Heat shock response of glacier microbiome

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Glacier ice occupies a significant area of the planet and is currently experiencing one of the most rapid and severe melting rate, associated with possible changes of microbiome composition due to exposure to temperature variations when passing to adjacent soil. Our study investigated the thermal response of total and active ice-contained microbiome from a Svalbard glacier ice core and arctic subglacial soil samples in order to identify an enzymatic biomarker. All the samples were submitted to a 7-day heat/freeze cycling experiment, and the total DNA and RNA was extracted and analyzed. Changes in the total and active microbiome composition after heat shock treatment was investigated by quantitation by qPCR of the aspartate transcarbamoylase (ATC) expression, a key enzyme of pyrimidine nucleotides biosynthesis which revealed associated changes in the microbiome DNA synthesis. Thermal response of pyrimidine gene expression was investigated in a parallel bacterial model experiment using psychrophilic Glaciibacter superstes. Analysis of the ATCase gene expression pattern in the psychrophilic bacterium and ice microbial community is currently carried out in order to propose an enzymatic biomarker for ice microbiome response to temperature variations when changing habitats due to glaciers melting.

Conclusions

- Psychrophilic bacteria revealed good surviving strategies based on structural and functional adaptations to extreme temperatures
- ATCase as key enzyme for survival, showing different gene expression pattern
- ATCase appears to be a good catalyst biomarker candidate for monitoring the effect of temperature alternation on microbial cells

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