



## OPINION

### Fungal taxonomy: Are we casual about species identification?

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In the first week of December 2023, SIES College of Arts, Science & Commerce, Mumbai hosted the First Annual Meeting of the Association of Fungal Biologists (AFB) and an International Conference on 'Biology, Biodiversity, and Biotechnology of Fungi'. Over the course of two days, there were more than 30 oral presentations by young doctoral students and faculty members. Most of these presentations showcased interesting and novel concepts, which significantly contributed to the conference's theme. It was noted that, with the exception of projects not focused on taxonomy, fungal species identification was not attempted meticulously in many of the reported studies. Accurate identification of fungal species is important in biological research. We aim to emphasize that in this communication with the help of recent taxonomic and molecular phylogenetic studies.

The sequencing of the internal transcribed spacer (ITS) region, designated as the first barcode of fungi, marks a significant advancement in the field of fungal taxonomy (White et al. 1990, Schoch et al. 2012). This development is coupled with the establishment of the "One Fungus = One Name" principle mooted by Taylor (2011). Additionally, the undertaking of multilocus sequence analysis has furthered the field of fungal taxonomy. Hibbett's classification of the Kingdom *Fungi* based on polyphasic data, including multilocus sequence information, was one of the most significant contributions to mycology and allied fields (Hibbett et al. 2007). Most recently, the introduction of genome-based phylogenetic analysis has emerged as an important milestone in the evolving journey of fungal taxonomy (Li et al. 2021).

There were some earlier publications that focused on educating young researchers by providing reviews and general articles, written in simple language, about the taxonomic principles of fungi (Guarro et al. 1999, Sharma et al. 2015, Naranjo-Ortiz and Gabaldón 2019). The current species concept and recognition criteria in fungi recommend a polyphasic taxonomic approach, incorporating molecular, morphological, physiological, and biochemical data, allowing for the improved characterization of a fungal species (Xu 2020, Stengel et al. 2022). Fungal species



identification can be achieved, more or less satisfactorily, through the sequencing and analysis of the fungal ITS region, with several service providers and government institutes available throughout the country. Today, DNA sequencing costs have come down, especially when compared to expensive services like scanning electron microscopy (SEM) or transmission electron microscopy (TEM). Additionally, MALDI-TOF represents a cost-effective technique for identifying human pathogenic fungi, with service costs averaging Rs. 300–500 per sample. This approach not only aids in the accurate identification of fungal species but also enhances the quality of research output.

Similar observations have been made with Arbuscular Mycorrhizal (AM) fungi belonging to *Glomeromycota*, where ITS, large subunit (LSU) or small subunit (SSU) rRNA gene sequencing is infrequently reported by Indian mycologists in their studies on various aspects of AM fungi (Oehl et al. 2011, Montoliu-Nerin et al. 2021). Given that not every laboratory possesses the necessary monographs for the morphological identification of fungal species, ITS sequencing emerges as the most viable solution. Furthermore, as most studies involve only a few fungal strains in applied research, ITS sequencing, therefore, could be a feasible option for young researchers. Unfortunately, it has been observed that phylogeny as a method of taxonomy has not been vigorously embraced by Indian mycologists as compared to other parts of the world.

Among the eukaryotes, the *Kingdom Fungi* is highly diverse, comprising unicellular yeasts, mycelial fungi, and macrofungi. Moreover, the taxonomy of fungi has progressed from morpho-taxonomy to molecular phylogeny and onto phylogenomics (Galindo et al. 2021). Fungi are so diverse in morphology, function, ecological roles, and genome constitution that it has been a challenge for scientists to resolve the taxonomic positions and evolutionary histories of many fungal taxa. This progression, however, has helped in resolving ambiguities surrounding some fungal groups, such as *Chytridiomycota*, *Neocallimastigomycota* and fungi-like organisms, such as *Myxomycota*, *Plasmodiophoromycota* and *Oomycota* (Powell and Letcher 2014). Recently, Strasser and Monaghan (2022) proposed a fungal tree of life based on phylogenomic analyses, which includes the recently reported lineage of *Sanchytriomycota* (Galindo et al. 2021).

