OUTLINE OF FUNGI

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Abbreviations:
benA – nuclear gene encoding β-tubulin protein
cal – nuclear gene encoding calmodulin protein
cytB – mitochondrial gene encoding cytochrome B
IGR – nuclear intergenic region of the rRNA gene cluster
ITS – nuclear internal transcribed spacers 1 and 2 of the rRNA gene cluster, includes 5.8S rRNA gene
LSU – nuclear large subunit, a gene encoding 28S rRNA
mtSSU – mitochondrial small subunit of the rRNA gene cluster
rpb1 – nuclear gene encoding RNA polymerase subunit B I of RPB1 protein
rpb2 – nuclear gene encoding RNA polymerase subunit B II of RPB2 protein
rRNA – ribosomal RNA
SSU – nuclear small subunit, a gene encoding 18S rRNA
tub – nuclear gene encoding β-tubulin protein

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Orders

Aulographales Crous, Spatafora, Haridas & I.V. Grig.

Haridas et al. (2020) introduced this order to accommodate the families *Aulographaceae* and *Rhizodiscinaceae* based on phylogenetic analysis.

Aureoconidiellales Hern.-Restr. & Crous

Hernández-Restrepo et al. (2020) introduced this order to accommodate the family *Aureoconidiellaceae* based on phylogenetic analysis.

Catabotryales K.D. Hyde & Senan.

The analysis of LSU, SSU, *tef1,* and *rpb2* gene data by Hyde et al. (2017) has led to the description of seven subclasses including the order *Catabotryales*. On the basis of evolutionary data, Hyde et al. (2017) has proposed this order resulting in 15 sub-orders and 65 families in the subclass *Diaporthomycetidae*, having its stem age estimated 172 MYA. *Catabotryales* comprises saprobic species on dead leaves and stems of tropical monocotyledons. This order is distinct from its sister orders in having astromatic ascomata, broad cylindrical asci and ellipsoidal to cylindrical ascospores without a mucilaginous sheath (Hyde et al. 2020).

Cladosporiales Abdollahz. & Crous

Based on the phylogenetic results, combined with morphology and ecology, Abdollahzadeh et al. (2020) introduced this new order to accommodate the family *Cladosporiaceae,* which was previously placed in *Capnodiales*.

Comminutisporales Abdollahz. & Crous

Based on the phylogenetic results, combined with morphology and ecology, Abdollahzadeh et al. (2020) introduced this new order to accommodate the family *Comminutisporaceae*.

Coniosporiales Crous, Spatafora, Haridas & I.V. Grig.

Haridas et al. (2020) introduced this order to accommodate the family *Coniosporiaceae* based on phylogenetic analysis.

Heitmaniales Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Lineolatales Crous, Spatafora, Haridas & I.V. Grig.

Haridas et al. (2020) introduced this order to accommodate the family *Lineolataceae* based on phylogenetic analysis.

Neophaeothecales Abdollahz. & Crous

Abdollahzadeh et al. (2020) introduced this order to accommodate the family *Neophaeothecaceae* based on the phylogenetic results, combined with morphology and ecology.

Racodiales Abdollahz. & Crous

The typification of the genus *Racodium* Fr. was discussed earlier by Hawksworth et al. (2011). Based on the results of Bayesian analysis of combined LSU, *tef1* and *rpb2* sequences of 193 taxa representing orders *Capnodiales* sens. lat., *Myrangiales* and *Dothideales*, the new order *Racodiales* was introduced by Abdollahzadeh et al. (2020) to include family *Racodiaceae* (based on genus *Racodium*).

Rosettozymales Q.M. Wang & F.Y. Bai

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Families

Aureoconidiellaceae Hern.-Restr. & Crous

Hernández-Restrepo et al. (2020) introduced this new family to accommodate the type genus *Aureoconidiella* Hern.-Restr. & Crous based on phylogenetic analysis.

Coniosporiaceae Crous, Spatafora, Haridas & I.V. Grig.

Haridas et al. (2020) introduced this new family to accommodate the type genus *Coniosporium* Link based on phylogenetic analysis.

Cylindrosympodiaceae Crous, M. Shen & Y. Zhang ter

Shen et al. (2020) introduced *Cylindrosympodiaceae* to accommodate the genera *Cylindrosympodium* W.B. Kendr. & R.F. Castañeda, *Pseudoanungitea* Crous, *Sympodiella* W.B. Kendr. and *Tothia* Bat. within the *Venturiales*.

Foliocryphiaceae C.M. Tian, N. Jiang & Crous

Revaluation of families in the pathogenic fungal order *Diaporthales* and the family *Cryphonectriaceae* has resulted in the separation of the latter into two subclades, 21 genera and 55 species, based on the phylogenetic studies on combined sequence data of ITS, LSU, *tef1*, and *rpb2* genes. The family *Foliocryphiaceae* is distinguished by its phylogeny and dimorphic conidia while *Mastigosporellaceae* can be differentiated by owning apical conidial appendages. A new genus, *Neocryphonectria* has also been described in the family *Foliocryphiaceae* which is characterized by fusoid, aseptate macroconidia. In total, 31 families have been validated under the order *Diaporthales* (Jiang et al. 2020).

Mastigosporellaceae C.M. Tian, N. Jiang & Crous

Revaluation of families in the pathogenic fungal order *Diaporthales* and the family *Cryphonectriaceae* has resulted in the separation of the latter into two subclades, 21 genera and 55 species, based on the phylogenetic studies on combined sequence data of ITS, LSU, *tef1*, and *rpb2* genes. The family *Foliocryphiaceae* is distinguished by its phylogeny and dimorphic conidia while *Mastigosporellaceae* can be differentiated by owning apical conidial appendages. A new genus, *Neocryphonectria* has also been described in the family *Foliocryphiaceae* which is characterized by fusoid, aseptate macroconidia. In total, 31 families have been validated under the order *Diaporthales* (Jiang et al. 2020).

Neocryphonectria C.M. Tian, N. Jiang & Crous

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Heitmaniaceae Q.M. Wang & F.Y. Bai

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Jianyuniaceae Q.M. Wang & F.Y. Bai

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Lineolataceae Crous, Spatafora, Haridas & I.V. Grig.

Haridas et al. (2020) introduced this new family to accommodate the type genus *Lineolata* Kohlm. & Volkm.-Kohlm. based on phylogenetic analysis.

Neoantennariellaceae Abdollahz. & Crous

Based on the phylogenetic results, combined with morphology and ecology, Abdollahzadeh et al. (2020) introduced *Neoantennariellaceae* to accommodate the genera *Fumiglobus* D.R. Reynolds & G.S. Gilbert, *Neoantennariella* Abdollahz. & Crous and *Neoasbolisia* Abdollahz. & Crous within the *Capnodiales*.

Neophaeothecaceae Abdollahz. & Crous

Abdollahzadeh et al. (2020) introduced this new family to accommodate the type genus *Neophaeotheca* Abdollahz. & Crous.

