically inactive state, ex-type CBS 15446 = XZ50B2).

Yurkovia longicylindrica Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828860. Fig. 19K, L.

Etymology: the specific epithet *longicylindrica* refers to the elongate cylindrical cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are elongate cylindrical, 2.5–4.5 × 7.5–15.9 µm and single, budding is polar (Fig. 19K), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, wrinkled and dull. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are allantoid, falcate or cylindrical, 1.4–2.6 × 7.1–12.9 µm (Fig. 19L).

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose, sucrose, trehalose, melibiose, melezitose, inulin, soluble starch (delayed and weak), D-arabinose, ethanol, ribitol, D-mannitol and D-glucitol are assimilated as sole carbon sources. L-sorbose, maltose, cellobiose, lactose, raffinose, D-xylose, L-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 22–23 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Yu. longicylindrica* differs from its closely related species *Yu. mendeliana* and *Yu. nerthusi* in its inability to assimilate L-sorbose, maltose, L-arabinose, glycerol and succinate and its ability to assimilate melibiose (Table S1.36).

Typus: **China**, Milin county, Tibet, obtained from a leaf of an unidentified plant, Sep. 2015, Q.-M. Wang (**holotype** CGMCC 2.5603^T preserved in a metabolically inactive state, ex-type CBS 15550 = GPS20.2C3).

Slooffia globosa Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828861. Fig. 19M.

Etymology: the specific epithet *globosa* refers to the globosal vegetative cells of the type strain.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are globosal, 4.1–5.9 × 4.8–5.9 µm and single, budding is polar (Fig. 19M), a sediment is present. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish cream, butyrous, slightly wrinkled and glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, cellobiose, trehalose, lactose (weak), melezitose (delayed and weak), ethanol, glycerol, D-mannitol, Methyl-α-D-glucoside (delayed and weak) and D-gluconate (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, N-Acetyl-D-glucosamine, methanol, erythritol, ribitol, galactitol, D-glucitol, salicin, succinate, DL-lactate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, L-lysine (weak), ethylamine hydrochloride and cadaverine dihydrochlorideare (delayed and weak) are assimilated as sole nitrogen sources. Sodium nitrite is not assimilated. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is negative. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Sl. globosa* differs from its closely related species *Sl. tsugae* in its inability to assimilate L-sorbose, D-xylose, D-glucitol, salicin, DL-lactate, succinate, citrate and sodium nitrite (Table S1.37).

Typus: **China**, Daxinganling, obtained from soil, Aug. 2015, Q.-M. Wang (**holotype** CGMCC 2.5822^T preserved in a metabolically inactive state, ex-type CBS 15573 = 4–6).

Colacogloea aletridis Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828862. Fig. 19N.

Etymology: the specific epithet *aletridis* refers to *Aletris*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are ellipsoidal and ovoid, 2.0–3.8 × 3.0–7.6 µm and single, budding is polar (Fig. 19N), a sediment is formed. After 1 mo at 17 °C, a ring and a sediment are present. On YM agar, after 1 mo at 17 °C, the streak culture is cream, butyrous, smooth and glistening. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose (weak), trehalose, melezitose, ethanol, ribitol (delayed), D-mannitol (weak), D-glucitol (weak) and Methyl-α-D-glucoside (weak) are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, melibiose, raffinose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, glycerol, erythritol, galactitol, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 30 ΄IC. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Co. aletridis* differ well from other *Colacogloe* species in its assimilation of carbon and nitrogen sources (Table S1.38).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Aletris pauciflora*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2766^T preserved in a metabolically inactive state, ex-type CBS 15459 = XZ31A1).

Colacogloea hydrangeae Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828863. Fig. 19O.

Etymology: the specific epithet *hydrangeae* refers to *Hydrangea*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical and ellipsoidal, 2.7–4.1 × 5.7–10.9 µm and single, budding is polar (Fig. 19O), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is yellowish cream, butyrous, smooth with partly wrinkled, glossy. The margin is entire. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, sucrose, maltose, trehalose, melezitose (delayed), D-glucosamine, ethanol, ribitol (delayed), D-mannitol, D-glucitol and salicin are assimilated as sole carbon sources. Galactose, L-sorbose, cellobiose, lactose, raffinose, melibiose, inulin, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, methanol, glycerol, erythritol, galactitol, Methyl-α-D-glucoside, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine and ethylamine hydrochloride are assimilated as sole nitrogen sources. Cadaverine dihydrochlorideare is not assimilated. Maximum growth temperature is 28 °C. Growth in vitamin-free medium is weak. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Co. hydrangeae* differs from its closely related species *Co. rhododendri* in its inability to assimilate glycerol and its ability to assimilate salicin (Table S1.38).

Typus: **China**, Lulang county, Tibet, obtained from a leaf of *Hydrangea heteromalla*, Sep. 2004, Q.-M. Wang (**holotype** CGMCC 2.2798^T preserved in a metabolically inactive state, ex-type CBS 15463 = XZ46B3).

Colacogloea rhododendri Q.M. Wang, F.Y. Bai & A.H. Li ***sp. nov.*** MycoBank MB828864. Fig. 19P.

Etymology: the specific epithet *rhododendri* refers to *Rhododendron*, the plant genus from which the type strain was isolated.

Culture characteristics: In YM broth, after 7 d at 17 °C, cells are cylindrical, 1.0–3.8 × 4.3–15.0 µm and single, budding is polar (Fig. 19P), a sediment is present. On YM agar, after 1 mo at 17 °C, the streak culture is prey-cream, butyrous, wrinkled and dull. The margin is entire or eroded. In Dalmau plate culture on corn meal agar, pseudohyphae are not formed. Sexual structures are not observed on YM, PDA, V8 and CM agar. Ballistoconidia are not produced.

