

VII Simpósio de Microbiologia Agrícola

Inovação e Sustentabilidade para transformar o campo

18 a 21 de maio de 2026



Microbial community structure responds to land use change and soil carbon fractions in the Cerrado

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The conversion of land use from natural areas to agricultural systems can alter soil carbon (C) stocks, influencing the structure and functioning of microbial communities. This study aimed to evaluate the effects of land use change on soil C content and on the structure of bacterial and fungal communities. Four land uses were sampled in the Cerrado biome: Crop-Livestock Integration (ICL), Livestock-Forest (ILF), Permanent Pasture (PP), and Native Forest (NF). Samples were collected at depths of 0-5 and 5-10 cm, where carbon fractions (mineral-associated organic matter (MAOM) and particulate organic matter (POM)) were evaluated, in addition to the characterization of microbial communities through amplicon sequencing. Soil physical attributes and enzymatic activity were also determined. The ICL system showed the lowest MAOM contents, while the other land uses did not differ from each other. For POM in the 0-5 cm layer, higher values were observed in NF. ICL presented a higher number of observed bacterial ASVs. Bacterial and fungal beta diversity was influenced by land use change. Arylsulfatase, soil density, moisture, and MAOM were the main variables associated with community structuring, explaining 46.8% and 26.99% of the variation for bacteria and fungi, respectively. Variance partitioning indicated a greater contribution of the physical component for bacterial communities, whereas for fungal communities there was an equivalent contribution of the physical, carbon, and biological components. Co-occurrence networks indicated greater connectivity between MOP and predicted carbon metabolic pathways. The results highlight the close relationship between microbial dynamics and soil C fractions under different land uses.

KEYWORDS: amplicon sequencing, particulate organic matter, integrated agricultural system, microbiome

FUNDING: São Paulo Research Foundation (FAPESP # 2022/09977-6) and RCGI – Research Centre for Gas Innovation, hosted by the University of São Paulo (USP) and sponsored by FAPESP (2014/50279-4 and 2020/15230-5) and Shell Brasil.