

HIGH ELEVATION MICROBIAL COMMUNITY SHIFTS FOLLOWING EXPOSURE TO FREEZE-THAW CYCLING

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Background:

High elevation soils are among some of the most extreme environments on Earth and microbial life dwelling in these environments is known to cope with a complex interplay of stresses, among which freeze-thaw cycling¹. Little is known on which microbial taxa are best suited to withstand natural freeze-thaw cycles and which molecular strategies come into play for resistance. We exposed microcosms from high elevation soils to prolonged freeze-thaw cycles in order to get an insight on how microbial communities shift in response to this stress.

We hypothesized that consortia from different locations that survive to freeze-thaw cycles are similar in terms of major phyla and consequently in their potential response to this environmental stress.

Methods:

Soil samples taken from 5 different high elevation sites across the globe were exposed to prolonged freeze-thaw cycles. Our approach used a chamber that replicates field freeze-thaw cycles (Fig. 1) closely mimicking the sub-zero cooling rate (Fig. 2). The chamber was run for 48 days, cycling to 27 °C during the day and -9 °C at night. DNA was then extracted, quantified and normalized for Illumina MiSeq sequencing.

Results:

Preliminary results from sequences retrieved from microcosms exposed to freeze-thaw cycling revealed a significant change in the community structure of all samples analyzed in both the Bacteria and Eukarya domains. Change in the structure was mainly associated with the shift in abundance of a few dominant taxa, while most of the less abundant taxa remained relatively unchanged. Predominant taxa in the communities following freeze-thaw cycling differed among the different high elevation sites.

Conclusions:

Our results show that microbial communities shift significantly upon exposure to freeze-thaw cycling and that the key taxa that are mostly responsible for the shift are different depending on the location. Our evidence may indicate that resistance to freeze-thaw cycling is not

strongly associated with specific taxa. Other environmental parameters and original community composition may have a key role in determining the differential survival among different sites.

This study lays the foundations for a better understanding on how microbial communities as a whole respond to freeze-thaw cycling in natural environments.

References:

1) R.C. Lynch, A.J. King, Mariá E. Farías, P. Sowell, Christian Vitry and S. K. Schmidt.

The potential for microbial life in the highest-elevation (>6000 m.a.s.l.) mineral soils of the Atacama region. *Journal of Geophysical Research*, Vol. 117, 2012.

Fig.1: Temperature data of freeze-thaw cycles in the chamber

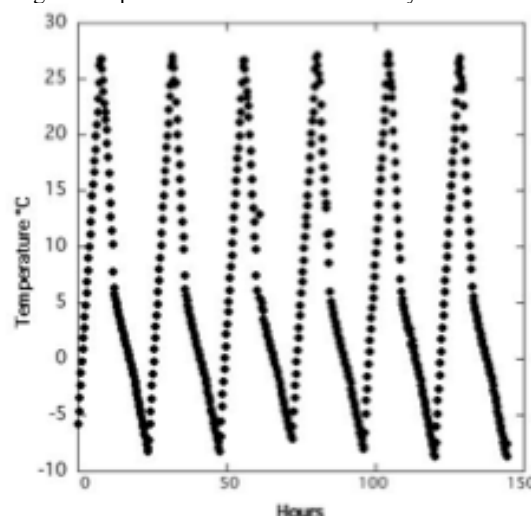


Fig.2: Sub-zero cooling rate of the incubator versus the field

