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POPULATION ANALYSIS IN HIGH-NITRATE WASTEWATER TREATMENT IN SEQUENCING BATCH REACTORS

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Abstract

The pickling liquor used in the stainless steel manufacturing process is a mixture of nitric and hydrofluoric acid which generates wastewater with nitrate concentrations ranging between 500 and 6000 mgNO₃⁻-N/L. In the present study, laboratory-scale anoxic Sequencing Batch Reactors (SBRs) were used to treat high nitrate wastewaters. Two different sludge inocula were tested: one from a Municipal Solid Waste Leachate Treatment Plant (LTP), and the other from a Sewage Treatment Plant (STP). Methanol and sugar-rich wastewater were assayed as alternative carbon sources for denitrification. The best results (removal of 700 mg NO₃-N/L in 6 hours of operating) were obtained when using methanol as external carbon source and inoculum from the LTP. Phylogenetic analysis of the bacteria present in the bioreactors using 16S rDNA sequences showed the presence of members of three bacterial phyla: Proteobacteria (Alfa, Gamma and Beta classes), Bacteroides and Actinobacteria. Bacteria belonging to the genera *Pseudomonas*, *Aeromonas*, *Comamonas*, *Flavobacterium* and *Tessaracoccus* were identified, *Paracoccus* being the most conspicuous denitrifying genus. Although most of the isolated bacteria harbour the *nosZ* denitrification gene, three of them, *Paracoccus* sp R-24665, *Paracoccus denitrificans* ATCC19367 and *Paracoccus* sp WB1, stood out in terms of their denitrifying capacity in both the synthetic and original wastewater, employing methanol as the carbon source. The results open the way to implementing and optimizing the full-scale treatment of industrial wastewater contaminated with nitrate.

Key words: denitrifying bacteria, microbiological analysis, nitrates, SBR, stainless steel wastewater

Received: March, 2012; *Revised final:* December, 2012; *Accepted:* December, 2012

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