Desalination and Water Treatment
www.deswater.com

doi: 10.5004/dwt.2021.26768

215 (2021) 23–30
March

Relationship between denitrification performance and microbial community structure in a PHBV-supported denitrification reactor

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Received 18 April 2020; Accepted 17 October 2020

ABSTRACT

Solid-phase denitrification systems using biodegradable polymers are promising for wastewater treatment; however, little is known about the relationship between microbial communities and effluent quality in these systems. In this study, we evaluated the performance of a poly(3-hydroxybutyrate-*co*-3-hydroxyvalerate) (PHBV)-supported denitrification system in the treatment of wastewater with high nitrate concentrations with respect to the microbial community structure and dominant bacteria. An average denitrification rate of 1.11 g/(L d) could be achieved at an influent NO_3^-–N concentration of 80 mg/L and hydraulic retention time (HRT) of 1.5 h. Compared to the HRT, the influent NO_3^-–N concentration had a greater effect on the denitrification efficiency at the same NO_3^-–N loading rate (NLR). Microbial community analysis using Miseq Illumina sequencing showed that the genera *Diaphorobacter* and *Dechloromonas* were predominant. The nitrate removal efficiency was positively correlated with the *Dechloromonas* abundance, and the NLR was negatively correlated with *Diaphorobacter*. Heatmap analysis showed that the denitrification function dominated over all stages, which may explain the good performance of the PHBV-supported denitrification system. These findings clarify the effect of the influent nitrate load on microbial functional abundance and community structure as well as the molecular determinants of solid-phase denitrification efficiency.

Keywords: Solid-phase denitrification; Poly(3-hydroxybutyrate-*co*-3-hydroxyvalerate); Microbial community; Functional analysis

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