**TEMPORAL BANDING VERSUS INTEGRATED TAXONOMY: HOW TO TRANSLATE MACROEVOLUTION INTO CLASSIFICATION USING CETRARIOID LICHENS AS CASE STUDY**

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Translating phylogenies into classifications provides challenges, since macroevolutionary forces that determine the phenotypic outfit of clades do not necessarily correlate with phylogeny. Besides homoplasy, phenotypic convergence, and phenotypic stasis, the conceptual problem of rank-based taxonomy adds an additional layer of complexity, since tree topologies do not offer objective solutions for ranking. While some workers have suggested to abandon rank-based classifications, an alternative of presumably objective ranking is temporal banding. In a recent study of class Lecanoromycetes, the largest class of lichen-forming fungi, temporal banding was employed to propose some profound changes to classifications at order, family, and genus level [Kraichak et al., Botanical Journal of the Linnean Society 188: 233–49 (2018)]. In a critical revision of the temporal banding concept [Lücking, Critical Reviews in Plant Sciences 38: 199–253 (2019)], it was argued that this approach is too mechanistic and does not properly reflect macroevolutionary processes such as disparate diversification of sister clades, phenotypic coherence above species level, and differential taxonomic resolution based on body plan complexity. Integrated taxonomy considers all these processes to produce more consistent classifications. This approach was tested using the cetrarioid core (Parmeliaceae) as an example, which for a long time had been divided into 12 genera, but based on the strict temporal banding approach was recently re-classified into just two genera, *Cetraria* and *Nephromopsis*. For rhe integrated taxonomic approach, 11 molecular markers were analyzed, for a total of 1,017 terminals in the concatenated dataset and 919 terminals in the ITS alone, and 70 phenotype characters were scored for all accepted species. The results, based on maximum likelihood tree search, molecular clock and ancestral character state analysis, phenotype-based phylogenetic binning, and multiresponse permutation procedure, suggest to distinguish a total of 28 genera, differing from any previous classification.