Physiological and biochemical characteristics: Glucose fermentation is absent. Glucose, galactose (variable), sucrose, maltose, cellobiose (variable), trehalose, melezitose, inulin (variable), D-glucosamine (weak), N-Acetyl-D-glucosamine (weak), ethanol, glycerol (delayed), ribitol (variable), D-mannitol, D-glucitol (variable) and D-gluconate are assimilated as sole carbon sources. L-sorbose, lactose, melibiose, raffinose, soluble starch, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, methanol, erythritol, galactitol, Methyl-α-D-glucoside, salicin, DL-lactate, succinate, citrate, myo-inositol and hexadecane are not assimilated. Ammonium sulfate, potassium nitrate (weak), sodium nitrite (variable), L-lysine, ethylamine hydrochloride and cadaverine dihydrochlorideare (variable) are assimilated as sole nitrogen sources. Maximum growth temperature is 26–27 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Growth on 50 % (w/w) glucose-yeast extract agar is negative. Urease activity is positive. Diazonium Blue B reaction is positive.

Physiologically, *Co. rhododendri* differs from its closely related species *Co. hydrangeae* in its inability to assimilate salicin and its ability to assimilate glycerol (Table S1.38).

Typus: **China**, Bomi county, Tibet, obtained from a leaf of *Rhododendron lulangense*, Sep. 2004, F.-Y. Bai (**holotype** CGMCC 2.2770^T preserved in a metabolically inactive state, ex-type CBS 15652 = XZ10F1).

New combination for *Colacogloea*

Colacogloea subericola (Belloch, Villa-Carv., Álv.-Rodríg. & Coque) Q.M. Wang & F.Y. Bai **com. nov.** MycoBank MB832093. *Basionym*: *Rhodotorula subericola* Belloch, Villa-Carv., Álv.-Rodríg. & Coque, Int. J. Syst. Evol. Microbiol. 57(7): 1670 (2007).

Validated Taxa

Usually the type culture of a new yeast species should be conserved in two or more collections when it was described. Thus, two or more collection numbers of type culture were always listed for new species by many yeast taxonomists but often without explicitely indicating the holotype, which, however, resulted in numerous invalidly described species according the Art. 40.7 of the Shenzhen Code (Turland *et al.* 2018) during the last ten years. In order to avoid this embarrassing situation, 70 invalidly described taxa were validated here.

Apiotrichum xylopini S.O. Suh, C.F. Lee, Gujjari & J.J. Zhou ex Kachalkin, Yurkov & Boekhout, ***sp. nov.*** MycoBank MB831708. For description see Int. J. Syst. Evol. Microbiol. 61(10): 2540 (2011).
Holotype: CBS 11841 (preserved in a metabolically inactive state).
Synonyms: *Trichosporon xylopini* S.O. Suh, C.F. Lee, Gujjari & J.J. Zhou, Int. J. Syst. Evol. Microbiol. 61(10): 2540 (2011), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Apiotrichum xylopini* S.O. Suh, C.F. Lee, Gujjari & J.J. Zhou ex Kachalkin, Yurkov & Boekhout, Stud. Mycol. 81: 142 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Bannozyma arctica Vishniac & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831713. For description see Int. J. Syst. Evol. Microbiol. 60(5): 1217 (2010).
Holotype: CBS 9278 (preserved in a metabolically inactive state).
Synonyms: *Rhodotorula arctica* Vishniac & M. Takash., Int. J. Syst. Evol. Microbiol. 60(5): 1217 (2010), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Bannozyma arctica* Vishniac & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 183 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Bulleribasidium panici Fungsin, M. Takash. & Nakase ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831675.
For description see Microbiol. Culture Coll. 19(1): 27 (2003).
Holotype: JCM 11819 (preserved in a metabolically inactive state).
Synonyms: *Bullera panici* Fungsin *et al.*, Microbiol. Culture Coll. 19(1): 27 (2003), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Bulleribasidium panici* Fungsin, M. Takash. & Nakase ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 123 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Bulleribasidium siamense Fungsin, M. Takash. & Nakase ex Q.M. Wang, F.Y. Bai, Boekhout & Nakase, ***sp. nov.*** MycoBank MB831676.
For description see Microbiol. Culture Coll. 19(1): 29 (2003).
Holotype: JCM 11820 (preserved in a metabolically inactive state).
Synonyms: *Bullera siamensis* Fungsin *et al.*, Microbiol. Culture Coll. 19(1): 29 (2003), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Mingxiaea siamensis* Fungsin, M. Takash. & Nakase ex Q.M. Wang, F.Y. Bai, Boekhout & Nakase, Int. J. Syst. Evol. Microbiol. 61: 214 (2011), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Bulleribasidium siamense* Fungsin, M. Takash. & Nakase ex Xin ZhanLiu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 123 (2015), *Nom. inval.*, Art. 40.6 (Shenzhen).

Carcinomyces arundinariae Fungsin, M. Takash. & Nakase ex Yurkov, ***sp. nov.*** MycoBank MB831698.
For description see Microbiol. Culture Coll. 18(2): 86 (2002).
Holotype: JCM 11818 (preserved in a metabolically inactive state).
Synonyms: *Bullera arundinariae* Fungsin, M. Takash. & Nakase, in Fungsin *et al.*, Microbiol. Culture Coll. 18(2): 86 (2002), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Carcinomyces arundinariae* Fungsin, M. Takash. & Nakase ex Yurkov, Stud. Mycol. 81: 133 (2015), *nom. inval.*, Art. 40.6 (Shenzhen).