Readerielliopsidaceae Abdollahz. & Crous

Abdollahzadeh et al. (2020) introduced *Readerielliopsidaceae* to accommodate the coelomycetous genera *Phaeoxyphiella* Bat. & Cif., *Readerielliopsis* Crous & Decock, *Scolecoxyphium* Cif. & Bat. and *Scorias* Fr. within the *Capnodiales*.

Rhizodiscinaceae Crous, Spatafora, Haridas & I.V. Grig.

Based on phylogenetic analysis, Haridas et al. (2020) introduced this new family to accommodate the type genus *Rhizodiscina* Hafellner.

Rosettozymaceae Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Rubikioideae Lücking, M. Cáceres & Aptroot

Cáceres et al. (2020) reanalyzed the phylogenetic placement of two non-lichenized fungi, namely *Furcaspora eucalypti* Crous & Verkley and *Rubikia evansii* Crous (*Graphidaceae*). Maximum likelihood tree of *Graphidaceae* based on the mtSSU, LSU, and *rpb2* concatenated markers showed the positions of *Furcaspora* Bonar and *Rubikia* H.C. Evans & Minter as separate, basally diverging clade. The new subfamily, *Rubikioideae*, was described by the authors.

Tricladiaceae P.R. Johnst. & Baschien

While circumscribing the family *Solenopeziaceae*, a novel family has been established which include the genera that have aquatic hyphomycete-like asexual morphs and sexual morphs comprising of shiny apothecia; such as *Cudoniella* Sacc., *Geniculospora* Sv., *Graddonia* Dennis, *Halenospora* E.B.G. Jones, *Mycofalcella* Marvanova, Om-Kalth. & J. Webster, *Spirosphaera* Beverw., and *Tricladium* Ingold. However, the family *Solenopeziaceae* comprised of *Lasiobelonium* Ellis & Everh., *Solenopezia* Sacc., *Trichopeziza* Fuckel, and *Trichopezizella* Dennis ex Raitv. all showing sexual morphs with smooth-walled hairs. The current proposed novel family has been evidenced by the phylogenetic analysis revealing the new family has monophyletic clade having relationships with other families *Pleuroascaceae* and *Helotiaceae* (Johnston & Baschien 2020).

Genera

Acidotalaromyces Houbraken, Frisvad & Samson

An updated review of the generic, subgeneric, sectional classification of the order *Eurotiales* have resulted in the description of new family *Penicillaginaceae* and few genera, mainly based upon the sequence-based studies using GenBank accession numbers of ITS, *benA*, *cal1* and *rpb2* gene sequences. In total, the order *Eurotiales* under *Ascomycetes* comprise of five accepted families, 28 genera and 1187 species (Houbraken et al. 2020).

Aphanodesmium Réblová & Hern.-Restr.

With evidence from the phylogenetic studies, Réblová et al. (2020) placed the four species of *Bactrodesmium* in three unrelated novel genera, *viz*., *Gamsomyces* (*Sclerococcales*), *Kaseifertia* (*Pleosporales*) and *Aphanodesmium* (*Helotiales*) the last of which had been originally described in Koukol & Kolářová (2010) and made several novel combinations *viz*., *A. gabretae* (Koukol & Kolářová) Réblová & Hern.-Restr, *G. longisporus* (M.B. Ellis) Hern.-Restr. & Réblová, *G. stilboideus* (R.F. Castaneda & G.R.W. Arnold) Hern.-Restr. & Réblová, *Helicoascotaiwania farinosa* (Linder) Réblová, Hern.-Restr. & J. Fourn., *K. cubense* (R.F. Castaneda & G.R.W. Arnold) Réblová, Hern.-Restr. & J. Fourn. The new sequence data for *B. longisporum* M.B. Ellis and *B. stilboideum* R.F. Castañeda & G.R.W. Arnold placed them in *Sclerococcales* (*Eurotiomycetes*), *B. cubense* (R.F. Castañeda & G.R.W. Arnold) Zucconi & Lunghini in *Dothideomycetes*, and *B. gabretae* Koukol & Kolářová in *Leotiomycetes* (Réblová et al. 2020).

Arboricolonus S. Bien & Damm

Multi-locus phylogenetic studies (LSU, ITS, *tub*, *tef1*) of fungi associated with wood necroses of *Prunus* L. in Germany, has led to the description of novel species, in a new genus *Arboricolonus* with the type *A. simplex* S. Bien & Damm, belonging in *Helotiales* (*Leotiomycetes*) with a collophorina-like asexual morph along with seven new species of *Cadophora* Lagerb. & Melin. The authors found the novel genus has similarities with *Glutinomyces* Nor Nakam., *Chalara* (Corda) Rabenh., *Hyalodendriella* Crous and *Polyphilus* D.G. Knapp, Ashrafi, W. Maier & Kovacs with ITS (90% for LC218288 with the strains of *Glutinomyces vulgaris*) and LSU (97% for EU040232 with the ex-type strain of *Hyalodendriella betulae*) similarity (Bein & Damm 2020) and has distinguishable asexual morphs.

Ascospirella Houbraken, Frisvad & Samson

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Atrophysma T. Sprib.

The genus was introduced by Spribille et al. (2020) to accommodate a single species of a cyanolichen which differs from *Placynthium* by simple ascospores, and from *Leciophysma* by producing dark blue-black pigments in the apothecia. Multi-locus DNA sequencing placed the new genus in *Pannariaceae*. So far, no genus with black pigments was known within *Pannariaceae*.

Aureoconidiella Hern.-Restr. & Crous

The monotypic genus *Aureoconidiella* was introduced by Hernández-Restrepo et al. (2020) with *A. foliicola* Hern.-Restr. & Crous as the type species. This genus is characterized by unbranched conidiophores, cicatrized and sympodial conidiogenous cells with thickened scars, producing sub-globose, verruculose, and golden-brown conidia.

Baidera Ertz & Diederich

Baidera containing a single species, *B. mauritiana,* was described from Mauritius by Diederich & Ertz (2020). A maximum-likelihood analysis based on the two *rpb2* sequences (MN989868 for Ertz 21443-hymenium, MN989869 for Ertz 21443-thallus) was used to place *Baidera* in a phylogeny of *Arthoniales*. The new genus forms a distinct lineage in *Roccellaceae*, being somewhat related to *Gyrographa* Ertz & Tehler and *Sigridea* Tehler. *Baidera* differs from all genera of *Roccellaceae* by a thick crustose, not byssoid thallus, lirelliform ascomata with a carbonized excipulum not covered by a thalline layer, a carbonized hypothecium extending down to the substrate, a pruinose and atomentose hymenial disc, ascospores without a distinct gelatinous sheath, and a chemistry with psoromic acid as a major substance.

Batnamyces Noumeur

A new endophytic genus *Batnamyces* belonging to *Chaetomiaceae* was described based on the morphological and molecular studies. It is phylogenetically related to *Stolonocarpus* X. Wei Wang & Houbraken and *Madurella* Brumpt. Besides the phylogenetic studies, biochemical analyses were also undertaken using NMR spectroscopy, HRESIMS and ECD techniques resulting in eight diketopiperazines. The strain has been isolated from the medicinal plant *Globularia alypum* L. collected in Algeria (Noumeur et al. 2020).

