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β-glucosidase, acid phosphatase, and arylsulfatase responses to agricultural management: reflections of microbial dynamics in the Cerrado

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The sustainability of soybean depends on the microbial community, the main source of extracellular enzymes that act as mediators of soil biogeochemical cycles. This study evaluated the impact of different managements on the activity of microbial enzymes linked to the carbon (C), phosphorus (P), and sulfur (S) cycles. The experiment compared four systems: Forest (natural reference), No-Till (NT), Regenerative Agriculture (RA), and Conventional Cultivation (CC), using soil samples (0-20 cm). The activities of β-glucosidase (C), acid phosphatase (P), and arylsulfatase (S) were determined via colorimetric assays (pNP). The results demonstrated that management practices strongly modulate the microbiome. RA stood out with β-glucosidase activity 27% higher than the Forest and 94% higher than CC, evidencing intense microbial degradation of cellulose due to the constant biomass input. For acid phosphatase, conservationist systems (NT and RA) outperformed CC by 64%, suggesting greater microbial induction for organic phosphorus mineralization. Noteworthy is arylsulfatase, an enzyme closely associated with fungal biomass, which presented activity 210% higher in managed areas compared to the Forest. This increase reflects significantly more dynamic nutrient cycling and rapid microbial turnover in agroecosystems, driven by crop succession and continuous residue addition. It is concluded that conservationist systems favor the proliferation of the microbiota and the stabilization of its enzymes in the soil. This dynamic results in cycling rates superior to the natural reference, consolidating biological health as the basis for soybean sustainability.

KEYWORDS: Soil microbiota, Enzymatic bioindicators, Conservation systems, Nutrient cycling.