Cystobasidium alpinum Turchetti, Selbmann, Onofri & Buzzini, ***sp. nov.*** MycoBank MB831749.
For description see Life 8 (2, no 9): 10 (2018).
Holotype: CBS 14809 (preserved in a metabolically inactive state).
Synonyms: *Cystobasidium alpinum* Turchetti, Selbmann, Onofri & Buzzini, Life 8 (2, no 9): 10 (2018), *nom. inval.*, Art. 40.7 (Shenzhen).

Cystobasidium portillonense (Laich, Vaca & R. Chávez) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***comb. nov.*** MycoBank MB831741.
Basionym: *Rhodotorula portillonensis* Laich, Vaca & R. Chávez, Index Fungorum 361: 1 (2018).
Synonyms: *Rhodotorula portillonensis* Laich, Vaca & R. Chávez, Int. J. Syst. Evol. Microbiol. 63(10): 3889 (2013), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Cystobasidium portillonense* Laich, Vaca & R. Chávez ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 173 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Derxomyces cylindricus F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, ***sp. nov.*** MycoBank MB831863.
For description see Int. J. Syst. Evol. Microbiol. 54(5): 1879 (2004).
Holotype: CGMCC AS 2.2308 (preserved in a metabolically inactive state).
Synonyms: *Bullera cylindrica* F.Y. Bai, Q.M. Wang & M. Takash., Int. J. Syst. Evol. Microbiol. 54(5): 1879 (2004), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Derxomyces cylindrica* F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, FEMS Yeast Res. 8(5): 804 (2008), *nom. inval.*, Art. 40.7 (Shenzhen).

Derxomyces hubeiensis F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, ***sp. nov.*** MycoBank MB831864.
For description see Int. J. Syst. Evol. Microbiol. 54(5): 1880 (2004).
Holotype: CGMCC AS 2.2466 (preserved in a metabolically inactive state).
Synonyms: *Bullera hubeiensis* F.Y. Bai, Q.M. Wang & M. Takash., Int. J. Syst. Evol. Microbiol. 54(5): 1880 (2004), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Derxomyces hubeiensis* F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, FEMS Yeast Res. 8(5): 805 (2008), *nom. inval.*, Art. 40.7 (Shenzhen).

Derxomyces nakasei F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, ***sp. nov.*** MycoBank MB831865.
For description see Int. J. Syst. Evol. Microbiol. 54(5): 1880 (2004).
Holotype: CGMCC AS 2.2435 (preserved in a metabolically inactive state).
Synonyms: *Bullera nakasei* F.Y. Bai, Q.M. Wang & M. Takash., Int. J. Syst. Evol. Microbiol. 54(5): 1880 (2004), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Derxomyces nakasei* F.Y. Bai, Q.M. Wang & M. Takash. ex F.Y. Bai & Q.M. Wang, FEMS Yeast Res. 8(5): 805 (2008), *nom. inval.*, Art. 40.7 (Shenzhen).

Dioszegia zsoltii F.Y. Bai, M. Takash. & Nakase, ***sp. nov.*** MycoBank MB831868.
For description see J. Gen. Appl. Microbiol., 48(1): 21 (2002).
Holotype: CGMCC AS 2.2089 (preserved in a metabolically inactive state).
Synonyms: *Dioszegia zsoltii* F.Y. Bai, M. Takash. & Nakase, J. Gen. Appl. Microbiol., 48(1): 21 (2002), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Dioszegia yunnanensis* F.Y. Bai, M. Takash. & Nakase, J. Gen. Appl. Microbiol., 48(1): 22 (2002), *nom. inval.*, Art. 40.7 (Shenzhen).

Genolevuria bromeliarum Landell & P. Valente ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831695.
For description see Int. J. Syst. Evol. Microbiol. 59(4): 911 (2009).
Holotype: CBS 10424 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus bromeliarum* Landell & P. Valente, Int. J. Syst. Evol. Microbiol. 59(4): 911 (2009), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Genolevuria bromeliarum* Landell & P. Valente ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 129 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Glaciozyma Turchetti, Connell, Thomas-Hall & Boekhout ex M. Groenew. & Q.M. Wang, ***gen. nov.*** MycoBank MB831869.
For description see Extremophiles 15 (5): 579 (2011).
Type species: Glaciozyma antarctica (Fell, Statzell, I.L. Hunter & Phaff) M. Groenew. & Q.M. Wang.
Synonym: *Glaciozyma* Turchetti, Connell, Thomas-Hall & Boekhout, Extremophiles 15 (5): 579 (2011), *nom. inval.*, Art. 40.1, see Arts 6.3, 12.1 (Melbourne).

Glaciozyma antarctica (Fell, Statzell, I.L. Hunter & Phaff) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831870.
Basionym: *Leucosporidium antarcticum* Fell, Statzell, I.L. Hunter & Phaff, Antonie van Leeuwenhoek 35 (4): 447 (1970).
Synonym: *Glaciozyma antarctica* (Fell, Statzell, I.L. Hunter & Phaff) Turchetti, Connell, Thomas-Hall & Boekhout, Extremophiles 15 (5): 579 (2011), *nom. inval.*, Art. 41.5, see Note 1 (Shenzhen).

