

Effect of environmental heat-shock stress on glacier microbiome

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Glacier ice covers a noteworthy area of the planet and is presently facing an accelerated melting rate, combined with a potential remodeling of the microbial composition as a result of exposure to a temperature variation when moving to a contiguous soil. We investigated the bacterial thermal response examining the changes in the gene expression pattern in the microbiome of a glacier ice core from Svalbard, and in the psychrophilic bacterial model *Glaciibacter superstes*, in order to determine the presence of an enzymatic biomarker. Thawed ice samples were submitted to a 7-day heat/freeze cycles experiment, followed by DNA/RNA extraction and investigation of the resilient microbial community and gene expression variations by Shotgun metagenomics and metatranscriptomics. Gene expression coding for aspartate transcarbamoylase (ATC), a key enzyme of pyrimidine nucleotides biosynthesis, was quantified by qPCR, showing changes in the microbial DNA synthesis. Cell viability was assessed after each step based on dead/live cell counting in order to correlate the specific increase in ATC expression with the cellular division. Corroboration of the ATCase gene expression pattern in both psychrophilic bacterium and ice microbiome is currently underway in order to propose an enzymatic biomarker for ice microbiome response to temperature variations when changing habitats due to glaciers' retreat.

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