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Intra-seasonal trends of cryoconite bacterial communities on an Alpine Glacier

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In the current context of climate change, the study of cryospheric environments is becoming increasingly important. While it was originally believed that these natural systems were unable to support life, it is now well known that they represent microbial biodiversity hot spots. To better understand the dynamics and drivers that regulate the cryospheric microbial communities inhabiting cryoconite holes throughout the melting season, 60 samples were collected from an alpine glacier (Jamtalferner, Austrian Alps), consisting of sediment and supernatant water from June to September 2022. The present study harnesses the power of long-read Nanopore 16S rRNA sequencing, flow cytometry for cell counting in supra-glacial water, and a technique for estimating bacterial productivity of cryoconite sediment based on ^{3}H-Leucine incorporation.

The results of bacterial abundance and productivity showed numbers ranging from 64.000 (early July) to 300.000 cells/mL (early August). Levels of bacterial productivity were shown peaking in early June and early August (ranging from 10^{-8} - 10^{-5} gC/g ww·h), especially at the beginning of the season and during late July - early August, but, unlike the community structure, they suggest no distinctive trends. On the other hand, the significance of the observed trends in microbial ecology was investigated by means of Generalized Linear (Mixed) Models. It revealed a globally increasing diversity along the season for all alpha diversity indices, and a strong presence of cyanobacteria, mainly belonging to the family Leptolyngbyales, which decreased along the season in favor of Proteobacteria (*Polaromonas* sp.) and Bacteroidetes (fam. Chitinophagaceae). This highlights a fully-fledged ecological succession despite the harsh environmental conditions and the relatively short intra-seasonal time frame.

The ongoing climate change scenario represents a clear threat to the communities inhabiting the supraglacial environments due to the faster ice melting rates observed on low altitude glacial tongues. While the long-term repercussions are somewhat difficult to envision and quantify, what we currently know is that the (deriving) functional losses encompass different aspects, such as carbon fixation by cyanobacteria (estimated in the tens of thousands of tons worldwide for non-Antarctic cryoconites alone). Also, bacteria are able to degrade persistent organic pollutants from agricultural use like pesticides, or, more generally, to handle a variety of compounds as growing substrates, due to the otherwise environmental scarcity they are subjected to. In this sense, along with the ice, a plethora of filter ecosystems are quickly disappearing. The natural continuation of

our study is to directly analyze the expressed activities compared to the genomic potential shown by these communities (genomics versus transcriptomics), extending the field of application to extreme latitudes (East Antarctica). Finally, to pinpoint the provenance of the various components of the aforementioned communities, sampling the bioaerosols insisting on these glacial areas and backtracking the air masses' trajectories will provide us with the last piece of the puzzle, to understand the assembly processes that lead to the observed ecological configurations.