Characterization of the bacterial diversity associated with a reverse osmosis membrane system by cultivation-independent methods

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The technology of reverse osmosis membranes systems has been seen as a clean technology with low environmental impact, and has been used by diverse industries, including oil refineries, in order to treat and reuse water, and consequently reduce discharge. However, these systems are constantly subjected to contamination by microorganisms in the form of biofilms, causing a decrease in efficiency, increase in operational and maintenance costs. Biofilms are microbial communities developed on surfaces which are formed by initial adhesion of planktonic bacteria or by bacteria that are incorporated onto the preformed biofilm. In this context, this work aimed to characterize the bacterial diversity present in a reverse osmosis system from an oil refinery in order to determine which microorganisms were related to the biofilm formation. For this, cultivation-independent methods were employed, i.e., 16S rRNA gene libraries, genetic fingerprinting by DGGE and Real Time PCR. One sample of the feedwater and ten different reverse osmosis membrane samples were analyzed. Three 16S rRNA gene libraries were constructed, one from the feed water (211 clones), and two from the membranes (73 and 57 clones). The membranes were also analyzed by DGGE, and 13 bands from different membranes were selected for identification. Furthermore, Real Time PCR quantification of total bacteria was carried out. Combined results of these assay experiments showed that the most representative genera found in the system were: Acidovorax, Bosea, Devosia, Microbacterium, Novosphingobium, Rhizobium, Shinella, Sphingobium, Sphingomonas, Sphingopyxis and Methylibium. Sphingomonas, for example, are important in the initial formation of biofilms on reverse osmosis systems. These results corroborate with the literature, some of these genera are found continuously in aquatic systems and are important in the initial biofilm formation on reverse osmosis systems. The knowledge of the diversity of microorganisms present in these systems may provide insights for understanding the ecology and dynamics of biofilm formation. allowing the development of more specific and efficient control strategies.

Keywords: Biofilms, Microbial Diversity, Wastewater Treatment, DGGE, Real Time PCR.

Funding Agency: PETROBRAS.