Microbial abundance and community structure in the winter sea ice of Franklin Bay, NWT

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ABSTRACT

Microbial communities in Arctic winter sea ice (presumably concentrated in the brine inclusions) are dominated by heterotrophic Bacteria that appear to undergo selection as the temperature and salinity of their micro-habitats harshen. Archaea have been detected microscopically in winter sea ice in small numbers (< 3% of the total population), but nothing is known about their phylogenetic affiliations, community dynamics, or capacity for persistence in sea ice. The CASES overwintering expedition provided a unique opportunity to examine microbial diversity and succession in sea ice in much greater spatial and temporal detail than possible in prior studies.

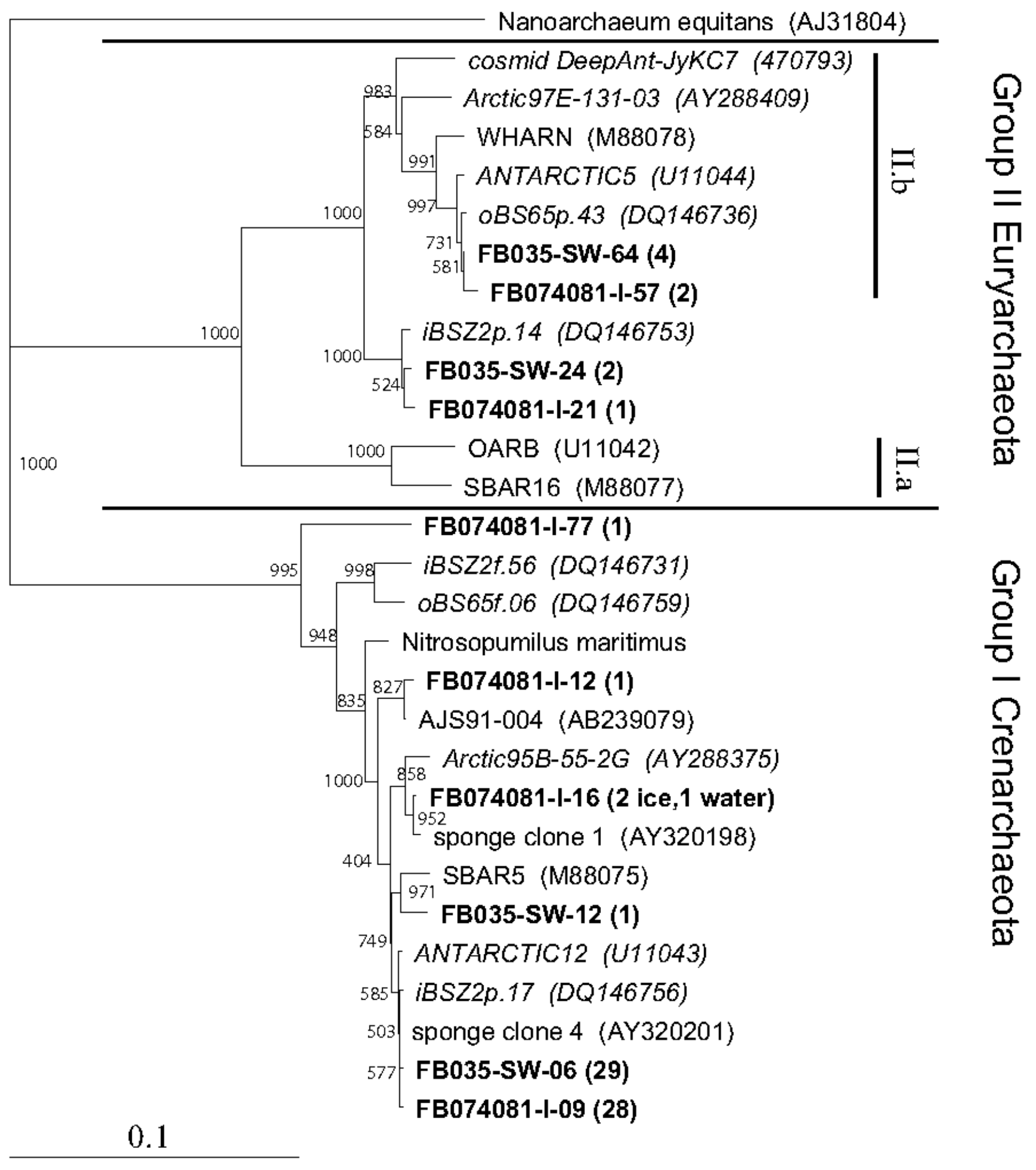

FIG 1
Neighbor-joining phylogenetic tree of environmental Archaeal 16S rRNA genes based on 1000 bootstrap replications (supporting values shown at bifurcation points). One sequence from each OTU (>98% similarity cutoff) from each clone library from this study is shown in bold, followed by the number of sequences in that OTU from seawater ("SW") or 25-cm depth-horizon ice ("I"). FB=Franklin Bay, numbers indicate day of year (or pooled days in the case of 074/081) the sample was collected. Reference sequences in italics originate from polar regions. Scale bar indicates 10 nucleotide substitutions per 100 base pairs.

