

# EXPLORING HTS TECHNOLOGY TO SEQUENCE 150-YEAR-OLD LICHEN SPECIMENS

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Natural history collections worldwide house immense numbers of lichen specimens, which are increasingly used for a variety of studies. Specimens collected during the big research expeditions in the 19<sup>th</sup> and 20<sup>th</sup> century represent essential information about the application of names. In some cases, these specimens comprise the single known collection of a species. In today's taxonomic research, comparative DNA sequence analysis has become an invaluable tool for identifying and delimiting species. The DNA of old specimens, however, is expected to be variously degraded and challenging to sequence. Rarely, DNA from specimens collected more than 30 years ago are successfully sequenced, leaving many lichens in natural history collections unavailable for molecular phylogenetic studies. To address these challenges, we applied a two-step PCR protocol followed by sequencing on an Ion Torrent PGM to obtain DNA sequence reads from the mtSSU of lichen specimens collected up to 155 years ago. We tested the hypotheses that DNA quality of lichens depends on (1) time since collection, (2) taxonomic affinity, and/or (3) habitat/ecology. Age showed to be the prime cause for sequencing failure followed by taxonomic affinity. With the data at hand, we could not find statistically significant correlations between autecology and sequencing success. The applied protocol proved successful for sequencing specimens up to 150 years old.