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of the 21st World Congress of Soil Science

VOLUME II



RIO18

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of Soil Science

SOCIEDADE BRASILEIRA DE CIÊNCIA DO SOLO
Viçosa, MG, Brazil - April 2019

PROCEEDINGS
of the 21st WORLD CONGRESS OF SOIL SCIENCE
Rio de Janeiro, August 12-17, 2018 BRAZIL

SOIL SCIENCE
Beyond Food and Fuel



RIO18

21st World Congress
of Soil Science

Rio de Janeiro August | 12 - 17

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Felipe Martins do Rêgo Barros¹; Victor Lucas Vieira Prudêncio de Araújo¹; José Petrônio Mendes Júnior¹; Tiago de Oliveira Santos¹; Giselle Gomes Monteiro Fracetto¹; Felipe José Cury Fracetto¹; Mario Andrade Lira Junior¹
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Intercropping tree legumes with forage grasses in a silvopastoral system can avoid the pastures degradation and recover them. This soil management has been successfully used in the recovery and maintenance of degraded pastures, with known results on the soil chemical quality, but without information about their influence on the soil microbial communities. We investigated the influence of the silvopastoral system on the community structure from soil total bacteria. The study area is located at the Experimental Station from Instituto Agronômico de Pernambuco (IPA), in Itambé municipality (Pernambuco state, Brazil). The experiment had nine plots of one hectare with tree legumes Sabiá (*Mimosa caesalpinifolia*) and Gliricidia (*Gliricidia sepium*), and a single Brachiaria (*Brachiaria decumbens*), in a randomized block design with three treatments: B + S (Brachiaria intercropping Sabiá); B + G (Brachiaria intercropping Gliricidia) and B (single Brachiaria), containing three replicates. The soil samples were collected at 0.20 m of depth, in June 2016 (winter season). In B+G and B+S the samples were collected at zero (0 m), four (4 m) and eight meters (8 m) from the legumes, while in B the samples were randomly collected. The structure of the total bacteria communities was evaluated by DGGE (Denaturing Gradient Gel Electrophoresis). The differences in structure of the total bacteria communities among the treatments have been assessed by similarity analysis (ANOSIM). The structure of the total bacteria communities was significantly influenced by silvopastoral system. The results of the ANOSIM pairwise test showed significant differences between B + S (collected at 4 m and 8 m) and B (R Statistical = 0.61 and 0.85, respectively; $p < 0.05$) and between B and B+G at all distances evaluated (R Statistical > 0.75 ; $p < 0.05$), indicating distinct bacterial communities. The analysis among the distances showed significant differences between 0 and 8 meters. Bacterial communities are stimulated by higher enzymatic activity and higher C and N concentration below the canopy of the trees, forming "hotspots". Furthermore, tree legumes in silvopastoral system influence the grazing intensity in the grass, promoting changes in the microbial community, explaining the differences between B + G (collected at 8 m) and B and B + S (collected at 8 m) and B. However, silvopastoral systems with tree legumes drive the soil community structure of total bacteria.

Keywords: intercropping; tree legumes; brachiaria; 16S rRNA

Financial support: CNPq and Apoio à Pesquisa Institucional – Universidade Federal Rural de Pernambuco, Edital 09/2014.

(6582 - 996) Soil Bacterial and Archaeal community largely reflects changes in soil properties induced by sheep grazing in an arid shrubland of Patagonia

Magali S. Marcos¹; Mónica B. Bertiller¹; Nelda L. Olivera¹
IPEEC - CONICET¹

The aim of this study was to analyze the diversity of Bacteria and Archaea in arid soils from the Patagonian Monte under different sheep grazing pressures, and their relation with soil physicochemical properties. Upper soil samples associated to vegetated patches (P) and inter-patches (IP) were collected at a grazed site (G) and a non-grazed site (NG) within the field "San Guillermo" (42°51'S, 64°54'W). Aliquots of the soil samples were used to determine soil moisture, pH, texture, organic C, total N, C/N ratio, and the concentration of ammonium, nitrate and nitrite. The diversity and community structure of Bacteria and Archaea in DNA extracted from soil samples was analyzed by MiSeq sequencing of 16S rRNA genes. Bioinformatic analyses were performed in QIIME2 software and sequences were