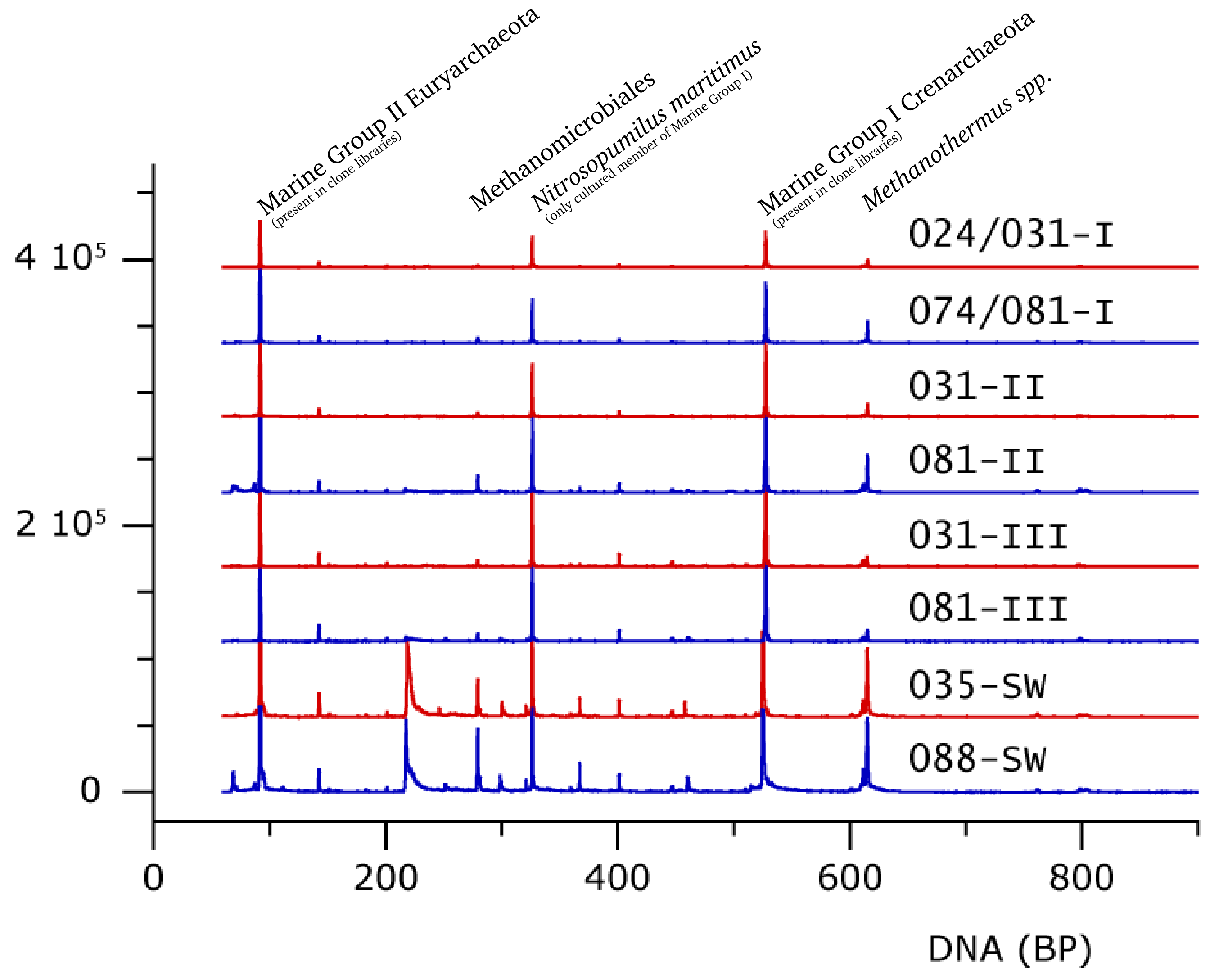

FIG 2
Representative electropherograms of terminal restriction fragment length polymorphism (T-RFLP) analysis from two sampling dates and four depths (3 ice, 1 seawater) using enzyme HpyCH4III. Y-axis scale is in relative fluorescent units. Samples are identified by: Day of Year – Section (I=25 cm, II=45 cm, III=65 cm, SW=seawater). Named peaks are best matches to in silico database of known Archaea (which were also identified using different primer/enzyme combinations); remaining peaks are unknown.

