# Distribution of prokaryotic communities in different compartments of an alpine rock glacier-pond system

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Rock glaciers (RGs) are slow-flowing mixtures of rocks and ice, representing one of the most common geomorphological features in high-elevation alpine environments. Due to their ubiquity and their capability to chemically and physically influence waters passing through them, RGs have recently become targets for studies on permafrost thawing and its effects on alpine headwaters. However, little attention has been paid so far to microbial communities inhabiting both RGs and connected water bodies, although their fundamental role in nutrients mobilization and availability has already been assessed in subglacial and permafrost ecosystems.

In this study, we follow a 16S rRNA-targeted sequencing approach to explore the microbial ecology of different compartments in an alpine rock glacier-pond system (Col d'Olen Rock Glacier Pond, Valle d'Aosta, Western Italian Alps). We consider lacustrine sediments, RG surface material and surrounding soil, in order to identify microbial markers potentially useful to give insights into the interactions among the three ecosystems (sediment-RG-soil).

A clear separation between communities belonging to different compartments was highlighted by beta diversity analysis for both Bacteria and Archaea and confirmed in terms of archaeal community composition. Conversely, considering the bacterial community, lacustrine sediment samples showed more similarities with RG surface material than with soil, both in terms of number of shared OTUs and taxonomic composition. In particular, sediments and RG material were characterized by higher proportions of *Betaproteobacteria*, *Anaerolineae*, *Gemmatimonadetes* and *Nitrospira* than soil and lower percentages of *Acidobacteria* and *Alphaproteobacteria*. However, the majority of the OTUs were shared among all the compartments.

These results outline how, in our model system, archaeal and bacterial communities follow different distribution patterns in the three compartments, suggesting Bacteria, in particular classes like *Gemmatimonadetes* and *Betaproteobacteria*, as a suitable target for further studies focused on RGs influence on connected water ecosystems and microbial-driven processes occurring at the rock-ice-water interface.