

**TITLE:** METHANOTROPHIC COMMUNITY CHANGES WITH DEFORESTATION IN AMAZON

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**ABSTRACT:**

Soils may be sink or sources of methane gas to the atmosphere. Primary forest soils in Amazon are commonly seen as sinks, while pastures as sources. The uptake of methane in soils is made by bacteria capable of using this gas as an energy source, so defined as methanotrophs. The well-known bacteria that perform this function in soils are defined as Type I (groups of Gamaproteobacteria) and Type II (groups of Alphaproteobacteria) (Knief et al. 2015). Type I methanotrophs assimilate formaldehyde by ribulose monophosphate, a more efficient assimilation reaction, while Type II methanotrophs use the serine pathway, which is less efficient in assimilating formaldehyde. To this study, in silico analysis were made with data obtained from Rodrigues et al. (2013) of primary forest and areas managed for 20 years with pasture in Ariquemes - RO. For taxonomic analysis, amplification reactions of the V4 region of the 16S rRNA gene were conducted with primers 577F and 926R. The amplicons were sequenced using the 454 Life Science sequencer, and the taxonomic identification of the sequences was done based on the Ribosomal Data Project - RDP database (<http://rdp.cme.msu.edu/index.jsp>), following an analysis of relative abundance of groups with Stamp software, and Canoco and R (multtest package) analysis to evaluate correlations with soil attributes. The frequency of each type of methanotrophic Type I and Type II was compared, identifying Methylocella, Methylosinus and Methylocystis as the most abundant in forest soils, and Methylocystis and Methylocella in the pasture soils. The analysis revealed a greater relative abundance of Type II methanotrophs compared to the abundance of Type I methanotrophs in both soils. The Type II methanotrophic groups in the forest soil indicated a greater spatial heterogeneity than in pasture soil, in agreement with the previous study of the entire bacterial community in the areas. The chemical factor in pasture soils that best explains the abundance of Methylocystis (Spearman, -56.7%, p-value 0.002) is the potential acidity of these soils, indicating a tendency of greater abundance in areas with less Al available. In forests, Methylosinus and Methylocystis respond negatively to C and N in soil (Spearman; <66.0%; p-value <0.0002), indicating a possible copiotrophic character of the groups. In an ongoing study, the response of these groups to corrections for base saturation (managing pH) will be evaluated.

**Keywords:** amazon, methanotroph, 454 pyrosequencing, microbial ecology

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