Metagenomic analysis on thermophilic biogas reactors fed with high load of Long Chain Fatty Acids (LCFA) - DTU Orbit (07/01/2019)

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In anaerobic digestion systems, the accumulation of long chain fatty acids (LCFA) leads to process instability and decrease of the methane production. This detrimental condition is known to be reversible depending on the concentration of the accumulated LCFA and mainly on the microbial consortium populating the biogas reactors. Therefore, the understanding of how the microbial communities change in response to LCFA pulses is essential to optimize the overall process. In this study two lab-scale continuously stirred reactors were used to characterize, via 16S rRNA gene analysis, the microbial shifts due to LCFA increase in the feedstock composition. The result shows that the addition of sodium oleate caused a reversible inhibition of reactor. The correlation between the microbial community’s profile and the reactors performance indicated that Syntrophomonas was the genus most likely involved in sodium oleate degradation. Other genera that were found abundant are Pseudomonas, Clostridium XI and Clostridium III. The relative abundance of these genera was not significantly affected by the addition of sodium oleate, and this indicates that they are probably involved in later steps of degradation. Methanoculleus was the main methanogen that was found in the reactors and its relative abundance was also not significantly affected by the addition of sodium oleate. This indicates that the main methanogenic pathway was not shifted with the addition of sodium oleate.

General information
State: Published
Organisations: Department of Environmental Engineering, Residual Resource Engineering, University of Padova
Number of pages: 4
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from 14th World Congress on Anaerobic Digestion, Viña del Mar, Chile.
Keywords: Anaerobic digestion, 16s rRNA gene, LCFA, Metagenomic analysis
Electronic versions:
Abstract_AD14.pdf
Source: PublicationPreSubmission
Source-ID: 118988257
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2015