**Supple Data 5.** **Detailed processes for phylogenetic analysis of the *Fuscoporia* datasets**

**Supple Data 5.1. Dataset collection and initial curation**

A total of seven references mentioned in table 1 of Cho et al. (2023) were utilized for database preparation (Brazee, 2015; Chen & Dai, 2019; Chen & Yuan, 2017; Chen et al., 2020; Du et al., 2020, Tchoumi et al., 2020; Vlasak et al., 2020). Sequences from Cho et al., labeled as “This study” were obtained directly from the *IMA Fungus* website and used as a query. Tables from references published in *Mycokeys* and *Mycologia* were directly parsed from the respective websites, while tables from references published in *Mycosphere* and *Phytotaxa* were extracted using ABBYY FineReader PDF (https://pdf.abbyy.com/) to prepare a database file. With Microsoft Excel, “genus / species” columns were split into separate “genus” column and “species” columns. The “Voucher” column was renamed to “ID”. Columns such as “nLSU” and “nrLSU” were unified under “LSU” for consistency. Also, subscripts following accession numbers (e.g., the asterisk in GenBank accession “XX000000\*”) were removed. The “Genus” and “Species” columns in the query file were removed to reproduce the situation of the original study, where the query sequences had not yet been identified.

**Supple Data 5.2. Iterative runs and curations**

**\* Note: See “~~~~~” refers to do designated file in the archived raw data of the article, as indicated in the ACKNOWLEDGEMENT (**https://doi.org/[10.5281/zenodo.14650006](https://zenodo.org/doi/10.5281/zenodo.13147233)**)**

The first run (run1) of FunVIP was conducted using fast mode. The run aborted with a total of 113+1 errors (See 300\_case\_study/run1/run1/log.txt). The additional error (indicated by “+1” in “133+1”) serves to inform users that errors occurred during the FunVIP run, resulting in termination. The 113 errors were caused by database conflicts, including species and sequence conflicts. Ten species conflicts were caused by six name updates in subsequent reference (one *F. ambigua* was re-identified as *F. ferruginosa*, one *F. gilva* was reidentified as *F. chinensis*, two *F.* *ferruginosa* were re-identified as *F. ambigua* and two *F. wahlbergii* were re-identified as *F. australasica*) and four orthographic variants (i.e., *F. setifera* was mistakenly typed as *F. setifer*, *F. septiseta* was mistakenly typed as *F. septoseta*). The remaining 103 sequence conflicts consisted of two partial sequences uploaded in different samples and 101 cases where sequence were added later (FunVIP detects conflict even when one of the sequences is blank). These database conflicts were resolved, and consequent FunVIP runs were conducted.

The second run (run2) was executed in fast mode. The number of inconsistent issues and polyphyly issues reported in each iteration of the run are described (Supple Table 5.1). The automatically visualized concatenated tree from the second run (see 300\_case\_study/run2/run2/07\_Tree/run2\_Fuscoporia\_concatenated.svg) revealed seven samples with long-branch problems and one branch with a taxonomically mislabeled sample at the genus level. To investigate the causes of the long-branch problem, the alignment file (see 300\_case\_study/run2/run2/05\_alignment/run2\_trimmed\_Fuscoporia\_concatenated.fasta) was examined using Geneious 9.1.8 software with the “sort by alignment length” function. As a result, the ITS and LSU sequences were interchangeably placed, and this was detected based on NCBI BLAST analysis.

**References**

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