Begerowomyces Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Bellamyces Crous, Coppins & U. Braun

Bellamyces, with *B. quercus* Crous, Coppins & U. Braun as the type species, was proposed by Shen et al. (2020) based on the multigene phylogenetic analysis, morphological and ecological characteristics. The genus is characterized by having solitary, and transversely multiseptate, rarely oblique conidia.

Bergerella Diederich & Lawrey

A new genus and species discovered from Austria, *Bergerella* with the species *B. atrofusca* Diederich & Lawrey belonging to the family *Hydnaceae* in the order *Cantharellales*. The phylogenetic studies by analyzing ITS and nuLSU rRNA revealed that novel species has similarities with the genus *Minimedusa* Weresub & P.M. LeClair of the same order *Cantharellales*. However, it was quite unique in neither having lichen association nor bulbilliferous species of the order (Lawrey et al. 2020).

Boekhoutia Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Bolbea Buaya & Thines

A novel holocarpic parasitoid oomycetes genus readily cultivable on malt-extract agar medium, belonging to the early *Saprolegniomycetes* in the order *Leptomitales*, has been reported from the Rebstock lake, Frankfurt, Germany. The absence of typical sacculate hyphal swellings and the "elephant hyphae" and the weak clustering with *Atkinsielladubia* (D. Atkins) Vishniac has resulted in describing this taxon as a novel genus. Phylogenetic analyses based on partial 18S rRNA gene (SSU) sequences were not conclusive in deriving contrasting topologies in minimum evolution (ME) and maximum likelihood (ML) analyses (Buaya & Thines 2020).

Bryoclavula H. Masumoto & Y. Degawa

The genus was introduced by Masumoto & Degawa (2020) for a species, *Bryoclavula phycophila* H. Masumoto & Y. Degawa, described from Japan. Maximum-likelihood analysis of LSU (D1/D2) sequences placed the new genus in a new lineage within *Cantharellales*. Morphologically the genus is similar to lichenized genus *Multiclavula* R.H. Petersen but differs by lacking a globular or bulbil-like thallus.

Burrowsia Fryday & I. Medeiros

The monotypic genus *Burrowsia* is proposed by Fryday et al. (2020) to accommodate the South African species *B. cataractae* Fryday & I. Medeiros. Maximum likelihood analysis of concatenated ITS, LSU, *rpb1* and *rpb2* sequences places the new species in the *Caliciaceae* outside related buellioid genera. Morphologically, *Burrowsia* is characterized by its pigmented, submuriform ascospores and asci with an apical tube-like structure.

Carneothele Fryday, T. Sprib. & M. Svenss.

Spribille et al. (2020) introduced this genus based on morphological traits. The single successful DNA extraction yielded ITS and 28S rRNA sequences which affinities to *Dothideomycetes* and *Sarea* Fr., respectively. However, these sequences could derive from another fungal material. Morphologically, the genus is close to *Thelocarpon* Nyl. by its minute ascomata with the occasional presence of a yellow pruina, and multi-spored asci that gradually taper to a narrow apex but differs by having red-brown ascomata with the wall pigment forming magenta crystals in 10% KOH.

Cladocillium Chun-Hao Chen & R. Kirschner

Based on evidence from DNA sequence data and morphology, Chen et al. (2020) introduced *Cladocillium* as a monotypic genus in *Mycosphaerellaceae*. The genus is typified by *C. musae* Chun-Hao Chen & R. Kirschner collected from leaves of *Musa itinerans* Cheesman in Taiwan. The genus is characterized by having macronematous, single, erect, unbranched or rarely branched, but with conidial chains arising in verticils along the conidiophore stipe, pigmented conidiophores, intercalary and terminal conidiogenous cells, in branched acropetal chains, pigmented, rough conidia (Chen et al. 2020).

Commelinaceomyces E. Tanaka

A novel false-smut fungal genus has been described from Japan that infects the flowers of *Murdannia keisak* (Hasskarl) Handel-Mazzetti (*Commelinaceae*) belonging to the family *Clavicipitaceae* of the order *Hypocreales* (*Ascomycota*) based on the multi-locus phylogenetic analysis of DNA sequences (18S, 28S, *tef1*, *rpb1*, and *rpb2*). The novel taxa varied from its close relative *Ustilago* (Pers.) Roussel in having conidia development at the apex of conidiogenous cells (Eiji et al. 2020).

Corylicola Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde

Wijesinghe et al. (2020) introduced the genus *Corylicola* in the family *Bambusicolaceae* (*Pleosporales*), to accommodate *C. italica* Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde isolated from *Corylus avellana* L. in Italy. This genus is characterized by scattered, globose to subglobose and ostiolate ascomata; anastomosing and branching pseudoparaphyses; cylindrical asci with a well-developed ocular chamber and short furcate pedicel; and single-septate ascospores. The coelomycetous asexual morph of *Corylicola* has holoblastic, phialidic conidiogenous cells and light brown conidia (Wijesinghe et al. 2020).

Cryphognomonia C.M. Tian & N. Jiang

A polyphasic approach including morphological, cultural data, and phylogenetic analyses of partial ITS, LSU, *tef1, rpb2,* and *tub2* gene sequences has resulted in description of novel species of *Cryphognomonia*, *C. pini* C.M. Tian & N. Jiang belonging to *Gnomoniaceae* from China. The new species is characterized by developed pseudostromata and ascospores with obvious hyaline sheath (Yang et al. 2020).

Diabolocovidia Crous

Diabolocovidia is the genus described during the lockdown period due to the COVID-19 pandemic from Gainesville, Florida, USA on the leaves of the palm *Serenoa repens* (W. Bartram) Small based on the collection of M J Wingfield. It is allied to *Vamsapriya* Gawas & Bhat in having brown, synnematous conidiophores, mono- to polytretic conidiogenous cells, and dark brown, septate conidia arranged in acropetal chains (Crous et al. 2020a).

Emmanuelia Ant. Simon, Lücking & Goffinet

The genus *Emmanuelia* was proposed to comprise twelve species previously recognized within polyphyletic subfamily *Lobarioideae* (*Peltigeraceae*) and restricted to the New World. Molecular phylogenetic analyses using ITS and mtSSU sequences show that *Emmanuelia* forms a well-supported monophyletic group within the *Lobaria sensu lat*o clade. Morphologically the genus is similar to *Ricasolia* D. Not., but differs by its apothecia, rimmed by overarching and often crenulate to lobulate margins, with the parathecium and the amphithecium apically separated and of a different structure (Simon et al. 2020).

