Diversity and microbe-mineral interaction in microbial mats of extreme environments: NE Antarctic Peninsula lakes

Introduction

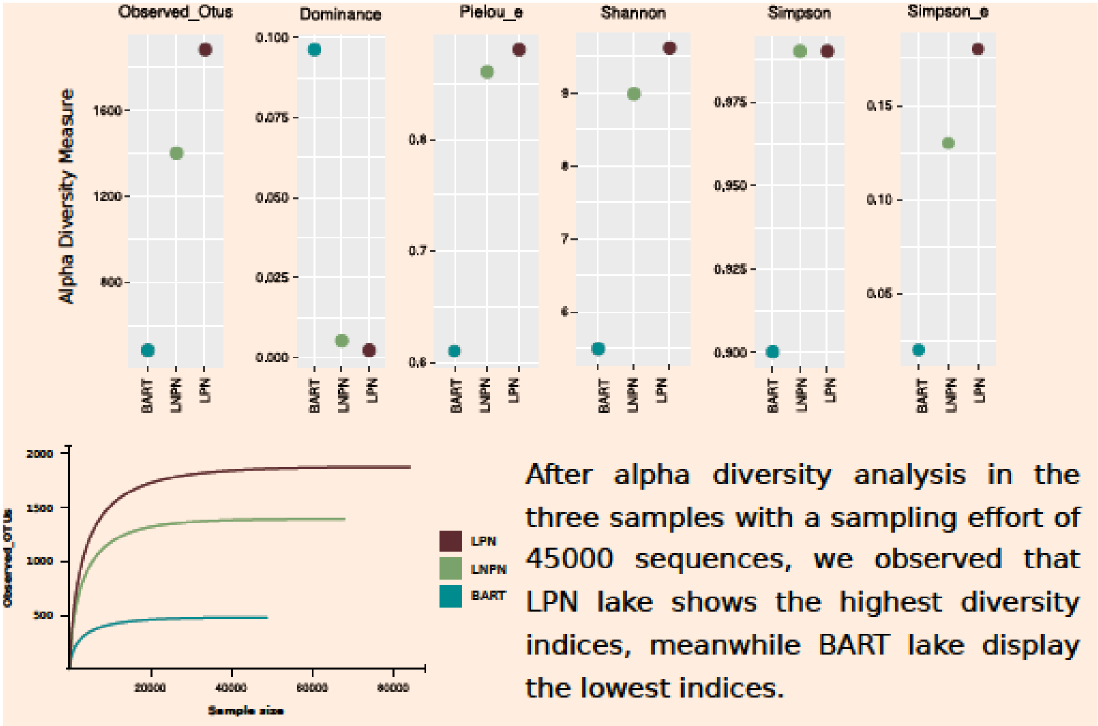
Microbial mats are dynamic and complex ecosystems exhibiting spatial and temporal heterogeneity. The Antarctic benthic areas that receive sufficient solar radiation are covered by microbial mats composed primarily of cyanobacteria, diatoms and bacteria [1-3]. These mats date back to the early Archaean: many of the major steps in early evolution probably took place at this point [4]. For thousands of years these microorganisms were challenged to extreme conditions, such as low temperatures, freezing-thawing periods, UV-irradiation, desiccation and changeable light conditions, salinities and nutrient concentrations [5-6]. In this context, many of them develop adaptations like anti-freeze proteins, cold-adapted enzymes, dehydration and salt tolerance. [7-9]. In consequence potential microorganisms belonging to endogenous taxa, as well as other not identified organisms can still be discovered [10-11]. This research plan is focused in the James Ross and Vega islands lakes (Antarctic Peninsula). The terrestrial vegetation in this region is limited to lichens and bryophytes, whereas microbial benthic mats are composed of algae and cyanobacteria [12]. However, no studies of the microbial diversity -using high-throughput sequencing technologies as well as the analysis of mineral precipitation and fossil mats record in these lakes- have been conducted.

