

**TITLE:** LINKING AVAILABLE PHOSPHORUS AND PHOSPHATASE ACTIVITY TO BACTERIAL COMMUNITY STRUCTURE IN FOREST AND PASTURE IN AMAZONIAN SOILS

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**ABSTRACT:**

Amazonian soils are generally highly weathered and have nutritional limitations to agricultural production, mainly in relation to phosphorus (P) content, due to low availability, precipitation with ionic forms of Fe and Al, and adsorption by Fe and Al oxy-hydroxides. In this sense, microorganisms, which produce most of the enzymes in the soil, represent the main facilitators for the availability of P for plants. Phosphatases are extracellular enzymes produced by microorganisms and plant roots that are related to the P cycle, being responsible for organic P mineralization and providing inorganic sources of P for plants. Therefore, our objective was to relate the P content of the soil to the activity of acid phosphatase (AP) and to identify which bacterial groups are related to the P transformations in the soil. For this, we investigated two land uses (primary forest and pasture) and two soil textures (clayey and sandy) at different depths (0-10, 10-20, 20-30, and 30-40 cm) in Amazonian Oxisols. Our results showed that the sandy forest, at all depths, showed more available P compared to the other treatments ( $p \leq 0.05$ ). In contrast, this soil showed the lowest AP activity, probably because this enzyme is produced mainly when the available P is at critical levels for plant and microbial growth. In relation to organic P, the clayey forest and clayey pasture have the highest values. The phosphatase activity decreased with increasing depth (average of 458.8 mg PNP kg<sup>-1</sup> soil h<sup>-1</sup> at 0–10 cm; 339.8 at 10–20 cm; 286.0 at 20–30 cm and 245.8 at 30–40 cm), which may be related to the lower labile carbon content and lower availability of O<sub>2</sub>, which decreases the number of aerobic microorganisms and their activity compared to the superficial layer. The taxonomical profile of the bacterial community related to P cycle was explored at the genus level through the high-throughput sequencing of the 16S rRNA gene. In general, community was more abundant in sandy pasture at the top layers. Interestingly, in clayey forest soil, the relative abundance of bacterial community was higher in depth soil layers. The genus *Bacillus* was the most abundant in the studied soils, followed by the genus *Bradyrhizobium*. However, switch in community composition was associated with the soil depths and texture, where the genus *Pseudomonas* was observed only in the depth layers, while the abundance of the genus *Rhizobium* was significantly higher in clayey soils, regardless of land use type.

**Keywords:** phosphorus cycle, land uses, soil texture, soil depths, microbial ecology

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