# Identification of Hydrolases Encoding Genes from the Metagenome of Cerrado Soil: A Source of Industrial Enzymes.

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The industrial use of enzymes is an alternative to the chemical industrial processes, in that they offer increased reaction specificity, product purity and reduced environmental impact. Therefore, the search for novel biocatalysts is very important to the identification of enzymes that can compete economically with the inexpensive, but pollutants, traditional chemical processes. The metagenomic approach has accelerated the discovery of novel hydrolases with activity and stability in a wide range of conditions (pH, temperature, organic solvents and salinity), making these technique a powerful tool to the identification of enzymes suitable for biotechnological application. In the present work, a metagenomic library from Cerrado soil was screened for lipases and proteases aiming the identification of novel genes with biotechnological interest. Expression screening of the library for lipases, based on the hydrolysis of tributyrin, resulted in the identification of three different positive clones with insert sizes ranging from 6000 to 8000 bp. The lipolytic activity of these clones was confirmed after retransformation in *Escherichia coli* EPI-300 and repeated screening. The positive clone pLIP3 shown the highest lipolytic activity on agar-plate assay and will be sequenced. Seven clones with proteolytic activity were identified after the agar-plate assay based on the hydrolysis of milk casein. These clones were stored at -80$^{o}$C for further analysis. Future studies include molecular characterization of the genes detected in this study, the expression and biochemical characterization of the metagenome derived-enzymes.

Keywords: Lipases, proteases and metagenome.

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