DISTRIBUTION OF BACTERIA IN SEDIMENTS FROM CONCEPCION BAY, CHILE

Chiang, O.[1]; González P.[1]; Green-Ruiz, C.[2]; Laverde-Castillo, J.[3]; Moraga, R.[4]; Palma, M.[1]; Rodríguez-Tirado, V.[2]; Santacruz-Reyes, R.[5]; Molina V. [1,7]; Ulloa O.[1,7]; Hanselmann, K.[6,7]

[1.]U. de Concepción (Chile); [2.]UNAM (México); [3.]U. del Magdalena (Colombia); [4.]U. Arturo Prat (Iquique, Chile); [5.]U. Técnica de Machala (Ecuador); [6.]Universidad de Zurich, Suiza; [7.]Course organizer.

Annual anoxia in deep waters and El Niño associated upwelling events, which are common along the South American Pacific coast, are strong ecosystem determinants of the inner continental shelf areas. Microbial population diversity allows the community to respond rapidly to variations in chemical and physical determinants associated with these environmentally driven events. Most notably, at certain times the sediments are covered with white veils consisting of trichome bundles of *Thioploca sp.* and by *Beggiatoa sp.*, at other times they are not.

During the Marine Microbiology Course (ECODIM 2003), a combination of molecular biological, physical and chemical techniques were employed to study the diversity and the interactions between microorganisms in sediments collected from stations 7 (mouth of Bay, 36 m depth) and 14 (inner continental shelf, 64m depth). To determine the vertical distribution of bacteria and their habitat conditions, nutrient concentrations, organic matter content and porosity in sediment cores were analyzed, bacterial production was estimated, DNA was extracted for the identification of bacterial groups based on 16S rDNA genes and enrichements were made for predominant bacteria. Total bacterial abundances were determined by flow cytometry after DNA staining with Sybr green I in samples from 3 depths of the two stations. Differences in community diversity were judged from RFLP patterns using 16S rDNA amplified with universal bacterial primer and digested with *EcoR1* and *HaeIII* restriction enzymes.

Abundance (Bact 10^3/mL) and bacterial secondary production (BSP by C^{14} Leucine incorporation) have the same patterns as the organic matter content (% MOT) in the sediment. The gradients in enrichment tubes suggest that reduction of Fe(III) and/or SO_4^{2-} occurrs. This is in accordance with the bacterial abundances observed. We were able to isolate total DNA from sediment mud and to amplify 16S rDNA fragements.

The nutrient profiles observed at both sampling stations were similar and *Beggiatoa* and *Thioploca* mats were sparse at both locations at the time of sampling. Bacterial abundance at station 7 decreased with depth, and samples from station 14 showed less abundance in comparison to those from station 7. This difference was confirmed by flow cytometric counting. Production rates reflect bacterial abundance and organic matter content. With the restriction enzymes employed, distinguishable patterns were obtained for both stations. Digestion with *EcoR1* gave the same pattern for all 3 levels, whereas fragments derived from digestion with *HaeIII* indicated gene polymorphism at the 3 depth levels. The enrichments for SRBs (sulfate reducing bacteria) were positive for station 14.

Sediments at the two locations are vertically structured ecosystems in which microbial abundance and activity is strongly influenced by the periodic availability of detrital organic matter settling to the ocean floor and by periodic changes in environmental conditions.