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Review Article

Red Listing lichenized fungi: best practices and future prospects

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Abstract

According to International Union for the Conservation of Nature (IUCN) guidelines, all species must be assessed against all criteria during the Red Listing process. For organismal groups that are diverse and understudied, assessors face considerable challenges in assembling evidence due to difficulty in applying definitions of key terms used in the guidelines. Challenges also arise because of uncertainty in population sizes (Criteria A, C, D) and distributions (Criteria A2/3/4c, B). Lichens, which are often small, difficult to identify, or overlooked during biodiversity inventories, are one such group for which specific difficulties arise in applying Red List criteria. Here, we offer approaches and examples that address challenges in completing Red List assessments for lichens in a rapidly changing arena of data availability and analysis strategies. While assessors still contend with far from perfect information about individual species, we propose practical solutions for completing robust assessments given the currently available knowledge of individual lichen life-histories.

Keywords: conservation assessment; extinction risk; generation time; IUCN; lifespan; mature individuals; red list; uncertain distribution

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Introduction

Standardizing and comparing measures of extinction risk are essential for global biodiversity conservation efforts. The process of categorizing the conservation status of species yields key information on threats, trends, distributions and conservation actions that can be used to positively alter long-term outcomes for species survival. The IUCN Red List is the best-established system for assigning extinction risk to species at global and regional (e.g. national) levels, and the published assessments are used to promote awareness and conservation needs of species (e.g. Niskanen *et al.* 2023). The Red List criteria (Box 1) rely on a series of quantitative thresholds that are applied to assign extinction risk categories to species. More than 150 000 species have been assessed according to Red List criteria, most of which are vascular plants, vertebrates, arthropods and molluscs (IUCN Standards and Petitions Subcommittee 2024). Recently, however, there have been more assessments in groups of species traditionally overlooked in conservation, including fungi (Mueller *et al.* 2022).

The intent of the Red List is that the criteria and guidelines are applicable and comparable across all multicellular taxa. Thus, all organisms are assessed against the same quantitative thresholds. Red Listing guidelines include substantial details, nuances, and examples of how to interpret and apply the criteria (IUCN Standards and Petitions Subcommittee 2024; hereafter 'guidelines'). While most of the criteria can be readily interpreted for most organisms, there are elements of the criteria and guidelines that require specialized interpretation incorporating the unique biology of a given group of organisms. Hence, papers have been published with suggestions for interpreting Red List criteria for lichens (Scheidegger & Goward 2002), other fungi (Dahlberg & Mueller 2011), and bryophytes (Bergamini *et al.* 2019) to standardize approaches for specific groups. This paper brings advice

> **Box 1.** Summary of IUCN Red List Criteria used to evaluate extinction risk of species
>
> Criterion
>
> A. Population Size Reduction measured over the longer of 10 years or 3 generations
>
> B. Geographic Range in the form of either extent of occurrence or area of occupancy
>
> C. Small population size and decline
>
> D. Very small or restricted population
>
> E. Quantitative analysis

for lichens up to date with current guidelines in light of new opportunities and understanding.

Lichens are symbiotic assemblages of dominant, exhabitant fungi with inhabitant photobionts that form stable, macroscopic, perennial structures (Fig. 1). The Latin names used for lichens apply to the dominant fungal partner, and there are *c.* 20 000 named species globally (Lücking *et al.* 2017). Lichens grow on a wide range of substrata, including soil, mosses, plant debris, tree bark and leaves, wood, rocks and human-made surfaces. Physiologically, they maintain equilibrium with the water content of their environments and can readily and rapidly dehydrate and rehydrate (Kershaw 1985; Honegger 2006). They are integral members of ecosystems globally where they serve as components of food webs, stabilize soil, fix substantial atmospheric nitrogen and carbon, and perform numerous other essential functions (Zedda & Rambold 2015; Asplund & Wardle 2017). Humans use lichens as biomonitors (Abas 2021) and as sources of secondary metabolites in medicine or food (Crawford 2019; Zhao *et al.* 2021) and for novel pharmaceutical and industrial applications (Goga *et al.* 2020). Lichens share many features of their biology with non-lichenized fungi, including microscopic life-history stages and endosubstratal hyphal networks, but they often, have non-overlapping sets of researchers. While often discussed with bryophytes, they are not plants.

Here we build on extant and accepted guidelines for groups that share aspects of biology or ecology with lichens (fungi, bryophytes) and present recommendations, reviews of relevant literature, and resources to aid in assessing the extinction risk of lichenized fungal species according to the guidelines. To this end, we: 1) address the use and application of key terms, including mature individuals and generation length; 2) provide recommendations for how to approach common challenges that arise in lichen Red Listing, including taxonomic and distributional uncertainty; 3) discuss future prospects with a focus on challenges for future conservation actions. For each topic, we provide examples to demonstrate the application of our recommendations.

Definitions and Applications of Key Terms

Appropriately applying Red List criteria requires the correct interpretation of a suite of specific definitions. For instance, a population according to the guidelines is 'the total number of individuals of the taxon' globally, which is distinct from the typical biological definition of the term as the total number of freely interbreeding individuals at a discrete location (e.g. Vandermeer & Goldberg 2013). While the majority of definitions in the guidelines require
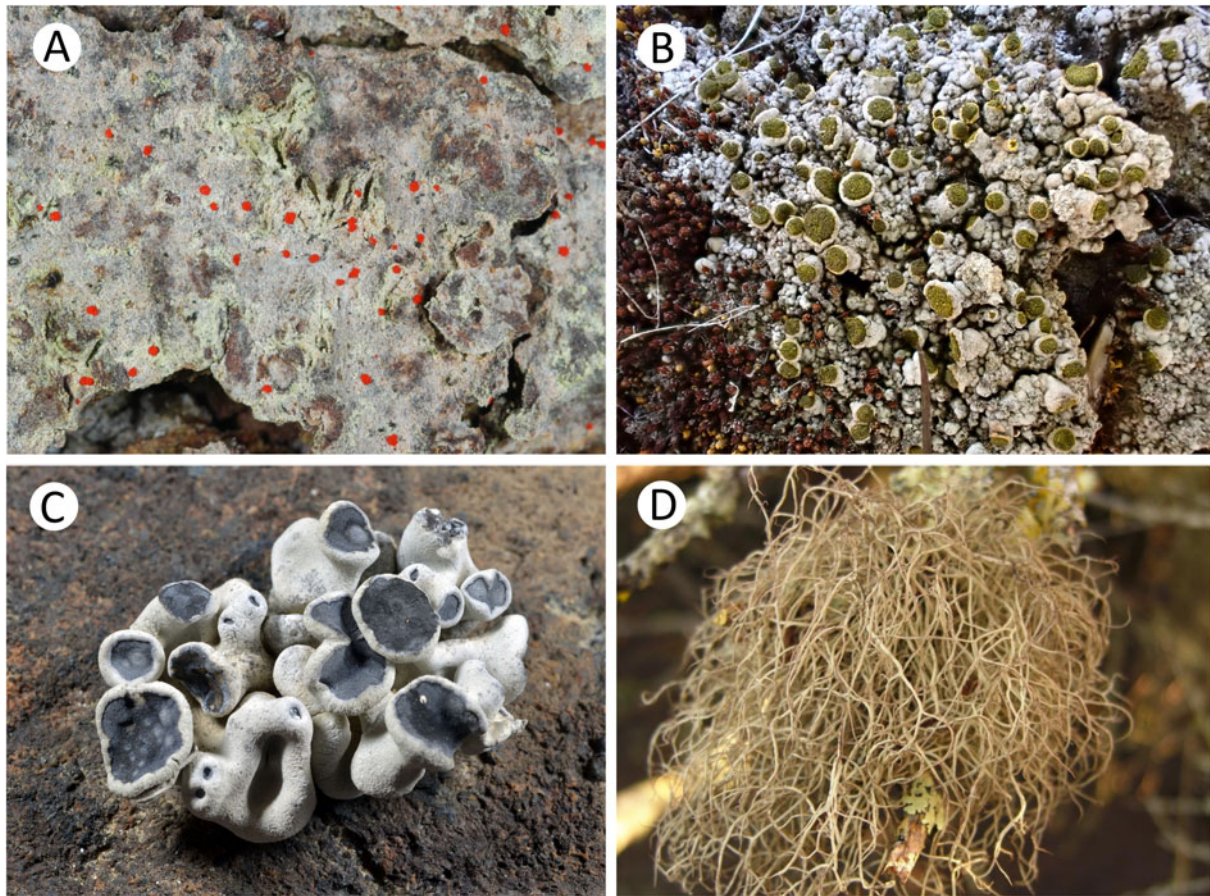
Figure 1. Examples of lichen species that are placed in threat categories. A, *Arthonia kermesina* is assessed as Critically Endangered. It is endemic to high elevations in the southern Appalachian Mountains of the south-eastern United States. Image: Erin Tripp. B, *Texosporium sancti-jacobi* is a soil crust-dwelling lichen that has a patchy distribution in arid western North America and is assessed as Endangered. C, *Mobergia calculiformis* is endemic to Baja California and Guadalupe Island. It is currently assessed as Endangered. D, *Sulcaria isidiifera* is a narrow endemic found only in San Luis Obispo County, California and is assessed as Critically Endangered. Image: Jason Hollinger.

