



First insights in bacteria diversity in headwaters emerging from Alpine rock glaciers.

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Abstract

Global warming exerts particularly pronounced effects on the European Alps. As the thawing rates of mountain permafrost ice is lower than for glacier ice, a shift from glacial/periglacial to paraglacial/periglacial dynamics is predicted for Alpine landscapes during the 21st century in relation to deglaciation. Poor knowledge exists on chemical and biological features of waters emerging from Alpine rock glaciers. A set of glacial- or permafrost-fed headwaters was investigated in the Eastern Italian Alps, aiming at exploring bacterial community composition and diversity in epilithic biofilm and sediments. Bacterial assemblages show significant differences according to water and sample type, and to catchment geology. Rock glacier-fed waters show enhanced conductivity and trace element concentrations, and their highly diverse bacterial assemblages significantly differ only from those of glacial streams. Further research will better outline the role of environmental features in modulating bacterial diversity of Alpine headwaters affected by progressing deglaciation.

Keywords: Alpine permafrost, glaciers, water chemistry, bacterial finger-printing, biofilm, surface sediment.

Introduction and Methods

Glacier retreat is a major effect of current global warming and 80-100% of the Alpine glaciers is predicted to vanish in the next few decades (Zemp *et al.*, 2006). As the thawing rate of permafrost ice is 10-100 times lower than for glacier ice, more subsurface permafrost ice will remain than surface glacier ice, and a shift from “glacial/periglacial to paraglacial/periglacial dynamics” is predicted for mountain landscapes in the next few decades (Haeberli *et al.*, 2017). Although rock glaciers (RG) are a common landform of mountain permafrost, both chemical and biological features of waters emerging from them are still poorly known (Thies *et al.*, 2013).

This work aims at characterizing the bacterial diversity in biofilm and sediments of Alpine headwaters directly affected by active RGs, and at exploring possible differences respect to headwaters of different origin. A headwater set (2027-2900 m a.s.l.) was surveyed in autumn 2016 (during base-flow conditions) in three metamorphic catchments of the Eastern Italian Alps

(EIA, Table 1). The water samples were analyzed for temperature, turbidity, pH, major ions, nutrients, and trace elements. Environmental DNA from epilithic biofilm (EPI), surface and deep sediment (SS: 0-2 cm depth, SD: ~5-10 cm) was extracted and analyzed by high throughput sequencing (MiSEQ Illumina) using the specific variable region V4 of 16S rRNA gene. Bioinformatic analyses were performed using the MICCA pipeline (Albanese *et al.*, 2015).

Table 1. Location, dominant geology, and number of headwaters sampled in the EIA in autumn 2016.

Range	Sub-catchment	Geology	nGL	nREF	nRG
Ortler	SU	Sc, Gn	2	0	2
Cevedale	MR	Gn, Sc	1	2	4
Presanella	AM	Gr	1	1	3

SU, MR, AM: Suldien, la Mare, Amola Valley, resp.: Sc, Gn, Gr: scists, orthogneiss, granite, resp. nGL, nREF, nRG: number of glacier-, rock glacier- and mainly precipitation-fed waters, resp.

Results and Discussion

RG-fed headwaters in MR and SU stand out for their low water temperature ($\leq 1^\circ\text{C}$), low turbidity (< 10 NTU) and higher electrical conductivity ($118\text{--}516 \mu\text{S cm}^{-1}$ 20°C) with respect to GL and REF waters in the same catchments (means 26 and $106 \mu\text{S cm}^{-1}$, respectively). All AM waters show very low conductivity ($11\text{--}19 \mu\text{S cm}^{-1}$) in relation to the granitic bedrock. All waters are poor in reactive P ($2\text{--}5 \mu\text{g L}^{-1}$), while $\text{NO}_3\text{--N}$ and SiO_2 are very low in the GL waters ($< 100 \mu\text{g L}^{-1}$ and $< 1 \text{ mg L}^{-1}$, resp.). All GL streams show high levels of total P ($70\text{--}428 \mu\text{g L}^{-1}$) and N (up to $\sim 4 \text{ mg L}^{-1}$), and varying levels of Fe ($17\text{--}250 \mu\text{g L}^{-1}$) and Al ($19\text{--}255 \mu\text{g L}^{-1}$). RG waters of MR and SU are enriched in Sr ($82\text{--}315 \mu\text{g L}^{-1}$), Ni ($12\text{--}60 \mu\text{g L}^{-1}$), As ($6\text{--}31 \mu\text{g L}^{-1}$).

The α -diversity of the bacterial assemblages in terms of number of observed OTUs and Shannon index (Fig. 1a-b, respectively) is much higher in both the SD and SS samples of the RG and REF streams. On the contrary, the epilithic samples do not show significant differences in bacterial diversity. The first three principal coordinates (PCo) based on weighted UniFrac distances outline significant differences (Wilcoxon rank-sum test with Bonferroni correction, $p < 0.001$) in 16S bacterial composition according to substrate type (PCo1), water origin (PCo2), and, to less extent, geographical location (PCo3, Fig. 1c).

The GL bacterial peculiarity is due to the co-dominance of Proteobacteria and Actinobacteria, followed by Bacteroidetes. Acidobacteria replace the last two phyla in RG samples. Epilithic samples from all water types show higher abundance in Cyanobacteria, while the geographical separation only produces rearrangements in the abundances of a few ubiquitous major phyla. Preliminary correlation analyses revealed significant relations between the abundance of several bacteria taxa and water turbidity, $\text{NO}_3\text{--N}$, SiO_2 , and metal concentrations.

The absence of significant differences between bacterial assemblages of RG-fed and mainly precipitation-fed REF waters suggests that chemical traits of RG-fed waters are not sufficient to select specific bacterial assemblages. In addition, further environmental variables need to be considered in future investigations of Alpine headwaters affected by permafrost degradation.

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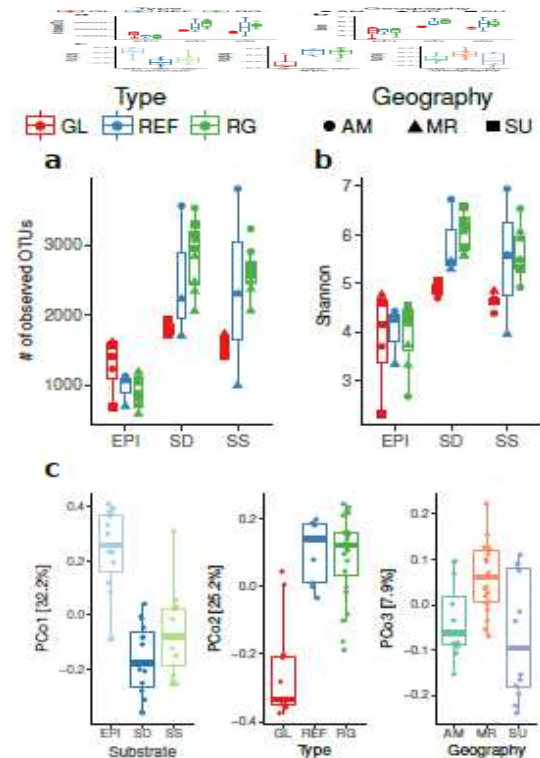


Figure 1. Number of observed bacterial OTUs (a) and Shannon Index values (b) in the sample collected from the headwater studied. (c) The first three principal coordinates (PCo) based on the weighted UniFrac distances outline differences in 16S bacterial composition between different substrates, water types, and sampling sites. Abbreviations as in Table 1.

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