Molecular phylogenetic studies not only facilitate the unambiguous assignment of fungal strains to the species level but also help in understanding their evolutionary relationships, which morpho-taxonomy alone may not infer (Sharma et al. 2015). The latest genome-scale phylogenies have also helped in resolving many taxon positions (Rahmat et al. 2021), but it might still take some time and data to establish itself as a gold standard. This shift in fungal taxonomy is also reflected in educational materials; school textbooks now generally cover the topic of phylogeny, while graduate syllabi delve into it in more detail, including concepts and laboratory practical involving software usage.

Relatively recently, in 2022 and 2023, the *Journal of Fungi* published a few special issues: 'Fungal Taxonomy, Phylogeny, and Ecology: A Themed Issue Dedicated to Academician Wen-Ying Zhuang', 'Phylogeny and Taxonomy of Ascomycete Fungi', and 'Recent Advances in



*Taxonomy, Phylogeny, and Evolution of Fungi*', highlighting the importance of fungal phylogeny (Garrido-Huésca et al. 2022, Gao and Cai 2023, Peng et al. 2023, Zitouni-Haouar et al. 2023). MycoIndia and MycoAsia journals have been conducting several online lectures and workshops to promote this field. In these events, various experts, including Prof. T. S. Suryanarayanan, Prof. K. R. Sridhar, Prof. N. S. Atri, Prof. D. J. Bhat, Dr. S. K. Deshmukh, and other prominent Indian mycologists, have delivered lectures on different, often emerging, topics in mycology for the benefit of young researchers. This emphasis is also echoed in some recent reviews (Borman and Johnson 2023, Lin et al. 2023, Zhou and May 2023).

It is beneficial for young researchers to consult experts (both national and international, which may be on platforms like MycoAsia and Fungi-ID, <https://fungi-id.org/>) to resolve their queries regarding basic fungal species identification, which contributes to the advancement of our collective knowledge in mycology. Faculty members in colleges and universities, who are working on fungal taxonomic or applied aspects of fungi can encourage students and young researchers to accurately identify the fungal species in their research projects.

## References

- Borman AM, Johnson EM (2023) Changes in fungal taxonomy: mycological rationale and clinical implications. *Clinical Microbiology Reviews* e00099-22. DOI: <https://doi.org/10.1128/cmr.00099-22>
- Galindo LJ, López-García P, Torruella G, Karpov S, Moreira D (2021) Phylogenomics of a new fungal phylum reveals multiple waves of reductive evolution across Holomycota. *Nature Communications* 12:4973. DOI: <https://doi.org/10.1038/s41467-021-25308-w>
- Gao C, Cai L (2023) Fungal taxonomy, phylogeny, and ecology. *Journal of Fungi*, p. 506. DOI: <https://doi.org/10.3390/books978-3-0365-6448-7>
- Garrido-Huésca E, González-Burgos E, Kirika PM, Boustie J, Ferron S, et al. (2022). A new cryptic lineage in *Parmeliaceae* (*Ascomycota*) with pharmacological properties. *Journal of Fungi* 8:826. DOI: <https://doi.org/10.3390/jof8080826>
- Guarro J, Gené J, Stchigel AM (1999) Developments in fungal taxonomy. *Clinical Microbiology Reviews* 12:454–500. DOI: <https://doi.org/10.1128/CMR.12.3.454>
- Hibbett DS, Binder M, Bischoff JF, Blackwell M, Cannon PF, et al. (2007) A higher-level phylogenetic classification of the fungi. *Mycological Research* 111:509–547. DOI: <https://doi.org/10.1016/j.mycres.2007.03.004>
- Li Y, Steenwyk JL, Chang Y, Wang Y, James TY, et al. (2021) A genome-scale phylogeny of the kingdom Fungi. *Current Biology* 31:1653–1665.e5. DOI: <https://doi.org/10.1016/j.cub.2021.01.074>
- Lin P, Kook M, Yi TH, Yan ZF (2023) Current fungal taxonomy and developments in the identification system. *Current Microbiology* 80:375. DOI: <https://doi.org/10.1007/s00284-023-03514-7>
- Montoliu-Nerin M, Sánchez-García M, Bergin C, Kutschera VE, Johannesson H, et al. (2021) In-depth phylogenomic analysis of arbuscular mycorrhizal fungi based on a comprehensive set of de novo genome assemblies. *Frontiers in Fungal Biology* 2:716385. DOI: <https://doi.org/10.3389/ffunb.2021.716385>





