Corrections to recent changes in the taxonomy of the Sordariales

Yasmina Marin-Felix1,2,Andrew N. Miller3

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Abstract
The classification of taxa belonging to the Sordariales has been problematic over the years. With the beginning of the DNA era, ascospore morphology, which was the main criterion for the delimitation of taxa in the Sordariales, was demonstrated to not be useful for inferring taxonomic relationships especially at the genus level. In the past decades, the combination of both morphological and molecular data allowed the reclassification of these taxa. Recently, a study of some often overlooked Diaporthomycetidae and Sordariomycetidae included a new taxonomic classification for members of the Sordariales, many of which were based on nomenclatural errors or which lacked sufficient data to support their hypotheses. The authors did not contribute any new DNA sequences, but instead relied on datasets generated by previous authors in their published phylogenetic studies. Surprisingly, different results were obtained contradicting these previous studies and, in an act of taxonomic vandalism, five new families were introduced without performing further molecular analyses to verify the incongruencies with these previous studies. Three of these new families, which we consider doubtful, are Bombardiaceae, Lasiosphaeridaceae and Zygospermellaceae. The family Strattoniaceae is here considered superfluous since it was introduced to accommodate only a single genus and delimited based on a species that is not the type species of Strattonia. The Neoschizotheciaceae was erected based on the new genus Neoschizothecium, which was introduced to accommodate members of Schizothecium since Huang et al. (2021) considered Schizothecium as a synonym of Podospora after misinterpreting their type species as the same. However, Schizothecium and Podospora have been two independent genera based on two different type species for half a century, making Neoschizothecium and Neoschizotheciaceae superfluous. Moreover, they proposed 32 new combinations, 16 of which are now superfluous or doubtful. Most of these taxonomic errors could have been avoided if a proper literature review had been performed. Two examples are the new superfluous combinations of Triangularia tarvisina and Cladorrhinum olerum, because the former is considered conspecific with Triangularia setosa, and the latter conspecific with Cladorrhinum foerundissimum, the anamorph of Arnium olerum. The focus of the current review is to provide a scientifically responsible alternative to the erroneous novelties proposed at the family, genus and species level in the recent classification of Sordariales.

Keywords Fungal classification · Integrative taxonomy · Podospora · Schizothecium · Sordariales · Sordariomycetes

Introduction
The order Sordariales is one of the most diverse groups in the Sordariomycetes and the classification of their members based solely on morphology has been problematic (Hawksworth and Eriksson 1986; Miller and Huhndorf 2004a, 2005; Huhndorf et al. 2004; Kruys et al. 2015). The taxonomic classification of taxa belonging to this order was traditionally based on ascospore morphology; however, Miller and Huhndorf (2005) demonstrated that this character is extremely homoplastic and not useful for inferring taxonomic relationships. Instead, the ascomatal wall morphology appears to be more phylogenetically informative, even though it has its limitation since not all taxa exhibit distinctive features in their ascomatal walls, and/or similar ascomatal wall characteristics are found in different monophyletic lineages.

For nearly two decades, extensive molecular studies have been combined with morphological data to delimit sordarialean taxa at the family, genus and species level (Miller and Huhndorf 2004a; Cai et al. 2005; Kruys et al. 2015; Wang...
et al. 2019a; Marin-Felix et al. 2020). Historically, the Sordariales has contained 7 to 14 families, depending on the authors’ concepts (Hawksworth and Eriksson 1986; Eriksson et al. 2001). Huhndorf et al. (2004) restricted the order to 3 families, i.e. Chaetomiaceae, Lasiosphaeriaceae and Sordariaceae, the first two of which were considered polyphyletic based on molecular data. The Chaetomiaceae has been extensively studied in recent years based on a polyphasic approach combining morphological and molecular data, resulting in its delimitation as a monophyletic lineage (Wang et al. 2019a, b). However, the polyphly of Lasiosphaeriaceae, which was the largest family of the order, remained problematic until it was recently partly resolved (Marin-Felix et al. 2020). Kruys et al. (2015) demonstrated the separation of the family into four different clades. Subsequently, Wang et al. (2019a) introduced the new family Podosporaceae to accommodate taxa belonging to clade IV in Kruys et al. (2015). Marin-Felix et al. (2020) delimited Lasiosphaeriaceae to clade III, which contained the type genus Lasiosphaeria. Moreover, the new families Diplogelasinosporaceae, Naviculisporaceae and Schizotheciaceae were introduced to accommodate three monophyletic lineages containing taxa resembling those in the Lasiosphaeriaceae. Once again, the morphological characters used to delimit these families turned out to be homoplastic and appeared independently in multiple lineages. Other lasiosphaeriaceous taxa were nested in an unsupported lineage (Lasiosphaeriaceae s. lat. I, Fig. 1), and therefore a new family was not introduced for this clade. Finally, another monophyletic lineage with two genera was shown as an unsupported sister group to Schizotheciaceae (Lasiosphaeriaceae s. lat. II, Fig. 1). However, a new family was not introduced until further studies including additional taxa and molecular data could be performed. Figure 1 shows the phylogenetic tree obtained from the study performed by Marin-Felix et al. (2020).

The genera belonging to this order have also been taxonomically challenging to delineate over the years. For example, the genera Gelasinospora and Neurospora, both in the Sordariaceae, were established based on different patterns of ascospore ornamentation. Garcia et al. (2004) demonstrated that this character was not phylogenetically informative and synonymized Gelasinospora under Neurospora. This observation agreed with Miller and Huhndorf (2005), who found that ascospore morphology was a homoplastic character throughout the order. The largest genera in the Chaetomiaceae have also been recently refined, i.e. Chaetomium, Humicola and Thielavia, resulting in the introduction of 17 new genera and more than 70 new combinations to accommodate taxa not included in the molecular-based monophyletic lineages of these recircumscribed genera (Wang et al. 2016a, 2019a, b). Genera traditionally placed in Lasiosphaeriaceae are currently being studied. For example, Wang et al. (2019a) delimited Cladorrhinum, Podospora and Triangularia, whereas Marin-Felix et al. (2020) established 5 new genera, i.e. Areotheca, Lundqvistomyces, Pseudoechria, Pseudoschizothecium and Rhypophila. These taxonomic changes were done to accommodate taxa previously placed in Cercophora, Podospora and Triangularia based on morphology, but that no longer occurred in the more narrowly defined, DNA-based monophyletic lineages representing these genera.

Recently, Huang et al. (2021) performed a phylogenetic study based on ITS, LSU, RPB2 and TUB2 sequences already available in GenBank, without generating a single new sequence. As a result, they introduced 5 new families, 1 new genus and 32 new combinations in the order Sordariales. However, most of these taxonomic novelties are based on errors of interpretation or lack sufficient data for their creation (Table 1). In order to compare the contradictory results between the phylogenetic study of Huang et al. (2021) and previous studies (Kruys et al. 2015; Marin-Felix et al. 2020), we tried to reanalyze the original molecular alignments generated by Huang et al. (2021). However, these alignments are not available in TreeBase even though they stated in their publication that final alignments and trees were deposited in TreeBase. Therefore, we had to download all sequences from GenBank to perform a phylogenetic analysis that included all sequences previously used in Marin-Felix et al. (2020) and Huang et al. (2021).

