

# MICROBIOLOGY OF A SUBGLACIAL LAKE: THE LAKE VOSTOK

Ferran Romero Blanch

## INTRODUCTION:

Lake Vostok is the largest and deepest subglacial body of water in Antarctica. It has an area of 14000Km<sup>2</sup> and a volume of 5600Km<sup>3</sup>. Nowadays, it is accepted that it has been buried under glacial ice for 14-15 millions of years (Figure 1). Discovered between 1950 and 1960, it has been recently reported that it forms a complex ecosystem with both prokaryotic and eukaryotic microorganisms<sup>1,2</sup>.

The living forms here have evolved to survive in an extremely **oligotrophic, hyperbaric, cold and dark environment**.

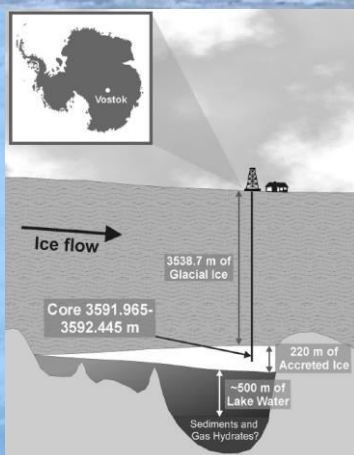


Figure 1. Location of lake Vostok under Antarctic glacial ice<sup>1</sup>.

## OBJECTIVES

The aim of the present review is to **describe the communities** present in a subglacial lake (the Lake Vostok).

It is also objective of this review to **describe the use of ice-binding proteins** as a method to survive in extremely cold environments.

### Main characteristics of Lake Vostok

**Temperature:** -2°C

**Pressure:** 350atm (as it is covered by a 4-kilometer-thick layer of glacial ice)

**Nutrient availability:** very slow

**Light:** absent

The ice above Lake Vostok freezes forming a 220m layer of accreted ice. It is generally accepted that this 220m layer of accreted ice reflects the contents into the lake and, because of this, it has been under study during the last 30 years. Ice accreting near the embayment has higher concentrations of ions, biomass and solid inclusions and it is known as **type I accretion ice**. The ice that forms over open water contains lower concentrations of biomass and ions and has been termed **type II accretion ice**<sup>3</sup> (Figure 2). Mainly because of this, type I accretion ice shows more richness and abundance of sequences.

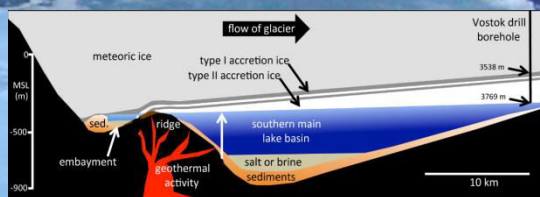


Figure 2. Location of type I and type II accretion ice above lake basin<sup>3</sup>.

As it is shown in the graphic (Figure 3), the main known phyla present in lake Vostok accretion ice are Firmicutes, Proteobacteria and Actinobacteria (determined by the sequence of 16S rDNA gene). The members of **Firmicutes** found in accretion ice include species such as *Paenibacillus* sp. and *Bacillus* sp. (soil inhabitants), *Carnobacterium* sp., *Macroccus* sp., and *Clostridium* sp. (water inhabitants usually associated with marine metazoan). **Proteobacteria** include species previously found in other Antarctic environments (*Sphingomonas* sp.) and symbionts such as *Aquabacterium* sp., *Pelomonas saccharophila*, *Comamonas* sp., *Verminephrobacter* sp. and *Curvibacter* sp. The phylum **Actinobacteria** it is also represented in lake Vostok accretion ice as it has been reported the presence of bacteria also found in seafood (*Brachybaetium* sp.) and a large number of fish-associated actinobacteria (*Mobilicoccus pelagius*, *Renibacter salmonarium* and *Mycobacterium marinum*). Several analyses of melted ice samples with both fluorescence and scanning microscopes have been carried out and a large number of different morphologies have been reported, as shown in the micrographs below<sup>1,2,3</sup> (Figure 4).

### Broad taxonomic proportions (type I accretion ice)

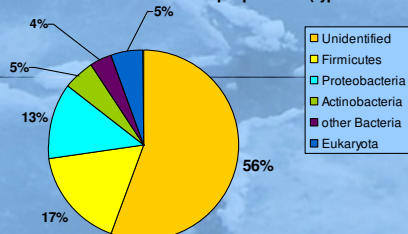


Figure 3. Taxonomic proportions from 16S rDNA metagenomic data including only sequences that have identities between 99 and 100%. Data from reference 3.

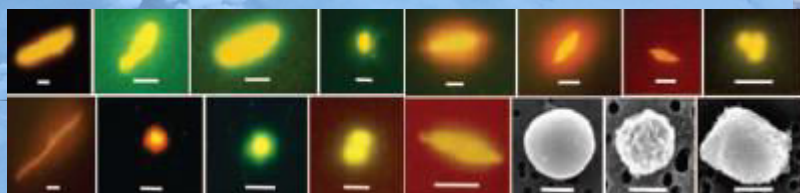


Figure 4. Fluorescence and scanning electron micrographs of cells found in accretion ice<sup>2</sup>.

**Ice-binding proteins (IBP)** are a useful method to cope with freezing conditions. IBP are peptides that specifically bind to and inhibit the recrystallization of ice. The recrystallization of ice is the growth of ice crystals and it has negative consequences to living forms. IBPs have been demonstrated to be produced by microbes from the family Flavobacteriaceae isolated from Vostok ice core and other organisms.

Its recrystallization inhibition (RI) activity has been determined by measuring the ability of a solution (containing the IBP) to prevent distortions in a growing ice crystal<sup>4</sup> (Figure 5).

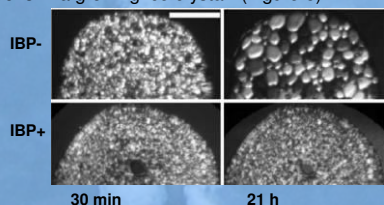


Figure 5. RI activity. In a solution containing ice-binding protein (IBP+) recrystallization of ice doesn't take place<sup>4</sup>.

## CONCLUSIONS:

Far from being sterile, lake Vostok accretion ice shows a diverse set of sequences related to eukaryotic and prokaryotic organisms despite the fact that it is a extremely cold, oligotrophic and hyperbaric environment. The majority of the sequences found are unidentified.

The **main** prokaryotic known phyla are:

- Actinobacteria
- Firmicutes
- Proteobacteria



Microbes living here have developed an efficient method to inhibit the recrystallization of ice, the production of a molecules that bind ice crystals called **ice-binding proteins (IBP)**