classified using the Greengenes database. Soil moisture was low ($< 3.6\%$), pH varied between 7.8 and 8.3, and texture was sandy loam. Soil organic C, total N, ammonium and nitrite concentrations were higher ($p < 0.05$) at NG (C: 5.79 ± 0.66 mg/g; N: 0.50 ± 0.03 mg/g; NH_4^+ : 2.25 ± 0.12 $\mu\text{g/g}$; NO_2^- : 0.30 ± 0.03 $\mu\text{g/g}$) than at G (C: 3.29 ± 0.68 mg/g; N: 0.30 ± 0.05 mg/g; NH_4^+ : 1.80 ± 0.16 $\mu\text{g/g}$; NO_2^- : 0.16 ± 0.03 $\mu\text{g/g}$), but nitrate concentration and the C/N ratio did not differ significantly among samples ($p > 0.05$). Two-way nested analysis of similarities based on the Bray Curtis index detected differences in microbial community composition at G and NG (global R: 0.59, significance 0.3%), and this result was also supported by cluster and MDS analyses. The families with higher contributions to these differences ($> 1\%$) were Gaiellaceae and Rubrobacteraceae (Actinobacteria), Nitrososphaeraceae (Thaumarchaeota), and unclassified families of the phyla Euryarchaeota, Acidobacteria, Proteobacteria and Actinobacteria. Four soil physicochemical variables (moisture, clay percentage, organic C and nitrite concentration) showed the highest correlation (Rho: 0.71, significance 1%) with the Bray Curtis resemblance matrix based on microbial community composition. No differences were detected between P and IP in physicochemical properties, nor in microbial community composition ($p > 0.05$). In this study, grazing disturbance exerted a major effect shaping soil Bacterial and Archaeal community, through their response to changes in soil physicochemical properties, both in vegetated patches and in bare soil areas.

Keywords: arid soils; Patagonia; microbial diversity; microbial community ecology

Financial support: ANPCyT, Project Numbers PICT 2013-1505 and PICT 2015-1689; and CONICET, Project Number PUE IPEEC 22920160100044

(4758 - 1434) Structure of the microbial community in a saline soil from semi-arid region of Pernambuco.

Emanuelle Maria da Silva¹; Maria Betânia Galvão dos Santos Freire¹; Giselle Gomes Monteiro Fracetto¹; Josimar Gurgel Fernandes²; Alcione Guimarães Freire¹; Felipe Martins do Rêgo Barros¹
UFRPE¹; IPA²

The knowledge of the microbial communities present in saline soils could represent a biotechnological potential for applications in the improvement and conservation of saline environments. Some research has focused on the isolation and characterization of these organisms, but more extensive studies have been needed on their ecology, structure, diversity, and functionality. In this study, the structure and diversity of the microbial communities were evaluated along a salinity gradient (High salinity - 17 dS m^{-1} , Average salinity - 8 dS m^{-1} , Low salinity - 4 dS m^{-1} , Native forest - 0.6 dS m^{-1}) in a degraded pasture area, unused for about 20 years, in the municipality of Caruaru (S $08^\circ 15'00.4''$ and W $035^\circ 52'38.0''$). At each salinity level, three samples were collected in the 0-20 cm layer, 2.5 m apart. DNA extraction from the soil was performed with the PureLink™ Microbiome DNA Purification Kit (Invitrogen). Bacterial communities were analyzed by the 16S rRNA gene using the 341f-GC and 518r primers and for the fungi, the ITS1 region of the 18S rRNA gene was amplified using primers EF4, ITS4, ITS1-F-GC and ITS2. DGGE was performed with a denaturing gradient of 30 to 60% for the 16S rRNA gene, from 30 to 55% for ITS. The similarity index was obtained by the analysis of similarity (ANOSIM). The diversity of the communities was evaluated by Shannon's diversity index (H') and Simpson's dominance index (D). ANOSIM pointed out that the four areas were not different from each other, indicating that the salinity was not determinant for the differentiation of the community structure. It is possible that the high variability of the areas has prevented the detection of differences between them. By the factorial analysis by main components, there was a positive correlation between EC and SAR with D index, and