A multitude of fungi and an advocacy for fungal taxonomy

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Abstract

Fungi are among the most diverse and ecologically significant organisms on our planet, yet their vast biodiversity remains underexplored and undervalued. This paper highlights the evolutionary success of fungi, owing to their unique reproductive strategies, filamentous growth form, and ecological versatility, and argues for a renewed urgency in fungal taxonomy. Despite their critical roles in ecosystem functioning, medicine, agriculture, and biotechnology, fewer than 10% of fungal species are currently described. The taxonomic impediment, particularly severe in mycology, is driven by structural underfunding, a shortage of trained taxonomists, geographic and conceptual biases, and limited access to data. Societal consequences of this shortfall are widespread, from inadequate nature conservation and emerging fungal diseases to unreliable DNA-based biodiversity assessments. This paper advocates for reversing institutional neglect, strengthening research infrastructures, and integrating molecular tools within an inclusive taxonomic framework. Only through coordinated global efforts can fungal taxonomy meet the demands of science and society in the 21st century.

An evolutionary success story

Fungi outnumber most other organisms on our planet and have endured here far longer than many other life forms. They cross the borders between macro – and microbiology given their often microscopic and hidden lifestyle. On the other hand, the largest organism in the world is most probably a fungus (Smith et al., 1992) and many species make themselves visible as very diverse, colourful fruiting bodies in an amazing variety of shapes: the mushrooms! After insects, fungi constitute the second-largest group of organisms. Estimates range from 650,000 (Mora et al., 2011) to 6 million species (Taylor et al., 2014; Hawksworth & Lücking, 2017). The high number of species of fungi reflects a huge evolutionary success.

First reason for this impressive evolutionary success is their ability to produce billions of spores per fruiting body. Spores can be either sexual (meiospores) or asexual (mitospores) reproductive units, most often uni-cellular and very small. Spores are encountered in many other groups of organisms, think plants, think bacteria, but fungal spores outrange the spores in other groups by numbers and by their very small sizes (Money, 2002). Designed to be transported by wind and convective currents in the air, they are often formed in specially designed structures, the ones we know as sporocarps of mushrooms. One fruitbody of *Langermannia gigantea* produces up to 7 trillion spores (Ingold, 1971), remaining inside the fungus until the wall degrades and the spore mass can be dispersed mainly by the wind. For the more iconic gilled mushrooms we know that they can produce up to 30.000 spores per second on special cells (basidia) that are present on the gills. Basidiospores are actively discharged from the basidia by a catapult mechanism (Money, 1998; Noblin et al., 2009). These sexually produced spores contain new genetic information and spread it around the environment. Fungi are also champions in forming asexual spores that are produced and discharged in high numbers to conquer and occupy new territory.

Another crucial factor is the entirely innovative body design. Unlike plants and animals, fungi are not composed of cells but consist of a network of delicate threads (hyphae) that can grow everywhere and in-between. Thanks to this network, they can feed and reproduce in a truly unique manner and they have access to almost every conceivable substrate. Their body is a continuum able to grow at all ends in every direction, wit no fixed form or format. Though the hyphae have a very small diameter the wall is rather rigid because it contains chitin. Extra support is also given by transversal septae dividing the mycelium into regular compartments. It is wrong however to compare these compartments with elongated well because the original design was threads (or rather tubes) without septae, and in all case (septate or aseptate) there is a continuous flux within the hyphae. Not only cytoplasma, but also organelles and nuclei are able to move along the length of the mycelium (Steinberg, 2007).

Fungi are not just a network; they also connect other organisms, especially plants, in a vast and ecologically vital network known as the wood-wide-web (Simard et al., 1997).

The reasons to study fungi are manyfold. They fulfill key roles in all ecosystems worldwide, as saprotrophs, mutualists and parasites. The services they provide to humanity are immense, including medicine, food production, fermentation, bioremediation, production of enzymes and biofuel (Hyde et al., 2019; Hawksworth et al., 2010).

