

TITLE: METHANE-CYCLER COMMUNITIES AT DIFFERENT SOIL DEPTH IN THE AMAZON RAINFOREST ACROSS FOREST-TO-PASTURE CONVERSION: THEIR RELATIONSHIP WITH EDAPHIC FACTORS

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Abstract

The Amazon rainforest is one of the most important biomes worldwide, that participates in the global climate regulation. Nevertheless, its preservation is threatened by deforestation that reached more than 15% of the area, of which 80% is used as pasture. The forest-to-pasture conversion turns upland soils from sinks to sources of atmospheric CH₄. This research aims to identify the shift patterns of the methane-cycling communities in terms of abundance and community composition throughout forest and pasture sites, as well their relationship with edaphic factors, addressed at different soil depths in sandy and clay soils. Measurements of continuous CH₄ fluxes and soil sampling were conducted during the rainy season (March) of 2018 in both land use systems at the Tapajos National Forest (Pará, Brazil). Two sampling sites from two soil textures (clay and sandy) were selected for each land use, and soil samples were collected at 0-10, 10-20, 20-30 and 30-40 cm. Quantification of methanogenic and methanotrophic microorganisms was made by qPCR, and the taxonomic characterization of those communities was based on bacterial and archaeal 16S rRNA amplicon sequencing. Methane fluxes were strongly associated with land use, as native forest soils maintained methane consumption at all depths (0-40 cm) while methane emissions were observed in the pasture soils. Within pasture soils, methane emissions in sandy soils were similar throughout the soil profile and were higher than in clayey soils on which the emissions were higher in the surface layers (0-20 cm). Pasture soils presented more abundance of methanogens, while methanotrophs were most abundant in the forest soils. Gene abundance varied with soil depth, being higher at the top layer (0-10 cm), while at other soil depths the gene abundances were influenced by soil texture. Shifts in the taxonomic profiles of methanotrophic bacterial communities were observed, in which the genus *Methylobacter* and *Alpha I Cluster* predominated in forest soils and *Methylocystis* in pasture soils. For methanogens, the most important variations among taxonomical profiles were the presence of several genera in pasture soils. The soil texture revealed as an important factor affecting the distribution of methane-cycler microorganisms in both forest and pasture soils (i.e., higher diversity in sandy soils). The integrated results of this work indicated that the diversity of these microbial communities is regulated by soil physical and chemical properties, such as bulk density, macroporosity, water-filled pore space (WFPS), pH and the content of Al, Fe, Cu and Ca. These results constitute evidence of the effect of deforestation on the soil methane-cycling communities and a reference for future programs aiming to reduce this phenomenon.

Keywords: deforestation, microbial ecology, soil methane cycle

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