

Dynamics of microbial populations responsible for biodegradation during the full-scale treatment of palm oil mill effluent

ABSTRACT

Despite efforts to address the composition of the microbial community during the anaerobic treatment of palm oil mill effluent (POME), its composition in relation to biodegradation in the full-scale treatment system has not yet been extensively examined. Therefore, a thorough analysis of bacterial and archaeal communities was performed in the present study using MiSeq sequencing at the different stages of the POME treatment, which comprised anaerobic as well as facultative anaerobic and aerobic processes, including the mixed raw effluent (MRE), mixing pond, holding tank, and final discharge phases. Based on the results obtained, the following biodegradation processes were suggested to occur at the different treatment stages: (1) Lactobacillaceae (35.9%) dominated the first stage, which contributed to high lactic acid production; (2) the higher population of Clostridiaceae in the mixing pond (47.7%) and Prevotellaceae in the holding tank (49.7%) promoted acetic acid production; (3) the aceticlastic methanogen Methanosaetaceae (0.6-0.8%) played a role in acetic acid degradation in the open digester and closed reactor for methane generation; (4) Syntrophomonas (21.5-29.2%) appeared to be involved in the degradation of fatty acids and acetic acid by syntrophic cooperation with the hydrogenotrophic methanogen, Methanobacteriaceae (0.6-1.3%); and (5) the phenols and alcohols detected in the early phases, but not in the final discharge phase, indicated the successful degradation of lignocellulosic materials. The present results contribute to a better understanding of the biodegradation mechanisms involved in the different stages of the full-scale treatment of POME.

Keyword: Bacterial community; Biodegradation; Methanogenic archaea; Palm oil mill effluent; Wastewater treatment

