Interdisciplinary Studies of a Marine Microbial Mat Ecosystem, Baja California, Mexico

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Introduction: Cyanobacterial mats in extensive seawater evaporation ponds at Guerrero Negro, Baja California, Mexico, have been excellent subjects for interdisciplinary research. Exportadora de Sal, S.A. (ESSA) has maintained this solar saltern since the 1950s. The following entities provided research support: NASA Exobiology (1984-1988), Precambrian Paleobiology Research Group (1986-1993), NAI (1998-2010), and Exobiology (2010-2016). This summary emphasizes research that was supported by the NAI and conducted by its teams.

Biogeochemistry: Permanently submerged *Microcoleus*-dominated cyanobacterial mats occur in the salinity range 65 to 120‰. They maintain rapid rates of biogeochemical processes and experience steep and rapidly changing environmental gradients at the mm scale. Light exhibited both a strong decline in intensity and a marked change in its spectral composition within a few mm from the mat surface. Minima in the spectra corresponded to the absorption maxima (430 and 670 nm) of cyanobacterial photosynthetic pigments. Longer-wavelength light, particularly longer than 900 nm, penetrated farthest into the mats. High rates of oxygenic photosynthesis in the mat's shallow photic zone created steep and variable gradients in pH and in concentrations of dissolved inorganic C (DIC) and O_2. O_2 diffused downward where it overlapped with sulfide diffusing up from below; abundant anoxygenic phototrophic bacteria and aerobic sulfide oxidizers typically inhabited this interval. Each evening the oxic zone collapsed quickly and the oxic-anoxic boundary approached the mat surface. ATP concentrations were more than four times greater in the oxic zone (defined as the topmost ~2 mm mat layer that becomes oxygenated during the day) than in the underlying anoxic zone (~2 to ~6 mm depth). Observations of the cycling of C, O and S illustrated the intimate interactions between mat processes. During the day most of the O_2 produced was recycled within the mat by O_2 respiration and, to a lesser degree, by sulfide oxidation. At night, O_2 was consumed principally by sulfide oxidation near the mat-water interface. The principal source of DIC at night was microbial sulfate reduction. During the day more DIC diffused into the mat than O_2 diffused out. At night more DIC diffused out of the mat than O_2 diffused into the mat. However both the net O_2 and the net DIC fluxes were balanced over the 24-hour cycle. The rates of the key processes that cycled C, O, and S all increased strongly with temperature by the same amount. High rates of photosynthetic C fixation fueled high rates of C oxidation in this closely coupled system. Rates of N_2 fixation were highly variable, with highest rates occurring at night. Recycled fixed N apparently provided most of the required N. Efficient oxidation of organic components regenerated nutrients that, in turn, maintained high rates of primary production.

Microbial populations: Genetic studies revealed an enormous microbial diversity as well as a highly structured spatial distribution of Bacteria, Archaea and Eukarya. Combined universal clone libraries from all mat layers indicated that the Bacteria/Archaea/Eukarya ratio was 57:7:1. When two quantitative estimators of richness were used to analyze the distribution of observed sequences, they indicated that >10,000 unique bacterial sequences were present. These assessments indicated that diversity of these mats was very high and most of it had not yet been described. The cyanobacterial genes attained their greatest relative abundance in the oxic zone, whereas *Chloroflexi*, *Proteobacteria* and *Bacteroidetes* maintained high relative abundances throughout the topmost 60 mm of mat. Populations of sulfate reducing bacteria (SRB) varied with depth in the mats. Archaea constituted about 1 to 4% of the uppermost 100 mm of mat. The relative abundance of Archaea increased with depth. Below 100 mm, archaeal lipids were twice as abundant as bacterial lipids. Archaeol was the most abundant archaeal lipid throughout the mat. Incubations of samples from near the mat photic zone were dominated by *Methanolobus* spp., whereas sediments from beneath the mat (>100 mm depth) yielded principally *Methanococcoides.* Only 15 species of Eukarya were found among 890 clones analyzed, indicating a remarkably low diversity. Nematodes constituted more than half of the total sequences and were dominated by members of the *Monhysteridae* and *Rhabdolaimidae* families. Other sequences represented an insect, a crustacean, and a stramenopile. One cluster had no kingdom-level affiliation with known sequences.

Significance: This research demonstrated how highly interdisciplinary teams contributed substantially to our understanding of these highly complex photosynthetic microbial mats. Current research is investigating the origins, transformations and fates of lipid biosignatures in benthic microbial mat ecosystems.

Reference: Des Marais, D.J. (2010) Marine hypersaline *Microcoleus*-dominated cyanobacterial mats in the saltern at Guerrero Negro, Baja California Sur, Mexico. In *Microbial Mats*, J. Seckbach, editor, Cellular Origins, Life in Extreme Habitats and Astrobiology (COLE) Series, Springer, pp. 401-420.