BACTERIAL AND ARCHEAL COMMUNITIES IN THE ANOXIC SEDIMENTS OF THE VENICE LAGOON

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Abstract

Sediments were sampled in nine stations representative of different ecosystems of the lagoon. The metabolic profile of each sediment was screened with AN-BiologâĎć for anaerobic bacteria. The structure of the bacterial communities was also analysed by Automated Ribosomal Intergenic Spacer Analysis (ARISA) allowing grouping the samples according to their similarity in community composition. One sample for each group was described in detail by the screening of 16S rRNA libraries, showing the dominance of Alteromonadales and Vibrionales, indicators of urban pollution around the city of Venice and Chioggia. Gamma-, Delta-Proteobacteria, Bacteroidetes and other minor taxa dominated the other stations. Among archaea, uncultivated and unidentified Euryarchaeota belonging to the Thermoplasmatales and Methanomicrobium groups were detected.

Keywords : Sediments, Anoxia, Bacteria, Biodiversity, Genetics.

Introduction

The lagoon of Venice is a large shallow water system (550 km2, mean depth 1m). It surrounds the city of Venice (Italy) and has been exploited for several purposes. During the last 20 years, the attention focused on the restoration of the lagoon equilibrium, planning a drastic decrease of nutrients and pollutants with a sensible beneficial effect on sediments, water, and biota quality. Lagoon sediments are are colonized mainly by anaerobic microorganisms. The aim of the work was to characterise the microbial communities of the lagoon sediments. This characterisation served to establish be a "state of reference"of the microbial sediment colonisation, useful to predict water anoxia, one of the most undesirable occurrences.

Methodology

The sediments were taken with a corer and the first 3 cm of three different cores were mixed to obtain a more representative sample of the station. Some environmental parameters such as pH and Eh were determined in situ, whereas the abundance of microbes were determined in the laboratory by microscope and total DNA analysis. Metabolic profiles of the microbial communities were screened with AN-BiologTM for anaerobes and analysed by Principal Component Analysis (PCA). The structure of the bacterial populations was analyzed with the PCR-fingerprinting technique Automated Ribosomal Intergenic Space Analysis (ARISA) [1]. PCA applied to the obtained fingerprints grouped the samples in three groups hosting similar bacterial communities. From selected stations, 16S rRNA libraries were constructed using bacteria- and archaea-specific primers.

Results and discussion

Seven out of nine stations were anoxic while 2 were hypoxic and all exhibited high microbial abundance ranging between 8.3x10exp7 and 5.7x10exp9 per volume??. Metabolic profiles of sediment microbial communities were screened from 10 stations of the lagoon of Venice with AN-BiologTM for anaerobes. PCA analysis of the profiles distinguished the samples in two different groups only on the basis of the microbial fermenting activity. Anaerobic respiration was not a differential metabolic feature among the samples. The structure of the bacterial populations was analyzed by ARISA fingerprinting. All the samples exhibited high species richness and Shannon index (respectively between 60 and 80, and 3.03 and 4.12) and very low dominance indexes (ranging from 0.021 to 0.081). PCA analysis of the fingerprints allowed to identify 3 stations representative of the groups of samples showing similar bacterial populations, that were subsequently described in detail by the screening of bacterial and archaeal 16S rRNA clone libraries (Figure 1). The composition of the bacterial communities differed between the three samples confirming the results obtained by ARISA. The bacterial communities appeared to be strongly influenced by anthropogenic activity. Areas adjacent to Venice and Chioggia showed the presence of *Alteromonadales* and *Vibrionales*, strong indicators of urban pollution. Gamma-, Delta-Proteobacteria, *Bacteroidetes* and other minor taxa dominated the other stations, where the gamma-Proteobacteria composition showed high concentrations of *Chromatiales*. These purple bacteria produce intracellular polymeric sulphur during the anoxygenic photosynthesis and probably were responsible in the past of "white waters"in the Venice Lagoon. Archaea were present in all the sediments of the lagoon. Most of the sequences present in the 16S rRNA libraries showed homology only with unidentified and uncultivated species retrieved from aquatic environments, belonging to the *Thermoplasmatales* and *Methanomicrobiales* groups of the *Euryarchaeota* order.
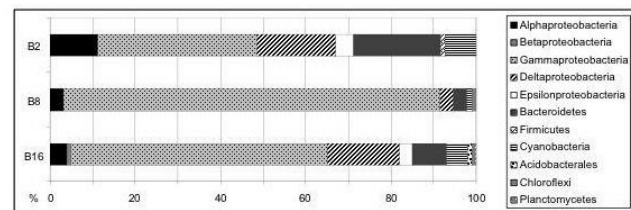

Fig. 1. Identification of representative phylogenetic groups detected from 16S rRNA clone libraries in 3 stations (B2, B8, B16) of the lagoon of Venice.

Reference

Cardinale, M., Brusetti, L., Quattrini, P., Borin, S., Puglia, A., M. Rizzi, A., Zanardini, E., Sorlini, C., Corselli, C., and Daffonchio D., 2004. Comparison of different primer sets for use in automated ribosomal intergenic spacer analysis of complex bacterial communities. *Appl. Environ. Microbiol.* 70: 6147-6156.