THE LIMNOLOGY OF LAKE VOSTOK

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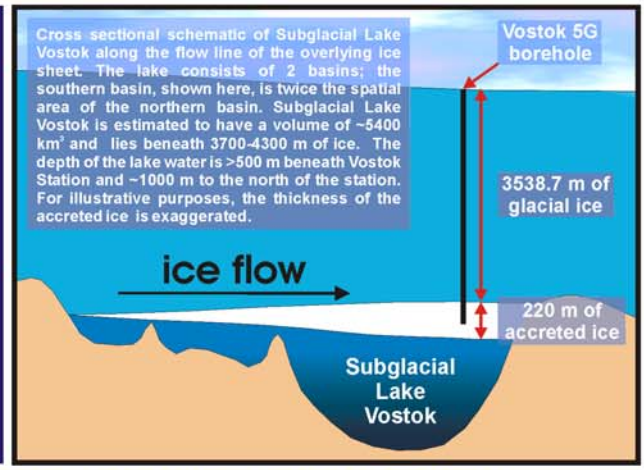
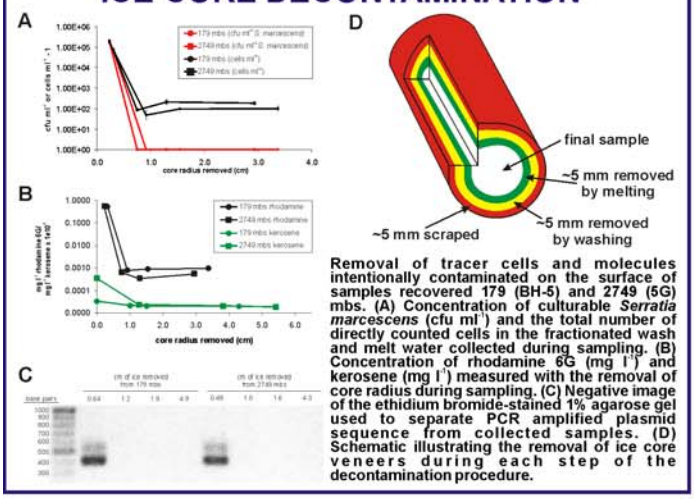
ABSTRACT

Recent geophysical surveys of the Antarctic subglacial environment have revealed the existence of more than 140 subglacial lakes, with Lake Vostok being the largest. Lake Vostok, lies below 4 km of ice, has a surface area of 14,000 km^2, a water volume of approximately 5400 km^3, and consists of 2 basins with depths approaching 800 m and 500 m, respectively. The primary input of allochthonous matter to the lake is from melting of the overlying ice sheet in the northern portion of the lake; the primary loss is from lake water that refreezes (accretes) to the bottom of the ice sheet and is carried away from the lake as the ice sheet moves over the lake. Based on studies of accretion ice obtained by the Russian Antarctic Expedition, the lake is thought to have a predominately heterotrophic assemblage of bacterioplankton that is related to the Proteobacteria. The bacterial density within the surface lake water is estimated to be 10,000 cells per ml and the DOC near 40 micromolar. Geochemical data implies that the surface waters are fresh and supercharged with oxygen.