Glaciozyma martinii Turchetti, Connell, Thomas-Hall & Boekhout, ***sp. nov.*** MycoBank MB831872.
For description see Extremophiles 15 (5): 579 (2011).
Holotype: CBS 10620 (preserved in a metabolically inactive state).
Synonym: *Glaciozyma martinii* Turchetti, Connell, Thomas-Hall & Boekhout, Extremophiles 15 (5): 579 (2011), *nom. inval.*, Arts 35.1, 40.7 (Shenzhen).

Glaciozyma watsonii Turchetti, Connell, Thomas-Hall & Boekhout, ***sp. nov.*** MycoBank MB831873.
For description see Extremophiles 15 (5): 582 (2011).
Holotype: CBS 10986 (preserved in a metabolically inactive state).
Synonym: *Glaciozyma watsonii* Thomas-Hall, Connell, Boekhout & Turchetti, Extremophiles 15 (5): 582 (2011), *nom. inval.*, Arts 35.1, 40.7 (Shenzhen).

Kockovaella mexicana Lopandić, O. Molnár & Prillinger ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831697.
For description see Microbiol. Res. 160(1): 8 (2005).
Holotype: CBS 8279 (preserved in a metabolically inactive state).
Synonyms: *Fellomyces mexicanus* Lopandić *et al.*, Microbiol. Res. 160(1): 8 (2005), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Kockovaella mexicana* Lopandić, O. Molnár & Prillinger ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 131 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Kondoa thailandica Fungsin, Hamam. & Nakase ex Q.M. Wang, M. Groenew., F.Y. Bai & Boekhout, ***sp. nov.*** MycoBank MB831742.
For description see Int. J. Syst. Evol. Microbiol. 51(3): 1210 (2001).
Holotype: JCM 10651 (preserved in a metabolically inactive state).
Synonyms: *Bensingtonia thailandica* Fungsin, Hamam. & Nakase, Int. J. Syst. Evol. Microbiol. 51(3): 1210 (2001), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Kondoa thailandica* Fungsin, Hamam. & Nakase ex Q.M. Wang, M. Groenew., F.Y. Bai & Boekhout, Stud. Mycol. 81: 171 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Kwoniella newhampshirensis K. Sylvester, Q.M. Wang & Hittinger, ***sp. nov.*** MycoBank MB828749.
For description see FEMS Yeast Research 15: 7 (2015).
Holotype: NRRL Y-63731 (preserved in a metabolically inactive state).
Synonyms: *Kwoniella newhampshirensis* K. Sylvester *et al.*, FEMS Yeast Res. 15: 7 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Kwoniella shandongensis R. Chen, Yuan M. Jiang & S.C. Wei ex M. Groenew. & Q.M. Wang, ***sp. nov.*** MycoBank MB828750.
For description see Int. J. Syst. Evol. Microbiol. 62: 2775 (2012).
Holotype: CGMCC 2.04458 (preserved in a metabolically inactive state).
Synonyms: *Kwoniella shandongensis* Chen *et al.*, Int. J. Syst. Evol. Microbiol. 62: 2775 (2012), *nom. inval.*, Art. 40.7 (Shenzhen).

Leucosporidium creatinivorum (Golubev) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831751.
Basionym: *Rhodotorula creatinivora* Golubev, Mikol. Fitopatol. 32(3): 8 (1998), as '*creatinovora*'.
Synonyms: *Leucosporidiella creatinivora* (Golubev) J.P. Samp., Mycol. Progr. 2(1): 66 (2003).
= *Leucosporidium creatinivorum* (Golubev) V. de García *et al.*, FEMS Yeast Research 15 (4): 9 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Leucosporidium fragarium (J.A. Barnett & Buhagiar) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831752.
Basionym: *Torulopsis fragaria* J.A. Barnett & Buhagiar, J. Gen. Microbiol. 67(2): 237 (1971).
Synonyms: *Leucosporidiella fragaria* (J.A. Barnett & Buhagiar) J.P. Samp., Mycol. Progr. 2(1): 66 (2003).
= *Leucosporidium fragarium* (J.A. Barnett & Buhagiar) V. de García *et al.*, FEMS Yeast Res. 15: 9 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Leucosporidium intermedium (Nakase & M. Suzuki) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831754.
Basionym: *Bullera intermedia* Nakase & M. Suzuki, J. Gen. Appl. Microbiol. 32(2): 150 (1986).
Synonyms: *Sporobolomyces intermedius* (Nakase & M. Suzuki) Nakase & M. Suzuki, J. Gen. Appl. Microbiol. 33(2): 193 (1987).
= *Bensingtonia intermedia* (Nakase & M. Suzuki) Nakase & Boekhout, J. Gen. Appl. Microbiol. 34(3): 435 (1988).
= *Leucosporidium intermedium* (Nakase & M. Suzuki) V. de García *et al.*, FEMS Yeast Res. 15: 9 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Leucosporidium muscorum (Di Menna) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831755.
Basionym: *Candida muscorum* Di Menna, J. Gen. Microbiol. 18: 269 (1958).
Synonyms: *Leucosporidiella muscorum* (Di Menna) J.P. Samp., Mycol. Progr. 2(1): 66 (2003).
= *Leucosporidium muscorum* (Di Menna) V. de García *et al.*, FEMS Yeast Res. 15: 9 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Leucosporidium yakuticum (Golubev) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831756.
Basionym: *Rhodotorula yakutica* Golubev, Mikol. Fitopatol. 32(3): 9 (1998).
Synonyms: *Leucosporidiella yakutica* (Golubev) J.P. Samp., Mycol. Progr. 2(1): 66 (2003).
= *Leucosporidium yakuticum* (Golubev) V. de García *et al.*, FEMS Yeast Res. 15: 9 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Naganishia onofrii Turchetti, Selbmann & Zucconi ex Yurkov, ***sp. nov.*** MycoBank MB831673.
For description see Extremophiles 19: 157 (2015).
Holotype: CBS 13732 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus onofrii* Turchetti *et al.*, Extremophiles 19: 157 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Naganishia onofrii* Turchetti, Selbmann & Zucconi ex Yurkov, Stud. Mycol. 81: 119 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Naganishia vaughanmartiniae Turchetti, Blanchette & Arenz ex Yurkov, ***sp. nov.*** MycoBank MB831674.
For description see Extremophiles 19: 157 (2015).
Holotype: CBS 13731 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus vaughanmartiniae* Turchetti *et al.*, Extremophiles 19: 157 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

