Microbial characterization in the WAIS divide ice core between the Last Glacial Maximum and the Mid- Holocene: Preliminary results.

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INTRODUCTION

The Quaternary period is unique in Earth's history owing to human habitation and the rapid and high magnitude of climatic and environmental changes. Proxies and evidence for Quaternary environmental conditions are more abundant, of higher resolution, and better preserved than those from any other period. Additionally, biological proxies and geological features are more similar to extant biological species and current features than those from other periods. Bacteria in terrestrial and aquatic environments respond quickly to environmental changes due to short generation time and play important roles in ecosystems as key drivers of elemental cycles. Consequently, microbial abundance in ice cores may provide a unique proxy for paleoclimatic and paleoenvironmental conditions on Earth.

MATERIAL AND METHODS

We used discrete samples from the West Antarctic Ice Sheet (WAIS) Divide ice core (Fig. 1). They were obtained from the continuous melting system operated by the McConnell Laboratory at the Desert Research Institute to reconstruct bacterial abundance from the Last Glacial Maximum (LGM) to the Mid-Holocene (~27000 to 6000 years before 1950; timescale WDC06A-6). An overarching goal of our work was to develop flow cytometric (Fig 4) and microscopic methods (Fig. 3) to accurately determine bacterial abundance in small volumes of melted ice and; to use this information to infer environmental patterns through time.

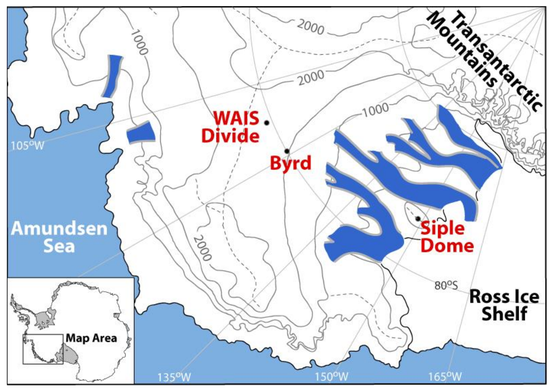

FIG. 1. Location. WAIS (West Antarctic Ice Sheet) Divide is a United States deep ice coring project in West Antarctica funded by the National Science Foundation (NSF). Source: Howard Conway, University of Washington.

BACKGROUND

Table 1. Some types of paleoenvironmental information from ice cores.

Indicator	Proxy: indirect measure of environmental conditions
$^{18}O/^{16}O$ and H^2/H^1 ratios	Past temperatures
Dust content	Past aeolian activity, aridity
Chemical composition	Past atmospheric circulation, pollution
Composition of trapped air	Past atmospheric concentration of CO_2, CH_4, N_2O, etc.
Bacterial abundance and composition	?

Before using bacteria as a Proxy of …….. these questions MUST be answered

Is there a signal?

NO SIGNAL | CYCLE | TREND | PERIODICITY

What aspects of climate and/or environment do the bacterial abundance record respond?

BACTERIAL SOURCES → TRANSPORT PROCESSES → DEPOSITION → POST-DEPOSITIONAL EFFECTS ON THE GLACIER

At what time scale does the bacterial abundance record respond to climate?

THAT DEPENDS ON GENERATION TIMES. FOR BACTERIA THAT MEANS HOURS, DAYS AND/OR MONTHS, BUT IT ALSO DEPENDS ON SCALE OF THE RECORDED PROCESS

What are the lags and complicated factors in response to climate and/or environment?

- MICROBIAL CONTAMINATION
- BACTERIAL GROWTH IN THE ICE
- TIME INTENSIVE METHODS, ETC.

How far back into the past can the record go?