Erichansenia S.Y. Kondr., Kärnefelt & A. Thell,

Results of the three gene phylogeny of the *Teloschistaceae* based on ITS, LSU and mtSSU sequences revealed the genus *Shackletonia* Søchting, Frödén & Arup to be polyphyletic and the new genus *Erichansenia* was proposed by Kondratyuk et al. (2020) to accommodate three species, namely *Caloplaca epithallina* Lynge, *S. cryodesertorum* Garrido-Ben., Søchting & Pérez-Ort. and *S. sauronii* (Søchting & Øvstedal) Søchting, Frödén & Arup. Morphologically, the new genus is similar to *Shackletonia*, but differs in having better developed thallus, black apothecia with a dark greenish blue outer exciple, *Lecidea*-green pigment in the cortex of thallus and exciple, as well as in geographic distribution.

Evansstolkia Houbraken, Frisvad & Samson

An updated review of the generic, subgeneric, sectional classification of the order *Eurotiales* have resulted in the description of new family *Penicillaginaceae* and few genera, mainly based upon the sequence-based studies using GenBank accession numbers of ITS, *benA*, *cal1* and *rpb2* gene sequences. In total, the order *Eurotiales* under *Ascomycetes* comprise of five accepted families, 28 genera and 1187 species (Houbraken et al. 2020).

Fagicola Crous, M. Shen & Y. Zhang ter

Fagicola was proposed by Shen et al. (2020) based on *F. fagi* (Crous & de Hoog) Crous, M. Shen & Y. Zhang ter (as *Fusicladium fagi* Crous & de Hoog), which was saprotrophic on leaves of *Fagus sylvatica* L. collected in the Netherlands.

Fraxinicola Crous, M. Shen & Y. Zhang ter

Shen et al. (2020) introduced this genus to accommodate two new species and two new combinations based on the multigene phylogenetic analysis, morphological and ecological characteristics. Currently, the genus comprises four species viz. *F. europaea* Crous, M. Shen & Y. Zhang ter, *F. fraxini* (Aderh.) Crous, M. Shen & Y. Zhang ter (the type species), *F. italica* Crous, M. Shen & Y. Zhang ter and *F. orni* (M. Ibrahim, M. Schlegel & T.N. Sieber) Crous, M. Shen & Y. Zhang ter (Shen et al. 2020).

Fulgogasparrea S.Y. Kondr., N.-H. Jeong, Kärnefelt, Elix, A. Thell & Hur

The genera *Fulgogasparrea* S.Y. Kondr., N.-H. Jeong, Kärnefelt, Elix, A. Thell & Hur and *Wetmoreana* Arup, Søchting & Frödén were introduced in 2013 by Kondratyuk et al. (2013) and Arup et al. (2013), respectively, for the *Caloplaca decipioides* group. The latter genus was accepted by Wijayawardene et al. (2020) while the former was considered to be a synonym. However, Mishra et al. (2020) accepted both *Fulgogasparrea* and *Wetmoreana* revealing genetical distance based on ITS sequences as well as morphological differences.

Fuscohilum Crous, M. Shen & Y. Zhang ter

Shen et al. (2020) introduced this genus within *Sympoventuriaceae* to accommodate *Fusicladium rhodense* Crous & M.J. Wingf. and *F. sicilianum* Koukol. Since *F. rhodense* and *F. sicilianum* formed a separate generic clade within *Sympoventuriaceae*, these two species were phylogenetically assigned to a new genus, *Fuscohilum*.

Gamsomyces Hern.-Restr. & Réblová

With evidence from the phylogenetic studies, Réblová et al. (2020) placed the four species of *Bactrodesmium* in three unrelated novel genera, *viz*., *Gamsomyces* (*Sclerococcales*, *Kaseifertia* (*Pleosporales*) and *Aphanodesmium* (*Helotiales*), the last of which had been originally described in Koukol & Kolářová (2010) and made several novel combinations such as *A. gabretae* (Koukol & Kolářová) Réblová & Hern.-Restr, *G. longisporus* (M.B. Ellis) Hern.-Restr. & Réblová, *G. stilboideus* (R.F. Castaneda & G.R.W. Arnold) Hern.-Restr. & Réblová, *Helicoascotaiwania farinosa* (Linder) Réblová, Hern.-Restr. & J. Fourn., *K. cubense* (R.F. Castaneda & G.R.W. Arnold) Réblová, Hern.-Restr. & J. Fourn. The new sequence data for *B. longisporum* M.B. Ellis and *B. stilboideum* R.F. Castañeda & G.R.W. Arnold placed them in *Sclerococcales* (*Eurotiomycetes*), *B. cubense* (R.F. Castañeda & G.R.W. Arnold) Zucconi & Lunghini in *Dothideomycetes*, and *B. gabretae* Koukol & Kolářová in *Leotiomycetes* (Réblová et al. 2020).

Halocryptosphaeria Dayarathne, *Devadatha,* V.V. Sarma & K.D. Hyde

Two new genera, *viz*., *Halocryptosphaeria*; *Halotestudina* belonging the families *Diatrypaceae* (*Xylariales*) and *Testudinaceae* (*Pleosporales*), respectively have been described from mangrove forests of India and Thailand. The genus *Halocryptosphaeria* shows similarities with *Cryptosphaeria* Ces. & De Not. however, differs morphologically from *Cryptosphaeria* in having light-brown ascospores containing oil droplets versus pale yellow ascospores; and dwelling in marine environment (Rappaz, 1987). The other genus *Halotestudina* differs from all other genera of the family in having brown muriform ascospores that are constricted at each septum. These genera have been described mainly on the morphological aids supported by phylogenetic evidences (Dayarathne et al. 2020).

Halotestudina Dayarathne & K.D. Hyde

Two new genera, *viz*., *Halocryptosphaeria*; *Halotestudina* belonging the families *Diatrypaceae* (*Xylariales*) and *Testudinaceae* (*Pleosporales*), respectively have been described from mangrove forests of India and Thailand. The genus *Halocryptosphaeria* shows similarities with *Cryptosphaeria* Ces. & De Not. however, differs morphologically from *Cryptosphaeria* in having light-brown ascospores containing oil droplets versus pale yellow ascospores; and dwelling in marine environment (Rappaz, 1987). The other genus *Halotestudina* differs from all other genera of the family in having brown muriform ascospores that are constricted at each septum. These genera have been described mainly on the morphological aids supported by phylogenetic evidences (Dayarathne et al. 2020).

Italiofungus Crous

A total of seven new genera, 26 new species, 10 new combinations have been described from different parts of the world by Crous et al. (2020b) providing genera and species descriptions. All of these genera have been recorded on *Phillyrea latifolia* L.*, Lonicera tatarica* L., *Tilia* sp., *Pinus sylvestris* L., *Caragana arborescens* Lam., *Prunus cerasus* L., *Muntingia calabura* L. respectively. The morphological studies were supported by molecular phylogeny analysis using the LSU and ITS (Crous et al. 2020b).

Jennwenomyces Goh & C.H. Kuo

A newly segregated hyphomycete genus *Jennwenomyces* has been described based on the morphological and molecular data from the freshwater streams of Taiwan. The novel genus is characterized by the presence of versicolored, straight, navicular to cylindrical euseptate phragmospores borne on multiple percurrently extending, annellate conidiophores. The phylogenetic analysis showed similarities with the species of *Dictyosporella* Abdel-Aziz, *Junewangia* W.A. Baker & Morgan-Jones, and *Sporidesmiella* P.M. Kirk in the family *Junewangiaceae* clustered together under *Sordariomycetes* (Goh & Kuo 2020).

