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380-1 Accessing lipases from soil metagenome as an aid for biofuel production

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Resume

Accessing lipases from soil metagenome as an aid for biofuel production Tavares, P.2; Bergmann, J. 3; Kruger, R.2; Noronha, E.2 and Quirino, B.1,3 1- Universidade de Brasilia, Brasilia, DF, Brazil; 2 - Embrapa Agroenergia, Brasilia, DF, Brazil; 3 - Universidade Catolica de Brasilia, Brasilia, DF, Brazil. The Brazilian Cerrado has a savanna-like vegetation and the soil has been the focus of very few studies about its microbial biological diversity. Soil is a habitat with high diversity of microorganisms and thus it can be used as a source of industrial enzymes. This genetic resource can be exploited for the identification of novel enzymes suitable for biofuel production Using metagenomics, namely microbial genetic material recovered directly from environmental samples, this biogenetic diversification can be accessed without the need to cultivate cells. The advantage of directly screening for enzymatic activities from metagenome libraries is that one can access previously unknown genes and their encoded enzymes without cultivation. Lipases are hydrolases with diverse applications in the process of biodiesel production. Metagenome expression libraries were constructed by inserting fragmented metagenomic DNA into low copy plasmid expression vectors and transformed into Escherichia coli. Functional screening of this metagenomic expression library resulted in the identification of three lipolytic clones. These clones show high activity against tributyrin and they were characterized and sequenced. The utilization of these new lipolytic genes in the biofuel industry will be discussed.

Keyword: lipases, soil metagenome, biofuel production