BACTERIAL AND ALGAL COMMUNITIES OF CRYOCONITE, DIFFERENCES BETWEEN ANTARCTICA AND THREE ALPINE GLACIER (MORTERATSCH, FORNI, AND ADAMELLO)

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Introduction: Glaciers represent harsh environments rich in life and are the largest reservoir of fresh water. Their study can be interesting for astrobiologists because water exists in the form of ice on many locations in the Solar System, from icy moons (like those of Jupiter and Saturn) to the craters of Pluto. Astrobiologists can thus gain insight into where we might find habitable environments by studying the mechanisms used by psychrophiles (organisms adapted to live in cold conditions) on Earth to survive extreme cold. On glaciers we can find different habitats, among which the habitat of cryoconite is probably the most teeming with life. Cryoconite is a granular sediment found on glacier surfaces composed of a mixture of minerals and organic materials, including bacteria and algae. It plays important roles in biogeochemical cycles and in lowering the albedo of a glacier surface [1], [2]. The heating of accumulated low-albedo particles (e.g., cells, dust, and minerals) brings the surrounding ice to melt, producing characteristic holes in the ice filled with liquid water and cryoconite itself (Fig. 1.). Such cryoconite holes are oases of microbial diversity on glaciers [3]. In addition, algae seem to contribute to a microbially driven reduction of glacier albedo because of algal blooms [4]. This contribution comes from the production of dark pigments by algae as a screening mechanism when exposed to high-intensity radiations typical of glacial environments. The associated darkening blooms can thus develop at the surface of glaciers and cover wide areas, involving both ice and snow [5]. While on ice and snow, we can easily recognize algal blooms, little is known about the presence of microalgae in cryoconite. Albedo reduction is both a cause and a consequence of biological activity. Indeed, one the one side the production of pigments and the aggregation of organic material decreases the albedo, on the other the reduced albedo provides liquid water availability and therefore life proliferation.

The aim of this study is to investigate the biodiversity of the bacterial communities in the cryoconite habitat of Antarctic blue ice fields (Hells Gate Ice Shelf, Nansen Ice Shelf, Priestley glacier, and Tarn Flat) and to compare them with the ones of three Alpine glaciers (Forni, Adamello, and Morteratsch). The algal community will be also characterized on Morteratsch and on the Antarctic glaciers [6]. With our results on the microbial communities in cryoconite holes we would like to answer two main questions: are cryoconite holes the reservoir and refugium from where algae initially spread during blooms of algae?

What are the differences between microbial communities in cryoconite holes on Antarctic and Alpine glaciers? To this aim, we used high-throughput sequencing of the 16S and 18S rRNA genes to describe the bacterial and algal community compositions respectively.

Expected results: The bacterial communities of cryoconite holes from Alpine glaciers have already been described, showing that the most abundant taxa are similar regardless the considered glacier. The comparison with the Antarctic environment, where seasonality is less pronounced and the environmental conditions are completely different, could provide more information on which factors promote the establishment of specific communities.

Fig. 1. Example of cryoconite holes.

Materials and methods: Cryoconite material was collected from cryoconite holes. Samples collection was carried out on the Forni Glacier (46°12’30’’ N, 10°13’50’’ E – July and August 2016), on the Adamello Glacier (46°09′22.06″N 10°29′46.9″E), and on the Morteratsch Glacier (46°24′34″N 9°55′54″E - 2016), in the Alps. And on the Nansen Ice Shelf (-74°50’5.66’’S; 163°5’2.02’’E) in Antarctica. Then in the laboratory we performed DNA extraction and characterized the communities with Illumina sequencing, and multivariate analyses.

Results and discussion:

So far, we characterized the bacterial communities of the three Alpine glaciers. As is shown in Fig. 4, one of the most abundant orders on all the three glaciers is the Oligoflexales (phylum Proteobacteria), which consists of filamentous bacteria.

Fig. 2. Sampling sites on the Alps: Morteratsch Glacier (Switzerland), Forni Glacier (Italy), Adamello Glacier (Italy)

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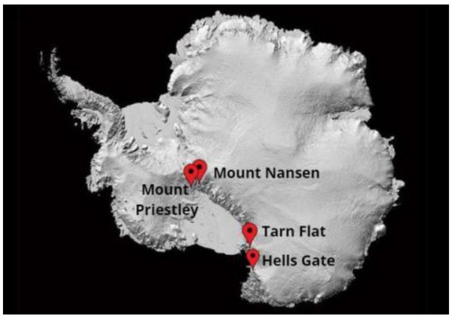

Fig. 3. Sampling sites: Nansen Ice Shelf (Antarctica).

On the Forni glacier there is a high relative abundance of Leptolyngbyales (phylum Cyanobacteria) and Sphingomonadales (phylum Alphaproteobacteria). On the Morteratsch glacier there is a high relative abundance of Holophagales (phylum Acidobacteriota) and Myxococcales (phylum Proteobacteria). On the Adamello glacier there is a dominance of Leptolyngbyales (phylum Cyanobacteria) and a high relative abundance of Oligoflexales (phylum Proteobacteria) (Fig. 4.).

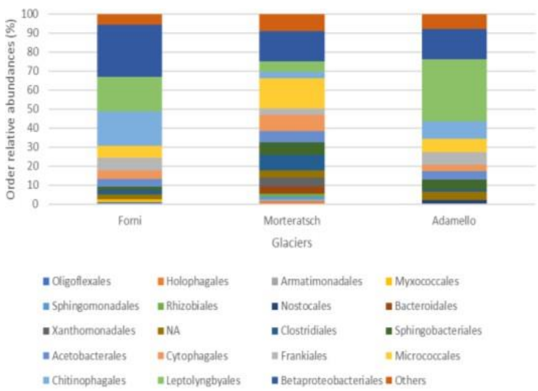

Fig. 4. Barplot showing the order relative abundances of the Forni, Morteratsch, and Adamello Glaciers. Orders less abundant than 1 % were grouped in "Others".

Results from literature show that these orders are present on glaciers in different areas around the world (e.g., the Himalaya, Andes, Alps, Arctic, and Antarctica) [7], [8], [9].

Despite some similarity, our first results about Alpine glaciers showed that the three communities differ significantly from each other as can be seen in Fig. 5.

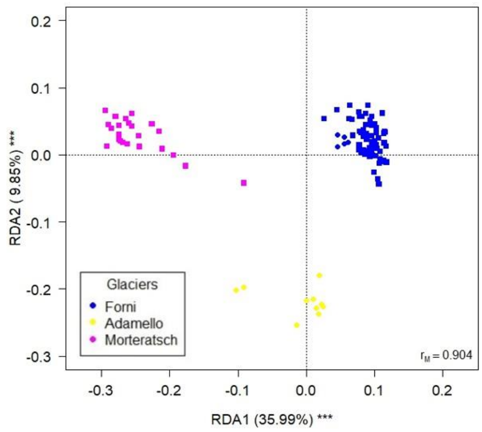

Fig. 5. Biplot from RDA on Hellinger-transformed bacterial ASVs on three different glaciers. The proportional amount of variance explained by each axis is reported. rM is the Mantel correlation coefficient between the distance among points in the graphs and the Hellinger distance between communities, Values close to 1 indicate that the graph can accurately represent the ecological distances among communities.

These results provided evidence that bacterial communities differ significantly also between geographically close glaciers of the same mountain chain. When data about Antarctica will be available, it will be possible to address biogeographical patterns at a larger scale and relate them to the glaciological contexts of polar and mountain glaciers.

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