



IDENTIFICATION OF THE MICROBIAL COMMUNITY INVOLVED IN BIOGAS PRODUCTION FROM POULTRY LITTER WITH USE OF BIOAUGMENTATION

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Anaerobic digestion is a complex process that occurs through the combination of metabolic activities of *Bacteria* and *Archaea*, which transform different types of biomass into biogas. Poultry litter is one of the materials used as biomass, and the biogas produced can be converted into energy or be used as vehicular fuel. Bioaugmentation, on the other hand, is characterized by the inoculation of microorganisms with specific catalytic capabilities and with the purpose of increasing the anaerobic digestion efficiency through microbial diversity improvement. The objective of this study was to identify the microorganisms involved in biogas production from poultry litter with and without the use of bioaugmentation, by means of DNA sequencing analysis and genomic database comparisons. The samples were extracted from bioassays using poultry litter (CA) at 60% (v/v) as substrate, with and without the addition of effluent treatment plant sludge (L) and a commercial product containing a microbial consortium (B). The microbiome identification process was initiated by the DNA extraction from the initial and final samples of the bioassays, followed by the amplification of the V3 and V4 regions of the 16S gene of rRNA of bacteria and archaea by Polymerase Chain Reaction. High-throughput sequencing was performed using the MiSeq Sequencing System (Illumina Inc., USA) and V2 kit, with 300 cycles and pair-end sequencing. The sequences were analyzed on *Qiime 2.0* and its identification was made using the *RDP Classifier* and *NCBI* databases. The most representative phyla found in the final sample of CA 60% were Firmicutes (84%), Actinobacteria (9%) and Bacteroidetes (5%), while in the sample CA 60% + B + L the most representative were Bacteroidetes (45%), Synergistetes (27%) and Firmicutes (16%). Though in the final sample of CA 60% the occurrence of 6 most representative genera was observed (such as *Tissierella* and *Clostridium*), in the final sample of the bioassay using bioaugmentation the genus *Petrimonas* was the only highly expressive one. Moreover, in the bioaugmentation samples representatives of Euryarchaeota were found, in which the genera *Methanobacterium* and *Methanolineae* are hydrogenotrophic methanogenic archaea, whereas *Methanosaeta* produces methane through the acetoclastic pathway. Overall, the microbiome profile changed through the course of the experiment, as well as the relationships between bacteria and archaea reflected on the success of biogas production.

Palavras-chave: Anaerobic digestion, Bioaugmentation, DNA sequencing

Apoio: UCS, CNPq