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## Functional diversity of yeast associated with sweet sorghum plants determined through the system Biolog

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Yeasts are unicellular ascomycetes fungi or basidiomycetes with high biotechnological potential due to its highly diversified metabolism. Physiological analyzes of different groups of microorganisms have been performed successfully using the Biolog system. This method consists in the ability of a microorganism used and oxidize a pre-selected amount of carbon sources, generating a specific metabolic profile. Moreover, the functional diversity of yeasts that colonize plant sweet sorghum, based on this usage pattern of different carbon substrates has not yet been reported. The purpose of this study was to characterize the functional profile of yeasts associated with plant sorghum via biolog system. 15 were studied yeast strains obtained from stem broth samples from five plant genotypes (three genotypes) were selected randomly based on macro and distinct Micromorphological characteristics. Initially, the strains were activated and tested for purity solid YEPD culture medium (1% glucose, 0.3% yeast extract, bacteriological peptone 0.5%, agar 2%) for 48 hours at 28 ° C. Thereafter, pure colonies were suspended in sterile saline solution (NaCl 0.85%). An aliquot of 120µl of the dilution 10<sup>-2</sup> of the suspension of each strain was transferred to Biolog® GN2 microplate containing sources of carbon and 95 control, which was incubated at 30 ° C in the dark for 72 hours of incubation. Then he performed the absorbance reading of the reactions with development of purple color in an ELISA plate reader (Labstems, Multiskan, MS) at 590 nm. Through readings, estimated the metabolic profile of each strain based on the parameters overall activity (sum of the activity values / plate) substrate wealth (S) number of substrates used / plate, Shannon index (H) diversity species in relation to the use of substrates and equity (E) similarity index between samples. The analysis of variance showed significant differences between the strains for the evaluated parameters. For total activity values ranged from 2660 to 68,630. Regarding (S), there was variation 5333-57666. The value of (M) ranged 0409-3030. To (E) there was variation 0536-0820. It was observed that all cell lines analyzed were capable of using substrates, L-Arabinose, D-Arabitol D-cellobiose, D-fructose, D-galactose, gentiobiose, α-D-Glucose, D-Mannose, β-methyl - D-Glucoside, D-Raffinose, Sucrose, D-trehalose, turanose. It was concluded that there are functional diversity in yeast associated with sorghum plants grown in the Brazilian cerrado.