A WINDOW TO THE PAST: CYANOBACTERIAL DIVERSITY AND BIOGEOGRAPHY IN HERBARIA SPECIMENS

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During the HERBA project, a pilot study of the past diversity and biogeography of cyanobacteria in polar and alpine regions (till ca. 100 years BP) was performed on cyanobacterial samples preserved in the Drouet herbarium, Smithsonian Institution, USA. Amplicons based on the 16S rRNA gene V3-V4 segment were used for High-throughput sequencing (HTS). In total, the diversity of 12 samples was obtained, of which 2 samples were sequenced both by the 454 pyrosequencing and Illumina (MiSeq, 2x300 bp) technologies. The 12 samples were collected from 1897 to 1964 in Antarctica, Alaska, Yellowstone Park, and Austrian, Swiss and American glaciers.

Both HTS technologies results were consistent and gave an identical dominant OTU.

For the 10 samples analysed by 454 pyrosequencing, we obtained 46,889 good quality cyanobacterial reads. They ranged from 67 reads to 16,434 reads per sample and 86 OTUs (threshold 99% 16S rRNA similarity) were obtained. All four samples analysed by Illumina sequencing gave at least about 20,000 reads after quality check.

Five of the 12 samples showed a complete identity between the morphological identification indicated on the label of the specimen and the dominant OTUs observed in the HTS sequencing data.

Three other samples could be considered as showing a congruence between the two types of identifications if the taxonomic label based on morphology could be adapted to modern classification, like the assumption that the morphotype of *P. laminosum* could correspond in fact to the sequence of *Leptolyngbya*, as found in the older specimen of 1898. Four other specimens do not show an agreement between the molecular diversity and the label.