Counter-diffusion biofilms have lower N2O emissions than co-diffusion biofilms during simultaneous nitrification and denitrification: Insights from depth-profile analysis

The goal of this study was to investigate the effectiveness of a membrane-aerated biofilm reactor (MABR), a representative of counter-current substrate diffusion geometry, in mitigating nitrous oxide (N2O) emission. Two laboratory-scale reactors with the same dimensions but distinct biofilm geometries, i.e., a MABR and a conventional biofilm reactor (CBR) employing co-current substrate diffusion geometry, were operated to determine depth profiles of dissolved oxygen (DO), nitrous oxide (N2O), functional gene abundance and microbial community structure. Surficial nitrogen removal rate was slightly higher in the MABR (11.0 ± 0.80 g-N/(m2 day) than in the CBR (9.71 ± 0.94 g-N/(m2 day), while total organic carbon removal efficiencies were comparable (96.9 ± 1.0% for MABR and 98.0 ± 0.8% for CBR). In stark contrast, the dissolved N2O concentration in the MABR was two orders of magnitude lower (0.011 ± 0.001 mg N2O-N/L) than that in the CBR (1.38 ± 0.25 mg N2O-N/L), resulting in distinct N2O emission factors (0.0058 ± 0.0005% in the MABR vs. 0.72 ± 0.13% in the CBR). Analysis on local net N2O production and consumption rates unveiled that zones for N2O production and consumption were adjacent in the MABR biofilm. Real-time quantitative PCR indicated higher abundance of denitrifying genes, especially nitrous oxide reductase (nosZ) genes, in the MABR versus the CBR. Analyses of the microbial community composition via 16S rRNA gene amplicon sequencing revealed the abundant presence of the genera Thauera (31.2 ± 11%), Rhizobium (10.9 ± 6.6%), Stenotrophomonas (6.8 ± 2.7%), Sphingobacteria (3.2 ± 1.1%) and Brevundimonas (2.5 ± 1.0%) as potential N2O-reducing bacteria in the MABR.

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