

Proposed best practices for taxonomic innovations in lichen and allied Fungi: A framework derived from analysis of more than 1,000 new taxa and new combinations

James C. Lendemer¹

Institute of Systematic Botany, The New York Botanical Garden, Bronx, NY 10458-5126, U.S.A.

ABSTRACT. Analyses of data associated with 1376 taxonomic innovations (703 new taxa, 673 new combinations and replacement names) published from 2018–2020 are presented. Taxonomic contributions represented 14.2% of the published literature for the period. Most registration numbers for new names were obtained from MycoBank, suggesting the community has coalesced behind this resource. The overwhelming majority of new taxa (85.1%) and combinations (94.1%) involved crustose lichens and lichenicolous fungi. But lichenicolous fungi, regarded as a major source of undetected biodiversity, represented less than a fifth of innovations. More than half of new taxa were described from Asia and South America. Fewer than half (39%) of new taxa were published with molecular data, mostly from the ITS region but often in combination with data from additional loci. The majority of new taxa were based on small numbers of specimens (34.1% from one specimen, 69.2% from five or fewer) from few locations (44.4% from one location, 80.7% from five or fewer). Although a large number of identification keys were published, many new taxa were described with limited ecological data, distribution data or range maps, or discussion of similar species or phenotypic variation. Many innovations based on previously published names did not cite the nomenclatural type (67.7%) and less than a tenth of all such names were newly typified. Based on these results a best practices framework is presented.

KEYWORDS. Biodiversity hotspot, biogeography, conservation, data gaps, natural history collections, taxonomy, systematics.



In an age of unprecedented global change and habit loss, there is an urgent need to document and describe biodiversity (Ceballos et al. 2015; Craven et al. 2019; Pimm et al. 2014; Tedesco et al. 2014). Study of natural history collections coupled with targeted biodiversity inventories and stakeholder outreach are recognized as core to such efforts (Funk 2018; Grieneisen et al. 2014; Lendemer et al. 2019; Meineke et al. 2018). It is well-established that the scale of taxonomic description and revision must expand substantially above historical baselines to address the vast amount of work that remains (Gemeinholzer 2020; Kim & Byrne 2006; Liu et al. 2019; Zhang 2011). Indeed, this is the case for lichen

and allied fungi (e.g., Lücking 2020). The urgent need for taxonomic effort that is greatly expanded in scale and scope provides an ideal opportunity to build a framework for best practices that can be implemented to address gaps in current practice (Edie et al. 2017; Hortal et al. 2015; Troudet et al. 2017). Here such a framework for best practices is proposed based on analyses of published data associated with 1377 taxonomic innovations in lichen and allied fungi between 2018 and 2020.

MATERIALS & METHODS

This study is based on data collected by the author in conjunction with his role as editor of *Recent Literature on Lichens* (RLL hereafter; Culberson et al. 2020). As part of indexing each

¹ Author's e-mail: jlendemer@nybg.org

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publication for that literature database, all new nomenclature is routinely itemized and appended to each entry so that information on orthography, taxonomic authorities and geographic provenance of new names are readily available. Beginning in April 2018 the author expanded this process to include a protocol to score metadata associated with each new name. Two datasets were created: one for all newly described species and infraspecific taxa, and a second for taxonomic innovations that involve previously published names (i.e., new combinations and replacement names).

Literature analysis. Each publication was examined for taxonomic innovations as part of being incorporated in RLL. After indexing, each publication was assigned a unique identifier (RLL Record Number) and archived under that identifier as a PDF by the author. The unique identifiers were then used in downstream data scoring to cross-reference both bibliographic data available via the RLL database (<http://nhm2.uio.no/botanisk/lav/RLL/RLL.HTM>) and archived digital media.

Dataset I: New species and infraspecific taxa. For each new species or infraspecific taxon the protologue was examined and the following data were recorded: 1) RLL record number, 2) citation style publication authorship (e.g., Lendemer, Lendemer & Harris, Lendemer et al.), 3) total number of publication authors, 4) genus name, 5) new species and/or infraspecific epithet, 6) number of authors of the new taxon, 7) registration identifier and source, 8) whether the new taxon was represented by ITS, mtSSU or nuLSC sequence data, 9) the names of up to five additional molecular markers, 10) the number of collections cited for the new taxon, 11) the number of unique sites the cited collections were derived from, 12) whether an identification key incorporating the new taxon was included, 13) geographic range of the taxon, 14) whether a distribution map was included, 15) the number of lines of text devoted to ecology and habitat or distribution, 16) the number of lines of text devoted to taxonomic discussion of similar species and identification, 17) the number of columns per page (to standardize number of lines in two column vs. one column text), and 18) whether an etymology was included.

