Identification of genes encoding for amylase activity with potential use in the ethanol industry

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Economical, political and environmental issues have motivated the search for new alternatives for energy sources and in particular for ethanol production. Today in Brazil ethanol is produced from sugarcane sucrose, while the U.S. uses corn starch. Despite the great success of the Brazilian ethanol program, in a large country with great regional and social contrast, other raw materials such as cassava starch may be an interesting option for ethanol production in the future. Starch is a glucose polymer that can be hydrolyzed by a-amylase and glucoamylase. Glucose monomers can then be fermented into ethanol. The availability of enzymes with different kinetic properties allows the improvement of industrial production processes. Molecular studies have shown that the vast majority of microorganisms is yet unknown. These microorganisms represent a wealth of metabolic pathways and therefore biocatalysts with industrial potential. The genes encoded by these microorganisms can be accessed using a metagenomic approach that involves recovery of DNA from a microbial community followed by cloning and functional screens for the activity of interest. The goat rumen is an anaerobic environment where microbial fermentation of the ingested feed including starch takes place. An expression library was constructed with DNA from goat rumen microorganisms and a functional screen for amylases was performed. Twenty-two clones exhibiting amylase activity were identified. Of these, only six clones showing a different restriction pattern on agarose gel were able to confer the amylase-positive phenotype to newly transformed *E. coli* cells. The genes responsible for the identified amylase activities are being cloned and molecularly characterized.

Keywords: ethanol, amylase and metagenome.

Financial support: CNPq, FAP-DF and UCB.