

Patterns of nitrogen fixation and related genetic diversity (*nifH*) in microbial mats and stromatolites from different environments. Y. Beltrán¹, C. Centeno¹, L.I. Falcón¹ ¹Instituto de Ecología, UNAM. Circuito Exterior sn, Ciudad Universitaria, México 04510. (yislem@gmail.com; centenocarla@hotmail.com; falcón@ecologia.unam.mx).

Introduction: Microbial mats and microbialites are organo sedimentary structures formed by the interaction of the microbial community and the physicochemical environment. These structures have been compared to micro scale ecosystems and their ecological and evolutive importance has been acknowledged. The aim of this study was to estimate the patterns of nitrogen fixation and the related genetic diversity (*nifH*) of microbial mats and microbialites on dial and temporal scales along a physicochemical and geographical gradient. The overall pattern of nitrogenase activity was similar, with the highest rates of activity occurring during the light period, suggesting the importance of cyanobacteria. All communities showed higher fixation rates in the summer coinciding with the increase of dissolved inorganic phosphorus. Stromatolites from crater-lake Alchichica, in central Mexico, had an order of magnitude greater rates of nitrogen fixation than all other sites, with stromatolites from Cuatro Ciénegas, in northern Mexico exhibiting the lowest rates. Nevertheless, the N:P ratio was proportional between communities that showed large differences in nitrogen fixation rates, suggesting that communities recycle P as an ecological strategy. The microbial C:N ratios showed that the N-content of microbial mass is low, but in summer with the increase in nitrogen fixation, C:N ratios decreased, suggesting the importance of diazotrophy in these communities. Statistical analysis revealed that communities are structured along a gradient in temperature, nitrogen fixation rates and dissolved inorganic forms of nitrogen. Genetic diversity of *nifH* sequences showed that phylogenotypes recovered from these mats pertained to Proteobacteria and Cyanobacteria, although each site had species specificity.