

TITLE: ANAEROBIC CO-DIGESTION OF COMMERCIAL LAUNDRY WASTEWATER AND DOMESTIC SEWAGE IN EGSB PILOT SCALE REACTOR: INFLUENCE OF SURFACTANT CONCENTRATION ON MICROBIAL DIVERSITY

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ABSTRACT:

Inadequate destination of wastewater containing LAS can lead to the formation of foams, which inhibit the natural processes of self-purification of rivers and lagoons, as well the aerobic and/or anaerobic process in sewage treatment plants. Due to high consumption of surfactants, especially LAS, and the impacts caused by their inadequate fate, there is a need to develop technologies to treat this macro pollutant. Microbiology is a valuable tool for attempt elucidates the consortium of microorganisms that participate in the degradation of the LAS molecule. Different molecular tools (PCR-DGGE, high-throughput sequencing of 16S rRNA gene and sequencing of *bamA* gene) were used to compare and assess the microbial diversity of an Expanded Granular Sludge Bed (EGSB) reactor in pilot scale applied to anaerobic co-digestion of commercial laundry wastewater and domestic sewage submitted to increasing concentrations of anionic surfactant. By using PCR-DGGE, a microbial stratification along the sludge bed of the reactor was observed. Moreover, it was, probably, related to size granule. 16S rRNA gene sequencing showed high diversity and richness of the samples, and the lowest Shannon value was obtained for the upper concentration of surfactant. For the Bacteria domain the genus *Bellilinea*, *Syntrophus*, *Syntrophohobacter*, *Cytophaga*, *Bacteroides*, and *Synergistes* were the most abundant; whereas for Archaea domain, the genus was *Methanosaeta* and *Methanolinea*. Only *Pseudomonas* genus is related to all steps of degradation and unique in the Ω -oxidation. In the other steps, a greater richness (> 6 different genera) was observed, indicating the need for a microbial syntrophism for complete LAS degradation. Also, *bamA* gene sequencing indicated the presence of *Syntrophorhabdus aromaticivorans*, *Desulfosarcine ketonica* and *Syntrophus aciditrophicus* with the genetic potential for the aromatic ring cleavage under anaerobic condition. Therefore, only future studies of reactors with biomass of these microorganisms can clarify the importance of this microbiome in the degradation of LAS.

Keywords: Linear alkylbenzene sulfonate (LAS); Expanded Granular Sludge Bed (EGSB); Illumina sequencing; microbial diversity.

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