



Phylogenomics and diversification of Sordariomycetes

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Abstract

The Sordariomycetes is a specious, morphologically diverse, and widely distributed class of the phylum Ascomycota that forms a well-supported clade diverged from Leotiomycetes. Aside from their ecological significance as plant and human pathogens, saprobes, endophytes, and fungicolous taxa, species of Sordariomycetes produces a wide range of chemically novel and diverse metabolites used in important fields. Recent phylogenetic analyses derived from a small number of genes have considerably increased our understanding of the family, order, and subclass relationships within Sordariomycetes, but several important groups have not been resolved well. In addition, there are various paraphyletic or polyphyletic groups. Moreover, the criteria used to establish higher ranks remain highly variable across different studies. Therefore, the taxonomy of Sordariomycetes is in constant flux, remains poorly understood, and is subject to much controversy. Here, for the first time, we have assembled a phylogenetic dataset containing 638 genomes representing the 156 genera, 50 families, and 17 orders and 5 subclasses of Sordariomycetes. This data set is based on 1124 genes and results in a well-resolved phylogenomic tree. We further constructed an evolutionary timeline of Sordariomycetes diversification based on the genomic data sets. Our divergence time estimate results are inconsistent with previous studies, suggesting estimates of node ages are less precise and varied. Based on these results, we discuss the higher ranks of Sordariomycetes and empirically propose an unprecedented taxonomic framework for the class.

Keywords – Ascomycota – divergence time – evolution – genomes – tree of life

Introduction

Sordariomycetes is the second-largest class of Ascomycota, with a worldwide distribution that mostly accommodates terrestrial taxa, although several can also be found in aquatic habitats Zhang et al. (2006). Some are phytopathogens that cause leaf, stem, and root diseases in a wide variety of hosts, while others cause diseases in arthropods and mammals (Jayawardena et al. 2019, Hyde et al. 2020). Fungal pathologists recently conducted a study in association with the journal *Molecular Plant Pathology* and nominated the top 10 fungal plant pathogens. The list includes four Sordariomycetes, namely *Magnaporthe oryzae*, *Fusarium graminearum*, *F. oxysporum* and *Colletotrichum* species, while the rice blast fungus *Magnaporthe oryzae* ranks number one (Dean et al. 2012). The members of Sordariomycetes are also frequently isolated as endophytes from a wide variety of plants (Perera et al. 2020). Some taxa are fungicolous (Liu et al. 2000, Sun et al. 2019,

2022), while many persist as saprobes involved in decomposition and nutrient recycling (Boonmee et al. 2021). Some species of Sordariomycetes are economically important biocontrol agents (Kaewchai 2009, Hyde et al. 2019), and others produce a wide range of chemically diverse metabolites that are important in agricultural, medicinal and other biotechnological industries (Helaly et al. 2018).

The class Sordariomycetes was established by Eriksson & Winka (1997), and the first main attempts at classifying all genera of Sordariomycetes were by Barr (1983, 1990) and Eriksson & Hawksworth (1986, 1993). These early efforts relied solely on morphology to classify what were poorly understood taxa at the time. Classification of the sexual morphs of Sordariomycetes was continued by Lumbsch & Huhndorf (2007, 2010), which incorporated morphology and available phylogenies. Maharachchikumbura et al. (2015, 2016) were among the first to include the asexual and sexual states as well as partial molecular data in the classification of Sordariomycetes. Hongsanan et al. (2017) used divergence time to support various class orders and families.

Eriksson & Winka (1997) erected the subclasses Hypocreomycetidae, Sordariomycetidae and Xylariomycetidae based on morphology and ribosomal RNA (rRNA) sequence data. Maharachchikumbura et al. (2015) used morphological features and combined sequence data to introduce the three subclasses Diaporthomycetidae, Lulworthiomycetidae and Meliolomycetidae. However, the subclass Meliolomycetidae was considered a synonym of Sordariomycetidae by Hongsanan et al. (2017), while Pisorisporiomycetidae and Savoryellomycetidae were introduced into the class Sordariomycetes (Hongsanan et al. 2017, Hyde et al. 2020). According to the latest outline by Wijayawardene et al. (2022), Sordariomycetes consists of 7 subclasses, 46 orders, and 172 families. Since then, an increasing number of new orders and families have been added to the Sordariomycetes, highlighting its growing importance (Hyde et al. 2021, Sun et al. 2021, Magyar et al. 2022, Sugita & Tanaka 2022).

Unclear resolution is expected in higher-level relationships of fungi when phylogenetic inferences rely upon a small number of loci. In Sordariomycetes, comparison between several loci of the genome is the only available option for resolving most nodes of the phylogenetic tree at the family level (Zhang et al. 2006, Maharachchikumbura et al. 2015, 2016, Hongsanan et al. 2017, Hyde et al. 2020). Current phylogenies mainly use four loci: the partial nuclear ribosomal small subunit rRNA (SSU), the partial nuclear ribosomal large subunit rRNA (LSU), the partial translation elongation factor 1-alpha (TEF) and the partial second-largest subunit of RNA polymerase II (RPB2), which have several disadvantages and do not provide enough phylogenetic information to fully support the Sordariomycetes families. This is common in many specious orders of Sordariomycetes, such as Diaporthales, Hypocreales and Xylariales, and many of their families consequently lack resolution (Senanayake et al. 2018, Voglmayr et al. 2018, Xavier et al. 2019, Hyde et al. 2020, Jiang et al. 2020, Samarakoon et al. 2022, Sun et al. 2022).

In recent years, the subclass Diaporthomycetidae has accommodated the newest families and orders in Sordariomycetes. However, the majority of orders in Diaporthomycetidae are given uncertain placements within the subclass in different studies, and the sister order relationships could not be located in most cases. For instance, Hongsanan et al. (2017) and Hyde et al. (2017) showed that Distoseptisporaceae is phylogenetically related to Magnaporthales. Hyde et al. (2017) further suggested that Distoseptisporaceae (121 million years ago, Mya) should be placed within Magnaporthales based on divergent time estimation. A later study by Luo et al. (2019) showed that Distoseptisporaceae is not related to Magnaporthales and raised it to Distoseptisporales. However, the placement of Distoseptisporales continually changes within the subclass Diaporthomycetidae across different studies (Dong et al. 2021, Hyde et al. 2021, Sugita & Tanaka 2022, Zhang et al. 2022). Furthermore, many of the higher ranks introduced in Diaporthomycetidae are not natural groupings and are likely composed of phylogenetically unrelated taxa. For example, the family placement in Atractosporales often changes across studies (Zhang et al. 2017a, Luo et al. 2019, Hyde et al. 2020, Maharachchikumbura et al. 2022), indicating that the familiar placement of Pseudoproboscisporaceae is more closely related to the Junewangiaceae and not to the Atractosporaceae. Higher morphological variation within the families of respective orders and

phylogenetic instability are good indicators of this. Therefore, Diaporthomycetidae is in need of urgent revisions in terms of re-evaluating the higher-rank boundaries, including missing fungal lineages, and filling in gaps in knowledge.

Several Sordariomycetes evolved independently and obtained similar traits in response to adapting to different geographical locations and various environmental forces, often resulting in polyphyletic genera. The situation within the orders like Sordariales and Phyllachorales are much more complex (Wanderlei-Silva et al. 2003, Huhndorf et al. 2004, Mardones et al. 2017, Marin-Felix et al. 2020). Taxa related to Sordariales are traditionally classified mainly based on morphology and host association. For example, *Neurospora* species have traditionally been based on the wall structure of ascospores (Dettman et al. 2001), but this practice remains incongruent with molecular data. Many of the traditionally defined genera in Lasiosphaeriaceae and Sordariaceae have been found to either be polyphyletic or paraphyletic (Wang et al. 2019, Marin-Felix et al. 2020, Huang et al. 2021a). Based on DNA sequence analyses, taxa initially classified under these families have been found not to be close relatives of these families (Cai et al. 2006). Several recent attempts have been made for the natural classification of the group; as a consequence, polyphyletic families have been divided and several new families have been introduced (Wang et al. 2019, Marin-Felix et al. 2020, Huang et al. 2021a). However, the majority of taxa related to these higher ranks continue to lack sequence data, as they have been described over several decades ago. Acremonium-like, arthrini-like, verticillium-like, nodulisporium-like, sporidesmium-like and geniculosporium-like asexual morphs are distributed across the Sordariomycetes, and some of them are even distributed in other ascomycete classes (Summerbell et al. 2011, Senanayake et al. 2015, Gams 2017, Yang et al. 2018, Wittstein et al. 2020, Maharachchikumbura et al. 2022). The morphology of these taxa has undergone convergent evolution and is not phylogenetically reliable.

Based on the morphology and sequence analysis of combined ITS and LSU regions, the subclass Xylariomycetidae was thought to comprise two orders, Amphisphaeriales and Xylariales (Smith et al. 2003, Tang et al. 2009, Senanayake et al. 2015). Jaklitsch et al. (2016) and Maharachchikumbura et al. (2016) considered Amphisphaeriales as a synonym of Xylariales. In their phylogenies, there was a lack of statistical support for the Amphisphaeriales and Xylariales as distinct orders within Xylariomycetidae. However, Samarakoon et al. (2016) and Hongsanan et al. (2017) provided phylogenetic and divergence time estimations for the subclass Xylariomycetidae and accepted Amphisphaeriales and Xylariales as distinct orders, a practice which was followed by Hyde et al. (2020). However, the placement of several families within respective orders was not consistent across different studies or even analyses in the same study. For instance, the phylogenetic placements of the families Oxydothidaceae and Polystigmataceae are inconsistent in two different analyses of Hyde et al. (2020), and these two families were accepted in Xylariales. However, previous phylogenetic placements of the families Oxydothidaceae and Polystigmataceae indicated that they belonged to Amphisphaeriales (Hongsanan et al. 2017). Furthermore, the order Delonicicolales was introduced to the Xylariomycetidae by Perera et al. (2017) based on the monotypic family Delonicicolaceae. Later, Voglmayr et al. (2019) based on morphology and phylogeny introduced Leptosilliaceae as a new family sister to Delonicicolaceae, while rejecting the order state of Delonicicolales. With the support of phylogeny and divergence time estimates (stem age of 165 Mya), Hyde et al. (2020) support the Delonicicolales establishment by Perera et al. (2017). Therefore, the lack of phylogenetic support and unstable placement is relatively more common in many families and orders of Sordariomycetes.

Several criteria have been used to introduce families and other higher ranks in the Sordariomycetes (Maharachchikumbura et al. 2015, Marin-Felix et al. 2020, Samarakoon et al. 2020, Hyde et al. 2021). However, the criteria used to introduce higher ranks have changed depending on the methods of different authors and studies. Traditionally, higher ranks have been introduced based solely on morphology and later based on phylogeny or morphology with phylogeny. Many studies have revealed that divergence times can provide additional criteria or support for ranking taxa. Yet, some studies give more priority to divergent time estimation when

introducing higher taxa. Consequently, there is no clear consensus regarding the determination of family and order levels in the Sordariomycetes.

Therefore, regardless of the exhaustive morphological documentation and phylogenetic analyses, fundamental uncertainties and phylogenetic instability remain constant across the family and higher ranks of the Sordariomycetes. We have identified four key areas of concern regarding family and higher ranks: 1) lack of resolution and/or support; 2) existing taxa have been shown to be polyphyletic or paraphyletic in many cases, which is not fully accounted for; 3) phylogenetic positions of several orders remain in dispute, and the taxa within these orders are not natural groups; and 4) ranks are not quantitatively equivalent between higher ranks, or criteria used to establish ranks are highly variable. Hence, the systematics of Sordariomycetes remain in a state of flux, and a standard and stable taxonomic framework is urgently required.

The work of the taxonomist has expanded over the years with the advent of new technological methods. The development of next-generation DNA-sequencing technologies to sequence complete genomes was a great boon to phylogenetic reconstructions and fungal systematics (Hyde et al. 2013, Zhang et al. 2017b). The cost of genome sequencing continues to decrease, and the number of genomes deposited into databases is on the rise (Maharachchikumbura et al. 2021), while Sordariomycetes has the highest number of available genome sequences for an ascomycetes class in public databases. Here, we present the first higher-level phylogenomics study for the Sordariomycetes and estimate its evolutionary history based on a genomic dataset. The study aims to deepen our understanding of the current taxonomic status and relationships among higher ranks of Sordariomycetes and propose an unprecedented taxonomic framework for the class.

Materials & Methods

Genome collection

To collect as comprehensive a genome data set of Sordariomycetes, a custom pipeline was used to obtain and select representative genomes. The search term “Ascomycota” was used to query the NCBI genome database (<https://www.ncbi.nlm.nih.gov/data-hub/genome/?taxon=4890>, 12 August 2022) for obtaining a metadata table that contains basic information including assembly accession, scientific name, size, sequencing technology and the submitter. Simultaneously, a taxonomic scheme table was prepared according to the latest outline of Wijayawardene et al. (2022), which covers all generic names and the corresponding lineage information. Besides, several changes were added in keeping with the latest literature (Sun et al. 2021, Magyar et al. 2022, Sugita & Tanaka 2022). The genus names as “baits” were used to retrieve all genomic sequences that belong to the class Sordariomycetes and further removed duplicated genomes by their strain names, identifiers and background description. With written permission, several genomes from JGI Genome Portal (Grigoriev et al. 2014) were also included. The genomes of lousy quality with BUSCO completeness below 80% were discarded. For the species with multiple genomes available, the reliability of the genome was checked (relevant publication records, collection information, NCBI project description) and selected no more than two genomes as representatives. The strain *Allantophomopsis lycopodina* (ATCC 66958) from class Leotiomycetes was selected as the outgroup taxon.

BUSCO assessment and phylogenomic data matrix construction

Evaluation of the quality of genome assemblies is of great importance to recognize possible issues during genomic studies (Manni et al. 2021a). The tool BUSCO (Benchmarking Universal Single-Copy Orthologs) uses universal single-copy orthologs to identify the homologous proteins in target genomes and further estimate completeness. In addition, the identified conserved BUSCO genes are ideal candidate barcodes for genome-scale phylogenomic analysis (Waterhouse et al. 2018, Manni et al. 2021b) and have been widely used in diverse eukaryotic lineages. In this study, all genome assemblies were assessed using BUSCO version 5.3.3 with the “ascomycota_odb10” as the benchmarking data set. BUSCO genes of all Sordariomycetes genomes and the outgroup were

assembled into single-copy protein datasets using an in-house python script. These datasets whose taxon coverage is below 80% were removed and multiple sequence alignment for each dataset was conducted using MAFFT version 7.310 with the option “--auto” (Kato et al. 2002). Poorly aligned regions were removed using trimAl version v1.4. rev15 based on the gappyout strategy (Capella-Gutiérrez et al. 2009). The alignments whose trimmed alignment length were below 300 were removed. The remaining trimmed alignments were concatenated using an in-house python script.

Phylogenetic analysis

The best-fitting amino acid substitution model for each BUSCO alignment, was inferred using IQ-TREE version 2.0.3 with options “-m TESTONLY --mset mrbayes” with the Corrected Akaike Information Criterion (Nguyen et al. 2015). The concatenation-based ML tree was inferred using IQ-TREE under a single evolutionary model “LG + G4”, as 899 of 1124 proteins favored “LG + G4” as the best-fit model. The topology of the concatenation-based tree was assessed using 1000 replicates for ultrafast bootstrap approximation (UFboot) (Hoang et al. 2018) and SH-like approximate likelihood ratio test (SH-aLRT) (Guindon et al. 2010). *Allantophomopsis lycopodina* (ATCC 66958) was used as the outgroup to root the phylogeny. The phylogenetic tree was visualized using the R package ggtree (Yu et al. 2017) and further edited in Adobe Illustrator 2020.

Time dating

Since the introduction of the molecular clock by Zuckerkandl & Pauling in 1965, many methods, including local molecular-clocks (Yoder & Yang 2000), the Bayesian technique (Kishino et al. 2001), the penalized likelihood approach (Sanderson 2002, 2003) and the RelTime method (Tamura et al. 2012) were developed to estimate divergence time. However, in the era of post-genomics, only the RelTime is capable of handling genome-scale datasets, and it has been proven to obtain similar and reliable results to other Bayesian approaches (Mello et al. 2016). The rare fossil of *Paleoophiocordyceps coccophagus* in Sordariomycetes was used to represent the genus *Ophiocordyceps* in previous molecular dating studies (Sung et al. 2008, Samarakoon et al. 2016). In this study, we used RelTime implemented in MEGA-X (Kumar et al. 2018) and the ML tree as input to inference the TimeTree. In order to minimize the difference in selecting the time calibrations with the previous studies, we followed the calibration scheme of Samarakoon et al. (2016) with slightly adjusted to suit the program. The origin of the class Sordariomycetes was set with normal distribution, mean = 250 Mya, SD = 45, and the origin of the genus *Ophiocordyceps* was set to at least 27.5 Mya (Samarakoon et al. 2016, Hyde et al. 2017, 2020).

Results & Discussion

Phylogenomics of Sordariomycetes

A total of 638 genomes of Sordariomycetes, which include 625 species covering 156 genera, 50 families, 17 orders, and five subclasses, were selected in this study. The concatenated dataset for up to 1224 conserved BUSCO protein sequences was assembled, and we obtained a consistent and well-supported phylogeny. The tree was rooted to *Allantophomopsis lycopodina* (ATCC 66958) from Leotiomycetes. When clades are discussed, the SH-aLRT values are followed by UFBoot values (Figs 1, 2). We use the following three terms to discuss support values in the phylogenomics trees: (1) nodes with ≥ 80 and ≥ 95 are described as fully supported; (2) nodes with < 80 & ≥ 95 are described as moderately supported and (3) nodes with ≥ 80 & < 95 ; < 80 & < 95 are described as weakly supported or could not come to a conclusion. Sordariomycetidae, Hypocreomycetidae, Xylariomycetidae, Diaporthomycetidae and Lulworthiomycetidae were described as in the previous treatment of Lumbsch & Huhndorf (2010) and Maharachchikumbura et al. (2015).

