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Bacteria and archaea under Greenland ice sheet: NGRIP ‘red’ ice issue

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The NGRIP project successfully finished in 2003 by reaching the bedrock beneath 3090 m thick Greenland ice sheet (75.1N, 42.3W). During this campaign the drill escaped from getting stuck because of a sudden basal meltwater inflow up to 45 m in the hole. In a year after the frozen meltwater containing a lot of reddish sediment particles was drilled again, and the so called ‘red’ ice core was obtained and sampled for a biological pilot study. This water may represent an environment isolated from the surface biota for a few millions of years.

Two studied ice samples were of moon-shaped ice from bag 4 (3039 m) and 15 (3045 m). First bag contained a rather dirty ‘reddish’ ice mixed heavily with a kerosene and HCFC fluid while the second bag was representing relatively clean ice (no kerosene film but still smelling kerosene odor) with reddish sediment inclusions. The ice samples were cleaned, decontaminated and finally rinsed with ultra-pure low DOC water according to Vostok ice core protocol (1). Meltwater was concentrated 10-20 times down keeping the sediment material, and gDNA was extracted using FastPrep device along with FastDNA kit.

Preliminary results of molecular microbiology studies of this basal ‘reddish’ meltwater showed the presence of microbial DNA. Common PCR with bacterial 16S rRNA gene targeting primers (590 bp amplicon) easily generated a lot of products for both ice samples and controls while with archaea only highly sensitive nested PCR scheme (630 bp final amplicon) gave positive signals and only for the bag 4 sample. If confirmed, this would be the first finding of archaea in deeply buried icy environments with respect to prior studies of glacier ice in Greenland and Antarctica and accretion

ice from Lake Vostok, East Antarctica (1, 2, 3).

Subsequent preliminary ribotyping showed 6 phylotypes of archaea (of 17 clones) for bag 4 red ice only, while a few specific non-overlapping phylotypes of bacteria (of 20 clones) for both red ice samples. Other bacterial phylotypes were proved to be contaminants as compared to controls. Unlike archaeal contents in NGRIP ice samples studying indigenous bacteria raises the problem, like with Vostok ice studies in deciphering the contribution from the forward contamination. It seems however the bacteria are not really abundant in both red ice samples giving some perspective of indigenous signal. Phylotypes representatives are now under gene sequencing. Identified bacteria and archaea along with their possible metabolic profiles will be then discussed in terms of possible (ancient) life strategies under the thick Greenland ice sheet.

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