Dataset II: New combinations and replacement names. For each new combination or replacement

name, the protologue was examined and the following data were recorded: 1) RLL record number, 2) citation style publication authorship (e.g., Lendemer, Lendemer & Harris, Lendemer et al.), 3) total number of publication authors, 4) newly combined genus name, 5) newly combined species or infraspecific epithet, 6) number of authors of new combination, 7) basionym genus name, 8) basionym species or infraspecific epithet, 9) number of authors of basionym, 10) registration identifier of the new combination or replacement name and its source, 11) whether the type was cited, 12) whether the name was newly typified, 13) whether the type material was indicated as having been seen by the authors of the publication, 14) whether an identification key incorporating the new name was included, 15) the number of lines of text devoted to ecology and habitat or distribution, 16) the number of lines of text devoted to taxonomic discussion of similar species and identification, 17) the number of columns per page (to standardize number of lines in two column vs. one column text); and 18) whether any information (including 15 and 16 above, but more generally about the taxon) was included.

Dataset refinement and analysis. In preparation for this study, the nutrition mode (lichen, non-lichen parasite, non-lichen ally) and growth form (crustose, foliose, fruticose; squamulose treated as foliose) for each indexed taxon was scored. Discrete data such as presence/absence of molecular markers, distribution maps, and identification keys were transformed to 0 = absent, 1 = present, ? = missing. The number of molecular markers (zero to eight) was quantified for each new species or infraspecific taxon. Distribution data for the new species and infraspecific taxa were transformed to a presence/absence matrix at the level of continent (Africa, Antarctica, Asia, Australasia/Pacific, Central America, Europe, North America, South America). The refined dataset is available online as **Supplementary Dataset S1**.

RESULTS AND DISCUSSION

Between April 2018 and October 2020, 1376 taxonomic innovations for lichens and lichen allies were published, comprising 703 newly described species and infraspecific taxa, and 673 new combinations or replacement names. These names were

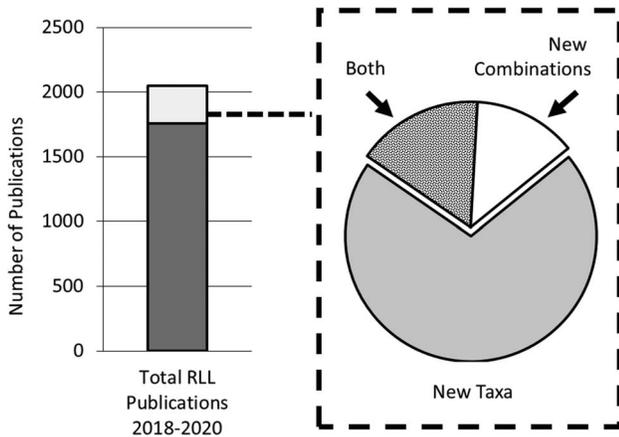


Figure 1. Quantification of publications containing new nomenclature relative to all lichen publications (left) and graphical breakdown of publications containing new taxa, new combinations or replacement names and both (right).

published in 292 contributions of which 252 (86.3%) included new species or infraspecific taxa while 89 (30.4%) included new combinations or replacement names. Only 13.7% (40 publications) included both types of innovations. The 292 publications represent 14.2% of the 2050 contributions published and indexed for the same period in RLL (**Fig. 1**). Of the 252 publications that described new species or infraspecific taxa, the majority (145, 57.5%) introduced only one new taxon and were responsible for publishing 20.6% of the names while only 36 publications introduced more than five new taxa and these accounted for nearly half of the names (348 names, 49.5%). Of the 89 publications that introduced new combinations or replacement names, 45 (50.6%) introduced one such innovation, accounting for 6.7% of the innovations, while 18 publications introduced more than five innovations, which accounted for 82.5%. The largest number of new taxa named in a single publication was 27 (3.8% of such taxa), and the largest number of new combinations or replacement names introduced in a single publication was 154 (22.8% of such names). The latter was a substantial outlier as the next largest number of innovations introduced in a single publication was 67 (9.9% of such names).

