

Molecular characterization of rock microbial communities from the Mars analogue MDRS

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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). This report details the microbial diversity derived from culture-independent techniques, such as polymerase chain reaction (PCR) and denaturing gradient gel electrophoresis (DGGE) analysis.

1. Introduction

The present environment on Mars is hostile for the widespread proliferation of life. However, microorganisms may still survive in habitats that can provide a favorable microhabitat protecting them from the harsh conditions on the surface, e.g., within or under rocks.

The interaction between rocks/soil and the microorganisms plays a very significant role in the overall survival strategy of potential extremophiles.

The objective of this study was to study the bacterial community colonizing rocks in the Mars Desert Research Station (MDRS) area, in Utah Desert (USA), a Mars analogue. Combining these data with mineralogical analysis of the samples we expect to gain some preliminary insight about the role of mineralogical elements in controlling endolithic microbial communities.

2. Materials and methods

2.1 Sample collection

Representative samples were collected during the campaign of Crew 104 from MDRS area at Cedar Mountain Formation (Early Cretaceous) and Carmel

Formation (Jurassic) (San Rafael Swell of Utah Desert, USA). Two lithologies are present at Cedar Mountain Formation: 1) a conglomerate unit consisting of poorly stratified, coarse, well rounded coarse pebbly sandstone, coarse gravelly sandstone to gravelly conglomerate; and 2) a fine to medium grained sandstone unit, with coarse grains cemented by silica with minor carbonate.

2.2 DNA extraction, PCR-amplification and pyrosequencing

Prior to analysis, samples were ground to a fine powder, under sterile conditions.

DNA extraction from samples was conducted using the PowerSoil DNA Isolation kit according to the recommendation of the manufacturer (MoBio Laboratories, Inc.). DNA was amplified with a nested PCR approach, using the barcoded fusion universal primer pairs: 27F/338R, Arc344_titF/Arc934_titR, and ITS2F/ ITS2R. Amplicons were sequenced by using a Roche GS FLX 454 System.

2.3 Phylogenetic analysis

Sequences of four libraries were calculated with DOTUR and those with similarity greater than 97% were grouped into one operational taxonomic unit (OTU). Blast analyses were carried out using the *Classifier* program of RDP. Sequences were assigned to the genus level grouping with 80% confidence. The closest neighbors were retrieved from the NCBI through blasting.

2.4 Mineralogical Analysis

Sequences of X-ray powder diffraction (XRD), using Cu-K α radiation at 45 kV and 40 mA.

3. Results

Rock communities were dominated by a few highly abundant OTUs on all samples. The most abundant OTUs were Actinobacteria (139 OTUs, 27,86%), Proteobacteria (97 OTUs, 19,44%), Cyanobacteria (74 OTUs, 14,83%), Acidobacteria (66 OTUs, 13,23%), and Bacteroidetes (42 OTUs, 8,42%).

The most represented OTUs were related to the genus *Rubrobacter*. The members of rare phyla included: *Deinococcus-Thermus*, *Nitrosperae*, *Verrucomicrobia*, *Gemmatimonadetes*, and *Armatimonadetes*.

Figure 1: Community structure of rock samples from MDRS area.

Observed richness and diversity indexes reported by the Shannon index (table 1 TO BE ADD)

Table 1: Richness and diversity indexes for MDRS rocks based on 16S rRNA gene sequence assignments (95% sequence similarity threshold)

Samples	OTUs	Shannon index
	observed richness	Estimated diversity

5. Summary and Conclusions

In the present investigation we continued previous studies of endoliths in the area of MDRS [2] [3].

The sampling efficiency was demonstrated to be a crucial steps on samples with high gypsum content.

The yield of highly similarity(/variability?) (TBC) found between microbial communities from different rocks suggests that other factors than exclusively the rock type and mineralogy must role the microbial distribution within desert habitats, and will be discuss in this presentation.

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