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VOLUME II

RIO18

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Viçosa, MG, Brazil - April 2019

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of the 21st WORLD CONGRESS OF SOIL SCIENCE

Rio de Janeiro, August 12-17, 2018 BRAZIL

S O I L S C I E N C E

Beyond Food and Fuel

RIO18
21st World Congress of Soil Science
Rio de Janeiro August | 12 - 17

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SUMMARY

RIO18
21st World Congress of Soil Science
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(6999 - 2888) DNA concentration of the soil may be affected by herbicide applications in high weathered soils

Marco Aurélio Pessoa-de-Souza[1]; Hugo Delleon da Silva[2]; Elisângela de Paula Silveira-Lacerda[2]; Evandro Novaes[2]; Virgínia Damin[2]
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Savanna Tropical soil has a tendency to be weathered due intensive climatic characteristic. These condition may offer a specifically condition of charges exposure contained in the external sites of the clay minerals. Herbicide, frequently used in Brazilian crop production, may interact with soil charges and microorganisms of the soil, and this relationship is dependent of molecular and soil physic-chemical profile. Microbiote is sensitive parameter and biological indicator to prognosticate soil management especially when assessments are at the molecular level. In this way, our aim was evaluate soil capacity to extraction Soil DNA when submitted to herbicide application. The experiment were established in factorial design 4 X 4 (three herbicides – Oxyfluorfen, Sulfentrazone e Diclosulam – and control, and four soil classes - LATOSSOLO VERMELHO Ácrico (LVw), LATOSSOLO VERMELHO Distrófico (LVd), GLEISSOLO MELÂNICO (GM) and NEOSSOLO QUARTZARENICO (RQ)). Soils were collected in 30 cm of profundity, sieved 2 mm and disposed in black vases with near of 1000 ± 20 g, considering soil density. Before DNA extraction procedure, samples were prepared by 8 months in semi controlled site, with application time intervals of the 2 months, with humidity control (60%) e temperature (30 ± 5°C). Extraction was procedure using Fast DNA^{TM} SPIN KIT for Soil$^{®}$ (MPBio), and DNA concentration was mesure by Digital Fluorimeter FD-570, 0.02 mg·L^{-1} precision. The main results point to two ways: soil and herbicide effects. Among the soils, the organic character (GM) was the most affect reached the highest levels of DNA concentration and with herbicide application low DNA levels. RQ had low DNA concentration. All herbicides decreased the DNA concentration for all studies soils, following the order GM > LVw > LVd > RQ. Finally, we conclude the herbicide may impact negatively DNA concentration and microbiota persistence.

Keywords: DNA Quantification, DNA interaction, Pesticides, Environment
Financial support: FAPEG

(5664 - 1181) Fish processing effluent discharges influenced chemical properties and microbial diversity in arid soils from Patagonia

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Even though fish processing industry uses large amounts of water, there is scarce knowledge about the possibility of its reuse for irrigation. In the arid Patagonian Monte, there are sites where fish processing effluents are discharged, resulting in a visible stimulation of native vegetation. We analyzed soil chemical properties and microbial diversity in a site where fish processing effluents are discharged (ES) and in a control site not disturbed (CS). At each site, 5 surface soil samples were randomly taken under plant-covered patches. We determined soil moisture, pH, electric conductivity (EC), sodium adsorption ratio (SAR), total C, inorganic C, total N, and concentrations of ammonium and nitrates+nitrites. Bacterial 16S V4 rDNA region was amplified and sequenced using MiSeq® Illumina platform. Operational taxonomic unit (OTU) clustering was performed with mothur using the Silva database. ES showed significantly higher values ($p<0.05$) of soil moisture (ES 12.9±0.7, CS 9.4±0.3%), EC (ES1.2±0.5, CS 0.6±0.2 mmhos/cm), total C (ES 0.86±0.10, CS 0.42±0.03%), inorganic C (ES 0.46±0.12, CS 0.10±0.02%), and nitrates+nitrites (ES 74.1±48.2, CS 4.26±0.13 µg/g) than CS. No significant differences were detected for pH, SAR, ammonium, and total N between sites. A total of 874,827 high quality reads were obtained for 10 samples (GOOD´s coverage > 94%). Effluent discharges induced a diminution of bacterial richness (OTUs) and diversity (Inverse Simpson). Dendrogram (Bray-Curtis distance) as well as principal co-ordinate analysis show that control samples clustered together, while some samples from ES clustered with control samples and others with themselves. LEfSE analysis showed 580 biomarker OTUs with significantly differential abundances between sites, which were classified into 16 phyla. This analysis showed that Archaea, mainly represented by *Nitrososphaeraceae*, were more abundant in CS. Besides, bacterial lineages enriched in CS included *Acidobacteria*, *Actinobacteria*, *Chloroflexi*, *Gemmatimonadetes*, *Nitrospirae*, *Planctomycetes*, *Alphaproteobacteria*, *Deltaproteobacteria*, and *Verrucomicrobia*. Biomarker OTUs from *Gammaproteobacteria* were more numerous in ES. Fish processing effluent discharges increased heterogeneity of soil chemical properties, reducing bacterial diversity and inducing shifts in the structure of the microbial community. This would be considered, and hence monitored, to preserve soil fertility when proposing fish effluent reuse for irrigation.

Keywords: fish processing effluents, microbial diversity, arid soils
Financial support: PICT 2015-1689 (FONCyT, Argentina) and PUE IPEEC 22920160100044 (CONICET-Argentina).

(7721 - 1593) In situ cultivation and 16S rRNA-based identification of rhizobacteria associated with wheat seedlings grown in a Chilean Andisol

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The use of next-generation sequencing technologies have revealed that rhizosphere harbours thousands of different bacterial taxa, which living in a constant interaction with the roots of their host plant. However, it is widely accepted that only a minor portion (≤1%) of rhizobacterial populations can be cultured under laboratory conditions. This limitation underestimates the total diversity of rhizobacteria, particularly of bacterial groups defined as 'rare taxa' or 'unculturable', and commonly present in low abundance. Novel culture techniques have recently been focused on mimicking of the natural environment to unravel the diversity, activity and biotechnological potential of rare or unculturable bacterial portion. In this sense, diffusion chambers for in situ cultivation is one of the most promissory advance for the cultivation and isolation of previously unculturable environmental bacteria. In this study, we used the in situ cultivation using micro-well chambers to isolate rhizobacteria associated with wheat seedlings grown in a Chilean Andisols. Samples of 1 g of rhizosphere soils were serially diluted in sterile distilled water. Distilled water supplemented with agar (1.5% and 60ºC) was used for 10^{-3} dilution, which was then inoculated into a micro-well chambers. The micro-well chambers were incubated in the rhizosphere of wheat seedlings (previously grown for 1 month) and maintained for 2 months under greenhouse conditions (2 months at 20ºC). A total of 236 isolates were obtained by in situ cultivation and 206 isolates were able to identified based on partial sequencing of 16S rRNA genes. Taxonomic analysis revealed that 70% of isolates were identificated as belonging to Proteobacteria, following by Firmicutes (24%), Actinobacteria (4.4%), and Bacteroidetes (1.5%). At the order level, higher abundance were predominated by isolates belonging primarily to Bacillales (24%), Pseudomonadales (22%), Burkholderiales (21%) and Xantomonadales (17%). Isolates with lower abundance (<10