

Characterization of novel marine denitrifying bacteria with versatile metabolic pathways for the degradation of trimethylamine

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Four denitrifying bacteria capable of degrading trimethylamine under both aerobic and denitrifying conditions were newly isolated from coastal sediments and a wastewater contaminated by marine water. All strains were in α -subclass of *Proteobacteria*. Strain GP43 was classified as genus *Paracoccus*, and strain PH32, PH34 and GRP21 were novel organisms with remote phylogenetic positions from other genus in this group. Among these four strains, strain PH32, PH34 and GRP21 were halophilic, which did not grow in the absence of sodium chloride in culture medium. During the anaerobic degradation of trimethylamine, all isolates reduced nitrate to nitrogen gas, indicating that the anaerobic degradation of trimethylamine was coupled with nitrate reduction. Cells grown under denitrifying conditions expressed trimethylamine dehydrogenase activity and dimethylamine dehydrogenase. This suggests that they directly demethylated trimethylamine to methylamine using these enzymes for the metabolism of trimethylamine under denitrifying conditions. In contrast, cells grown under aerobically condition possessed two different enzymes for oxidation of trimethylamine, trimethylamine dehydrogenase and trimethylamine monooxygenase. This is a novel feature in denitrifying organisms capable of degrading trimethylamine. The newly isolated strains may be the first halophilic bacteria to degrade trimethylamine under denitrifying condition.