**PHOTOBIONT DIVERSITY AND SPECIFICITY IN CYANOLICHENS OF THE *Dictyonematinae* SUBTRIBE**

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Based on recent phylogenetic studies of the basidiolichen subtribe *Dictyonematinae*, 149 species are now accepted in five genera, with hundreds of species remaining to be described. The identified photobionts of these species are members of a remarkable clade of cyanobacteria called *Rhizonema*, found predominantly associated with lichens, both basidiolichens and ascolichens (e.g., *Coccocarpia*, among others). To investigate the levels of photobiont diversity and specificity in this group, we generated 16S rDNA and *rbc*LX sequences from over 600 specimens representing all major clades within *Dictyonematinae* and an additional 21 ascolichens suspected to contain *Rhizonema*. This dataset contains samples collected from 18 countries, mainly from the Neotropics and Paleotropics. All lichens were found to harbor one of three putative species of *Rhizonema*: *R. andinum*, *R. interruptum* or *R. neotropicum*. There was no indication of photobiont-mycobiont co-evolution at the species level in any of the clades in *Dictyonematinae*; however, one of the three lineages of *Rhizonema*, *R. andinum*,appears to partner primarily with one of the two larger *Cora* clades, specifically the clade mostly composed of northern Andean taxa. *Rhizonema* *interruptum* was represented by a much larger number of haplotypes and associates with mycobionts from many clades, and an ancestral photobiont association reconstruction for *Dictyonematinae* indicated an early mycobiont association with this cyanobiont lineage. Based on the reconstruction of both fungal and cyanobacterial molecular clocks, we found that *Rhizonema* is much older than the Basidiomycota they associate with and was likely present in much older ascolichen clades (e.g., *Coccocarpiaceae*) before associating with basidiolichens. Our results for *Dictyonematinae* confirm other findings that the diversity of photobionts is far lower than that of the mycobionts, a view that lends further support to the “fungal farmers” hypothesis, in which photobiont lineages are under strong selection driven by lichenization.

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