ONCE UPON A TIME: CYANOBACTERIAL DIVERSITY AND BIOGEOGRAPHY IN HERBARIA SPECIMENS

Wilmotte, A.1, Pessi, I.S2, Velazquez D3, Durieu B4, Lara Y5, Laughinghouse H.D6

1. BCCM/ULC cyanobacteria collection, InBios Research Unit, University of Liege, Belgium; 2. Marine and Freshwater Solutions, Finnish Environment Institute (SYKE), Finland; 3. Department of Biology, Universidad Autonoma de Madrid, Spain; 4. InBios, University of Liege, Belgium; 5. Early Life Traces and Evolution, UR Astrobiology, University of Liege, Belgium; 6. Agronomy Department, Ft. Lauderdale Research and Education Center, University of Florida - IFAS, Florida, USA.

During the FNRS 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 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). The 12 samples studied were collected from 1897 to 1964 in Antarctica, Alaska, Yellowstone Park, and Austrian, Swiss and American glaciers. 2 samples were sequenced both by the 454 pyrosequencing and Illumina (MiSeq, 2x300 bp) technologies that gave an identical dominant OTU.

For the 10 samples analysed by 454 pyrosequencing, 86 OTUs (threshold 99% 16S rRNA similarity) were obtained.

Five of the 12 samples showed a complete identity between the name 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. Four other specimens do not show an agreement between the molecular diversity and the label.