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Influence of soil properties on the differential abundance of prokaryotes in silvopastoral systems in the western Amazon

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Livestock-forestry systems (ILFSs) may improve soil health by promoting diverse microbial communities. The soil microbiome is influenced by soil chemical and physical properties. Understanding this influence is important in explaining differential abundance and in defining management practices. The objective of this study was to analyze the correlation between soil environmental variables and prokaryote community structure in two ILFSs and a native forest fragment (NF) located in Porto Velho, Rondônia State, Brazil. Soil samples were taken from the 0-10 cm layer from two ILFSs (0.00 and 5.25 m from the trees) and a NF fragment (Am climate, Udox soil, clay texture), with five replicates, totaling 25 samples. Both ILFSs consisted of long-established pastures in which Samanea tubulosa (ILFS-ST) and Eucalyptus pellita (ILFS-EP) strips were planted. The soil DNA was extracted, and the 16S rRNA gene was sequenced. The sequences were grouped into OTUs and classified taxonomically. The influence of sixteen soil chemical and physical properties on the microbial community was analyzed using the dbRDA function of the microeco package for R, with Bray distance and grouping by area. The soil properties accounted for 83.43% of the variance in the community composition among areas, excluding moisture, available P and K (p>0.05). Aluminum, exchangeable Ca and Mg, clay content, and pH were the soil properties with the strongest influence. The native forest had the most distinct microbial community, likely due to its higher acidity. This study suggested that ILFS practices can influence soil microbial communities, potentially impacting soil health, especially by reducing acidity.

KEYWORDS: 16S rRNA gene sequencing, ICLFS, Soil microbiome, Soil quality

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