

Assessing diversity and patterns of association in *Trebouxia*

Matthew P. Nelsen

Integrative Research Center - The Field Museum, Chicago, USA

Over the past 15+ years, the ITS has become the most-sequenced locus of *Trebouxia* algae. Sequencing efforts have revealed substantial diversity – far greater than was previously appreciated. Here we synthesize publicly available ITS sequence data and summarize our efforts to characterize OTU diversity, geographic richness and range of *Trebouxia* OTU's, and patterns of association with lichen mycobionts. We assess how close we are as a community to capturing the diversity of *Trebouxia* algae, and emphasize research avenues that will further contribute to our understanding of this lineage of algae.