**THE GOLDEN ERA OF LICHEN GENOMICS: A CHROMOSOMAL-SCALE GENOME ASSEMBLY OF *Xanthoparmelia***

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With the advent of next-generation sequencing and increasing computational powers over the past decades, science’s capacity of understanding and utilizing genomic data dramatically increased. Compiling chromosomal-scale genomes (“gold genomes”) for non-model organisms is an innovative challenge that can now be addressed in a cost-effective way. Here we present a combination of sequencing strategies and assembly approaches to build a chromosomal-scale genome of a *Xanthoparmelia* lichen fungus. We used a combination of cutting-edge sequencing methods including ultra-long-read Nanopore sequencing, Illumina reads for polishing, chromosome conformation capture with Hi-C technology, and short scaffolding with transposase enzyme linked long-read sequencing (Tell-Seq). Many steps in the various protocols were optimized to best fit lichens, including a successful and inexpensive high molecular weight DNA extraction prep. The methodologies described here, from DNA extraction to sequencing and assembly, will provide a novel protocol for genome sequencing under a lichen-focused framework. The assembled gold genomes will provide ideal reference genomes that lay the groundwork for the next level of lichen genome research.