

Contribution Details

Microbial community dynamics during the anaerobic digestion of aromatic compounds

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Talk

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Abstract

Using organic waste products from food industry or from agriculture for biogas production can be an ethically permissible, economically effective and sustainable way to meet the increasing energy demand and the concurrent efforts to reduce greenhouse gas emissions from fossil fuel combustion. One drawback of using organic wastes, which are often pre-treated nowadays [1], is the release of aromatic compounds like phenyl acids. These acids have diverse and yet marginally understood effects on the overall biogas process. Hence, a closer look on microbial community dynamics during anaerobic digestion (AD) of aromatic compounds is pending to better understand the overall microbial dynamics. In batch reactors, meso- and thermophilic communities were fed with lignocellulosic or proteinaceous substrates (containing relatively high amounts of aromatic compounds) under different overload conditions. The reactors were monitored biochemically (biogas, volatile fatty acid (VFA) and phenyl acid concentrations) as well as microbiologically (amplicon sequencing, qPCR) for 28 days. Raw sequences were qualitatively checked and processed via mothur [2]. Microbial biomarkers for high phenyl acid concentrations were assessed via the command LEfSe. Especially syntrophic VFA oxidising microorganisms, like *Syntrophomonas* spp., *Clostridia* D8A-2, *Syntrophaceticus* spp. or *Tepidanaerobacter* spp., and hydrogenotrophic methanogens like *Methanoculleus* spp. were shown to be biomarkers for high phenyl acid concentrations. By contrast, acetoclastic methanogens like *Methanothrix* spp. were more susceptible towards high phenyl acids concentrations [3,4]. These results are the basis for further investigations regarding the direct and/or indirect involvement of syntrophic VFA oxidisers (and their H₂ consuming partners) during the AD of aromatic compounds.

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