

Bacteria and Archea biodiversity in sediments of Venice Lagoon and their impact on sediment anoxia

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Introduction: During the last decades administrators and scientists focused on ecosystem processes designing and implementing a large program of actions targeted to reduce pollution and restore morphology and hydrodynamics of the Venice lagoon. While a very large programme investigations and studies was carried out on environmental and engineering issues, very little was done to assess the state of microbial communities in the lagoon and to explore possible future changes of those communities. The aim of this study was the description of the structure and phylogenetic composition of bacterial and archaeal communities of the lagoon sediments as the best markers for evaluating environmental changes and impact on this ecosystem.

Methods: sediments were collected in nine stations of the Venice lagoon, located in the four main sub-basins[1]. Sediments were characterized for grains-size and nutrients contents. Bacteria were microscopically counted after DAPI staining and total DNA was extracted and purified [1]. Amplified Ribosomal Intergenic Spacer Analysis (ARISA) fingerprinting was performed on the extracted DNA as described elsewhere [2] and the obtained electropherograms were statistically compared by Principal Component Analyses (PCA). 16S rRNA genes were amplified from sediment DNA, using universal primers for bacteria and archaea [3, 4] A total of 343 clones were sequenced from six clone libraries Phylogenetic affiliation of each sequence was determined by alignment with public sequence databases (BLASTN and Ribosomal Database Project websites).

Results and Discussion: Microbial community structure and diversity in the wide and shallow Venice lagoon were assessed in nine stations representative of different four sub-basins previously selected on the basis of international guidelines for sediment quality. The sediments were mostly anoxic and colonized by microbial communities whose species richness was quantitatively correlated with low redox potential. ARISA fingerprinting clustered the stations in three groups colonised by similar

bacterial communities. One station for each group has been hence analyzed in detail for bacterial and archaeal diversity by the screening of 16S rRNA gene clone libraries. The dominance of Gamma proteobacteria (84% of the clones with a high proportion of *Vibrionaceae*, indicator of urban pollution) determined a significant divergence of the station adjacent to industrial and metropolitan areas. *Bacteroidetes* were widespread especially where prairies of aquatic plants are located. The other two analysed stations were dominated by bacterial taxa involved in the sulphur cycle: the anoxygenic photosynthetic *Chromatiales*, sulphate and sulphur reducing Delta proteobacteria (*Desulfobacterales* and *Desulfuromonadales*) and members of the Alpha and Epsilon proteobacteria. The sequences present in the archaeal libraries belonged to *Euryarchaeota* (56-92%) and *Crenarchaeota* (8-44%). Besides *Thermoprotei*, known to comprise anaerobes and sulphur reducers[5], the majority of the archaeal sequences in all the samples belonged to unidentified classes. Results showed the presence of a complete sulphur cycle in the lagoon sediments, and indicated urban wastes as the major important impacting factor on microbial biodiversity. This research represents also a good baseline to assess evolutionary trends of microbial communities.

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