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Prevalence of Red List DD Species Limits the Application of the EDGE Approach for Fungi

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ABSTRACT

Despite their importance, fungi remain underrepresented in global conservation priorities and largely absent from indicators established for monitoring progress within the Global Biodiversity Framework. One indicator, the Evolutionarily Distinct and Globally Endangered (EDGE) Index, tracks the conservation status of evolutionarily distinct species, but no EDGE list exists for fungi. To help address this gap, we assessed the extinction risk of 94 fungal species in monotypic genera, expected to have high evolutionary distinctiveness. Using IUCN Red List Criteria, most species were categorized as Data Deficient (56), 28 as Least Concern, with only nine assigned to threatened or near threatened categories, and one Not Evaluated. The prevalent data deficiency reflects severe knowledge gaps in fungal distribution, ecology, and taxonomy that impede evidence-based policy-making. We discuss challenges constraining fungal Red Listing and emphasize how basic mycological research is crucial to capture phylogenetic diversity in conservation priorities and ensure adequate representation of fungi in biodiversity policy and conservation.

1 | Introduction

Fungi make up a significant part of the planet's biodiversity, with an estimated 2.5 million species, and play crucial roles in ecosystems and various aspects of human life. Yet, they remain among the most understudied organisms, with up to 95% still unknown to science (Niskanen et al. 2023). This is reflected in the attention given to their protection. Despite being susceptible to extinction threats, fungi have so far been largely neglected in conservation efforts (Gross 2025).

The IUCN Red List of Threatened Species (henceforth Red List) is widely used to monitor the state of biodiversity and inform conservation priorities (Stuart et al. 2010). It categorizes species according to their extinction risk, applying criteria based on, for example, population size and trends, threats or geographic range. Categories range from Critically Endangered, Endangered and Vulnerable (threatened) to Near Threatened and Least Concern, as well as extinct categories. Species lacking sufficient information, making both Critically Endangered and Least Concern plausible, are categorized as Data Deficient (DD) (IUCN 2024). While the number of published fungal assessments has risen significantly since 2013, reaching 1300 (IUCN 2025), most species remain unassessed. Those assessed so far are also biased in taxonomic representation, distribution, ecology, and risk categories, with a high proportion of species in threatened categories due to prioritizing for assessment those already suspected to be threatened (Mueller et al. 2022).

Because less than 1% of species have been assessed for the Red List (Niskanen et al. 2023), fungi are often overlooked in conservation research and action (Di Marco et al. 2017; Guénard et al. 2025). Moreover, though fungi are vital to achieving the goals outlined in the Kunming-Montreal Global Biodiversity Framework (Fungal Conservation Network 2024), fungal species are largely absent from its monitoring framework (CBD Secretariat 2022). Indicators such as the Red List Index (Butchart et al. 2025) or genetic diversity indicators (Mastretta-Yanes et al. 2024) are, in theory, applicable to fungi, but the lack of comprehensively assessed and reassessed groups in the Red List (IUCN 2025) and challenges concerning fungal population genetics complicate their application. Another indicator, the Evolutionarily Distinct and Globally Endangered (EDGE) Index, tracks the conservation status of evolutionarily distinct species (Gumbs et al. 2023). The EDGE score, the basis of the index, highlights threatened species from evolutionarily distinct lineages, whose extinction would represent a substantial loss of evolutionary diversity. Its calculation combines a score for a species' degree of isolation on the tree of life with an extinction risk score based on the Red List (Gumbs, Gray, et al. 2023; Isaac et al. 2007). Given the absence of comprehensive data for species isolation or extinction risk, no EDGE list for fungi currently exists, but key steps toward it can be identified and piloted.

Knowledge of fungal diversity and evolutionary history has increased significantly in recent decades (James et al. 2020). Current trends, including the sequencing of fungaria specimens (Varga et al. 2026) and the increasing inclusion of molecular data in protologues (Miralles et al. 2020), may provide the necessary phylogenetic diversity data in the future. Comprehensive phylogenies of fungal clades, such as Varga et al. (2019)'s phylogeny of Agaricomycetes, are essential to estimate the evolutionary distinctiveness of species. Concurrently, since the growth in Red List assessments is relatively recent, many more are needed to increase the number of species for which we can compute EDGE scores.