Fig. 1 Schematic RAxML phylogram based on ITS, LSU, RPB2 and TUB2 sequences obtained in the phylogenetic study performed by Marin-Felix et al. (2020) (adapted from Charria-Girón et al. 2022)
No sequences in *Chaetomiaceae* were included since no novelties were proposed in this family (Table 2). The maximum likelihood (ML) and Bayesian inference (BI) analyses including the four loci were performed as described by Harms et al. (2021). The lengths of the individual alignments used in the combined dataset were 556 bp (ITS), 916 bp (LSU), 978 bp (*RPB2*) and 618 bp (*TUB2*), and the final combined alignment was 3068 bp. A poorly aligned ambiguous region was manually deleted from the ITS1 region. Figure 2 shows the most likely tree obtained from the RAxML analysis of the combined dataset generated in our study. It is identical in the topology of the 95% majority-rule consensus tree generated by the Bayesian analysis. It is unfortunate that Huang et al. (2021) did not indicate the GenBank accession numbers of the sequences they used to produce their trees, making it very difficult for...
the scientific community to reproduce their results. It should have been mandatory to indicate which sequences were incorporated in their phylogenetic study, as well as to cite the underlying papers giving proper attribution to the authors that generated those data, as recommended in Aime et al. (2020), a recent ICTF-sponsored paper on best practices in taxonomy. Surprisingly, the second author of Huang et al. (2021) is also a co-author of the Aime et al. (2020) paper, yet he does not follow his own recommendation.

New families superfluously introduced or without sufficient evidence

The family Schizotheciaceae was recently introduced by Marin-Felix et al. (2020) to accommodate lasiosphaeraceous taxa occurring in a well-supported monophyletic lineage phylogenetically distant from both the Podosporaceae and the clade containing the type genus Lasiosphaeria. However, Huang et al. (2021) erroneously changed its name to Neoschizotheciaceae based on taxonomic errors by Wang et al. (2019a). Both papers incorrectly assumed that the genera Schizothecium and Podospora shared the same type species, and thus, should be synonymized. Therefore, the new genus Neoschizothecium was introduced with N. curvisporum as its type species to accommodate species of Schizothecium outside the Podosporaceae. Huang et al. (2021) designated Neoschizothecium as type genus of their new family Neoschizotheciaceae.

The complex nomenclatural histories surrounding the type species of Podospora and Schizothecium have been discussed in detail (Lundqvist 1972; Ament-Velásquez et al. 2020; Vogan et al. 2021). Briefly, two distinct type specimens representing two distinct type species exist for each genus: the conserved non-originale type specimen of Podospora fimiseda (Ces. & De Not.) Niessl. (in Hedwigia 22: 156. Oct 1883) and the lectotype illustration of Schizothecium fimicola Corda (in Icon. Fung. 2: 29, tab. 13, fig. 105, Jul 1838). This segregation, which was based on morphological data and discussed by Lundqvist (1972), was later supported by molecular data (Cai et al. 2005). Wang et al. (2019a) overlooked the conserved type of Podospora (i.e. Sordaria fimicola Ces. & De Not.) and incorrectly cited S. fimicola Corda as type species. To further complicate matters, Wang et al. (2019a) designated an epitype specimen (CBS H-24048) for S. fimicola that was induced to produce fertile ascomata in culture (CBS 482.64), but this epitype represents P. fimiseda, not S. fimicola! We have examined the ex-epitype culture (CBS 482.64) and could not reproduce the fruiting of ascomata in culture. The epitype specimen was also examined, but no ascomata were found to study their morphology in detail, despite images of mature ascomata fruiting in culture provided in Wang et al. (2019a).

According to the pictures of the epitype shown by Wang et al. (2019a), this specimen produces hyphal-like ascomatal hairs surrounding the entire ascoma, which match P. fimiseda (Miller 2003). Schizothecium fimicola has swollen agglutinatet ascomatal hairs only in the upper part of the ascomata. Thus, the type species of Schizothecium should be conserved as S. fimicola (typ. cons. pending). The ascomal wall of CBS 482.64 needs to be studied to verify that it is pseudo-bombardioid and matches the description of P. fimiseda (Miller 2003) and, therefore, it is a suitable epitype for this later species. If the conservation proposal to change the type species of Podospora from P. fimiseda to P. anserina (Vogan et al. 2021) is accepted, this would also bring additional resolution to the complicated and often confused nomenclatural history of these two genera. Since Podospora and Schizothecium are clearly not synonyms as Wang et al. (2019a) and Huang et al. (2021) believed, there was no reason to create a new family (i.e. Neoschizotheciaceae) for Schizotheciaceae. Thus, Neoschizotheciaceae is nomenclaturally illegitimate (Art. 14.3, Shenzhen Code) and a superfluous synonym of Schizotheciaceae.

It is worthwhile to mention that one should always attempt to make decisions that lead to as few taxonomic name changes and reduce the possibility of publishing taxonomically superfluous names, as recommended in the recent guidelines for publishing new fungal species or names, version 3.0 (Aime et al. 2020). This is especially important in this group of fungi, in which many names are not represented by DNA sequences of type material and many new combinations are possible. Therefore, the proposal to introduce a new genus with numerous subsequent new combinations for an established lineage should have never been accepted and was easily avoidable if a review of the literature was performed.