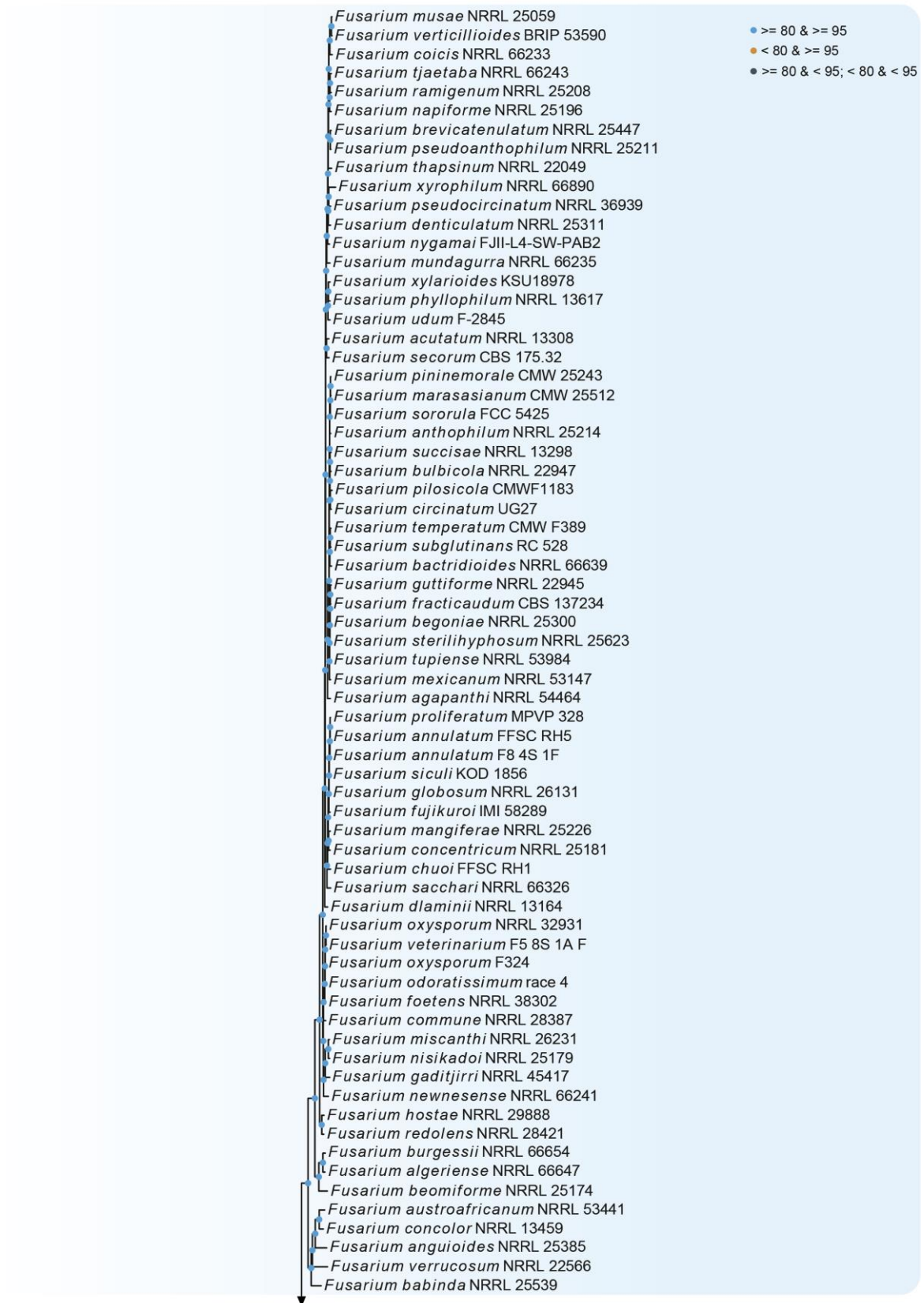


Figure 1 – The concatenation-based ML tree (lnL = -134234602.321) based on 1124 single-copy orthologous proteins for the analyzed Sordariomycetes isolates. Genera are indicated in dark and light blue-coloured blocks and polyphyletic groups are indicated in dark grey-coloured blocks. ultrafast bootstrap approximation (UFboot) and SH-like approximate likelihood ratio test (SH-aLRT) are given at the nodes. The tree is rooted with *Allantophomopsis lycopodina* (ATCC 66958).

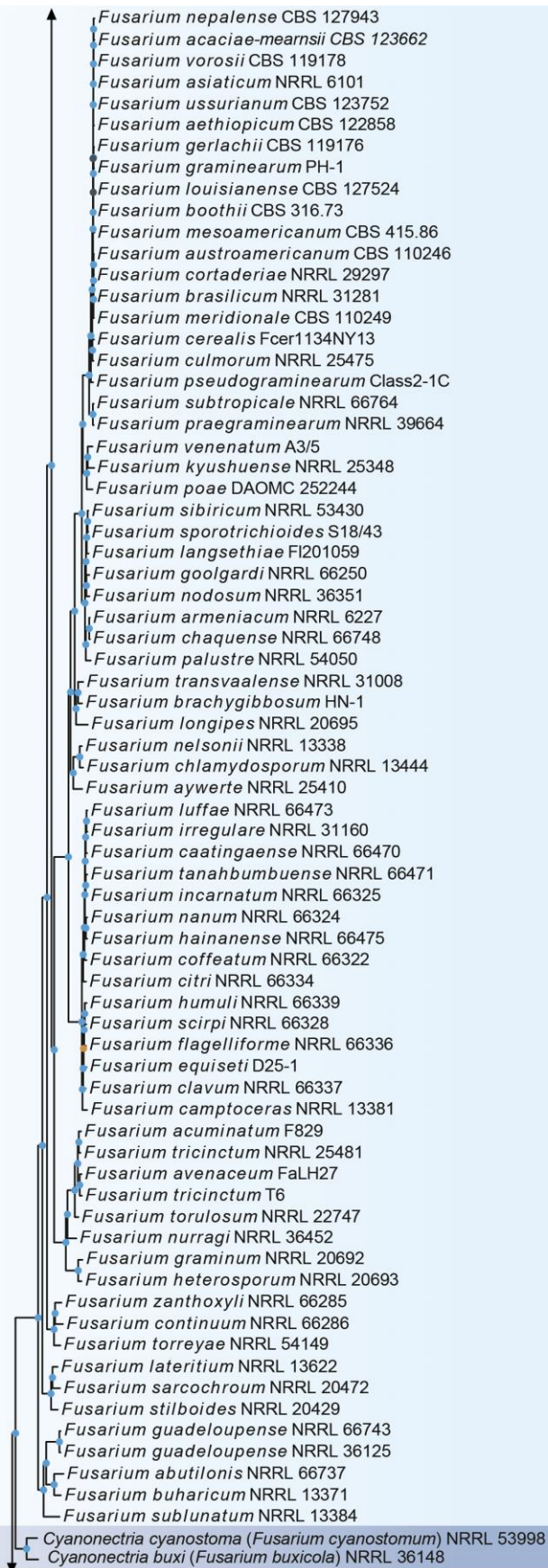


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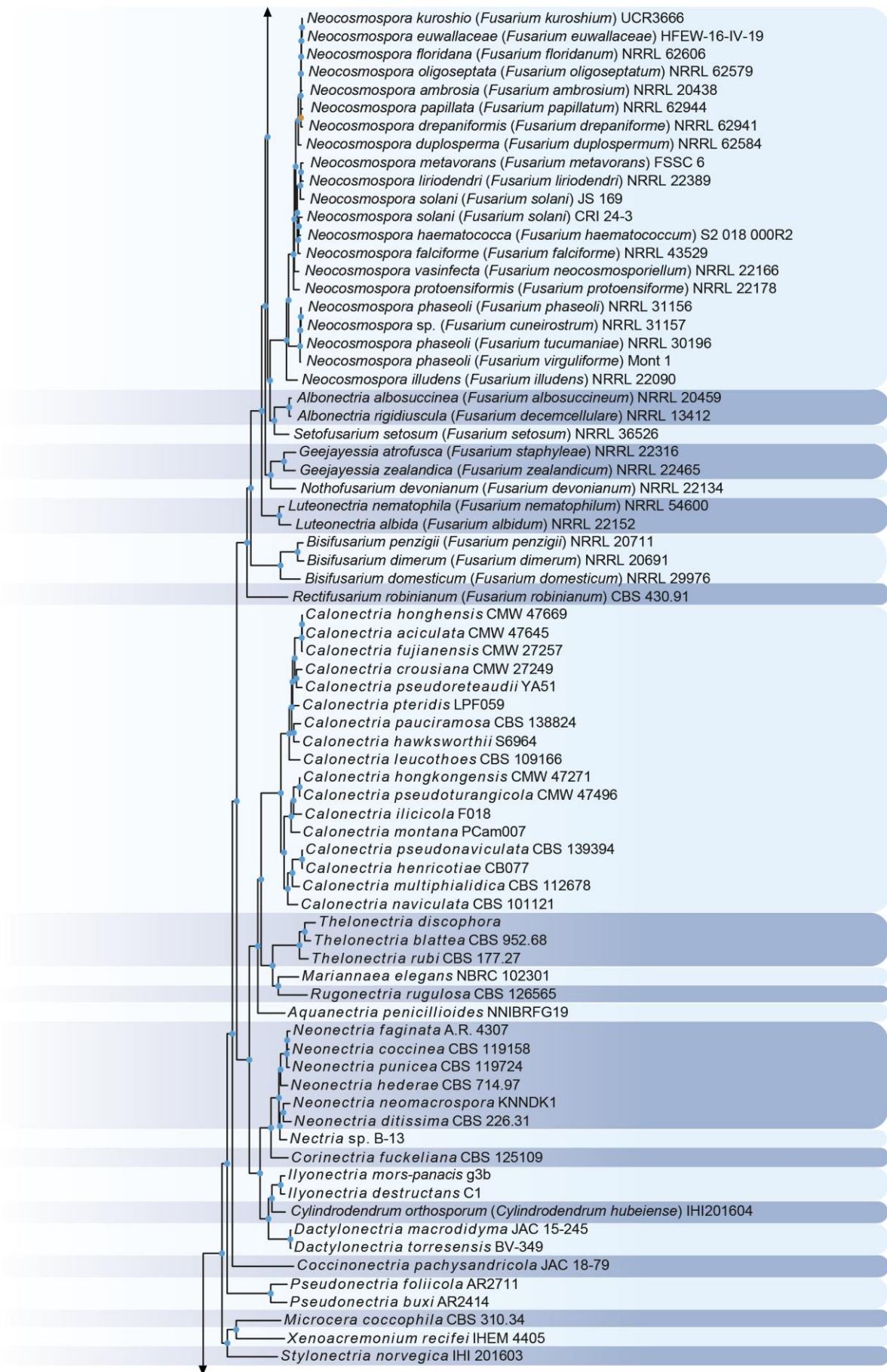


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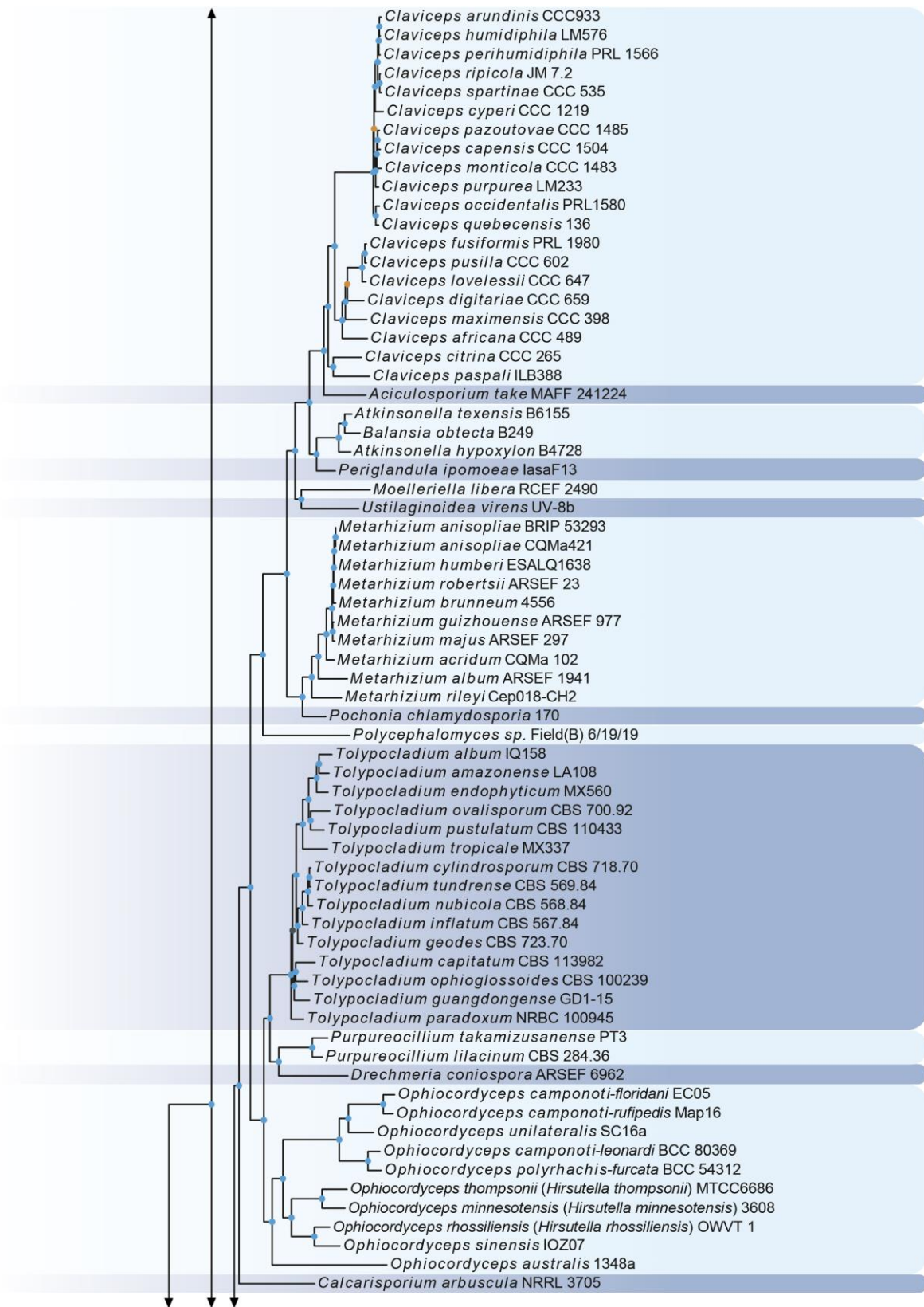


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Divergence time estimation

The divergence time of fungal lineages supports significantly in understanding the processes of fungal evolution and optimizing the current taxonomic scheme (Divakar et al. 2017, Hyde et al. 2017, 2020, Zhao et al. 2017, Dayarathne et al. 2019, He et al. 2019).

