ECOLOGICAL CO-OCCURRENCE MORE THAN SOIL PHYSICOCHEMICAL FACTORS DRIVERS ARCHAEAL COMMUNITY IN AMAZON SOILS UNDER DIFFERENT LAND USE SYSTEMS

CHAVES, M.G.1*; MERLOTI, L.F.1; DE SOUZA, L. F.1; TSAI, S.M.1; NAVARRETE, A.A1,2

¹Cell and Molecular Biology Laboratory, Center for Nuclear Energy in Agriculture, University of São Paulo USP, Piracicaba, SP, Brazil

²Department of Environmental Sciences, Federal University of São Carlos, Sorocaba, SP, Brazil

Deforestation of tropical rainforests in the Amazon for the establishment of pasture and cultivation areas has resulted in structural and functional changes in the soil archaeal community. This study aimed to evaluate which factors, if whether the occurrence of archaeal taxonomic groups or whether those related to soil physicochemical characteristics, has a greater relevance in structuring the community of this microbial domain. Soil samples were collected in the Solimões river basin, in the state of Amazonas, Brazil, in agricultural systems of indigenous people, cattle pasture, primary forest and secondary forest (5-20 years old). The archaeal community composition was revealed based on high throughput amplicon sequencing of the 16S rRNA gene. Sequence data was analyzed using bioinformatics tools (QIIME), and then combined with soil physicochemical factors using statistical analysis. The results revealed greater co-occurrence of archaeal taxonomic groups at the Class level, where two groups were formed: between the Thaumarchaeotas class SAGM (Gold Mine of South Africa), SCG (Soil Crenarchaeotic Group) and the Euryarchaeotas Thermoplasmatas (positive Spearman correlation rank P <0,05); among Bathyarchaeotas and Euryarchaeotas Methanomicrobia and Methanobacteria (positive Spearman correlation rank P <0.05). The Methanomicrobia class were the only that presented correlation with phycochemical factors: P (potassium), silt and coarse sand, all negative Spearman correlation rank (P < 0.05). These results suggest that possible interactions are occurring between classes belonging to different archaeal phyla, mainly among the methanogenic Bathyarchaeota and the methanogenic Methanomicrobia and Methanobacteria, possibly to supply energy necessary in environments under stress.

KEYWORDS: Archaea, tropical rain forest, 16S rRNA gene amplicon sequencing, soil agriculture.

^{*} mgchaves@usp.br