

Life in Oligotrophic Desert Environments: Contrasting Taxonomic and Functional Diversity of Two Microbial Mats with Metagenomics. G. Bonilla-Rosso¹, M. Peimbert², G. Olmedo³, L.D. Alcaraz³, LE Eguarte¹ and V. Souza¹. ¹Depto. Ecología Evolutiva, Instituto de Ecología, UNAM., ²Depto. Ingeniería Celular y Biocatálisis, Instituto de Biotecnología, UNAM, ³Depto. Ingeniería Genética, CINVESTAV-Irapuato. (germanbr@gmail.com)

Introduction: Cuatrociénegas Basin is an enclosed endovaporitic basin that harbors an extensive system of springs and pools in the heart of the Chihuahuan desert. Despite being an arid system with very low available phosphorus concentrations [1], it hosts a large degree of bacterial diversity [2] along with a wide array of complex communities forming microbialites and bacterial mats [3].

In order to shed some light on how such an oligotrophic environment can sustain complex communities, we chose two microbial mats from two physico-chemically contrasting ponds within the basin. These ponds also represent two contrasting conditions of environmental variability, one being fairly permanent and stable (PG) and the other being a variable desiccation pond (PV). We built 16SrRNA clone libraries and pyrosequencing for each mat in an effort to assess and compare the taxonomic composition and functional potential of the two communities.

Community Structure and Composition: Both clone libraries and metagenomic markers show a high diversity in both mats, though the nature of the diversity is different in each case: PG displays a high diversity at phylum level with little to no dominance of any specific taxa, while PV has a large diversity within a single taxonomic group. The most abundant taxa in PV is the *Pseudomonas* group, while in PG these are Cyanobacteria, GN02, OP11 and Chlorobi. Even though the two mats share phyla, only 9 OTU's are shared between communities and community structure and composition is statistically different. This suggests that seasonal disturbances deeply impact diversity at phylum level while it promotes diversification of specific groups at species/genus level.

Functional Potential: As reported for other microbialites from the basin [3], a very low percentage of reads could be assigned to functional categories (24.61% for PG and 28.27% for PV), and the most abundant category in both mats was Clustering-Based Subsystems, which is not an actual category.

The second most abundant category in both mats is Carbohydrate metabolism, where both mats are dominated by Serine-glyoxylate cycle, mainly by reads hitting proteins related to malate interconversion, and Maltose/Maltodextrin utilization. In this category a significant difference can be observed: the most abundant pathways in PG are all related to aerobic (TCA cycle, aerobic dehydrogenase complexes, PEP

anaplerotic reactions, glucolysis) and oxygenic photosynthesis (CO₂ uptake, Calvin cycle, carboxysomes), while in PV fermentations (Lactate, glycolate and isositol degradation).

Differences in fermenting pathways are a preference for the pentose-phosphate pathway in PG and glyoxylate/glycolate cycle in PV, and a large abundance of phosphoglucomutases from the Sucrose metabolism in PG. All this suggests that PG dynamics are mainly sustained by photoautotrophic organisms, while PV is dominated by chemoorganotrophic organisms.

Other remarkable differences are an elevated proportion of virulence, stress response, motility/chemotaxis and cell signaling in PV, revealing a large investment in metabolisms related to communication between cells (probably from biofilm production in *Pseudomonas*) and a fast response to rapidly changing environmental conditions, while in PG cell housekeeping is more abundant (Protein, amino acids, cofactors and vitamins). Finally, a large increase of Aromatic Compounds metabolism, mainly benzoate and phenylpropanoid, is observed in PV.

PG displays a slightly larger abundance of P metabolism, mostly related with alkaline phosphatases, exopolyphosphatases, inorganic phosphatases and phosphate transport systems, while in PV P-metabolism is dominated by acyltransferases and phosphate kinases. In both systems, inorganic phosphate metabolism is more abundant than organophosphorus compound metabolism.

Metagenomic analysis opens an unprecedented opportunity to simultaneously analyze taxonomic composition and functional potential of natural microbial communities. The present work sets a precedent to the analysis of complex microbial communities in low-phosphorus environments, revealing relevant differences in both community composition and metabolism.

References:

- [1] Elser J. et al. (2005) *Freshw Biol*, 50, 1808–1825. [2] Souza V. et al. (2006) *PNAS*, 103, 6565–6570 [3] Breitbart M. et al. (2008) *Environ Microbiol*, 11, 16–34.