The aim of this project was to characterize the microbial community of lakes from James Ross and Vega islands and the study of subfossil microbial mats and their association with mineral precipitates.

Results

The study area is located in James Ross archipelago, in the NE of Weddell Sea. Microbial mats samples were obtained from sediments of three fresh water systems: BART lake is located in Vega island (63°58’03,30”S- 57°54’02,10”W) meanwhile Pan Negro (LPN) and Norte Pan Negro (LNPN) lakes are located in Lamb Cape, Vega Island (63°52’04,60”S - 57°37’12,60”W and 63°52’02,10”S - 57°37’25,20”W, respectively). Geochemical parameters were measured in each sampling sites in a campaign field from 2014; besides, the samples for metagenome sequencing where keep it at -20 °C until used.

DNA extraction was performed using a DNeasy Power soil (Qiagen) kit, and the amplicon sequences of the 16S gen of the RNAr was analyzed by Illumina Miseq. The sequences annotations data were analyzed with Qiime2. Over 385.984 sequences considered the following richness and diversity indexes were calculated (Figure 1).



After alpha diversity analysis in the three samples with a sampling effort of 45000 sequences, we observed that LPN lake shows the highest diversity indices, meanwhile BART lake display the lowest indices.

Figure 1: Microbial diversity indexs

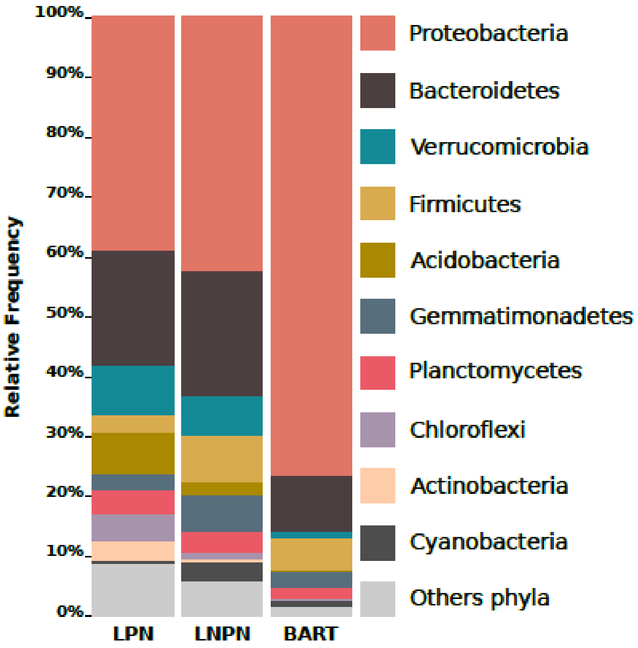


Figure 2: Proteobacteria is the prominent phylum, with 42.6% for LPN, 42.7% for LNPN and 78.3% for LB. Besides, Bacteroidetes,Verrucomicrobia, Planctomycetes and Cyanobacteria were also observed.