We aimed to contribute to the evidence base for the future development of a fungi EDGE list/Index by assessing species in monotypic genera and families expected a priori to score highly for evolutionary distinctiveness. An additional goal was to contribute extinction risk assessments that, through a different approach for selecting species for assessment, could help redress the bias within fungi currently on the Red List. Here, we give an overview of candidate species for a future EDGE list for fungi and discuss how data shortfalls hinder the application of the EDGE approach and fungal conservation more broadly.

2 | Methods

To identify species in monotypic lineages in the class Agaricomycetes, we used Index Fungorum (https://www.indexfungorum.org). We selected species in commonly recognized orders in Agaricomycetes to ensure feasibility while maintaining taxonomic diversity. This included all species in monotypic genera in Boletales, Cantharellales, Russulales, and in monotypic families in Agaricales and Polyporales, totaling 114 species (Table S1). Nomenclature was verified through literature review, resulting in the removal of 20 nonmonotypic species and follows Index Fungorum at the time of assessment (2022–2023). Of the 94 selected species, eight were already published on the Red List. The remaining 86 species were assessed in this study, following IUCN Red List criteria and specific recommendations for fungi (IUCN 2024; Dahlberg and Mueller 2011). Of these, 76 have since been published on the Red List, nine have been submitted to the Red List Unit for future publication, and one was not evaluated because its protologue and other information were unavailable. In assessments, estimates of population size and distribution were based on occurrence data from the Global Biodiversity Information Facility (https://www.gbif.org) and MyCoPortal (https://www.mycoportal.org), together with protologue information on specimens and habitat requirements to estimate multipliers for unknown sites. Population declines were calculated based on published estimates of habitat loss, when available, and forest loss data from Global Forest Watch (https://www.globalforestwatch.org) (Hansen et al. 2013).

For data analysis, we assigned ecological guilds and growth forms based on species assessments and associated literature, as well as the FunGuild database (Nguyen et al. 2016), and determined geographical distribution by the countries of occurrence recorded in assessments. Given the importance of phylogenetic distinctiveness in calculating EDGE scores, we also characterized species according to the available information that indicated their monotypic status. We distinguished three categories of evidence: phylogenetic data, morphological characteristics alone, or isolation due to a taxonomic revision that reassigned all other species in the genus. For DD species, we identified the reason for this category assignment following the justification tags recommended by Bland et al. (2017), with amendments reflecting guidelines for fungi (Dahlberg and Mueller 2011) (see Table 1). Although multiple reasons could sometimes apply, only the primary reason was recorded. For threatened species, threats identified in assessments were recorded based on the highest level of the Red List Threats Classification Scheme (version 3.3) (IUCN 2022), splitting where appropriate, consistent with Mueller et al. (2022), and allowing multiple threats per species. Finally, we recorded "research-needed" tags identified during the assessments (IUCN 2012).

Data were analyzed using R 4.4.0 (R Core Team 2024) and the packages rnaturalearth 1.0.1 (Massicotte and South 2023) and ggplot2 3.5.1 (Wickham 2016).

3 | Results

Of the 94 species analyzed, 56 were assessed as DD, 28 as Least Concern, eight in threatened categories, one as Near Threatened, and one could not be evaluated (Figure 1a). The selected species represented various geographical regions, ecological guilds, and growth forms (Figure 2). However, guild could not be determined for 15 of the 94 species due to a lack of available information. Similarly, it was not possible to attribute a growth form to 10 species.

TABLE 1 | Definitions of terms used as the main reason for the assignment of the Data Deficient (DD) category in assessments.[a]

Term	Definition
Type series	Species only known from specimens cited in the protologue.
New species	Species described within 10 years before the date of assessment.
Few records	Species known from very few records (e.g., two to four), in the absence of further data that allows for the estimation of unknown sites.
Taxonomic uncertainty	Species for which uncertainty regarding taxonomy directly leads to paucity of data on distribution, population status, ecology, and threats.
Old records	Species is only known from records older than 50 years at the time of assessment. A threshold of 50 years corresponds to the three-generation period used in assessment criteria for ectomycorrhizal fungi and matches the upper limit of the 20- to 50-year interval used for wood-inhabiting fungi, and soil and litter fungi (Dahlberg and Mueller 2011).
Uncertain provenance	Species is only known from specimens with no or extremely uncertain locality information.

