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**Resumo:1475-2**

## Poster (Painel)

### 1475-2 **Accessing lipases from soil metagenoma and their application for microbial biofuel production**

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## Resumo

The Brazilian Cerrado has 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. The genetic resource can be explored for the identification of novel enzymes suitable for biofuel applications. Using metagenomics, namely genetic material recovered directly from environmental samples, this biogenetic diversification can be accessed without the need to cultivate cells. Metagenome expression libraries are constructed by inserting fragmented metagenomic DNA into expression vectors based on plasmids, cosmids, fosmids, or phages, after which gene expression is examined in a suitable host system. With this method, the biotechnological potential of cultivated and uncultivated microorganisms in a specific biological sample can be exploited. The advantage of directly screening for enzymatic activities from metagenome libraries is that researcher could access previously unknown genes and their encoded enzymes. Screenings of metagenomic libraries can be performed aiming the bioprospection of enzymes of biotechnological interest. The functional screening of this library resulted in the identification of three lipase activity producing clones that were subsequently sequenced. They revealed ORFs with functions related to lypolitic activity. In addition, these enzymes will be produced in heterologous expression systems so that they can be further characterized for their kinetic parameters and properties suitable for use in biofuel. