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MOLECULAR MONITORING OF BACTERIAL AND ARCHAEAL DOMAINS DURING THE ANAEROBIC MINERALIZATION OF BIOMASS-ASSOCIATED LCFA

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The anaerobic digestion of effluents with high lipid content can be energetically attractive due to their theoretical methane yield. Recently Pereira *et al.* (1) showed that for an efficient mineralization of Long Chain Fatty Acids (LCFA), a sequential process may be advantageous over the continuous operation. After a first step of LCFA accumulation onto the sludge, the feeding is suppressed and a second step of mineralization of the biomass-associated LCFA is promoted. Knowledge about the microbial populations involved in the accumulation and degradation steps of LCFA can give more insight into the mechanisms of LCFA conversion. The aim of this work was to compare the microbial diversity of Bacteria and Archaea present in anaerobic sludge after LCFA accumulation and degradation steps, using a molecular approach.

METHODOLOGY

Two Expanded Granular Sludge Bed (EGSB) reactors were inoculated with anaerobic suspended sludge previously acclimated with oleic acid. Oleic acid and palmitic acid were fed to reactors RO and RP, respectively, as the sole carbon source, during about 40 days (HRT=1 day, influent COD=4 g/L). After this continuous operation, sludge samples containing 4570±257 and 5200±9 mg COD-LCFA/g VSS were collected from reactors RO and RP, respectively (samples RO_l and RP_l). Each sample was incubated in batch assays and the methane production from the mineralization of the biomass-associated LCFA was monitored for 45 days. These final sludge samples were designated RO_b and RP_b. Total DNA was extracted from homogenized sludge samples (RO_l, RP_l, RO_b, RP_b and inoculum (I)), and conserved regions of bacterial and archaeal 16S rRNA genes were amplified for Denaturing Gradient Gel Electrophoresis (DGGE) using Polymerase Chain Reaction (PCR).

RESULTS AND DISCUSSION

The obtained DGGE profiles are presented in Figure 1. The differences for the archaeal domain between the inoculum (I), RO_l and RP_l are less prominent than those observed for the bacterial domain. After batch degradation of the accumulated LCFA (RO_b and RP_b) the change in microbial composition is evident for both domains, with a decrease in intensity of some bands and a possible enrichment of specific microorganisms.

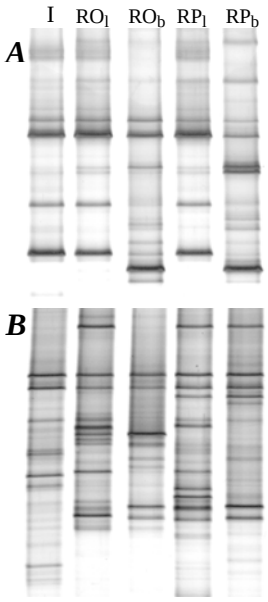

Figure 1
DGGE profiles (A-Archaea; B-Bacteria).

CONCLUSION

A shift in bacterial and archaeal community composition was observed when anaerobic sludge was submitted to a cycle of feeding and batch degradation of two different LCFA. These changes could be related with an enrichment of specific populations in the consortium that may be involved in LCFA degradation.

(1) Pereira, M.A., Pires, O.C., Mota, M., Alves, M.M. (2002) Water Science and Technology 45, 139-144.