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Microbial dynamics in anaerobic digestion (AD) reactors with sodium oleate in the substrate

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In AD systems, the accumulation of long chain fatty acids (LCFA) leads to process instability and decrease of the methane production. 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 used to characterize, via 16s rRNA gene analysis, the microbial shifts due to LCFA increase in the feedstock composition. Genera that had relative abundance higher than 1% or increased more than 2 folds after sodium oleate addition are chosen for discussion. The result shows that the average methane yield was 150 ± 4 ml CH₄/gVS for cattle manure and 380 ± 37 ml CH₄/gVS for manure with sodium oleate addition. 75% of the added sodium oleate was utilized to produce methane. The addition of sodium oleate caused a slight decrease on the methane yield with a concomitant increase of VFA. In average, 1.6 million sequencing reads were generated from each sample and 20% of the reads were identified using RDP classifier. Results showed that 4 genera had relative abundance higher than 1% after the LCFA addition, suggesting that these members involved in the LCFA degradation process. The relative abundance of *Pseudomonas*, *Clostridium* XI and *Clostridium* III was not significantly affected (changed less than 2 folds) by the addition of LCFA, suggesting that these genera are not directly involved in the β -oxidation process but probably in later steps of the degradation process, i.e. the metabolism of VFA. This observation consists with the previous study where *Pseudomonas* has been reported to have versatility in catabolizing esoteric organic compounds (von Graevenitz 1976), and *Clostridium* III has been found playing important role in the efficient operation of anaerobic reactors (Shiratori, Ikeno et al. 2006). *Syntrophomonas* increased significantly after the addition of sodium oleate and became the most abundant genus. Several members of *Syntrophomonas* genus have been proven to be specialized in performing β -oxidation on LCFA (Sousa, Smidt et al. 2009). The significant increase of *Syntrophomonas* found in this experiment confirmed that this genus is a key player in the LCFA degradation under thermophilic anaerobic conditions. As for methanogens, *Methanoculleus* was found to be the most abundant genus, with no significant change before and after sodium oleate addition.

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