[a]Adapted from Bland et al. (2017) and IUCN (2024), considering assessment guidelines developed specifically for fungi (Dahlberg and Mueller 2011).

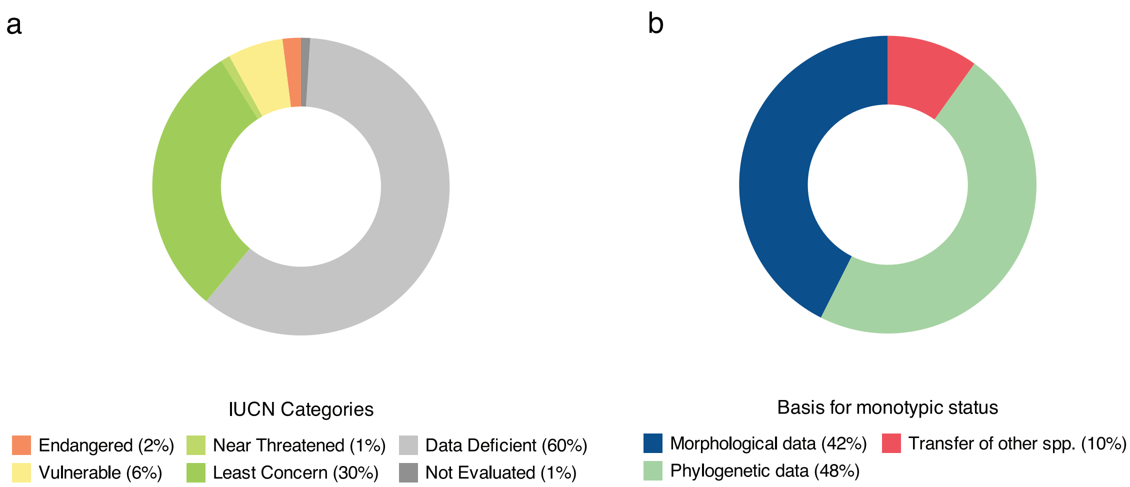

FIGURE 1 | Percentage of monotypic fungal species ($n = 94$) according to their (a) Red List category and (b) type of research used as a basis for the assignment of the species to a monotypic genus. "Transfer of other species" was applied when species were not included in taxonomic changes, leaving them isolated.

Phylogenetic data were the basis for the monotypic status of the genus in 48% of species (Figure 1b), while 43% were considered to represent monotypic genera based on morphological characteristics alone. Approximately 10% were treated as monotypic because they had become isolated in a genus after taxonomic reviews that did not consider them—primarily due to specimen unavailability—but transferred all other species to other genera or families. Very little information was available in these cases, and ultimately, they were all assessed as DD. Of the species for which genetic data were available, only 14 were included in Varga's comprehensive Agaricomycete phylogeny.

3.1 | Threatened Species

Only eight species were classified as threatened (two as Endangered, six as Vulnerable) and one as Near Threatened (Table 2). They were distributed in different global regions, with the highest counts, three each, in Malaysia and Japan (Figure 3a). All the Red List's main criteria (A–D) were applied except for criterion E, as there were insufficient data for the required quantitative analysis of extinction risk. Threats also varied, with logging and agriculture as the most frequently recorded (Figure 3b).

Regarding phylogenetic information, five of these species were not included in Varga's comprehensive phylogeny. Moreover, one had no phylogenetic data available, having been classified in a monotypic genus based on morphological characteristics alone.

3.2 | Causes of Data Deficiency

Most DD assessments were due to a lack of records (Figure 4a). For 11 species, this was attributed to their recent description as species new to science within 10 years of the assessment date, resulting in relatively little available information. However, more