Jocatoa R. Miranda

The new genus *Jocatoa* was introduced by Miranda-González et al. (2020) to accommodate the single species *J. agminalis* (Nyl.) Lücking, Herrera-Camp. & R. Miranda previously included in the polyphyletic genus *Medusulina* Müll. Arg. which is no longer valid. The new monospecific genus strongly resembles species of *Diorygma* Eschw. but maximum likelihood analysis of SSU, LSU, and *rpb2* sequences put the genus *Jocatoa* outside the *Diorygma* clade. From *Diorygma* the new genus differs by having simple paraphyses tips that do not form an epithecium.

Juncomyces Crous

Crous et al. (2020a) introduced *Juncomyces* to accommodate *J. californiensis* Crous (the type species) collected from leaves of *Juncus effuses* L. This genus is closely related to *Graminopassalora* U. Braun, C. Nakash., Videira & Crous but differs in having solitary conidiophores (rarely fascicles of 2–3), and multiseptate, obclavate conidia.

Kaseifertia Réblová & Hern.-Restr. & J. Fourn.

With evidence from the phylogenetic studies, Réblová et al. (2020) placed the four species of *Bactrodesmium* in three unrelated novel genera, *viz*., *Gamsomyces* (*Sclerococcales*), *Kaseifertia* (*Pleosporales*) and *Aphanodesmium* (*Helotiales*) the last of which had been originally described in Koukol & Kolářová (2010) and made several novel combinations *viz*., *A. gabretae* (Koukol & Kolářová) Réblová & Hern.-Restr, *G. longisporus* (M.B. Ellis) Hern.-Restr. & Réblová, *G. stilboideus* (R.F. Castaneda & G.R.W. Arnold) Hern.-Restr. & Réblová, *Helicoascotaiwania farinosa* (Linder) Réblová, Hern.-Restr. & J. Fourn., *K. cubense* (R.F. Castaneda & G.R.W. Arnold) Réblová, Hern.-Restr. & J. Fourn. The new sequence data for *B. longisporum* M.B. Ellis and *B. stilboideum* R.F. Castañeda & G.R.W. Arnold placed them in *Sclerococcales* (*Eurotiomycetes*), *B. cubense* (R.F. Castañeda & G.R.W. Arnold) Zucconi & Lunghini in *Dothideomycetes*, and *B. gabretae* Koukol & Kolářová in *Leotiomycetes* (Réblová et al. 2020).

Keithomyces Samson, Luangsa-ard & Houbraken

A phylogenetic framework is reconstructed for the *Clavicipitaceae* focusing on *Metarhizium* Sorokin through increased taxon-sampling using five genomic loci (SSU, LSU, *tef1*, *rpb1*, *rpb2*) and the barcode marker ITS rRNA resulted in describing six new genera of monophyletic clades subtending the core *Metarhizum* clade, 19 new species and several novel combinations (Mongkolsamrit et al. 2020).

Kosmimatamyces Bianchin., Reinoso-Fuentealba, Rodr.-Andr., Cano & Stchigel

Crous et al. (2020a) introduced *Kosmimatamyces* as a monotypic genus in *Capnodiaceae*. The genus is typified by *K. alatophylus* Bianchin., Reinoso-Fuentealba, Rodr.-Andr., Cano & Stchigel collected from soil of the salt marsh in Argentina.

Kukwaea Suija, Motiej. & Zhurb.

On the basis of morphological and phylogenetic studies, a novel genus, *Kukwaea*, found associated with *Cetraria islandica* (L.) Ach. has been described from Russia. The newly described fungus, characterized by its cupulate, brown ascomata with grey to blackish disc surrounded by brownish grey pubescence, exciple of textura angularis type, with crystals in the lower part, with granulose excipular hairs obtuse at the tips, simple to forked paraphyses, *Calycina*-type asci, and hyaline, aseptate ascospores. The genetic analysis proved that it belongs to the order *Helotiales* (Suija et al. 2020).

Lendemeriella S.Y. Kondr.

The genus *Lendemeriella* was proposed by Kondratyuk et al. (2020) for seven species of the *Caloplaca reptans* Lendemer & B.P. Hodk. group on the basis of the analysis of ITS, LSU and mtSSU sequences. *Lendemeriella* forms the separate robust branch in sister position to the genera *Olegblumia* S.Y. Kondr., Lőkös & Hur, *Rufoplaca* Arup, Søchting & Frödén and *Usnochroma* Søchting, Arup & Frödén. Authors mentioned that some contradictive data exist, and additional molecular data are needed to clarify position of these and other possible *Lendemeriella* species.

Linosporopsis Voglmayr & Beenken

A new genus *Linosporopsis* belonging to the order *Xylariales* has been described based on the basis of molecular phylogenetic and morphological studies from the leaves of *Fagus sylvatica* L. The multi-locus matrix of partial ITS-LSU rRNA, *rpb2* and *tub2* gene sequences as well as morphological investigations revealed that both species, *Linospora ischnotheca* (Desm.) Sacc. and *L. ochracea* Sacc. are unrelated to the diaporthalean genus *Linospora* Fuckel, but belong to *Xylariaceae* sens. str. Thus, along with *Linospora carpini* J. Schrot. and *Linospora magnagutiana* Speg. these four species have been accommodated in the new genus (Voglmayr & Beenken 2020).

Longiseptatispora L.W. Hou & Crous

Crous et al. (2020b) introduced this genus to accommodate two new species based on the DNA phylogeny and morphological characters. The genus is typified by *L. curvata* Crous & Bulgakov collected from leaves of *Lonicera tatarica* L. in Russia.

Marquandomyces Samson, Houbraken & Luangsa-ard

A phylogenetic framework is reconstructed for the *Clavicipitaceae* focusing on *Metarhizium* Sorokin through increased taxon-sampling using five genomic loci (SSU, LSU, *tef1*, *rpb1*, *rpb2*) and the barcode marker ITS rRNA resulted in describing six new genera of monophyletic clades subtending the core *Metarhizum* clade, 19 new species and several novel combinations (Mongkolsamrit et al. 2020).

Meniscomyces Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Muriphila Jurjevic, Cmoková & Hubka

Crous et al. (2020a) introduced *Muriphila* as a monotypic genus in *Teratosphaeriaceae*. This genus is characterized by velvety, dark olivaceous to black, convex, radially wrinkled to crateriform colonies, septate, with smooth to verrucous walls hyphae, rectangular to asymmetrical, and disintegrates into fragments at maturity hyphal cells (Crous et al. 2020a).

Neoantennariella Abdollahz. & Crous

The monotypic genus *Neoantennariella* was erected by Abdollahzadeh et al. (2020) with *N. phylicae* Abdollahz. & Crous as the type species. Morphologically similar to *Antennariella* Bat. & Cif., but different in conidiomatal and conidium morphology (Abdollahzadeh et al. 2020).

