

TITLE: CHANGES IN COMMUNITIES OF METHANOGENIC ARCHAEA DUE TO CHANGES IN THE LAND USE IN AMAZONIA

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ABSTRACT

Amazonian forest conversion into agricultural and livestock areas has been driven in recent decades by population growth in the region. This land use change disrupts processes related to carbon stock, being considered, after the fossil fuels burning, the activity contributes most to the greenhouse gases emission, of which is methane. Thus, we aim to monitor methanogenic archaeal communities by population enrichment from soil samples collected in primary forest, secondary forest and pasture of the Amazon region. Monitoring was performed by methane emission analysis and enrichment driven by morphological characterization. Sampling was carried in the Tapajos National Forest in Santarém-PA and around. Soil samples were placed into serum sterile flasks with Zinder Basal Medium and separately received acetate, methanol and H₂:CO₂ to stimulate the three metabolism types (acetoclastic, methylotrophic and hydrogenotrophic). Flasks atmosphere was formed using the Simultaneous Gas Distribution System, where enrichment was made on carbon dioxide as carbon source received H₂:CO₂ gas atmosphere in the 80:20 ratio, further filled with gaseous nitrogen. Emissions of methane were monitored by Gas Chromatography, every 7 days. Enriched communities were characterized morphologically by fluorescence microscopy. Methane emission average in soil from pasture sample was higher than the primary and secondary forest samples. The higher emission was observed for all carbon substrates. Analyzing the methane emission by the three types of carbon sources in the three soil samples, the methanol enrichments presented a higher methane yield than the acetate samples and much larger than cultures with H₂:CO₂. These results indicate that methylotrophic pathway, although considered as an alternative, may be important in methane production in the Amazonian soil. The phenotypic characterization of enrichments revealed aggregated cells, characteristic of the genus *Methanosarcina* sp. Cells in cocci and bacilli formats were also observed. Future analyses should include *mcrA* quantification and sequencing of V4 region of the archaeal 16S rRNA.

Keywords: Enrichment; Gas Chromatography; Methanogen

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