

TITLE: MICROBIAL PROFILE IN SWEET SORGHUM GENOTYPES

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ABSTRACT:

The ethanol production is growing in the last decades, is expected to increase more than twice the current production to 55 Bi.L⁻¹ to meet all estimated future demand. However, the processing of sugarcane will not be enough to meet this demand and there will be a need for the use of complementary raw materials. The sweet sorghum has been highlighted as promising and economically viable to ethanol produce. In this context, this research evaluated the microbial characterization of the sweet sorghum juice from the sorghum genotypes BRS 508 and BRS 511. The research was carried out in the 2017 harvest, a randomized complete block design with 4 replicates, evaluating the genotypes. Microbial counts were carried out on various media by the plating technique on the extracted sweet sorghum juice. MRS was used for the quantification of lactic acid bacteria, WLN (with added ampicillin and nalidixic acid at 50 mg.L⁻¹ each) for yeasts and total yeasts determination, and PCA for total microbial counts. The average of results for the genotype BRS 508 for the total microbial counts it was 8.28 x 10⁵ CFU.mL, this represents 100% of the microbial presents in the juice. 71.90% of this it was lactic acid bacteria, 26.37% it was yeasts, and 1.72% it was others microbial counts presents in the sweet sorghum juice. However, for the BRS 511 the total microbial counts it was 1.06 x 10⁷ CFU.mL but just 16.47% of this it was lactic acid bacteria, 1.05% of yeasts, and 82.48% it was others microbial counts. When you compare the raw material that arrives from the field to the industry is directly linked to the quality of the final product, in the sugarcane process, the main contamination presents are some bacteria's from the class *Bacillus* and *Lactobacillus*, other contaminants are the yeasts from the class *Schizosaccharomyces*, *Debaryomyces*, *Candida*, *Pichia*, and *Kloeckera*. This contamination microbial are undesirable for the process because they use the sugars presents and produce undesirable metabolic and instead, could produce ethanol. For can control the contamination in the process, first is necessary to identify the main microorganisms present in the juice. It can be concluded that the presence of different contamination microbial in the sweet sorghum juice, especially for the genotype BRS 511.

Keywords: Bacteria; Biofuels; Contamination; *Sorghum bicolor* (L.) Moench; Yeasts.

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