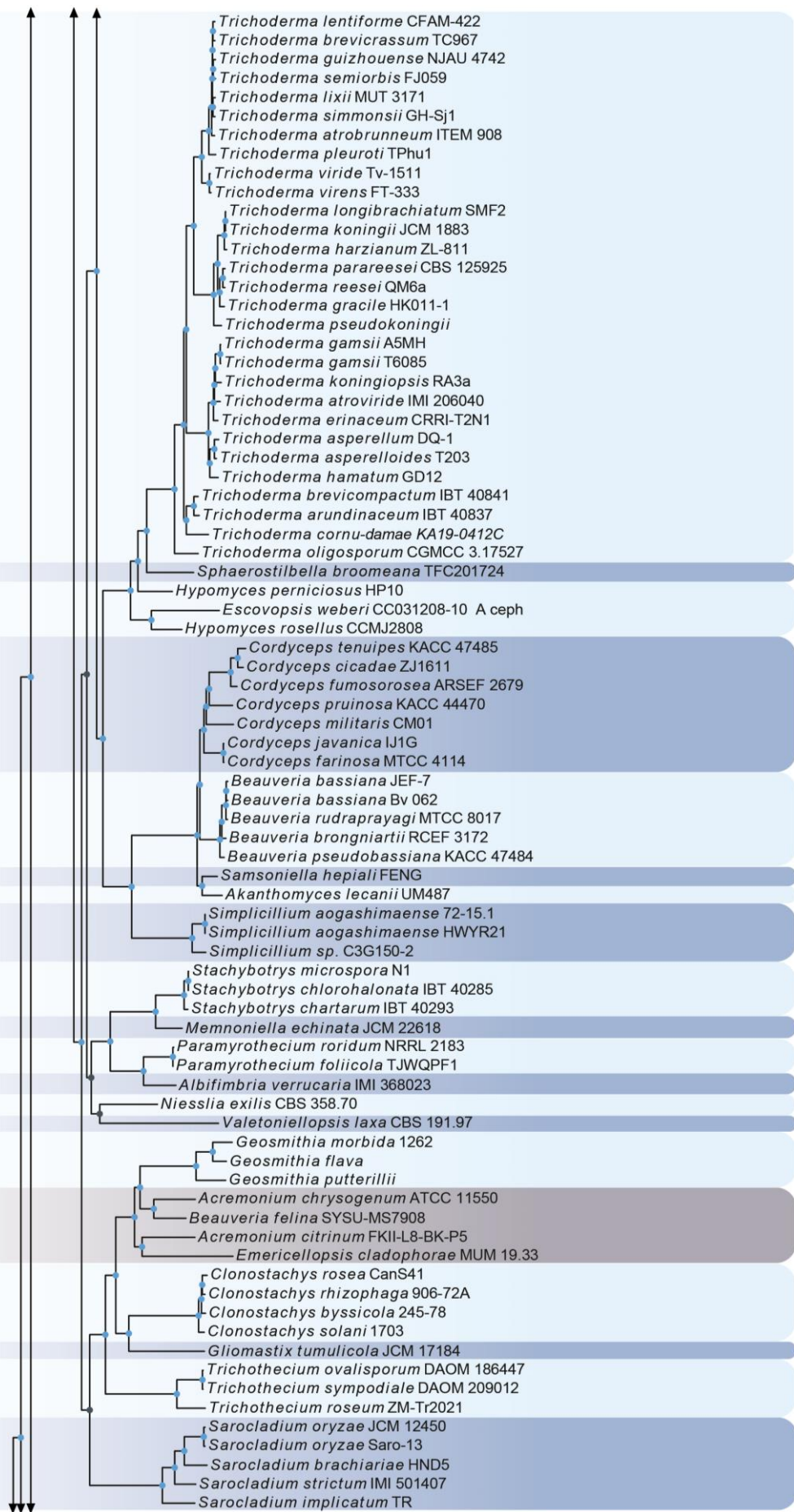


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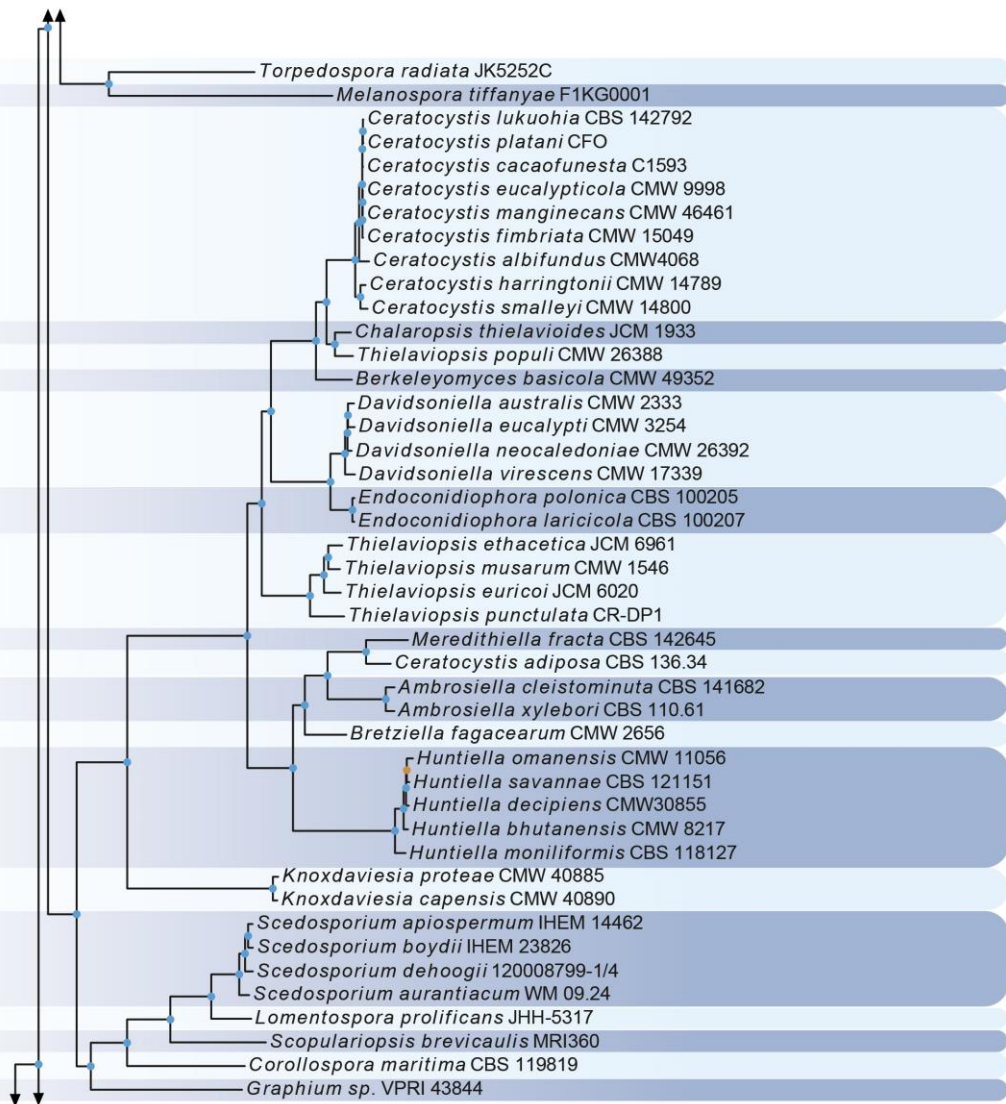


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However, divergence time estimation obtains the genetic distances of the extant taxa displayed as branch length, then scales the branch length to time scale with time calibrations, the accuracy of which depends on multiple factors, including the number of loci (Dos Reis & Yang 2013), clock calibrations selected (Roger & Hug 2006, Hug & Roger 2007), evolutionary model (Kelchner & Thomas 2007, Schenk & Hufford 2010), and the level of taxon sampling (Linder et al. 2005). In this study, we selected representative genomes to include as many genera as possible, and a total of 1224 conserved protein sequences to calculate the genetic distance and obtained a TimeTree of Sordariomycetes. Although the accuracy does not increase indefinitely with the number of loci (Dos Reis & Yang 2013, Morris et al. 2018), we confirmed that our genome-scale dataset provided more sites to calculate and optimize the branch lengths than previous molecular dating studies that used few barcodes. Furthermore, studies dating the tree of life using genome-scale data are becoming more and more (Ohm et al. 2012, Morris et al. 2018, Karpinski et al. 2020, Shen et al. 2020, Álvarez-Carretero et al. 2022), and the divergence times of most taxonomic groups inferred from genome-scale datasets are broadly aligned with the current taxonomic scheme and genome sequence divergence at higher level (Li et al. 2021).

Despite the reliable datasets, time dating often remains difficult in selecting convincing calibration points for many groups that lack fossil records (Rutschmann et al. 2007, Schenk 2016). *Paleoophiocordyceps coccophagus* was the reference fossil for estimating divergence times, which is from Hypocreales and resembles the asexual forms of *Hirsutella* and *Hymenostilbe* (Sung et al.

2007). These genera are synonymized under *Ophiocordyceps* by Quandt et al. (2014), and was followed by subsequent studies (Maharachchikumbura et al. 2015, 2016, Simmons et al. 2015a, b, Wang et al. 2018).

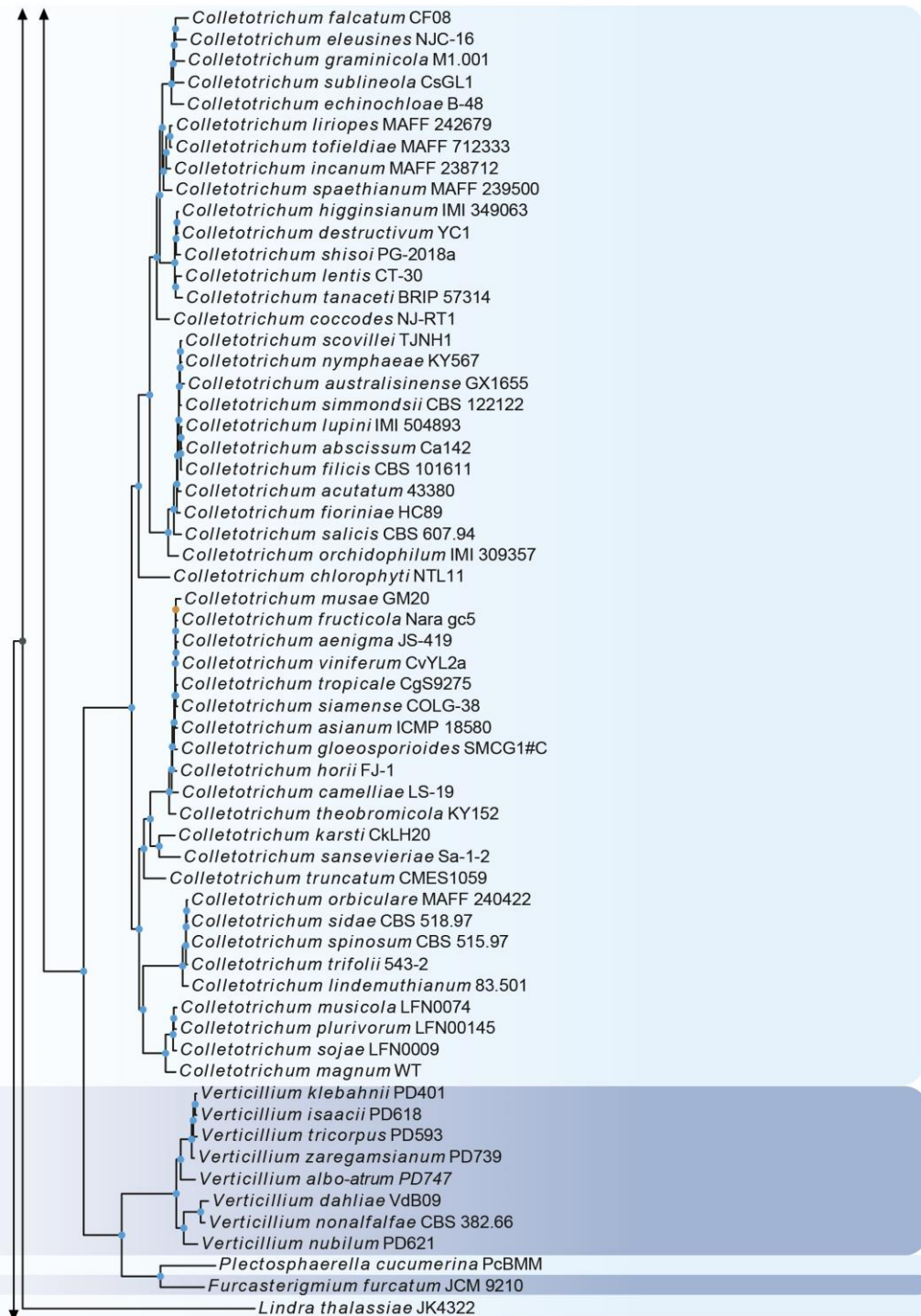


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However, Hyde et al. (2020) accepted *Hirsutella* and *Hymenostilbe* as distinct genera without giving a specific reason. Another fossil record is *Spataporthe taylori*, which provides a calibration time for the order Diaporthales at least 136 Mya (Bronson et al. 2013). We tested these calibrations during initial analyses, and the divergence times are generally older than the previous studies of Samarakoon et al. (2016) and Hyde et al. (2020). Considering the remarkable results of previous molecular dating studies and comparative analysis, we followed Quandt et al. (2014) and accepted

Paleoophiocordyceps, *Hirsutella*, and *Hymenostilbe* as a synonym of *Ophiocordyceps* and set the *Ophiocordyceps* crown at least 27.5 Mya. The secondary calibration of the crown age of Sordariomycetes at ~ 250 Mya, which is widely used calibration in the molecular clock studies of Ascomycota, was used to constrain the time scale. According to the molecular clock analysis, the crown age of the extant Sordariomycetes dates to ~250 Mya (95% HPD = 187–312 Mya), which is similar to the estimate (233, 95% HPD = 182–316 Mya) of Beimforde et al. (2014), whereas (Taylor & Berbee 2006) accepted the calibration of minimum age for Sordariomycetes at 400 Mya. In this study, we are not trying to investigate the influences of calibrations but to provide a genome-scale TimeTree for Sordariomycetes and compare the divergence time of main groups with the previous studies.

Subclasses

Seven subclasses are accepted in Sordariomycetes, and genomics data are available for the subclasses Diaporthomycetidae, Hypocreomycetidae, Lulworthiomycetidae, Sordariomycetidae and Xylariomycetidae.

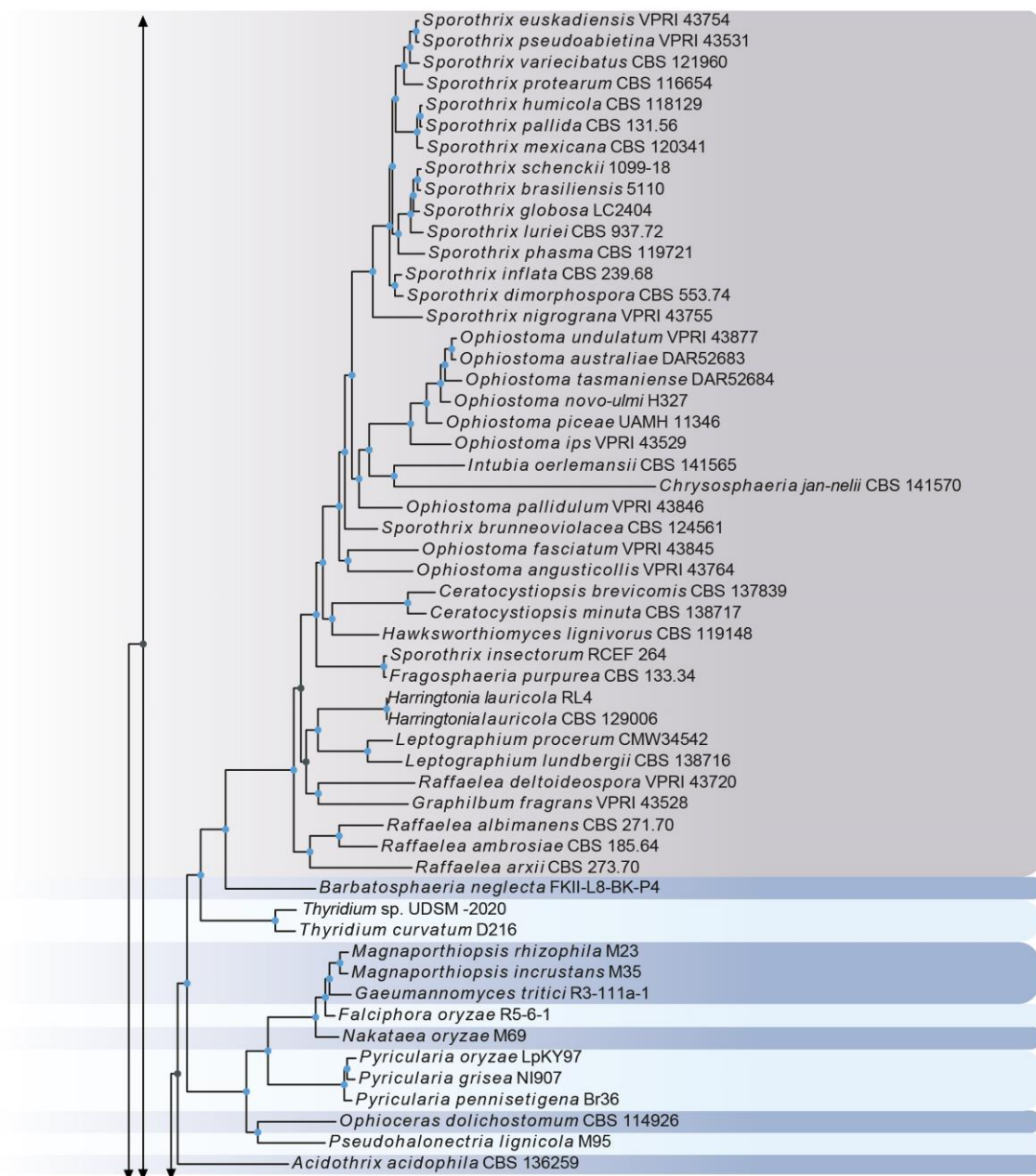


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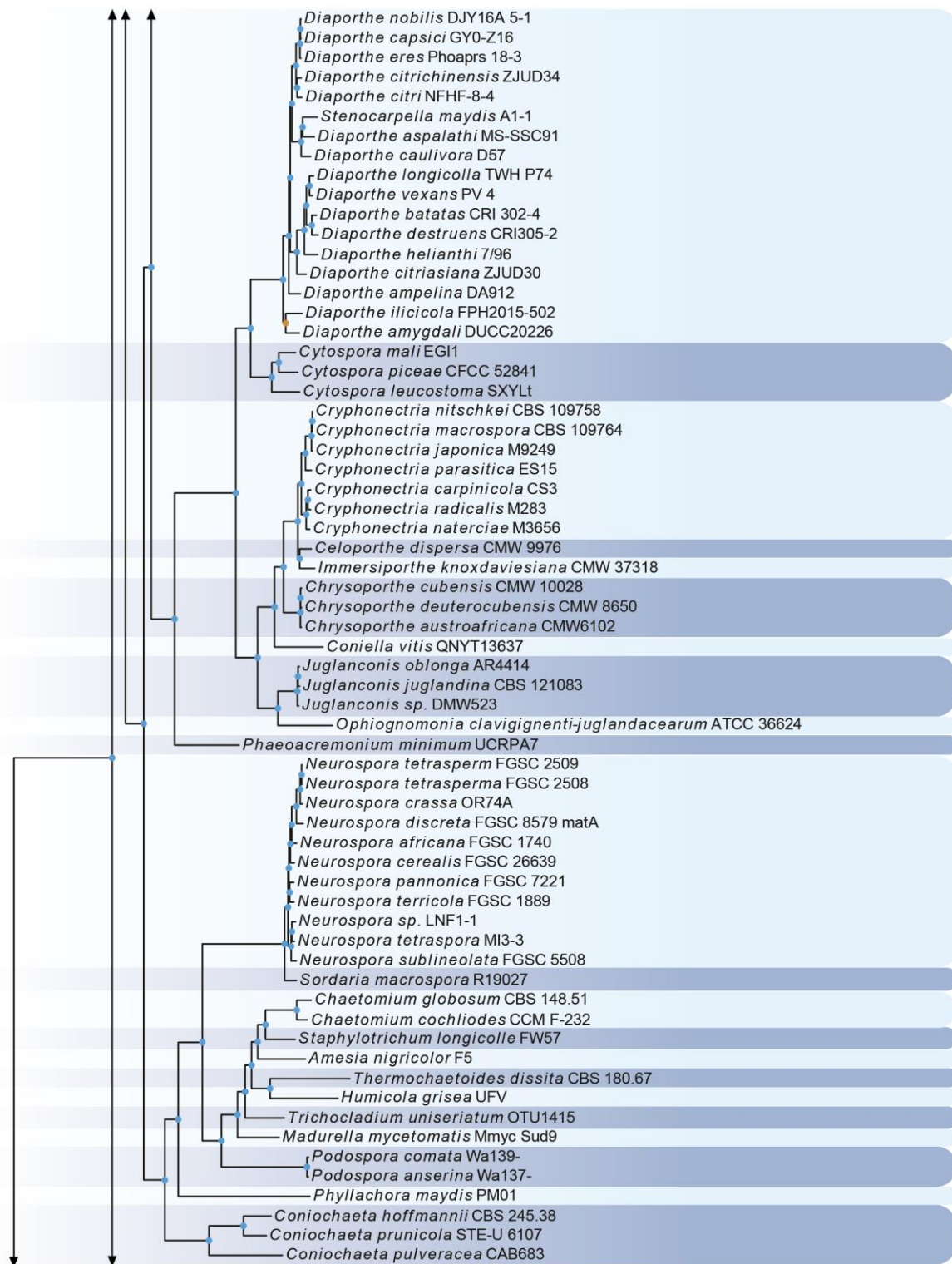


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Diaporthomycetidae

Maharachchikumbura et al. (2015) introduced the subclass as a segregation from Sordariomycetidae. Diaporthomycetidae comprises 15 orders and 59 families, and genomic data are available for 5 orders and 14 families. Our calibrated tree reveals that the Diaporthomycetidae crown and stem ages date to ~193 Mya (95% HPD = 113.59–309.79 Mya) and ~205 Mya (95% HPD = 130.04–309.79 Mya), respectively, lower ages than what has been found in previous studies (Samarakoon 2016, Hyde et al. 2017, 2020, 2021). These previous molecular dating analyses from the 4 loci dataset showed that Diaporthomycetidae is the youngest subclass of Sordariomycetes. We

estimate that more validation studies that incorporate additional genome data may be required for clarifying the status of Diaporthomycetidae as a distinct subclass or to place it under the subclass Sordariomycetidae.

