

A Microbial Community in Sediments beneath the Western Antarctic Ice Sheet, Ice Stream C (Kamb)



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Abstract:

In 2000, an ice-drilling project focusing on the "sticky spot" of Ice Stream C recovered cores of sub-glacial sediments from beneath the Western Antarctic Ice Sheet. We have characterized several chemical and microbiological parameters of the sole intact sediment core. Pore waters extracted from these sediments were brackish and some were supersaturated with respect to calcite. Ion chromatography demonstrated the presence of several organic acids at low, but detectable, levels in the pore water. DAPI direct cell counts were approximately 10^3 cells g^{-1} . Aerobic viable plate counts were much lower than direct cell counts; however, they were two orders of magnitude higher on plates incubated at low temperature ($4^\circ C$; 3.63×10^5 CFU ml^{-1}) than at higher temperatures (ca. $22^\circ C$; 1.5×10^3 CFU ml^{-1}); no colonies were detected on plates incubated anaerobically at either temperature. 16S rDNA clone library analysis indicates extremely limited bacterial diversity in these samples; six phylogenetic clades were detected. No Archaeal PCR product could be obtained. The three dominant bacterial phylogenetic clades in the clone libraries (252 clones total) were most closely related to *Thiobacillus thioarvens* (180 clones), *Polaromonas vacuolata* (34 clones), and *Gallionella ferruginea* (35 clones) and their relatives; one clone each represented the other three phylogenetic clades (most closely related to *Ralstonia pickettii*, *Lyso bacter antibioticus*, and *Xylophaga fastidiosa*, respectively). These sequences match closely with sequences previously obtained from other subglacial environments in Valdez, Alaska and Ellesmere Island, Canada. Implications of this microbial community to subglacial chemistry and microbial biogeography will be discussed.

Introduction:

Recent studies have provided evidence that active and abundant microbial ecosystems are present in subglacial Arctic and alpine environments (Sharp et al., 1999; Skidmore et al., 2000; Foght et al., 2004). These communities may play significant roles in biogeochemical cycling and chemical weathering processes in these environments. The possibility of similar microbial ecosystems in subglacial systems in Antarctica has been proposed, and there is indirect evidence of a microbial ecosystem in Lake Vostok, a subglacial lake beneath the East Antarctic Ice Sheet (Karl et al., 1999; Priscu et al., 1999). However, no direct microbiological study of Antarctic subglacial sediments has been performed.

The Western Antarctic Ice Sheet currently is losing mass primarily by drainage into the Ross and Weddell Seas. The flow of ice from the grounded part of WAIS to the ocean occurs predominantly in fast-moving ice streams (Figure 1; Oppenheimer, 1998). To examine the mechanisms by which ice streams flow faster than the surrounding ice and to determine the reason for the slow down of one of the Ross Sea ice streams, Ice Stream Kamb, holes were drilled in the ice and samples of ice, subglacial water, and sediment cores were collected in 2000 (see <http://skua.gps.caltech.edu/hermann/upc/upc.htm> for pictures and data). These sediments have a marine origin and are remnants of the Pleistocene collapse of the WAIS (Scherer, et al., 1998). We took advantage of the existence of these cores by sampling the sole fully intact core for characterization of chemical and microbiological parameters to determine a) whether a microbial community is present in this environment, b) whether the community is active, and c) whether that activity has a significant impact on the geochemistry of the subglacial environment.

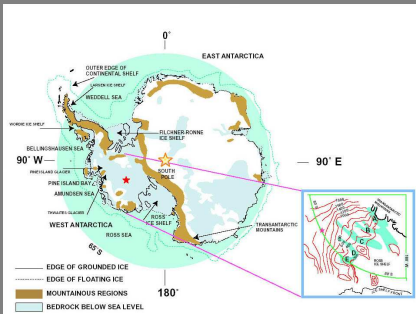


Figure 1: Map of the Western Antarctic Ice Sheets. The Western Antarctic Ice Sheet (WAIS) is located to the left of the transantarctic mountains. The inset is an enlargement of the highlighted region showing the five main ice streams that feed the Ross Sea, including the focus of this study, Ice Stream C, recently renamed Ice Stream Kamb. Figure from Oppenheimer (1998).



