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## Lithic microbial communities from a Mars analogue site in Utah desert

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### Abstract

Several rock samples have been collected as part of a Mars field analogue campaign (NASA DOMEX-ILEWG EuroMoonMars) at Mars Desert Research Station (MDRS) area (Utah Desert, USA), and were analyzed with respect to the microbial diversity they support; a culture-independent approach resulted in DGGE band profiles descriptive of the composition of the 3 domains, Bacteria, Archaea and Eukarya.

### **1. Introduction**

As the potential presence of life on the surface of Mars today is limited by the extreme conditions, the strategy in looking for evidence of life on Mars will focus beneath Martian surface (underground, permafrost and rocks). Therefore, the overall survival strategy of endoliths gained special attention for Mars exploration, due to their potential as analogs for possible extinct and extant life on the planet. Mineralized endolithic communities could provide a biosignature of past life on Mars [1].

The endolithic habitat offers a quite stable habitat in extreme environments, providing protection from UV radiation flux, extreme temperature variations, and desiccation [1] [2]. However these microhabitats are limited by the oligotrophic and light conditions [3].

In this study we examined the microbial community composition associated with a hypolith and several endolith samples (Fig. 1) from the Mars Desert Research Station (MDRS) vicinity, in order to understand if rock type or other site characteristics influence the phylogenetic composition of the endolithic communities. Samples were collected between April-May 2011, during the campaign performed by Crew 104.

We characterized these micro-habitats in terms of microbial community distribution by culture independent techniques, such as polymerase chain reaction (PCR) and denaturing gradient gel electrophoresis (DGGE) analysis.



Figure 1:Endoliths from the vicinity of MDRS.

### 2. Methods

#### 2.1 Field sampling

The campaign took place in MDRS area, which is located in the southern San Rafael Swell area near Hanksville, Utah (USA), on Jurassic flood plain deposits. Samples were collectedfrom different locations: an overturned conglomerate boulder at Kissing Camel Ridge (Morrison Formation), Cedar Mountain Formation, Mancos Shale and Carmel Formation. The rocks are diverse, from naturally organic rich(coals and marine shales) to naturally organic poor (oxidized sandstones and shales). Mineralogyincludes sulphates, carbonates, quartzose rocks andclays.

With the exception of the hypolith and a gypsum sample, the rocks presented a superficial dark, thin layer, known as desert varnish on the surface, which was harvested from the rock and separately analyzed.

### **2.2 DNA Extraction**

PowerSoil DNA Isolation Kit (MOBIO Laboratories, Inc.)used according to the manufacturer's instructions.

# 2.3 Primers for 16S and 18S rDNAamplification and sequencing

Bacteria: 27F and 1492R ( $1^{st}$  set); 338F-GC and 518R ( $2^{nd}$  set); Archaea: 344F and 934R ( $1^{st}$  set);344F-GC and 518R ( $2^{nd}$  set); Eukarya: Euk 1A and 516R-GC ( $1^{st}$  and  $2^{nd}$  sets); Fungi: ITS1F-GC and ITS2 ( $1^{st}$  and  $2^{nd}$  sets).

### **2.4 DGGE Fingerprinting**

Denaturing gradients used for small subunit ribosomal RNA profiling: Bacteria 30-60%; Archaea 30-50%; Fungi 20-50% and Eukarya 20-35%.

### **3. Results**

The PCR-DGGE analyses reveal presence of microorganisms from the three domains (Bacteria, Archaea and Eukarya), with the exception of the hypolith were Archaea was not represented.

The band profiles describing the microbial communities from the desert varnish and the respective endolith did not display relevant differences.

The phylogenetic diversity is higher within the Bacteria. Regarding Archaea and Eukarya, the band profiles are less complex when compared to those describing the diversity of Bacteria, thus indicating a lower diversity within these two domains. Also Archaea and Eukarya communities are similar in samples collected from different sites.

### 4. Summary and Conclusions

In the present investigation we extend a previous study ofendoliths [4] to a larger area than the vicinity of MDRS.

The similarity found between microbial communities fromdifferent sites suggests that other factors than exclusively the rock composition must role the microbial distribution within desert habitats. Ambient irradiance, total organic content, water availability, and rock texture have been investigated [5][6].

A detailed characterization of the microbial communities and mineralogy of these rocks is indispensable to enhance our understanding of the correlations between microbesand rocks on terrestrial Mars analogues.Our biological data will be complemented by mineralogical characterization of samples using X-Ray Diffraction (XRD) analysis.

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