



PERSPECTIVE

Can we create a truly unified fungal taxonomy portal?

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Abstract

Fungal taxonomy remains fragmented and inadequately resourced, lacking a unified, sequence-validated, and clinically actionable framework akin to the List of Prokaryotic names with Standing in Nomenclature (LPSN). As fungal pathogens pose growing threats to global health, agriculture, and ecosystems, an integrated taxonomy platform is urgently needed, one that links nomenclature, DNA barcodes, type strains, literature, and metadata. This article proposes a Unified Fungal Taxonomy Portal (UFTP), grounded in open-access principles, international collaboration, and bioinformatic interoperability. The UFTP would improve species identification, enhance diagnostic precision, and support antifungal stewardship, meeting

taxonomic, medical, and non-medical imperatives of the 21st century.

Keywords: Bioinformatics, Diagnostics, Fungus, Mycology, Taxonomy

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1. Introduction

Fungi represent one of the largest and most functionally diverse biological kingdoms, with an estimated 2.2–3.8 million species, yet fewer than 150,000 have been formally described (Hawksworth & Lücking, 2017; Hyde, 2022). Despite their biographic, ecological, industrial, and medical relevance, fungal taxonomy remains hindered by inconsistent data standards, limited integration, and a lack of centralized, and curated platforms.

Unlike bacterial taxonomy, which benefits from resources such as the *List of Prokaryotic names with Standing in Nomenclature* (LPSN) (<https://lpsn.dsmz.de/text/introduction>) (Parte et al. 2020; Meier-Kolthoff et al. 2022), fungal classification lacks a comparable, sequence-informed infrastructure. This lacuna hampers reproducibility, diagnostic accuracy, and the tracking of emerging agriculture and medical pathogens. Existing nomenclatural databases, though foundational, are poorly connected to the molecular, ecological, and clinical demands of modern fungal research, forecasting, and diagnostics. Although fungal taxonomy is much more complex than bacterial

taxonomy, a systematic approach for data maintenance will not only help taxonomists but also help ecologists (Sharma et al., 2015).

2. Challenges with Existing Databases

MycoBank (<https://www.mycobank.org>) is a major resource for registering fungal names under the International Code of Nomenclature (ICN) for algae, fungi, and plants. It is managed by the International Mycological Association (IMA), Westerdijk Fungal Biodiversity Institute (WFDI), and German Mycological Society (Deutsche Gesellschaft für Mykologie / DGfM). However, it does not mandatorily require deposition of culture and molecular data such as ITS, LSU, *TEF1α*, or other protein-coding regions used for characterizing the species, limiting its utility in validating species or establishing phylogenetic relationships (Hibbett et al., 2016).

Index Fungorum (<http://www.indexfungorum.org>), managed by The Royal Botanic Gardens, Kew, UK, and CABI, UK, maintains an extensive nomenclatural archive but similarly lacks integration with molecular, cultural, etymological, nomenclatural, and

bibliographic data (Hawksworth, 2011). This database does not directly link to databases like GenBank, or EMBL, which also contain several invalidated or inconsistently annotated sequences (Nilsson et al., 2019), and repositories like ATCC, DSMZ, JCM, etc., thus affecting the overall systematics of fungi.

Other platforms like UNITE (Kõljalg et al., 2013), MycoCosm, FungiDB, and BOLD house extensive sequence data but lack formal taxonomic oversight (Grigoriev et al., 2011; 2014; Alvarez-Jarreta et al., 2024; Ratnasingham & Hebert, 2007, 2013; Ratnasingham et al., 2024). Culture collections such as CBS, ATCC, DSMZ, JCM, and MTCC maintain valuable type materials but are rarely synchronized with nomenclatural databases, complicating taxon validation, and strain traceability. Taxonomists still face these problems with difficulty, but for ecologists, they pose serious problems when annotating Operational Taxonomic Units (OTUs) or identifying strains and confirming their ecological functionality.

The clinical implications of this fragmentation are significant. Misidentification of species like *Aspergillus fumigatus*, *Candida auris*, or cryptic *Mucorales* taxa can lead to diagnostic errors, ineffective treatments, and uncontrolled outbreaks (Fisher et al., 2020; Lockhart et al., 2017). Internal transcribed spacer (ITS) remains the gold standard for fungal identification, but curated sequences linked to type strains are often difficult to access (Schoch et al., 2012).

Similarly, the agriculturally important, non-clinical fungi have also faced several issues due to segregated information related to fungal taxonomy. *Akanthomyces lecanii* is an example of problems faced by companies manufacturing this entomopathogenic fungus as biopesticides due to a change in nomenclature or taxonomic position within the family (Zhang et al., 2020). This not only affects the approval procedures (bureaucrats with little knowledge of taxonomy) but also makes it difficult to convince the end users and stakeholders.

3. Toward Integration: Lessons from LPSN

The LPSN model demonstrates the feasibility of a centralized, peer-reviewed taxonomy that integrates type strains, molecular data, literature, nomenclature, and etymology (Parte et al., 2020). Each bacterial species entry includes not only information related to type strain deposition, 16S rRNA gene sequence accession numbers, synonym, basionym, etymology, gender of species name, reference citations, and cross-references to genome data and culture collections, enhancing transparency and reproducibility, but also

has hyperlinks to the culture collection numbers, NCBI accession numbers, etc. It also has an excellent hierarchical taxon browsing system and provides links to almost every external data mentioned on the website, be it a culture collection number or an NCBI accession number (<https://lpsn.dsmz.de/>).

