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## MS-016

**METAGENOMIC ANALYSIS OF MICROBIAL MATS FROM BRAVA AND TEBENQUICHE LAKES**

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In this work, nucleic acid-based molecular methods, geochemical measurements and physico-chemical characteristics were combined to investigate microbial sedimentary ecosystems of Laguna Tebenquiche and Laguna Brava. Molecular diversity of two hypersaline microbial mats was compared by WGS sequencing of environmental DNA from the mats. Brava and Tebenquiche are lakes in the Salar de Atacama, Chile, where microbial communities are growing in extreme conditions, including high salinity, high solar insolation, and high levels of metals such as lithium, arsenic, magnesium, and calcium. Evaporation creates hypersaline conditions in these lakes and mineral precipitation is a characteristic geomicrobiological feature of these benthic ecosystems. Microsensor measurements on the mats allowed determination of depth profiles of O<sub>2</sub> and sulfide, showing active production and respiration. The mat from Brava was more rich and diverse, with a higher number of different taxa and with species more evenly distributed. At the phylum level, Proteobacteria, Cyanobacteria, Chloroflexi, Bacteroidetes and Firmicutes were the most abundant, including ~75% of total sequences. At the genus level, the most abundant sequences were affiliated to anoxygenic phototrophic bacteria from the genera *Roseoflexus*, *Chloroflexus* and *Oscillochloris*, followed by cyanobacterial genera such as *Microcoleus*, *Cyanothece* and *Nostoc*. In Tebenquiche mats, Proteobacteria and Bacteroidetes covered ~70% of the sequences, with Cyanobacteria and Firmicutes including 5% each. Over 13% of the sequences were affiliated to *Salinibacter* genus, thus addressing the lower diversity. Other Bacteroidetes genera with more than 1% abundance included *Rhodothermus* and *Bacteroides*. Finally, the Alphaproteobacteria *Rhodospirillum* was also important. In spite of the differences at the taxonomic level, the two mats were functionally similar. Thus, similar roles could be fulfilled by different organisms. For example, primary production, performed mainly by photosynthetic organisms from the phyla Cyanobacteria and Chloroflexi in Brava, is performed by members of Alphaproteobacteria in Tebenquiche. Further comparison with other microbial mats will allow identifying unique genes from these environments related to their extreme characteristics.

## MS-017

***Rhodopseudomonas palustris* AZUL: A NEW MEMBER OF THE ELECTRO-ACTIVE BACTERIA CLUB?**

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Among current alternatives for non-polluting electricity generation, some depend on the activity of biological catalysts. The use of electrogenic bacteria in bio-electrochemical systems is a good example that calls particular attention due to its low cost, innocuousness and potential applications. In the last years, the search for microorganisms capable of exchanging electrons with a polarized electrode has become significant when aiming at improving the production of electrical energy in such systems. In this work, we explore the capacity of an autochthonous strain of *Rhodopseudomonas palustris* (AZUL strain) of growing in continuous culture electrochemical bioreactors interacting with an electrode. *R. palustris* belongs to the group of purple non-sulphur photosynthetic bacteria and has an extraordinary metabolic versatility which allows it to grow under any of the four modes of metabolism: photoautotrophic, photoheterotrophic, chemoautotrophic and chemo-heterotrophic. A phylogenetic analysis based on 23S rRNA gene indicated that strain AZUL has a closest match to CGA009, TIE-1 and DX-1. The latter two are strains which interaction with an electrode has been previously reported. *R. palustris* AZUL was capable of growing in bioreactors, forming biofilms on graphite electrodes under photoheterotrophic conditions. Electrochemical assays showed that biofilms formed on electrodes under various applied potentials (polarized) had specific redox signals which varied with light, polarization time and potential value. Despite these signals, current obtained from biofilms in chronoamperometric assays did not overcome 9.5 μA/cm<sup>2</sup>; moreover, we could not see any relationship between current magnitude and biomass accumulation on the electrode. At least two well defined redox pairs centered at 0,4 and 0,6V (Ag/AgCl- 3M NaCl) were detected whose amplitude depended on imposed conditions. On the other hand, SEM images revealed differences in the structure of biofilms grown on polarized and non-polarized control electrodes. These results indicate that *R. palustris* AZUL possesses extracellular electron transfer mechanisms which do not seem to be directly related to cellular respiration, but probably to a mechanism of protection against oxidative stress. Due to its ease of culture in laboratory and its extraordinary metabolic versatility, the study of optimal conditions in which this bacterium exchanges electrons to a polarized electrode in a bioelectrochemical system, deserves to be extended aiming at developing technological applications.