BACTERIAL DEGRADATION IN THE ICE

RESULTS

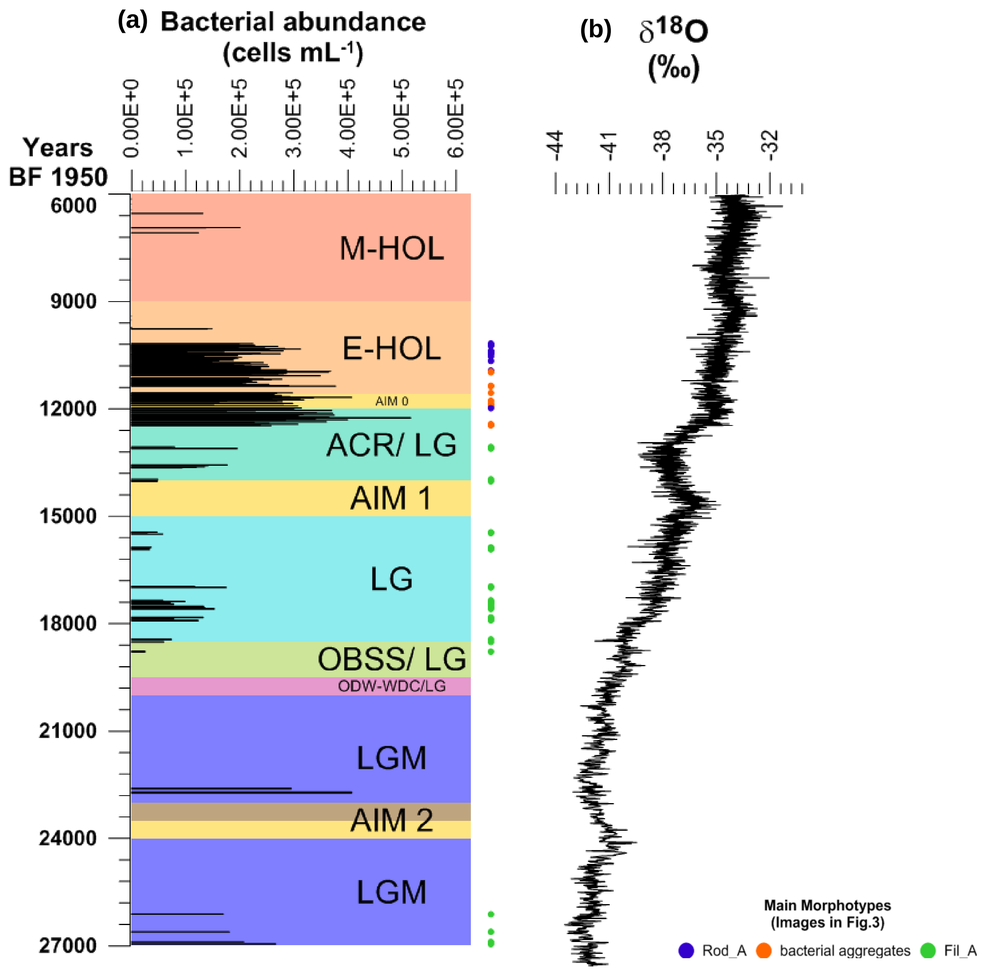

FIG. 2. Bacterial record in WAIS Divide Ice core. **(a)** bacterial abundance (cells mL^{-1}) profile with climatic periods and events between 6,000 and 27,000 years before 1950. **Climatic periods and events**: Mid-Holocene **(M-HOL)**, Early-Holocene **(E-HOL)**, Antarctic Isotope Maximum **(AIM 0, AIM 1, and AIM 2)**, Antarctic Cold Reversal **(ACR),** Late Glacial **(LG)**, Onset of "Bipolar See-Saw" **(OBSS),** Onset Deglacial Warming WAIS Divide ice core **(ODW-WDC)**, and Last Glacial Maximum **(LGM)**. The dominant bacterial morphotypes through the ice core are represented with colored circles at the right of the profile (see details in legend). **(b)** water isotope ratio $\delta^{18}O$ of ice (‰) from WAIS Divide ice core (WAIS Divide Project Members, 2013). Both records are at original resolution.

Initial results reveal that both methods yielded cellular densities ranging from ~10 to $4.83x10^5$ cells mL^{-1} in a discrete set of spanning the period of study. Highest bacterial density occurred during the LGM (mean=$2.39x10^5$, n=6) and Early Holocene (mean= $2.11x10^5$, n=99), whereas bacterial abundance was slightly lower during the deglaciation/late glacial period (mean=$1.67x10^5$, n=52) and one order of magnitude lower in the mid-Holocene (mean=$6.67x10^4$, n=10) (Fig.1). Bacterial abundance record shows dramatic changes between 6000 and 10000 years before 1950 (~10 to 1.15 $x10^5$cells mL^{-1}). Morphological diversity was low during the LGM, increased with the onset of deglaciation until the Early Holocene, and was again low in the Mid-Holocene. Distinct cellular aggregates were evident during the deglaciation period whereas free-bacteria dominated the assemblage during other periods. Dominated bacterial morphotypes (Fig. 3) were plotted against time periods showing a temporal succession signal (Fig. 2).

