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Microbial populations description in Deception Island (Antarctica): exploring the surface and the permafrost using an antibody microarray

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Abstract

We performed assays with a Life Detector Chip (so called LDChip300) to study on site the microbial diversity on the surface and the permafrost from a Deception Island borehole. LDChip300 contains more than 300 antibodies developed against bacterial and archaeal strains, crude extracts from environmental samples, proteins, peptides and other biological polymers [1,2,3]. Superficial and core permafrost samples were analyzed by sandwich microarray immunoassays (SMI) with LDChip300 by using a cocktail of 300 different fluorescent antibodies. Pyroclasts and rocks from the surface and the top layer of the permafrost showed positive antigen-antibody reactions against Alpha-, Delta- and Gamma-proteobacteria, Actinobacteria, Bacteroidetes, Firmicutes, archaeal species and proteins and peptides involved in nitrogen fixation and methanogenic processes, iron homeostasis and ABC transporters. Immunoarray results were validated on site with an oligonucleotide microarray for prokaryotic diversity and then in the laboratory through 16S and 23S rRNA gene sequence analysis, aerobic viable counts and microscopy studies. Those results revealed Acidobacteria, Actinobacteria, Proteobacteria, Bacteroidetes and phototrophs as dominant groups in the top active layer of the Deception Island permafrost [4].

1. Introduction

Cold environments are abundant in the Solar System, from the Earth to the moons of the giant planets, or even Mars in the present, with widespread permanently frozen grounds. Thus, permafrost environments are considered suitable terrestrial analogues for astrobiological habitability studies. Many researches have been done on permafrost, however, mostly on Arctic. Deception Island, a glaciated active stratovolcano island, located at the South Shetland Islands archipelago from the Antarctic Peninsula, is an excellent scenario to study permafrost, which is continuous throughout most of the island. In this work, we analyzed the microbiology and the biomarker immunoprofiling associated to different depths of the frozen ground at an elevated flat plain to contribute the understanding of the ecology and the evolution of the permafrost on Earth and as terrestrial analog for searching for life in other permafrost-containing planetary bodies. Our research could also contribute to understand how a potential microbiota have colonized, survived and evolved after past volcanism events.

2. Figures

Fig. 1: Lateral view of a core obtained at depth of 60-80 cm, with relatively high water content and big ice crystals.

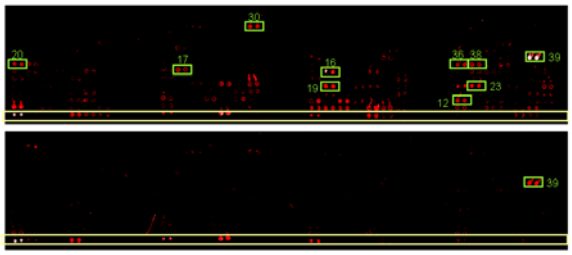

Fig. 2: Scanned chip images after SMI with a sample from the top active layer (from 0 to -4 cm) (top panel) and the negative control (bottom panel). The most relevant positive reactions are marked with a number over the spots.

3. Summary and Conclusions

We demonstrate the potentiality of LDChip300 to characterize the diversity of natural microbial communities by *in situ* analysis in the context of the permafrost environment.

LDChip300 results together with phylogeny analysis confirmed a diverse microbial community colonizing the surface of the permafrost.

Surface samples and the top active layer (0-4 cm depth) revealed positive immunoreactions with antibodies raised against cellular and extrapolymeric biopolymers from environmental extracts of an acidic environment, psychrophiles from Gamma-proteobacteria, Delta-proteobacteria, Firmicutes, other psychrophiles from the Bacteroidetes and Actinobacteria groups and some archaea. The phylogenetic analysis results were consistent with the immunological analysis in the top layer, which by these technique revealed a high level of prokaryotic diversity, mainly dominated by Actinobacteria, Cyanobacteria (*Nostoc* spp.), Acidobacteria and Proteobacteria (Alpha > Beta > Gamma > Delta subdivisions).

Lack of immunoreactions were detected below the top active layer, while phylogenetic surveys indicated a gradual increase in Beta-proteobacteria from 2 to 4,2 m of depth [4].

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