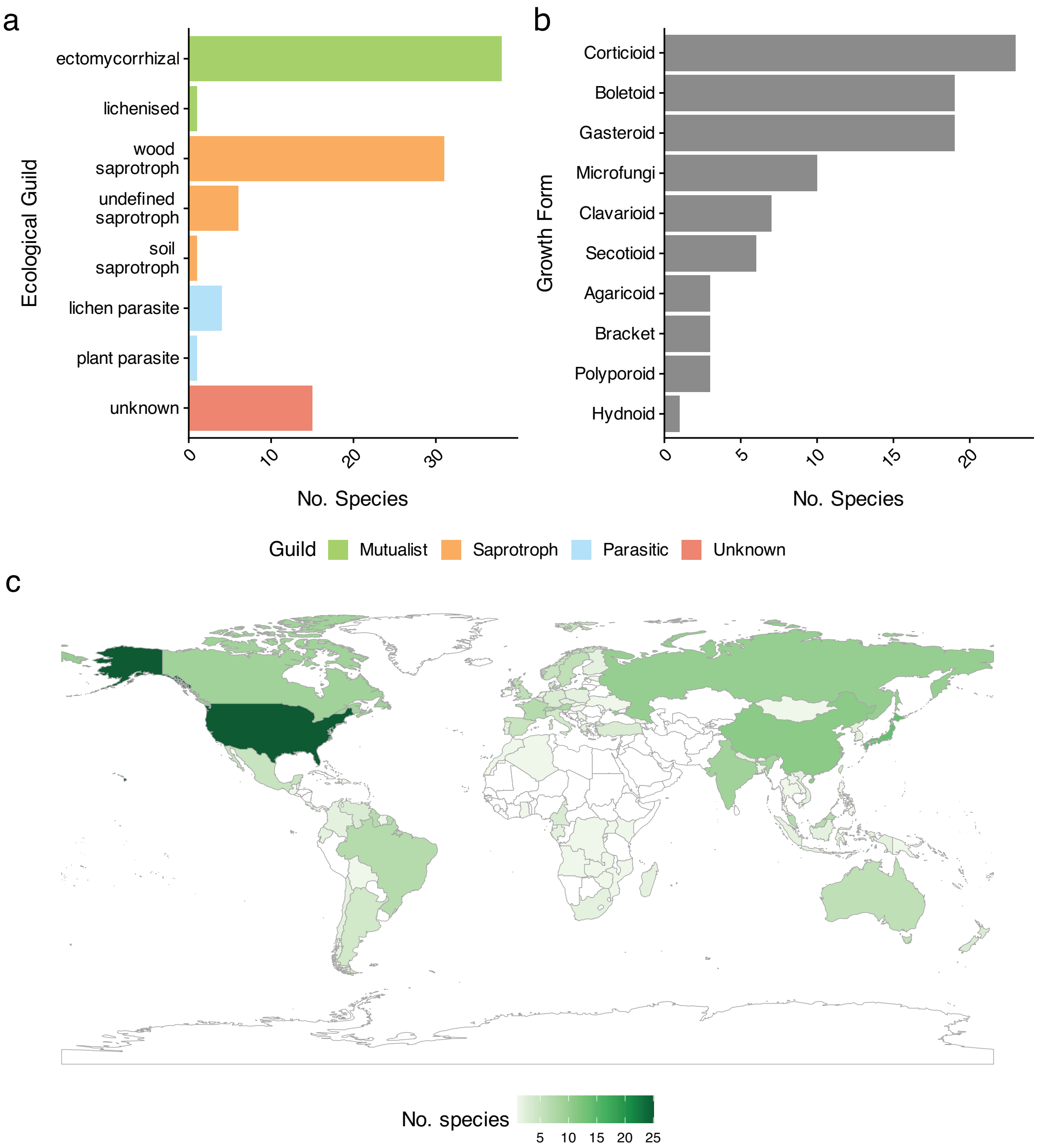

FIGURE 2 | Number of species included in the study according to their (a) ecological guilds, (b) growth forms, and (c) countries of occurrence. Both ecological guilds and growth forms are based on species assessments and associated literature, as well as FunGuild classifications (Nguyen et al. 2016). Where appropriate, species were categorized under multiple ecological guilds and countries.

time elapsed since the description did not necessarily result in a greater number of records. Twenty-nine species were only known from their description more than 10 years ago and specimens cited therein (Type Series, Table 1), with no further records being made since, while for a further 10 species, the number of records available was still very limited (e.g., two or three known collections or sites). For two species, all records were more than 50 years old, which prevented the evaluation of their conservation status in the absence of evidence of targeted search attempts. The justification "Taxonomic uncertainty" was applied to three species, for which a taxonomic revision is needed to clarify whether specimens from different locations are conspecific and allow for a calculation of population size and distribution range. Finally, "Uncertain Provenance" was applied to one species due to high uncertainty regarding its locality information. Though most prevalent for DD species, the lack of information was a recurring issue in the full dataset, as evidenced by the frequent use of "research needed" tags in assessments related to taxonomy, threats and, especially, population and ecology (Figure 4b).

