**GENOME SKIMMING BY SHOTGUN SEQUENCING TO ADDRESS LONGSTANDING QUESTIONS OF SPECIES DIVERSITY IN *Lecanora polytropa***

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Genome skimming can provide cost-effective strategies for generating phylogenomic datasets, particularly for organisms with relatively small genomes, including fungi. Inferring robust phylogenies and species boundaries can be facilitated by these genome-scale datasets. Here we explore the utility of genome skimming for inferring species boundaries in the cosmopolitan taxon *Lecanora polytropa.* As the specific epithet suggests, this nominal taxon is morphologically variable, with distinct populations occurring in montane to alpine/polar habitats on all seven continents. To initially delimit candidate species-level lineages in this group, we compiled ITS sequence data – the standard DNA barcoding marker – from GenBank and newly generated sequences from populations occurring in alpine habitats in western North America (*n*=129, total). Species partitions were empirically delimited using ASAP, a new method to build species partitions from single locus alignments. Representative samples for species partitions inferred from ITS sequence data were selected for high-throughput short-read, shotgun sequencing using Illumina. We generated alignments for 1209 single-copy nuclear genes (2.27 Mb, total), in addition to an alignment of spanning most of the mitochondrial genome (65.4 Kb). Phylogenomic species delimitation analysis using the 1209 gene trees using SODA. Candidate species partitions inferred from the ITS data were consistent with reciprocally monophyletic clades inferred from both the nuclear and mitochondrial phylogenomic alignments. Specimens from western North America represented up to 19 species, with different mountain ranges having only partly overlapping species. Similarly, most species diversity sampled in western North America was not represented by ITS sequence data currently available on GenBank, suggesting interesting biogeographic patterns in this complex. Species inferred from phylogenomic data were generally morphologically variable, and no diagnostic secondary metabolites were observed. Our results demonstrate that genome skimming can provide powerful data to help resolve longstanding questions of species boundaries in well-known, taxonomically challenging groups. Funding: SDL (Canyonlands Natural History Association).