

Title: CHARACTERIZATION OF BACTERIA ISOLATED FROM SOILS ASSOCIATED TO SUGARCANE CROP.

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Abstract:

Sugarcane (*Saccharum spp.*) crop is used on the production of edible sugar and alcohol fuel and its production generates wastes, which pollute the environment when dismissed as *in natura*. The introduction of those compounds in the environments changes the natural microbiome leading to impacts that transform the diversity and richness of microorganisms populations. However, the wastes generated by sugarcane industry sectors also aggregate essential nutrients that could be applied as manure to the sugarcane crop itself, rising the productivity and decreasing the costs involved in fertilizers. Stillage application in fertirrigation is used as a total or partial substitute for mineral fertilizers. In addition, stillage could be utilized as supplement to microbial inoculants acting on the aggregation of microbial communities that in turn participate on the degradation of hydrocarbonates present in some poor nitrogen and phosphate sludge. Thus, these microorganisms play an important role in the generation of micronutrients that plant root system can uptake. The main aim of this work consisted in access the microbial community in sugarcane crop soils under different agricultural management, viewing the isolation of bacteria able to phosphorus solubilization and their respective identification by molecular characterization of 16S rRNA gene. Four bacteria isolates (LGA01-EV05, LGA02-EV08, LGA03-V20B, and LGA04-V20G) from different area irrigate with stillage were characterized regarding their: (i) growth profile on NBrip medium, (ii) pH, (iii) phosphate solubilization ($\text{CaCO}_3(\text{PO}_4)_2$), and (iv) complete DNA sequencing of 16S rRNA amplicon. All of isolates have presented satisfactory results regarding phosphate solubilization, while LGA02-EV08 has highlighted when grown for 72 hours (O.D. 250) on 0.2 mg/ml $\text{CaCO}_3(\text{PO}_4)_2$. In spite of that, there was little variation on pH during the development of growth-curve. Finally, the dendrogram has shown that LGA01-EV05 belongs to Actinobacteria (Microbacteriaceae) while LGA03-V20B and LGA04-V20G belong to Actinobacteria (Micrococcaceae). LGA02-EV08 has shown similarity with Firmicutes. The analysis of microbial diversity faced to stillage applications is important and sustainable for posterior studies focusing on the isolation of functional genes of biotechnological interest.

Key-words: Phosphorus solubilizing, stillage, soil bacteria, agricultural management.

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