Based on the above, while the number of new names for lichens and lichen allies introduced is high, these publications represent less than a fifth of the lichen literature published during this period. Likewise, the number of newly introduced taxa did not differ substantially from the number of

innovations based on previously published names. Nonetheless more than half the papers describing new taxa introduced a single new taxon and there was an overall trend of fewer publications describing larger numbers of taxa (only two introduced more than 20). In contrast, far fewer publications introduced innovations based on previously published names and a small number of publications accounted for the vast majority of such innovations. In other words, many papers described a single new taxon, while a small number of papers introduced most new combinations.

Results of more detailed analyses and discussion of trends uncovered from these analyses are presented below and organized within a framework of the following topics: registration of names, traits, geographic provenance, use of molecular data, taxon rarity and range size, inclusion of identification resources, inclusion of ecological and biogeographic context, and inclusion of key information in taxonomic innovations.

MycoBank is the most used registration system.

Registration numbers have been required for valid publication of new names of fungi since 2013 (Art. F.5.1; May et al. 2019). Beginning in 2019 registration numbers were also required for valid designation of replacement or interpretative types (i.e., epitypes, lectotypes, neotypes; Art. F.5.4; May et al. 2019). At present no repository has been formally designated as the sole source for registration numbers. All of the 1376 names included in this study were published with a registration number and the majority of these (97.7% for newly described taxa, 76.5% of innovations) obtained the registration number from MycoBank. Two other registration systems were used, IndexFungorum (0.7% new taxa, 23.5% innovations) and Fungal-Names (1.6% of new taxa, zero innovations). The above suggests the community has coalesced behind MycoBank as the primary source for registration numbers and that this repository could be prioritized as the source for registration numbers in fungi. Nonetheless further improvements and investment in the system are needed, for instance, inclusion of fields for data associated with herbarium specimens as is typical of lichen and allied fungi (e.g., standard herbarium acronym for the type, accession number or barcode number, collector and collection number). While MycoBank is widely used to obtain registration identifiers, this should in no way be

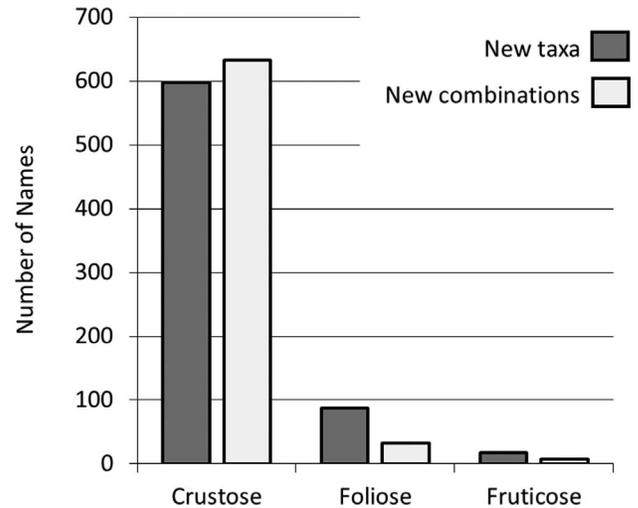
Table 1. Tabular summary of names analyzed for this study classified by major growth forms and life strategies.

	New Species/Infraspecifics	New Combinations
Growth Form		
Crustose	526 (85.9%)	614 (94.3%)
Foliose	73 (11.9%)	29 (4.5%)
Fruticose	13 (2.1%)	8 (1.2%)
Nutrition Mode		
Lichen-forming	535 (87.4%)	562 (86.3%)
Non-lichenized	77 (12.6%)	89 (13.7%)
Parasitic		
Lichen-forming	75 (12.3%)	93 (14.3%)
Non-lichenized	166 (27.1%)	168 (25.8%)

interpreted as an obsolescence of IndexFungorum. The latter is a simplified, easy to navigate system that is commonly used to query nomenclatural information about fungal names. Both MycoBank and IndexFungorum likely fill essential, complementary roles in lichen systematics.