The new family Strattoniaceae was erected to accommodate the genus Strattonia. Surprisingly, the genus was redefined without the study of any material of the type species (St. tetraspora), but based only on the already available sequences of the type strain of another species, St. oblecythiformis. The redefinition was made only on morphological characters even though it has already been clearly demonstrated that taxonomists must be careful proposing any taxonomic reclassification of members of the Sordariales and that a polyphasic approach based on both morphological and molecular data is required (Miller and Huhndorf 2004a; Kruys et al. 2015; Marin-Felix et al. 2020). It is of note that no cultures of St. tetraspora are available in any recognized culture collection. Therefore, it is of utmost importance to recollect this species and include it in phylogenetic analyses to confirm the monophyly of Strattonia. Huang et al. (2021) argued that the characteristics of Strattonia should be reduced to those species producing ascospores with an upper cell surrounded by a gelatinous sheath. On the other hand, taxa that have no sheath have been demonstrated to belong to different genera, i.e. Jugulospora.
| Taxa                                      | Strain          | GenBank accession #  | References                                      |
|-------------------------------------------|-----------------|----------------------|------------------------------------------------|
| **Amesia atrobrunnea**                    | CBS 379.66<sup>T</sup> | MH870470 MH858833 KX976798 | Wang et al. (2016a), Vu et al. (2019)          |
| **Anopodium amphilacum**                  | MIR 40/07       | KF557662 - - KF557701 | Kruys et al. (2015)                            |
| **Apiosordaria microcarpa**               | CBS 692.82<sup>T</sup> | MK926841 MK926841 MK876803 | Wang et al. (2019a)                           |
| **Apodospora gutlandica**                 | E00204952       | KF557664 - - KF557703 | Kruys et al. (2015)                           |
| **Apodospora peruviana**                  | CBS 118394      | KF557665 EU573703 - - | Kruys et al. (2015), Debuchy et al. (unpubl. data) |
| **Apodospora simulans**                   | Kruys 701       | KF557666 - - KF557704 | Kruys et al. (2015)                           |
| **Apodus deciduus**                       | CBS 506.70<sup>T</sup> | AY681165 AY681199 | Cai et al. (2006)                             |
| **Apodus oryzae**                         | CBS 376.74      | AY681166 - - -       | Cai et al. (2006)                             |
| **Areotheca areolata**                    | UAMH 7495       | AY587936 AY587911 AY600275 AY600252 | Miller and Huhndorf (2004b)                  |
| **Arnium caballinum**                     | Lundqvist 7098-e | KF557672 - - -       | - Kruys et al. (2015)                         |
| **Arnium cirriferum**                     | CBS 120041      | KF557673 - - KF557709 | Kruys et al. (2015)                           |
| **Arnium japonense**                      | SANK 10273      | KF557680 - - KF557713 | Kruys et al. (2015)                           |
| **Arnium mendax**                         | Lundqvist 20874-c E00122117 | KF557688 - - KF557717 | Kruys et al. (2015)                           |
| **Bellojisia rhynchostoma**               | CBS 118484      | EU999217 - - -       | Réblová (2008)                                |
| **Bombardia bombarda**                    | AR1903 CBS 3391 | AY780052 - - AY780152 | Miller and Huhndorf (2005)                     |
| **Boothiella tetraspora**                 | CBS 334.67<sup>T</sup> | AY780057 - - AY780167 | Wang et al. (2019), Wang et al. (2019a)       |
| **Camarops amorpha**                      | SMH 4821        | AY780053 - - AY780156 | Miller and Huhndorf (2005), Miller and Huhndorf (2005) |
| **Cercophora appalachianensis**           | HKUCC 3711      | AF132328 AF177155 - - | Ranghoo et al. (unpubl. data)                 |
| **Cercophora aquatica**                   | JF 06314<sup>T</sup> | JN673036 KX179147 - - | Raja et al. (2011)                            |
| **Cercophora mirabilis**                  | CBS 120402      | KP981429 TP784128 KP981611 KP981556 | Marin-Felix et al. (2020)                 |
| **Cercophora newfieldiana**               | SMH 3303        | AY780062 - - AY780167 | Miller and Huhndorf (2005)                     |
| **Cercophora scortea**                    | JF 00229        | AY87936 - - AY87912  | Vu et al. (2019), Wang et al. (2019a)          |
| **Cercophora sulphurella**                | SMH 2531        | AY87938 AY87913 AY600276 AY600254 | Miller and Huhndorf (2004b)                  |
| **Chaeotium globosum**                    | CBS 160.62<sup>T</sup> | MH869713 KT214565 KT214666 | Vu et al. (2019), Wang et al. (2016b)          |
| **Cladorrhinum brunnescens**              | CBS 643.75A<sup>T</sup> | FR692346 FM955446 - - | Madrid et al. (2010, 2011)                     |
| **Cladorrhinum coprophilum**              | SMH 3794        | AY780058 - - AY870162 | Miller and Huhndorf (2005)                     |
| **Cladorrhinum foecundissimum**           | CBS 180.66<sup>T</sup> | MK926856 MK926856 MK876818 | Wang et al. (2019a)                          |
| **Cladorrhinum olerum**                   | CBS 120012      | KF557689 - - KF557718 | Kruys et al. (2015)                           |
| **Cladorrhinum globosporum**              | CBS 120013      | MT731524 GQ925544 MT731556 MT173156 | Geydan et al. (2012), Ament-Velásquez et al. (2020) |
| **Cladorrhinum hyalocarpum**              | SMH 322.70<sup>T</sup> | MK926857 MK926857 MK876819 | Wang et al. (2019a)                          |
| **Cladorrhinum hyalocarpum**              | FMR 13412       | KP981428 MT784129 KP981610 KP981555 | Marin-Felix et al. (2020)                  |
| **Cladorrhinum intermedium**              | CBS 433.96<sup>T</sup> | MK926859 MK926859 MK876821 | Wang et al. (2019a)                          |
| **Cladorrhinum leucotrichum**             | CBS 463.61      | MH869684 MH858107 - - | Vu et al. (2019)                              |
| **Cladorrhinum terricolum**               | ATCC 200395     | AY780067 - - AY870170 | Miller and Huhndorf (2005)                     |
| **Cladorrhinum tomentosum**               | Francoise Candoussau KF557691 | - - KF557720 | Kruys et al. (2015)                           |
| **Corynascus sepedonium**                 | CBS 111.69<sup>T</sup> | MH871003 MH859271 FJ666394 | Vu et al. (2019), Greif et al. (2009)         |
| **Dichomopilus fucicola**                 | CBS 159.52<sup>T</sup> | MH868497 MH856976 KX976856 | Wang et al. (2016a), Vu et al. (2019)          |
| **Diplogelasinospora grovesii**           | CBS 340.73<sup>T</sup> | MH872401 MH860693 - - | Vu et al. (2019)                              |
| **Diplogelasinospora inaequalis**         | CBS 436.74<sup>T</sup> | AY681167 AY681201 - - | Cai et al. (2006)                             |
| Taxa                        | Strain                | GenBank accession #         | References                                      |
|-----------------------------|-----------------------|----------------------------|-------------------------------------------------|
| **Diplogelasinospora moalen**sis** | CBS 136018T          | KP981430 HG514152          | Crous et al. (2014), Marin-Felix et al. (2020)  |
| **Diplogelasinospora princeps** | FMR 154414           | KP981431 MT784131          | Marin-Felix et al. (2020)                       |
| **Echria gigantospora**      | F77-1                 | KP557574                   | Kruys et al. (2015)                             |
| **Echria macrothec**         | Lundqvist 2311        | KP557664                   | Kruys et al. (2015)                             |
| **Episternus onthophagi**    | KRAM 585223T          | KP903375 KP903374          | Görz and Boroń (2018)                           |
| **Fimetariella rubra**       | Lundqvist 20410-e     | KP557694                   | Kruys et al. (2015)                             |
| **Immersiella caudata**      | SMH 3298              | AY436407 - AY780161        | Miller and Huhndorf (2004a, 2005)               |
| **Immersiella hirta**        | E00204950             | KP557675 - KF557711        | Kruys et al. (2015)                             |
| **Immersiella hirta**        | E00204847             | KP557676 - KF557712        | Kruys et al. (2015)                             |
| **Jugulospora antarctica**   | CBS 380.86 (type of  | MH873659 MH861966          | Vu et al. (2019)                                |
| **Jugulospora vestita**      | CBS 135.91T           | MT785872 MT784135 MT783824 MT783825 | Marin-Felix et al. (2020) |
| **Lasioglossa glabrata**     | TL 4529               | AY436410 AY587914 AY600277 AY600255 | Miller and Huhndorf (2004a, 2004b) |
| **Lasioglossa lanuginosa**   | SMH 3819              | AY436412 AY587921 AY600283 AY600262 | Miller and Huhndorf (2004a, 2004b) |
| **Lasioglossa miniovina**    | SMH 2392T             | MH700179                   | Crous et al. (2018)                             |
| **Lasioglossa ovina**        | SMH 1538              | AY436414 AY587926 AY600287 AF66046 | Fernández et al. (1999, 2006), Miller and Huhndorf (2004b) |
| **Lasiosphaeria rugulosa**   | CBS 126299            | MH875422 MH863967          | Vu et al. (2019)                                |
| **Lasiosphaeria similisor**  | SMH 1518              | AY436414 AY587933 AY600294 AY600272 | Miller and Huhndorf (2004a, 2004b) |
| **Lasiosphaeria sorb**       | CBS 885.85            | AY436416 AY587935 AY600296 AY600274 | Miller and Huhndorf (2004a, 2004b) |
| **Lasiosphaeria arenicola**  | ANM 1080              | JN673037 JN673037          | Raja et al. (2011)                              |
| **Lasiosphaeria hispida**    | SMH 1543              | AY436417 - AY780179        | Miller and Huhndorf (2004a, 2004, 2005)         |
| **Lasiosphaeria hispida**    | JS 0218               | AY436418 - AY780180        | Miller and Huhndorf (2004a, 2004, 2005)         |
| **Lasiosphaeria hispida**    | CBS 955.72            | MH872327 AY681203          | Cai et al. (2006), Vu et al. (2019)             |
| **Lundqvistomyces karachiensis** | CBS 657.74         | KP918447 MK266850 KP918360 KP918147 | Wang et al. (2019a), Marin-Felix et al. (2020) |
| **Lundqvistomyces tanzaniensis** | TRTC 51981            | KP780081 MH682260 AY780197 AY780143 | Miller and Huhndorf (2005), Vu et al. (2019) |
| **Mammaria echinochory**     | CBS 277.63            | MH869889 MH858283          | Vu et al. (2019)                                |
| **Mammaria echinochory**     | CBS 458.65            | MH870308 MH856868          | Vu et al. (2019)                                |
