

**Title: BIOPROSPECTION AND MOLECULAR CHARACTERIZATION OF ENZYMES INVOLVED IN PLANT BIOMASS DECONSTRUCTION FROM SOIL METAGENOMES.**

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**Abstract:**

In order to overtake the foreign technology and increment the national technological development, universities and private enterprises invest money and efforts on the way to increase energy production through sugarcane application without the increment on crop area, avoiding thus the competition with other edible crops. After harvesting and processing, sugarcane presents a high economic as well as energetic value for new researches based on waste plant biomass, as straw and bagasse, which are mostly constituted by cellulose, hemicellulose and lignin. After the deconstruction of lignin and hemicellulose matrix, cellulose become able to be converted in simple sugars that leads to obtainment of second generation ethanol through their fermentation by certain yeasts. Thus, waste plant biomass encounters a noble application faced to currently fate of it. However, this process presents some bottlenecks concerning economic viability and application of more powerful enzymes that have become the matter of research regarding new or alternative pathways for plant biomass conversion. Microbiologists appoint some difficulty to grown mostly of microbiome present in soils, supported by reports showing that just 0.1 – 1.0 % of soil microorganisms could be cultivated by traditional techniques. In this concern, metagenomics could be considered the most accurate technology to unveil the ecological niche. The main aim of this research is the application of metagenomics on soil samples under sugarcane cultivation in order to prospect new enzymes able to break down lignocellulolytic array to generate fermentable sugars to yeasts. This is important to supplement fermenter from alcohol plants. The approaches applied were (i) screening by PCR using specific primers for glycosidases on metagenomics DNA, and (ii) biochemical assays based on cellulolytic substrates to identify positive clones from metagenomics clone library. We have found until now four positive clones expressing cellulolytic activities. The perspective of this work is characterize and express the enzymes showing high ability on plant biomass deconstruction and more thermostability, viewing their application in large scale in biotechnological processes.

**Key-words:** Sugarcane, Agricultural soils, Microbiomes, Carboxymethylcellulose, Cellulase.

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