Analysis of Microbial Communities Responsible for Enhanced Biological Phosphorus Rremoval in an Anaerobic/Aerobic SBR Rreactor using Stable Isotope Probing Approaches

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Abstract

Microbial communities responsible for enhanced biological phosphorus removal (EBPR) were analyzed using DNA-stable isotope probing (SIP)[1] and RNA-SIP[2] approaches in an anaerobic/aerobic sequencing batch reactor (SBR) supplied with acetate as sole carbon source. The SBR was inoculated with activated sludge from a wastewater treatment facility performing just carbon removal. SBR was operated with a cycle of fill, anaerobic, aerobic, settling, and drawing phases. Phosphate release during the anaerobic period and phosphate uptake in the aerobic period gradually increased with time. After about 2-month, steady state operation with complete phosphorus removal could be achieved. At 3-month operation, the enriched microbial community was subjected to SIP with ^{13}C-labled sodium acetate to biomark the DNA of phosphorus accumulating microorganisms. The extracted DNA and RNA were fractionated using CsCl and CsTFA ultracentrifugation, respectively. The fractionated [^{13}C] DNA and RNA from the SIP experiment were separately subjected to t-RFLP and rRNA gene sequence analyses. Small subunit ribosomal DNA inserts from two 16S rRNA gene libraries were PCR amplified and digested using *Hae*III and *Hha*I to analyze restriction fragment length polymorphism (RFLP). The dominant clones (11 of 42 clones) in the [^{13}C] DNA clone library was closely related to *Dechloromonas* with low sequence identity within the *betaproteobacteria*, while the dominant clones (25 of 41 clones) in the [^{13}C] RNA clone library were affiliated into uncultured *betaproteobacteria* from environmental samples.

References

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