no additional interpretation for lichens, three definitions do require special attention: mature individuals, generation length and severe fragmentation. Here we discuss each of these terms, interpret them in light of the unique biology of lichens, and give a standardized set of suggestions for their application.

Mature individuals

Counts of mature individuals are used for assessing species under criteria C and D (see Box 1), where C requires knowledge of the number of mature individuals and documentation of a decline, and D may be used in cases of extremely small numbers of mature individuals even in the absence of a decline. According to the Red List guidelines, mature individuals include only those that are able to, or are inferred to be able to, reproduce. For clonal organisms, the definition is modified to encompass any unit that can survive on its own and reproduce either sexually or asexually. Thus, reproductive biology and maturity are foundational to counting individuals. Counting mature individuals is also intrinsically tied to survival. If a species is completely dependent on another taxon or substratum for its continued survival, counting the unit of dependence may serve as a count of 'mature individuals' for the focal taxon (IUCN Standards and Petitions Subcommittee 2024, §4.1). Lichens can be both partially or fully clonal organisms and are often completely dependent on their substrata for their continued survival; we therefore opt for counting functional individuals as mature individuals following Scheidegger & Goward (2002), Scheidegger & Werth (2009), and Dahlberg & Mueller (2011). Our implementation of counts of functional individuals is dependent on the growth habits and substrata of individual species, with the units described in Table 1 all being equivalent to one functional individual for the purpose of counting mature individuals; for example, a single occupied tree is counted as a single functional individual for an epiphytic lichen. For functional counts of species on potentially extensive surfaces, such as soil or pebbles or rock outcrops or cliffs, we follow the example of the European Bryophyte Red List (Bergamini *et al.* 2019) of using 1 m² as 'individual equivalents'. This estimate allows for uncertainty in the identity and potential spread of genetic individuals (genets) and simultaneously captures what is probably a better estimate of extinction risk than counting individual thalli.

Common challenges that may arise in applying this method for counting mature individuals include detection uncertainty, deriving counts from herbarium specimens, and integrating functional individual counts with other methods of counting individuals. As with all data compiled for Red List assessments, different levels of uncertainty can be accommodated in counting

Table 1. Best practice methods for counting mature functional individuals in lichens.

Occupied substratum	Unit for count	Example
Epiphytic, including leaf-dwelling species	One phorophyte (e.g. tree or shrub)	*Bryoria salazinica*, restricted to < 30 trees in the Canadian Maritimes
Epixylic	One log or snag	*Carbonicola anthracophila*, restricted to old dead standing trees and stumps (not assessed globally)
Saxicolous	One boulder or 1 m^2 occupied rock-face	*Lepra andersoniae*, restricted to rock faces in high southern Appalachian Mountains
Terricolous, including vagrant species	1 m^2 occupied area	*Cladonia perforata*, unattached on bare sand in fossil dunes in Florida, USA
Lichenicolous	Same as for host lichen	*Tremella wirthii*, specific to the epiphyte *Protoparmelia oleagina*, is counted by the inhabited phorophytes

mature individuals, and it is advisable to incorporate ranges of plausible values for mature individuals, rather than using a single value (IUCN Standards and Petitions Subcommittee 2024, §3.2). Since species are almost never detected without error (Britton *et al.* 2014; von Hirschheydt *et al.* 2024), models have been developed to account for imperfect detection (see 'Uncertainty in species distributions, data and occurrences' section below for further discussion). Most often, assessors will count functional individuals for sites where a species' presence is documented only by herbarium specimens. For *Bryoria salazinica* Brodo & D. Hawksw. (CR), for example, whose distribution is largely based on historical collection data, it was possible to estimate the number of functional mature individuals using a combination of locality data and abundance notes from labels (Paquette *et al.* 2021). Historical specimens with poor label data will increase this challenge, but inferences from any known localities or additional fieldwork can be used to fill data gaps.

When a census-focused survey is newly undertaken, it is possible to include an estimate of observed abundance (counts of discrete individual thalli, patches, cover, etc.) and to simultaneously translate those counts using the standardized functional individual framework presented here. For example, counts of 100+ thalli on each of five trees equals 500 individual thalli, but for a Red List assessment this would equate to five functional individuals. It is axiomatic that the extinction risk of the lichens on those five trees would be higher than that of the same number of individuals spread over a larger number of trees (e.g. five individuals on each of 100 trees). In fact, this example illustrates that the functional individual method of counting is likely to be conservative, since evidence from repeated surveys of discrete habitat patches such as trees or stumps demonstrates that extinction rates due to stochastic events exceed those of the patches themselves (Caruso *et al.* 2010; Öckinger & Nilsson 2010); we therefore recommend including both types of data where possible (abundance and functional individual counts).

Generation length and life history strategies

Criteria A and C (subcriterion C1; IUCN Standards and Petitions Subcommittee 2024) (Box 1) rely on measures of generation length in considering time spans over which population size reductions occur. There are multiple generation length definitions according to the Red List Guidelines: 1) 'average age of parents of the current cohort'; 2) 'mean age at which a cohort of newborns produce offspring'; 3) 'age at which 50% of total reproductive output is achieved'; 4) 'mean age of parents in a population at the stable age distribution'; 5) 'time required for the population to increase by replacement rate' (IUCN Standards and Petitions Subcommittee 2024, §4.4). When considering the biology of lichens and elements of their demographics that are accessible to observation and measurement, in many cases the simplest definition to apply is the age at which 50% of the reproductive output is achieved. Considering that lichens produce reproductive structures (e.g. asexual lichenized propagules and/or ascospores) continuously as the thallus grows, we can infer that reproductive output will continue to increase over the lifespan of the lichen. Then there would probably be a steep decline at the end of the lifespan of the thallus. Thus, lichens in general will have fairly long generation length to lifespan ratios compared to other groups of organisms where reproductive rate decreases with age (e.g. mammals).

Selecting the values for generation length therefore requires knowledge of lichen lifespans. Although it is not logistically feasible to conduct empirical studies of generation length for every species of lichen, the guidelines state that it is permissible to use generation length data from well-characterized species and apply them to similar taxa (IUCN Standards and Petitions Subcommittee 2024, §4.4). The Bryophyte Specialist Group has developed and applied life-history categories (Bergamini *et al.* 2019) where shared suites of traits, reproductive biology, lifespan, growth rate, substrata, and habitats can be referred to as 'life history strategies.' These life-history categories refer to the characteristics of the life cycle that influence how a species interacts with its environment, and for lichens, several of these have been applied based on different traits (Topham 1977; Rogers 1990; During 1992; Deduke *et al.* 2014). Unfortunately, although life-history strategies and life cycles strongly determine species responses to changes in the environment and are of vital importance when assessing extinction risks (Goudie *et al.* 2011), relatively few species have been studied in detail (e.g. Jahns & Ott 1997; Scheidegger *et al.* 1997, 2023; Sanders 2002, 2014). The study of life cycles in lichens is partly impeded by the problem of identifying individuals. Terricolous species forming mats (such as those of the genus *Cladonia*), crustose species forming joint thalli originating from the fusion of different lichenization events (Jahns 1993; Sanders 2014), or the presence of hybrids (Keuler *et al.* 2020) pose significant challenges to the study of life cycles in lichen-forming fungi.