TABLE 2 | Threatened and Near Threatened species assessed in this study according to their Red List category and criteria, type of data available for monotypic assignment, and inclusion in Varga et al. (2019) comprehensive phylogeny.

Species[a]	Category	Criteria	Data available	Varga et al. (2019)
Bondarcevomyces taxi	VU	C2a(i)	Phylogenetic	Yes
Chlorogaster dipterocarpi	VU	A2c+4c	Morphological	No
Cupreoboletus poikilochromus	VU	C2a(i)	Phylogenetic	No
Durianella echinulata	VU	A2c+4c	Phylogenetic	No
Echinodontiellum japonicum	EN	B1ab(i, iii, iv, v); C2a(i)	Phylogenetic	No
Fevansia aurantiaca	EN	B2ab(ii, iii, iv, v); C2a(i)	Phylogenetic	Yes
Gymnogaster boletoides	VU	A3c+4c	Phylogenetic	Yes
Haloaleurodiscus mangrovei	VU	D1+2	Phylogenetic	Yes
Spongispora temasekensis	NT	A2c	Phylogenetic	No

Abbreviations: EN, Endangered; NT, Near threatened; VU, Vulnerable.
[a]*Echinodontiellum japonicum* is published on the Red List (IUCN 2025) as *Echinodontium japonicum*, and *Cupreoboletus poikilochromus* as *Cyanoboletus poikilochromus*.

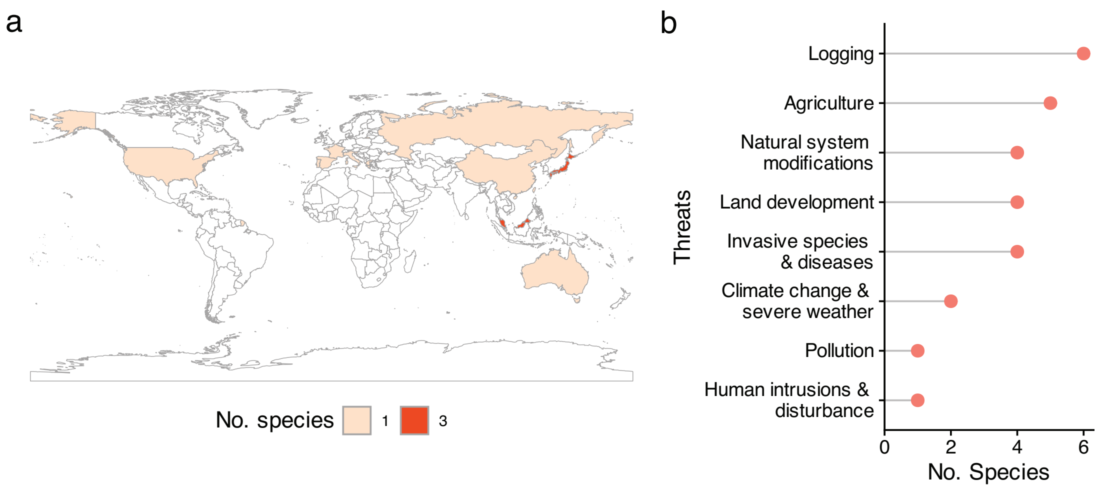

FIGURE 3 | Overview of the nine threatened and Near Threatened species assessments in this study. (a) Number of threatened species assessed per country, (b) frequency of threats recorded in their assessments. For some species, multiple threats are recorded. Threat categories are adapted from IUCN's Threats Classification Scheme (IUCN 2022), following Mueller et al. (2022).

4 | Discussion

This study resulted in 85 new global Red List assessments for species in monotypic genera from various geographies and ecologies. However, of these, only four have the necessary threat status and phylogenetic information for the application of the EDGE approach. The relatively small percentage of threatened species in this dataset was expected since our selection process did not favor those suspected to be at risk. However, the high percentage of species assessed as DD was unexpected (60%).