= *Naganishia vaughanmartiniae* Turchetti, Blanchette & Arenz. ex Yurkov, Stud. Mycol. 81: 119 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Nielozyma Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***gen. nov.*** MycoBank MB831677.
For description see Stud. Mycol. 81: 123 (2015).
Type species: *Nielozyma melastomatis* Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout.
Synonym: *Nielozyma* Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 123 (2015), *nom. inval.*, Art. 40.1 (Shenzhen).

Nielozyma formosana Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831678.
For description see Syst. Appl. Microbiol. 27(5): 562 (2004).
Holotype: JCM 12154 (preserved in a metabolically inactive state).
Synonyms: *Bullera formosana* Nakase *et al.*, Syst. Appl. Microbiol. 27(5): 562 (2004), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Nielozyma formosana* Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 123 (2015), *nom. inval.*, Art. 40.6 (Shenzhen).

Nielozyma melastomatis Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831679.
For description see Syst. Appl. Microbiol. 27(5): 560 (2004).
Holotype: JCM 12153 (preserved in a metabolically inactive state).
Synonyms: *Bullera melastomatis* Nakase *et al.*, Syst. Appl. Microbiol. 27(5): 560 (2004), as '*melastomae*', *nom. inval.*, Art. 40.6 (Shenzhen).
= *Nielozyma melastomatis* Nakase, Tsuzuki, F.L. Lee & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 123 (2015), as '*melastomae*', *nom. inval.*, Art. 40.6 (Shenzhen).

Oberwinklerozyma silvestris Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831743.
For description see Int. J. Syst. Evol. Microbiol. 60(10): 2504 (2010).
Holotype: CBS 11420 (preserved in a metabolically inactive state).
Synonyms: *Rhodotorula silvestris* Golubev & Scorzetti, Int. J. Syst. Evol. Microbiol. 60(10): 2504 (2010), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Oberwinklerozyma silvestris* Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 185 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Oberwinklerozyma straminea Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831744.
For description see Int. J. Syst. Evol. Microbiol. 60(10): 2505 (2010).
Holotype: CBS 10976 (preserved in a metabolically inactive state).
Synonyms: *Rhodotorula straminea* Golubev & Scorzetti, Int. J. Syst. Evol. Microbiol. 60(10): 2505 (2010), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Oberwinklerozyma straminea* Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 185 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Papiliotrema aspenensis (Ferreira-Paim *et al.*) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***comb. nov.*** MycoBank MB831707.
Basionym: *Cryptococcus aspenensis* Ferreira-Paim *et al.*, PLoS ONE 9(9): e108633, 10 (2014).
Synonym: *Papiliotrema aspenensis* (Ferreira-Paim, *et al.*) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 126 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Papiliotrema baii Yurkov, M.A. Guerreiro & Á. Fonseca ex Yurkov, ***sp. nov.*** MycoBank MB831705.
For description see PLoS ONE 10(4): e0126996, 15 (2015).
Holotype: PYCC 6352 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus baii* Yurkov, M.A. Guerreiro & Á. Fonseca, in Yurkov *et al.*, PLoS ONE 10(4): e0126996, 15 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Papiliotrema baii* Yurkov, M.A. Guerreiro & Á. Fonseca ex Yurkov, Stud. Mycol. 81: 126 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Papiliotrema frias V. de García, Zalar, Brizzio, Gunde-Cim. & van Broock ex Yurkov, ***sp. nov.*** MycoBank MB831685.
For description see FEMS Microbiology Ecology 82(2): 537 (2012).
Holotype: EXF-5992 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus frias* V. de García *et al.*, FEMS Microbiol. Ecol. 82(2): 537 (2012), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Papiliotrema frias* V. de García, Zalar, Brizzio, Gunde-Cim. & van Broock ex Yurkov, Stud. Mycol. 81: 126 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Papiliotrema hoabinhensis D.T. Luong, M. Takash., Ty, Dung & Nakase ex Yurkov, ***sp. nov.*** MycoBank MB831686.
For description see J. Gen. Appl. Microbiol. 51(6): 340 (2005).
Holotype: JCM 10835 (preserved in a metabolically inactive state).
Synonyms: *Bullera hoabinhensis* D.T. Luong *et al.*, J. Gen. Appl. Microbiol. 51(6): 340 (2005), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Papiliotrema hoabinhensis* D.T. Luong, M. Takash., Ty, Dung & Nakase ex Yurkov, Stud. Mycol. 81: 126 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Papiliotrema japonica J.P. Samp., Fonseca & Fell ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831687.
For description see Int. J. Syst. Evol. Microbiol. 54(3): 990 (2004).
Holotype: CBS 2013 (preserved in a metabolically inactive state).
Synonyms: *Bullera japonica* J.P. Samp. *et al.*, Int. J. Syst. Evol. Microbiol. 54(3): 990 (2004), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Papiliotrema japonica* J.P. Samp., Fonseca & Fell ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 126 (2015), *nom. inval.*, Art. 40.6 (Shenzhen).

