

Prokaryotic Diversity in Upflow Anaerobic Biodigestors Treating Slaughterhouse Waste

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Anaerobic biodigestion is a method widely used in industrial wastewater treatment in order to reduce the high concentration of organic matter before discharging as effluent into running water. The removal of organic compounds is due to prokaryotic activity in industrial biodigestors. Thus, in this work, the prokaryotic diversity present in the following three upflow anaerobic biodigestors operated with different supports was compared: polypropylene rings (A), polyurethane foam (B) and clay brick (C), in slaughterhouse wastewater treatment. In the Hydraulic Retention Time of one day, libraries of the 16S rRNA of archaea and bacteria were built by using as template the total isolated DNA of the mud fixed to the different supports. The diversity was analyzed by RFLP, digesting the clones of the library with the restriction enzymes *RsaI* and *HinfI*. Such analyses showed that reactor C contained the least archaeal diversity, consistent with the results obtained previously using ARDRA analyses. Nevertheless, since the reactor C achieved the highest organic matter removal, it is believed that the performance of this system is a result of a specific prokaryotic population selected by its support. In order to identify the microorganisms of each reactor, the clones of the libraries are being sequenced. Up to the present, the following common methanogens found in anaerobic biodigestors were identified *Methanospirillum* sp, *Methanothrix* sp, *Methanofollis* sp and *Methanoplanus* sp.

Palavras Chaves: Anaerobic biodigestion, prokaryotic diversity, 16S rDNA.

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