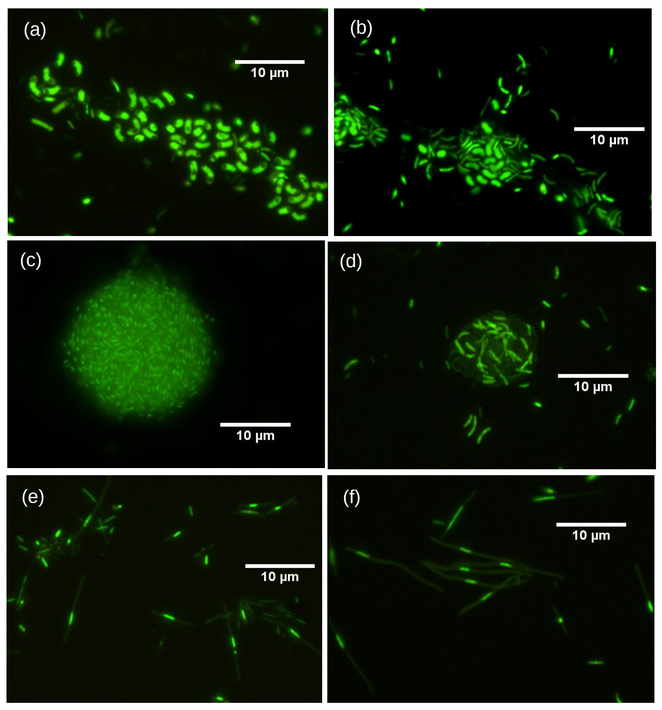

FIG. 3. Epifluorescent microscopy images of dominant bacterial morphotypes from WAIS divide ice core. (a-b) Morphotype Rod_A from the Early Holocene, **(c-d)** bacterial aggregates present during the LGM and late glacial periods, **(e-f)** Morphotype Fil_A from the LGM and Late Glacial periods. DNA stain: SYTOX Green (2.5 µM final concentration)

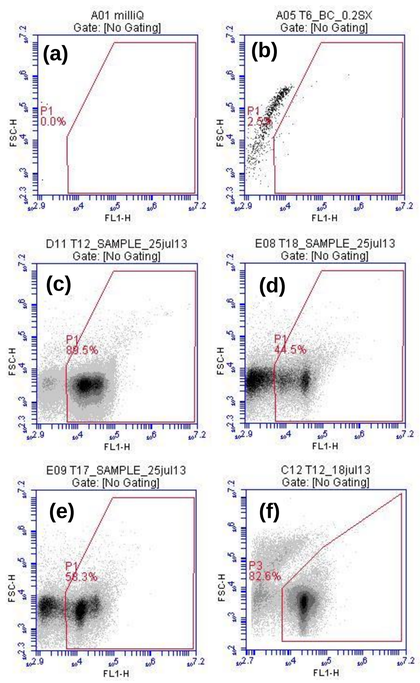

FIG. 4. Flow cytometry plots (FSC-H vs. FL1-H). (a) Milli-Q water control, **(b)** 0.2 µm filtered and stained sample (background control)**, (c-f)** stained WAIS samples**.** DNA stain: SYTOX Green (0.05 µM final concentration).

DISCUSSION

Our preliminary data show that:

(i) there is a temporal signal of bacterial abundance and morphological diversity in WDC through the LGM to Mid-Holocene,

(ii) the temporal variability of bacterial abundance appears to be linked to dust proxy, which may be a reflection of changes in deposition mechanism and/or bacterial sources,

(iii) dramatic changes in bacterial abundance are observed through the transition from Early-Holocene (~6,000-9,000 years before 1950) and Mid-Holocene (~9,000-12,000 years before 1950).

We will continue to process discrete samples through the ice core, refine our estimates of abundance and morphological diversity and construct statistical models. To ensure that the bacteria in our samples are not contaminants from the DRI melting and/or storage protocols, we will examine discrete samples that have not been subjected to them.

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