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XXIX Encontro de Jovens Pesquisadores
e XI Mostra Acadêmica de Inovação e Tecnologia

De 5 a 7/10

Local: UCS - Cidade Universitária,
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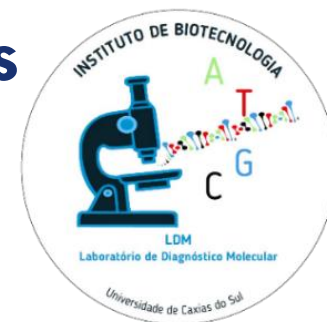


Identification of the microbial community involved in biogas production from poultry litter with use of bioaugmentation

METANOGÊNICAS

PIBIC/CNPq

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INTRODUCTION

Anaerobic digestion is a complex and efficient microbial process that occurs through the association of metabolic activities of *Bacteria* and *Archaea*, which transform different types of biomass into biogas [1, 2], while bioaugmentation is a technique where microorganisms with specific catabolic capabilities are inoculated in the experiment with the purpose of enhancing anaerobic digestion's efficiency through microbial diversity improvement [3]. Brazil's poultry production was the third biggest worldwide in 2020, and our country was also the biggest poultry exporter in the same year, with 4.231 million tonnes exported, generating a big amount of residues [4]. Therefore, the objective of the present study was to identify the microorganisms involved in biogas production from a bioassay using only poultry litter and another one with the use of bioaugmentation, which had higher methane production, by means of DNA sequencing analysis and genomic database comparisons.

MATERIALS AND METHODS

1



Substrate

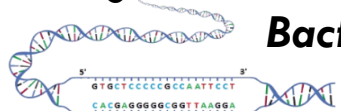
Poultry litter (CA) 60% v/v
Effluent sludge treatment plant (L) 10% v/v
Commercial consortium (B) 10% v/v

2 DNA extraction

Initial/Final samples
CA 60% (CA1; CA2)
CA 60% + B + L (CA3; CA4)

3 Polymerase Chain Reaction

V3/V4 regions of 16S gene of rRNA
Bacteria • Archaea
341F / 806R



4 High-throughput sequencing

MiSeq Sequencing System (Illumina Inc., USA)
V2 kit • 300 cycles • Pair-end sequencing



5



6

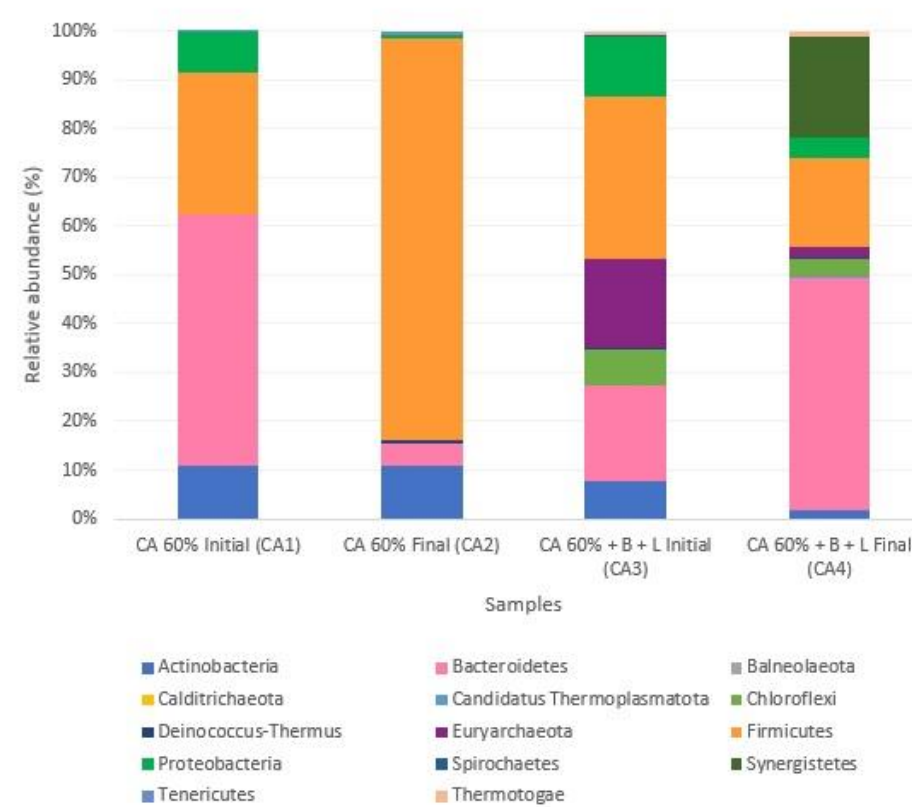


RESULTS AND DISCUSSION

The most representative phyla found in CA1 were Bacteroidetes, Firmicutes and Actinobacteria, respectively, while in the CA2 sample the most prevalent were Firmicutes, Actinobacteria and Bacteroidetes (Figure 1). A possible linkage between Bacteroidetes and Firmicutes was previously shown suggesting that Firmicutes is the dominant phylum in the bacterial community during stable process performance [5], and Bacteroidetes is known for its importance during hydrolysis and volatile fatty acids production in the anaerobic digestion process [6]. Both CA3 and CA4 samples showed Firmicutes and Bacteroidetes abundance, however while

the third most abundant phylum in CA3 was Euryarchaeota, in CA4 it was Synergistetes.

Figure 1 Phyla identified in the initial and final samples of CA 60% (CA1; CA2) and of CA 60% + B + L (CA3; CA4)



Moreover, in CA2 5 genera stood out, but only the genus *Petrimonas* had a highly significant abundance in the final sample CA4. *Petrimonas* can ferment many sugars into methane precursors, such as acetic acid, propionic acid, H₂ and CO₂ [7]. Euryarchaeota was represented by the genera *Methanobacterium*, *Methanolinea* and *Methanosaeta* in CA3, of which only the genus *Methanobacterium* was also found in CA4. *Methanobacterium* and *Methanolinea* are hydrogenotrophic methanogenic archaea, converting CO₂ and H₂ to CH₄. *Methanosaeta*, on the other hand, produce methane through the acetoclastic pathway, and are responsible for great part of methane production in reactors [8].

CONCLUSIONS

The present study showed that 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.

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Acknowledgments

