



## **Influence of natural and anthropogenic disturbances on benthic communities in four lagoons of the Po delta system: focus on microbial assemblages**

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Benthic communities inhabiting river lagoons are subjected to several natural (e.g. hypoxia and anoxia events) and anthropogenic disturbances such as excessive organic and nutrient loads from urban, industrial and agricultural discharges and high contamination levels. To investigate how benthic microbial communities (prokaryotes and microphytobenthos-MPB) respond to these disturbances, in the framework of the Project RITMARE, surface sediments from four coastal lagoons of the Po River delta were sampled in May 2016 (3 sampling sites in each lagoon): two with more marine features (Scardovari and Caleri) and two more directly affected by the Po River flow (Canarin and Vallona-Marinetta). Prokaryotes distribution was analyzed by hybridization techniques (CARD-FISH); MPB by inverted light microscopy (400x final magnification). The abundance and structure of benthic communities were related to physical-chemical parameters (grain-size, Organic C and synthetic organic contaminants: PAHs, PCBs, DDX).

High densities of Bacteria and Archaea were observed at sites directly influenced by the freshwater input and a significant correlation between prokaryotes abundance and Organic C was highlighted. Delta-, Alpha- and Gamma-Proteobacteria were the dominant classes at all sites. Deltaproteobacteria, that include sulfate reducers typical of anoxic conditions, were more abundant in Canarin. Beta-Proteobacteria, a typically freshwater class, displayed the highest abundances at sites characterized by the lowest salinity where also Gamma-Proteobacteria, that include pathogens of fecal origin (e.g. *Escherichia coli*), were well represented.

MPB abundances in Marinetta-Vallona and Canarin were almost double ( $81600 \pm 22735$  and  $81200 \pm 50938$  cells  $\text{cm}^{-3}$ , respectively) compared to Scardovari and Caleri ( $42350 \pm 19131$  and  $48700 \pm 10086$  cells  $\text{cm}^{-3}$ , respectively) likely due to freshwater nutrient loads. In Marinetta-Vallona and Canarin, the higher relative abundance of Chlorophyceae, Cyanobacteria and freshwater planktonic diatoms was a clear signature of the major river inflow. Cluster and nMDS analyses highlighted different MPB communities both at the intra-lagoonal level (among stations within the same lagoon), and inter-lagoonal level (among the four lagoons). Diversity indices revealed that the MPB community was more biodiverse at stations closest to the sea due to the concomitant presence of marine and brackish species, compared to the innermost stations where the lowest biodiversity was observed. Under organic enrichment conditions, as those encountered in Marinetta-Vallona due to intensive clam farming, *Nitzschia tryblionella* that prefers high organic loads was the most represented species (RA =19.1%). The benthic diatom community, through the selection of specific living forms, appeared to be affected by contaminants to some extent. In Canarin, the most contaminated lagoon, diatom living forms that are scarcely or not at all associated with the sediments prevailed over the typical benthic forms, suggesting a negative influence attributed to contaminants accumulated in the sediments.

However, the contamination levels in Canarin did not seem to severely affect the microbial benthic communities that showed to be overall stimulated by the combined effect of high organic and nutrient loads.