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Molecular profiling of microbial communities in anaerobic bioreactors treating oleic acid rich wastewater

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Abstract

Anaerobic treatment of long-chain fatty acids (LCFA) rich effluents, such as dairy effluents, can result in a high methane production. LCFA are degraded by syntrophic bacteria to hydrogen and carbon dioxide and also to acetate, which are consumed by methanogenic *archaea* to produce methane. A better knowledge of the microbial communities involved in the process is of utmost importance, because it can contribute to improve bioreactors performance and enhance methane production efficiency. In this work, the composition and dynamics of an anaerobic microbial community was studied during the high rate operation of a bioreactor treating a synthetic wastewater made up of sodium oleate and skim milk. The bioreactor was operated with a step feeding during 213 days and in continuous thereafter, with organic loading rates from 5 to 31 kg COD m⁻³ day⁻¹. Reactor performance improved during the step feeding start-up, achieving a maximum methane yield of 91 % and a COD removal efficiency of 97 % (Cavaleiro et al., 2009). Accumulation of LCFA onto the sludge was observed only during the first 62 days of operation. During the continuous period COD removal averaged 99 % and a maximum methane yield of 98 % was reported. Fifteen biomass samples were collected during the 665 days of operation. Total DNA was extracted and 16S rRNA gene was amplified for DGGE fingerprint analysis and for cloning/sequencing analysis. According to DGGE profiles, shifts in microbial composition were more evident during the first 100 days of the step feeding start-up. Dominant bacterial and archaeal ribotypes prevailed in the system, even when working in continuous high-rate mode. Archaeal 16S rRNA gene sequences showed higher identity to those of *Methanobacterium* and *Methanosaeta* genera. On the other hand, bacterial 16S rRNA gene sequences were most similar to those of uncultured bacteria and were assigned to phylum Firmicutes, Chloroflexi and Bacteroidetes. In conclusion, the microbial community developed during the start-up of the bioreactor was able to efficiently convert high oleate loads to biomethane, and remained stable until the end of the experiment.

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