

UNKNOWN WIDELY-SPREAD Fe REDOX CYCLING BACTERIA BENEATH THE EAST ANTARCTIC ICE SHEET

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The main objective was to recover bacterial life existing beneath the thick East Antarctic Ice Sheet (EAIS) using the sequencing of bacterial 16S rRNA genes recovered in the ice samples containing bedrock source mineral inclusions. The samples included the accretion (lake water source) ice of the Vostok ice core (the Russian intra-continental station Vostok) containing small numerous mineral inclusions (ice type I). Three ice samples from the same depth horizon (3607-3608 m deep; age about 16 kyr) were obtained from 3 parallel boreholes (5G-1, 5G-2 and 5G-3). Another sample was the glacier ice segment containing numerous big in size reddish rock sediments of moraine source from the D10 ice core (East Antarctic coastal area, nearby the French station Dumont d' Urville). The sample was recovered from 230 m depth and aged by about 20 kyr. The samples were strictly decontaminated and treated under 'clean room' conditions (IGE, CNRS-University Grenoble Alpes).

The comprehensive DNA analyses (constrained by Ancient DNA research criteria) of three Vostok accretion ice samples have confidently revealed three phylotypes of iron-oxidizing beta-proteobacteria belonging to Gallionellaceae. Two related phylotypes from boreholes 5G-2 and 5G-3 samples have had the closest relative at the genus level *Sideroxydans lithotrophicus*, while the remaining phylotype from the borehole 5G-3 sample - *Ferriphaselus amnicola*. The 3rd ice sample originated from the borehole 5G-1 has gave only contaminants.

The similar analysis of the D10 ice core sample has confidently recovered also three phylotypes. The 1st phylotype has proved to be the same bacterium already detected in the Vostok ice core (borehole 5G-3 sample) –the iron-oxidizing bacterium of Gallionellaceae with the closest relative at the genus level *Sideroxydans lithotrophicus*. Two other related phylotypes have showed rather low family level similarity (92%) with the acidophilic thermotolerant facultative anaerobic Fe- and S-oxidizing gamma-proteobacterium *Acidiferrobacter thiooxydans*. However, due to status 'unidentified' they were removed from the further discussion on their possible involvement in the Fe redox cycling.

Thus, three confident phylotypes of iron-oxidizing beta-proteobacteria of Gallionellaceae related to *Sideroxydans lithotrophicus* and *Ferriphaselus amnicola* were revealed in Vostok and D10 ice cores meaning that unknown bacterial Fe redox cycling communities widely exist beneath the EAIS.

Of them, one phylotype (population) related to *Sideroxydans lithotrophicus* was surprisingly found out in both Russian Vostok 5G-3 and French D10 ice cores. The age of both ice sample types is nearly the same while their origin is evidently different - Vostok accretion (lake water source) ice vs. Dumont d' Urville glacier ice. The storage time periods for ice samples (before to be treated in a laboratory) are quite different (0.5 year for Vostok ice samples vs. 40 years for D10 ice sample) as well as the time frame for the ice treatment (in a range of 1-5 years –D10 ice core sample was treated in a year after the last Vostok 5G-3 ice sample) meaning no cross-contamination could happen. The ice coring sites (Vostok and Dumont d' Urville) are far away (more than 1000 km) with no evident hydrological links beneath the EAIS meaning no bacterium 'flow' could occur. How to explain such a coincidence in findings? It seems that the presence of bedrock minerals containing Fe(II) under similar physical-chemical conditions featured by the existence of unfrozen water might provide the plausible scenario.

Keywords: East Antarctic Ice Sheet, Bedrock-originating mineral inclusions, Vostok ice core, D10 ice core, 16S rRNA genes, Iron-oxidizing bacteria