PROFILING MICROBIAL BIOMARKERS IN CHANGING LAKES IN DEGLACIATION AREAS.

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Introduction: With global temperature rising, ice retreats and thins worldwide. Glacial lakes are highly sensitive markers of environmental variability, and especially vulnerable to climate change as dissolved organic carbon (DOC) concentration is strongly affected by lower and more acid precipitations, increased temperature and snow melting [1]. Early in the deglaciation (phase 1), the high silt content of water provides protection from UV. With time, as meltwater discharge and sediment load decrease, transparency and UV levels increase in the water column (phase 2), creating an optical environment detrimental to plankton and limiting biodiversity [2]. Oligotrophic water is a main feature of glacial Andean lakes, with low organic carbon and microbial biomass. Although some works have reported on the microbial content, photosynthetic activity or geochemistry of the water column of these lakes [3], very little is actually known about the sediments of these changing lakes.

Objectives: Understanding the sedimentation as well as the geomicrobiological processes associated to it may give us clues on the evolution of these important ecosystems, from the standpoints of ecology and as analogue for deglaciation processes in other planetary bodies. Our objective is to investigate whether there is any particular microbial succession or biomarker profile in the sediments or water column associated to the different phases of deglaciation.

Methods: As part of the NASA-ASTEP funded Planetary Lake Lander (PLL) project, we sampled and investigated the microbial and molecular biomarkers in the sediments and the water column from two oligotrophic Andean lakes: Laguna Negra and Lo Encañado (Región Metropolitana, Santiago, Chile). The biomarker and microbial profiling were obtained on site and in the laboratory by using LDChip, an antibody microarray-based biosensor [4,5]. Current LDChip contains 450 antibodies produced to whole microbial strains (archaea and bacteria), extracellular polymers, environmental extracts from terrestrial analogues, proteins and peptides. The study was complemented with geochemical analysis as well as DNA sequencing for microbial diversity.

Results: Samples of sediments from the shore and lakebed at different depths, as well as samples from the water column (0, 5, 10 and 20 m depth) were collected during the 2011 and 2012 field campaigns. On site and laboratory analysis by sandwich microarray immunoassays with LDChip allowed us to detect different microbial markers from sulfate reducing bacteria, methanogenic archaea and exopolymeric substances from Gammaproteobacteria. We also detected members of different cyanobacterial genera (Figure 1), showing changing pattern along the water column. Sequencing the bacterial and archaeal 16S rRNA gene confirmed and expanded the immunological results by detecting Alpha, Beta, Gamma, and Deltaproteobacteria, as well as cyanobacteria and methanogenic archaea.

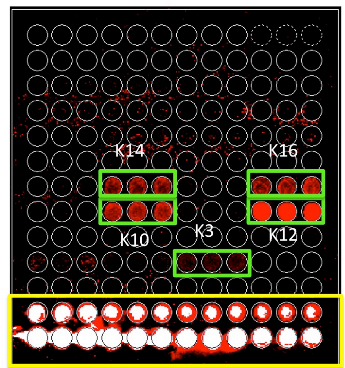

Figure 1. Cyanobacterial biomarkers by LDChip at 5 m depth at Lo Encañado: K3, *Mycrocystis* sp.; K10, *Leptolyngbya* sp. ; K12, *Aphanizomenon* sp.; K14, *Anabaena* sp.; and K16, *Tolypotrix* sp.

Geochemical analysis by Ion Chromatography showed an unexpected concentration of sulphate (SO4=) and chloride (Cl-) anions in some of the sediment samples. Although Laguna Negra is an oligotrophic lake, the results suggest a rich microbial diversity with active sulfate reduction and methanogenic activities in its shore and shallow sediments. Sedimentation of sulfate-rich deposits from the surrounding volcanic terrains during the fist deglatiation phase may explain the observed microbial pattern. Our results constitute a starting reference for monitoring deglatiation process through the microbial biomarkers in the sediments and the water columns in these Andean lakes, and a proxy to understand similar events in other planets.

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