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ANCIENT BACTERIA AND THEIR FUNCTIONAL GENES PRESERVED IN ANTARCTIC GLACIAL ICE

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Total genomic DNA was extracted from ancient Antarctic glacial ice for molecular analyses on the trapped microbial community. Ice samples were from the Dry Valley region, and the age dating by ^{40}Ar/^{39}Ar analysis on the volcanic ashes deposited *in situ* indicated the samples are ca. 300,000 (sample DLE) and 8 million yrs (sample EME) old. Parallel assay proved the ice survived freeze-thaw cycles or other re-working processes. EME, which was from a small lobe of the basal Taylor glacier, is the oldest known ice on Earth. Microorganisms, preserved frozen in glacier ice and thus isolated from the rest of the world over a geological time scale, can provide valuable info for the diversity, distribution, survival strategy, and evolutionary relationships to the extant relatives. From the 16S gene cloning study, we detected no PCR amplicons with Archaea- or Eukarya-specific primers, however we found many phylotypes belonging to Bacteria divisions, e.g., Actinobacteria, Acidobacteria, Proteobacteria (α, β, and γ), Firmicutes, and

Cytophaga-Flavobacterium-Bacteroid. End-sequencing of the cloned genomic DNA revealed genes highly identical to known protein codings, e.g., membrane protein, phenylacetic acid degradation protein, chromosome segregation ATPases, cold shock protein B, Fe-superoxide dismutase, recombinational DNA repair protein, and transposase, which suggests the presence of virus. Incubations of the freshly melt ice water with added radio isotope-labelled substrate demonstrated that the viable cells instantaneously responded to the added substrates, utilizing them without delay. We also recovered culturable cells from the DLE sample on solid media, and characterized them by their 16S rDNA sequences. Further investigations on the survivorship and functional genes of the prokaryotic cells from the past should help unveil the propagation and evolution of life on Earth, or elsewhere, if any.