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Sugarcane trash levels in soil affects the fungi but not bacteria in a short-term field experiment

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ABSTRACT

The sugarcane in Brazil is passing through a management transition that is leading to the abolition of pre-harvest burning. Without burning, large amounts of sugarcane trash is generated, and there is a discussion regarding the utilization of this biomass in the industry versus keeping it in the field to improve soil quality. To study the effects of the trash removal on soil quality, we established an experimental sugarcane plantation with different levels of trash over the soil (0%, 50% and 100% of the original trash deposition) and analyzed the structure of the bacterial and fungal community as the bioindicators of impacts. The soil DNA was extracted, and the microbial community was screened by denaturing gradient gel electrophoresis in two different seasons. Our results suggest that there are no effects from the different levels of trash on the soil chemistry and soil bacterial community. However, the fungal community was significantly impacted, and after twelve months, the community presented different structures among the treatments.

Introduction

Brazil is the largest sugarcane producer in the world, with a cultivated area of 9 million ha that is mainly used for the production of sugar and ethanol.[1,2] Traditionally, sugarcane crops are burnt before harvest. However, this procedure results in the emission of particulate matter and smoke, resulting in poor air quality and a problem for public health.[3]

The government and other organizations proposed the elimination of pre-harvest burning, which resulted in the input of 10,000–30,000 kg of dry mass ha^{-1} of sugarcane trash over the soil.[4–6] This biomass can be used for energy generation,[7,8] for cellulosic ethanol or bio-oil production,[9,10]

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Table 1 – Chemical characterization of the soil samples from the studied areas.

Treatments	pH H_2O	Ca	Mg	H + Al	K	P	SB	CEC	V	Organic matter
			$cmol_c\ dm^3$		$mg\ dm^{-3}$		$cmol_c\ dm^{-3}$		%	$g\ kg^{-1}$
0%	6.38	7.16	3.00	3.68	0.52	2.64	10.69	14.37	74.38	34.60
50%	6.32	7.03	2.90	3.80	0.42	2.59	10.35	14.15	73.14	39.70
100%	6.35	7.12	3.05	3.70	0.47	2.68	10.66	14.36	74.20	38.95
Cerrado	6.47	10.02	3.30	3.35	0.63	3.41	13.96	17.31	80.62	52.25

* Available P and K; exchangeable Ca, Mg and H + Al; SB, sums of bases; CEC, cation exchange capacity; and V, percent base saturation. The exchangeable Al content was below the detection limit in all of the treatments.

or it could be maintained on the field to improve the soil quality.[11–13]

Several studies have reported the influence of the burnt versus green harvest managements on the soil properties.[11–22] They showed that the conversion of burnt to green harvest can positively influence several soil properties, such as C stocks, microbial biomass, soil enzyme activity and soil aggregation. It can also significantly modify the total bacterial community and the nitrifying and denitrifying gene diversity.

However, these studies involved several other factors, such as fire occurrence and the mechanical versus manual harvest, in addition to the sugarcane trash content. Therefore, there is a lack of information regarding the specific impacts of removing versus keeping the sugarcane trash on the soil. The biological attributes of soil, such as the microbial community structure, biomass, diversity, soil enzymes activities, soil respiration and qCO_2, are very sensitive to land use changes and crop management. Typically, biological properties change faster when compared to physical or chemical properties,[12,19,23–25] and could be used as an early evaluation of some adverse management practices, which also allows the early adoption of corrective practices.

In this context, we studied the influence of the different levels of sugarcane trash over the soil on the structure of soil bacterial and fungal communities in two contrasting seasons. We hypothesized that the sugarcane trash is an important factor influencing the microbial community in the soil, and its removal can significantly impact the structure of both the bacterial and fungal communities.

Materials and methods

Field description, experiment design and sampling

The experiment site was located at Cristal Farm, property of Unialco Company, in Dourados, Mato Grosso do Sul state, Brazil. The climate of the region is Cwa, according to Köppen's classification (temperate humid with hot summer and dry winter), with an annual average temperature of 23 °C and an average annual precipitation of 1635 mm.

The experiment was set in a randomized block design, with three treatments and three replications. Treatments were defined as different levels of trash left over the soil (0% – all trash on the ground was removed; 50% – half of the trash was maintained; and 100% – all trash was maintained). Each plot had an area of 5 m × 20 m. The treatments were set in January 2009, two years after the sugarcane crop establishment. The area was previously cultivated with corn, wheat and soybean.

The samplings were performed in January 2010 and July 2010 during the wet and dry seasons, respectively (after 12 and 19 months after treatments implementation, respectively). In each plot, five soil samples (0–10 cm) were randomly collected and combined into a composite sample. To compare the community with the natural condition of the soil, in each season, three composite soil samples were collected in an adjacent area under native Cerrado vegetation (Brazilian savana-like vegetation) and similar soil and topographic conditions. The soil of the area was classified as Rhodic Eutrudox, according to Soil Taxonomy,[26] and as Latossolo Vermelho Eutroférico, according to the Brazilian System of Soil Classification (SiBCS).[27] Table 1 presents some soil chemical properties of the sampled soil.

Bacterial and fungal community analysis

Soil DNA was extracted using the FastDNA Spin Kit for Soil and a FastPrep equipment (Bio 101, CA, USA), according to the manufacturer's instructions. We used the universal primers for the domain bacteria and fungi to analyze the microbial community structure. All of the primers and cycles and PCRs used for this analysis are specified in the supplementary material (Table S1).

The amplified fragments were analyzed via denaturing gradient gel electrophoresis (DGGE),[28] as described by Rachid et al.[19] The gel concentration and the denaturing gradients were, respectively, 6% and 45–65% for bacteria and 8% and 30–60% for fungi.

Data analysis

The differences in the microbial community structures were analyzed by non-metric multidimensional scaling (NMS) using the PC-ORD statistical package V5 (MjM Software, Gleneden Beach, OR). The DGGE band profiles were digitalized and inserted into the data matrices using the Bionumerics v6.5 package (Applied Maths), according to the manufacturer's instructions.

Each matrix was ordinated by NMS using the Sørensen distance[29] and a random initial configuration. The significance of the matrix data structure was assessed with the Monte Carlo test with randomized data. The final result of the NMS analyses was restricted to two dimensions to simplify the data analyses and discussion.

To confirm the existence of the groupings generated by the NMS analysis, we performed a blocked Multi-Response