MICROBIAL SNOW PACK COMMUNITIES: IDENTIFICATION AND PHYLOGENETIC RELATIONS

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Discoveries

- A search for microorganisms in cold-extreme habitats (ice, snow) revealed an amazing number of known and new microorganisms.
- They are transported to high-altitude sites via the atmosphere together with dust particles.
- Some of them will multiply during snowmelt, others remain dormant but stay alive in newly formed ice (see poster P53 by S. Wüst et al.).

Introduction

Snow is an oligotrophic ecosystem characterized by extremes of dryness and low temperatures. How can microorganisms thrive under the extreme conditions near the triple point of water?
Here, we report on microbial community compositions in snow and air at Jungfraujoch (3500m a.s.l) and “red snow” at Jöri LakeXIII (2640m a.s.l).

Methods

Snow samples were collected at different depths in the snow pack at Jungfraujoch. Coloured surface snow was sampled in May 2003 close to Jöri Lake XIII.
(Fig.1 and Fig.2).

Fig.1: Snowfield at Jungfraujoch, were the samples were collected.

Fig.2:“Red snow“ Carotenoid-pigmented eukaryotic flagellates predominate.

Air samples were drawn directly onto a nutrient agar plate or through a filter. Community composition was analysed by characterising the rRNA-genes amplified from total genomic DNA employing PCR. Bacterial and archaeal primer sets were used.
PCR-products were separated by cloning and the restriction enzymes *HaeIII* and *HinfI* were used to analyse fragment length polymorphism (RFLP). DNA from clones showing different RFLP-patterns (Fig3.) were selected for sequencing and sequences were compared using cluster analysis employing the Phylip program available from RDP.
(http://www.rdp.cme.msu.edu/html)

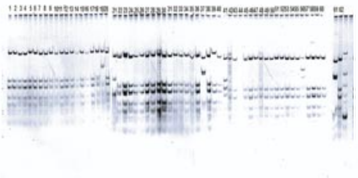
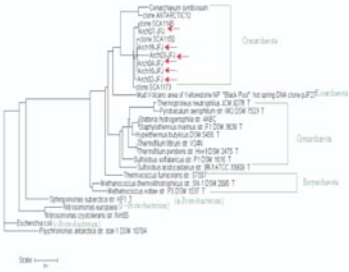


Fig.3: RFLP patterns of different clones.

Results

The snow pack on Jungfraujoch contained many *Archaea* which belong to the subgroup of the *Crenarchaeota.*
Most of the bacterial species belong to the subgroups *Actinobacteria* and *Proteobacteria* (Fig.4).

Archaea



Bacteria

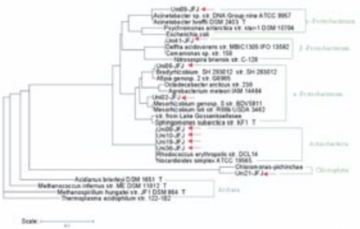


Fig.4: Phylogenetic trees based on clones of Archaea and Bacteria obtained from Jungfraujoch snow. Red arrows show the microorganisms present in the snow samples.

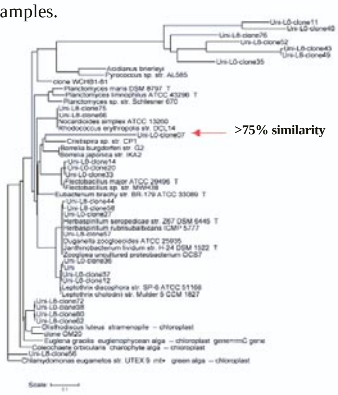


Fig.5: Phylogenetic tree of microorganisms present in „red snow“ near Jöri Lake XIII. The distinct cluster containing uni-L8-clone52 represents eukaryotes.

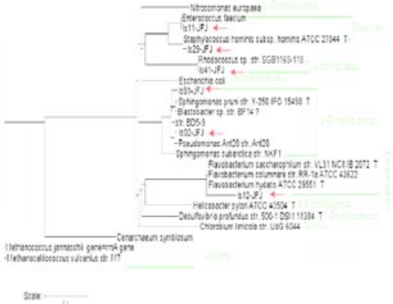


Fig.6: Phylogenetic tree based on clones obtained from air samples which were collected on Jungfraujoch. Red arrows indicate the microorganisms found in the air. The thick red arrow indicates a novel organism which has not been described before.

Conclusions

The clones found in air samples fall into the groups *Proteobacteria, Bacteroides, Actinobacteria* and *Firmicutes* (Fig.6).

A sequence from a newly discovered air isolate showing a similarity of 94% to the closest cultivated strain belongs to a Flavobacterium which has not been described before.

In the samples form Jöri Lake snow, a new group of microorganisms was found.