Communities of metanotrophs associated with changes in land use of Amazon soils

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Amazonia hosts the largest biodiversity in the world. However, the increased human activities in the Amazonia during the last decades have been causing irreparable losses in the resident biological diversity. One of the consequences of these changes is the shifts in the release of gases related to the greenhouse effect, such as methane. Here we aim to measure the bacterial communities that are able to consume methane produced in soils - named methanotrophs. This assessment was conducted by comparing the bacterial communities of soils of primary and secondary forest with those from pastures sampled in the region of Tapajós National Forest (Brazil). Soil samples with 4 biological repeats were enrichmented with approximant 20% methane, followed by DNA extracted and the 16S IonTorrent sequencing. The results show that groups of Alphaproteobacteria and Verrucomicrobia are more abundant in Forest soil than in pasture soil, whereas Actinobacteria, Chloroflexi, and Firmicutes were more abundant in pasture. Focusing on methanotrophs communities, we observed that the abundance relative of forest soils were higher than pasture. These communities revealed differences in the composition, where the groups of methanotrophs were more abundant in soil forest than pasture. When these soils were enrichmented, we observed an increase of methanotrophs abundance in all soil samples, but in the pasture, we found a remarkable growth of Gammaproteobacteria methanotrophs. These results suggest that pasture soil harbor a distinct metanothopic community than forest, what is important to improve our knowledge about methane emission in the Amazonia. In combination, these results point to a strong effect of changes in land use on bacteria that act in the methane oxidation in Amazonian soils.

Methane; Amazonian; soil; bacteria; enrichment

1800-2500 caracteres com espaços