Despite the challenges presented when inferring lifespans and generation lengths of lichens, empirical data are available for a variety of species to support generation length ranges (Box 2, Fig. 2, Supplementary Material Table S1, available online).

Box 2. Generation length categories with examples for lichens with varying life histories. Supplementary Material Table S1 (available online) provides an extensive list of published generation lengths and Red List assessments.

Short-lived: ephemerals and foliicolous species

Description: species whose lifespan depends on environmental conditions and/or persistence of their substratum. For example, reproductive structures and even the thallus may disappear during dry, hot periods, and reappear when conditions improve. The lifespan of foliicolous lichens is completely dependent on the length of time each leaf is retained by the phorophyte.
Example species: *Strigula smaragdula*, *Thelocarpon* spp.
Generation length range: < 1–3 years
Relevant citations: Poelt & Vězda 1990; Sanders & Lücking 2002

Medium-lived: early colonizers and monocarpic species

Description: generalists are able to colonize new substrata and reproduce relatively fast. Early colonizers are often weak competitors.
Example species: *Candelaria concolor*, *Cladonia floerkenan*, *Evernia prunastri*
Generation length range: 4–12 years
Relevant citations: Stone 1989; Armstrong & Bradwell 2011

Long-lived: slow-growing, long-term stable substratum associates

Description: specialist species generally take longer to start reproducing. Longer generation time requires more stable substrata (e.g. large rocks or older tree trunks).
Example species: *Cliostomum corrugatum, Lobaria pulmonaria, Xanthoparmelia cumberlandia*
Generation length range: 13–50 years
Relevant citations: Pringle *et al.* 2003; Lättman *et al.* 2009

Very long-lived: extremophiles

Description: species with very slow growth rates possibly caused by limited availability of water for photosynthesis. These species are often found in extreme environments such as Antarctica or very dry deserts. Most, if not all, species in this category are crustose.
Example species: *Buellia frigida*, *Rhizocarpon* spp.
Generation length range: > 50 years
Relevant citations: Sancho *et al.* 2007; Armstrong & Bradwell 2010; Green *et al.* 2012

Some species are known to complete their life cycles in short periods of time, a small number of years (1–3) or even months. This is the case of ephemeral lichens (Poelt & Vězda 1990; Scheidegger 1995), which occur in disturbed habitats or on dynamic substrata, such as leaves or open soil, where competition is scarce (e.g. *Sarcosagium campestre* (Fr.) Poetsch & Schied. or species in the genera *Absconditella*, *Thelocarpon* or *Vezdaea*). Within the category of species with short life cycles are the foliicolous species, which, due to the transitory nature of their substrata, are obliged to have short life cycles (Lücking 2001; Sanders 2014; Sanders & de los Ríos 2015). When assessing the extinction risks of foliicolous lichens, aspects of their life cycles and the phenology of their hosts must be considered.

Unlike ephemeral and foliicolous species, most other lichenized fungi are capable of living for longer periods of time (Fig. 2). Among these species, it is important to distinguish
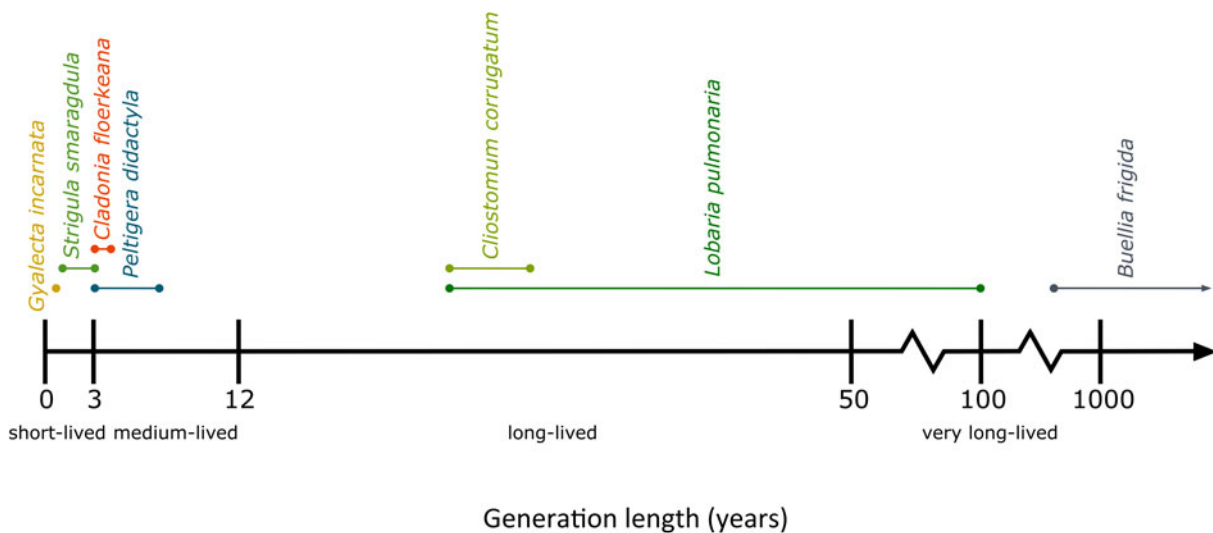

Figure 2. Generation length categories informed by life history strategies with specific examples. The generation lengths are calculated as the age at which 50% of reproductive output is reached for a species. A table with generation lengths, lifespans, and growth rates for numerous species is included in Supplementary Material Table S1 (available online).

between those that are monocarpic and those that are polycarpic. In monocarpic species, individuals die after sexual reproduction. This is the case for *Cladonia floerkeana* (Fr.) Flörke whose thalli die after ascospore production, which has been estimated at 3–4 years (Jahns & Ott 1997). In polycarpic species, sexual reproduction does not imply the death of the individual. This is the case for *Cladonia rangiferina* (L.) Weber, with a lifespan of 20–30 years, which can produce sexual propagules throughout its lifespan once apothecia are produced, or species such as *Lobaria pulmonaria* (L.) Hoffm. or *Ramalina fraxinea* (L.) Ach. (Jahns & Ott 1997). Many crustose saxicolous species may live for hundreds of years, with the extreme cases of individuals of *Buellia frigida* Darb. and *Rhizocarpon geographicum* (L.) DC. growing in polar regions having thalli estimated to survive for thousands of years (Miller & Andrews 1972; Green *et al.* 2012). In these cases, reproduction does not imply developmental arrest or thallus death. In addition, many species have well-documented high variability among individuals and across sites (Supplementary Material Table S1).

Based on published lifespan, ecological and demographic literature on lichen species, we propose the following generation length categories: 1) short-lived species: < 1–3 years (e.g. foliicolous species); 2) medium-lived species: 4–12 years (e.g. early colonizers and monocarpic species); 3) long-lived species: 13–50 years (e.g. slow-growing, long-term stable substratum associates); 4) very long-lived species: > 50 years (e.g. polar species with exceptionally long lifespans). See Box 2 for details and examples.

Dispersal distances and severe fragmentation

Severe fragmentation is applied to cases in which more than 50% of the global population of a species exists in small, isolated subpopulations. By definition, these subpopulations are isolated in terms of gene flow and dispersal, which results in increased risk of extinction and reduced probability of recolonization (IUCN Standards and Petitions Subcommittee 2024, §4.8).

In terms of assessing extinction risk, it is imperative to parse naturally fragmented populations from species whose isolation has resulted in diminished gene flow and increased extinction risk. In the case of the former, species with naturally fragmented distributions are not necessarily at risk of extinction; the arctic-alpine species *Flavocetraria nivalis* (L.) Kärnefelt & A. Thell and *F. cucullata* (Bellardi) Kärnefelt & A. Thell have widely disjunct distributions in arctic and alpine habitats, yet sampled individuals from across Eurasia and North America provided evidence for continuing gene flow at large geographical scales (Geml *et al.* 2010). This does not discount the evidence for some small and isolated mountain subpopulations of other widespread arctic-alpine species to be at local or national risk of extinction, for example in tropical isolated subpopulations of *Cetraria aculeata* (Schreb.) Fr. (Lutsak *et al.* 2016); however, in this species, those isolated and at-risk subpopulations make up less than 50% of the global population. For species globally restricted to a small number of widely separated localities, these naturally fragmented populations are affected by limited gene flow and are at risk of extinction globally due to both their small size and isolation and are therefore correctly described as severely fragmented. Examples include the disjunct occurrences of *Lethariella togashii* (Asahina) Krog on five widely separated mountain massifs in Japan and Far East Russia, where the former population at the southernmost point had completely disappeared (Ohmura *et al.* 2018), or the few remnant stable occurrences of *Mobergia calculiformis* (W. A. Weber) H. Mayrhofer & Sheard, fragmented by habitat loss and degradation (Herrera-Campos *et al.* 2020; Fig. 1C).

