

From barcode to “blueprint”: what is in a species of lichens?

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Accurate estimation of species diversity is central to conservation, biomonitoring, and understanding the evolutionary dynamics of lichens. Molecular data, spanning from single-locus barcodes to multi-locus markers, have expanded our understanding of lichen diversity, demonstrated homoplasy of numerous phenotypic traits and challenged traditional species concepts. Thus, despite its central meaning for lichenology, the species concept remains a matter of debate and taxonomic uncertainty, and we still do not know if further, genome-scale approaches — such as RADseq, phylogenomics, and metagenomics — will resolve this situation by revealing previously inaccessible information. This symposium brings together researchers across these scales to consider questions such as: How much of the genome is enough to delineate species? What new insights arise when we move beyond barcoding to the genomic “blueprint” of species, including regulatory loci, gene architecture, and structural variation? Topics to be presented in this symposium may cover hidden diversity, methodological advancements, functional genomic insights, and the wider consequences of precise species delimitation and genomic discoveries, ranging from ecological monitoring to habitat conservation. Together, we seek to map the next frontier in decoding lichen biodiversity—from barcodes to blueprints.