Microbial Diversity in Different Stages of the Ethanol Production Process Using Traditional Techniques and Molecular Biology

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INTRODUCTION: Biofuels are renewable and cleaner energy sources that can reduce our current dependence on fossil fuels. Brazil is one of the largest producers of sugarcane in the world and the second largest producer of ethanol. Although the ethanol production process from sugarcane is well established, microbial contamination can be a major obstacle to high productivity. The objective of this work is to identify and characterize the main microbial contaminants in the bioethanol production process using microbiology and molecular biology techniques. MATERIAL AND METHODS: Triplicate samples were collected from different stages of the ethanol production process: cane juice, mixed juice, clarified juice, evaporated juice, must and wine. Each sample was diluted and plated on four culture media: PCA, MRS, Czapek and YPD. Colonies were counted, isolated and stored in glycerol. Total DNA of each sample was extracted and the DNA used to amplify ribosomal genes for the construction and sequencing of DNA libraries. DISCUSSION AND RESULTS: We isolated 47 bacteria, 31 yeasts and 17 filamentous fungi. They were stored and will be identified by sequencing the gene coding for rRNA. The total DNA extracted will be used for amplification of the gene encoding the 16S rRNA of the domains *Bacteria*, *Archaea* and 18S for *Fungi*. DNA libraries will be constructed and the clones will be sequenced. The obtained sequences will be used to construct phylogenetic trees for each of the domains. CONCLUSION: We expect to identify and characterize the contaminating microorganisms present in the sugarcane ethanol production process by traditional and molecular biology techniques.

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