The phylogenomic tree supports all the orders (Barbatosphaeriales, Magnaporthales, Diaporthales, Togniniales, Ophiostomatales and Thyridiales) of Diaporthomycetidae except Amplistromatales (Fig. 1). The order Amplistromatales was introduced by Maharachchikumbura et al. (2015), and since it appears to have a distant relationship with Meliolomycetidae (now synonymized under Sordariomycetidae) and Sordariomycetidae, it was placed in Sordariomycetes order *incertae sedis*. The placement of Amplistromatales is doubtful in preceding studies, which suggests that this order is unstable and treated in different subclasses, Diaporthomycetidae and Sordariomycetidae (Hyde et al. 2017, 2020, 2021). Even though the sister order relationship cannot be fully clarified in this study, Amplistromatales clusters as an internal clade of Diaporthomycetidae, and we accordingly suggest treating it under Diaporthomycetidae.

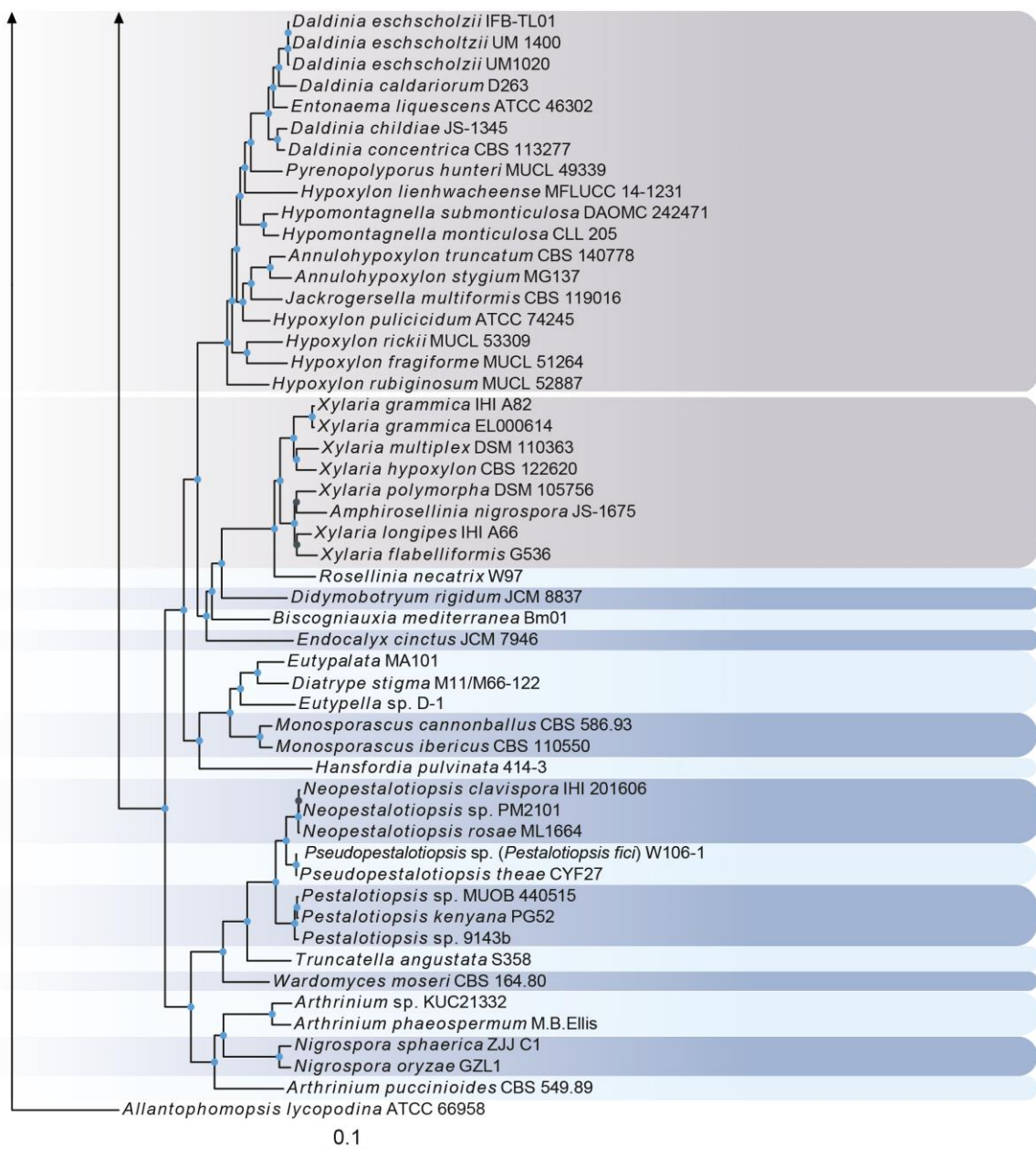


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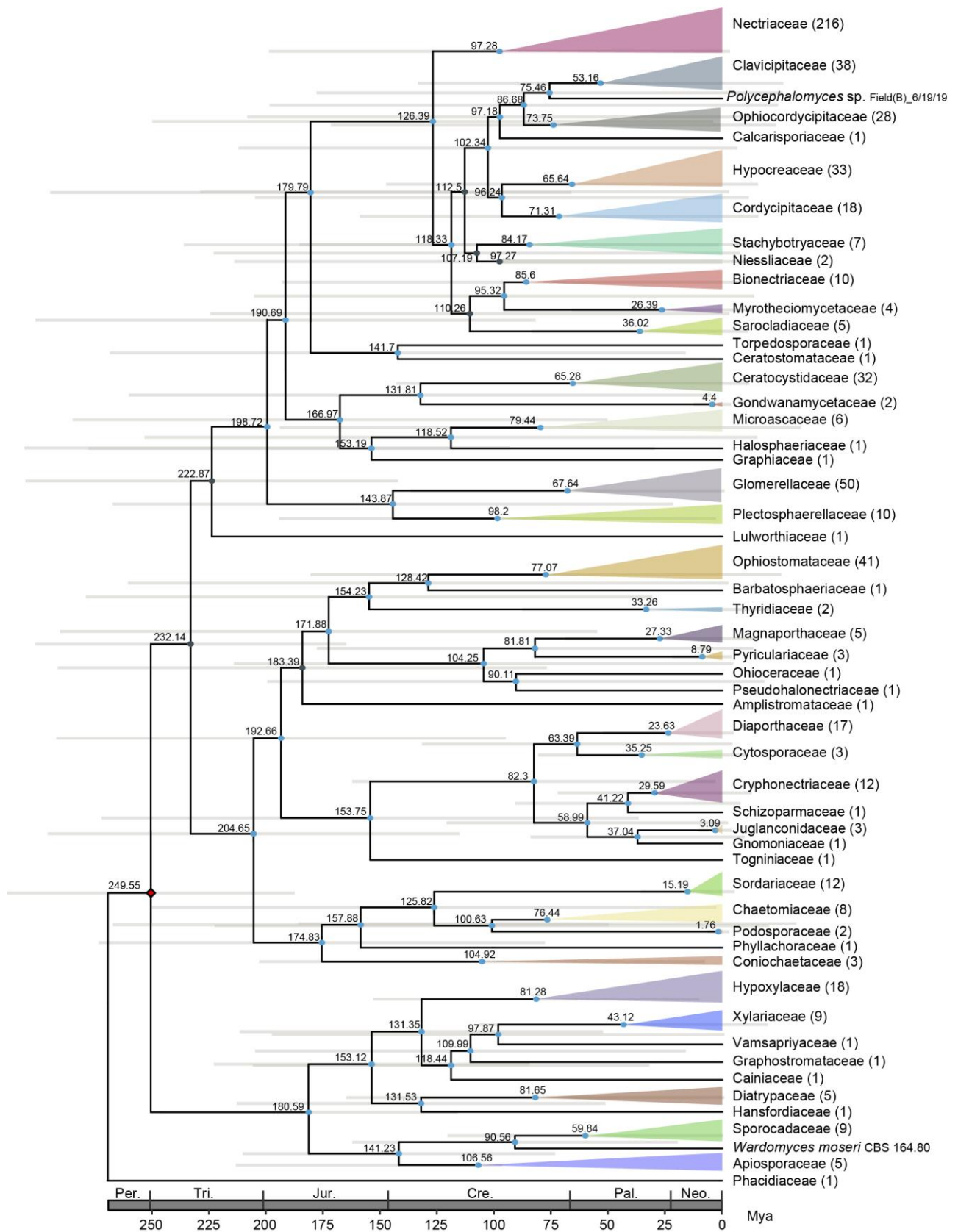


Figure 2 – The maximum clade credibility (MCC) tree from the RelTime analysis, using the same dataset from Fig. 1. Calibration points are noted using red, whereas fossil calibration at the genus level was not displayed due to the collapse. Node ages are given at the nodes, and divergence times are shown in millions of years. Light grey bars correspond to the 95% highest posterior density (HPD) intervals. The number after the family name represents the number of taxa. Neo.: Neogene, Pal.: Paleogene, Cre.: Cretaceous, Jur.: Jurassic, Tri.: Triassic, Per.: Permian.

The stem age of order Amplistromatales is ~183 Mya (95% HPD = 309.79 – 96.31 Mya). According to molecular clock analysis, Thyridiales diverged from Barbatosphaeriales + Ophiostomatales ~154 Mya (95% HPD = 309.79–62.51 Mya). The family Thyridiaceae has long been treated in the Sordariomycetes families *incertae sedis*. Sugita & Tanaka (2022) revised the family Thyridiaceae and synonymized Phialemoniopsidaceae, which was introduced by Hyde et al. (2021) under Thyridiaceae, and the new order Thyridiales in Sordariomycetes was established to accommodate it. The orders Barbatosphaeriales and Ophiostomatales have similar ages dating back ~128 Mya (95% HPD = 309.79–47.65 Mya). The age of Barbatosphaeriales is somewhat younger than recent studies of Hyde et al. (2021) (177 Mya) but broadly consistent with Hyde et al. (2020) (135 Mya). Hyde et al. (2021) noted that Magnaporthales is the oldest order within Diaporthomycetidae, with a stem age of 204 Mya; however, in the present study, the stem age of Magnaporthales is somewhat younger than Hyde et al. (2021) at ~172 Mya (95% HPD = 309.79 – 75.17 Mya) but consistent with Hyde et al. (2020) at (190 Mya). Stem age of the Diaporthales is younger than estimates from most other researchers (Hyde et al. 2017, 2020, 2021) at ~154 Mya (95% HPD = 309.79–75.42 Mya). The stem age of Togniniales, ~154 Mya (95% HPD = 309.79–75.42 Mya), is more consistent with other previous molecular estimates (Hyde et al. 2017, 2020, 2021).

All the families of Diaporthomycetidae are highly supported in phylogenomics analysis, and stem ages range from ~37 Mya to ~183 Mya. The Amplistromataceae is the oldest family, while Juglanconidaceae and Gnomoniaceae are the youngest.

Hypocreomycetidae

Currently, there are seven orders (Coronophorales, Falcocladales, Glomerellales, Hypocreales, Microascales, Parasymphodiellales and Torpedosporales) and 37 families in this subclass, and genomics data are available for 5 orders and 20 families. Fungal species belonging to Hypocreomycetidae are characterized by diverse life modes, and many members are well-known plant animal and human pathogenic species (Huang et al. 2021b). Therefore, subclass Hypocreomycetidae has the highest amount of genomic data in public databases. The stem age for Hypocreomycetidae has been estimated at ~223 Mya (95% HPD = 309.79–147.13 Mya) (Fig. 2), which is slightly younger (~256.5 Mya) than Hyde et al. (2020).

All the orders of Hypocreomycetidae are well-supported in the phylogenomic analysis, while most of the families are well-supported, excluding the Niessliaceae and Sarocladiaceae in Hypocreales (Figs 1, 2). Glomerellales is the oldest order of Hypocreomycetidae, with a stem age of ~199 Mya (95% HPD = 309.79–97.97 Mya) that is in agreement with a previous divergence time estimation by Hyde et al. (2020) (~216 Mya), despite being younger than Hyde et al. (2017) (~256 Mya). We found the origin of Microascales features a stem age of ~191 Mya (95% HPD = 309.79–91.56 Mya), which is in large agreement with a previous divergence time estimation by Hyde et al. (2020) (~216 Mya). The origin of orders Coronophorales and Torpedosporales were dated to a stem age of ~180 Mya (95% HPD = 309.79–58.40 Mya). Previous analysis by Hyde et al. (2020) showed the origin of these orders within the same age (Torpedosporales: 185 Mya; Coronophorales: 192 Mya). The divergence time for Hypocreales, the largest order, has been estimated as ~180 Mya (95% HPD = 309.79–82.42 Mya), which is younger than estimates from Hyde et al. (2020) who estimated the age of the order to be 229 Mya. Molecular dating analysis showed the origin of families of Hypocreomycetidae occurring between ~75 Mya to ~180 Mya, with the Nectriaceae as the oldest family and Clavicipitaceae the youngest.

Lulworthiomycetidae

The subclass Lulworthiomycetidae was introduced by Maharachchikumbura et al. (2015), and it accommodates the two orders Koraliastetales and Lulworthiales and the two families Koraliastetaceae and Lulworthiaceae (Dayarathne et al. 2019). A single genome sequence is available for the group *Lindra thalassiae* from Lulworthiales. The molecular dating analysis (Fig. 2) from the genomic dataset showed the split between Lulworthiomycetidae and

Hypocreomycetidae occurred around ~223 Mya (95% HPD = 309.79–147.13 Mya). Hyde et al. (2020) and Dayarathne et al. (2019) estimated the divergence time for Lulworthiomycetidae at 257 Mya and 310 Mya, respectively. Members of Lulworthiomycetidae are distinct from taxa belonging to other orders in Sordariomycetes as many of them are restricted to marine habitats, and some members, such as Koralionastetales, form antheridia on their germinating ascospores (Zhang et al. 2006). Previously, the order Pisorisporiales was also included in Lulworthiomycetidae (Maharachchikumbura et al. 2015), while Hyde et al. (2020) transferred it to the newly introduced subclass Pisorisporiomycetidae. Due to insufficient genome samples and missing ranks, Lulworthiomycetidae still requires substantial rank filling in future studies.

Sordariomycetidae

Sordariomycetidae is the earliest subclass of Sordariomycetes, accommodating eight orders and 18 families. Genomic data are available for the Coniochaetales, Phyllachorales and Sordariales as well as families Chaetomiaceae, Coniochaetaceae, Phyllachoraceae, Podosporaceae and Sordariaceae. The stem age for Sordariomycetidae has been estimated at ~205 Mya (95% HPD = 309.79–130.04 Mya) (Fig. 2), when it split from the members of Diaporthomycetidae, which was found to be younger than the estimation in previous study of Hyde et al. (2020) (247 Mya). The crown group age of Sordariomycetidae dates to ~175 Mya (95% HPD = 297.52–102.73 Mya). Based on available genomic data, Coniochaetales is the oldest order of Sordariomycetidae, with a stem age of ~175 Mya (95% HPD = 297.53–102.73 Mya) which is consistent with Hongnan et al. (2017) (176 Mya), though it is older than estimates from Hyde et al. (2020) (131 Mya). The stem leading to the Phyllachorales is estimated at ~158 Mya (95% HPD = 297.53–81.26 Mya) and consistent with the estimations of Hyde et al. (2020) (168 Mya). The order Sordariales has a similar stem age as Phyllachorales and is older than the estimation of Hyde et al. (2020) (128 Mya). The origin of families of Sordariomycetidae occurred between ~101 Mya to ~175 Mya (stem ages), and Coniochaetaceae is the oldest family, while Chaetomiaceae and Podosporaceae are the youngest. In phylogenomic analysis, all orders and families are well-supported (Fig. 1).

Xylariomycetidae

The orders Amphisphaeriales, Delonicicolales and Xylariales are presently included in the subclass Xylariomycetidae, and genome data are available only for Amphisphaeriales and Xylariales. Molecular dating analysis from the present study revealed that the stem age of Xylariomycetidae dated back to ~250 Mya (95% HPD = 312.68–187.11 Mya), which is slightly younger than the estimation of Hyde et al. (2020) (278 Mya). The orders Amphisphaeriales and Xylariales split around ~181 Mya (95% HPD = 256.96–126.92 Mya). The crown ages of Amphisphaeriales and Xylariales are estimated at ~141 Mya (95% HPD = 225.09–88.61 Mya) and ~153 Mya (95% HPD = 236.75–99.03 Mya), respectively, and in agreement with Samarakoon et al. (2016) and Hyde et al. (2020). Molecular dating analysis showed that the origin of families of Xylariomycetidae occurred between ~91 Mya to ~141 Mya (stems ages), and the Apiosporaceae is the oldest, while Xylariaceae and Vamsapriyaceae are the youngest.

The phylogenomic analysis supports all the orders and families of Xylariomycetidae (Fig. 1). Hyde et al. (2017) treated Cainiaceae under families *incertae sedis* in Xylariomycetidae, since it formed a distinct lineage from Amphisphaeriales and Xylariales. However, in later studies, Cainiaceae was treated as a family of Xylariales (Hyde et al. 2020, Samarakoon et al. 2022), and our phylogenomics study confirms its placement in Xylariales.