Taxonomic innovation is dominated by crustose lichens. Each of the 1376 names analyzed here was classified based on the growth form, nutrition mode and life strategy of the taxon it applies to (Table 1). Most newly described taxa (598, 85.1%) and innovations (633, 94.1%) involved species with crustose growth forms (Fig. 2). In contrast, only 14.9% of the newly described taxa were foliose or fruticose macrolichens and even fewer (5.9%) innovations involved such taxa (Fig. 2). This may support the belief that foliose and fruticose microlichens have been more completely described and documented historically in comparison to macrolichens. It may also reflect a greater diversity of crustose microlichens relative to macrolichens, although this has yet to be studied in detail across large geographic areas outside of Europe (Bergamini et al. 2005; Lendemer et al. 2016). At the same time, it may also reflect an increased focus on crustose lichens by current taxonomists and a widely held belief that macrolichens are completely known even though detailed studies often lead to the recognition of previously overlooked taxa (Lücking et al. 2014).

Interestingly, although lichenicolous fungi have been suggested to be an important source of previously overlooked fungal diversity (Hawksworth & Rossman 1997; Hawksworth & Lücking 2017), these accounted for 11% of the newly described taxa and 14.2% of the innovations. Only 77 new lichenicolous fungi were described during this

**Figure 2.** Graphical breakdown of new taxa and new combinations by growth form (lichenicolous and non-lichen fungi included in crustose growth form).

period, a number far outpaced by the number of crustose lichens. It is possible that this reflects a smaller research community and that research on lichenicolous fungi is an area that would benefit from targeted support. Given the comparatively small number of lichenicolous taxa involved, it is not surprising that 11.1% of the new taxa and 14% of the innovations involved non-lichenized fungi. This is because the majority of such taxa treated by lichenologists are lichenicolous, and that there are relatively few non-lichen fungi treated by lichenologists (e.g., Mycocaliciaceae, some Arthoniaceae s.l., selected pyrenocarpous fungi; Lücking et al. 2017).

Asia and South America are hotspots of new taxa. A breakdown of the geographic provenance of newly described taxa demonstrates that more than half (53.6%) are from Asia (26.7%, 188 taxa) and South America (26.8%, 189 taxa). The number of new taxa described from purportedly well-studied areas such as Europe (11.8%, 83 taxa) and North America (14.5%, 102 taxa) is somewhat surprising, but likely reflects the high concentrations of lichen taxonomists in those regions (e.g., Lücking 2020). In contrast, the small number of taxa described from Africa (4.1%, 29 taxa) almost certainly reflects a lack of lichenological attention rather than a completely documented biota. These results largely correlate with those previously observed for all groups of organisms (Grieneisen et al. 2014).

It is interesting to note that 97.4% (685 taxa) of new taxa were described from a single continent,

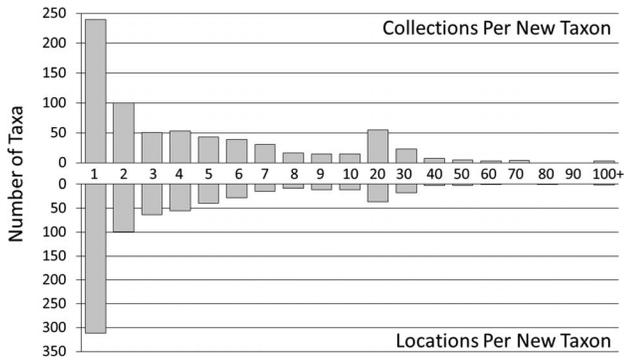


Figure 3. Graphical summary of the number of collections (top) and locations (bottom) each newly described taxon was based on. Note that x-axis labels greater than 10 refer to the span of values between labels (i.e., 20 = 11–20; 30 = 21–30).

while none were found to occur on more than three continents. This could reflect real continental range limits for most lichens, or it may reflect spatial limitations wherein most studies focus on small geographic areas and rarely span multiple continents.