Even without genetic data, using species-specific life-history data can inform the distribution of population genetic structure and therefore fragmentation on a case-by-case basis. A species' distribution in combination with its occupancy, turnover, habitat persistence and reproductive mode can be used to infer potential population structure (O'Brien *et al.* 2022). Species that rely on habitats or microhabitats which themselves display turnover (e.g. epiphytes, lignin-dwelling specialists) must be subject to metapopulation dynamics including extinctions and re-colonizations, and evidence for external factors limiting new colonizations must be offered as evidence of restrictions to dispersal among locations if severe fragmentation is to be considered. On the other hand, tests of old-growth indicator lichens confirm that dispersal limitation plays an important role in restricting potential colonizations (Johansson *et al.* 2012; Jüriado *et al.* 2012; Ellis *et al.* 2022) and contributing to extinction risk. For some specialist species, dispersal kernels are shorter for larger asexual propagules (Eaton 2018), which also colonize new trees more slowly (Johansson *et al.* 2012). Similarly, experimental introduction of *Cladonia* and *Stereocaulon* shows high survival rates but low colonization of new sites, resulting in regional assessments of threat for species that do not colonize new sites, even with suitable habitat (Sparrius & Kooijman 2011).

Challenges and Opportunities

Apart from the careful application of key terms and definitions described above, we believe it is timely to consider further challenges and opportunities provided by the large-scale data-driven exercise of assessing the Red List status of lichens which exemplify these themes. We discuss approaches to species with uncertain distributions, including using digital data as well as those from preserved collections, completing assessments in hyperdiverse but understudied areas, and taxonomic challenges.

Uncertainty in species distributions, data, and occurrences

Distribution data are used to evaluate designations such as severe fragmentation, and to calculate key metrics such as the Area of Occupancy (AOO), Extent of Occurrence (EOO) and, in combination with threat information, number of locations. However, gathering and refining distributional data are some of the most difficult tasks in writing an assessment for lichens. Challenges arise in assessing data quality and cleaning data from online repositories (see 'Best practice for collating data from large repositories' section below), determining survey effort and how that may vary from region to region (see 'Detection error and absences' below), and how taxonomic changes and uncertainties may influence the distributional data (see 'Taxonomic challenges' section below). Many of these challenges can be addressed through tasks such as examining herbarium specimens, contacting regional experts, and even conducting targeted surveys, with remaining uncertainty accounted for with explicit terminology described in the IUCN guidelines (observed, estimated, inferred, suspected) and ranges of values which reflect upper and lower bounds for these quantities.

Best practice for collating data from large repositories.
Distributional datasets can be generated from both physical and digital biodiversity data repositories. Preserved herbarium or fungarium collection data, such as those aggregated by the Global Biodiversity Information Facility (GBIF; GBIF 2024), the

Box 3. Strategic precautions for inferring distributions from record data

✓ Records based on observations (e.g. photographs) must only be considered if the species in question can reliably be identified from images alone; for the majority of lichenized fungi, this is not the case.

✓ Specimens which have been recently annotated, cited in the scientific literature, or identified as part of a recent inventory might be considered more reliable compared to those for which no additional information or specimens are available.

✓ All distribution records must generally be screened for unusual patterns or outliers; highly disjunct distributions are not common, even for lichens that are assumed to be widely distributed.

• Consider comparing AOO/EOO calculations which account for disjunct areas of the distribution far from the type locality with ones that exclude them.

• Re-examine outlier specimens or check locality data for those specimens deemed least likely to be correctly identified.

• Ensure habitat and climate for the record locality are suitable for the species.

✓ Historic records are often based on problematic, outdated concepts; this is particularly true for poorly known taxonomic groups; they require taxonomic research before any of the records should be trusted.

✓ Details of survey effort or gaps in surveys, where known, should be included in the narrative sections.

Consortium of Lichen Herbaria (Consortium of Lichen Herbaria 2023), ITALIC (Nimis 2023), PlutoF (Abarenkov *et al.* 2010) and similar, provide occurrence records based on specimens deposited in natural history collections, as well as datasets from country-level specialist societies and citizen scientist platforms. Since these datasets are not the product of systematic sampling, they largely consist of presence-only records which are typically biased due to spatial and temporal variation in sampling effort (Bird *et al.* 2014; Isaac & Pocock 2015; Mair & Ruete 2016), in addition to both oversampling of rare species and under-sampling of common ones (ter Steege *et al.* 2011; Lõhmus *et al.* 2023). When using presence-only data for a Red List assessment, there are two possible approaches. The first approach is relatively simple and consists of making a qualitative but critical judgement of the available record data (Box 3) to assess the likelihood of correct presences. The second approach is to use presence data to model distributions (see section on 'Model-based distributions and trends' below).

Record data form the foundation for the understanding of distribution data in some countries, where these are carefully curated by experts, but caution needs to be applied for such observations from uncurated sources. Although photographs can and have alerted taxonomists to the existence of new species, populations and range extensions (Mesaglio & Callaghan 2021; Mesaglio *et al.* 2021; Rosa *et al.* 2022; Gómez-Bolea *et al.* 2023), records from community scientist platforms such as iNaturalist, which base observations largely on photographs, can rarely be verified (McMullin & Allen 2022). Unless identifications are unequivocal, such records should usually be excluded by applying filters such that only specimen-based records are included in Red List assessments. In some cases, data from citizen science platforms and campaigns can be used when observations are verified by experts. For example, the exTRICATe project (Gómez-Bolea *et al.* 2023) was set up to link citizen scientists to a specific conservation goal, and one of the eight citizen-science observations resulted in the discovery of a new population of a nationally rare species. Likewise, the Ready! Set! Lichen! citizen science campaign for lichens (Lõhmus *et al.* 2023) contributed observations which were later expert-verified to be species of conservation concern, including nationally protected lichen species.

Model-based distributions and trends. The second approach for evidencing species distributions is to estimate these using appropriate statistical models. A model combines the available geographical information on environmental conditions relevant to the species (habitat type, climatic conditions, availability of suitable substratum, etc.) and predicts its distribution in a chosen area. Species distribution models frequently permit better estimates of distributions than occurrences alone or expert-drawn maps due to their ability to balance the likelihoods of presences and absences (Syfert *et al.* 2014), though understanding their application and limitations is crucial (Velazco *et al.* 2020). If utilized, the software should be mentioned in the range description as well as whether the data are observed, estimated, projected, or inferred. If possible, ground truthing based on real specimens should be undertaken. In addition to providing estimates of current distributions, models have also been used to forecast changes in distributions or continuing declines due to known or predicted habitat or climate changes (e.g. Ellis *et al.* 2007; Allen & Lendemer 2016; Allen *et al.* 2020). It is important to remember that the data available for modelling (known distribution and ecology) are the result of two processes: the occurrence of the species (ecological process) and the sampling that led to the data (detection or observation process). While we are really interested in the ecological processes resulting in a distribution, we must either make assumptions about the observation process or account for it explicitly in the model (e.g. Outhwaite *et al.* 2020; von Hirschheydt *et al.* 2024). For further guidance, see also the reviews by Pearce & Boyce (2006), Tingley & Beissinger (2009), Guillera-Arroita (2017), Miller *et al.* (2019) and Valavi *et al.* (2022). Data from models may be used for criteria that require documentation of population reductions or decline (A, B2b, C; IUCN Standards and Petitions Subcommittee 2024, §4.5–4.6).

