Two-year microbial adaptation during hydrogen-mediated biogas upgrading process in a serial reactor configuration

Microbial dynamics in an upgrading biogas reactor system undergoing a more than two years-period at stable operating conditions were explored. The carbon dioxide generated during biomass degradation in the first reactor of the system was converted to methane into the secondary reactor by addition of external hydrogen. Considering the overall efficiency, the long-term operation period resulted in an improved biogas upgrading performance (99% methane content). However, a remarkable accumulation of acetate was revealed, indicating the enhancement of homoacetogenic activity. For this reason, a shift in the anaerobic digestion microbiome was expected and evaluated by 16S rRNA amplicon analysis. Results demonstrated that the most abundant archaeal species identified in the first time point, Candidatus Methanoculleus thermohydrogenotrophicum, was replaced by Methanothermobacter thermautotrophicus, becoming dominant after the community adaptation. The most interesting taxonomic units were clustered by relative abundance and six main long-term adaptation trends were found, characterizing functionally related microbes (e.g. homoacetogens).

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