| **Mischaria vermicul**       | ANM 734              | KX171943 KX171948          | Miller (unpubl. data)                           |
| **Morinagamyces vermicul**   | CBS 303.81T           | KP981427 MT904879 KP981609 KP981554 | Harms et al. (2021)                             |
| **Naviculopsis terrestr**    | CBS 137295T           | KP981439 MT784136 KP981622 KP981567 | Marin-Felix et al. (2020)                       |
| **Neurospora crassa**        | ICMP 6360             | AY681158 AY681193          | Cai et al. (2006)                               |
| **Neurospora hispaniola**    | FGSC 8817T            | FR774257                   | Ngren et al. (2011)                             |
| **Neurospora metzenbergii**  | FGSC 8847             | FR774263                   | Ngren et al. (2011)                             |
| **Neurospora pannoica**      | TRTC 51327            | AY780070 - AY780185        | Miller and Huhndorf (2005)                      |
| **Neurospora sitophila**     | CBS 112.19            | MH866192 MH854676          | Vu et al. (2019)                                |
| **Neurospora tetrasperma**   | CBS 225.38            | MH867446 MH855950          | Vu et al. (2019)                                |
| **Podospora appendiculata**  | CBS 212.97            | AY780071 MH862644 AY780186 AY780129 | Miller and Huhndorf (2005), Vu et al. (2019) |
| **Podospora bulbillosa**     | CBS 304.90T           | MK266861 MK266861 MK876823 | Wang et al. (2019a)                             |
| **Podospora bulu**           | CBS 115576T           | MK874548 DJ66960          | Bell et al. (2016), Vu et al. (2019)            |
| **Podospora communis**       | CBS 118393T           | MH874584 MH863031          | Vu et al. (2019)                                |
| **Podospora costaricensis**  | SMH 4021              | AY780059 - AY780163        | Miller and Huhndorf (2005)                      |
| **Podospora cupiformis**     | CBS 246.71T           | AY999102 AY999125          | Cai et al. (2005)                               |
| Taxa                        | Strain         | LSU accession #       | ITS accession #       | RPB2 accession #       | TUB2 accession #       | References                                      |
|-----------------------------|----------------|-----------------------|-----------------------|------------------------|------------------------|------------------------------------------------|
| *Podospora dacyroidinea*    | INTA-AR 70^T   | KT312976              | KT321062              | -                      | -                      | Carmarán et al. (2015)                          |
| *Podospora didyma*          | CBS 232.78     | AY999100              | AY999127              | -                      | -                      | Cai et al. (2005)                               |
| *Podospora excentrica*      | CBS 118392     | MH874583              | MH863030              | -                      | -                      | Vu et al. (2019)                                |
| *Podospora fabiformis*      | CBS 112043^T   | MK926843              | MK926843              | MK876805               | -                      | Wang et al. (2019a)                             |
| *Podospora fibrinocaudata*  | CBS 315.91^T   | MK926844              | MK926844              | MK876806               | -                      | Wang et al. (2019a)                             |
| *Podospora fimiseda*        | TRTC 48343     | AY780074              | AY780188              | AY780131               | -                      | Miller and Huhndorf (2005)                      |
| *Podospora fimicola*        | CBS 482.64^ET  | KP981440              | MK926862              | KP981623               | KP981568               | Wang et al. (2019a), Marin-Felix et al. (2020) |
| *Podospora flexuosa*        | FMR 10415^T    | FN662477              | FN662474              | -                      | -                      | Madrid et al. (2011)                           |
| *Podospora hamata*          | CGMCC 3.15230^T| KP878304              | KP878306              | -                      | -                      | Vu et al. (2016)                                |
| *Podospora inflata*         | CBS 413.82     | MH873254              | MH861508              | -                      | -                      | Vu et al. (2019)                                |
| *Podospora intestinacea*    | CBS 113106     | AY999104              | AY999121              | -                      | -                      | Cai et al. (2005)                               |
| *Podospora jamaicensis*     | CBS 672.70^T   | MT731527              | MH859895              | MT731556               | MT731534               | Vu et al. (2019), Ament-Velásquez et al. (2020) |
| *Podospora leporina*        | CBS 365.69     | MH871063              | MH859324              | -                      | -                      | Vu et al. (2019)                                |
| *Podospora macrospora*      | CBS 286.86^T   | MT731528              | MH861958              | MT731558               | MT731532               | Vu et al. (2019), Ament-Velásquez et al. (2020) |
| *Podospora minicauca*       | CBS 227.87     | MH873757              | MH862068              | -                      | -                      | Vu et al. (2019)                                |
| *Podospora petrogale*       | CBS 109409^T   | MH874419              | AY071831              | -                      | -                      | Bell (1999), Vu et al. (2019)                   |
| *Podospora prethopodalis*   | CBS 121128     | MH874659              | MH863103              | -                      | -                      | Vu et al. (2019)                                |
| *Podospora sacchari*        | CBS 713.70^T   | KP981425              | MK899105              | KP981607               | KP981552               | Vu et al. (2019), Marin-Felix et al. (2020)     |
| *Podospora serotina*        | CBS 252.71     | MH871878              | MH860102              | -                      | -                      | Vu et al. (2019)                                |
| *Podospora spinosa*         | CBS 265.71^T   | MH877809              | -                      | -                      | -                      | Vu et al. (2019)                                |
| *Podospora striatiptora*    | CBS 154.77^T   | KP981426              | MT784137              | KP981608               | KP981553               | Marin-Felix et al. (2020)                      |
| *Pseudoechria curvicolla*   | IFO 8548       | AY999099              | AY999122              | -                      | -                      | Cai et al. (2005)                               |
| *Pseudoechria decidua*      | CBS 259.69     | MH871036              | MH859302              | -                      | -                      | Vu et al. (2019)                                |
| *Pseudoechria longicollis*  | CBS 365.68^T   | MK926847              | MK926847              | MK876809               | -                      | Wang et al. (2019a)                             |
| *Pseudoechria prolifica*    | CBS 250.71^T   | MK926848              | MK926848              | MK876810               | -                      | Wang et al. (2019a)                             |
| *Pseudoneurospora amorphoporcorata* | CBS 626.80 | FR774287              | -                      | -                      | FR774294               | Nygren et al. (2011)                            |
| *Pseudoneurospora canariensis* | FMR 12156^T | MH877580              | -                      | -                      | HG423208               | Crous et al. (2014), Vu et al. (2019)            |
| *Pseudorhypophila mangenotii* | CBS 419.67T | MK926851              | MK926851              | MK876813               | -                      | Wang et al. (2019a)                             |
| *Pseudorhypophila marina*   | CBS 155.77^T   | MK926851              | MK926853              | MK876815               | -                      | Wang et al. (2019a)                             |
| *Pseudorhypophila pilifera* | CBS 413.73^T   | MK926852              | MK926852              | MK876814               | -                      | Wang et al. (2019a)                             |
| *Pseudoschizothecium atropurpureum* | SMH 2961 | AY999097              | AY999123              | -                      | -                      | Cai et al. (2005)                               |
| *Ramophialophora globispora* | SMH 3073      | AY780057              | AY780160              | AY780100               | -                      | Miller and Huhndorf (2005)                      |
| *Ramophialophora humicola*  | CGMCC 3.17940  | KU746745              | KU746699              | KY883252               | -                      | Zhang et al. (2017, 2018)                        |
| *Ramophialophora petraea*   | FMR 9523^T     | FR692337              | FM955449              | -                      | -                      | Madrid et al. (2010, 2011)                       |
| *Ramophialophora vesiculosa*| CBS 110629^T   | KU746747              | KU746701              | KY883254               | -                      | Zhang et al. (2017, 2018)                        |
| *Rinaldiella pentagonospora*| CBS 132344^T   | MK926452              | MK926866              | -                      | -                      | Vu et al. (2019)                                |
| *Rhypophila cochleariformis*| CBS 249.71     | AY999098              | AY999123              | -                      | -                      | Cai et al. (2005)                               |
| *Rhypophila decipiens*      | CBS 258.69     | AY780073              | KX171946              | AY780187               | AY780130               | Miller and Huhndorf (2005), Miller (unpubl. data) |
| *Rhypophila myriaspora*     | TNM F17211     | -                     | EF197083              | -                      | -                      | Chang et al. (2010)                             |
| *Rhypophila pleiospora*     | TNM F16889     | -                     | EF197084              | -                      | -                      | Chang et al. (2010)                             |
| *Schizothecium aloides*     | CBS 879.72     | AY999097              | AY999120              | -                      | -                      | Cai et al. (2005)                               |
| *Schizothecium carpinicola* | CBS 228.87^T   | AY999095              | AY999118              | -                      | -                      | Cai et al. (2005)                               |
| *Schizothecium conicum*     | CBS 434.50     | MH868218              | MH856702              | -                      | -                      | Vu et al. (2019)                                |
Table 2 (continued)

