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Halophilic denitrifying bacteria for high-rate denitrification of saline industrial wastewater

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Summary

Denitrification system for saline wastewater utilizing halophilic denitrifying bacteria has not been developed so far. Our previous study revealed that denitrification performance at 10% salinity was higher than that at 1% salinity in denitrification system for saline metal refinery wastewater. Terminal restriction fragment length polymorphisms (T-RFLP) profiles and clone analysis based on 16S rRNA encoding gene in sludge of denitrification system with 10% salinity indicated that γ -Proteobacteria, especially *Halomonas* spp., was predominant, suggesting that these bacterial member showed high denitrification activity under high saline condition. However, these phenomena have prospects of particularity at denitrification system for saline metal refinery wastewater. In this study, to examine whether these phenomena are general, denitrification performance and microbial community of denitrification system using Na₂SO₄- and NaCl-based synthetic wastewater under low and high saline conditions were investigated. Continuous denitrification experiment showed that denitrification performance at 10% salinity was higher than that at 1% salinity in the same manner as saline metal refinery wastewater. T-RFLP profiles and clone analysis indicated that *Halomonas* spp. was predominant. The direct counting of cells stained by fluorescent *in situ* hybridization (FISH) revealed that the percentages of *Halomonas* spp. increased with an increment of the denitrification rate in the system irrespective of salt components at 10% salinity. These results indicated that the phenomenon that *Halomonas* spp. is predominant under high saline condition is not specific for saline metal refinery wastewater, suggesting that these bacterial members show high denitrification activity under high saline condition irrespective of salt components in the industrial wastewaters.