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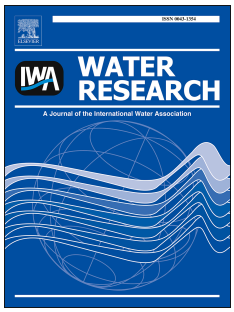

Anaerobic digester bioaugmentation influences quasi steady state performance and microbial community

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Anaerobic digester bioaugmentation influences quasi steady state performance and microbial community

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Abstract

Nine anaerobic digesters, each seeded with biomass from a different source, were operated identically and their quasi steady state function was compared. Subsequently, digesters were bioaugmented with a methanogenic culture previously shown to increase specific methanogenic activity. Before bioaugmentation, different seed biomass resulted in different quasi steady state function, with digesters clustering into three groups distinguished by methane (CH_4) production. Digesters with similar functional performance contained similar archaeal communities based on clustering of Illumina sequence data of the V4-V5 region of the 16S rRNA gene. High CH_4 production correlated with neutral pH and high *Methanosarcina* abundance, whereas low CH_4 production correlated to low pH as well as high *Methanobacterium and DHVEG 6* family abundance. After bioaugmentation, CH_4 production from the high CH_4-producing digesters transiently increased by 11±3% relative to non-bioaugmented controls ($p < 0.05$, n=3), whereas no functional changes were observed for medium and low CH_4 producing digesters that all had pH higher than 6.7. The CH_4 production increase after bioaugmentation was correlated to increased relative abundance of *Methanosaeta* and