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Land-use change and forest degradation affect the structure and functional diversity of the Amazonian soil microbiome

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Land-use conversion and forest degradation (such as logging and fires) are major drivers of tropical forest and carbon loss. Anthropogenic land-use changes, in particular, alter the soil microbiome, along with its physicochemical properties, contributing to climate change and increasing the vulnerability of tropical forests. Here, we evaluated forest degradation and land-use change impacts on the structure and functional potential of soil microbial communities. We sampled six areas in the Eastern Amazon, ranging from primary forest to forests experiencing varying levels of degradation (fire and logging), as well as a soybean field and pasture, and used 16S rRNA sequencing and quantitative PCR of methane-related genes (*pmoA*: methanotrophs, *mcrA*: methanogens). Non-metric multidimensional scaling distinguished bacterial and archaeal communities of forest soils (stress < 0.15), associated with higher organic matter, cation exchange capacity, moisture, and clay content, from agricultural soils, which were drier, sandier, and more alkaline. Land-use conversion affected methane-cycling genes: pasture soils showed more copies of *mcrA* (9.46×10^3) and *pmoA* (7.30×10^2) compared to other land uses, indicating higher methane emission potential. Soybean soils also showed almost 57 times more methanogenic (2.51×10^3) than methanotrophic (4.43×10^1) genes. Bacterial abundance was lower in soy in comparison to all other areas, pasture differed from burning-logging forest, and forest areas did not differ from each other. Pseudomonadota and Chloroflexota dominated the communities: 43-60% and 6-26% of relative abundance, respectively. Richness increased along the degradation gradient, with lowest values observed in primary forest, intermediate values in degraded forests, and the highest richness and evenness in agricultural areas. Land-use change was the main factor shaping community composition and methane-cycling genes, strongly increasing methanogenic potential in converting areas, followed by forest degradation. Distinct profiles were observed among degraded and deforested sites, particularly between pasture and soybean systems.

KEYWORDS: methane-cycling, quantitative PCR, methanogenic, methanotrophic, deforestation