While data deficiency was sometimes attributable to recent species descriptions, in most cases, it reflected a severe lack of targeted research, as evidenced by the frequent use of "research needed" tags in assessments. This high percentage is consistent with a similar figure found in the Red List assessment of macrofungi in China (Yi et al. 2020), but considerably higher than the 4.5% estimated for plants in monotypic genera (Brown et al. 2025) and is potentially concerning. High percentages of DD species have been predicted to be threatened with extinction in well-known groups, such as amphibians, reptiles, or mammals (Borgelt et al. 2022). Although no such studies exist for fungi, the high DD percentage and its underlying causes should be carefully considered.

Red List assessments rely on information on taxonomy, population, distribution, ecology, and threats, often based on preserved specimens and field records (IUCN 2024). Although these are frequently lacking for fungi, contextual information on ecology, conspicuousness, search efforts, and overall distribution can be used to estimate population size parameters (Dahlberg and Mueller 2011). Therefore, species with few records sometimes qualified as threatened when sufficient search efforts were evidenced, while others were categorized as Least Concern when

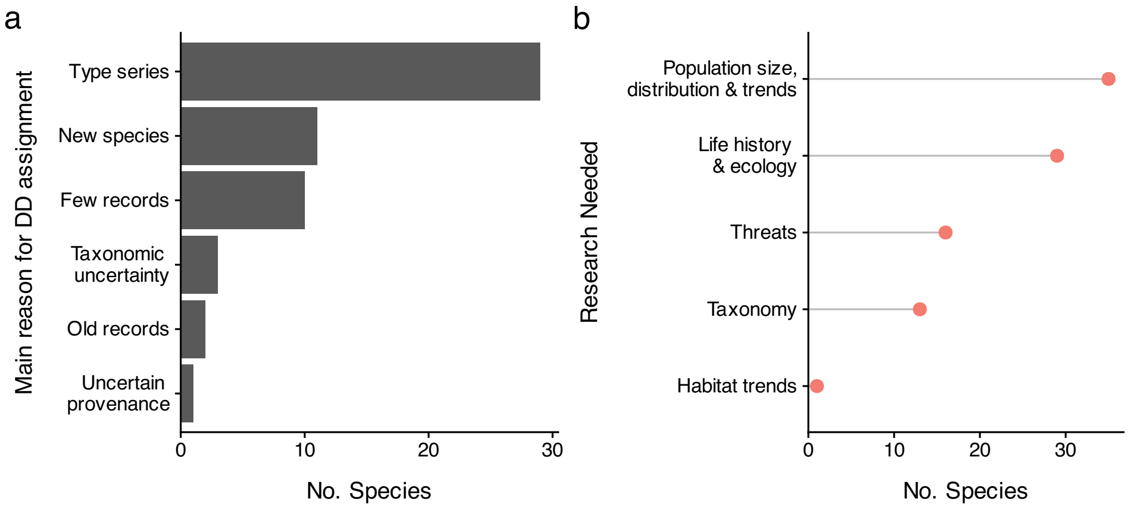

FIGURE 4 | Knowledge gaps identified in the assessments of the monotypic species in this study. (a) Primary reason for assigning species to the Data Deficient (DD) category, following schema adapted from Bland et al. (2017), considering assessment guidelines for fungi (Dahlberg and Mueller 2011) (Table 1) ($n = 56$). Though multiple reasons may apply, only the main reason was recorded. (b) Frequency of research needed classifications (IUCN 2012) recorded across all species evaluated ($n = 93$).

evidence suggested a large distribution and no significant threats. Because the DD category should be avoided whenever possible and is intended as a last resort (Butchart and Bird 2010), different Red List criteria were also used along with indirect data and threat information to avoid assessing species as DD. In particular, criterion A enabled the assessment of species as threatened even in the absence of detailed data due to a suspected decrease in population size from habitat decline and the use of published estimates and remote sensing information (Hansen et al. 2013). This was the case for *Chlorogaster dipterocarpi* and *Durianella echinulata*, both restricted to Malaysian forests, including Borneo, a deforestation hotspot (Gaveau et al. 2016). Nonetheless, a strong link between a species and an exclusive habitat is not always possible to establish, and information on targeted search efforts was not often available, leaving most species as DD.