Neoasbolisia Abdollahz. & Crous

Based on the phylogenetic results, combined with morphology and ecology, the monotypic genus *Neoasbolisia* was erected by Abdollahzadeh et al. (2020) with *N. phylicae* Abdollahz. & Crous as the type species.

Neofusicladium Crous, M. Shen & Y. Zhang ter

Shen et al. (2020) introduced this genus within *Sympoventuriaceae* to accommodate three new combinations. The genus is typified by *N. eucalypti* (Crous & R.G. Shivas) Crous, M. Shen & Y. Zhang ter collected from leaves of *Eucalyptus* sp.

Neolamproconium Crous & Akulov

A total of seven new genera, 26 new species, 10 new combinations have been described from different parts of the world by Crous et al. (2020b) providing genera and species descriptions. All of these genera have been recorded on *Phillyrea latifolia* L.*, Lonicera tatarica* L., *Tilia* sp., *Pinus sylvestris* L., *Caragana arborescens* Lam., *Prunus cerasus* L., *Muntingia calabura* L. respectively. The morphological studies were supported by molecular phylogeny analysis using the LSU and ITS (Crous et al. 2020b).

Neophaeotheca Abdollahz. & Crous

The monotypic genus *Neophaeotheca* was erected by Abdollahzadeh et al. (2020) with *N. salicorniae* (Crous & Roets) Abdollahz. & Crous as the type species based on the phylogenetic results, combined with morphology and ecology.

Neoshiraia H.A. Ariyaw.

Ariyawansa et al. (2020) introduced this new genus in *Shiraiaceae* to accommodate two coelomycetous species isolated from *Camellia sinensis* L. based on multi-gene phylogenetic inference and morphological interpretations. *Shiraia* Henn. can be distinguished from *Neoshiraia* in having fusiform, muriform, asymmetrical, hyaline to light brown conidia whereas *Neoshiraia* possesses hyaline, aseptate, obovoid to ellipsoidal conidia (Ariyawansa et al. 2020).

Neosorocybe Crous & Akulov

A total of seven new genera, 26 new species, 10 new combinations have been described from different parts of the world by Crous et al. (2020b) providing genera and species descriptions. All of these genera have been recorded on *Phillyrea latifolia* L.*, Lonicera tatarica* L., *Tilia* sp., *Pinus sylvestris* L., *Caragana arborescens* Lam., *Prunus cerasus* L., *Muntingia calabura* L. respectively. The morphological studies were supported by molecular phylogeny analysis using the LSU and ITS (Crous et al. 2020b).

Neotorrubiella Tasan., Thanakitp. & Luangsa-ard

Two new fungal genera, *Neotorrubiella* and *Pechia*, on insects has been described in the *Hypocreales* from Thailand. A multi-locus molecular phylogenetic analysis involved SSU, LSU, *tef1*, *rpb1*, and *rpb2* together with the nuclear intergenic region (IGR) for 67 sequences.

Neotorrubiella resembles *Torrubiella* Boud. in the absence of a stipe and can be distinguished by the production of whole ascospores, which are not commonly found in *Torrubiella* (Thanakitpipattana et al. 2020).

Nothoseiridium Crous

A novel pathogenic fungus infecting *Podocarpus* L'Heritier ex Persoon has been discovered and described from Cape Town, South Africa. This novel genus produces black-colored, round, flattened acervular conidiomata with many brownish wall layers. The conidiophores, reduced to conidiogenous cells are colorless, smooth, subcylindrical to ampuliform, annellidic and are arising from the base of the stroma. The conidia are fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline; apical and basal appendage filiform, flexuous, unbranched, excentric. Type species: *N. podocarpi* Crous (Crous et al. 2020a).

Nothoseptoria Crous & Bulgakov

Crous et al. (2020b) introduced this new genus in the family *Mycosphaerellaceae* (*Mycosphaerellales*), to accommodate *N. caraganae* (Henn.) Crous & Bulgakov collected from living leaves of *Caragana arborescens* Lam. in Russia.

Ochraceocephala Voglmayr & Aiello

Aiello et al. (2020) described the monotypic genus *Ochraceocephala* to accommodate *O. foeniculi* Voglmayr & Aiello within *Leptosphaeriaceae*. It is phylogenetically closely related to *Plenodomus* Preuss, from which it deviates substantially in morphology. *Plenodomus* species are characterized by pycnidial phoma-like asexual morphs, and while in two *Plenodomus* species [*P. chrysanthemi* (Zachos, Constantinou & Panag.) Gruyter, Aveskamp & Verkley, *P. tracheiphilus* (Petri) Gruyter, Aveskamp & Verkley] simple hyphomycetous, phialophora-like synanamorphs have been recorded (Boerema et al. 1994), these are very different from the complex conidiophores of the present fennel pathogen (Aiello et al. 2020).

Papiliomyces Luangsa-ard, Samson & Thanakitp.

A phylogenetic framework is reconstructed for the *Clavicipitaceae* focusing on *Metarhizium* Sorokin through increased taxon-sampling using five genomic loci (SSU, LSU, *tef1*, *rpb1*, *rpb2*) and the barcode marker ITS rRNA resulted in describing six new genera of monophyletic clades subtending the core *Metarhizum* clade, 19 new species and several novel combinations (Mongkolsamrit et al. 2020).

Parafusicladium Crous, M. Shen & Y. Zhang ter

Based on a multigene phylogenetic analysis, Shen et al. (2020) introduced the genus *Parafusicladium* with three new combinations in *Sympoventuriaceae*. Currently, the genus comprises three species viz. *P. amoenum* (R.F. Castañeda & Dugan) Crous, M. Shen & Y. Zhang ter (the type species), *P. intermedium* (Crous & W.B. Kendr.) Crous, M. Shen & Y. Zhang ter and *P. paraamoenum* (Crous, Jacq. Edwards & P.W.J. Taylor) Crous, M. Shen & Y. Zhang ter (Shen et al. 2020).

Parathyridariella Prigione, A. Poli, E. Bovio & Varese

Poli et al. (2020) introduced the genus *Parathyridariella*, typified by the new species *P. dematiacea* Prigione, A. Poli, E. Bovio & Varese within *Thyridariaceae*. This genus is characterized by septate, hyaline to lightly pigmented hyphae; numerous, mostly in chain, intercalary or solitary, globose to subglobose, from brownish to dark brown chlamydospores (Poli et al. 2020).

Parvomorbus Wen Wang & S.F. Chen

Studies on the pathogenic fungal family *Cryphonectriaceae* in the southern China on different members of higher plants of the order *Myrtales* has resulted in the discovery of eight species of four genera and a novel genus *Parvomorbus* with two novel species. The novelty has been supported by DNA sequences of the partial LSU, ITS, two regions of the β-tubulin (*tub2/tub1*) gene, and *tef1* gene region (Wang et al. 2020).