Papiliotrema terrestris Crestani, Landell, Faganello, Vainstein, Vishniac & P. Valente ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831688.
For description see Int. J. Syst. Evol. Microbiol. 59(3): 635 (2009).
Holotype: CBS 10810 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus terrestris* Crestani *et al.*, Int. J. Syst. Evol. Microbiol. 59(3): 635 (2009), *nom. inval.*, Art. 40.7 (Shenzhen).

= *Papiliotrema terrestris* Crestani, Landell, Faganello, Vainstein, Vishniac & P. Valente ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 121 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Papiliotrema wisconsinensis K. Sylvester, Q.M. Wang & Hittinger ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831712.
For description see FEMS Yeast Res. 15(3): 7 (2015).
Holotype: CBS 13895 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus wisconsinensis* K. Sylvester, Q.M. Wang & Hittinger, FEMS Yeast Res. 15(3): 7 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Papiliotrema wisconsinensis* K. Sylvester, Q.M. Wang & Hittinger ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 127 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Piskurozyma fildesensis T.T. Zhang & Li Y. Yu ex Yurkov, ***sp. nov.*** MycoBank MB831672.
For description see Int. J. Syst. Evol. Microbiol. 64(2): 676 (2013).
Holotype: CBS 12705 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus fildesensis* T.T. Zhang & Li Y. Yu, in Zhang *et al.*, Int. J. Syst. Evol. Microbiol. 64(2): 676 (2013), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Piskurozyma fildesensis* T.T. Zhang & Li Y. Yu ex Yurkov, Stud. Mycol. 81: 121 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Piskurozyma taiwanensis Nakase, Tsuzuki & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831670.
For description see J. Gen. Appl. Microbiol. 48(6): 349 (2002).
Holotype: JCM 11143 (preserved in a metabolically inactive state).
Synonyms: *Bullera taiwanensis* Nakase *et al.*, J. Gen. Appl. Microbiol. 48(6): 349 (2002), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Cryptococcus taiwanensis* Nakase, Tsuzuki & M. Takash. ex Golubev, in Golubev & Tomashevskaya, Mikrobiologiya 79 (3): 408 (2010), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Piskurozyma taiwanensis* Nakase, Tsuzuki & M. Takash. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 121 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Pseudoleucosporidium V. de García *et al.* ex M. Groenew. & Q.M. Wang, ***gen. nov.*** MycoBank MB831877.
For description see FEMS Yeast Res. 15: 11 (2015).
Type species: Pseudoleucosporidium fasciculatum (Babeva & Lisichk.) M. Groenew. & Q.M. Wang.
Synonyms: *Pseudoleucosporidium* V. de García *et al.*, FEMS Yeast Research 15 (4): 11 (2015), *nom. inval.*, Art. 40.1 (Shenzhen).

Pseudoleucosporidium fasciculatum (Babeva & Lisichk.) M. Groenew. & Q.M. Wang, ***comb. nov.*** MycoBank MB831878.
Holotype: VKM Y-2869 (preserved in a metabolically inactive state).
Basionym: *Leucosporidium fasciculatum* Babeva & Lisichk., Mikrobiologiya 69(6): 801 (2000).
Synonym: *Pseudoleucosporidium fasciculatum* (Babeva & Lisichk.) V. de García, *et al.*, FEMS Yeast Res. 15: 11 (2015), *nom. inval.*, Art 41.5 (Shenzhen).

Pseudotremella lacticolour Satoh & Makimura ex Yurkov, ***sp. nov.*** MycoBank MB831696.
For description see Antonie van Leeuwenhoek 104(1): 90 (2013).
Holotype: JCM 15449 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus lacticolour* Satoh & Makimura, Antonie van Leeuwenhoek 104(1): 90 (2013), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Pseudotremella lacticolour* Satoh & Makimura ex Yurkov, Stud. Mycol. 81: 130 (2015) *nom. inval.*, Art. 40.7 (Shenzhen).

