**Phylogenomics of lichens: Using alternative next-generation sequencing approaches to reveal various levels of phylogenetic relationships in lichen-forming fungi**

Felix Grewe1\*, H Thorsten Lumbsch1

1 Grainger Bioinformatics Center, The Field Museum, Chicago, IL, USA; \*E-mail: fgrewe@fieldmuseum.org

Revolutionary advancements in sequencing technologies and bioinformatics over the past decade have paved the way for the current era of “big data.” These changes have dramatically affected current lichen genome research, in which researchers can now use whole-genome datasets for phylogenomic analyses. However, sequencing entire genomes can be still challenging and expensive, especially since lichens, as symbiotic organisms, contain at least two partners with different genomes: the mycobiont and the photobiont. In addition, the metagenomic sequence pool can contain additional organisms, including endolichenic and lichenicolous fungi which complicate the phylogenetic analyses. Therefore, we developed and applied three different next-generation sequencing methods and made them suitable for use with lichens. The first technique, named HybSeq, physically selects for the DNA strands of target genes prior to sequencing. In the other methods, Restriction site associated DNA markers (RADseq) and *de novo* sequencing, we bioinformatically filtered metagenomic sequences of the fungal partner after sequencing the total lichen. HybSeq and RADseq are very cost effective reduced-genome representation methods. In this presentation, we will exemplify the power of the new sequencing technology by presenting representative studies at different phylogenetic levels from higher-level relationships to population biology within species. We successfully combined target enrichment with manually extracted genes from *de novo* assemblies to build a comprehensive phylogenomic dataset and were able to reconstruct the phylogeny of Parmeliaceae. Moreover, we present the results of RADseq from hundreds of individuals of *Usnea*, in which we used thousands of molecular markers for phylogenetic, barcoding, and species delimitation approaches. Although the availability of whole genome data opens unforeseen avenues into lichen genome research, new challenges emerge using big data. Therefore, we will further discuss how whole genome data demands new solutions to existing phylogenetic and statistical models, as well as the current progress in bioinformatics methods.