- Naranjo-Ortiz MA, Gabaldón T (2019) Fungal evolution: diversity, taxonomy and phylogeny of the fungi. *Biological Reviews* 94:2101–2137. DOI: <https://doi.org/10.1111/brv.12550>
- Oehl F, Sieverding E, Palenzuela J, Ineichen K, da Silva GA (2011) Advances in Glomeromycota taxonomy and classification. *IMA Fungus* 2:191–199. DOI: <https://doi.org/10.5598/imafungus.2011.02.02.10>
- Peng L, Zhang YW, Wang HY, Dong CB, Chen WH, Liang JD, Han YF (2023) Taxonomy and phylogeny of eight new *Acrophialophora* species (*Sordariales*, *Chaetomiaceae*) from China. *Journal of Fungi* 9:645. DOI: <https://doi.org/10.3390/jof9060645>
- Powell MJ, Letcher PM (2014) Chytridiomycota, Monoblepharidomycota, and Neocallimastigomycota. *Systematics and Evolution: Part A*, 141–175. DOI: [https://doi.org/10.1007/978-3-642-55318-9\\_6](https://doi.org/10.1007/978-3-642-55318-9_6)
- Rahmat E, Park I, Kang Y (2021) The whole-genome sequence of the novel yeast species *Metschnikowia persimmonesis* isolated from medicinal plant *Diospyros kaki* Thunb. G3:11(11), jkab246. DOI: [10.1093/g3journal/jkab246](https://doi.org/10.1093/g3journal/jkab246)
- Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, et al. (2012) Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for fungi. *Proceedings of National Academy of Science* 109:6241–6246. DOI: <https://doi.org/10.1073/pnas.1117018109>
- Sharma R, Polkade AV, Shouche YS (2015) 'Species concept' in microbial taxonomy and systematics. *Current Science* 108:1804–1814.
- Stengel A, Stanke KM, Quattrone AC, Herr JR (2022) Improving taxonomic delimitation of fungal species in the age of genomics and phenomics. *Frontiers in Microbiology* 13:847067. DOI: <https://doi.org/10.3389/fmicb.2022.847067>
- Strasser JF, Monaghan MT (2022) Phylogenomic insights into the early diversification of fungi. *Current Biology* 32:3628–3635. DOI: <https://doi.org/10.1016/j.cub.2022.06.057>
- Taylor JW (2011) One fungus= one name: DNA and fungal nomenclature twenty years after PCR. *IMA Fungus* 2:113–120. DOI: <https://doi.org/10.5598/imafungus.2011.02.02.01>
- White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics, 315–322. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Editors), *PCR Protocols: A guide to methods and applications*, Academic Press, New York.
- Xu J (2020) Fungal species concepts in the genomics era. *Genome* 63:459–468. DOI: <https://doi.org/10.1139/gen-2020-002>
- Zhou LW, May TW (2023) Fungal taxonomy: current status and research agendas for the interdisciplinary and globalisation era. *Mycology* 14:52–59. DOI: <https://doi.org/10.1080/21501203.2022.2103194>
- Zitouni-Haouar FEH, Bidartondo MI, Moreno G, Carlavilla JR, Manjón JL, et al. (2023) Bioclimatic origin shapes phylogenetic structure of *Tirmania* (*Pezizaceae*): New species and new record from North Africa. *Journal of Fungi* 9:532. DOI: <https://doi.org/10.3390/jof9050532>