Rhynchogastrema complexa (Landell *et al.*) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, ***comb. nov.*** MycoBank MB831689.
Basionym: *Bandoniozyma complexa* Landell, *et al.*, in Valente *et al.*, PLoS ONE 7(10): e46060, 9 (2012).
Synonym: *Rhynchogastrema complexa* (Landell, *et al.*) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, Stud. Mycol. 81: 127 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Rhynchogastrema fermentans (C.F. Lee) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, ***comb. nov.*** MycoBank MB831690.
Basionym: *Bandoniozyma fermentans* C.F. Lee, in Valente *et al.*, PLoS ONE 7(10): e46060, 9 (2012).
Synonym: *Rhynchogastrema fermentans* (C.F. Lee) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, Stud. Mycol. 81: 127 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Rhynchogastrema glucofermentans (S.O. Suh & M. Blackw.) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, ***comb. nov.*** MycoBank MB831691.
Basionym: *Bandoniozyma glucofermentans* S.O. Suh & M. Blackw., in Valente *et al.*, PLoS ONE 7(10): e46060, 9 (2012).
Synonym: *Rhynchogastrema glucofermentans* (S.O. Suh & M. Blackw.) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, Stud. Mycol. 81: 127 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Rhynchogastrema nanyangensis F.L. Hui & Q.H. Niu ex Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, ***sp. nov.*** MycoBank MB831692.
For description see Curr. Microbiol. 65(5): 619 (2012).
Holotype: CBS 12474 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus nanyangensis* F.L. Hui & Q.H. Niu, in Hui *et al.*, Curr. Microbiol. 65(5): 619 (2012), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Rhynchogastrema nanyangensis* F.L. Hui & Q.H. Niu ex Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, Stud. Mycol. 81: 127 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Rhynchogastrema tunnelae (Boekhout, Fell, Scorzetti & Theelen) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, ***comb. nov.*** MycoBank MB831693.
Basionym: *Bandoniozyma tunnelae* Boekhout, Fell, Scorzetti & Theelen, in Valente *et al.*, PLoS ONE 7(10): e46060, 9 (2012).
Synonym: *Rhynchogastrema tunnelae* (Boekhout, Fell, Scorzetti & Theelen) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, Stud. Mycol. 81: 128 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Rhynchogastrema visegradensis (G. Péter & Dlauchy) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout & Yurkov, ***comb. nov.*** MycoBank MB831694.
Basionym: *Bandoniozyma visegradensis* G. Péter & Dlauchy, in Valente *et al.*, PLoS ONE 7(10): e46060, 10 (2012).
Synonym: *Rhynchogastrema visegradensis* (G. Péter & Dlauchy) Xin Zhan Liu, F.Y. Bai, M. Groenew., Boekhout &

Yurkov, Stud. Mycol. 81: 128 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Ruinenia diospyri Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831745.
For description see J. Gen. Appl. Microbiol. 51(5): 280 (2005).
Holotype: JCM 12157 (preserved in a metabolically inactive state).
Synonyms: *Sporobolomyces diospyri* Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. J. Gen. Appl. Microbiol. 51(5): 280 (2005), as '*diospyroris*', *nom. inval.*, Art. 40.7 (Shenzhen).
= *Ruinenia diospyri* Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 171 (2015), as '*diospyroris*', *nom. inval.*, Art. 40.7 (Shenzhen).

Ruinenia pyrrosiae Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831746.
For description see J. Gen. Appl. Microbiol. 51(5): 284 (2005).
Holotype: JCM 12159 (preserved in a metabolically inactive state).
Synonyms: *Sporobolomyces pyrrosiae* Nakase, *et al.*, J. Gen. Appl. Microbiol. 51(5): 284 (2005), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Ruinenia pyrrosiae* Nakase, Tsuzuki, F.L. Lee, Jindam. & M. Takash. ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 171 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Saitozyma ninhbinhensis (D.T. Luong, M. Takash., Dung & Nakase) Yurkov, ***comb.*** **nov.** MycoBank MB831700.
For description see J. Gen. Appl. (Special Issue) Biotechnol.: 36 (2002).
Holotype: VTCC 10184 (preserved in a metabolically inactive state).
Basionym: *Bullera ninhbinhensis* D.T. Luong, M. Takash., Ty, Dung & Nakase, Journal of Genetics and Applications (Special Issue) Biotechnology: 36 (2002).
Synonyms: *Saitozyma ninhbinhensis* D.T. Luong, M. Takash., Ty, Dung & Nakase ex Yurkov, Stud. Mycol. 81: 134 (2015), *nom. inval.*, Art. 41.5 (Shenzhen).

Saitozyma paraflava Golubev & J.P. Samp. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831704.
For description see J. Gen. Appl. Microbiol. 50(2): 68 (2004).
Holotype: VKM Y-2923 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus paraflavus* Golubev & J.P. Samp., in Golubev *et al.*, J. Gen. Appl. Microbiol. 50(2): 68 (2004), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Saitozyma paraflava* Golubev & J.P. Samp. ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 134 (2015), *nom. inval.*, Art. 40.6 (Shenzhen).

Tremella basidiomaticola Xin Zhan Liu & F.Y. Bai, ***sp. nov.*** MycoBank MB831876.
For description see Mycokeys 47: 80 (2019).
Holotype: CGMCC 2.5724 (preserved in a metabolically inactive state).
Synonym: *Tremella basidiomaticola* Xin Zhan Liu & F.Y. Bai, Mycokeys 47: 80 (2019), *nom. inval.*, Art. 40.8 (Shenzhen).

