MICROBIAL SNOW PACK COMMUNITIES: IDENTIFICATION AND PHYLOGENETIC RELATIONS

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In spring, snow surfaces sometimes turn pink or golden brown due to mass developments of pigmented microorganisms. How can microorganisms thrive under the extreme conditions near the triple point of water and what are their nutrient sources? Snow is an oligotrophic ecosystem, which imposes extremes of dryness and temperature. No growth can take place at temperatures below freezing, but it will resume when snowmelt begins. Resting stages quickly turn into vegetative cells, which propagate into large populations once liquid water becomes available. The changing conditions - freezing at night and thawing during the day – still pose challenging conditions for survival, however. It is of ecological and biotechnological interest to investigate the microbial populations of the snow habitat, to find out where they come from and to study their living strategies.

We report on the microbial community composition in snow and air in high mountain environments. The study sites were located at Jungfraujoch (3500m) and at Jöri Lake XIII (2640m).

Snow samples were collected aseptically at different depths in the snow pack at Jungfraujoch. Coloured surface snow was sampled in May 2003 on Jöri Lake XIII. For air sampling, a defined volume of air was drawn directly onto a nutrient agar plate or through a filter. Snowmelt water was filtered and DNA was extracted from the residues on the filter.

Community composition was analysed by characterizing rRNA-genes amplified from total genomic DNA employing the Polymerase Chain Reaction (PCR) with universal (0519s-1392as), archaeal (0089s-0915as), bacterial (0008s-1524as) and eukaryotic (0008s-1512as) primer pairs. PCR products were separated by cloning and the restriction enzymes *Hae*III and *Hinf*I were used to analyse fragment length polymorphism (RFLP). DNA from clones with different RFLP patterns were selected for sequencing and sequences were compared using cluster analysis employing the Phylip program. The results are presented in the form of a phylogenetic tree based on comparison with sequence data available in the RDP and the ARB 16S rRNA gene libraries.

Most of the Archaea among the large variety of microorganisms found in the snow pack belong to the Crenarchaeota. One group branches off distinctly from all others. Predominant bacterial species belong to the subgroups Actinobacteria and Proteobacteria. Phylogenetically, the air isolates fall into the groups of the Proteobacteria, Bacteroides, Actinobacteria and Firmicutes. Air samples collected on plates yielded a number of microbes, which can be classified within the same groups. A sequence from a newly discovered air isolate from Jungfraujoch showing a similarity of 94% belongs to a Flavobacterium which has not been described before.