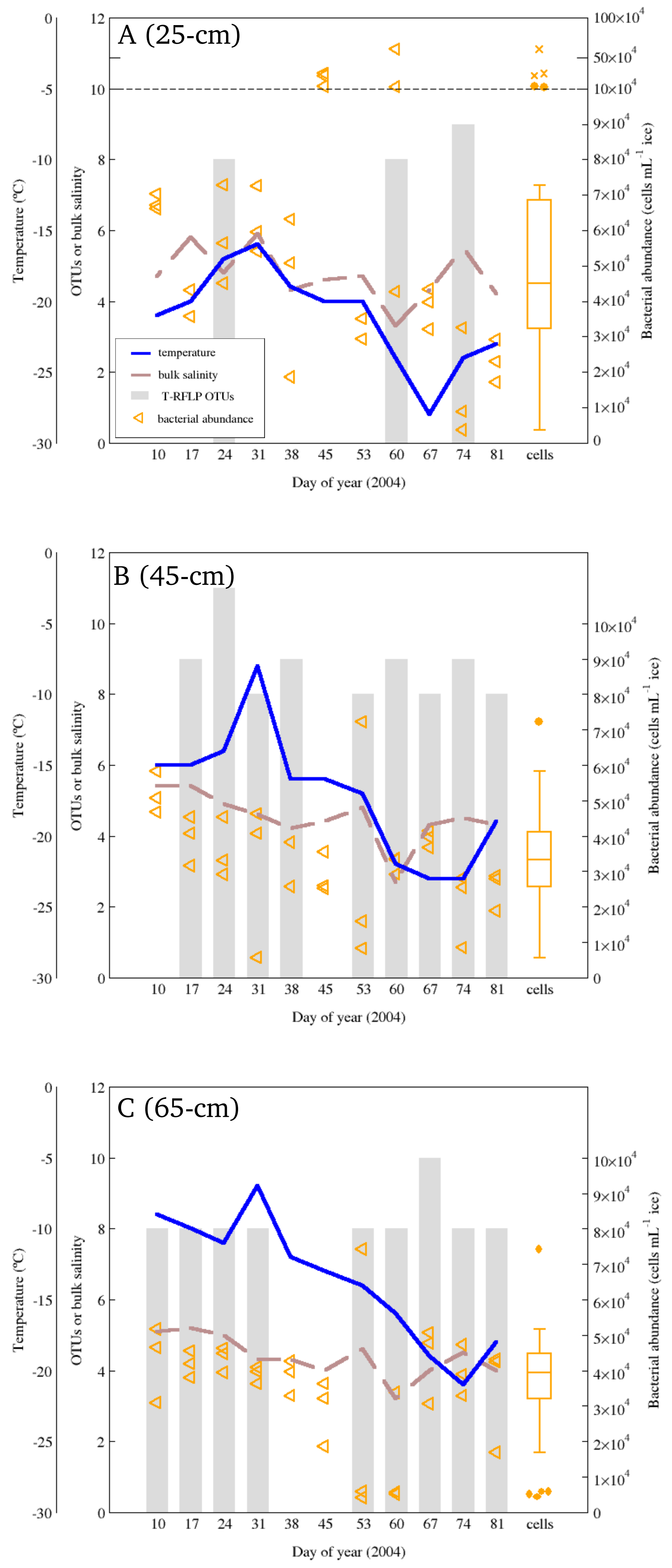

FIG 3
Temperature (blue solid line), bulk salinity (brown dashed line), total bacterial abundance (orange triangles), and OTUs determined by T-RFLP (grey bars) in A) 25-cm depth horizon, B) 45-cm depth horizon, and C) 65-cm depth horizon over time. The box-and-whisker plot recapitulates the total count data ("dot" is 1.5–3.0 IQRs from the quartiles, "x" is >3.0 IQRs from the quartiles). Note the change in scale for bacterial abundance in the 25-cm depth horizon.

RESULTS

Archaeal 16S rRNA genes in under-ice seawater and winter ice of Franklin Bay were predominantly Marine Group I Crenarchaeota, with a minority of Marine Group II Euryarchaeota (Fig. 1; environmental cloning).

Methane-cycling groups (Methanomicrobiales and Methanothermus) were inferred from community fingerprinting (Fig. 2; T-RFLP).

Archaeal community richness and structure in sea ice fluctuated slightly over time but a core group persisted unchanged through the winter (Fig. 2 & 3; T-RFLP).