Trimorphomyces sakaeraticus Fungsin, M. Takash. & Nakase ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831699.
For description see Microbiol. Culture Coll. 19(1): 37 (2003).
Holotype: JCM 11900 (preserved in a metabolically inactive state).
Synonyms: *Bullera sakaeratica* Fungsin, M. Takash. & Nakase, Microbiol. Culture Coll. 19(1): 37 (2003), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Trimorphomyces sakaeraticus* Fungsin, M. Takash. & Nakase ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 134 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vanrija meifongana C.F. Lee ex Kachalkin, Yurkov & Boekhout, ***sp. nov.*** MycoBank MB831709.
For description see Antonie van Leeuwenhoek 99(3): 647 (2011).
Holotype: CBS 11424 (preserved in a metabolically inactive state).
Synonyms: *Asterotremella meifongana* C.F. Lee, in Liu *et al.*, Antonie van Leeuwenhoek 99(3): 647 (2011), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Vanrija meifongana* C.F. Lee ex Kachalkin, Yurkov & Boekhout, Stud. Mycol. 81: 142 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vanrija nantouana C.F. Lee ex Kachalkin, Yurkov & Boekhout, ***sp. nov.*** MycoBank MB831710.
For description see Antonie van Leeuwenhoek 99(3): 648 (2011).
Holotype: CBS 10890 (preserved in a metabolically inactive state).
Synonyms: *Asterotremella nantouana* C.F. Lee, Antonie van Leeuwenhoek 99(3): 648 (2011), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Vanrija nantouana* C.F. Lee ex Kachalkin, Yurkov & Boekhout, Stud. Mycol. 81: 142 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vanrija thermophila Vogelmann, S. Chaves & C. Hertel ex Kachalkin, Yurkov & Boekhout, ***sp. nov.*** MycoBank MB831711.
For description see Int. J. Syst. Evol. Microbiol. 62(7): 1719 (2012).
Holotype: CBS 10687 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus thermophilus* Vogelmann, S. Chaves & C. Hertel, Int. J. Syst. Evol. Microbiol. 62(7): 1719 (2012), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Vanrija thermophila* Vogelmann, S. Chaves & C. Hertel ex Kachalkin, Yurkov & Boekhout, Stud. Mycol. 81: 142 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vishniacozyma foliicola Q.M. Wang & F.Y. Bai ex Yurkov, ***sp. nov.*** MycoBank MB831680.
For description see J. Gen. Appl. Microbiol. 57(5): 287 (2011).
Holotype: CGMCC AS 2.2471 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus foliicola* Q.M. Wang & F.Y. Bai, J. Gen. Appl. Microbiol. 57(5): 287 (2011), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Vishniacozyma foliicola* Q.M. Wang & F.Y. Bai ex Yurkov, Stud. Mycol. 81: 124 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vishniacozyma heimaeyensis Vishniac ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831682.
For description see Canad. J. Microbiol. 48(5): 464 (2002).
Holotype: CBS 8933 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus heimaeyensis* Vishniac, Canad. J. Microbiol. 48(5): 464 (2002), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Vishniacozyma heimaeyensis* Vishniac ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 124 (2015), *nom. inval.*, Art. 40.6 (Shenzhen).

Vishniacozyma psychrotolerans V. de García, Zalar, Brizzio, Gunde-Cim. & Van Broock ex Yurkov, ***sp. nov.*** MycoBank MB831684.

For description see FEMS Microbiology Ecology 82(2): 535 (2012).
Holotype: EXF-7039 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus psychrotolerans* V. de García, Zalar, Brizzio, Gunde-Cim. & Van Broock, FEMS Microbiol. Ecol. 82(2): 535 (2012), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Vishniacozyma psychrotolerans* V. de García, Zalar, Brizzio, Gunde-Cim. & Van Broock ex Yurkov, Stud. Mycol. 81: 124 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vishniacozyma taibaiensis Q.M. Wang & F.Y. Bai ex Yurkov, ***sp. nov.*** MycoBank MB831681.
For description see J. Gen. Appl. Microbiol. 57(5): 288 (2011).
Holotype: CGMCC AS 2.2444 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus taibaiensis* Q.M. Wang & F.Y. Bai, J. Gen. Appl. Microbiol. 57(5): 288 (2011), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Vishniacozyma taibaiensis* Q.M. Wang & F.Y. Bai ex Yurkov, Stud. Mycol. 81: 124 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

Vishniacozyma tephrensis Vishniac ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831683.
For description see Canad. J. Microbiol. 48(5): 466 (2002).
Holotype: CBS 8935 (preserved in a metabolically inactive state).
Synonyms: *Cryptococcus tephrensis* Vishniac, Canad. J. Microbiol. 48(5): 466 (2002), *nom. inval.*, Art. 40.6 (Shenzhen).
= *Vishniacozyma tephrensis* Vishniac ex Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 124 (2015), *nom. inval.*, Art. 40.6 (Shenzhen).

Yamadamyces Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***gen. nov.*** MycoBank MB831747.
For description see Stud. Mycol. 81: 178 (2015).
Type species: Yamadamyces rosulatus Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout.
Synonym: *Yamadamyces* Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 178 (2015), *nom. inval.*, Art. 40.1 (Shenzhen).

Yamadamyces rosulatus Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, ***sp. nov.*** MycoBank MB831748.
For description see Int. J. Syst. Evol. Microbiol. 60(10): 2503 (2010).
Holotype: CBS 10977 (preserved in a metabolically inactive state).
Synonym: *Rhodotorula rosulata* Golubev & Scorzetti, Int. J. Syst. Evol. Microbiol. 60(10): 2503 (2010), *nom. inval.*, Art. 40.7 (Shenzhen).
= *Yamadamyces rosulatus* Golubev & Scorzetti ex Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout, Stud. Mycol. 81: 178 (2015), *nom. inval.*, Art. 40.7 (Shenzhen).

CONTRIBUTIONS

F.-Y.B. and Q.-M.W. conceived and designed the project. Q.-M.W., F.-Y.B., P.-J.H. and L.-D. G. performed sampling and yeast isolation. A.-H. Li, F.-X.Y. and Q.-M.W. performed phenotypic characterisation and analysed the molecular data. L.K. run the emboss water analysis. A.Y. analysed the D1/D2 data. K.B. registered the taxa in MycoBank and handled the invalid taxonomic names. Q.-M.W., M.G. and F.-Y.B. wrote the paper. Q.-M.W., M.C.A., A.Y. and K.B. revised the paper. A.Y., M.T., J.P.S., B.F., S.J., M.C.A., B.T., J.I. supported the sequences and physiological data or strains generated and conserved in their laboratory.

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APPENDIX A. SUPPLEMENTARY DATA

Supplementary data to this article can be found online at https://doi.org/10.1016/j.simyco.2020.01.002.

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