Denitrification with glucose as an external carbon source and investigation of microbial communities in a sequencing batch reactor treating reverse osmosis concentrate produced by a coking wastewater treatment plant

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In this study, a biological denitrifying process with glucose as an external carbon source was employed for the treatment of reverse osmosis (RO) concentrate with a conductivity of 17,539 ± 851 µs/cm generated from coking wastewater using a sequencing batch reactor (SBR). The average chemical oxygen demand and nitrate removal efficiencies during 60 d of stable SBR operation were 79.2% and 92.8%, respectively. Different microbial communities were identified by sequencing the V1–V3 region of the 16S rRNA gene on the MiSeq platform. The most abundant bacterial phyla in the SBR were Proteobacteria and Bacteroidetes, which could be responsible for biological denitrification of the RO concentrate. The core genera that played an important role in nitrate reduction were *Thauera*, *Hyphomicrobium*, *Flavobacterium*, and *Methyloversatilis*, accounting for 5.4%–8.0%, 2.0%–8.6%, 1.2%–1.6%, and 0.8%–3.4%, respectively, throughout the stable operational period. The quantitative real-time PCR was used to quantify the absolute abundances of the denitrifying genes *narG*, *nirS*, *nirK*, and *nosZ* during the entire operational period. The abundances of *narG*, *nirK*, and *nosZ* were lower during stable operation than start-up. Among these genes, *nirS* played relatively more important role than *nirK* in the reduction of nitrite to nitric oxide.

Keywords: Coking wastewater; RO concentrate; Denitrification; Microbial community; SBR

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