Figure 2: Sampling the core.

- The core was stored at $4^\circ C$ for 18 months prior to sampling
 - Likely shift in microbial community relative abundance, but not composition
- Interior of core unlikely to be contaminated during initial collection due to low porosity
 - Hydraulic diffusivity ($10^{-8} m^2 s^{-1}$) and hydraulic conductivity ($10^{-10} m s^{-1}$) indicate ~ 2 years to penetrate 1 cm of sediment (S. Tulaczyk, per. comm.).
 - Outer 1-2 cm discarded; all subsampling performed with sterile instruments
- All sampling was performed in a laminar flow hood, and indicator R2A plates were left open during the entire sampling procedure (no contamination was detected).

Table 1: Selected ionic composition of WAISC sediment pore water

	Top porewater (μM)	Bottom porewater (μM)	Dilution factor (relative to standard seawater) - Top porewater	Dilution factor (relative to standard seawater) - Bottom porewater
Na ⁺	19654	22318	23.8	21.0
K ⁺	592	708	17.2	14.4
Mg ²⁺	3075	3876	17.2	13.7
Ca ²⁺	6418	8749	1.6	1.2
Mn ²⁺	1	14	0.0003	0.00003
Si ⁴⁺	24	30	3.7	3.0
Cl ⁻	1062	1468	513.9	371.7
SO ₄ ²⁻	17061	20193	1.6	1.4
HCO ₃ ⁻	4099	6509		

*Determined by charge balance

- Pore water is clearly not just a dilution of seawater by ice melt; different elements have different dilution factors relative to seawater
- Appears to be significant cation exchange, as evidence by high Na⁺ relative to Ca²⁺ and Mg²⁺
 - Probably due to initial gypsum dissolution followed by ion exchange in clay rich sediments
- Extremely elevated Mn²⁺ levels relative to seawater, with the bottom showing an order of magnitude higher than top
 - Reason unknown
- Currently underway:
 - $\delta^{13}C$ of DIC and TOC
 - Dissolved iron
- Proposed:
 - $\delta^{34}S$ to determine source (i.e. gypsum dissolution vs. sulfide oxidation)

Table 2: Total and viable microbial abundance in WAISC sediments

	Upper	Lower
DAPI direct counts ¹	27400 ± 1390	15000 ± 523
Viable plate counts (incubation time) ²		
Aerobic, RT (5 weeks)	1.5 ± 1.1	ND ³
Aerobic, 4 ^o C (5 months)	363 ± 140	56 ± 6.3
Anaerobic, RT (5 months)	0	ND
Anaerobic, 4 ^o C (5 months)	0	0
Viable fraction ⁴		
Aerobic, RT (5 weeks)	0.00055	ND
Aerobic, 4 ^o C (5 months)	0.0132	0.0037

¹ Cells $g^{-1} \times 10^3 \pm$ one standard deviation
² Colony forming units (CFU) $g^{-1} \times 10^3 \pm$ one standard deviation
³ ND = not determined
⁴ CFU \div total direct counts

- Moderately abundant microbial community present
- Two order of magnitude higher viable cell counts at low temperature than at high temperature: viable portion of community is cold adapted
- No viable anaerobic microbes detected by growth on R2A agar
 - May be due to lack of terminal electron acceptors
- As in many other systems, viable fraction is $\sim 1\%$
- Top section of core has significantly higher viable counts than bottom

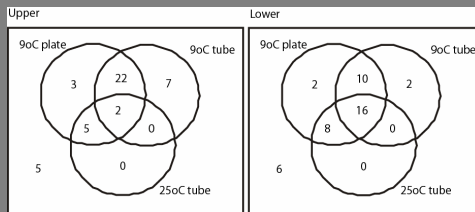


Figure 3: Temperature-dependent growth characteristics of isolates

- All isolates are psychrotolerant; some appear to be psychrophilic
- Preliminary data - must be confirmed
- Currently testing full growth range and cardinal temperatures of isolates

Table 3: Preliminary identification of isolates based on partial 16S rRNA gene sequences