| Taxa                                | Strain              | GenBank accession #                     | References                                      |
|--------------------------------------|---------------------|----------------------------------------|------------------------------------------------|
|                                      |                     | LSU | ITS | RPB2 | TUB2 |                        |
| Schizothecium curvipesorum (Neoschizothecium curvipesorum) | CBS 507.50          | AY999096 | AY999119 | -     | -                     | Cai et al. (2005)             |
|                                      | ATCC 36709          | AY346300 | -     | AY780192 | AY780136 | Huhndorf et al. (2004), Miller and Huhndorf (2005) |
| Schizothecium fimbuti (Neoschizothecium fimbuti) | CBS 144.54          | AY780075 | AY999115 | AY780189 | AY780132 | Cai et al. (2005), Miller and Huhndorf (2005) |
| Schizothecium glutinans (Neoschizothecium glutinans) | CBS 134.83          | AY999093 | AY999116 | -     | -                     | Cai et al. (2005)             |
| Schizothecium inaequale (Neoschizothecium inaequale) | CBS 356.49<sup>T</sup> | MK926846 | MK926846 | MK876808 | -       | Wang et al. (2019a)    |
| Schizothecium selenosporum (Neoschizothecium selenosporum) | CBS 109403<sup>T</sup> | MK926849 | MK926849 | MK876811 | -       | Wang et al. (2019a)    |
| Schizothecium tetrasporum (Neoschizothecium tetrasporum) | CBS 394.87          | MH873776 | MH862087 | -     | -                     | Vu et al. (2019)              |
| Sordaria fimicola                      | SMH 4106            | AY780079 | -     | AY780194 | AY780138 | Miller and Huhndorf (2005) |
| Sordaria islandica                    | CBS 512.77<sup>T</sup> | MH872859 | MH861097 | -     | -                     | Vu et al. (2019)              |
| Sordaria nodulisfera                  | NBRC 32551<sup>T</sup> | LC146761 | LC146761 | -     | -                     | Ban et al. (unpubl. data)     |
| Sordaria tamaensis                    | NBRC 32552<sup>T</sup> | LC146762 | LC146762 | -     | -                     | Ban et al. (unpubl. data)     |
| Strattonia obliechiformis<sup>*</sup>  | CBS 110305<sup>T</sup> | MH874449 | MH862861 | -     | -                     | Vu et al. (2019)              |
| Triangularia allahabadensis           | CBS 724.68<sup>T</sup> | MK926865 | MK926865 | MK876827 | -       | Wang et al. (2019a)    |
| Triangularia anserina                 | CBS 433.50          | MK926864 | MK926864 | MK876826 | -       | Wang et al. (2019a)    |
| Triangularia arizonensis              | Saintsess 18211-c    | KF557668 | -     | -     | -       | Kruys et al. (2015)    |
|                                      | Krusys 724          | KF557669 | -     | -     | -       | Kruys et al. (2015)    |
|                                      | E00204509           | KF557670 | -     | -     | -       | Kruys et al. (2015)    |
|                                      | CBS 120289          | KU955584 | -     | -     | -       | Debuchy et al. (unpubl. Data) |
| Triangularia backusii                 | CBS 539.89<sup>sp</sup> | MK926866 | MK926866 | MK876828 | -       | Wang et al. (2019a)    |
| Triangularia backusii                 | FMR 12439           | KP981423 | MT784138 | KP981605 | KP981550 | Marin-Felix et al. (2020) |
| Triangularia backusii                 | FMR 13591           | KP981424 | MT784139 | KP981606 | KP981551 | Marin-Felix et al. (2020) |
| Triangularia bambusae                 | CBS 352.33<sup>T</sup> | MK926868 | MK926868 | MK876830 | -       | Wang et al. (2019a)    |
| Triangularia battistae                | CBS 381.68<sup>T</sup> | KP981443 | MT784140 | KP981626 | KP981577 | Soil, Brazil             |
| Triangularia longicaudata             | CBS 252.57<sup>T</sup> | MK926871 | MK926871 | MK876833 | -       | Wang et al. (2019a)    |
|                                      | FMR 12365           | KP981448 | MT784141 | KP981631 | KP981474 | Marin-Felix et al. (2020) |
| Triangularia microsclerotigena        | CBS 290.75<sup>T</sup> | FN662476 | FN662475 | -     | -       | Madrid et al. (2011)   |
| Triangularia nanopodalidis<sup>*</sup> | CBS 113680          | MH874504 | MH862937 | -     | -       | Vu et al. (2019)       |
| Triangularia ovina                    | CBS 671.82<sup>T</sup> | MT731512 | MH861539 | MT731574 | MT731553 | Vu et al. (2019), Ament-Velásquez et al. (2020) |
| Triangularia pauciseta                | CBS 451.62          | MK926870 | MK926870 | MK876832 | -       | Wang et al. (2019a)    |
| Triangularia phialophoroides          | CBS 301.90<sup>T</sup> | MK926871 | MK926871 | MK876833 | -       | Wang et al. (2019a)    |
| Triangularia samala                   | CBS 307.81<sup>T</sup> | MH873104 | MH861345 | -     | -       | Vu et al. (2019)       |
| Triangularia setosa                   | FMR 12782           | KP981449 | MT784142 | KP981632 | KP981475 | Marin-Felix et al. (2020) |
|                                      | CBS 265.70          | MT731516 | MH859600 | MT731573 | MT731552 | Vu et al. (2019), Ament-Velásquez et al. (2020) |
| (Triangularia tarvisina)              | CBS 251.71<sup>T</sup> | MH871877 | MH860101 | -     | -       | Vu et al. (2019)       |
|                                      | (Triangularia praecox) | SMH 3431 | -     | AY780065 | AY780169 | AY780108 | Miller and Huhndorf (2005) |
|                                      | SMH 4036            | KX348038 | AY780066 | -     | -       | Miller and Huhndorf (2005), Miller (unpubl. data) |
| Triangularia tetraspera               | CBS 245.71          | MH860097 | MH871873 | -     | -       | Vu et al. (2019)       |
| Triangularia unicaudata               | CBS 313.58<sup>T</sup> | MT731513 | MH857799 | MT731575 | MT731554 | Vu et al. (2019), Ament-Velásquez et al. (2020) |
| Triangularia verruculosa              | CBS 148.77          | MK926874 | MK926874 | MK876836 | -       | Wang et al. (2019a)    |
| Triangularia yaeyamensis              | NBRC 31170<sup>T</sup> | LC146720 | LC146720 | -     | -       | Ban et al. (unpubl. data) |
| Zopfiella attenuata<sup>*</sup>       | CBS 266.77<sup>T</sup> | KP981445 | MH861060 | KP981628 | KP981572 | Vu et al. (2019), Marin-Felix et al. (2020) |
| Zopfiella erosetra<sup>*</sup>        | CBS 255.71          | AY999110 | AY999133 | -     | -       | Cai et al. (2005)      |
| Zopfiella latipes<sup>*</sup>         | IFO 9826           | AY999107 | AY999129 | -     | -       | Cai et al. (2005)      |
Table 2 (continued)