Future progress

Phylogenomic studies not only clarify the higher-level taxonomy of Sordariomycetes but also provide a deeper understanding and diversification of species-level phylogenies. For instance, there has long been disagreement between authors regarding the assigning of taxa of the *Fusarium solani* species complex to *Neocosmospora* (Lombard et al. 2015) and segregating new genera that were formerly treated as *Fusarium* (O'Donnell et al. 2020, Geiser et al. 2021). Crous et al. (2021), based

on multifaceted evidence, emphasized that the broad circumscription of *Fusarium sensu stricto* is fuzzy and treated those genera as distinct. In the present study, we included nine genera (*sensu lato*), including three newly segregated genera *Luteonectria*, *Nothofusarium* and *Setofusarium*, and these nine nodes are well-supported in the present phylogenomic tree and distinct from *Fusarium*.

It is estimated that at least 20 unrelated genes or 8000 randomly selected orthologous nucleotides are required to reconstruct a reliable systematic framework for fungi (Rokas et al. 2003). Phylogenetic analysis using large numbers of genes from multiple independently evolving regions across the genome maximizes information content and limits stochastic errors, thus improving phylogenetic accuracy (Zhang et al. 2017b). Genomic data not only increase our understanding of the systematics of fungi but also provide new insights into speciation, diversity, virulence, and biosynthetic potential at the species level (Maharachchikumbura et al. 2021).

The accurate classification of Sordariomycetes taxa at the family and higher levels remains a challenging task. Inconsistencies are frequently observed within various lower-number gene phylogenies and shared phenotypic characteristics between these higher-level taxonomic ranks, resulting in a highly subjective classification scheme, and phylogenetic relationships among many higher ranks have been disordered for some time. Our phylogenomic analysis provides new insights into the higher ranks of Sordariomycetes, and most of the nodes are well-supported. However, the same cannot be said about divergent time estimations. Our analysis and previous studies (Samarakoon et al. 2016, 2022, Hongsanan et al. 2017, Hyde et al. 2017, 2020, 2021, Dayarathne et al. 2019) have provided mixed results and highly inconsistent divergent time estimates, which have been debated extensively. Furthermore, sister group relationships among families and orders of Sordariomycetes remain a long-standing problem.

Therefore, in order to obtain a reliable taxonomic framework for the higher ranks of class, we should consider a range of empirical criteria/approaches for defining higher lineages of the Sordariomycetes. To avoid inherent biases associated with single methodological approaches when resolving or introducing higher ranks, there is great potential in the application of more promising polyphasic approaches. Wherever possible, families in orders could be separated by similar types of characteristics. For example, authors who introduce a new family should strive to ensure that the types of characteristics make it distinguishable are comparable to those that distinguish other families in the same order. Therefore, it is necessary to study the taxonomic criteria used in a given group before establishing a new rank within it to ensure that they are natural groups. Several genomes from each family should be sequenced to fill the ranks. It is quite clear that increased sampling and more robust genomic data are likely to strengthen the backbone of Sordariomycetes and reduce the long-branch attraction, which will also help determine sister group relationships and accurately resolve the ranks with unstable placements that have been placed in Sordariomycetes *incertae sedis*. Applying a strict timescale to higher ranks of Sordariomycetes is implausible. Therefore, when introducing a new rank, rather than enforcing a strict scale for the origin of families, orders, and subclasses of Sordariomycetes, we should adopt a more empirical scale based on each individual study and compare results with the already well-established, stable and higher ranks that have adequate sampling such as Hypocreales. The crown age, stem age, and stability of the sister groups in witness from different studies and methods will contribute to the standardization of delineated taxonomic ranks.

Conclusion

Hierarchical classification systems are not definitive and can be impacted by arbitrary practices; therefore, taxonomists have been developing methods to help standardize taxonomic ranks. Until recently, most molecular studies of Sordariomycetes consisted of limited taxonomic sampling. It is quite clear that a detailed study of both the molecular phylogeny and divergence times of Sordariomycetes requires additional taxonomic sampling, complete sets of SSU, LSU, TEF and RPB2 loci and additional genomic data, especially for families that lack genomes. In this study, we include 638 genome sequences of Sordariomycetes isolates to provide a backbone tree for the class. Our generated phylogenomic tree is sufficiently robust, and our study sheds light on

the higher-level relationships in Sordariomycetes. Divergent time estimation provides inconsistent results compared to previous studies that suggest enforcing a strict scale for the origin of higher ranks, which we believe to be inadequately complete. This backbone tree needs to expand in future studies to include missing lineages and representative genomes from each family, which we are currently undertaking. Through this, we hope to eventually derive a stable and natural classification of the class using multifaceted evidence.