Majority of new taxa lack accompanying molecular data. The increasing incorporation of molecular data into studies of lichens over the last decade has already been discussed and quantified (Hoffman & Lendemer 2018). As such one would expect newly described taxa to be routinely accompanied by molecular data, especially for commonly used loci. Yet of the 703 new taxa included in this study, less than half (39%, 274 taxa) were published with accompanying molecular data. It is important to highlight that this study did not discern whether molecular data had previously been published separately for a given species, although it did attempt to take into account any citation of molecular data even if they were not explicitly analyzed. Of these new taxa introduced with molecular data, the vast majority (81.8%, 224 taxa) included ITS sequence data, following the already recognized emphasis of these data in molecular studies of lichens (Hoffman & Lendemer 2018). The only other two loci that were commonly employed were mtSSU (46.7%, 128 taxa) and nucLSU (35%, 92 taxa). Interestingly, many of the studies that included molecular data for new taxa, used data from two or three loci (1 locus: 33.5%; 2 loci 34.3%, 3 loci 22.2%). Only 27 new taxa were published with data for more than three loci (3–6 loci: 9.9% of all names published with molecular data) and only one

was published with metagenomic data and a complete organellar genome (Anderson Stewart et al. 2018).

Most new taxa are based on few specimens from few locations. More than a third of new taxa were described from a single specimen (34.1%, 240 taxa) or location (44.4%, 312 taxa), and the majority were described from five or fewer specimens (69.2%, 487 taxa) or locations (80.7%, 568 taxa) (**Fig. 2**). Less than a fifth of all taxa were described from ten or more specimens (16.4%, 115 taxa) or locations (10.5%, 74 taxa). It should be noted that for this study, given divergence in specimen citation styles and lack of distribution maps (see below), “locations” were delimited liberally such that almost any difference in location data between two collections was treated as distinguishing an additional location. While this almost certainly means that locations were over-counted in many cases, it also suggests that the metrics cited above are conservative.

These results raise a number of questions about rarity and endemism. That so many taxa are based on a small number of specimens, or even one specimen, could reflect the rarity of the lichens involved. Indeed, many species appear to be rare, even if they are geographically widely distributed (McMullin et al. 2019). There are also narrowly endemic species with highly restricted ranges (e.g., Allen et al. 2018; Simon et al. 2018). However, the overwhelming majority of descriptions of new taxa did not contextualize rarity and endemism by discussing the depth and scale of sampling, either in a geographic sense or in terms of material available for study in natural history collections. Thus, it was typically not possible to determine whether species described from small numbers of specimens and locations may reflect actual rarity and small range sizes rather than sampling limitations. Inclusion of such data could fundamentally transform lichen conservation and identify conservation priorities, as has been demonstrated in vascular plants (Treurnicht et al. 2017).

Limited ecology and distribution information is often presented. Understanding the ecology and distributions of species is key to many aspects of the biological sciences (Bortolus 2008; Crisci & Katinas 2009; Sutherland et al. 2013). Yet 12.2% (86 taxa) of new taxa and 88.6% (596 names) of new combinations were introduced without any such accompa-