| Taxa                        | Strain          | GenBank accession #          | References                           |
|-----------------------------|-----------------|-----------------------------|--------------------------------------|
|                             |                 | LSU | ITS | RPB2 | TUB2 |
| **Schizotheciaceae**        |                 |     |     |      |      |
| Zygopleurage zygospora*     | CBS 518.70T     | K981450 | MT784145 | K981633 | K981476 | Marin-Felix et al. (2020) |
| Zopfiella tabulata          | CBS 230.78      | MK926854 | MK926854 | MK876816 | -         | Wang et al. (2019a)       |
| Zopfiella tardicicans*      | CBS 670.82T     | MK926855 | MK926855 | MK876817 | -         | Wang et al. (2019a)       |
| **Zygospermellaceae**       |                 |     |     |      |      |
| Zygospermella insignis      | Lundqvist 2444  | KF557698 | - | - | KF557722 | Kruis et al. (2015)       |
| Zygospermella insignis      | E00204312       | KF557699 | - | - | KF557723 | Kruis et al. (2015)       |

ATCC, American Type Culture Collection, VA, USA; CBS, Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; FMR, Facultad de Medicina, Reus, Spain; FGSC, Fungal Genetics Stock Center, University of Kansas Medical Center, Kansas City, USA; HKUCC, University of Hong Kong Culture Collection, Department of Ecology and Biodiversity, Hong Kong, China; IFO, Biological Resource Center, Chiba, Japan; IML, International Mycological Institute, CABI-Bioscience, Egham, UK; KRAM, National Biodiversity Collection – Herbarium KRAM, Kraków, Poland; SANK, Research laboratories of the Daichi Sanko Pharmaceutical Co., Ltd., Tokyo, Japan; TNRM, Herbarium of National Museum of Natural Science, Taiwan; TRTC, Royal Ontario Museum, Toronto, Canada; UAMH, UAMH Center for Global Microfungal Biodiversity, University of Toronto, Canada; AR, Francoise Candoussau, GJS, JF, HHH, Kruys, Lundqvist, MRR, Santensoon, SMH, TL: personal collections of Amy Rossman, Francoise Candoussau, Gary J. Samuels, Jacques Fournier, Harold H. Bursdal, Åsa Kruys, Nils Lundqvist, Michael J. Richardson, Sweden R. Santesson, Sabine M. Huhndorf, Thomas Lessoe, respectively; n/a: not available. ET, IsoT and T indicate ex-epitype, ex-isotype and ex-type strains, respectively. *Taxa with generic names applied in the broad sense (sensu lato), not necessarily reflecting molecular phylogenetic relationships

and Lundqvistomyces (Marin-Felix et al. 2020). Therefore, the presence or absence of an ascospore sheath is polyphyletic and one cannot assume that all species with ascospores surrounded by a sheath are going to belong to the same monophyletic lineage. In fact, other species characterized by ascospores surrounded by a gelatinous sheath are placed in different genera, such as Echria (Schizotheciaceae), Fimetariella (Lasiosphaeraceae s. lato) and Sordaria (Sordariaceae). This family is erected based on a clade containing only two species, S. oblecythiformis and the new combination S. petrogale, but both species only contain sequences from the internal transcribed spacer region (ITS) and the nuclear rDNA large subunit (LSU) from the study of Vu et al. (2019). For these reasons, we reject the family Strattoniaceae until additional taxa, including the type species, and additional genes (i.e. RPB2 and TUB2) have been studied.

The families Lasiosphaeridaceae and Zygospermellaceae, erected for only one and two genera, respectively, are also points of contention since they were proposed based on limited taxon sampling and poor taxonomic practices. In the recent phylogenetic studies from Kruys et al. (2015) and Marin-Felix et al. (2020), both clades now considered independent families by Huang et al. (2021) were clustering together in a well-supported clade. Huang et al. (2021) prematurely introduced both families since they formed two independent lineages in their phylogenetic study. However, both families are included in the Schizotheciaceae clade in our Bayesian phylogenetic study (0.97 pp) (Fig. 2). More taxa and sequences should be incorporated in further phylogenetic analyses to verify if the Lasiosphaeridaceae and Zygospermellaceae are two independent lineages or belong to the Schizotheciaceae. For these reasons, we reject these families until more data can be analysed and we refer to both lineages as Lasiosphaeridaceae s. lato.

In our phylogenetic study, the only family not supported is Lasiosphaeridaceae s. str. However, the conflicts may be caused by the high number of taxa in which only the ITS and LSU sequences are available, which most likely influences the backbone relationships and support for these phylogenetic relationships resulting in misleading higher-level classifications. Although most strains included in Huang et al. (2021) are available in the CBS collection, and therefore additional loci could have been sequenced, they chose not to generate these critical sequence data for their phylogenetic analyses.