Patellariopsidaceae Karun., Camporesi & K.D. Hyde

A new family under the polyphyletic *Ascomycetes* order *Helotiales* has been described from Italy on the basis of morphology and molecular phylogeny. The novel family is represented with an asexual morph of *Patellariopsis atrovinosa* (A. Bloxam ex Curr.) Dennis while a new record of *Cheirospora botryospora* (Mont.) Berk. & Broome (*Vibrisseaceae*) on *Fagus sylvatica* L. (*Fagaceae*) has also been reported. Phylogenetic analyses based on a combined sequence dataset of LSU and ITS were used to infer the phylogenetic relationships within the *Helotiales* and thus confirmed its identity (Karunarathna et al. 2020)

Penicillaginaceae Houbraken, Frisvad & Samson

An updated review of the generic, subgeneric, sectional classification of the order *Eurotiales* have resulted in the description of new family *Penicillaginaceae* and few genera, mainly based upon the sequence-based studies using GenBank accession numbers of ITS, *benA*, *cal1* and *rpb2* gene sequences. In total, the order *Eurotiales* under *Ascomycetes* comprise of five accepted families, 28 genera and 1187 species (Houbraken et al. 2020).

Petchia Thanakitp., Mongkols. & Luangsa-ard

Two new fungal genera, *Neotorrubiella* and *Pechia*, on insects has been described in the *Hypocreales* from Thailand. A multi-locus molecular phylogenetic analysis involved SSU, LSU, *tef1*, *rpb1*, and *rpb2* together with the nuclear intergenic region (IGR) for 67 sequences. *Neotorrubiella* resembles *Torrubiella* Boud. in the absence of a stipe and can be distinguished by the production of whole ascospores, which are not commonly found in *Torrubiella* (Thanakitpipattana et al. 2020).

Pinaceicola Crous, M. Shen & Y. Zhang ter

Based on a multigene phylogenetic analysis, Shen et al. (2020) proposed the genus *Pinaceicola* with two new combinations in *Sympoventuriaceae*. Currently, the genus comprises two species viz. *P. pini* (Crous & de Hoog) Crous, M. Shen & Y. Zhang ter (the type species) and *P. cordae* (Koukol) Crous, M. Shen & Y. Zhang ter (Shen et al. 2020).

Pisutiella S.Y. Kondr., Lokös & Farkas

The phylogenetic analysis of the *Teloschistaceae* based on ITS, LSU and mtSSU sequences supported recognition new genus, *Pisutiella*, to accommodate six species of the *Caloplaca conversa* (Kremp.) Jatta group (Kondratyuk et al. 2020). The genus *Pisutiella* is positioned as a strong branch between *Rufoplaca* Arup, Søchting & Frödén and *Usnochroma* Søchting, Arup & Frödén.

Protographum Le Renard, Upchurch, Stockey & Berbee

The fossil fungus *Protographum* was described by Le Renard et al. (2020) from cuticle of unidentified conifer. *P. luttrellii* Le Renard, Upchurch, Stockey & Berbee is distinguished from other fossil taxa by pseudomonopodial dichotomous branching in a scutellum initiated by multiple generator hyphae (Le Renard et al. 2020).

Pruniphilomyces Crous & Bulgakov

Crous et al. (2020b) introduced this monotypic genus *Pruniphilomyces* to accommodate the plant pathogenic fungus *P. circumscissus* (Sacc.) Crous & Bulgakov collected from living leaves of *Prunus cerasus* L. in Russia.

Pseudobactrodesmium H. Zhang, W. Dong & K.D. Hyde

A couple of new species resembling *Bactrodesmium longisporum* M.B. Ellis were collected from the Greater Mekong Subregion and is described under new genus *Pseudobactrodesmium*. They have fasciculate conidiophores, enteroblastic conidiogenous cells and subulate to fusiform, phragmoseptate conidia with a tapering apical cell and sheath. On the basis of analyses of LSU, SSU, ITS and *rpb2* sequence data, the novel genus is placed under the family *Dactylosporaceae* (*Eurotiomycetes*) (Dong et al. 2020).

Pseudohamigera Houbraken, Frisvad & Samson

An updated review of the generic, subgeneric, sectional classification of the order *Eurotiales* have resulted in the description of new family *Penicillaginaceae* and few genera, mainly based upon the sequence-based studies using GenBank accession numbers of ITS, *benA*, *cal1* and *rpb2* gene sequences. In total, the order *Eurotiales* under *Ascomycetes* comprise of five accepted families, 28 genera and 1187 species (Houbraken et al. 2020).

Pseudosterigmatospora Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Purpureomyces Luangsa-ard, Samson & Thanakitp.

A phylogenetic framework is reconstructed for the *Clavicipitaceae* focusing on *Metarhizium* Sorokin through increased taxon-sampling using five genomic loci (SSU, LSU, *tef1*, *rpb1*, *rpb2*) and the barcode marker ITS rRNA resulted in describing six new genera of monophyletic clades subtending the core *Metarhizum* clade, 19 new species and several novel combinations (Mongkolsamrit et al. 2020).

Rhagadodidymellopsis Fern.-Brime, Gaya, Llimona & Nav.-Ros.

The lichenicolous fungus *Rhagadodidymellopsis* growing on the thallus of the terricolous lichen *Endocarpon pusillum* Hedw. was introduced by Fernández-Brime et al. (2020) with *R. endocarpi* Fern.-Brime, Gaya, Llimona & Nav.-Ros. as the type species. *R. endocarpi* is characterized by its almost completely superficial stromatic ascomata with a coarse and irregular surface, and an ascomatal wall of very irregular thickness, and ascospores smaller than those of *Didymellopsis perigena* (Nyl.) Grube & Hafellner (Fernández-Brime et al. 2020).

Robertozyma Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Rosettozyma Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Sajamaea Flakus, Piatek & Rodr. Flakus

The mycoparasitic fungus *Sajamaea* was proposed by Piatek et al. (2020) with *S. mycophila* Flakus, Piątek & Rodr. Flakus as the type species within *Dictyosporiaceae* based on molecular and morphological characters.

Serusiauxia Ertz & Diederich

The genus accommodates a single species, *S. inexpectata* Ertz & Diederich, found on Mauritius. Maximum likelihood and Bayesian inference analyses based on the four mtSSU sequences put the fungus in a clade including *Lithothelium septemseptatum* (R.C. Harris) Aptroot, the genus *Anthracothecium* Hampe ex A. Massal. and several species of *Pyrenula* Ach. (including type species, *P. nitida* Weigel) Ach. Based on the unique morphological and chemical characters, namely a sorediate thallus and producing the gyrophoric acid, the genus *Serusiauxia* was proposed by Diederich & Ertz (2020).

Serusiauxiella S.H. Jiang, Lücking & J.C. Wei

The genus *Serusiauxiella* was introduced by Jiang et al. (2020) to accommodate three species, all new to science and known from (sub-)tropical Asia. Maximum likelihood analysis based on four markers (SSU, LSU, *tef1*, and *rpb2*) revealed a well-supported novel lineage within *Strigula sens. lat.* for which the name *Serusiauxiella* was proposed. From *Strigula* sens. str. the genus differs in the *Trentepohlia* Mart. photobiont and the extremely long macroconidial appendages.

