THE GREAT DIVERSITY OF MICROORGANISMS PRESENT IN NIVAL LAKES ALLOWS THE COMMUNITY TO RAPIDLY ADAPT TO ENVIRONMENTAL CHANGES

M. Yuhana, G. Iqbal and K. Hanselmann

University of Zürich, Microbial Ecology Group, Zollikerstr. 107, 8008 Zürich www.microeco.unizh.ch

We are studying the planktonic microbial communities in Jöri Lake XIII (2640 m), an ecologically young high-mountain lake, and discovered new groups of prokaryotes as well as interesting seasonal population changes by analyzing 16S-rRNA-gene sequences of bacteria and following algal populations microscopically.

Aquatic ecosystems in the nival zone experience variable environmental conditions. They change seasonally between freezing temperatures in winter to diurnal temperature fluctuations between 0°C and 15°C in the summer, between long periods of darkness at greater water depths while the lake is ice covered to strong UV radiation during ice melt in the height of summer, and between nutrient deprivation during stratification in winter and mesotrophic conditions in late fall.

Temporal Temperature Gradient Gel Electrophoresis (TTGE) of PCR-amplified 16S-rDNA was used to monitor the microbial populations and their seasonal dynamics at different depths in the water column. Cloning of 16S-rRNA genes from total community DNA and sequencing them allowed us to genotypically identify the clones which revealed dominant TTGE bands.

TTGE using 600 bp fragments of 16S-rRNA gene sequences turned out to be a powerful tool for the analysis of the planktonic community structure. While the lake was stratified it yielded distinct banding patterns for different depths. TTGE profiles of samples taken during summer up-welling events indicated identical patterns over the entire water column. The TTGE patterns from total community DNA were compared with the library of cloned 16S-rDNA fragments in order to identify population migration of predominant species. The majority of the TTGE bands were well represented by fragments from the gene library. Out of 45 TTGE bands, 32 were unique whereas the remaining 13 were strains present during more than one sampling period.

Sequence analysis of 38 TTGE bands showed 88 to 99% similarity to16S rRNA gene sequences present in the RDP and ARB databanks. 15 of those belong to newly discovered bacteria. Cluster analysis revealed that the predominant bacteria belong to five phylogenetic groups: Actinobacteria, Verrucomicrobia, Planctomycetes, Proteobacteria ($\propto$-, β-, and δ-group), the candidate division BD and to chloroplasts of a unicellular green alga. The highest bacterial diversity stems from the group of the β-Proteobacteria which also showed the highest seasonal dynamic in Lake Jöri XIII.