Applying this model to fungi would require mandatory deposition of barcoding sequences (e.g., ITS, LSU, *TEF1α*, *RPB1/2*, etc.), integration with major culture collections (e.g., CBS, ATCC, DSMZ, JCM, MTCC and others), and linking to full-text literature via DOIs and PubMed IDs. This unified approach would not only align taxonomy with genomic and clinical utility, especially for medically significant taxa, but also benefit non-clinical fungi.

4. Barriers to Clinical Relevance

Clinical limitations of fungal taxonomy stem from the lack of integrated sequence data, inconsistent linkage to type cultures, and poor bibliographic traceability or record. These issues hinder reliable identification of cryptic or resistant species (e.g., *Aspergillus lentulus*), obstruct access to validated material, and complicate clinical decision-making (Chowdhary et al., 2013).

Nomenclatural redundancy and asynchronous updates between MycoBank and Index Fungorum create further confusion. Such discrepancies directly impact epidemiology, pharmacovigilance, and antifungal stewardship. As fungal infections rise and resistance spreads, reliance on outdated, siloed systems becomes increasingly untenable.

5. Proposal: A Unified Fungal Taxonomy Portal (UFTP)

The proposed Unified Fungal Taxonomy Portal (UFTP) would address current deficiencies by integrating nomenclature, morphology, molecular data, type strains, siloed geographic distribution, and literature in a single platform. Key components will include:

1. **Sequence and Morphological Integration:** Each species entry would include high-resolution images of type cultures, mandatory DNA barcode sequences (ITS, LSU, *TEF1α*, *RPB1/2*, and so on), and curated GenBank accessions (Schoch et al., 2012; Nilsson et al., 2019). It will also include whole genome sequence data, if any.

2. **Taxonomic Metadata and Literature:** including full hierarchical classification, synonym tracking, and protologue citations and DOIs, and full-text links to original descriptions, ensuring traceability.

3. Culture Collection Linkage: including cross-referencing with CBS, ATCC, MTCC, DSMZ, and others, and growth protocols, availability data, and ordering links (Kwon-Chung & Sugui, 2013). It will also mention whether a fungus is deposited as culture or herbarium.

4. Interactive Phylogenetic Tools: including tree visualization, BLAST, MLSA, and species delimitation tools, aiding diagnostics and research.

5. Interoperable API Framework: including synchronization with UNITE, GBIF, NCBI, and culture databases and real-time updates, reducing redundancy and facilitating data sharing.

6. Governance and Sustainability

A globally coordinated consortium comprising taxonomists, clinicians, data scientists, and public health stakeholders should oversee UFTP development. The portal would adhere to ICN standards and incorporate the proposed MycoCode (May et al., 2019; Yurkov et al., 2021). A peer-reviewed, auditable feedback mechanism would ensure transparency and community-driven accuracy (Parte et al., 2020).

Funding could come from bodies such as the WHO, NSF, GBIF, CDC, and international collections (e.g., DSMZ, ATCC, JCM, CBS, CABI, WDCM, WFCC, and others). A tiered access model offering open-access core infrastructure with optional advanced tools could sustain long-term operations.

7. Conclusions

The UFTP represents a transformative vision for modern fungal taxonomy that is comprehensive, interoperable, and clinically actionable. Much like LPSN has become a cornerstone of bacterial nomenclature, the UFTP would unify fungal names, sequences, and reference materials while serving a diverse user base across clinical, agricultural, and ecological sectors. LPSN is a free-to-use service founded by Jean P. Euzéby in 1997 and later maintained by Aidan C. Parte. LPSN is now also recognized by the Global Biodata Coalition (<https://globalbiodata.org/>)

Its benefits include enhanced diagnostic accuracy for pathogenic fungi, improved epidemiological tracking, correct nomenclature of fungi commercially used for biopesticidal and biofertilizer use, and antifungal resistance surveillance, reliable identification of environmental and industrial strains, and bridging gaps between taxonomic theory and practical application.

Real-world challenges, such as those experienced during *Verticillium–Lecanicillium* reclassification in biofertilizer approvals (Malusá & Vassilev, 2014) and the increase in multidrug-resistant *Candida auris* strains highlight the urgent need for taxonomic clarity. With coordinated global action, institutional support, and community participation, the UFTP can catalyse a new era in fungal systematics, one rooted in accuracy, accessibility, and interdisciplinary relevance.

Present-day molecular taxonomy and whole-genome sequencing data have enhanced our understanding of fungal diversity. It has also helped in the discovery of previously unrecognized lineages. A prominent example is the identification of *Cryptomycota*, a divergent fungal group that has so far evaded detection and recognition through traditional methods of morphotaxonomy (Jones et al., 2011). Environmental DNA sequencing and phylogenetic analysis have helped in the recognition of this group, thus highlighting the power of molecular tools in unveiling cryptic fungal taxa.

Clinically, the proposed Unified Fungal Taxonomy Portal (UFTP) could improve species identification and diagnostic accuracy, particularly for emerging pathogens such as *Candida auris* and mucormycosis-causing fungi. Beyond clinical settings, the UFTP would streamline bioinformatic pipelines, support antifungal resistance surveillance, and facilitate broader applications. Taxonomists and ecologists could also frame their research within this integrated system, enhancing the portal's overall utility.

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