Siphulopsis Kantvilas & A.R. Nilsen

Maximum likelihood analyses based on combined ITS and LSU sequences indicated that *Icmadophila* is not monophyletic. The new genus *Siphulopsis* was introduced to comprise a single rare Australian species, *S. queenslandica* (Kantvilas) Kantvilas & A.R. Nilsen, which had previously been placed in *Knightiella* Müll. Arg. Morphologically it resembles a species of *Siphula* Fr. but differs by lacking the basal rhizines characteristic of the genus (Ludwig et al. 2020).

Sterigmatospora Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Sterila Crous, M. Shen & Y. Zhang ter

Shen et al. (2020) introduced this new genus in the family of *Sympoventuriaceae* (*Venturiales*), to accommodate *S. eucalypti* Crous, M. Shen & Y. Zhang ter collected from leaves of a *Eucalyptus* sp. based on the multigene phylogenetic analysis, morphological and ecological characteristics.

Sungia Luangsa-ard, Samson & Thanakitp.

A phylogenetic framework is reconstructed for the *Clavicipitaceae* focusing on *Metarhizium* Sorokin through increased taxon-sampling using five genomic loci (SSU, LSU, *tef1*, *rpb1*, *rpb2*) and the barcode marker ITS rRNA resulted in describing six new genera of monophyletic clades subtending the core *Metarhizum* clade, 19 new species and several novel combinations (Mongkolsamrit et al. 2020).

Synnematotriadelphia Chuaseehar., Somrith., Nuankaew & Boonyuen

Based on the molecular phylogenetic analyses of nuclear ribosomal DNA and partial sequence of *rpb2*, the species of *Triadelphia* Shearer & J.L. Crane bifurcated into two monophyletic clades having the type species along with different others, *viz*., *T. heterospora* Shearer & J.L. Crane*, T. diversa* Tzean & J.L. Chen*, T. loudetiae* Maggi, Bartoli & Rambelli*, T. hexaformisspora* Chuaseehar., Somrith. & Boonyuen, and *T. romanica* Constant. & Samson while the other clade comprised of *T. moubasheri* Abdel-Sater & Soliman*, T. pulvinata* Maggi, Bartoli & Rambelli, and *T. disseminata* Madrid & Edathodu leaving the other two species, *Triadelphia stilboidea* Mercado & R.F. Castañeda and *T. synnematofera* Matsush. in a separate clade for which the authors assigned them under the proposed novel genus (Chuaseeharonnachai et al. 2020).

Teunia Q.M. Wang & F.Y. Bai

On the basis of multi-locus phylogenetic analyses combined with the clustering optimisation analysis revealed that there has been tremendous diversity of the Basidiomycetous yeasts in the Chinese soils. An exhaustive list of 107 new species have also been described including newly proposed two orders, three families and eight new genera and three combinations. The phylogenetic studies involved analyses of D1/D2 domain of LSU, SSU, ITS, and protein-coding genes (*rpb1*, *rpb2*, *tef1*, and *cytB*), and physiological comparisons (Li et al. 2020).

Trichophoma Magaña-Dueñas, Cano & Stchigel

Trichophoma was proposed by Crous et al. (2020a) with *T. cylindrospora* Magaña-Dueñas, Cano & Stchigel as the type species. Based on the phylogenetic analysis of the ITS, LSU and *tef1* combined dataset, the closest relative of *T. cylindrospora* is *Forliomyces uniseptata* Phukhams., Camporesi & K.D. Hyde. *F. uniseptata* differs from *T. cylindrospora* in producing shorter and broader conidia (10–15 × 5–8 µm vs 18–20 × 2–3 µm), which are brown-coloured when mature (hyaline in *T. cylindrospora*) (Phukhamsakda et al. 2016).

Triseptata Boonmee & Phookamsak

Boonmee et al. (2020) introduced this new genus in the family *Latoruaceae* based upon the morphological and phylogenetic evidences. This new genus is characterized by immersed, uni- to multi-loculate ascomata, filamentous pseudoparaphyses, bitunicate, fissitunicate, cylindrical-clavate asci and 3-septate, light brown spores, with asymmetrical ends, in its sexual form. The LSU, ITS and SSU showed that *Triseptata* has distinct lineage than other genera of the family.

Tylocliostomum van den Boom & Magain

The Bayesian analysis of ITS, mtSSU and *rpb1* sequences confirmed the genus *Bacidina* Vězda to be paraphyletic (see Kistenich et al. 2018) and the new genus *Tylocliostomum* was introduced by van den Boom & Magain (2020) to accommodate a single species, *T. viridifarinosum* van den Boom & Magain. Within the *Ramalinaceae*, *Tylocliostomum* forms a well-supported group with *Tylothallia biformigera* (Leight.) P. James & H. Kilias and two accessions of *Cliostomum haematommatis* (Keissl.) D. Hawksw., Earl.-Benn. & Coppins, which most probably do not represent *Cliostomum* sens. str. as it was assumed by authors.

Vandijckomycella Hern.-Restr., L.W. Hou, L. Cai & Crous

Hou et al. (2020) introduced the genus *Vandijckomycella* to accommodate two new species isolated from soil samples within *Didymellaceae* based on morphological and molecular data. *V. joseae* Hern.-Restr., L.W. Hou, L. Cai & Crous is characterized by producing pycnidia with longer whitish hyphal outgrowths, and with elongated necks.

Vesiculozygosporium Crous

A total of seven new genera, 26 new species, 10 new combinations have been described from different parts of the world by Crous et al. (2020b) providing genera and species descriptions. All of these genera have been recorded on *Phillyrea latifolia* L.*,* *Lonicera tatarica* L., *Tilia* sp., *Pinus sylvestris* L., *Caragana arborescens* Lam., *Prunus cerasus* L., *Muntingia calabura* L. respectively. The morphological studies were supported by molecular phylogeny analysis using the LSU and ITS (Crous et al. 2020b).

Wetmoreana Arup, Søchting & Frödén

The genera *Fulgogasparrea* S.Y. Kondr., N.-H. Jeong, Kärnefelt, Elix, A. Thell & Hur and *Wetmoreana* Arup, Søchting & Frödén were introduced in 2013 by Kondratyuk et al. (2013) and Arup et al. (2013), respectively, for the *Caloplaca decipioides* group. The latter genus was accepted by Wijayawardene et al. (2020) while the former was considered to be a synonym. However, Mishra et al. (2020) accepted both *Fulgogasparrea* and *Wetmoreana* revealing genetical distance based on ITS sequences as well as morphological differences.

Yosiokobayasia Samson, Luangsa-ard & Thanakitp.

A phylogenetic framework is reconstructed for the *Clavicipitaceae* focusing on *Metarhizium* Sorokin through increased taxon-sampling using five genomic loci (SSU, LSU, *tef1*, *rpb1*, *rpb2*) and the barcode marker ITS rRNA resulted in describing six new genera of monophyletic clades subtending the core *Metarhizum* clade, 19 new species and several novel combinations (Mongkolsamrit et al. 2020).

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