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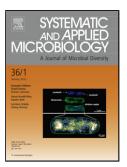
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## ACCEPTED MANUSCRIPT

Integrated diversity analysis of the microbial community in a reverse osmosis system from a Brazilian oil refinery

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Accession numbers: All partial sequences of the 16S rRNA genes obtained in this study were deposited in GenBank with the accession numbers KX254965 to KX255001 (isolates) and KX270024 to KX270202, MH027471 to MH027512; MH027521 to MH027577, MH040122 to MH040166 (library clones).

#### **ABSTRACT**

Oil refineries are known for the large volume of water used in their processes, as well as the amount of wastewater generated at the end of the production chain. Due to strict environmental regulations, the recycling of water has now become a viable alternative for refineries. Among the many methods available to treat wastewater for reuse, the use of membranes in reverse osmosis systems stands out due to several economic and environmental benefits. However, these systems are vulnerable to contamination and deposition of microorganisms, mainly because of the feedwater quality. In this

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