About 154,000 species of fungi (circa 6% of estimated total diversity) are currently described (Banki et al., 2023). This large gap between estimated and actual described number of species, known as the Linnean shortfall (Hortal et al., 2015), is a reality for all species on earth, but especially striking for fungi. This is confirmed by analysing environmental DNA, where one single soil sample might reveal hundreds of potential new species (Tedersoo et al., 2014; Bahram et al., 2018).

Such staggering diversity calls for an accelerated investment in fungal taxonomy and a more efficient effort from fungal taxonomists. Particularly, institutions that have historically played a significant role in taxonomic research in fungi have a moral obligation to maintain and, where possible, expand that knowledge. Assessment of the biodiversity with eDNA is only possible when supported by a solid taxonomic framework (Nilsson et al., 2019).

"Taxonomy (the science of classification) is often undervalued as a glorified form of filing—with each species in its folder, like a stamp in its prescribed place in an album; but taxonomy is a fundamental and dynamic science, dedicated to exploring the causes of relationships and similarities among organisms. Classifications are theories about the basis of natural order, not dull catalogues compiled only to avoid chaos." Stephen Jay Gould

The taxonomic impediment and the multiple hurdles for fungal taxonomy

1. On top of the global taxonomic challenge, there is a specific mycological obstacle. The inadequate state of knowledge regarding mycological diversity has various causes linked to the aforementioned general gaps but is characterized by specific disparities compared to other branches of taxonomy. The needs in terms of professional mycologists, knowledge of biodiversity hotspots, exploration of specific niches, capacity building in developing countries, and theoretical foundation are even more extensive and explicit than in other taxa (Ainsworth & Gaya, 2020). There is a significant discrepancy between these needs and available taxonomists: traditionally, fewer mycotaxonomists are active in institutes, universities, etc., compared to, for example, botanists or entomologists (Blackwell, 2011).
2. Funding discrepancies. The allocation of funds for fungal taxonomic research is correspondingly severely limited (Castaño et al., 2023; Hawksworth et al., 2020).
3. Geographic under-exploration: The most biodiverse biota and hotspots for fungal diversity are underexplored. For instance, an estimated 75% of fungi are believed to be endemic to the tropics (Hyde et al., 2020). The low level of exploration likely means that the majority of unknown diversity is tropical (Fröhlich & Hyde, 1999).
4. Capacity inequalities: The overwhelming majority of taxonomists, taxonomic collections, and associated taxonomic knowledge are currently located in industrialized countries, while the bulk of fungal diversity is found in developing countries (Vázquez-Baeza et al., 2016).
5. Gap in information provision. Taxonomic information is often only available in formats and languages that are not suitable or accessible to the countries of origin given that specimens from (often) developing countries are studied in industrialized countries. Access restrictions due to journal paywalls present an added obstacle (Chan et al., 2021).
6. Discrepancy regarding unexplored niches: due to their diffuse body (hyphae) and unique physiology (external digestion), fungi can colonize almost all substrates. Numerous examples exist of exploratory research projects on new substrates that reveal a plethora of new species: endophytes in plant leaves (with their diverse array of compounds that can play a crucial role in medicine and healthcare), fungi associated with insects, marine fungi, lichens (Amend et al., 2019; Hawksworth & Rossman 1997; Fröhlich & Hyde 1999; Taylor et al. 2000a; Sipman & Aptroot 2001; Lawrey & Diederich 2003; Arnold & Lutzoni 2007).
7. Conceptual discrepancy. Fundamentally, fungal taxonomy still largely operates from the organism level, broadly conceived from a narrow morphological approach that is generally characterized by the traditional use of the morphological species concept (alongside, for example, host associations). This results in an underestimation of the actual number of species, especially in groups with relatively simple morphological

features. About 2.000 new species are described each year (Cheek et al. 2020), with more than half still being described without molecular data (Lücking et al., 2020).

