

MOLECULAR PROFILING OF MICROBIAL COMMUNITIES DEVELOPED IN HIGH-RATE ANAEROBIC TREATMENT OF OLEIC ACID RICH WASTEWATER

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Background: Long-chain fatty acids (LCFA) are attractive for biogas production since they have a twofold theoretical methane yield when compared to proteins or carbohydrates. Efficient anaerobic treatment of lipids/LCFA rich wastewaters at industrial scale, without risk of overload and inhibition, is still considered a challenge. In this context, increased knowledge on the microbial populations involved is of utmost importance to enhance CH₄ production from LCFA.

Objectives: The aim of this work was to study the microbial communities developed in an anaerobic reactor treating high loads of oleic acid based wastewater.

Methods: Biomass samples were collected from a mesophilic up-flow anaerobic reactor, operating with a step feeding during 213 days and in continuous thereafter, with organic loading rates from 5 to 31 kgCOD m⁻³ day⁻¹ (Cavaleiro et al, 2009). DNA was extracted and 16S rRNA gene amplified for DGGE fingerprint analysis and for cloning/sequencing analysis.

Results and conclusions: After the step feeding operation, efficient methane recovery from oleate degradation was achieved. A maximum methane yield of 98% was reached for 12 kgCOD m⁻³ day⁻¹. According to DGGE profiles, shifts in microbial composition were more pronounced during the first 100 days. Dominant bacteria and archaea ribotypes prevailed in the system, even when working in continuous high-rate mode. The operating strategy applied resulted in the development of a stable microbial community able to efficiently convert high oleate loads to biomethane.

References: Cavaleiro AJ, Salvador AF, Alves JI, Alves M. 2009. Continuous High Rate Anaerobic Treatment of Oleic Acid based Wastewater is Possible after a Step Feeding Start-up. *Environ Sci Technol*. In press.

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