Detection error and absences. In addition to documenting where a species is present, it is essential to determine the areas where absence of a species can reasonably be inferred, and which areas should be considered as 'presence uncertain' or 'possibly extant'. There is growing evidence that some 'absences' are in fact false absences, that is, sites where the species occurs but was simply not detected (for lichen examples see; McCune *et al.* 1997; Vittoz *et al.* 2010; Britton *et al.* 2014; Casanovas *et al.* 2014; Bhatti 2021). A short discussion about detection probability may be appropriate for some species and may affect levels of uncertainty about distribution data. Large and conspicuous species tend to be more often reported when sampling opportunistically (Cáceres *et al.* 2008; Vondrák *et al.* 2016; von Hirschheydt *et al.* 2024), but for smaller or difficult taxa, the experience of the person who made the identification has been shown to correlate with the probability of discovery (McCune *et al.* 1997; Brunialti *et al.* 2012; von Hirschheydt *et al.* 2024). When resources are limited for a survey, or when species require microscopy, thin-layer chromatography (TLC), or even genetic analyses for accurate identification, such species tend to have substantially fewer records (Cáceres *et al.* 2008; Lõhmus & Lõhmus 2009; von Hirschheydt *et al.* 2024). Likewise, a locally common species (occurring with many individuals) is much more likely to be detected than a locally rare species (Chen *et al.* 2009; Garrard *et al.* 2013), reinforcing the need to incorporate ranges of plausible values for distribution estimates (and count data; see 'Mature individuals' above).

Distribution patterns obtained from data repositories must carefully be screened with such inferences of absences in mind, especially for taxa that are readily misidentified. If habitat or climate are unlikely to be suitable, inferring absence may be justified, keeping in mind that habitat and microhabitat preferences can vary from region to region and across climate gradients and must be considered carefully across large areas (Ellis 2013). If a suitable area has been surveyed generously with an effort adapted to the conspicuousness and identifiability of the species, and by people capable of identifying it, inferring absence may be justified. Special care should be taken when inferring the absence of a species from areas where it has historically been reported. It takes enormous effort to be certain of the local disappearance of a species, even when revisitation resurveys are conducted specifically for this purpose (Kéry 2002, 2004; Garrard *et al.* 2008). When a local disappearance can be confirmed (e.g. by habitat conversion), this should be accounted for as a change in AOO or EOO if relevant, and if there is reason to believe that further losses should be expected, a continuing decline can be inferred.

Best practice for handling uncertain distributions. Even with the best efforts to fill data gaps, uncertainty about the complete distribution of a species will probably remain, and not all assessments will be able to include statistical models of species distributions. Where quantitative analysis is not possible, we recommend the following approaches. First, use ranges of values for AOO, EOO, and the number of locations, all of which are especially important in criteria A, B, and D (subcriterion D2; IUCN Standards and Petitions Subcommittee 2024) (Box 1). The lower limit for all these values will probably be the current numbers calculated based on empirical data. Estimating the upper limit will require the assessors to consider survey effort and detectability, along with quantity and quality of potentially available habitat where the species could occur. With this information available, the assessors may then determine if the species' distribution is well known, and then they may add only a small upper buffer to the values for the key metrics. Alternatively, they may determine that there could be many currently undocumented sites where the species could occur and opt for much larger ranges of values. Next, once the value ranges are assigned, it is then up to the assessors to determine the most likely value to use for the quantitative thresholds. If the ranges of values are so large that a category cannot be assigned to the species, it is then considered Data Deficient (DD). It is also possible to assign a coding of 'Presence Uncertain' to any country or subnational unit both in coding the distribution in the Species Information System (SIS), the Red List database management system, and in the actual map files. Points or polygons that are designated as 'Presence Uncertain' will show up with distinct symbology on the Red List website.

Examples of species with uncertain distributions include *Xanthaptychia aurantiaca* (R. Br.) S. Y. Kondr. & Ravera (Sokoloff & McMullin 2020; as *Seirophora aurantiaca*) and *Allophoron farinosum* Nádv (Moncada *et al.* 2023). Assessors exclusively utilized herbarium data ($n = 18$) to delimit the geographical range of *X. aurantiaca*, growing in arctic areas with difficult access yet considered very well surveyed. Ultimately, the species was evaluated as Endangered (EN) under criterion A3c due to its inferred susceptibility to major climate change impacts and loss of habitat. The suspected endemic *A. farinosum*, described in 1942, is known only from the type collection in *Quercus humboldtii* forest in the vicinity of Bogotá, Colombia.

Several studies have been conducted over the last 30 years to explore the *Q. humboldtii*-related lichen biota across Colombia, but *A. farinosum* has not been re-found. The continuing decline of its habitat is evidenced by the ongoing logging of *Q. humboldtii* and the urban expansion of Bogotá, for which reasons the phorophyte has lost over 40% of its potential Colombian extent and is currently covering only 10–40% of its inferred pre-Colombian distribution in the northern Andes (Aguilar-Garavito *et al.* 2023). Thus, a plausible and precautionary approach lists the species under Critically Endangered (CR) using the criterion B2abiii.

New methods for generating more robust distribution data. Apart from individual cases exemplified above, data from preserved collections can and are being used for assessing extinction risk in various ways, from building traditional checklists to building reference databases for metabarcoding. Checklists are typically published for countries or specific regions. Traditionally, these lists are static and not regularly or easily updated, but increasingly, checklists are available online, consecutively curated, and more regularly updated. In continental North America for example, the online checklist by Esslinger is published at irregular intervals (Esslinger 2021), while some European examples are continuously updated (e.g. ITALIC 7.0; Nimis 2023). However, these checklists do not typically provide direct access to specimen records and instead refer to secondary literature, meaning that species distribution patterns are not easily inferred. Exceptions are voucher-based checklists, where reports of species are linked directly to selected and verified specimens. An example was recently presented by Yánez-Ayabaca *et al.* (2023a), who discussed best practices using the biodiversity data platform *Consortium of Lichen Herbaria* to compile a checklist of lichen-forming, lichenicolous, and allied fungi of Ecuador (Consortium of Lichen Herbaria 2023; Yánez-Ayabaca *et al.* 2023b). Built on the software Symbiota, the Consortium provides sophisticated tools to include species in a checklist not only based on literature, but also linking them to vouchers (i.e. selected verified specimens). Symbiota checklists can be downloaded and their distribution data analyzed. For individual species or species groups, these lists of verified vouchers do not yet exist at the global scale, but the tools should be explored further for their potential to base Red Listing assessments on more reliable records of individual species distributions.