Group*	# isolates	% of total isolates	Nearest Neighbor†	Phylogenetic group	Similarity†
A	43	68.3	Clone RA13C6 / <i>Polaromonas vacuolata</i>	Comamonas and relatives	98%
B	11	17.5	Aflipia genom. 14	Caulobacter (α -proteobacteria)	98%
C	9	14.2	<i>Microbacterium phyllosphaerae</i>	Actinobacteria	97%

*Based on *HhaI* and *MspI* RFLP patterns of nearly full-length 16S rRNA genes
 †Based on BLAST similarity of partial 16S rRNA gene sequences of clones representing each group to sequences available in the Genbank database. Similarity is based on partial sequences ranging from ~ 500 to ~ 750 bp in length

- Isolates show minimal diversity
- One group abundant in culture collection is also abundant in clone library (Comamonas and relatives; Figure 5)
- Two other groups in isolates do not match the dominant groups as indicated by non-culture based methods

Acknowledgements: We would like to thank Barclay Kamb, Hermann Engelhardt, and Slawek Tulaczyk for access to samples and continued collaborative support, and Stefan Vogel for assistance in sampling. Louisa Hanna assisted in the temperature characterization of the isolates. This work was funded by NSF grant 0314293 to BL.

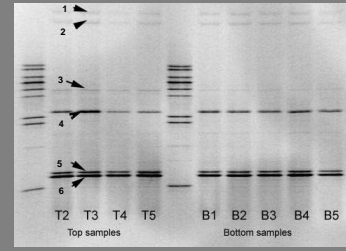


Figure 4: DGGE analysis of replicate extractions from the top and bottom of the core. Arrows indicate bands excised and cloned for sequencing.

- Diversity is extremely limited
- Sequencing indicates the presence of only three dominant phylogenetic groups (see figure 5)
- Sequences for bands 1, 2 and 4 are identical to each other, as are bands 5 and 6
 - 1 and 2 likely heteroduplexes

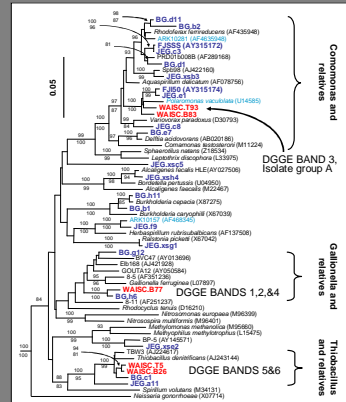


Figure 5: Phylogenetic analysis of WAISC 16S rRNA gene clones PCR amplified from DNA extracted directly from sediment samples.

- WAISC sequences are indicated in **bold red**, sequences from other subglacial systems are indicated in **bold blue** (BG = Bench Glacier, Alaska (Skidmore et al. in prep), JEG = John Evans Glacier, Nunavut, Canada (Skidmore et al. in prep), and FJ = Franz Joseph Glacier, New Zealand (Foght, et al. 2004)), and those from icy systems are indicated in **bold light blue**. Identity of DGGE bands (see Figure 2) are indicated.
- The WAISC community is similar to that observed in other subglacial and icy systems.
- The largest group of isolates is very similar to a group of gene sequences that are abundant in both the top and bottom clone libraries (i.e. Comamonas and relatives).
- Dominant sequence clusters are related to heterotrophs and iron or sulfur oxidizing microbes, perhaps providing some insight into possible energy sources in this environmentally isolated system.

Results and Conclusions:

- The porewater of the subglacial environment shows indications of biogeochemical alteration; however, it is currently unclear whether microbial activity plays a significant role in these alterations.
- A small, but easily detectable, microbial community is present in sediments from beneath the Western Antarctic Ice Sheet. This is the first study showing the presence of microbes in such an environment.
- A fraction of the microbial community can be cultured, including one of the dominant groups based on non-culture methods. This will be a target of future study.
- Culturable microbes are cold-adapted, and some are psychrophilic.
- Based on 16S rRNA gene studies, the bacterial community diversity is extremely limited in this system, but the members of this community are highly similar to those found in other subglacial environments.
- No Archaea could be detected by PCR of 16S rRNA genes

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