

**TITLE:** EVALUATION OF SPECIFIC METHANOGENIC ACTIVITY (SMA) IN ANAEROBIC SLUDGE RESULTING OF THE WASTEWATER TREATMENT PLANT AT FEDERAL UNIVERSITY OF LAVRAS, LAVRAS, MINAS GERAIS, BRAZIL.

**AUTHORS:** COSTA, A. D.; PAEZ, S.; MATOS, M. P.; SINISCALCHI, L. A. B.

**INSTITUTION:** UNIVERSIDADE FEDERAL DE LAVRAS, LAVRAS, MG (AVENIDA DR. SYLVIO MENICUCCI, 1001, LAVRAS, MG. CEP: 37200-000)

**ABSTRACT:**

This study assessed a Specific Methanogenic Activity (SMA) test of the sludge mixture of two (2) of the six (6) Upflow Anaerobic Sludge Blanket (UASB) reactors, installed in the Sewage Treatment Plant at the Universidade Federal de Lavras, in order to evaluate the maximum capacity of the sludge, under anaerobic conditions, in laboratory scale bioreactors, in converting organic substrates to methane gas. After the sampling of sludge in the two UASB reactors, the concentration of Total Volatile Solids (TVS) was measured and the TVS added on the antibiotics flasks. The flasks were sealed with rubber bung and aluminium sealing, maintaining anaerobic atmosphere, incubated at 30°C, being one set of reactors with addition of acetate, and another one without acetate. For both, a food / microorganism ratio of 0.5 gDQO (gSTV)<sup>-1</sup> was applied. The volume produced daily was measured using a ground syringe, and the biogas composition from the standard 85% CH<sub>4</sub> gas curve, measured by gas chromatography (GC), until the stabilization of generation. It was observed that the addition of acetate as a substrate favored SMA, having an average value of 0.011526432 gDQO.(gSTV.d)<sup>-1</sup> compared to 0.000164077 gDQO.(gSTV.d)<sup>-1</sup> for the non-acetate tests. This result is reasonable because the acetogenesis, one of the four (4) phases of the anaerobic degradation, the volatile organic acids formed are oxidized in hydrogen and acetate, direct substrates for the methanogenics. It should also be noted that acetate bacteria is responsible for about 60 to 70% of methane production. In the present study, Next Generation Sequencing (NGS), by the Illumina Miseq Sequencing platform, of the 16S ribosomal RNA genes were used to investigate the anaerobic sludge. The result showed a microbial diversity community and 4.8% of the Euryarchaeta phylum. The anaerobic sludge sample was high abundance of the *Methanobacterium* (3.9%), a genus of hydrogenotrophic archaea, dominant in anaerobic reactors. Others archaeal genus with lower relative abundance

were found such as *Methanobrevibacter*, *Methanolinea*, and *Methanosaeta*. Although the presence of archaea was detected by NGS, the result of the SMA found is below the expected, indicating that could be possible to find problems in the operation of the system, such as over sizing, or inhibitors compounds presence in the effluent ,which could be affecting the methanogenic activity performed by the methanogenic microorganisms contained in the sludge of the UASB reactor.

**Keywords:** Methane, *Methanobacterium*, sludge, UASB, Specific Methanogenic Activity