Figure 2 summarizes a general phylum-level diversity found in each microbial mat

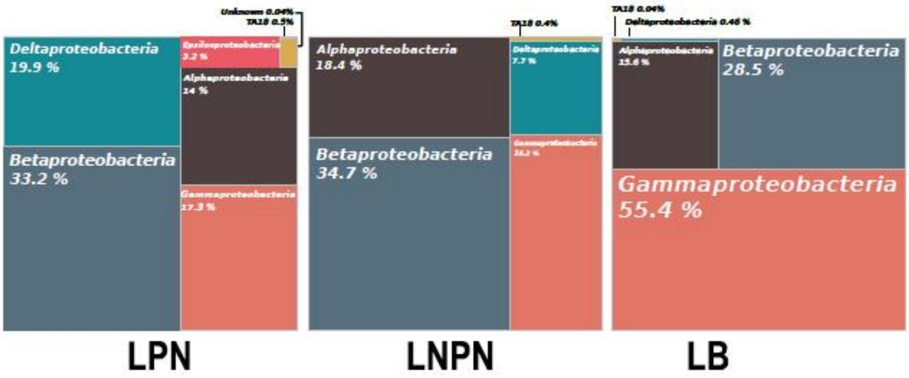


Figure 3: Inside the Proteobacteria phylum, Gammaproteobacteria, Betaproteobacteria and Alphaproteobacteria were the most abundant for LB; Betaproteobacteria, Alphaproteobacteria y Gammaproteobacteria for LNPN and for LPN Betaproteobacteria, Alphaproteobacteria, Deltaproteobacteria y Gammaproteobacteria respectively. Besides, Epsilonproteobacteria was also observed only in this lagoon. This observation was also corroborated by Fluorescence in situ hybridization with probes specially design for the detection of Alphaproteobacteria, Betaproteobacteria, Deltaproteobacteria and gammaproteobacteria.

In a first approximation to the relation microorganisms-mineral precipitation, we analyzed the microbial mats by electronic microscopy (SEM-EDS) and X ray diffraction (DRX). SEM analysis showed that all the lakes where very similar in its composition, except for LB where acicular forms of iron and phosphorous were observed (Figure 4C). Besides, in all the images an expolimeric substances (EPS) surrounding the minerals were detected, plus diatoms, most pennals, and some filamentous microorganisms that could correspond to cyanobacterias. The DRX analysis showed a similitude between all the lakes except for LB where sodium aluminum silicates were also observed.

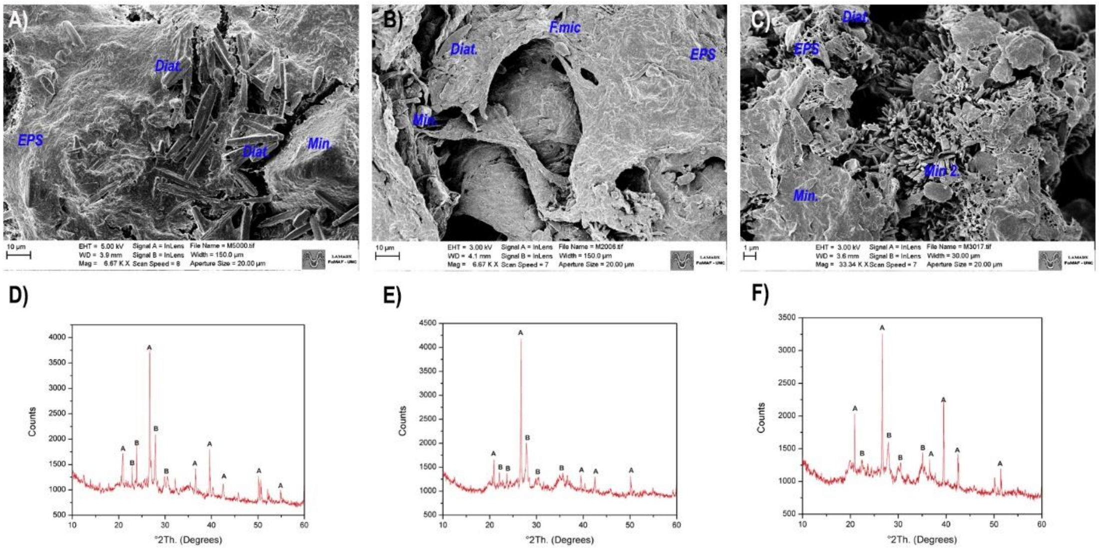


Figure 4: SEM and DRX images respectively, A and D correspond to LPN, B and E to LNPN and finally C and F to LB. A and B for DRX graph correspond to silicates, oxides and silicates of aluminum

Future

All this results are still in develop with focus to the mineral interaction, the next step is go to confocal microscopy and make Fluorescence in situ hybridization and the detection of the possible bacteria associated to the minerals forms. Besides, we already isolated two strains of cyanobacteria from LPN and LB, so next step will be to identify and see if could correspond to a new species and to make some in vitro experiments related to UV expositions. This results are going to be presented in the First Latin-American ISME meeting, in Chile (11-13 of September).

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