

# Exploring metabolic interactions of highly diverse archaea in microbial mats from the Atacama desert

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Since the recognition of the Archaea as a third domain of life in the late 1970s, a wide diversity of archaeal lineages without cultures representatives has been, and is still being, uncovered by 16S rRNA-based environmental exploration. Many of these lineages may carry out key ecological roles in ecosystems, such as the nitrifying Thaumarchaeota, and/or hold clues for understanding evolutionary history, such as the eukaryotic-like Asgard archaea. Getting genomic information about uncultured archaeal groups is an affordable way to access information about their function, ecology and evolution. Recently, we carried out a 16S/18S rRNA-based metabarcoding study to characterize the diversity of microorganisms belonging to the three domains of life in four microbial mats (and different layers) distributed along sharp physicochemical gradients (depth, oxygen, salinity and temperature) in a warm shallow pond of the salar of Llamara (Atacama, Chile). Archaea were highly diverse and, in the deeper, anoxic layers, they made up to 40% of the microbial diversity. We detected members of various uncultured clades, notably Pace- and Woesearchaeota, but also Thor- and Lokiarchaeota along with six novel archaeal lineages. phyla (Saghaï et al). Since microbial mats are highly complex communities where many metabolic syntrophic interactions take place, we carried out co-occurrence networks to identify potential partners of archaeal lineages. To further understand potential metabolic interactions that operate in these mats, we have generated metagenomic data from different layers in the four microbial mats under study. After metagenomic assembly and annotation, we looked for diagnostic genes of key metabolic pathways that are operating in these systems (e.g. photosynthesis, sulfur and nitrogen cycles) and carried out co-occurrence networks of these metabolic genes. Our data indicate that methanogenesis, hydrogen transfer and iron dependence are essential processes in the anoxic layers of these microbial mats and suggest potential interactions between specific lineages.

SAGHAÏ A, GUTIÉRREZ-PRECIADO A, DESCHAMPS P, MOREIRA D, BERTOLINO P, RAGON M & LÓPEZ-GARCÍA P. Unveiling microbial interactions in stratified mat communities from a warm saline little pond. *Environ Microbiol*, in press