Total bacterial abundance decreased significantly over time in the 25-cm and 45-cm horizons but not in the 65-cm horizon (Fig. 3; DAPI staining).

Particulate EPS increased significantly in all horizons, but was very low (Fig. 4; Alcian Blue staining).

More variability and higher abundances of bacteria, particles, and EPS were observed in the upper 25-cm depth horizon, possibly due to growth history as consolidated ice (Fig. 3 & 4).

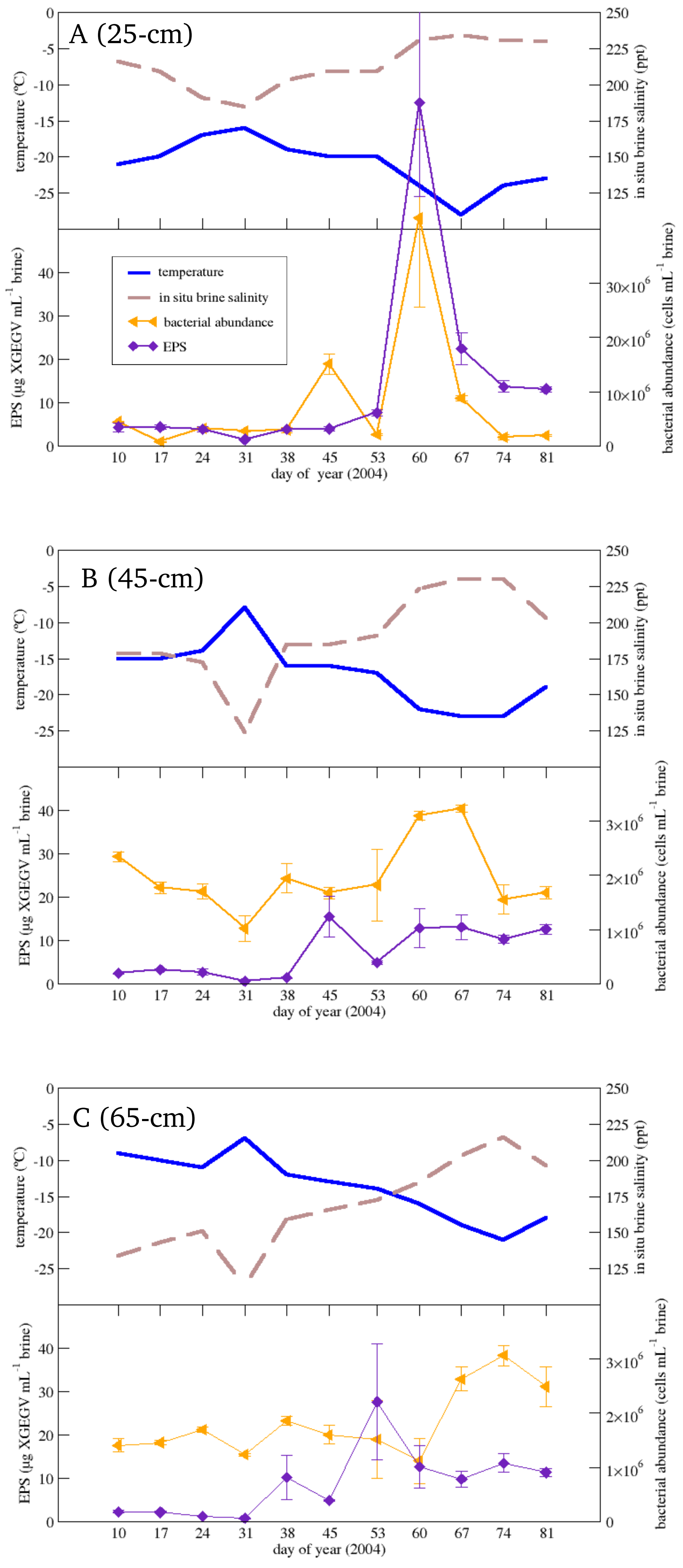

FIG 4
Temperature (blue solid line), in situ brine salinity (brown dashed line), total bacterial abundance scaled to brine volume (orange triangles), and EPS scaled to brine volume(blue diamonds) in A) 25-cm depth horizon, B) 45-cm depth horizon, and C) 65-cm depth horizon over time. Note the change in scale for bacterial abundance in the 25-cm depth horizon.

CONCLUSIONS

Significant decreases in total bacterial abundance were observed in the upper horizons of Arctic winter sea ice, but were not closely correlated to temperature or salinity changes in the ice. One possible biological explanation is viral lysis, as observed by Wells and Deming (2006). The phylogenetic richness of the Archaea in the ice did not change in response to the environmental extremes of low temperature and high salinity, suggesting that