

DIVERSITY AND DISTRIBUTION OF PROKARYOTIC COMMUNITIES IN A COASTAL LAGOON INFLUENCED BY SEASONAL UPWELLING

Guadalupe Hernández^{1,2}, Silvia Pajares¹, Guillermo Samperio³

¹ Institute of Marine Science and Limnology, National Autonomous University of Mexico, Mexico.

² Postgraduate in Biological Sciences, National Autonomous University of Mexico, Mexico.

³ Institute of Oceanological Research, Autonomous University of Baja California, Baja California Mexico.

E-mail: guadalupeangeles.hl@gmail.com, spajares@cmarl.mx

Coastal lagoons are dynamic transitional ecosystems influenced by hydrodynamic and biogeochemical processes. Their sediments host a wide variety of microbial communities that play important roles in biogeochemical cycles and sequestration of organic matter and contaminants. However, there is still little information about the composition and distribution of these communities in relatively pristine coastal lagoons. In this study, we used 16S rRNA gene sequencing (Illumina MiSeq) to analyze the diversity and distribution of prokaryotic communities in sediments from San Quintín Bay, a shallow lagoon with minimal anthropogenic impact and seasonal upwelling, on the Pacific coast of Mexico. Sediment samples were collected from four sectors (outer mouth, inner mouth, transition zone, and head), two habitats (with and without *Zostera marina*), and two contrasting upwelling seasons (relaxation: October 2021; intense upwelling: June 2022). Gammaproteobacteria, Deltaproteobacteria, Alphaproteobacteria, Flavobacteria, and Actinobacteria were the most abundant taxa. Despite strong physicochemical gradients, preliminary results suggest that these sediments host highly diverse and relatively stable prokaryotic communities across different sites, habitats, and seasons. This stability may be related to the relatively pristine conditions of the system. This study offers a useful baseline to understand microbial ecology in coastal sediments shaped mainly by natural oceanographic processes.