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Supplementary Table 1 Genome information of 639 genomes and BUSCO completeness.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|---|-------------------|------------------------|------------------------|
| <i>Aciculosporium take</i> | MAFF 241224 | GCA_000222935.2 | 95.1 |
| <i>Acidothrix acidophila</i> | CBS 136259 | NA | 97.5 |
| <i>Acremonium chrysogenum</i> | ATCC 11550 | GCA_000769265.1 | 97.6 |
| <i>Acremonium citrinum</i> | FKII-L8-BK-P5 | GCA_022814615.1 | 97.7 |
| <i>Akanthomyces lecanii</i> | UM487 | GCA_001653215.1 | 81.0 |
| <i>Albifimbria verrucaria</i> | IMI 368023 | GCA_020081605.1 | 82.2 |
| <i>Allantophomopsis lycopodina</i> | ATCC 66958 | GCA_024752465.1 | 98.3 |
| <i>Ambrosiella cleistominuta</i> | CBS 141682 | GCA_017139545.1 | 95.7 |
| <i>Ambrosiella xylebori</i> | CBS 110.61 | GCA_002778035.1 | 96.9 |
| <i>Amesia nigricolor</i> | F5 | GCA_004802645.1 | 97.8 |
| <i>Amphirosellinia nigrospora</i> | JS-1675 | GCA_004123355.1 | 80.1 |
| <i>Annulohypoxylon stygium</i> | MG137 | GCA_003314315.1 | 98.4 |
| <i>Annulohypoxylon truncatum</i> | CBS 140778 | GCA_902805465.1 | 97.5 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|--------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Aquanectria penicillioides</i> | NNIBRFG19 | GCA_003415625.1 | 95.1 |
| <i>Arthriniium phaeospermum</i> | M.B.Ellis | GCA_006503535.1 | 94.7 |
| <i>Arthriniium puccinioides</i> | CBS 549.89 | GCA_022414665.1 | 96.3 |
| <i>Arthriniium</i> sp. | KUC21332 | GCA_017163955.1 | 97.8 |
| <i>Atkinsonella hypoxylon</i> | B4728 | GCA_000729835.1 | 97.3 |
| <i>Atkinsonella texensis</i> | B6155 | GCA_001008035.1 | 97.4 |
| <i>Balansia obtecta</i> | B249 | GCA_000709145.1 | 97.2 |
| <i>Barbatosphaeria neglecta</i> | FKII-L8-BK-P4 | GCA_022813145.1 | 93.6 |
| <i>Beauveria bassiana</i> | Bv 062 | GCA_003337105.1 | 96.6 |
| <i>Beauveria bassiana</i> | JEF-007 | GCA_002871155.1 | 97.9 |
| <i>Beauveria brongniartii</i> | RCEF 3172 | GCA_001636735.1 | 97.7 |
| <i>Beauveria felina</i> | SYSU-MS7908 | GCA_016490725.1 | 97.7 |
| <i>Beauveria pseudobassiana</i> | KACC 47484 | GCA_003267905.1 | 96.1 |
| <i>Beauveria rudraprayagi</i> | MTCC 8017 | GCA_000733645.1 | 97.8 |
| <i>Berkeleyomyces basicola</i> | CMW 49352 | GCA_003671435.1 | 97.4 |
| <i>Biscogniauxia mediterranea</i> | Bm01 | GCA_018398605.1 | 97.1 |
| <i>Bretziella fagacearum</i> | CMW 2656 | GCA_002018255.1 | 96.4 |
| <i>Calcarisporium arbuscula</i> | NRRL 3705 | GCA_009828645.1 | 93.3 |
| <i>Calonectria aciculata</i> | CMW 47645 | GCA_013406995.1 | 97.8 |
| <i>Calonectria crousiana</i> | CMW 27249 | GCA_013406985.1 | 97.7 |
| <i>Calonectria fujianensis</i> | CMW 27257 | GCA_013406965.1 | 97.5 |
| <i>Calonectria hawksworthii</i> | S6964 | GCA_020975415.1 | 97.8 |
| <i>Calonectria henricotiae</i> | CB077 | GCA_004380935.1 | 93.5 |
| <i>Calonectria honghensis</i> | CMW 47669 | GCA_013403855.1 | 97.5 |
| <i>Calonectria hongkongensis</i> | CMW 47271 | GCA_017140755.1 | 98.1 |
| <i>Calonectria ilicicola</i> | F018 | GCA_024515735.1 | 97.2 |
| <i>Calonectria leucothoes</i> | CBS 109166 | GCA_002179835.1 | 97.8 |
| <i>Calonectria montana</i> | PCam007 | GCA_022606435.1 | 98.2 |
| <i>Calonectria multiphialidica</i> | CBS 112678 | GCA_020623665.1 | 97.6 |
| <i>Calonectria naviculata</i> | CBS 101121 | GCA_003031705.1 | 97.5 |
| <i>Calonectria pauciramosa</i> | CBS 138824 | GCA_017140785.1 | 98.2 |
| <i>Calonectria pseudonaviculata</i> | CBS 139394 | GCA_001696505.1 | 98.0 |
| <i>Calonectria pseudoreteauidii</i> | YA51 | GCA_001879505.1 | 97.5 |
| <i>Calonectria pseudoturangicola</i> | CMW 47496 | GCA_013403825.1 | 97.7 |
| <i>Calonectria pteridis</i> | LPF059 | GCA_022837005.1 | 97.7 |
| <i>Celoportha dispersa</i> | CMW 9976 | GCA_016584495.1 | 92.5 |
| <i>Ceratocystiopsis brevicomis</i> | CBS 137839 | GCA_002778105.1 | 91.6 |
| <i>Ceratocystiopsis minuta</i> | CBS 138717 | GCA_001676865.1 | 93.5 |
| <i>Ceratocystis adiposa</i> | CBS 136.34 | GCA_001640685.1 | 96.8 |
| <i>Ceratocystis albifundus</i> | CMW4068 | GCA_002742255.2 | 96.0 |
| <i>Ceratocystis cacaofunesta</i> | C1593 | GCA_002776505.1 | 97.5 |
| <i>Ceratocystis eucalypticola</i> | CMW 9998 | GCA_001513815.1 | 97.6 |
| <i>Ceratocystis fimbriata</i> | CMW 15049 | GCA_012652265.1 | 96.7 |
| <i>Ceratocystis harringtonii</i> | CMW 14789 | GCA_002018265.1 | 96.7 |
| <i>Ceratocystis lukuohia</i> | CBS 142792 | GCA_023509845.1 | 97.4 |
| <i>Ceratocystis manginecans</i> | CMW 46461 | GCA_006408425.1 | 97.4 |
| <i>Ceratocystis platani</i> | CFO | GCA_000978885.1 | 97.3 |
| <i>Ceratocystis smalleyi</i> | CMW 14800 | GCA_003449175.1 | 97.0 |
| <i>Chaetomium cochliodes</i> | CCM F-232 | GCA_001752565.1 | 86.8 |
| <i>Chaetomium globosum</i> | CBS 148.51 | GCF_000143365.1 | 90.0 |
| <i>Chalaropsis thielavioides</i> | JCM 1933 | GCA_001599435.1 | 97.4 |
| <i>Chrysoportha austroafricana</i> | CMW6102 | GCA_016071805.1 | 97.7 |
| <i>Chrysoportha cubensis</i> | CMW 10028 | GCA_001282315.2 | 97.9 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|---------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Chrysosporthe deuterocubensis</i> | CMW 8650 | GCA_001513825.2 | 97.7 |
| <i>Chrysosphaeria jan-nelii</i> | CBS 141570 | GCA_020002325.1 | 94.9 |
| <i>Claviceps africana</i> | CCC 489 | GCA_018360145.1 | 95.0 |
| <i>Claviceps arundinis</i> | CCC933 | GCA_004016465.1 | 96.9 |
| <i>Claviceps capensis</i> | CCC 1504 | GCA_018360045.1 | 97.5 |
| <i>Claviceps citrina</i> | CCC 265 | GCA_018360365.1 | 92.4 |
| <i>Claviceps cyperi</i> | CCC 1219 | GCA_018360075.1 | 97.2 |
| <i>Claviceps digitariae</i> | CCC 659 | GCA_018360205.1 | 96.8 |
| <i>Claviceps fusiformis</i> | PRL 1980 | GCA_000223055.1 | 96.4 |
| <i>Claviceps humidiphila</i> | LM576 | GCA_018360465.1 | 97.2 |
| <i>Claviceps lovelessii</i> | CCC 647 | GCA_018360185.1 | 93.1 |
| <i>Claviceps maximensis</i> | CCC 398 | GCA_018360255.1 | 97.5 |
| <i>Claviceps monticola</i> | CCC 1483 | GCA_018360055.1 | 97.2 |
| <i>Claviceps occidentalis</i> | PRL1580 | GCA_004016105.1 | 95.7 |
| <i>Claviceps paspali</i> | ILB388 | GCA_013435705.1 | 97.5 |
| <i>Claviceps pazoutovae</i> | CCC 1485 | GCA_018360065.1 | 96.8 |
| <i>Claviceps perihumidiphila</i> | PRL 1566 | GCA_004016475.1 | 97.3 |
| <i>Claviceps purpurea</i> | LM233 | GCA_018360655.1 | 97.2 |
| <i>Claviceps pusilla</i> | CCC 602 | GCA_018360225.1 | 93.9 |
| <i>Claviceps quebecensis</i> | 136 | GCA_004016085.1 | 96.6 |
| <i>Claviceps ripicola</i> | JM_7.2 | GCA_004016175.1 | 97.0 |
| <i>Claviceps spartinae</i> | CCC 535 | GCA_018360215.1 | 96.7 |
| <i>Clonostachys byssicola</i> | 245-78 | GCA_902006505.2 | 97.3 |
| <i>Clonostachys rhizophaga</i> | '906-72A' | GCA_902077795.2 | 96.7 |
| <i>Clonostachys rosea</i> | CanS41 | GCA_015832225.1 | 89.4 |
| <i>Clonostachys solani</i> | 1703 | GCA_902141235.2 | 97.1 |
| <i>Coccinonectria pachysandricola</i> | JAC 18-79 | GCA_013283235.1 | 97.2 |
| <i>Colletotrichum abscissum</i> | Ca142 | GCA_023376855.1 | 97.7 |
| <i>Colletotrichum acutatum</i> | 43380 | GCA_020465775.1 | 97.7 |
| <i>Colletotrichum aenigma</i> | JS-0419 | GCA_022496045.1 | 97.3 |
| <i>Colletotrichum asianum</i> | ICMP 18580 | GCA_009806415.1 | 97.9 |
| <i>Colletotrichum australisinense</i> | GX1655 | GCA_014706365.1 | 87.3 |
| <i>Colletotrichum camelliae</i> | LS-19 | GCA_018853505.1 | 90.7 |
| <i>Colletotrichum chlorophyti</i> | NTL11 | GCA_001937105.1 | 97.5 |
| <i>Colletotrichum coccodes</i> | NJ-RT1 | GCA_002249775.1 | 97.4 |
| <i>Colletotrichum destructivum</i> | YC1 | GCA_009900065.1 | 97.9 |
| <i>Colletotrichum echinocloae</i> | B-48 | GCA_016618095.1 | 97.7 |
| <i>Colletotrichum eleusines</i> | NJC-16 | GCA_016807845.1 | 97.9 |
| <i>Colletotrichum falcatum</i> | CF08 | GCA_019425465.1 | 92.5 |
| <i>Colletotrichum filicis</i> | CBS 101611 | GCA_023376865.1 | 97.8 |
| <i>Colletotrichum fioriniae</i> | HC89 | GCA_002930455.1 | 97.8 |
| <i>Colletotrichum fructicola</i> | Nara gc5 | GCA_000319635.2 | 97.8 |
| <i>Colletotrichum gloeosporioides</i> | 'SMCG1#C' | GCA_003243855.1 | 97.8 |
| <i>Colletotrichum graminicola</i> | M1.001 | GCF_000149035.1 | 97.8 |
| <i>Colletotrichum higginsianum</i> | IMI 349063 | GCF_001672515.1 | 97.8 |
| <i>Colletotrichum horii</i> | FJ-1 | GCA_019693695.1 | 97.5 |
| <i>Colletotrichum incanum</i> | MAFF 238712 | GCA_001855235.1 | 97.3 |
| <i>Colletotrichum karsti</i> | CkLH20 | GCF_011947395.1 | 97.5 |
| <i>Colletotrichum lentis</i> | CT-30 | GCA_003386485.1 | 97.4 |
| <i>Colletotrichum lindemuthianum</i> | 83.501 | GCA_001693015.2 | 97.2 |
| <i>Colletotrichum liriopes</i> | MAFF 242679 | GCA_022179045.1 | 92.5 |
| <i>Colletotrichum lupini</i> | IMI 504893 | GCF_023278565.1 | 97.8 |
| <i>Colletotrichum magnum</i> | WT | GCA_022457145.1 | 97.8 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|-------------------------------------|-------------|-----------------|------------------------|
| <i>Colletotrichum musae</i> | GM20 | GCA_002814275.1 | 87.2 |
| <i>Colletotrichum musicola</i> | LFN0074 | GCA_014235935.1 | 97.8 |
| <i>Colletotrichum nymphaeae</i> | KY567 | GCA_014705095.1 | 97.3 |
| <i>Colletotrichum orbiculare</i> | MAFF 240422 | GCA_000350065.2 | 97.8 |
| <i>Colletotrichum orchidophilum</i> | IMI 309357 | GCF_001831195.1 | 97.5 |
| <i>Colletotrichum plurivorum</i> | LFN00145 | GCA_014235945.1 | 97.4 |
| <i>Colletotrichum salicis</i> | CBS 607.94 | GCA_001563125.1 | 97.4 |
| <i>Colletotrichum sansevieriae</i> | Sa-1-2 | GCA_002749775.1 | 95.8 |
| <i>Colletotrichum scovillei</i> | TJNH1 | GCF_011075155.1 | 97.6 |
| <i>Colletotrichum shisoii</i> | 'PG-2018a' | GCA_006783085.1 | 97.2 |
| <i>Colletotrichum siamense</i> | COLG-38 | GCA_011426375.1 | 95.9 |
| <i>Colletotrichum sidae</i> | CBS 518.97 | GCA_004367935.1 | 97.6 |
| <i>Colletotrichum simmondsii</i> | CBS 122122 | GCA_001563135.1 | 97.4 |
| <i>Colletotrichum sojae</i> | LFN0009 | GCA_014235955.1 | 97.7 |
| <i>Colletotrichum spaethianum</i> | MAFF 239500 | GCF_022836535.1 | 92.6 |
| <i>Colletotrichum spinosum</i> | CBS 515.97 | GCA_004366825.1 | 98.0 |
| <i>Colletotrichum sublineola</i> | CsGL1 | GCA_020631755.1 | 97.8 |
| <i>Colletotrichum tanacetii</i> | BRIP 57314 | GCA_005350895.1 | 96.9 |
| <i>Colletotrichum theobromicola</i> | KY152 | GCA_014705415.1 | 93.4 |
| <i>Colletotrichum tofieldiae</i> | MAFF 712333 | GCA_022836555.1 | 97.2 |
| <i>Colletotrichum trifolii</i> | 543-2 | GCA_004367215.1 | 97.7 |
| <i>Colletotrichum tropicale</i> | CgS9275 | GCA_013201785.1 | 97.5 |
| <i>Colletotrichum truncatum</i> | CMES1059 | GCF_014235925.1 | 97.2 |
| <i>Colletotrichum viniferum</i> | CvYL2a | GCA_020226115.1 | 98.0 |
| <i>Coniella vitis</i> | QNYT13637 | GCA_011317545.1 | 97.6 |
| <i>Coniochaeta hoffmannii</i> | CBS 245.38 | GCA_002798055.1 | 89.8 |
| <i>Coniochaeta prunicola</i> | STE-U 6107 | GCA_007388105.1 | 98.1 |
| <i>Coniochaeta pulveracea</i> | CAB683 | GCA_003635345.1 | 98.1 |
| <i>Cordyceps cicadae</i> | ZJ1611 | GCA_010211705.1 | 97.3 |
| <i>Cordyceps farinosa</i> | MTCC 4114 | GCA_000733625.1 | 97.3 |
| <i>Cordyceps fumosorosea</i> | ARSEF 2679 | GCF_001636725.1 | 96.9 |
| <i>Cordyceps javanica</i> | IJ1G | GCA_006981985.1 | 97.8 |
| <i>Cordyceps militaris</i> | CM01 | GCF_000225605.1 | 97.4 |
| <i>Cordyceps pruinosa</i> | KACC 44470 | GCA_003025255.1 | 94.4 |
| <i>Cordyceps tenuipes</i> | KACC 47485 | GCA_003025305.1 | 96.2 |
| <i>Corinectria fuckeliana</i> | CBS 125109 | GCA_019137255.1 | 97.8 |
| <i>Corollospora maritima</i> | CBS 119819 | NA | 96.7 |
| <i>Cryphonectria carpinicola</i> | CS3 | GCA_014849955.1 | 97.3 |
| <i>Cryphonectria japonica</i> | M9249 | GCA_014851275.1 | 97.7 |
| <i>Cryphonectria macrospora</i> | CBS 109764 | GCA_004802535.1 | 97.4 |
| <i>Cryphonectria naterciae</i> | M3656 | GCA_014850565.1 | 97.9 |
| <i>Cryphonectria nitschkei</i> | CBS 109758 | GCA_006503525.1 | 97.5 |
| <i>Cryphonectria parasitica</i> | ES15 | GCA_018104285.1 | 97.6 |
| <i>Cryphonectria radicalis</i> | M283 | GCA_014849355.1 | 97.9 |
| <i>Cylindrodendrum hubeiense</i> | IHI 201604 | GCA_014621425.1 | 96.5 |
| <i>Cytospora leucostoma</i> | SXYLt | GCA_003795295.1 | 98.5 |
| <i>Cytospora mali</i> | EGII | GCA_023079475.1 | 97.7 |
| <i>Cytospora piceae</i> | CFCC 52841 | GCA_016508685.1 | 97.4 |
| <i>Dactylonectria macrodidyma</i> | JAC 15-245 | GCA_000935225.1 | 97.9 |
| <i>Dactylonectria torresensis</i> | BV-349 | GCA_011426265.1 | 97.3 |
| <i>Daldinia caldariorum</i> | D263 | GCA_018842695.1 | 98.7 |
| <i>Daldinia childiae</i> | JS-1345 | GCF_008694065.1 | 97.0 |
| <i>Daldinia concentrica</i> | CBS 113277 | GCA_902805455.1 | 98.7 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Daldinia eschscholtzii</i> | UM 1400 | GCA_000751375.2 | 98.0 |
| <i>Daldinia eschscholtzii</i> | UM1020 | GCA_000261445.1 | 86.9 |
| <i>Daldinia eschscholtzii</i> | IFB-TL01 | GCA_001951055.1 | 95.9 |
| <i>Davidsoniella australis</i> | CMW 2333 | GCA_009806335.1 | 93.4 |
| <i>Davidsoniella eucalypti</i> | CMW 3254 | GCA_004009845.1 | 95.9 |
| <i>Davidsoniella neocaledoniae</i> | CMW 26392 | GCA_009806295.1 | 93.4 |
| <i>Davidsoniella virescens</i> | CMW 17339 | GCA_001513805.1 | 97.1 |
| <i>Diaporthe ampelina</i> | DA912 | GCA_001006365.1 | 97.7 |
| <i>Diaporthe amygdali</i> | DUCC20226 | GCA_021655905.1 | 97.9 |
| <i>Diaporthe aspalathi</i> | MS-SSC91 | GCA_001447215.1 | 98.3 |
| <i>Diaporthe batatas</i> | CRI 302-4 | GCF_019321695.1 | 98.3 |
| <i>Diaporthe capsici</i> | GY-Z16 | GCA_013364905.1 | 97.8 |
| <i>Diaporthe caulivora</i> | D57 | GCA_023703485.1 | 97.8 |
| <i>Diaporthe citri</i> | NFHF-8-4 | GCF_014595645.1 | 97.2 |
| <i>Diaporthe citriasiana</i> | ZJUD30 | GCA_014872975.1 | 98.2 |
| <i>Diaporthe citrichinensis</i> | ZJUD34 | GCA_014872995.1 | 98.0 |
| <i>Diaporthe destruens</i> | CRI305-2 | GCA_016859255.1 | 98.4 |
| <i>Diaporthe eres</i> | Phoaprs 18-03 | GCA_022225955.2 | 98.0 |
| <i>Diaporthe helianthi</i> | 7/96 | GCA_001702395.2 | 97.9 |
| <i>Diaporthe ilicicola</i> | FPH2015-502 | GCA_023242295.1 | 98.4 |
| <i>Diaporthe longicolla</i> | TWH P74 | GCA_000800745.1 | 98.5 |
| <i>Diaporthe nobilis</i> | DJY16A 5-1 | GCA_023078575.1 | 98.0 |
| <i>Diaporthe vexans</i> | PV 4 | GCA_021188095.1 | 97.8 |
| <i>Diatrype stigma</i> | M11/M66-122 | GCA_022225965.1 | 97.5 |
| <i>Didymobotryum rigidum</i> | JCM 8837 | GCA_001600575.1 | 97.9 |
| <i>Drechmeria coniospora</i> | ARSEF 6962 | GCF_001625195.1 | 97.0 |
| <i>Emericellopsis cladophorae</i> | MUM 19.33 | GCA_022114955.2 | 96.2 |
| <i>Endocalyx cinctus</i> | JCM 7946 | GCA_001600455.1 | 98.4 |
| <i>Endoconidiophora laricicola</i> | CBS 100207 | GCA_001640655.1 | 97.3 |
| <i>Endoconidiophora polonica</i> | CBS 100205 | GCA_001856765.1 | 97.3 |
| <i>Entonaema liquescens</i> | ATCC 46302 | GCA_902805475.1 | 95.5 |
| <i>Escovopsis weberi</i> | CC031208-10 A | GCA_001278495.1 | 96.4 |
| | ceph | | |
| <i>Eutypa lata</i> | MA101 | GCA_022661535.1 | 93.1 |
| <i>Eutypella</i> sp. | D-1 | GCA_023313575.1 | 97.5 |
| <i>Falciphora oryzae</i> | R5-6-1 | GCA_000733355.1 | 97.1 |
| <i>Fragosphaeria purpurea</i> | CBS 133.34 | GCA_002778095.1 | 96.1 |
| <i>Furcasterigmium furcatum</i> | JCM 9210 | GCA_001599815.1 | 96.6 |
| <i>Fusarium abutilonis</i> | NRRL 66737 | GCA_021655885.1 | 97.6 |
| <i>Fusarium acaciae-mearnsii</i> | CBS 123662 | GCA_017657115.1 | 97.4 |
| <i>Fusarium acuminatum</i> | F829 | GCA_013363215.1 | 94.3 |
| <i>Fusarium acutatum</i> | NRRL 13308 | GCA_012932015.1 | 98.0 |
| <i>Fusarium aethiopicum</i> | CBS 122858 | GCA_017657045.1 | 98.1 |
| <i>Fusarium agapanthi</i> | NRRL 54464 | GCA_001654545.1 | 97.6 |
| <i>Fusarium albidum</i> | NRRL 22152 | GCA_013618265.1 | 91.3 |
| <i>Fusarium albosuccineum</i> | NRRL 20459 | GCA_012931995.1 | 97.1 |
| <i>Fusarium algeriense</i> | NRRL 66647 | GCA_002982055.1 | 97.0 |
| <i>Fusarium ambrosium</i> | NRRL 20438 | GCA_003947045.1 | 97.4 |
| <i>Fusarium anguioides</i> | NRRL 25385 | GCA_012977745.1 | 98.0 |
| <i>Fusarium annulatum</i> | FFSC RH5 | GCA_022627115.1 | 97.9 |
| <i>Fusarium annulatum</i> | F8_4S_1F | GCA_019189765.1 | 98.3 |
| <i>Fusarium anthophilum</i> | NRRL 25214 | GCA_013364935.1 | 98.0 |
| <i>Fusarium armeniacum</i> | NRRL 6227 | GCA_013623825.1 | 97.5 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|----------------------------------|-------------------|-----------------|-------------------------------|
| <i>Fusarium asiaticum</i> | NRRL 6101 | GCA_001717845.1 | 98.2 |
| <i>Fusarium austroafricanum</i> | NRRL 53441 | GCA_012932025.1 | 97.6 |
| <i>Fusarium austroamericanum</i> | CBS 110246 | GCA_017657035.1 | 98.4 |
| <i>Fusarium avenaceum</i> | FaLH27 | GCA_000769295.1 | 97.5 |
| <i>Fusarium aywerte</i> | NRRL 25410 | GCA_013186375.1 | 97.6 |
| <i>Fusarium babinda</i> | NRRL 25539 | GCA_013184435.1 | 97.2 |
| <i>Fusarium bactridioides</i> | NRRL 66639 | GCA_013623355.1 | 97.5 |
| <i>Fusarium begoniae</i> | NRRL 25300 | GCA_013186755.1 | 97.5 |
| <i>Fusarium beomiforme</i> | NRRL 25174 | GCA_002980475.2 | 98.1 |
| <i>Fusarium boothii</i> | CBS 316.73 | GCA_017656985.1 | 96.9 |
| <i>Fusarium brachygibbosum</i> | HN-1 | GCA_018886245.1 | 98.2 |
| <i>Fusarium brasiliicum</i> | NRRL 31281 | GCA_013184295.1 | 98.0 |
| <i>Fusarium brevicatenuatum</i> | NRRL 25447 | GCA_013363135.1 | 97.8 |
| <i>Fusarium buharicum</i> | NRRL 13371 | GCA_014822075.1 | 97.3 |
| <i>Fusarium bulbicola</i> | NRRL 22947 | GCA_013186765.1 | 97.1 |
| <i>Fusarium burgessii</i> | NRRL 66654 | GCA_002980515.1 | 98.4 |
| <i>Fusarium buxicola</i> | NRRL 36148 | GCA_014899095.1 | 96.1 |
| <i>Fusarium caatingaense</i> | NRRL 66470 | GCA_013624355.1 | 96.8 |
| <i>Fusarium camptoceras</i> | NRRL 13381 | GCA_004367475.1 | 97.3 |
| <i>Fusarium cerealis</i> | Fcer1134NY13 | GCA_012600195.1 | 89.8 |
| <i>Fusarium chaquense</i> | NRRL 66748 | GCA_020137375.1 | 97.7 |
| <i>Fusarium chlamydosporum</i> | NRRL 13444 | GCA_014898915.1 | 98.2 |
| <i>Fusarium chuoi</i> | FFSC RH1 | GCA_022627125.1 | 97.9 |
| <i>Fusarium circinatum</i> | UG27 | GCA_021513755.1 | 95.7 |
| <i>Fusarium citri</i> | NRRL 66334 | GCA_004367485.1 | 98.0 |
| <i>Fusarium clavum</i> | NRRL 66337 | GCA_004367155.1 | 98.0 |
| <i>Fusarium coffeatum</i> | NRRL 66322 | GCA_004367465.1 | 97.9 |
| <i>Fusarium coicis</i> | NRRL 66233 | GCA_013781345.1 | 97.6 |
| <i>Fusarium commune</i> | NRRL 28387 | GCA_013618355.1 | 98.0 |
| <i>Fusarium concentricum</i> | NRRL 25181 | GCA_014824425.1 | 97.7 |
| <i>Fusarium concolor</i> | NRRL 13459 | GCA_013184415.1 | 98.3 |
| <i>Fusarium continuum</i> | NRRL 66286 | GCA_013184455.1 | 97.6 |
| <i>Fusarium cortaderiae</i> | NRRL 29297 | GCA_013184305.1 | 97.7 |
| <i>Fusarium culmorum</i> | NRRL 25475 | GCA_013618375.1 | 97.5 |
| <i>Fusarium cuneirostrum</i> | NRRL 31157 | GCA_001680505.1 | 88.1 |
| <i>Fusarium cyanostomum</i> | NRRL 53998 | GCA_014824385.1 | 96.6 |
| <i>Fusarium decemcellulare</i> | NRRL 13412 | GCA_013266205.1 | 95.7 |
| <i>Fusarium denticulatum</i> | NRRL 25311 | GCA_013396175.1 | 97.3 |
| <i>Fusarium devonianum</i> | NRRL 22134 | GCA_017140155.1 | 97.3 |
| <i>Fusarium dimerum</i> | NRRL 20691 | GCA_013623525.1 | 97.1 |
| <i>Fusarium dlamini</i> | NRRL 13164 | GCA_013186775.1 | 97.8 |
| <i>Fusarium domesticum</i> | NRRL 29976 | GCA_013618395.1 | 97.6 |
| <i>Fusarium drepaniforme</i> | NRRL 62941 | GCA_012978555.1 | 92.9 |
| <i>Fusarium duplospermum</i> | NRRL 62584 | GCA_003946985.1 | 97.7 |
| <i>Fusarium equiseti</i> | D25-1 | GCA_003313175.1 | 97.5 |
| <i>Fusarium euwallaceae</i> | HFEW-16-IV-019 | GCA_002168265.2 | 97.8 |
| <i>Fusarium falciforme</i> | NRRL 43529 | GCA_013363125.1 | 96.7 |
| <i>Fusarium flagelliforme</i> | NRRL 66336 | GCA_004367175.1 | 98.3 |
| <i>Fusarium floridanum</i> | NRRL 62606 | GCA_003947005.1 | 95.3 |
| <i>Fusarium foetens</i> | NRRL 38302 | GCA_013623845.1 | 95.3 |
| <i>Fusarium fracticaudum</i> | CBS 137234 | GCA_003353625.1 | 98.0 |
| <i>Fusarium fujikuroi</i> | IMI 58289 | GCF_900079805.1 | 97.4 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Fusarium gaditjirri</i> | NRRL 45417 | GCA_013266175.1 | 98.2 |
| <i>Fusarium gerlachii</i> | CBS 119176 | GCA_017656835.1 | 98.1 |
| <i>Fusarium globosum</i> | NRRL 26131 | GCA_013396165.1 | 97.3 |
| <i>Fusarium goolgardi</i> | NRRL 66250 | GCA_014899075.1 | 97.8 |
| <i>Fusarium graminearum</i> | PH-1 | GCA_020991245.1 | 98.3 |
| <i>Fusarium graminum</i> | NRRL 20692 | GCA_013266165.1 | 97.7 |
| <i>Fusarium guadeloupense</i> | NRRL 36125 | GCA_021655875.1 | 97.4 |
| <i>Fusarium guadeloupense</i> | NRRL 66743 | GCA_021655865.1 | 97.5 |
| <i>Fusarium guttiforme</i> | NRRL 22945 | GCA_013186795.1 | 97.3 |
| <i>Fusarium haematococcum</i> | S2_018_000R2 | GCA_004026385.1 | 93.4 |
| <i>Fusarium hainanense</i> | NRRL 66475 | GCA_013618405.1 | 97.8 |
| <i>Fusarium heterosporum</i> | NRRL 20693 | GCA_013396295.1 | 97.4 |
| <i>Fusarium hostae</i> | NRRL 29888 | GCA_013184365.1 | 97.7 |
| <i>Fusarium humuli</i> | NRRL 66339 | GCA_004366955.1 | 97.6 |
| <i>Fusarium illudens</i> | NRRL 22090 | GCA_013623515.1 | 97.0 |
| <i>Fusarium incarnatum</i> | NRRL 66325 | GCA_004367075.1 | 97.9 |
| <i>Fusarium irregulare</i> | NRRL 31160 | GCA_004367085.1 | 97.9 |