Integrating molecular data with specimens can increase the accuracy of identifications. A recent study used phylogeny-based predictive niche modelling of preserved specimen records available in GBIF confirmed by ITS barcoding to confirm the identity of records (Smith *et al.* 2016). This work argues that reports of *Usnea longissima* Ach. from the tropics should be considered erroneous, representing misidentifications of morphologically similar species and leading to an estimated ten-fold reduction in the global distribution of this species. Although assessors can rarely access such molecular data across a species range, recent studies have demonstrated that it is possible to obtain DNA from historic collections (Sohrabi *et al.* 2010; Redchenko *et al.* 2012; Bendiksby *et al.* 2014; Schmull *et al.* 2014; Gueidan *et al.* 2019; Kistenich *et al.* 2019; Gueidan & Li 2022), and high-throughput sequencing has been proposed as a viable option for the routine DNA barcoding of even large historical collections (Dal Forno *et al.* 2022). Metabarcoding or genome skimming using high-throughput techniques, even for single specimens, can offer new ways of obtaining sequence data for older or mixed collections. It is therefore likely that these tools will
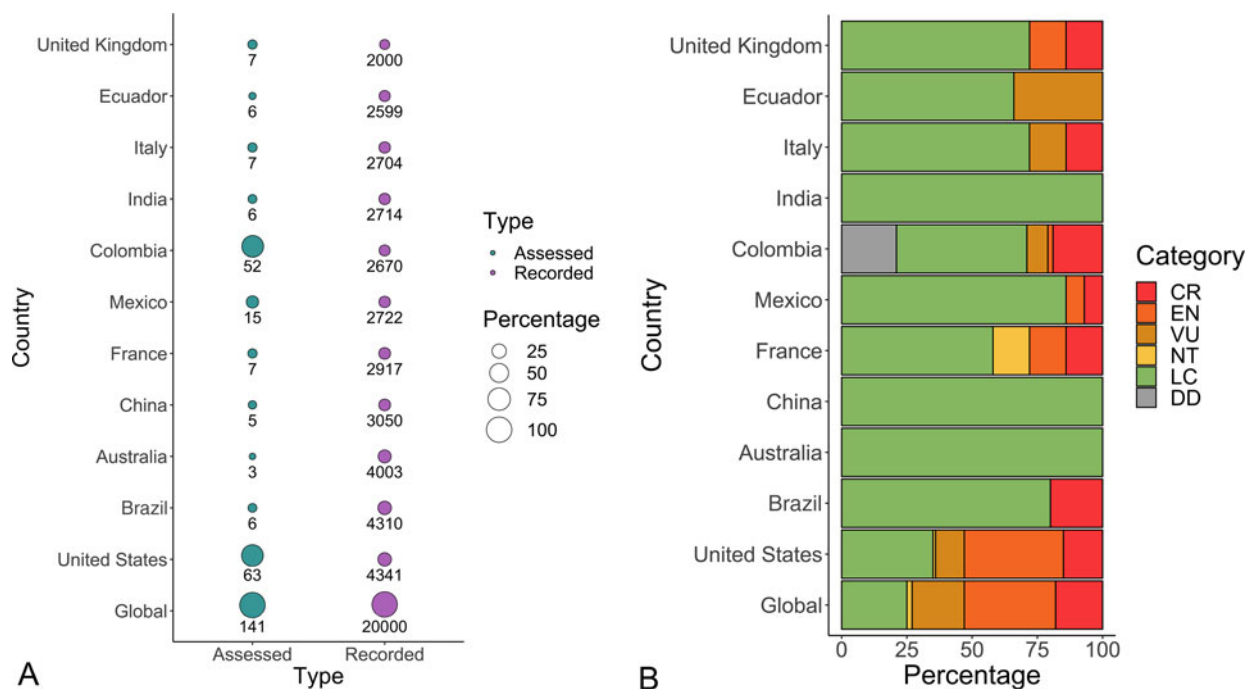
Figure 3. Global Red List assessments of lichens for selected countries, contrasting the best-studied countries (with respect to lichen biota) and some of the 'megadiverse' countries. A, number and proportion of Recorded species versus Assessed species. B, proportion of each listing category in Red Listed lichens per selected country, ordered by declining number of assessed species.

eventually allow for more accurate specimen records, updating even large digital biodiversity data repositories collected over hundreds of years across many thousands of localities.

Completing assessments in understudied, hyperdiverse regions

Despite having thousands of lichen species, megadiverse countries are poorly represented in the Global Red List (GRL). For example, so far 67 lichen species of the current total of 141 currently published assessments (IUCN 2023) have been assessed for Brazil, China, Colombia and Mexico. Brazil, with 4310 lichen species reported (Aptroot 2021), has only six species published in the GRL, while China, with 3050 species currently reported, has only five species published (Wei 2020; IUCN Standards and Petitions Subcommittee 2024). Similarly, Mexico (2722) has 15 published (Simijaca *et al*. 2023), and Colombia (2670) has 52 published (Simijaca *et al*. 2022). In contrast, most of the listed species occur in Western Europe (Italy, United Kingdom) or the United States (Fig. 3), regions where the lichen biota is better studied but less diverse (Moncada *et al*. 2022). This situation mirrors that of plants, where species richness and the number of species assessed are inversely correlated (the 'Red List deficit'; Bachman *et al*. 2019).

All species groups are vulnerable to increasing threats from large-scale land use change, but for understudied areas and species groups, we also risk missing the chance to find and study unique species before they are lost (Stropp *et al*. 2020). In addition to the example of *Allophoron farinosum* above, *Cora timucua* Dal Forno *et al*. is a recently described but already potentially extinct species presumably endemic to the south-eastern United States, not collected in the past 39 years, and with known collecting localities all lost to urbanization and agriculture (Lücking *et al*. 2020; Dal Forno *et al*. 2021). In these cases of suspected

endemism, local knowledge is sufficient to assess a species. However, most lichen distributions span multiple countries, and addressing the challenges of assessing threatened species requires global cooperation, an open exchange of data, tools, technology, and government support. This allows the integration of diverse initiatives to successfully assess tranches of species in understudied and hyperdiverse areas (Box 4).

Box 4. Red Listing in hyperdiverse regions: Colombian case study

Assessment of lichen priority species in Colombia was motivated by the initiative of modifying the Colombian regulation on environmental impact studies for infrastructural projects. The suggested modifications are likely to affect both Colombian ecosystems and biodiversity (República de Colombia 1977) and are based on an agreement among government and academic partners (MADS 2019). Under this agreement, for a set of putatively endemic species selected with preliminary research, a list of georeferenced records was refined and standardized for each, allowing calculation of the extent of occurrence (EOO) and area of occupancy (AOO) (Dauby *et al*. 2017). The set of information on each species was analyzed with several environmental and geographic layers to detect and describe the potential threats. Finally, in a workshop held in November of 2019, Colombian lichenologists discussed each case and assessed each species for each criterion, achieving the first national Red List of lichens of Colombia (CEIBA 2019), later submitted for evaluation by the IUCN Lichen Specialist Group as global assessments. The preliminary assessment resulted in 150 assessed species, of which 57 are considered threatened (CR, EN, VU) and 9% are Data Deficient (DD) (Simijaca *et al*. 2022). The agreement has recently resulted in the addition of more than 80 lichen species to the official threatened list of species in Colombia and is also the first time Funga is included in Colombian regulation (Decree 0126; República de Colombia 2024). This initiative of workshops to simultaneously evaluate several species (Mueller *et al*. 2022) allows the mycological community in hyperdiverse areas to build a network, connect with the Specialist Group, get feedback on the species assessment process and build better visibility for lichens.

Taxonomic challenges

Arguably one of the most significant challenges in gathering evidence for Red List assessments is that the taxonomic stability one would wish for in an authoritative checklist has not yet been achieved for all species. However, guidelines from the IUCN are clear: authors of assessments may either choose to regard species with taxonomic challenges as good species and assess them, or choose not to assess them for the Red List (IUCN Standards and Petitions Subcommittee 2024, §10.3.2), that is, apply the category Not Evaluated (NE) by default. Each case is taken on its own merits, and assessors must determine if a plausible case can be made with existing data. It is important to remember, however, that Red Listing should adopt a precautionary approach (IUCN Standards and Petitions Subcommittee 2024, §3.2.4) and that the change to a different taxonomic placement may or may not alter the evidence of threat.

Taxonomic challenges related to lichenized fungi encompass a range of problems, including the many cases where species' boundaries within a complex have not been reliably phylogenetically clarified, when a species is extremely rare and therefore without much scope for comparative work, or in the case of newly described species. One of the most common problems is the case of species complexes and cryptic species, when multiple, probably closely related taxa that may deserve species-level recognition are still referred to as a single-named entity (Hawksworth & Lücking 2017); in lichens, examples are numerous (e.g. Lücking *et al.* 2014, 2017, 2021; Corsie *et al.* 2019; Mark *et al.* 2019). Still, when the phylogenetic status has been clarified within a species complex and the ecological and distribution data can be gathered separately, the distinct species should be assessed independently. For example, the *Cetrelia olivetorum* species complex representing a common morphotype (Obermayer & Mayrhofer 2007) has been demonstrated to consist of four independent species distinguished chemically (*C. cetrarioides* (Duby) W. L. Culb. & C. F. Culb., *C. chicitae* (W. L. Culb.) W. L. Culb. & C. F. Culb., *C. monachorum* (Zahlbr.) W. L. Culb. & C. F. Culb. and *C. olivetorum* (Nyl.) W. L. Culb. & C. F. Culb. s. str.) (Mark *et al.* 2019); consequently, the extinction risk of each of the four species can be assessed individually. This has already been done in some national Red Lists, for example in Estonia (Lõhmus *et al.* 2019), Finland (Pykälä *et al.* 2019) and Germany (Wirth *et al.* 2011), but it will be a challenging task globally, possibly relying on an assessment of the complex in the broad sense and therefore underplaying threats to real but difficult to assess entities until more is known.