Finally, the family Bombardiaceae was introduced by Huang et al. (2021), even though the ML bootstrap support was only 76% and there was no Bayesian inference support for this clade. Huang et al. (2021) explained that Marin-Felix et al. (2020) discussed the low support of this lineage, and for that reason no family was introduced to accommodate it. Nonetheless, they considered this lineage to be well-supported in their phylogenetic study, and therefore the new family Bombardiaceae was introduced to represent it. In our phylogenetic study (Fig. 2), which included the same sequences that Huang et al. (2021) used, the clade representing this family is not supported (42% bs/0.89 pp), so we do not accept the Bombardiaceae as a justifiable family.
Fig. 2 RAxML phylogram obtained from the combined ITS, LSU, RPB2 and TUB2 sequences belonging to the families Chaetomiaceae, Diplogelasinosporaceae, Lasiosphaeriaceae, Naviculisporaceae, Podosporaceae, Schizotheciaceae, and Sordariaceae. Camarops amorpha SMH 1450 was used as an outgroup. Bootstrap support values ≥70/Bayesian posterior probability scores ≥0.95 are indicated along branches. Branch lengths are proportional to distance. Ex-epitype, ex-isotype and ex-type strains of the different species are indicated with ET, IsoT and T, respectively. Type species of the different genera are shown in bold. Alignment available in Supplementary Information.
We take this opportunity to clarify that most of the outgroups used in Huang et al. (2021) do not belong to the family Microascales as they erroneously indicated, but rather to the Coronophorales (syn. Melanosporales) as in the case of all the Microthecium spp. included, as well as Thielavia basicola.

**New genera superfluously introduced or redefined based on poor taxonomic practice**

As mentioned above, *Neoschizothecium* is a superfluous genus based on misinterpretation of the type species of *Podospora* and *Schizothecium* so it is nomenclaturally illegitimate (Art. 14.3, Shenzhen Code) and thus, a superfluous synonym under *Schizothecium*. The delimitation of *Strattonia* based on a single species is a poor taxonomic decision since the type species of the genus was not included in the study of Huang et al. (2021). Finally, the delimitation of *Cercophora* is also based on poor taxonomic practice since Huang et al. (2021) chose a dubious candidate to represent the type species of *C. mirabilis* in their analyses but thankfully, they did not designate an epitype. It is impossible to confirm the morphological identification of this strain (CBS 120402) because it does not sporulate in culture as mentioned by Marin-Felix et al. (2020). Therefore, it is not a suitable representative of the type species of *Cercophora* and a suitable epitype must be studied and designated before this genus can be properly delimited. The placement of *Cercophora* spp. in different lineages and families support the necessity of a detailed study of this genus and the careful designation of...
an epitype for the type species in order to determine the proper taxonomic placement of *Cercaphora* within the order.

**New combinations superfluously introduced or failing to follow good taxonomic practice**

The new combination of *Cladorrhinum olerum* proposed to accommodate *Arnium olerum* is superfluous because Marin-Felix et al. (2020) already synonymized this latter name under *Cl. foecundissimum*. The nucleotide similarity between both species is 99.81% for ITS, 100% for LSU, 98.60% for *RPB2* and 100% for *TUB2*, suggesting that these represent the asexual and sexual morphs of the same taxon.

The new combination *T. tarvisina* is superfluous since this species shows morphological and molecular similarity greater than 99.5% of the four loci (ITS, LSU, *RPB2* and *TUB2*) between both species according to a BLAST comparison. Therefore, this new combination was made in error due to the failure of a proper literature review by Huang et al. (2021). Likewise, the new combination *T. praecox* is also superfluous since this species shows morphological and molecular similarity also with *T. setosa*, and therefore *P. praecox* is here considered a synonym to this later species. The description of *T. setosa* is here emended to incorporate the sizes observed in *P. praecox* when it was introduced, which are similar to *T. setosa* except for the ascus dimensions (up to 190 μm wide in *P. praecox* vs. up to 60 μm in *T. setosa*) (Cailleux 1969; Lundqvist 1972; Wang et al. 2019a).

**Triangularia setosa** (G. Winter) X. Wei Wang & Houbraken, Stud. Mycol. 93: 243. 2019. emend. Y. Marin & A.N. Mill. MB829894

*Basionym: Sordaria setosa* G. Winter, Abh. Naturf. Ges. Halle 13: 97. 1873.

*Synonyms: Philocopia setosa* (G. Winter) Sacc., Syll. Fung. 1: 249. 1882.

*Podospora setosa* (G. Winter) Niessl, Hedwigia 22: 156. 1883.

*Pleuroge setosa* (G. Winter) Kuntze, Revis. Gen. Pl. 3: 505. 1898.

*Cladochaete setosa* (G. Winter) Sacc., Ann. Mycol. 10: 318. 1912.

*Philocopia setosa* subsp. *tarvisina* Sacc., Syll. Fung. (Abellini) 1: 250. 1882.

*Philocopia setosa* var. *tarvisina* (Sacc.) Traverso, Fl. Ital. Crypt. (Florence) 1: 437. 1907.

*Philocopia tarvisina* (Sacc.) J.H. Mirza & Cain, Can. J. Bot. 47: 2041. 1970.

*Podospora tarvisina* (Sacc.) J.H. Mirza & Cain, Can. J. Bot. 47: 2041. 1970.

The new combination *T. tarvisina* is superfluous since *T. setosa* is here considered a synonym to this later species. The description of *T. setosa* is here emended to incorporate the sizes observed in *P. praecox* when it was introduced, which are similar to *T. setosa* except for the ascus dimensions (up to 190 μm wide in *P. praecox* vs. up to 60 μm in *T. setosa*) (Cailleux 1969; Lundqvist 1972; Wang et al. 2019a).

**Triangularia tarvisina** (Sacc.) S.K. Huang & K.D. Hyde, Fungal Divers. 111: 515. 2021.

**Podospora praecox** Cailleux, Cahiers de La Maboké 7: 102. 1969.

**Triangularia praecox** (Cailleux) S.K. Huang & K.D. Hyde, Fungal Divers. 111: 515. 2021.

Ascomata superficial, mouse grey in reflected light, solitary, ovoid to ampulliform with a short, black beak, ostiolate, 230–900 μm high, 185–800 μm diam; ascomatal wall brown, opaque, of *textura intricata* or *epidermoidea* in surface view; ascomatal hairs arising mainly around the lower half, hyphal-like, erect or flexuous, brown, 1.5–3 μm diam near base. Asci fasciculate, fusiform or elongated fusiform, 170–430 × 25–60(–190) μm, without a conspicuous apical ring, stipitate, stipe 21.5–62 μm long, containing numerous irregularly- and densely-arranged ascospores, evanescent. Ascospores at first one-celled, hyaline, becoming transversely septate and two-celled; upper cell olivaceous brown to brown, ellipsoidal to broadly fusiform, equilateral, with an apical germ pore, (15–)17–21.5(–22) × (9–)10.5–13 μm; lower cell hyaline, elevate to cylindrical, 8–12 × 2–3 μm; apical and basal mucilaginous appendages mostly present, up to 120 μm long. Asexual morph not observed (adapted from Lundqvist 1972 and Wang et al. 2019a).

Huang et al. (2021) proposed the new combination *Jugulospora minor* to accommodate *Strattonia minor*. Even though we consider the transference of this species to *Jugulospora* necessary, Huang et al. (2021) did not demonstrate whether it is an independent species or if it should be synonymized with *J. rotula* as happened with *Apiosordaria globosa*, *A. hispanica* and *Rhexosporium terrestrum* (Marin-Felix et al. 2020). *Strattonia minor* is similar to *J. rotula*, differing only by the size of the upper cell of the ascospores and the width of the asci (Lundqvist 1972; Marin-Felix et al. 2020). In our phylogenetic study (Fig. 2), the type strain of this species occurred in the moderately well-supported clade (82% bs/0.98 pp) representing *J. rotula*. Therefore, *J. minor* is here considered a synonym of *J. rotula*, whose description is here emended to incorporate the new sizes of ascus and ascospores.