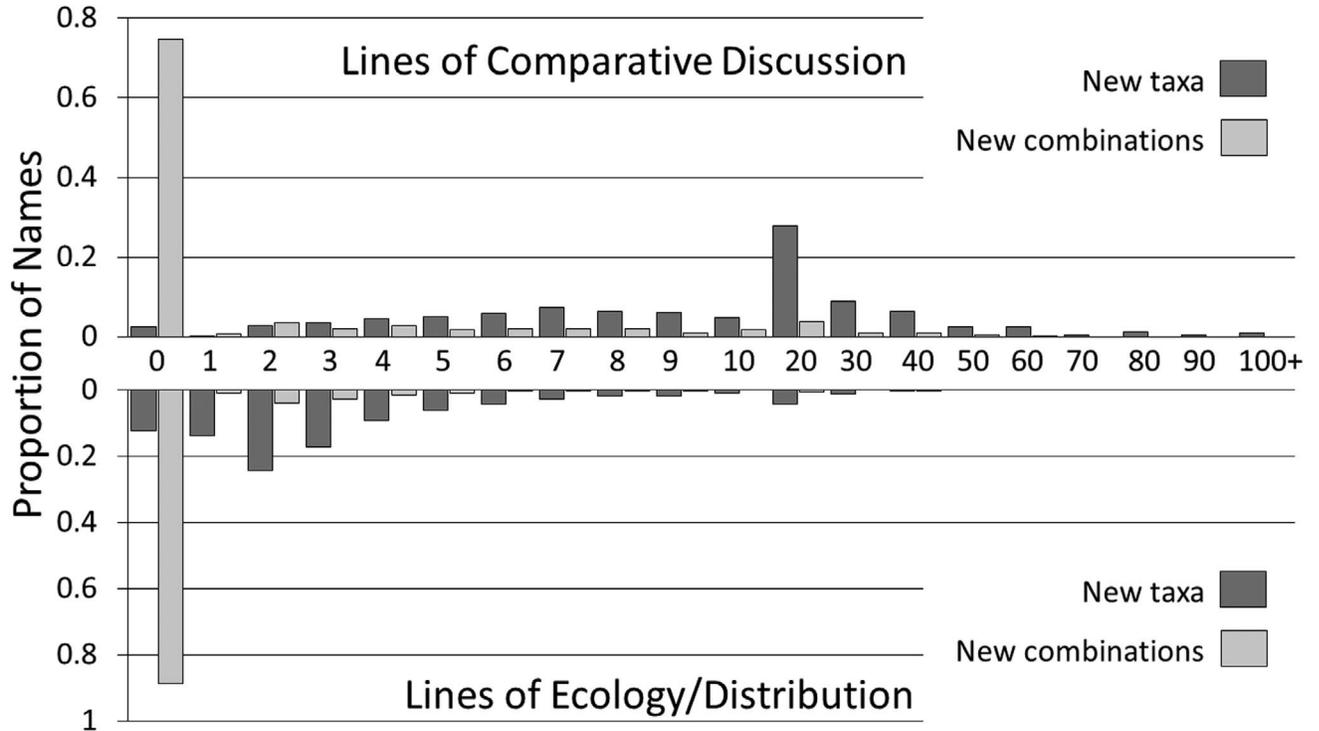


Figure 4. Graphical summary of length (in lines) of ecological information (bottom) and taxonomic or comparative discussion (top) presented for each newly described taxon and new combination. Note that x-axis labels greater than 10 refer to the span of values between labels (i.e., 20 = 11–20; 30 = 21–30).

nying information (**Fig. 4**). This may not be surprising for new combinations of names for taxa that had already been described, presumably with ecological and distributional data presented in earlier publications. However, it is remarkable that so many newly described taxa would lack such information. Further, when such information was included, it was typically very limited in scope. This is evidenced by the fact that 13.9% (98 taxa) of new taxa were introduced with only one line of ecological discussion and 82.1% (577 taxa) were introduced with between one and ten lines of ecological discussion (**Fig. 4**). A further illustration of the lack of distributional information is the fact that 93.8% (660 taxa) of new taxa were described without an accompanying range map. The above means that the majority of new taxa were described with little, if any, context as to where they live, what they grow on and how these factors may relate to other lichens and other groups of organisms.

Many identification keys but little comparative discussion for new taxa. In strong contrast to the overall paucity of data on ecology and distribution, dichotomous identification keys were included with

the descriptions of 38.5% (274 taxa) of newly described taxa. Although this study did not attempt to distinguish between taxonomically versus geographically defined identification keys, the fact that so many new taxa were published with such resources suggests that they are valued by the community and expected by reviewers. Given such an emphasis on information to aid in identification, it is interesting that nearly half (46.2%, 325 taxa) of new taxa were associated with comparative discussions one to ten lines in length and the majority (74.1%, 521 taxa) were introduced with between one and twenty lines of discussion. It must be acknowledged that the amount of text is at best only a rough approximation for the amount of information conveyed, and some information may have been presented separately in a collected results section of a given publication (vs. directly associated with the taxon). However, one must admit that it is difficult to contain within ten lines of text, a discussion of phenotypic variability, detailed and comprehensive comparison with related species, and comparison with sympatric or otherwise confusable species.