Newly described species form another difficult category, and their inclusion on the IUCN Red List is recommended to be addressed on a case-by-case basis (IUCN Standards and Petitions Subcommittee 2024, §2.1.1). An example among recently described lichens is *Parmotrema bifidum* A. A. Spielm. & Marcelli, collected in 1894 by G. O. Malme but formally described only in 2020. Only one year later, the species was globally assessed as CR (B1ab[iii] + 2ab[iii], D), with an additional comment that it may be extinct (Spielmann *et al.* 2022). The taxon, known only from the type locality in the highlands of central Brazil where it is considered endemic, has not been recorded again despite it being very conspicuous and despite several lichen collectors having visited the type locality. Other lichen-forming fungi for which extinction risk has been globally assessed soon after their description are two species of *Acanthothecis* in the *Graphidaceae* (*A. leucoxanthoides* Lendemer & R. C. Harris and *A. paucispora* Lendemer & R. C. Harris),

distributed in the Coastal Plain of south-eastern North America. Both taxa were described in 2014 and assessed in 2017 upon completion of a thorough biodiversity inventory of the region (Lendemer & Allen 2018*a*, *b*). This is especially important in cases when the species is known only from a habitat with high rates of loss along with strong continuing declines, and there is reasonable concern that the new taxon may be globally threatened. In some cases, it may be important to raise conservation awareness of such taxa, but for others, it may be more prudent to wait a number of years until more information is available about the species distribution. If, in time, new surveys discover additional localities for species on the Red List, assessments can be revised.

New taxa can be preliminarily globally assessed when they are described if their authors themselves undertake the job; such a practice is widespread in some branches of systematics, with preliminary conservation assessments recommended as a standard part of a new species description (plants: Bachman *et al.* 2018, amphibians: Tapley *et al.* 2018). We recommend that a provisional Red List assessment be written for all new species, as the authors are best placed to compile known information about distribution and potential threats.

Future Prospects

National Red Lists

The standardized, quantitative approach taken by the IUCN for the global Red List can be applied at regional scales with some slight modifications (Gärdenfors *et al.* 2001; IUCN Standards and Petitions Subcommittee 2024). However, national or regional Red Lists cannot always be directly translated into global assessments or drive global conservation priorities for several reasons. First, countries may have dissimilarities in methodology and approach. For instance, some countries assess the threat status for as many species as possible (e.g. Czech Republic (Liška & Palice 2010), Estonia (Randlane *et al.* 2024), Finland (Pykälä *et al.* 2019), Norway (Norwegian Biodiversity Information Centre 2021), Sweden (SLU Artdatabanken 2020), Switzerland (Scheidegger *et al.* 2002), United Kingdom (Woods & Coppins 2012)), while others address only nationally protected or rare species (e.g. Bulgaria (Shivarov *et al.* 2023), Latvia (Degtjarenko *et al.* 2024)) or transform Red Listing threat categories into officially protected state categories (e.g. Belarus; Kachanovski *et al.* 2015). Second, the ranges of species cross political boundaries, so species threatened with extinction in one country or region may experience no threats and have large, stable populations in others. Third, some national conservation assessments do not use the categories or criteria of the IUCN, such as Canada, Germany, or some parts of Russia, making international comparisons impossible.

Red Listing and conservation activities are two different systems in most countries. National Red Lists and Red Data Books in themselves do not provide legal protection for lichens, but they are an invaluable tool for stakeholders to carry out proper conservation and management, provide information, and increase public awareness of lichens. In countries such as Spain and Russia, which lack national Red Lists, the development of regional Red Lists has made it possible to decree the legal protection of some lichens (e.g. in Galicia and Catalonia: Zavarzin *et al.* 2003; ICHN 2010; Gencat 2023). As such, the development of separate regional assessments should be considered relevant for future national conservation policies.

The accessibility of information made possible by regional and national Red Lists allows the establishment of networks among Red List experts, the comparison of trends across geographical areas, and the use of trends for informing habitat protection and revising conservation policies. A number of national and regional Red Lists or conservation assessments for lichens have been produced (reviewed in Thor 1995; Scheidegger & Goward 2002; Niskanen *et al.* 2023), most of which now employ IUCN criteria (14 of 21 national assessments in Niskanen *et al.* (2023)). Regional Red Lists are useful in establishing conservation priorities within a given geographically defined area and can feed into global assessments (e.g. through the Global Fungal Red List Initiative), often highlighting conservation needs of nationally or regionally endemic species, for which global assessments are therefore fairly straightforward to assemble.

Use of population genetics and genomics in biodiversity assessment

Population genetics and genomics are powerful tools for investigating dispersal, molecular diversity and speciation in lichenized fungi (Werth & Sork 2010; Allen *et al.* 2018; Alonso-García *et al.* 2021; Lagostina *et al.* 2021; Moncada *et al.* 2021). Molecular characterization can both reveal (Crespo *et al.* 2002, 2020; Molina *et al.* 2004; Crespo & Lumbsch 2010; Schultz 2017) and deconstruct (Garrido-Benavent *et al.* 2022) lichen species boundaries, and molecular-driven taxonomic revision within groups of conservation interest may give rise to hitherto unrecognized priority taxa. Molecular methods are not routinely used in Red List assessments (Garrido-Benavent *et al.* 2022), and although molecular characterization of lichens should not be a prerequisite, it may still be used to supplement existing assessments and inform a conservation status where molecular diversity is known. Where population genetics and genomics approaches are to be used, accurate calculation of molecular diversity is a trade-off between number of loci, population size and the number of populations studied (Aguirre-Liguori *et al.* 2020). For example, Werth & Scheidegger (2011) determined that when using three microsatellite loci, *c.* 20 individuals are sufficient to recover diversity within a single population, while as many as 400 individuals over 30 populations are necessary to establish lichen diversity at a landscape scale. In plants, no more than eight individuals are required to establish genetic diversity within a population when a dataset contains >1000 single nucleotide polymorphisms (SNPs), and as few as two individuals with >1500 SNPs (Nazareno *et al.* 2017). Importantly, in highly threatened populations, conservation of those individuals that remain should be prioritized over determining genetic diversity by sacrificing the few surviving thalli.

Photobionts

Our current understanding of lichen distributions relies on recognition of their symbiotic phenotype, usually understood to be driven by the dominant fungal partner, and conservation assessments are therefore intrinsically fungal-focused. However, lichen-forming fungi associate with a relatively high diversity of green and yellow-green microalgae and cyanobacteria as their main photosynthetic partners (Sanders & Masumoto 2021), and thalli host a multiplicity of other microalgae that do not represent the main photobionts (Moya *et al.* 2017). Photobionts are essential members of the lichen symbiosis. To date, however, lichen photobiont diversity and species richness have been investigated only in a limited number of the existing lichen symbioses (Muggia *et al.* 2018, 2020, and references therein), and few photobionts have been studied in enough detail to make generalizations about photobiont associate conservation consequences. For example, while a number of lichen fungal genera and species appear to be relatively specific towards their *Trebouxia* photobiont partners (e.g. *Hypotrachyna, Lecanora, Tephromela, Xanthoparmelia*: Muggia *et al.* 2014; Kosecka *et al.* 2022), these same photobionts are often shared widely among different lichen-forming fungi, suggesting little role in limiting the distributions of the fungi. On the other hand, for cyanobacteria, although a meta-analysis and accepted nomenclature is still wanting, some studies consider the distribution of photobionts to be potentially constraining the distribution of lichens, particularly for ecological specialist species (Rikkinen 2002; Fedrowitz *et al.* 2011; Otálora *et al.* 2012; Belinchón *et al.* 2014). In addition, *Trentepohlia*-associated lichens appear to have a higher level of rarity than other photobionts in some regions (Manzitto-Tripp *et al.* 2022).

