The Brazilian technology for the production of ethanol biofuel from sugarcane is consolidated. However, Brazil stays quite behind countries like USA concerning the utilization of green sources of power, as starch and lignocellulosic biomass to biofuel production. In this context, this work aims the search of genes coding for biomass degradation enzymes in an insect transcriptome database, which could be used in biotechnological programs for bioethanol production. The transcriptome of Sugarcane Giant Borer (*Telchin licus licus*), previously obtained by our team, was used in a search for contigs which contained total or partial gene sequences coding for biomass degradation enzymes. Nucleotide sequences of biomass degradation enzymes from NCBI databank were used as queries in a multiblast alignment towards Sugarcane Giant Borer transcriptome. Eleven contigs were found to contain sequences of genes coding for biomass degradation enzymes, among them a β-glucosidase and a Xylose reductase genes, which were cloned in pGAPZα-B vector for heterologous expression in *Pichia pastoris*. After expression and purification such enzymes will be assay for activity over sugar from plant biomass. According to the coming results, the digestive enzymes of Sugarcane Giant Borer could encompass a suitable choice for biotechnological programs aiming plant biomass degradation for biofuel production.

Key-words: Biofuel; Plant Biomass; Enzymes
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