

TITLE: EVALUATION OF BACTERIAL COMMUNITY IN PAMPA BIOME AREAS UNDER DIFFERENT PASTURE GRAZING PRESSURE LOAD

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ABSTRACT:

Pampa Biome is one of the richest biome in diversity of species. It is located in the southern region of South America and occupies areas in Brazil, Uruguay, and Argentina. Despite the ecological importance, it is estimated that half of the original vegetation has been already removed and part of the land is used for livestock production, once the natural pasture on the region favors livestock activities. However, the excessive grazing or cattle load may generate major impact for the soil microbial diversity. Studies have shown that higher microbial diversity can increase resistance and resilience of microbial processes while the microbial diversity loss affects nutrient cycling. Therefore, the aim of the study was compare the bacterial community of grasslands controlled soils under different pasture grazing pressure load in a long term UFRGS control study areas, using high throughput sequencing: High Grazing Pressure (HP), with 4% herbage allowance (HG); Moderate Grazing Pressure (MG), with 12% HA; Low Grazing Pressure (LG), with 16% HA; and a control area (CG) with regenerated vegetation undisturbed since 1988. The sequencing of the V4-V5 16S rRNA gene of the soil DNA samples yielded 4,384,037 good quality sequences. Preliminary analysis show that although the soil bacterial community did not suffer differentiation in the presence/absence of bacterial groups, we were able to detect statistically significant changes in each different grazing pastures treatments, especially in the MG that differed in relation to other grazing pressures and to the CG in all analysis performed. There are forty-three different bacterial groups at the phylum level, and the most frequent phyla were Proteobacteria, Acidobacteria and Actinobacteria. Verrucomicrobia, Bacteroidetes and Gemmatimonadetes are highly frequent in CG, LG and HG, and less frequently found in MG. In contrast, Nitrospirae is highly frequent in MG while it has a low frequency in CG, LG and HG. More than six hundred genera were found in this study and twelve genera were statistically different among samples. *Syntrophobacteraceae*, *Koribacteraceae* and *Conexibacteraceae* were found mostly in MG unlike other groups, such as *Solibacteraceae*, *Edaphobacter*, *Acidobacteriaceae* and *Bacillales* found in lower frequency in MG. Our preliminary results provide the first insights into the range of microbial diversity on the soils with different pasture grazing pressures load in a long-term experiment in the Brazilian Pampa.

Keywords: Pampa, pasture, grazing pressure load, bacteria, high throughput sequencing.

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