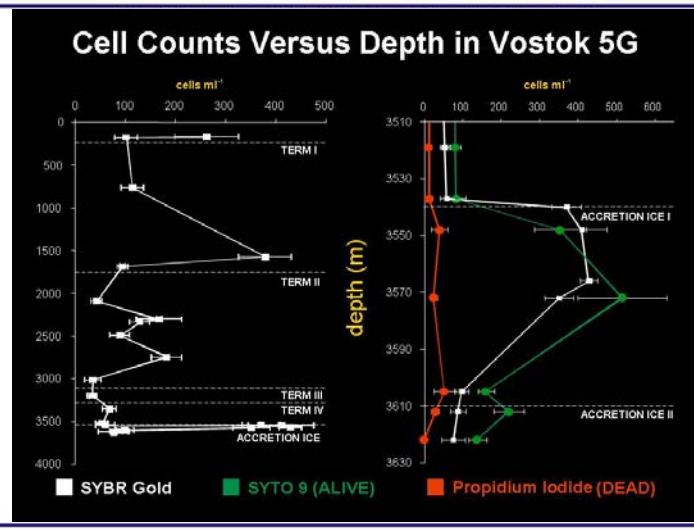


ICE CORE DECONTAMINATION

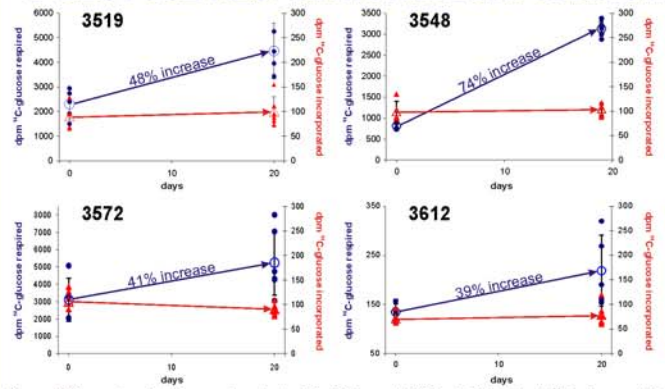


Removal of tracer cells and molecules intentionally contaminated on the surface of samples recovered 179 (BH-5) and 2749 (5G) mbs. (A) Concentration of culturable *Serratia marcescens* (cfu ml^{-1}) and the total number of directly counted cells in the fractionated wash and melt water collected during sampling. (B) Concentration of rhodamine 6G (mg l^{-1}) and kerosene (mg l^{-1}) measured with the removal of core radius during sampling. (C) Negative image of the ethidium bromide-stained 1% agarose gel used to separate PCR amplified plasmid sequence from collected samples. (D) Schematic illustrating the removal of ice core veneers during each step of the decontamination procedure.

Cell Counts Versus Depth in Vostok 5G

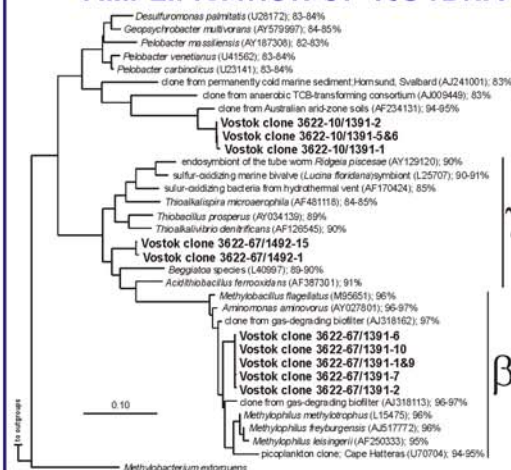


^{14}C-GLUCOSE RESPIRATION/INCORPORATION



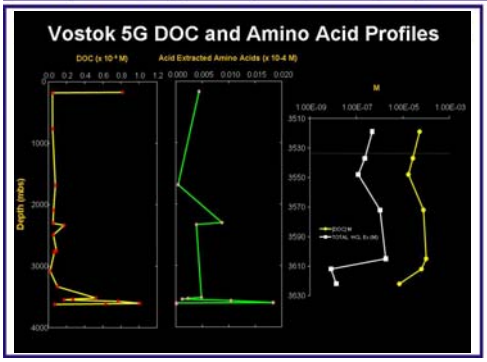
Five milliliters of melted ice was incubated for 20 days at 10°C with 0.8 μCi of U^{14}C-glucose (80 μM). At 0 and 20 days, incorporation into TCA-precipitated material and ^{14}C-CO_2 trapped on phenethylamine-saturated wicks was quantitated by liquid scintillation counting. Measurable levels of respiration (in blue) occurred in all samples except 3605 and 3622 (not shown). However, very little, if any, incorporation (in red) occurred over this time frame.

AMPLIFICATION OF 16S rDNA SEQUENCES



Phylogenetic analysis of β–, γ–, and δ-proteobacterial 16S rDNA sequences from sample 3622 (accretion ice II) by maximum likelihood (fastDNAml). A nested PCR, with primers corresponding to nucleotides 27 to 1492 or 1525 and 515 to 1391 or 1492 of the *E. coli* 16S rDNA, was used for amplification. Sequences were manually checked for covariance, aligned based on secondary structure, and a phylogenetic tree was constructed using an 820 nucleotide mask of unambiguously aligned positions. The nearest phylogenetic neighbors are indicated, along with GenBank accession numbers and the percent similarity to the nearest Vostok clone (in bold). The scale bar represents 0.10 fixed substitutions per nucleotide position.

Vostok 5G DOC and Amino Acid Profiles



RECOVERY OF VIABLE MICROORGANISMS FROM VOSTOK ACCRETION ICE

Strain ID/ Depth	% Similarity	Closest Relative	Isolation Location
V3572-1	98	*Bacillus circulans*	Ubiquitous
V3572-3	96	*Agrobacterium* sp.	Common in soil
V3572-4	99	*Agrobacterium albertimagni*	Common in soil
V3605-1	95	*Chelatococcus asaccharovorans*	Soil crusts of the Colorado Plateau
V3605-2	98 95	*Devosia neptunia* *Glacial Ice bacterium*	Aquatic root nodule Subglacial Sediments from New Zealand
V3605-5	98	*Kytococcus* sp.	Aquatic ecosystem
V3605-6	96	Unclassified bacterium	Antarctic soils
V3605-7	95	Unclassified bacterium	No information
V3605-8	90	Uncultured bacterium clone	Ross Island, Antarctica
V3622-3	90 89	*Subtercola pratensis* Antarctic bacterium	Actinobacteria
V3622-5	99	*Dietzia* sp.	No information

SUMMARY

Data collected from Vostok accretion ice indicate that Lake Vostok contains a viable microbial assemblage whose metabolism is supported in part by organic matter released into the subglacial environment from overlying meteoric ice. The phylotypes within the ice imply the potential for both heterotrophic and chemotrophic activity in the lake water. Actual sampling of the water column is needed to discern the vertical physical, chemical and biological structure of the lake.