Poster presentation

Competition poster

Planktonic community of southern Chile lakes: Phytoplankton, zooplankton and bacteria

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In this study we focused on evaluating the planktonic eukaryote and bacterial community structure in less studied south Chilean lakes (51-53°S) during the austral summer month of January (2016). At the present scenario of climate change, the climate-related environmental factors together with the spatial location of the lakes structuring these communities were studied. The study was carried out using Illumina based high-throughput sequencing (MiSeq) of hypervariable regions V1-V3 and V4 of 16S and 18S ribosomal RNA (rRNA), respectively, to access the community structure and distribution pattern of bacteria and eukaryotes in 27 littoral samples from southern Chile lakes. The samples were selected based on their position on the latitudinal scale, and to a span of wide environmental gradients across 27 lakes.

Sequenced data of these samples revealed the dominance of green and golden microalgae along with dinoflagellates phytoplanktonic communities, Arthropoda-Crustacea (Calanoid copepod and Ostracoda species Notodromas monacha) zooplanktonic communities, and Bacteroidetes, Actinobacteria, Cyanobacteria, Proteobacteria and Verrucomicrobia bacterial communities, which correlated with previous microscopy and denaturing gradient gel electrophoresis (DGGE) -based observations. Variation partition analysis revealed that the littoral planktonic communities are influenced by both environmental and spatial factors, among which temperature, electric conductance (salinity) and turbidity are of major importance. These three groups of environmental variables have previously been shown to change drastically in glacial settings.

Together, these results have obvious importance in the assessment of biodiversity changes in changing climatic conditions and calls for a continuous assessment of the unique though an understudied region of southern Chile.

Keywords: Phytoplankton; Zooplankton; Bacterial community; High-throughput sequencing; Quantitative ecology; Southern Chile lakes