Photobiont associations and specificity are essential traits to consider in evaluating the extinction risk faced by lichens. For instance, lichen recolonization can be a long process; a time span of 150–180 years was required for epiphytic lichen communities to reach a diversity similar to that of old-growth forests (Gjerde *et al.* 2012; Spake *et al.* 2015). Although mycobiont specialization towards the photobiont is a species-specific trait (Pérez-Ortega *et al.* 2023; Berlinches de Gea *et al.* 2024), it may be modulated to some extent by habitat quality (Berlinches de Gea 2024). Specialization is also a major factor contributing to the slow re-establishment of certain lichen communities, along with other factors such as host tree specificity and forest age (Singh *et al.* 2016). While in some cases there are sufficient data available for a species or closely related species to incorporate photobiont identity and diversity into a Red List assessment, for most species, data are currently lacking. One example of especially vulnerable types of interactions among lichen species that share a specific photobiont species is photobiont-mediated guilds. *Ricasolia amplissima* (Scop.) De Not., *R. virens* (With.) H. H. Blom & Tønsberg and *Lobaria pulmonaria* share the specific photobiont *Symbiochloris reticulata*. Threats that lead to a decline in the guild's core species (i.e. *L. pulmonaria*), which can spread the photobiont through vegetative propagules, will inevitably cause an even stronger decline in the guild's fringe species *R. amplissima* and *R. virens*. These fringe species reproduce with ascospores only and depend on the availability of the photobiont at the new habitat (Scheidegger *et al.* 2015, 2023). A declining core species is therefore likely to cause a severe extinction vortex in fringe species, a so far largely neglected process in lichen conservation biology (Allen & Scheidegger 2022). Investigating mycobiont-photobiont relationships in the context of conservation is a major research need.

Threats

Threats to lichens can be either direct (e.g. thermal damage caused by extreme temperatures) or indirect (e.g. habitat degradation) and occur on a wide range of scales, from global climate or sea-level changes to very local impacts such as recreation or construction projects. Since lichen species diversity, as with other taxonomic groups, does not necessarily mirror patterns of diversity in other organismal groups (Vessby *et al.* 2002; Dorey *et al.* 2017; but see Negi & Gadgil 2002), our community of scientists

is often responsible for raising the alarm in relative isolation. A recent summary of the first *c.* 600 fungal Red List assessments showed the largest fraction of newly assessed lichens list climate change as an important threat, followed by development and human disturbance (Mueller *et al.* 2022). Local extinction of species can occur with a substantial delay following habitat loss or degradation as explained by the theory of extinction debt (Kuussaari *et al.* 2009), and this phenomenon has been demonstrated to also influence lichens (Ellis & Coppins 2019; Randlane *et al.* 2024). The effects of such potentially diffuse changes can be assessed using the flow chart in the Red List guidelines (IUCN Standards and Petitions Subcommittee 2024, §12.1) by focusing on changes in distribution, demography, or habitat suitability, for example. Conducting a thorough literature review to seek evidence for the impacts of threats to guilds of species and in specific regions increases efficiency in assembling assessments to treat groups of species with similar distributions and threats at the same time.

Treating species with commercial value

Certain lichens are collected and commercially traded for use as food, spices, medicine, dyeing material and perfume ingredients (Casselman 2001; Devkota *et al.* 2017; Yang *et al.* 2021). In some instances, large quantities are being traded (e.g. Devkota *et al.* 2019) and lichens are now available widely on e-commerce platforms. Lichens such as the mat-forming *Cladonia stellaris* (Opiz) Pouzar & Vězda are harvested in large quantities for ornamental use or as fodder for semi-domestic reindeer herds. In India alone, lichens measured in hundreds of kilos are traded and, as a result, have been recommended for inclusion in CITES agreements for their protection (Upreti *et al.* 2005). *Roccella linearis* (Ach.) Vain., used for dyeing material, might be extremely rare or extinct in the Cape Verde Islands due to over-collecting for commercial purposes (Follmann & Mies 1988). *Lethariella*, distributed at *c.* 3700–4300 m elevation in the Himalayas, is used as an important component of Tibetan incense because of its special fragrance (Yang *et al.* 2021) and is mainly sold in China, where there is special demand for Tibetan material due to its holy provenance. 'Black stone flower' is a mixture of lichens mainly containing *Parmotrema* spp. under different names such as Kalpasi, Dagad Phool, Chadila Herb, Organic Dried Stone Flower and Patthar Phool, and can be purchased for INR 100–INR 3000 (*c.* $1–35) per kg, even internationally. Many species that are currently perceived as common may not remain so if current levels of exploitation continue (Heinrich *et al.* 2020). Some sellers require the purchase of a minimum quantity of 100–500 kg, which indicates the species are harvested illegally and uncontrollably (Devkota *et al.* 2019). At the same time, those species are also considered threatened by other factors, such as climate change and habitat loss, leading to substantially increased extinction risk. Completing assessments for lichen species with substantial economic value should be prioritized along with continued research on the impacts of harvesting.

Lichenicolous fungi

Lichenicolous fungi are highly specialized organisms that form obligate associations with lichens (Lawrey & Diederich 2003). Most are host-specific parasites while others are broad-spectrum pathogens, saprotrophs, or commensals (Diederich *et al.* 2018). Some lichenicolous fungi cause host discoloration or thallus

damage, reduced fitness and changes in secondary metabolite biosynthesis (Asplund *et al.* 2018; Merinero & Gauslaa 2018). Since lichenicolous fungi are closely associated with their hosts, but unlikely to have colonized all host specimens, they present a special challenge for Red List assessments. If the host lichen is listed in a threat category, a host-specific lichenicolous fungus will invariably be even more scarce than the host and should receive a threat status of at least that of the host (Woods & Coppins 2012). As mentioned earlier, lichenicolous fungi are counted as their host lichen in terms of number of functional individuals. Generation lengths logically must be shorter than that of the host to enable the lichenicolous fungi to recolonize other host specimens. Currently, no lichenicolous fungi have been evaluated, but assessments of four host-specific fungal plant pathogens, which present similar challenges, have been published (Denchev & Denchev 2019*a*, *b*, 2022; Smith *et al.* 2020).

Recommendations and Conclusions

The choice of which species to assess is one of the first that must be considered in compiling threat assessments. So far, in the global IUCN lichen Red List assessments, a large proportion of assessed species have been regional endemics because the distributions and threats of such species are well known. Another tranche of Least Concern species has been assessed to try to provide a balance between threatened and non-threatened species, and a tool for rapid Least Concern assessments is under construction (G. M. Mueller, personal communication). However, many more species are widely distributed, threatened in parts of their ranges, and challenged by a combination of poor distribution and threat information, leaving overall assessments rather difficult to assemble. Nevertheless, increasingly available digital information for species distributions along with international networks of collaborations have facilitated an upsurge in global species assessments (Mueller *et al.* 2022). We call for authors of national, regional and international Red List assessments and authors of new species to follow the recommendations in this paper, summarized in Box 5.

An important part of the growth in engagement and Red Listing activity has been the huge success of the community-led

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Box 5. Main recommendations for Red Listing lichens

- Follow the most recent IUCN guidelines for regional and national Red Lists to ensure comparability and standardization.
- Describe uncertainty for each estimated quantity in assessments, including ranges of values for numeric estimates.
- Count functional individuals alongside other population size estimates in survey work for rare species.
- Follow precautions in Box 3 when using occurrence records from large biodiversity repositories (i.e. it is necessary to carefully review these occurrence records for identification accuracy; observation records not based on specimens and those that are far outside the general range of the species should very rarely be trusted).
- Carefully consider a possible lack of survey effort when interpreting data gaps in spatial distributions.
- Draft provisional Red List assessments when new species are described.
- Gather or compile environmental data to inform species distribution models and survey efforts where ecological and distribution information is lacking for rare species.
- Understand the threats that lichens face while drafting Red List assessments as an important part of the process and crucial for driving conservation efforts.

platform Global Fungal Red List Initiative (GFRLI), allowing local and regional experts to add to the general pool of knowledge, resulting in both a remarkable upsurge in fungal (including lichen) Red List assessments and the development of international networks for collaboration. The close collaboration between GFRLI and the IUCN Red List Unit, which oversees the final reviews and publishes updates to the IUCN Red List, means that there is now an almost seamless transfer of information between the two systems, increasing efficiency, engaging a broader community, and speeding up the processes of assessment and publication. The number of countries and regions using IUCN guidelines for threat assessments and increasing calls for fungal threat assessments (e.g. Nic Lughadha *et al.* 2020; Niskanen *et al.* 2023) confirm that building these collaborations is valued by the international conservation community, and we hope that this contribution further promotes global engagement.

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