



Bacteria at glacier surfaces: microbial community structures in debris covered glaciers and cryoconites in the Italian Alps

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Supraglacial debris has an important role in the glacier energy budget and has strong influence on the glacial ecosystem. Sediment derives generally from rock inputs from nesting rockwalls and are abundant and continuous at the surface of debris-covered glaciers (i.e. DCGs; glaciers where the ablation area is mainly covered by rock debris) and sparse and fine on debris-free glaciers (DFGs). Recently, evidence for significant tongue darkening on retreating debris-free glaciers has been drawing increasing attention.

Fine particles, the cryoconite, are locally abundant and may form cryoconite holes that are water-filled depressions on the surface of DFGs that form when a thin layer of cryoconite is heated by the sun and melts the underlying ice. There is increasing evidence that cryoconite holes also host highly diverse microbial communities and can significantly contribute to global carbon cycle. However, there is almost no study on microbial communities of the debris cover of DCGs and there is a lack of data from the temporal evolution of the microbial communities in the cryoconites. To fill these gaps in our knowledge we characterized the supraglacial debris of two Italian DCGs and we investigated the temporal evolution of microbial communities on cryoconite holes in DFG.

We used the Illumina technology to analyse the V5 and V6 hypervariable regions of the bacterial 16S rRNA gene amplified from samples collected distances from the terminus of two DCGs (Miage and Belvedere Glaciers - Western Italian Alps). Heterotrophic taxa dominated bacterial communities, whose structure changed during downwards debris transport. Organic carbon of these recently exposed substrates therefore is probably provided more by allochthonous deposition of organic matter than by primary production by autotrophic organisms. We used ARISA fingerprinting and quantitative PCR to describe the structure and the evolution of the microbial communities and to estimate the number of the total bacteria and the copy of Rubisco genes found on cryoconite holes collected on a wide Italian DFG (Forni Glacier - Central Alps).

The structure of the microbial communities in cryoconite holes seem to be determined mainly by a turnover process.

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