Abundance, viability and diversity of the indigenous microbial populations at different depths of the NEEM Greenland ice core

Vanya Miteva, Kaitlyn Rinehold , Todd Sowers, Aswathy Sebastian, Jean Brenchley Department of Biochemistry and Molecular Biology, The Pennsylvania State University, University Park, PA 16802, USA

Corresponding author:

Dr. Vanya Miteva vim1@psu.edu

Supplementary Material

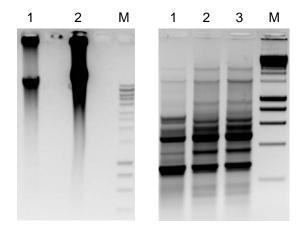


Fig. S1. Comparison of REPLI-g amplified genomic DNA from a NEEM ice core. A. REPLI-g amplification for 2.5 h (1) and for 5h; B. ERIC PCR profiles of original DNA (1), 2.5 h REPLI-g product (2) and 5h REPLI-g product (3).

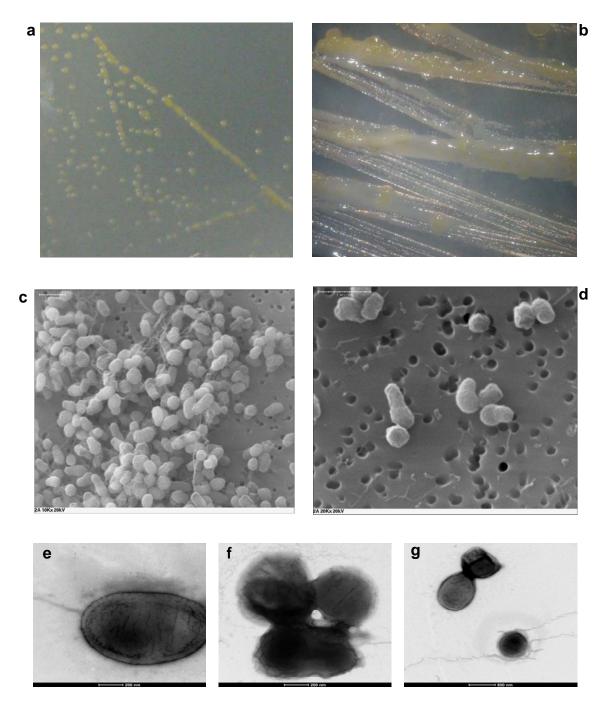


Fig. S2. Colony and cell morphology of isolate 633.05-i2a from 633.05 m deep NEEM ice core. Panels a and b: Colonies grown on TSA (left) and R2A (right, 10x magnification) at 25°C. Panels c and d: Scanning electron micrograph obtained using JEOL microscope, model JEM 5400, Peabody, MA at 20 kV, bar 1 μ m. Panels e and f: Transmission electron micrographs of cells, negatively stained with uranyl acetate (2%), showing long flagella, bars correspond to 200 and 500 nm, respectively. Images were taken under JEOL microscope, model JEM 1200 EXII, Peabody, MA) at 80 kV.