

BACTERIAL AND ARCHAEOAL COMMUNITIES IN METHANOGENIC SLUDGE: 16S rRNA ANALYSIS DURING BIOCHEMICAL METHANE POTENTIAL (BMP) ASSESSMENT

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Abstract

This study was designed to evaluate the microbial profiling in sewage sludge (SW) during anaerobic digestion (AD) in a Biochemical Methane Potential (BMP) assay operating at 37±1°C monodigestion. BMP of a specific substrate defines the maximum amount of methane that can be produced by AD. The sludge was taken from a Municipal Wastewater Treatment Plant (WWTP) in Rio de Janeiro. The microbial community diversity and structure were characterized with Illumina MiSeq (a molecular biology tool) using the 16S rRNA. The taxonomic composition of total bacteria and archaeal community in BMP AD reactors was investigated. Clear changes were observed in the bacterial diversity after the BMP assay in a lab-scale reactor. The most represented phyla in terms of number of operational taxonomic unit (OTU) in SW before AD treatment were: *Proteobacteria* (15248 OTU) > *Bacteroidetes* (4749 OTU) > *Actinobacteria* (2495 OTU) > *Firmicutes* (1619 OTU) > *Chloroflexi* (1183 OTU). After AD BMP assay the bacterial community changed regarding relative abundance. A new dominant community configuration emerged in the system, as following: *Firmicutes* (65368 OTU) > *Synergistota* (8182 OTU) > *Proteobacteria* (4010 OTU) > *Actinobacteriota* (2235 OTU) > *Desulfobacterota* (1077 OTU), which has been consistently reported in several previous studies, suggesting the existence of a general signature of the AD microbiome. At Genus level, the dominance of methanogenic groups was represented by *Methanosaeta* (34497 OTU) > *Methanolinea* (16261 OTU) > *Methanofastidiosum* (6836 OTU) > *Methanospirillum* (3739 OTU) > *Methanosarcina* (1521 OTU) > *Methanobrevibacter* (1422 OTU) before AD treatment and *Methanobacterium* (62398 OTU) > *Methanosaeta* (2617 OTU) after AD treatment. The changes observed in methanogenic profiles indicate a shift in the metabolic pathway for methane production from acetoclastic to hydrogenotrophic metabolism. The physicochemical parameters required for both methanogenic metabolisms have clear and remarkable differences. The results and conclusions of this study are expected to increase the knowledge on the ecology and function of the involved microbial consortia, and thus, allow a better control and optimization of AD at WWTPs. The findings obtained in this study are expected to help opening the microbial 'black-box' providing useful clues for process optimization of AD systems treating sludge.

Keywords: sewage sludge, anaerobic digestion, bacteria total, archaeal community