

Exploring the possibility of multiple *Trebouxia* lineages in individual lichen thalli using next-generation sequencing

Steven LEAVITT

Integrative Research Center, Science & Education, The Field Museum, 1400 S. Lake Shore Drive, Chicago, IL 60605, USA

Microbial symbionts are instrumental to the ecological and long-term evolutionary success of their hosts, and the central role of symbiotic interactions is increasingly recognized across the vast majority of life. Lichens provide an iconic group for investigating patterns in species interactions; however, the iconic perspective of lichen thallus comprised of a single mycobiont associating with a single photobiont has recently been challenged. The occurrence of multiple photobiont species-level lineages occurring in individual lichen thalli - intrathalline photobiont plurality - has been detected across a number of lichens groups. In this study, we implement a shotgun sequencing approach to characterize potential intrathalline photobiont plurality in members of Lecanoraceae and Parmeliaceae. We demonstrate that high throughput sequencing provides a powerful tool for assessing intrathalline algal diversity, in addition to generating phylogenomic datasets for inferring evolutionary relationships.

Inferring a phylogenetic hypothesis for *Trebouxia* to better characterize diversity in this important photobiont genus

Steven LEAVITT

Herbarium of Non-vascular Cryptogams, Department of Biology, Brigham Young University, 4143 LSB, Provo, UT 84602, 801 422-4879

The algal genus *Trebouxia* is comprised of diverse symbiotic algae, representing perhaps the most commonly associated lichen photobiont. Research into this important algal genus has provided vital perspective into symbiotic interactions in lichens, and symbiosis in general. However, in spite of the central role of *Trebouxia* in many lichen symbioses, a robust phylogenetic hypothesis of relationships has not yet been reconstructed for the genus. In this study, we assembled *Trebouxia* sequence data from over 1000 specimens (lichens and pure algal cultures) representing the currently known phylogenetic diversity in the genus. We generated sequence data from the nuclear ribosomal ITS, a fragment of the protein-coding *rbcL* chloroplast gene, and a fragment of the mitochondrial COX2 gene. Our phylogenetic reconstructions support four major clades previously recognized in *Trebouxia* and the monophyly of many of the candidate species level lineages. This study provides a key foundation for advancing our understanding of evolutionary processes, patterns of species interactions, and species delimitation in *Trebouxia*.