Lack of records was the main challenge for most assessments. However, gaps in records were especially pronounced in some geographic regions. This likely reflects both the availability of local mycologists and the presence of digitization initiatives. For example, the project "Macrofungi Collection Consortium" allowed for the digitization and publication of macrofungal fungarium records in the United States (Thiers and Halling 2018). Similarly, data collection portals and regional Red Lists in Northern Europe, such as the Finnish and Swedish platforms FinBIF (https://laji.fi) and SLU Artdatabanken (https://www.artdatabanken.se), provide large amounts of local data. In contrast, African taxa were often represented by broad, country-level information in local guides, making estimation of ranges and population size difficult.

Phylogenetic information was available for almost half of our selected species, but many lacked molecular data or were seemingly overlooked in taxonomic reviews. Still, species lacking molecular data may have been over-represented in the dataset because of the selection process. That is, the focus on monotypic genera might have inadvertently favored inclusion of species that have become isolated artificially through their omission from taxonomic revisions and even included species that have been forgotten by science. Therefore, although it highlights the prevalence of data lacunae for fungi, the DD percentage reported here should not be considered representative of all fungi. Moreover, while the percentage of genetic data in this study is promising, DNA data has led to substantial changes in previously established fungal classifications (Niskanen et al. 2023), suggesting that some of the species without genetic data included here could still prove not to be monotypic.

High percentages of DD are not unique to fungi, and have been reported for other poorly known groups, particularly invertebrates, along with strategies to address data deficiency (Hochkirch et al. 2021). Nonetheless, our findings illustrate how data deficiency can represent a significant barrier to the establishment of conservation indicators and result in the exclusion of fungi from conservation goals. Further investment in taxonomic research and field surveys is urgently needed. Cryptic fungi and evolving species concepts make the delimitation of species for assessment and record attribution difficult without reliable taxonomic information. Moreover, research into fungal diversity is essential not only for improving species distribution and population data but also for the description of species unknown to science that may need conservation measures. This research can be accelerated by cross-taxonomic sampling projects that integrate fungi with plant or animal collections and provide information on both distribution and ecology (Antonelli et al. 2025). Environmental DNA can also help elucidate species' distribution, and its use in Red Listing holds considerable potential for improving location estimates in assessments (Copoț et al. 2024). However, before widespread use of eDNA data as evidence in assessments, further discussion and new guidelines are needed to address important caveats. These include the detection of nonviable DNA, since Red List estimates are based on mature reproducing individuals, and also limitations related to the reliability of reference databases at species-level resolution (Meiklejohn et al. 2019).

Additionally, new scientific collections should be complemented by building capacity within local communities to document mycological diversity in underexplored regions, where mycological expertise is absent or under-resourced. Capacity building can include citizen science initiatives that capture fungal diversity while engaging local participants (Haelewaters et al. 2024). Accessibility of historic collections is improving as more fungaria digitize their collections (Thiers and Halling 2018). However, since records are often held in private databases and collections (Marinho and Beech 2020), stronger collaboration between taxonomists and fungal assessors is needed, particularly in reviewing Red List assessments. Lastly, the use of assessment justification tags (Bland et al. 2017) helps prioritize species based on the type of research needed before an assessment is possible. For example, species with few or old records are potential candidates for citizen science projects that target rare species such as the "FUNDIS Rare Fungi Challenges" or the "Lost and Found Fungi" project (Haelewaters et al. 2024). In contrast, species known only from their type series may have been overlooked since their description, so a taxonomic revision to confirm their validity should precede any search effort. Monotypic genera with no molecular data available should be prioritized in molecular studies, especially if they are threatened. Finally, recently described species should be reassessed promptly after new data become available.

Overall, the high DD percentage in our dataset highlights challenges for global fungal diversity metrics and the importance of basic mycological research. The true proportion of DD species across fungi known to science is recognized to be greater than documented in the early fungal assessments published on the global Red List (Mueller et al. 2022). Our adoption of a novel selection process not centered on well-known species, and the resulting prevalence of DD species in our results, underscores the extent and impact of data gaps on the establishment of conservation priorities. It is urgent that these knowledge gaps are addressed in order to establish conservation priorities that consider phylogenetic distinctiveness and prevent fungi from being overlooked in biodiversity indicators.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available in the Supplementary Materials of this article.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.

Supplementary Materials: conl70041-sup-0001-TableS1.xlsx