

TITLE: COMPOSITION AND POTENTIAL FUNCTION OF ARCHAEAS IN RESPONSE TO LAND USE CHANGE IN EASTERN AMAZON SOILS

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ABSTRACT:

The Amazon rainforest is characterized as one of Earth's most important biodiversity hotspots. However, deforestation and the subsequent conversion of forest-to-agriculture have impacts that have not yet been elucidated in the soil microbial community. The aim of this study was to evaluate the taxonomic profile and abundance of *Archaea* communities across land use changes at different time-scale in tropical soils of Eastern Amazon. Soil samples were collected in Nacional Forest of Tapajós and adjacent agricultural fields established at 2, 5 and 20 years ago respectively. A greenhouse experiment was carried out to grow soybean plants in soils under influence of land use over time. The soil samples were chemically characterized, and, DNA were extracted from rhizosphere, bulk and forest soils. The taxonomic profile of *Archaea* was characterized by sequencing of *16S rRNA* gene (MiSeq – 600c), and, real-time PCR was realized to quantify the abundance of *16S rRNA* and *amoA* genes of *Archaea*. More than 98% of relative abundance of *Archaea* sequences were classified as Thaumarchaeota phylum. Redundancy analysis showed P and Zn as the main soil chemical parameters responsible for distribution of samples. The forest samples were grouped independently of rhizosphere and agriculture samples. The Thaumarchaeota phylum was positively related with pH, P, Cu and Zn and negatively with H + Al, B and Fe. The Shannon index revealed a greater diversity of *Archaea* in forest soils than agriculture and rhizosphere. The number of copies of *16S rRNA* gene from *Archaea* was higher in bulk soil of 2 years ($1,53 \times 10^8$ Nº of DNA copies/ soil gram) and rhizosphere of 20 years ($1,03 \times 10^8$) when compared to rhizosphere of 5 years ($8,71 \times 10^8$). The abundance of *amoA* gene, related of *Archaea* ammonia oxidizers, was higher in rhizosphere of 2 and 5 years ($7,30$ and $5,95 \times 10^6$ respectively) than bulk soil of 5 ($1,39 \times 10^6$), 20 years ($1,85 \times 10^6$) and forest soil ($2,58 \times 10^6$). In conclusion, land use over time influenced the *Archaea* abundance and land use change altered your composition and diversity. Thaumarchaeota showed to be the dominant phylum in all soils. The results suggest a predominance of ammonia oxidizers in all soils mostly in rhizosphere soils.

Keywords: Forest-to-agriculture conversion; 16S rRNA sequencing; Real-time PCR; Microbial ecology

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