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MS-008

CHARACTERIZATION OF MINERAL-ASSOCIATED MICROBIAL ECOSYSTEMS (EMAM) IN LAGOONS OF THE ANDEAN PUNA

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The Andean Microbial Ecosystems Associated with Minerals (EMAM) are associations of bacteria, cyanobacteria and Haloarchaea that influence or induce the precipitation of minerals in lagoons, hydrothermal vents, fumaroles of volcanoes and Puna salares. They include microbial mats, microbialites, biofilms and endoevaporites. Those in the Puna are the highest described so far and due to the extreme conditions that give rise to altitude (high UV radiation, low O2 pressure, abrupt temperature changes, oligotrophy, etc.) these ecosystems are the most similar to the primitive Earth that is known in the planet. The general objective of this work is to characterize microbial ecosystems of different high altitude lagoons (Ojos de campo, Pozo Bravo, and a fumarola near the Diamond Lagoon) from the province of Catamarca, Argentina, including microbial mats and microbialites of sites not previously studied. DNA isolation of the samples were performed using different protocols, including CTAB, methods used for saline sediments, and kits for processing microbial mats (MoBIO). Subsequently a DNA quality analysis was performed by electrophoresis and UV absorption spectroscopy. The success of the methods employed was confirmed by PCR reactions with oligonucleotides to amplify the 16S rDNA gene (F27 and R1492). Amplicons libraries from the V4 region of the 16S rDNA gene, using the Bakt-341F and Bakt_805R oligonucleotides were constructed. These libraries were sequenced on the Illumina platform. Diversity data by 16S rDNA were analyzed using the QIIME software. This analysis allowed to define the biodiversity of the microbial ecosystems under study. The results indicate the presence of archaea and bacteria in these samples. A comparison of the study environments with other Puna environments previously analyzed shows that they are grouped with other microbial mats, differentiating them from other microbial communities with structures such as evaporites, but a clear difference is not seen with the microbialites. Some specific groups are more abundant in evaporite mats, such as the genus *Salinivibrio*. Microbial mats are divided into two classes. In the first group, there are abundant *Alphaproteobacteria* of the family *Rhodobacteraceae* and *Gammaproteobacteria* of the family *Marinicellaceae*, whereas in the second group there are important *Deltaproteobacteria* of the family *Desulfobacteraceae*. This work represents a new contribution to the bioprospecting of Andean Puna environments, and will help to select sites for further exploration.

MS-009

SELECTION OF VINASSE-DEGRADING MICROORGANISMS

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One of the main problems of the sugar-alcohol industries is the generation of large volumes of vinasse. The release of this acid effluent generated during the alcoholic distillation causes an undesirable environmental impact as consequence of the high content of organic matter and other toxins. Many technologies based on vinasse conditioning by microbial pathways are continuously evaluated in order to mitigate their environmental impact. In the current study, a preliminary selection of microorganisms from the soil with the potential to grow and degrade effectively the sugarcane vinasse was performed. To perform the isolation, two vinasse concentrations in distilled water (10 and 30%, v/v) added with 2% agar (w/v) were used as selective solid media (VS10 and VS30). An aqueous suspension obtained from a sugarcane vinasse-contaminated soil was inoculated in the VS media. A suspension obtained from same soil but without vinasse was also inoculated in these media to be used as controls. After 48 h of incubation at 30ºC, spores of the microorganisms developed in the VS media were harvested and quantified to be inoculated in a liquid medium consisting of 30% vinasse in distilled water (VL30). At the 72 h of incubation in VL30 at 30ºC, 150 rpm, the biomass concentration was measured by estimation of the dry weight at 80°C, while the biological oxygen demand was quantified by BOD5 standard method. Under the current assay conditions, microbial growth was not detected in the VS media from the soil samples without vinasse. However, two types of colonies from soil exposed to raw vinasse were isolated using VS30 as a selective medium. Microscopical observations of the two isolates denoted as V1 (spores pink) and V2 (green spores), revealed sparsely branched and septate hyphae as well as the presence of aspergillary heads. Both isolates were able to grow in VL30 and remove over 50% of the biodegradable organic matter, suggesting a proportional reduction in the effluent toxicity. This finding could be promising in terms of the future application of both strains for recovery of effluents with high load organic like vinasse. Supported by PICT 2015 Nº 0297 and CONICET.