

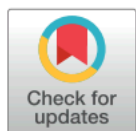
RESEARCH ARTICLE

The microbiome of modern microbialites in Bacalar Lagoon, Mexico

Alfredo Yanez-Montalvo^{1,2}, Selene Gómez-Acata¹, Bernardo Águila¹, Héctor Hernández-Arana², Luisa I. Falcón^{1*}

1 UNAM, Instituto de Ecología, Parque Científico y Tecnológico de Yucatán, Sierra Papacal, Yucatán, México, **2** El Colegio de la Frontera Sur Unidad Chetumal, Chetumal, Quintana Roo, Mexico

* falcon@ecologia.unam.mx



Abstract

Microbialites are highly diverse microbial communities that represent modern examples of the oldest life forms, stromatolites (dated >3.7 Ga). Bacalar Lagoon, in Mexico, harbors the largest freshwater microbialite occurrences of the world; yet diverse anthropogenic activities are changing the oligotrophic conditions of the lagoon. The objective of this work was to perform a spatial exploration of the microbialites of Bacalar Lagoon, analyze their prokaryote diversity, following a high throughput sequencing approach of the V4 region of the 16S rDNA, and correlate to the environmental parameters that influence the structure of these communities. The results indicate the presence of microbialites throughout the periphery of the lagoon. The microbiome of the microbialites is composed primarily of Proteobacteria (40–80%), Cyanobacteria (1–11%), Bacteroidetes (7–8%), Chloroflexi (8–14%), Firmicutes (1–23%), Planctomycetes (1–8%), and Verrucomicrobia (1–4%). Phylogenetic distance analyses suggests two distinct groups of microbialites associated with regions in the lagoon that have differences in their environmental parameters, including soluble reactive silicate (in the north), bicarbonates and available forms of nitrogen (ammonium, nitrates and nitrites) (in the south). These microbialite groups had differences in their microbiome composition associated to strong anthropogenic pressure on water quality (agriculture, landfill leachate, lack of water treatment infrastructure and intensive tourism), which were related to a loss of microbial diversity.

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Introduction

Bacteria and Archaea (prokaryotes) represent the most diverse and abundant organisms on the planet [1]. They are involved in maintaining and controlling biogeochemical cycling of the fundamental elements of life (H, C, N, O, S and P) [2]. Understanding the multiple ecological and evolutionary processes that are related to the distribution and structure of prokaryote diversity at the local and global scales is a main interest of microbial ecology [3–4]. The formation of biogeographic distribution patterns in prokaryotes is determined by environmental heterogeneity (ecological factor) and dispersion (historical factor) [5]. At the local scale, factors that include pH, habitat heterogeneity, system productivity, and more recently, human