

Anammox bacteria: lab-scale enrichment culture and pilot-scale application for saline sewage treatment

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Abstract:

The discovery of marine Anammox bacteria (MAB) provides direct elucidation of the marine nitrogen cycle and also expands the Anammox-based technology into saline sewage treatment. Heretofore adequate genomic studies have been conducted to decipher the features, genetic blueprint, versatile metabolism, and evolutionary history of the freshwater Anammox bacteria (FAB), which is not the case for MAB. According to the up-to-date genome database of Anammox bacteria from JGI and NCBI, only four draft genome assemblies affiliated with three MAB species have been reported, i.e., *Candidatus Scalindua brodae*, *Ca. Scalindua rubra* BSI-1, *Ca. Scalindua* sp. husup-a2. The current state of the art in engineering application of the Anammox-based technology confines to freshwater wastewater treatment. Genomic study of MAB and application of Anammox-based technology for saline sewage treatment are of great significance. In the present study, MAB was successfully cultivated and enriched in a lab-scale bioreactor and 16S rRNA gene sequencing was performed on Illumina MiSeq platform to diagnose the microbial community and dynamics. The lab-scale bioreactor realized a moderate nitrogen removal performance in long-term operation, i.e., over 80% nitrogen removal efficiency at the nitrogen load of 0.4 Kg N/m³/d. The enriched Anammox bacterium was identified as *Ca. Scalindua* sp. (i.e., 25.1% of the total sequences) based on 16S rRNA gene sequencing result. A pilot-scale anaerobic fluidized bed membrane bioreactor (AfMBR) was applied to implement one-stage partial nitrification/Anammox for saline sewage treatment under mainstream conditions. The pilot-scale AfMBR obtained delightful nitrogen removal performance in relatively short period with seeding activated sludge originated from local saline sewage treatment works. Surprisingly, 16S rRNA gene sequencing analysis indicated species affiliated with the typical FAB, i.e., *Ca. Kuenenia* sp., was the corresponding Anammox bacteria in the PN/A system while treating saline sewage. *Nitrosomonas* was detected as the corresponding microbe executing ammonia oxidation. The PN/A process is being projected for long-term operation to further consolidate process stability while treating saline sewage. Metagenomics approach will be conducted to decipher the genetic blueprint and the intriguing metabolism versatility of MAB.