| <i>Fusarium kuroshium</i> | UCR3666 | GCA_003698175.1 | 93.5 |
| <i>Fusarium kyushuense</i> | NRRL 25348 | GCA_013184315.1 | 98.2 |
| <i>Fusarium langsethiae</i> | FI201059 | GCA_001292635.1 | 97.8 |
| <i>Fusarium lateritium</i> | NRRL 13622 | GCA_014898835.1 | 97.5 |
| <i>Fusarium liriiodendri</i> | NRRL 22389 | GCA_023509735.1 | 96.8 |
| <i>Fusarium longipes</i> | NRRL 20695 | GCA_003012285.1 | 97.3 |
| <i>Fusarium louisianense</i> | CBS 127524 | GCA_017656825.1 | 98.3 |
| <i>Fusarium luffae</i> | NRRL 66473 | GCA_013184325.1 | 97.3 |
| <i>Fusarium mangiferae</i> | NRRL 25226 | GCA_013758935.1 | 97.9 |
| <i>Fusarium marasasianum</i> | CMW 25512 | GCA_022833035.1 | 98.0 |
| <i>Fusarium meridionale</i> | CBS 110249 | GCA_017656785.1 | 98.4 |
| <i>Fusarium mesoamericanum</i> | CBS 415.86 | GCA_017656745.1 | 98.4 |
| <i>Fusarium metavorans</i> | FSSC_6 | GCA_001633045.1 | 95.9 |
| <i>Fusarium mexicanum</i> | NRRL 53147 | GCA_013396015.1 | 97.8 |
| <i>Fusarium miscanthi</i> | NRRL 26231 | GCA_014898875.1 | 97.7 |
| <i>Fusarium mundagurra</i> | NRRL 66235 | GCA_013396205.1 | 97.7 |
| <i>Fusarium musae</i> | NRRL 25059 | GCA_013623345.1 | 97.7 |
| <i>Fusarium nanum</i> | NRRL 66324 | GCA_004367095.1 | 97.8 |
| <i>Fusarium napiforme</i> | NRRL 25196 | GCA_013396005.1 | 97.0 |
| <i>Fusarium nelsonii</i> | NRRL 13338 | GCA_014898925.1 | 98.0 |
| <i>Fusarium nematophilum</i> | NRRL 54600 | GCA_013623595.1 | 95.4 |
| <i>Fusarium neocosmosporiellum</i> | NRRL 22166 | GCA_006518225.1 | 96.9 |
| <i>Fusarium nepalense</i> | CBS 127943 | GCA_017656675.1 | 97.7 |
| <i>Fusarium newnesense</i> | NRRL 66241 | GCA_013184375.1 | 92.0 |
| <i>Fusarium nisikadoi</i> | NRRL 25179 | GCA_013623555.1 | 98.0 |
| <i>Fusarium nodosum</i> | NRRL 36351 | GCA_014898975.1 | 98.1 |
| <i>Fusarium nurragi</i> | NRRL 36452 | GCA_012977755.1 | 97.7 |
| <i>Fusarium nygamai</i> | FJII-L4-SW-PAB2 | GCA_022813395.1 | 98.1 |
| <i>Fusarium odoratissimum</i> | race 4 | GCA_000350365.1 | 97.9 |
| <i>Fusarium oligoseptatum</i> | NRRL 62579 | GCA_003946995.1 | 93.3 |
| <i>Fusarium oxysporum</i> | F324 | GCA_013423235.1 | 98.2 |
| <i>Fusarium oxysporum</i> | NRRL 32931 | GCF_000271745.1 | 98.2 |
| <i>Fusarium palustre</i> | NRRL 54050 | GCA_014899045.1 | 97.8 |
| <i>Fusarium papillatum</i> | NRRL 62944 | GCA_013186395.1 | 85.9 |
| <i>Fusarium penzigii</i> | NRRL 20711 | GCA_013623535.1 | 97.2 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|-----------------------------------|-------------------|-----------------|-------------------------------|
| <i>Fusarium phaseoli</i> | NRRL 31156 | GCA_001680515.1 | 93.4 |
| <i>Fusarium phyllophilum</i> | NRRL 13617 | GCA_013396025.1 | 98.0 |
| <i>Fusarium pilosicola</i> | CMWF1183 | GCA_020615335.1 | 91.8 |
| <i>Fusarium pininemorale</i> | CMW 25243 | GCA_002165215.1 | 98.0 |
| <i>Fusarium poae</i> | DAOMC 252244 | GCF_019609905.1 | 98.4 |
| <i>Fusarium praegraminearum</i> | NRRL 39664 | GCA_002093855.1 | 98.1 |
| <i>Fusarium proliferatum</i> | MPVP 328 | GCA_017309895.1 | 98.1 |
| <i>Fusarium protoensiforme</i> | NRRL 22178 | GCA_011320165.1 | 96.9 |
| <i>Fusarium pseudoanthophilum</i> | NRRL 25211 | GCA_013395995.1 | 97.4 |
| <i>Fusarium pseudocircinatum</i> | NRRL 36939 | GCA_013396035.1 | 97.5 |
| <i>Fusarium pseudograminearum</i> | 'Class2-1C' | GCA_016952305.1 | 97.8 |
| <i>Fusarium ramigenum</i> | NRRL 25208 | GCA_013186855.1 | 97.8 |
| <i>Fusarium redolens</i> | NRRL 28421 | GCA_019843785.1 | 98.1 |
| <i>Fusarium robinianum</i> | CBS 430.91 | GCA_024115165.1 | 97.7 |
| <i>Fusarium sacchari</i> | NRRL 66326 | GCA_013759005.1 | 98.0 |
| <i>Fusarium sarcochroum</i> | NRRL 20472 | GCA_013266185.1 | 97.0 |
| <i>Fusarium scirpi</i> | NRRL 66328 | GCA_004367495.1 | 97.7 |
| <i>Fusarium secorum</i> | CBS 175.32 | GCA_024112715.1 | 98.6 |
| <i>Fusarium setosum</i> | NRRL 36526 | GCA_013623625.1 | 94.2 |
| <i>Fusarium sibiricum</i> | NRRL 53430 | GCA_014898995.1 | 98.3 |
| <i>Fusarium siculi</i> | KOD 1856 | GCA_019843635.1 | 98.2 |
| <i>Fusarium solani</i> | JS-169 | GCA_002215905.1 | 94.1 |
| <i>Fusarium solani-melongenae</i> | CRI 24-3 | GCA_023101225.1 | 97.8 |
| <i>Fusarium sororula</i> | FCC 5425 | GCA_017579625.1 | 97.9 |
| <i>Fusarium sporotrichioides</i> | S18/43 | GCA_019054615.1 | 98.3 |
| <i>Fusarium staphyleae</i> | NRRL 22316 | GCA_017140175.1 | 96.9 |
| <i>Fusarium sterilihyphosum</i> | NRRL 25623 | GCA_013186845.1 | 97.3 |
| <i>Fusarium stilboides</i> | NRRL 20429 | GCA_014822085.1 | 97.6 |
| <i>Fusarium subglutinans</i> | RC 528 | GCA_012070385.1 | 98.2 |
| <i>Fusarium sublunatum</i> | NRRL 13384 | GCA_013623665.1 | 97.7 |
| <i>Fusarium subtropicale</i> | NRRL 66764 | GCA_003670145.1 | 97.2 |
| <i>Fusarium succisae</i> | NRRL 13298 | GCA_013186925.1 | 98.0 |
| <i>Fusarium tanahbumbuense</i> | NRRL 66471 | GCA_012977735.1 | 97.7 |
| <i>Fusarium temperatum</i> | CMW F389 | GCA_001513835.1 | 98.3 |
| <i>Fusarium thapsinum</i> | NRRL 22049 | GCA_013186935.1 | 97.8 |
| <i>Fusarium tjaetaba</i> | NRRL 66243 | GCF_013396195.1 | 98.2 |
| <i>Fusarium torreyae</i> | NRRL 54149 | GCA_014824505.1 | 97.5 |
| <i>Fusarium torulosum</i> | NRRL 22747 | GCA_013623875.1 | 97.4 |
| <i>Fusarium transvaalense</i> | NRRL 31008 | GCA_013623685.1 | 97.9 |
| <i>Fusarium tricinctum</i> | T6 | GCA_003045085.1 | 97.7 |
| <i>Fusarium tricinctum</i> | NRRL 25481 | GCA_012977725.1 | 97.8 |
| <i>Fusarium tucumaniae</i> | NRRL 30196 | GCA_021730365.1 | 96.4 |
| <i>Fusarium tupiense</i> | NRRL 53984 | GCA_013364945.1 | 97.3 |
| <i>Fusarium udum</i> | F-02845 | GCA_002194535.1 | 96.5 |
| <i>Fusarium ussurianum</i> | CBS 123752 | GCA_017656685.1 | 98.2 |
| <i>Fusarium venenatum</i> | A3/5 | GCF_900007375.1 | 98.2 |
| <i>Fusarium verrucosum</i> | NRRL 22566 | GCA_013623715.1 | 98.0 |
| <i>Fusarium verticillioides</i> | BRIP 53590 | GCA_003316995.2 | 98.0 |
| <i>Fusarium veterinarium</i> | F5_8S_1A_F | GCA_019191175.1 | 97.9 |
| <i>Fusarium virguliforme</i> | Mont-1 | GCA_000585705.1 | 95.9 |
| <i>Fusarium vorosii</i> | CBS 119178 | GCA_017656575.1 | 98.0 |
| <i>Fusarium xylarioides</i> | KSU18978 | GCA_013183765.1 | 98.1 |
| <i>Fusarium xyrophilum</i> | NRRL 66890 | GCA_008711575.1 | 95.9 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|---------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Fusarium zanthoxyli</i> | NRRL 66285 | GCA_013623745.1 | 98.0 |
| <i>Fusarium zealandicum</i> | NRRL 22465 | GCA_013266195.1 | 96.9 |
| <i>Gaeumannomyces tritici</i> | R3-111a-1 | GCF_000145635.1 | 96.8 |
| <i>Geosmithia flava</i> | NA | GCA_900188565.1 | 97.0 |
| <i>Geosmithia morbida</i> | 1262 | GCF_012550715.1 | 97.5 |
| <i>Geosmithia putterillii</i> | NA | GCA_900188575.1 | 97.9 |
| <i>Gliomastix tumulicola</i> | JCM 17184 | GCA_001599755.1 | 97.5 |
| <i>Graphilbum fragrans</i> | VPRI 43528 | GCA_019925655.1 | 97.4 |
| <i>Graphium</i> sp. | VPRI 43844 | GCA_019925285.1 | 97.5 |
| <i>Hansfordia pulvinata</i> | 414-3 | GCA_006538405.1 | 94.9 |
| <i>Hawksworthiomyces lignivorus</i> | CBS 119148 | GCA_002917075.1 | 96.9 |
| <i>Hirsutella minnesotensis</i> | 3608 | GCA_000956045.1 | 95.4 |
| <i>Hirsutella rhossiliensis</i> | OWVT-1 | GCA_004142005.1 | 96.7 |
| <i>Hirsutella thompsonii</i> | MTCC 6686 | GCA_000472125.2 | 97.2 |
| <i>Humicola grisea</i> | UFV | GCA_011316235.1 | 97.5 |
| <i>Huntia bhutanensis</i> | CMW 8217 | GCA_002018275.1 | 96.1 |
| <i>Huntia decipiens</i> | CMW30855 | GCA_003032515.1 | 96.4 |
| <i>Huntia moniliformis</i> | CBS 118127 | GCA_000712465.1 | 96.1 |
| <i>Huntia omanensis</i> | CMW 11056 | GCA_000833645.1 | 90.1 |
| <i>Huntia savannae</i> | CBS 121151 | GCA_001483325.1 | 96.1 |
| <i>Hypomontagnella monticulosa</i> | CLL 205 | GCA_902825475.1 | 98.3 |
| <i>Hypomontagnella submonticulosa</i> | DAOMC 242471 | GCA_902806495.1 | 97.3 |
| <i>Hypomyces perniciosus</i> | HP10 | GCA_008477525.1 | 97.0 |
| <i>Hypomyces rosellus</i> | CCMJ2808 | GCA_011799845.1 | 97.6 |
| <i>Hypoxyton fragiforme</i> | MUCL 51264 | GCA_902806515.1 | 98.3 |
| <i>Hypoxyton lienhwacheense</i> | MFLUCC 14-1231 | GCA_902806505.1 | 98.2 |
| <i>Hypoxyton pulicidum</i> | ATCC 74245 | GCA_902806525.1 | 98.8 |
| <i>Hypoxyton rickii</i> | MUCL 53309 | GCA_902806535.1 | 98.5 |
| <i>Hypoxyton rubiginosum</i> | MUCL 52887 | GCA_902806565.1 | 98.1 |
| <i>Ilyonectria destructans</i> | C1 | GCA_001913115.1 | 97.4 |
| <i>Ilyonectria mors-panacis</i> | g3b | GCA_002991585.1 | 90.4 |
| <i>Immersiportia knoxdavesiana</i> | CMW 37318 | GCA_021117315.1 | 92.5 |
| <i>Intubia oerlemansii</i> | CBS 141565 | GCA_020002355.1 | 96.9 |
| <i>Jackrogersella multififormis</i> | CBS 119016 | GCA_902806575.1 | 98.6 |
| <i>Juglanconis juglandina</i> | CBS 121083 | GCA_003012975.1 | 92.5 |
| <i>Juglanconis oblonga</i> | AR4414 | GCA_003012965.1 | 96.2 |
| <i>Juglanconis</i> sp. | DMW523 | GCA_003013055.1 | 95.2 |
| <i>Knoxdavesia capensis</i> | CMW 40890 | GCA_001510575.1 | 97.1 |
| <i>Knoxdavesia proteae</i> | CMW 40885 | GCA_001510565.1 | 93.6 |
| <i>Leptographium lundbergii</i> | CBS 138716 | GCA_001455505.1 | 96.9 |
| <i>Leptographium procerum</i> | CMW34542 | GCA_000806385.1 | 92.2 |
| <i>Lindra thalassiae</i> | JK4322 | NA | 97.2 |
| <i>Lomentospora prolificans</i> | JHH-5317 | GCA_002276285.1 | 97.1 |
| <i>Madurella mycetomatis</i> | Mmyc_Sud9 | GCA_022530565.1 | 97.6 |
| <i>Magnaporthiopsis incrustans</i> | M35 | GCA_003049425.1 | 96.0 |
| <i>Magnaporthiopsis rhizophila</i> | M23 | GCA_003049465.1 | 96.6 |
| <i>Mariannaea elegans</i> | NBRC 102301 | GCA_930272665.1 | 97.7 |
| <i>Melanospora tiffanyae</i> | FIKG0001 | NA | 94.6 |
| <i>Memnoniella echinata</i> | JCM 22618 | GCA_001599555.1 | 97.3 |
| <i>Meredithiella fracta</i> | CBS 142645 | GCA_023677585.1 | 89.3 |
| <i>Metarhizium acridum</i> | CQMa 102 | GCF_000187405.1 | 97.6 |
| <i>Metarhizium album</i> | ARSEF 1941 | GCF_000804445.1 | 97.3 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|--|-------------------|-----------------|-------------------------------|
| <i>Metarhizium anisopliae</i> | BRIP 53293 | GCA_000426965.1 | 96.9 |
| <i>Metarhizium anisopliae</i> | CQMa421 | GCA_013839505.1 | 97.4 |
| <i>Metarhizium brunneum</i> | 4556 | GCA_013426205.1 | 97.1 |
| <i>Metarhizium guizhouense</i> | ARSEF 977 | GCA_000814955.1 | 97.1 |
| <i>Metarhizium humberi</i> | ESALQ1638 | GCA_020102295.1 | 97.1 |
| <i>Metarhizium majus</i> | ARSEF 297 | GCF_000814945.1 | 97.6 |
| <i>Metarhizium rileyi</i> | Cep018-CH2 | GCA_007866325.1 | 97.6 |
| <i>Metarhizium robertsii</i> | ARSEF 23 | GCF_000187425.2 | 97.2 |
| <i>Microcera coccophila</i> | CBS 310.34 | GCA_024112705.1 | 97.7 |
| <i>Moelleriella libera</i> | RCEF 2490 | GCA_001636675.1 | 96.7 |
| <i>Monosporascus cannonballus</i> | CBS 586.93 | GCA_004155895.1 | 97.8 |
| <i>Monosporascus ibericus</i> | CBS 110550 | GCA_004154915.1 | 98.1 |
| <i>Nakataea oryzae</i> | M69 | GCA_003049435.1 | 96.6 |
| <i>Nectria</i> sp. | B-13 | GCA_002682825.1 | 97.5 |
| <i>Neonectria coccinea</i> | CBS 119158 | GCA_019137265.1 | 97.3 |
| <i>Neonectria ditissima</i> | CBS 226.31 | GCA_019137815.1 | 96.4 |
| <i>Neonectria faginata</i> | A.R. 4307 | GCA_019137275.1 | 98.2 |
| <i>Neonectria hederiae</i> | CBS 714.97 | GCA_003385265.1 | 97.5 |
| <i>Neonectria neomacrospora</i> | KNNDK1 | GCA_917563905.1 | 97.5 |
| <i>Neonectria punicea</i> | CBS 119724 | GCA_003385315.1 | 96.8 |
| <i>Neopestalotiopsis clavispora</i> | IHI 201606 | GCA_014621435.1 | 95.5 |
| <i>Neopestalotiopsis rosae</i> | ML1664 | GCA_023078685.1 | 98.0 |
| <i>Neopestalotiopsis</i> sp. | PM2101 | GCA_023628335.1 | 98.2 |
| <i>Neurospora africana</i> | FGSC 1740 | GCA_000604205.2 | 96.5 |
| <i>Neurospora cerealis</i> | FGSC 26639 | GCA_009801525.1 | 98.0 |
| <i>Neurospora crassa</i> | OR74A | GCF_000182925.2 | 97.9 |
| <i>Neurospora discreta</i> | FGSC 8579 matA | GCA_009805215.1 | 97.9 |
| <i>Neurospora pannonica</i> | FGSC 7221 | GCA_009805235.1 | 89.7 |
| <i>Neurospora</i> sp. | LNF1-1 | GCA_009805225.1 | 98.1 |
| <i>Neurospora sublineolata</i> | FGSC 5508 | GCA_000604185.2 | 95.9 |
| <i>Neurospora terricola</i> | FGSC 1889 | GCA_009805285.1 | 95.1 |
| <i>Neurospora tetrasperm</i> | FGSC 2509 | GCA_000213195.1 | 98.1 |
| <i>Neurospora tetrasperma</i> | FGSC 2508 | GCF_000213175.1 | 98.3 |
| <i>Neurospora tetraspora</i> | MI3-3 | GCA_009802755.1 | 92.9 |
| <i>Niesslia exilis</i> | CBS 358.70 | NA | 97.4 |
| <i>Nigrospora oryzae</i> | GZL1 | GCA_016758845.1 | 98.0 |
| <i>Nigrospora sphaerica</i> | ZJJ_C1 | GCA_018287875.1 | 98.2 |
| <i>Ophioceras dolichostomum</i> | CBS 114926 | GCA_003049485.1 | 97.2 |
| <i>Ophiocordyceps australis</i> | '1348a' | GCA_002591405.1 | 95.4 |
| <i>Ophiocordyceps camponoti-floridani</i> | EC05 | GCA_012980515.1 | 96.8 |
| <i>Ophiocordyceps camponoti-leonardi</i> | BCC 80369 | GCA_003339455.1 | 97.4 |
| <i>Ophiocordyceps camponoti-rufipedis</i> | Map16 | GCA_002591395.1 | 93.2 |
| <i>Ophiocordyceps polyrhachis-furcata</i> | BCC 54312 | GCA_001633055.2 | 96.1 |
| <i>Ophiocordyceps sinensis</i> | IOZ07 | GCA_012934285.1 | 97.5 |
| <i>Ophiocordyceps unilateralis</i> | SC16a | GCA_001272575.2 | 96.3 |
| <i>Ophiognomonium clavignenti-juglandacearum</i> | ATCC 36624 | GCA_003671545.1 | 97.3 |
| <i>Ophiostoma angusticollis</i> | VPRI 43764 | GCA_019925545.1 | 97.2 |
| <i>Ophiostoma australiae</i> | DAR52683 | GCA_022392945.1 | 97.9 |
| <i>Ophiostoma fasciatum</i> | VPRI 43845 | GCA_019925495.1 | 96.5 |
| <i>Ophiostoma ips</i> | VPRI 43529 | GCA_019925475.1 | 97.8 |
| <i>Ophiostoma novo-ulmi</i> | H327 | GCA_000317715.1 | 97.8 |
| <i>Ophiostoma pallidulum</i> | VPRI 43846 | GCA_019925425.1 | 97.2 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|--|-------------------|-----------------|-------------------------------|
| <i>Ophiostoma piceae</i> | UAMH 11346 | GCA_000410735.1 | 97.9 |
| <i>Ophiostoma tasmaniense</i> | DAR52684 | GCA_022392925.1 | 98.3 |
| <i>Ophiostoma undulatum</i> | VPRI 43877 | GCA_022392935.1 | 97.9 |
| <i>Paramyrothecium foliicola</i> | TJWQPF1 | GCA_023375755.1 | 97.0 |
| <i>Paramyrothecium roridum</i> | NRRL 2183 | GCA_003012165.1 | 94.6 |
| <i>Periglandula ipomoeae</i> | IasaF13 | GCA_000222875.2 | 95.9 |
| <i>Pestalotiopsis fici</i> | W106-1 | GCF_000516985.1 | 98.1 |
| <i>Pestalotiopsis kenyana</i> | PG52 | GCA_018092595.1 | 98.3 |
| <i>Pestalotiopsis</i> sp. | '9143b' | GCA_023701735.1 | 95.5 |
| <i>Pestalotiopsis</i> sp. | MUOB 440515 | GCA_021199905.1 | 98.6 |
| <i>Phaeoacremonium minimum</i> | UCRPA7 | GCF_000392275.1 | 97.2 |
| <i>Phialemoniopsis</i> sp. | UDSM-2020 | GCA_018873225.1 | 98.0 |
| <i>Phyllachora maydis</i> | PM01 | GCA_011801745.1 | 95.8 |
| <i>Plectosphaerella cucumerina</i> | PcBMM | GCA_014636675.1 | 96.2 |
| <i>Pochonia chlamydosporia</i> | 170 | GCF_001653235.2 | 97.6 |
| <i>Podospora anserina</i> | Wa137- | GCA_017654855.1 | 96.3 |
| <i>Podospora comata</i> | Wa139- | GCA_017354895.1 | 96.8 |
| <i>Polycephalomyces</i> sp. | Field(B)_6/19/19 | GCA_018831705.1 | 94.0 |
| <i>Pseudohalonectria lignicola</i> | M95 | GCA_003049395.1 | 96.9 |
| <i>Pseudonectria buxi</i> | AR2414 | GCA_003693545.1 | 97.3 |
| <i>Pseudonectria foliicola</i> | AR2711 | GCA_002911195.1 | 97.4 |
| <i>Pseudopestalotiopsis theae</i> | CYF27 | GCA_015881745.1 | 97.5 |
| <i>Purpureocillium lilacinum</i> | CBS 284.36 | GCA_023168085.2 | 96.9 |
| <i>Purpureocillium takamizusanense</i> | PT3 | GCF_022605165.1 | 97.4 |
| <i>Pyrenopolyporus hunteri</i> | MUCL 49339 | GCA_902806595.1 | 98.5 |
| <i>Pyricularia grisea</i> | NI907 | GCF_004355905.1 | 98.3 |
| <i>Pyricularia oryzae</i> | LpKY97 | GCA_012272995.1 | 97.0 |
| <i>Pyricularia pennisetigena</i> | Br36 | GCF_004337985.1 | 97.6 |
| <i>Raffaelea albimanens</i> | CBS 271.70 | GCA_002778245.1 | 97.2 |
| <i>Raffaelea ambrosiae</i> | CBS 185.64 | GCA_002778195.1 | 97.2 |
| <i>Raffaelea arxii</i> | CBS 273.70 | GCA_002778165.1 | 97.0 |
| <i>Raffaelea deltoideospora</i> | VPRI 43720 | GCA_019925385.1 | 96.1 |
| <i>Raffaelea lauricola</i> | CBS 129006 | GCA_004153705.1 | 96.4 |
| <i>Raffaelea lauricola</i> | RL4 | GCA_014183025.1 | 96.5 |
| <i>Rosellinia necatrix</i> | W97 | GCA_001445595.3 | 96.9 |
| <i>Rugonectria rugulosa</i> | CBS 126565 | GCA_023509875.1 | 97.6 |
| <i>Samsoniella hepiali</i> | FENG | GCA_001455915.2 | 97.7 |
| <i>Sarocladium brachiariae</i> | HND5 | GCA_008271525.1 | 96.4 |
| <i>Sarocladium implicatum</i> | TR | GCA_021176775.1 | 96.4 |
| <i>Sarocladium oryzae</i> | Saro-13 | GCA_001605845.1 | 96.5 |
| <i>Sarocladium oryzae</i> | JCM 12450 | GCA_001972265.1 | 97.0 |
| <i>Sarocladium strictum</i> | IMI 501407 | GCA_900290465.1 | 97.3 |
| <i>Scedosporium apiospermum</i> | IHEM 14462 | GCF_000732125.1 | 97.3 |
| <i>Scedosporium aurantiacum</i> | WM 09.24 | GCA_000812075.1 | 94.6 |
| <i>Scedosporium boydii</i> | IHEM 23826 | GCA_002221725.1 | 96.5 |
| <i>Scedosporium dehoogii</i> | 120008799-01/4 | GCA_002812735.1 | 96.9 |
| <i>Scopulariopsis brevicaulis</i> | MRI360 | GCA_017657125.1 | 96.9 |
| <i>Simplicillium aogashimaense</i> | 72-15.1 | GCA_012273805.1 | 97.8 |
| <i>Simplicillium aogashimaense</i> | HWYR21 | GCA_019843555.1 | 98.1 |
| <i>Simplicillium</i> sp. | C3G150-2 | GCA_022702485.1 | 97.9 |
| <i>Sordaria macrospora</i> | R19027 | GCA_008692325.1 | 98.2 |
| <i>Sphaerostilbella broomeana</i> | TFC201724 | GCA_930272545.1 | 97.6 |
| <i>Sporothrix brasiliensis</i> | 5110 | GCF_000820605.1 | 97.3 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|--------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Sporothrix brunneoviolacea</i> | CBS 124561 | GCA_021396205.1 | 95.4 |
| <i>Sporothrix dimorphospora</i> | CBS 553.74 | GCA_021397985.1 | 97.5 |
| <i>Sporothrix euskadiensis</i> | VPRI 43754 | GCA_019925375.1 | 98.6 |
| <i>Sporothrix globosa</i> | LC2404 | GCA_021396195.1 | 97.6 |
| <i>Sporothrix humicola</i> | CBS 118129 | GCA_021396245.1 | 98.2 |
| <i>Sporothrix inflata</i> | CBS 239.68 | GCA_021396225.1 | 97.1 |
| <i>Sporothrix insectorum</i> | RCEF 264 | GCA_001636815.1 | 92.5 |
| <i>Sporothrix luriei</i> | CBS 937.72 | GCA_021398005.1 | 95.9 |
| <i>Sporothrix mexicana</i> | CBS 120341 | GCA_021396375.1 | 98.1 |
| <i>Sporothrix nigrograna</i> | VPRI 43755 | GCA_019925305.1 | 97.6 |
| <i>Sporothrix pallida</i> | CBS 131.56 | GCA_021396235.1 | 97.8 |
| <i>Sporothrix phasma</i> | CBS 119721 | GCA_011037845.1 | 97.8 |
| <i>Sporothrix protearum</i> | CBS 116654 | GCA_016097115.2 | 81.7 |
| <i>Sporothrix pseudoabietina</i> | VPRI 43531 | GCA_019925295.1 | 98.4 |
| <i>Sporothrix schenckii</i> | 1099-18 | GCF_000961545.1 | 97.5 |
| <i>Sporothrix variecibatus</i> | CBS 121960 | GCA_016097105.2 | 82.2 |
| <i>Stachybotrys chartarum</i> | IBT 40293 | GCA_000732565.1 | 97.5 |
| <i>Stachybotrys chlorohalonata</i> | IBT 40285 | GCA_000732775.1 | 97.7 |
| <i>Stachybotrys microspora</i> | N1 | GCA_020085135.1 | 96.8 |
| <i>Staphylotrichum longicolle</i> | FW57 | GCA_019096155.1 | 96.4 |
| <i>Stenocarpella maydis</i> | A1-1 | GCA_002270565.1 | 97.2 |
| <i>Stylonectria norvegica</i> | IHI 201603 | GCA_014621405.1 | 93.5 |
| <i>Thelonectria blattea</i> | CBS 952.68 | GCA_024115155.1 | 97.6 |
| <i>Thelonectria discophora</i> | NA | GCA_911649645.1 | 97.8 |
| <i>Thelonectria rubi</i> | CBS 177.27 | GCA_013420875.1 | 97.4 |
| <i>Thermochaetoides dissita</i> | CBS 180.67 | GCA_011800035.1 | 83.6 |
| <i>Thielaviopsis ethacetica</i> | JCM 6961 | GCA_001599055.1 | 97.4 |
| <i>Thielaviopsis euricoi</i> | JCM 6020 | GCA_001599615.1 | 97.5 |
| <i>Thielaviopsis musarum</i> | CMW 1546 | GCA_001513885.1 | 97.0 |
| <i>Thielaviopsis populi</i> | CMW 26388 | GCA_017591655.1 | 96.6 |
| <i>Thielaviopsis punctulata</i> | CR-DP1 | GCA_000968615.1 | 96.8 |
| <i>Thyridium curvatum</i> | D216 | GCF_004353045.1 | 97.4 |
| <i>Tolypocladium album</i> | IQ158 | GCA_024341135.1 | 97.2 |
| <i>Tolypocladium amazonense</i> | LA108 | GCA_024340795.1 | 96.9 |
| <i>Tolypocladium capitatum</i> | CBS 113982 | GCA_002901185.1 | 96.3 |
| <i>Tolypocladium cylindrosporum</i> | CBS 718.70 | GCA_024340765.1 | 95.4 |
| <i>Tolypocladium endophyticum</i> | MX560 | GCA_024339985.1 | 97.1 |
| <i>Tolypocladium geodes</i> | CBS 723.70 | GCA_024340515.1 | 97.2 |
| <i>Tolypocladium guangdongense</i> | GD1-15 | GCA_022114105.1 | 96.5 |
| <i>Tolypocladium inflatum</i> | CBS 567.84 | GCA_003945565.1 | 97.0 |
| <i>Tolypocladium nubicola</i> | CBS 568.84 | GCA_024340505.1 | 96.1 |
| <i>Tolypocladium ophioglossoides</i> | CBS 100239 | GCA_001189435.1 | 96.3 |
| <i>Tolypocladium ovalisporum</i> | CBS 700.92 | GCA_024340015.1 | 97.4 |
| <i>Tolypocladium paradoxum</i> | NRBC 100945 | GCA_002916505.1 | 95.2 |
| <i>Tolypocladium pustulatum</i> | CBS 110433 | GCA_024340155.1 | 97.2 |
| <i>Tolypocladium tropicale</i> | MX337 | GCA_024340005.1 | 97.5 |
| <i>Tolypocladium tundrense</i> | CBS 569.84 | GCA_024340025.1 | 96.0 |
| <i>Torpedospora radiata</i> | JK5252C | NA | 96.3 |
| <i>Trichocladium uniseriatum</i> | OTU1415 | GCA_017139535.1 | 97.6 |
| <i>Trichoderma arundinaceum</i> | IBT 40837 | GCA_003012105.1 | 97.3 |
| <i>Trichoderma asperelloides</i> | T203 | GCA_021066465.1 | 98.5 |
| <i>Trichoderma asperellum</i> | DQ-1 | GCA_017945965.1 | 96.3 |
| <i>Trichoderma atrobrunneum</i> | ITEM 908 | GCA_003439915.1 | 94.7 |

