ABSTRACT:
The humus forms represent the distribution of organic and holorganic layers on top of the soil profile, and they are important sources of matter and energy for soil organisms. The humus forms are widely studied in temperate regions, unlike tropical regions, where little is known about the occurrence of these formations and their associated microbiota. Due to the anthropic pressures suffered by the Amazon forest, it becomes important to know these formations, their microbial diversity and functions. The objective of this study was to evaluate the bacterial distribution in a humus form found in the Brazilian Amazon rainforest. Layers representing different degrees of organic matter decomposition were sampled in a forest and a pasture located in São Joaquim do Ituquara, in the municipality of Baião (PA). In the forest, the layers were: whole leaves; fragmented leaves; fragmented leaves mixed with roots; a root-dominated layer; a layer containing abundant, highly fragmented organic matter; the transition between the organic layers and the mineral soil; and the mineral soil. In the pasture, the layers were: whole leaves; fragmented leaves; the mineral soil; and the rhizospheric soil. The composition of the bacterial communities was evaluated by sequencing of the 16S rRNA gene in the MiSeq Illumina platform. The data were processed with the Dada2 pipeline implemented in the R Studio software. Forest communities were clearly distinct from those in the pasture. A vertical distribution of bacterial groups was observed. Litter communities were distinct from soil communities in both land uses. This difference was discrete in the pasture, while a gradient in the composition of communities was observed in the forest, probably as a consequence of the gradual transformation of the organic material. These results indicate that the humus forms should be taken into account in studies of soil microbial diversity.

Keywords: bacterial distribution, diversity, humus form, MOR.

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