ANAEROBIC MICROBIAL COMMUNITY DYNAMICS DURING DISCONTINUOUS TREATMENT OF A SYNTHETIC DAIRY WASTEWATER

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Background and aims: Anaerobic digestion is an opportunity to generate energy from treatment of effluents with high lipid content. Nevertheless, long-chain fatty acids (LCFA) usually accumulate within reactors causing biomass washout and microbial inhibition. Discontinuous operation was suggested as the optimal strategy to treat LCFA-rich wastewater. In this work, microbial community dynamics was investigated, during the discontinuous operation of an anaerobic reactor treating a synthetic dairy wastewater.

Methods: An anaerobic lab scale reactor was operated in cycles, with OLR ranging from 4 to 8 $kgCODm^{-3}day^{-1}$. Feeding was composed of sodium oleate and skim-milk. Eight biomass samples were collected during the reactor operation and after DNA extraction, microbial community was studied by means of PCR-DGGE of the 16S rRNA gene fragments.

Results: DGGE-fingerprints of *Archaea* and *Bacteria* showed that bacterial community was more affected by the operating conditions imposed than the archaeal one. Shifts in microbial community correlate well with the reactor performance and point out to microbial acclimation, since overall COD removal efficiency and methane yield increased along time up to 98% and 91%, respectively. Specific methanogenic acetoclastic and hydrogenotrophic activities increased from 2 and 56 $mlCH_{4(STP)}gVS^{-1}d^{-1}$ at the beginning to 246 and 512 $mlCH_{4(STP)}gVS^{-1}d^{-1}$ at the end of the operation, respectively.

Conclusions: The results obtained show that the discontinuous operation applied promoted gradual development of a specialized microbial consortium able to efficiently treat LCFA-rich wastewater.

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