Supplementary Table 1 Continued.

| Species | Identifier | Assembly | BUSCO completeness (%) |
|------------------------------------|-------------------|-----------------|-------------------------------|
| <i>Trichoderma atroviride</i> | IMI 206040 | GCA_019297715.1 | 98.2 |
| <i>Trichoderma brevicompactum</i> | IBT 40841 | GCA_003012085.1 | 97.5 |
| <i>Trichoderma brevicrassum</i> | TC967 | GCA_017311225.1 | 98.2 |
| <i>Trichoderma cornu-damae</i> | 'KA19-0412C' | GCA_020631695.1 | 97.8 |
| <i>Trichoderma erinaceum</i> | CRRI-T2N1 | GCA_013365115.1 | 98.4 |
| <i>Trichoderma gamsii</i> | A5MH | GCA_002894205.1 | 98.0 |
| <i>Trichoderma gamsii</i> | T6085 | GCF_001481775.2 | 98.1 |
| <i>Trichoderma gracile</i> | HK011-1 | GCA_020002365.1 | 98.0 |
| <i>Trichoderma guizhouense</i> | NJAU 4742 | GCA_002022785.1 | 97.8 |
| <i>Trichoderma hamatum</i> | GD12 | GCA_000331835.2 | 97.8 |
| <i>Trichoderma harzianum</i> | ZL-811 | GCA_021186515.1 | 97.0 |
| <i>Trichoderma koningii</i> | JCM 1883 | GCA_001950475.1 | 97.8 |
| <i>Trichoderma koningiopsis</i> | RA3a | GCA_022985005.1 | 98.4 |
| <i>Trichoderma lentiforme</i> | CFAM-422 | GCA_011066345.1 | 98.0 |
| <i>Trichoderma lixii</i> | MUT 3171 | GCA_014468695.1 | 97.9 |
| <i>Trichoderma longibrachiatum</i> | SMF2 | GCA_000332775.1 | 98.0 |
| <i>Trichoderma oligosporum</i> | CGMCC 3.17527 | GCA_015266385.1 | 97.3 |
| <i>Trichoderma parareesei</i> | CBS 125925 | GCA_001050175.1 | 97.9 |
| <i>Trichoderma pleuroti</i> | TPhu1 | GCA_001721665.1 | 93.0 |
| <i>Trichoderma pseudokoningii</i> | NA | GCA_943193705.1 | 97.6 |
| <i>Trichoderma reesei</i> | QM6a | GCA_002006585.1 | 98.6 |
| <i>Trichoderma semiorbis</i> | FJ059 | GCA_020045945.2 | 98.1 |
| <i>Trichoderma simmonsii</i> | GH-Sj1 | GCA_019565615.1 | 98.0 |
| <i>Trichoderma virens</i> | FT-333 | GCA_020647705.1 | 91.0 |
| <i>Trichoderma viride</i> | Tv-1511 | GCA_007896495.1 | 96.5 |
| <i>Trichothecium ovalisporum</i> | DAOM 186447 | GCA_003012195.1 | 96.8 |
| <i>Trichothecium roseum</i> | ZM-Tr2021 | GCA_022701375.1 | 97.0 |
| <i>Trichothecium sympodiale</i> | DAOM 209012 | GCA_003012115.1 | 97.0 |
| <i>Truncatella angustata</i> | S358 | GCA_021193595.1 | 94.8 |
| <i>Ustilaginoidea virens</i> | 'UV-8b' | GCF_000687475.1 | 97.0 |
| <i>Valetoniellopsis laxa</i> | CBS 191.97 | NA | 97.5 |
| <i>Verticillium albo-atrum</i> | PD747 | GCA_002851705.1 | 96.3 |
| <i>Verticillium dahliae</i> | VdB09 | GCA_018982765.1 | 80.3 |
| <i>Verticillium isaacii</i> | PD618 | GCA_002851775.1 | 95.6 |
| <i>Verticillium klebahnii</i> | PD401 | GCA_002851715.1 | 95.9 |
| <i>Verticillium nonalfalfae</i> | CBS 382.66 | GCA_019553885.1 | 95.7 |
| <i>Verticillium nubilum</i> | PD621 | GCA_002851675.1 | 96.3 |
| <i>Verticillium tricorpus</i> | PD593 | GCA_002851695.1 | 96.3 |
| <i>Verticillium zaregamsianum</i> | PD739 | GCA_002851755.1 | 95.8 |
| <i>Wardomyces moseri</i> | CBS 164.80 | GCF_022829205.1 | 98.9 |
| <i>Xenoacremonium recifei</i> | IHEM 4405 | GCA_012184525.1 | 98.0 |
| <i>Xylaria flabelliformis</i> | G536 | GCA_007182795.1 | 97.9 |
| <i>Xylaria grammica</i> | IHI A82 | GCA_004014815.1 | 94.1 |
| <i>Xylaria grammica</i> | EL000614 | GCA_004353285.2 | 97.6 |
| <i>Xylaria hypoxylon</i> | CBS 122620 | GCA_902806585.1 | 96.5 |
| <i>Xylaria longipes</i> | IHI A66 | GCA_003426265.1 | 91.7 |
| <i>Xylaria multiplex</i> | DSM 110363 | GCA_011057905.1 | 95.1 |
| <i>Xylaria polymorpha</i> | DSM 105756 | GCA_003426235.1 | 93.8 |

Note: Outgroup is displayed in bold. NA means 'Not applicable'.