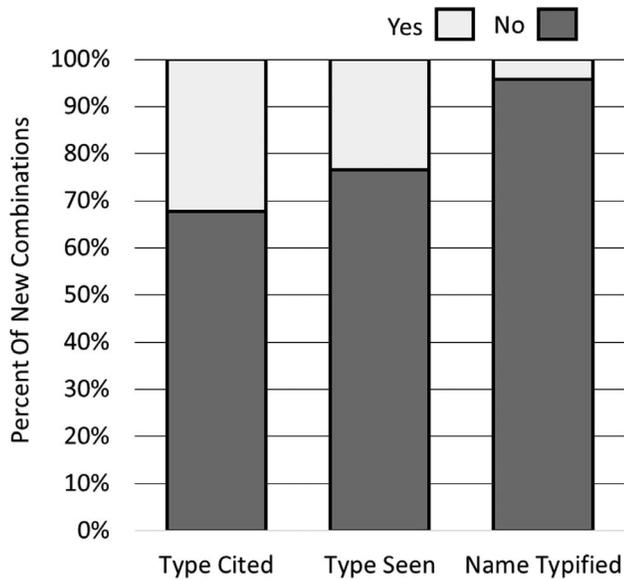


Figure 5. Summary of type specimen information presented for new combinations and replacement names.

Most new combinations lack key information.

Of the 673 new combinations and replacement names included in this study, more than half (67.7%, 456 names) did not cite the type specimen (Fig. 5). Moreover, 76.5% (515 names) either did not indicate whether the type had been seen or did not do so in an explicit manner (Fig. 5). Perhaps more surprising, only 4.3% (29 names) were newly typified in conjunction with taxonomic innovation (Fig. 5). While it is likely that many names had already been typified, the small percentage of cited types, coupled with the smaller percentage of types indicated as seen by the authors of the innovations, is surprising. Names are applied based on nomenclatural types, and decreasing examination, let alone citation of types raises the possibility of names becoming untethered from the things that define them.

Beyond citations of the types that define the names being newly combined or replaced, fully 70.4% (474 names) of such innovations did not include specific information about the taxon in terms of ecology, distribution, morphological characters or comparison of similar species. Likewise, 85.1% (573 names) of such innovations were not associated with an identification key. The lack of broader discussion and supporting identification information is surprising given 82.5% of the innovations were made in only 20.2% of the publications, suggesting that many names were

combined in the context of comparative studies, or floristic treatments of discrete geographic regions.

PROPOSED BEST PRACTICES

In light of the results presented in the proceeding section, a series of best practices is proposed to address apparent gaps in current taxonomic practice for lichen and allied fungi.

1. Comply with requirement to register new names and new typifications. Almost all new taxa and combinations are published with registration numbers, and errors in those identifiers are treated as automatically correctable (Art. F.5.6; May et al. 2019). Nonetheless a small number are still published without registration numbers, typically in journals where the editorial staff may be unfamiliar with the unique rules of fungal nomenclature. Registration numbers are also required for all new typifications (epitypifications, lectotypifications, neotypifications; Art. F.5.4; May et al. 2019). This latter rule appears to be less widely recognized. In the absence of a registration number, any new name or typification is invalid and must be republished with an identifier in order to be validated. To avoid this, authors should always obtain a registration number and given the widespread use of MycoBank, this source is a logical choice. Registration numbers should be obtained after manuscript acceptance and prior to publication, as is recommended by the *Code* (Rec. F.5.A; May et al. 2019).

2. Publish molecular data when available. There are many instances wherein molecular data cannot be easily generated as part of a taxonomic study. More importantly, such data are not necessarily required when new taxa or new combinations are well-supported by analyses of other data types (e.g., phenotypic characters). However, if molecular data are available, especially for newly described taxa, these should always be explicitly discussed, made available in a public repository, and the identifiers from that repository should be cited. This applies to sequence data (e.g., an ITS sequence should be deposited in NCBI and the identifier cited in the publication) as well as to any data that were analyzed (e.g., an alignment of ITS sequences used to infer a phylogeny should be deposited in a public repository and the identifier cited in the publication, or included as a supplemental file with the published manuscript). Descriptions of new taxa, and new

combinations of existing names, should not be based on unpublished sequence data that are not publicly available at the time of publication.