Societal relevance

The fundamental and academic usefulness of addressing the specific fungal taxonomic challenge may be clear from the above figures. The enormous diversity of species is further reflected in functional, physiological and ecological diversity. Fungi are undeniably key organisms in any ecosystem. Ecosystem services as primary production are inconceivable without fungi that form mycorrhizal associations, and the carbon cycle crucially depends on fungi that can break down lignin. As a result, the knowledge gaps have far-reaching consequences with regard to a large number of socially relevant fields:

Nature conservation: fine-tuning or resetting? In the conservation, management, and development of natural areas and the associated biodiversity, fungal diversity is hardly taken into account, correspondingly to the limited knowledge. Thus, by definition, the management effects cannot be properly evaluated. The problem is independent of the scale: a handkerchief redevelopment in a heathland reserve or a "replanting" of tropical forest will both gain in essential management efficiency when the various impacts of fungi on the ecosystem in question are taken into account (Castaño et al., 2023; Heilmann-Clausen et al., 2015).

Healthcare: *Bad taxonomy kills!* Given the annual number of incidents, it goes without saying that it is essential to know the toxicology of the various taxa in detail. Even within a number of well-known taxa, the current state of taxonomic knowledge does not always allow for the correct qualification of incidents. The problem is as pertinent in industrialized countries as it is in developing countries (Hyde et al., 2018; Fisher et al., 2012).

Neobiota: a ticking ecosystem bomb? Knowledge about the impact of neomycetes (fungal species that are newly introduced to an area where they are not native, typically as a result of human activity, whether intentional or accidental) on humans and communities in general is still in its infancy. Impact studies, measures, and control campaigns are pre-eminently based on specific species knowledge. Current strategies focus on macrofauna and flora, while neomycetes, inherent in their character, include an insidious and not to be underestimated problem, which is only becoming larger and more threatening in the context of the current climate change (e.g., mass mortality of *Salamandra salamandra* in the Netherlands by the parasite *Batrachochytrium salamandrivorans*, recently introduced in the Netherlands and only described in 2013, population crashes of many North American bats by *Pseudogymnoascus destructans*, the causal agent of white-nose syndrome, described in 2009 (Fisher et al., 2020).

Metabarcoding: an inflation of mysterious data. Ecologists are now increasingly using metabarcoding to quantify biodiversity in ecosystems/environmental samples. At first sight, it seems to be a faster and more efficient method than a traditional species recognition approach. Unfortunately, this often results in unreliable and misleading insights (many "new" DNA sequences) without a clear link to fundamental taxonomic research. There is an urgent need for more taxonomists to bridge this metabarcoding research (Nilsson et al., 2019).

Catching up

Given the critical role of fungi in both scientific research and broader societal contexts, and in light of the growing need to resolve the discrepancies outlined above, it is imperative not only to accelerate investment in fungal taxonomy, but also to confront the troubling trend of institutional neglect. The recent decision by Duke University to close its herbarium starkly illustrates the diminishing value placed on taxonomy in today’s academic climate. Rather than allowing such essential infrastructure to disappear, we must urgently reverse this trajectory. Institutions equipped for state-of-the-art taxonomic research should be supported, maintained, and, wherever possible, strengthened — not dismantled.In order to successfully close the gap, the above challenges must be tackled one by one and a synergistic offensive must be created:

a significant increase in the number of PhD and postdoc positions;
a significant increase in funds to boost research in these fields;
prioritizing the collection and study areas according to expected fungal diversity;
capacity building in developing countries;
improve accessibility of databases, specimen collections and mycological information and bridge the gap between metabarcoding and modern taxonomic research;
prioritizing research in new substrates.

New era: further development of the conceptual framework

The availability of molecular tools provides access to myriad of genetic information. Hand in hand with genotyping of new species, phylogenetic studies reveal many new genera and higher lineages. Morphologically similar taxa often appear to represent completely different lines of evolution, sometimes down to the familial level (and higher) (Lücking et al., 2020). This new knowledge should lead to an instrumental, pragmatic species approach, characterized by the use of an integrated taxonomy approach in which independent lineages of information (e.g., morphology, ecology, biogeography, DNA) together solidify the species descriptions.

In summary, it can be said that with a concerted effort with regard to mandates and operating funds, both prioritized according to the outlined scientific and societal

objectives, mycotaxonomists will further enable communication in the fundamental and applied scientific directions as well as in the broad social debate.

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