**Jugulospora rotula** (Cooke) N. Lundq. emend. Y. Marin & A.N. Mill. MB315972

*Basionym: Sphaeria rotula* Cooke, Handb. British Fungi 2: no. 2598. 1871.

*Synonyms: Strattonia minor* N. Lundq., Symb. Bot. Upsal. 20: 271. 1972.

**Jugulospora minor** (N. Lundq.) S.K. Huang & K.D. Hyde, Fungal Divers. 111: 95. 2021.

**Rhexosporium terrestrum** Udagawa & Furuya, Trans. Mycol. Soc. Japan 18: 303. 1977.
Apiosordaria globosa Dania García, Stchigel & Guarro, Mycologia 95: 137. 2003.
Apiosordaria hispanica Dania García, Stchigel & Guarro, Mycologia 95: 134. 2003.

Ascomata ostiolate, superficial or immersed, scattered to aggregated, pale brown to brown, pyriform, 350–770 × 200–540 μm, covered with pale brown, septicale phyphal-like hairs, 1–5 μm diam; neck brown to dark brown, cylindrical to conical, papillate, 80–280 μm long, 90–250 μm wide; ascomatal wall membranaceous, semi-transparent, brownish-orange to brown, 3–9-layered, 15–45 μm thick; outer layers textura angularis and textura intricata; inner layers textura epidermoidea. Paraphyses and periphyses filiform, up to 2 μm in diam. Asci unitunicate, eight-spored, cylindrical, 145–250 × 8–28 μm, stipitate, with a thin apical ring, evanescent. Ascospores at first one-celled, hyaline, clavate, becoming transversely septate and two-celled; upper cell dark brown, obvoid to globose, truncate at the base, ornamented with warts arranged uniformly or forming longitudinal ridges or large spots, (12–)13–18(–29) × 6–27 μm, with an apical to lateral germ pore 0.5–3 μm in diam.; lower cell hyaline, conical, smooth-walled to slightly warted, 1–6 μm long, collapsing; gelatinous caudae absent. Asexual morph present. Conidia hyaline to pale-colored, almost smooth-walled, ovate to elongate, 2–6 × 1.5–2.5 μm, produced laterally or terminally on undifferentiated hyphae, solitary (adapted from Marin-Felix et al. 2020).

As mentioned above, the genus Strattonia is delimited based on the non-type species S. oblecythiformis, which should not be accepted due to the difficulty of delimiting genera in the Sordariales based on only morphological data (for further details, see section “New families superfluously introduced or without sufficient evidence”). For this reason, the new combination S. petrogale should not be taken up until further studies that include the type species confirm the correct taxonomic placement of the lineage representing Strattonia.

The nine new combinations in the newly erected genus Neoschizothecium proposed for accommodating the species previously belonging to Schizothecium are also here considered superfluous for the same reasons the family Neoschizotheciaceae is invalid. Moreover, N. minicauda was introduced to accommodate P. minicauda. However, the strain included in the phylogenetic study does not represent type material and its morphology was not studied. Therefore, the transfer of this species to Schizothecium should await further studies.

Cladorrhinum brunnescens is transferred to Podospora as P. brunnescens. However, in our phylogenetic study, this species is not placed in the well-supported clade (99% bs/1 pp) representing Podospora. Only ITS and LSU sequence data of the type strain are available. Therefore, the other two loci should be sequenced and additional analyses conducted before this combination is accepted.

Finally, two additional new combinations that followed poor taxonomic practices are Cl. leucotrichum and T. nannopodalis, which were proposed based on strains that do not represent type material and whose morphology was not studied.

Limitation in the morphological study

Huang et al. (2021) performed morphological studies of type material for several taxa belonging to the Sordariales, although they mostly repeated what can already be found in the literature without providing any new information while at the same time destroying irreplaceable type material. Examination of type material is important, but generating sequence data from types or designating epitypes with molecular data is a higher priority. No molecular data were generated in Huang et al. (2021). Due to the difficulty of delimiting species and genera of this order based only on morphology, it is much more important to generate sequences from these types of materials to incorporate in phylogenetic analyses instead of re-examining material that has previously been studied and well documented. This is the case of Triangularia horridula, a new combination proposed after a morphological and molecular study of the holotype from the fungarium of Saccardo (Forin et al. 2021). Using next-generation sequencing techniques, the generation of molecular data from type material is possible and essential to improve taxonomic classifications.

Conclusions and final remarks

In conclusion, it is clear that the authors of Huang et al. (2021) were not able to fully appreciate or understand the problems surrounding the reclassification of the order Sordariales, which has been studied using a combination of meticulous morphological and molecular analyses by various workers for more than a decade. Even in the last few years, chemotaxonomic data have been combined with morphological and molecular data to verify some taxonomic relationships. For example, Shao et al. (2020) demonstrated that different specimens and strains of Jugulospora produced the same xanthoquinodins compounds, corroborating the redefinition of the genus performed by Marin-Felix et al. (2020). Moreover, the new genus Pseudorhypophila was introduced based on the production of the same class of compounds, i.e. zopfinol and derivatives, by members of the same monophyletic lineage (Harms et al. 2021). In this later work, they observed that producers of sordarins, which are a class of natural antifungal agents, were all located in the Naviculisporaceae, supporting the introduction of this family based on molecular data by Marin-Felix et al. (2020). The taxonomy of the Sordariales should not be rearranged.
following the results of a single phylogenetic study and numerous new family names should not be introduced without careful consideration. The study of Huang et al. (2021) is reminiscent of those of Raymond Hoser (Kaiser et al. 2013; Rhodin et al. 2015; Wüster et al. 2021) or Alexander Doweld (2001), who frequently practice taxonomic vandalism by formally naming clades based on the work of previous workers. The introduction of unnecessary families, genera and species for unstable and unsupported clades that will eventually change justifies the criticisms of other mycological disciplines. These claim fungal taxonomists only want to constantly change names and make systematic mycology a more difficult field. New scientific names will remain in databases forever even if they are proven to be invalid or superfluous and have the potential to be used by future careless workers and further populated in the literature making them appear as valid and accepted names. Therefore, the introduction of new taxa should be done responsibly by following the best taxonomic practices available, such as a thorough review of past literature, conducting polyphasic studies to corroborate initial hypotheses and collaborating with experts in the group of fungi under study (Aime et al. 2020; Lücking et al. 2020).

Furthermore, it is possible that DNA-based phylogenies can be misleading in the recognition of species just like morphological studies alone. Polymorphisms can interfere in species identification based only on morphology, but also the lack of loci or the use of loci inappropriate for the fungal taxa under study can also lead to the wrong conclusions (Lücking et al. 2020). This is the case for some of the new combinations proposed by Huang et al. (2021) based only on ITS and LSU sequences. Therefore, both phenotypic and molecular approaches should be combined for a more robust taxonomic classification.

It is worthy to mention that according to the recent guidelines for publishing a new fungal species or name provided by Aime et al. (2020), it is strongly recommended to examine the types of the basionyms before making changes and include notes on how to differentiate the new recombined species from other similar species in that genus. Even though one of the co-authors of this guideline was also one of the authors of all new combinations proposed, none of these recommendations were followed in any of the new combinations performed by Huang et al. (2021).

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**Declarations**

**Conflict of interest** The authors declare no competing interests.

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