3. Describe sampling limitations. In describing new taxa, workers typically consult many resources to determine phenotypic variation, substrate preferences, microhabitat and geographic range. The range of resources consulted, and potential limitations of this sampling should be explicitly discussed as part of the publication. This discussion should include i) how well studied the overall geographic region is for lichens and botanical organisms in general, ii) whether large numbers of lichen natural history collections have been previously made in the region and if they were examined to search for additional records of the new taxon, and iii) the extent of overall sampling carried out for the study and how it relates to the total number of occurrences found for the new taxon. Such information provides essential context for other workers, particularly in ecology, biogeography and conservation.

4. Publish a range map. Understanding geographic distribution and broader spatial context is a key component of describing new taxa. Even if a taxon is described from a single location, or set of spatially clustered locations, it is important to provide visual documentation in the publication. High quality range maps can easily be produced online (e.g., Simplemapp; Shorthouse 2010), free-ware (e.g., QGIS), and through standard GIS software. All new taxa should be accompanied by a range map.

5. Provide ecological and biogeographic context. There is a vast body literature on the ecology and biogeography of organisms, especially sessile taxa such as vascular plants. Yet, lichen and allied fungi are poorly integrated with patterns and processes of other organismal groups. A crucial step in advancing integration is more discussion of broader ecological and biogeographic patterns within taxonomic contributions. At minimum, detailed discussions of the ecology and distributions of the lichen taxon involved should be provided. These details may be hypotheses due to sampling limitations, but such hypotheses should be supported by citation of relevant literature. Ideally, ecological and distributional information for a given species should be placed in a broader context of other lichens (e.g., related, co-occurring or sympat-

ric species) and other organisms or factors (e.g., host substrates, natural communities, ecosystems or geological patterns).

6. Discuss both similar and confusable species. As is evidenced by the number of contributions that include identification keys, a core use of taxonomic literature is to identify and compare new or existing material and taxa. Therefore, new taxa should be accompanied by a detailed discussion of how the taxon differs from related species, especially sympatric taxa and those that are most morphologically and ecologically similar. It should also include a detailed discussion of how the taxon differs from superficially similar or otherwise confusable, co-occurring taxa that are not necessarily closely related. In cases where potential available names for a taxon were studied, and subsequently excluded for one reason or another, this should also be discussed.

When information such as the above has been previously published for a taxon whose name is newly combined or replaced, those sources should be cited to provide more complete context to the user community. In cases of new combinations and replacement names for taxa that do not have such previously published resources, then that information should be included as part of the discussion of the new name. There will be exceptional instances when a name must be transferred or replaced without a detailed understanding; however, such data deficiencies should also be highlighted to stimulate future research.

7. Include both differential diagnoses and descriptions of new taxa. Names of new species or infraspecific taxa must be accompanied by a diagnosis or description, or reference to one previously published, in order to be validly published (Art. 38; Turland et al. 2018). While only one of these is required, it can be helpful to include both when describing a new taxon. Indeed, differential diagnoses are recommended by the *Code* (Rec. 38.1.B; Turland et al. 2018) and can complement both a detailed description and a comprehensive comparative discussion. A differential diagnosis succinctly outlines the key differences between the new taxon and one or more that are most similar to it, providing a quick reference to the reader.

8. Fully cite primary types. In the case of new combinations and replacement names the nomenclatural type should always be cited with an

indication of whether it has been examined in person (“!”), examined digitally (e.g., “digital image!”), or not been examined (e.g., “n.v.”). In cases where the name has previously been typified, that typification should be directly cited. If a name has not been typified previously and is not then typified when it is newly combined, a justification for this should be provided.

CONCLUSION

The need to document and describe the global diversity of lichen and allied fungi has never been more urgent. The scale and scope of taxonomic work required to achieve this goal is immense. It has been suggested that this requires rapid increases in the amount of taxonomic output and decreases in the timeline to produce such output. However, such efforts must balance speed and quantity on one hand, with quality and utility on the other (Bortolus 2008; Carvalho 2008). Few would argue that the core goals of the lichen taxonomic community should be to: i) provide accessible identification tools and taxonomies that are relevant to user communities outside narrow group of lichen experts, ii) more fully integrate ecological and biogeographic knowledge across lichen taxa and across organismal groups, and iii) establish a clear basis for conservation and management of threatened or endangered species. It is hoped that the best practices outlined here provide a framework to further advance these goals.

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Supplementary documents online:

Supplementary Dataset S1. Study dataset scored and compiled from taxonomic literature, with associated tabulated values.