**FULL CHROMOSOME ASSEMBLY OF LICHENZIED FUNGAL GENOMES FROM WHOLE THALLUS EXTRACTS USING NANOPORE SEQUENCING**

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Growing lichenized fungi in axenic culture is challenging, slow, or impossible for many species. Furthermore, the mycobiont grows embedded in diverse microorganismal communities, so shotgun sequencing samples from nature yields rich and complex metagenomes. Filtering reads and assembling target fungal genomes from short-read sequences can be challenging. In this talk I will present a workflow for reliably generating high-quality lichenized fungal genomes using the Oxford nanopore MinION platform. To develop this protocol, whole lichen extracts were sequenced and genomes assembled from complex, metagenomic data, and all work was completed in-house with students at Eastern Washington University. Genomes of five species of lichenized fungi from five different families were assembled and all genomes were high quality. One genome, *Lepraria neglecta*, was assembled to whole chromosomes. Nanopore sequencing is a promising approach for generating high-quality references genomes in lichenized fungi.