

# Antarctic cyanobacterial communities : baseline data on their diversity and distribution

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## Introduction

The permanent inhabitants of the Antarctic continent are mainly microorganisms. Among them, the cyanobacteria are the dominant phototrophs in aquatic and terrestrial ecosystems. Their highest biomasses are found in microbial mats (laminated biofilms) on the bottom and littoral zones of ponds and in meltwaters (Vincent, 2000).

As emphasised by the IPCC Working Group 2 report (2007) on 'Impacts, Adaptation and Vulnerability', there will be important impacts of climate change on the polar regions. These impacts will also affect the microbial communities that are very important components of these particular biotopes, where higher organisms are scarce due to the extreme conditions. In the lakes and terrestrial environments, the microorganisms are the main actors in photosynthesis, food chains and biogeochemical cycles. Due to the remote, unique and extreme conditions in the polar regions, they can be expected to have developed specific adaptations and to be endemic (present only in a limited area). Therefore, their biodiversity should be taken into account in the impact assessments and their role should be better understood.

## Sampling



Fig.1 - Location of the sampling regions



Fig.2 - Forlidas Pond in the Transantarctic Mountains

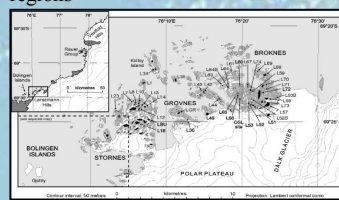


Fig.3 - Detailed view of lakes in Prydz Bay (Eastern Antarctica)

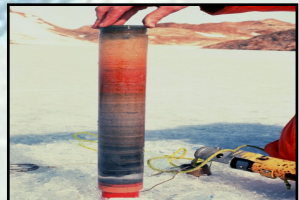


Fig.4 - Taking samples through the lake ice cover

Microbial mat samples were collected from 12 lakes and meltwaters located in 4 very different Antarctic regions: i) coastal lakes (freshwater and saline), in Eastern Antarctica (EA) ii) lake Fryxell in McMurdo Dry Valleys (DV), iii) meltwaters of the Antarctic Peninsula (AP) and iv) the Transantarctic Mountains (82°S) (TM)

## Conclusions

The higher cyanobacterial diversity in the DV, AP and non-saline EA lakes indicates that there is a gradient of stress severity, and that the selection is less harsh in coastal freshwater lakes and on the Peninsula than in the middle of the continent (TM) or in the saline lakes. This study allowed to us to obtain more information about the biogeographical distribution, through a genotypic approach for diversity study.

Constructing such a baseline data of characterised genotypes obtained from a large range of sites and regions is essential for the use of these communities in the future, as indicators of environmental changes, in the frame of long-term observations.

## Clone libraries

A 'cultivation-independent' approach, based on direct retrieval of sequences has been performed. The PCR-products (16S rRNA+ITS) obtained by amplification of the environmental DNA with the primer pairs 16S27F/359F and 23S30R (Taton et al. 2003, 2006) were cloned in *E. coli* and sequenced.

## Biogeographical distribution of cyanobacteria

A total of 831 new 16S rRNA gene sequences was obtained. The new sequences were compared to the already existing ones in the international databases. We defined OTUs (Operational Taxonomic Units) as group of sequences sharing more than 97,5% of similarity, thus corresponding to at least one bacterial genospecies. 79 OTUs were found. Results for the coastal lakes of low salinity in EA showed a high diversity (5 to 12 OTUs). Similar results were found for the Fryxell lake (DV) and the meltwaters (AP). In each new sample, 3 to 4 new OTUs were found on average. In contrast, saline lakes (EA) and the Transantarctic Mountains biotopes yielded a lower diversity

The relative abundance of each OTU in the clone libraries is detailed in fig. 5. The suffix 'Ant' indicates that the OTUs are found only in Antarctica, 'New' tags the OTUs that we are the first to find. The other OTUs were found outside Antarctica. Globally, about 2/3 of the OTUs seem to be endemic to Antarctica.

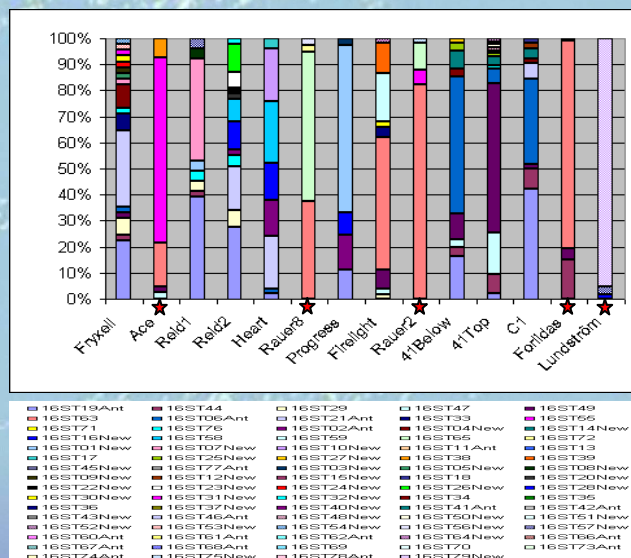


Fig. 5 - Histogram showing the relative abundance of each OTU in the clone libraries of the different lakes. The red star indicates hypersaline lakes (EA) and the Transantarctic Mountains' ponds (TM).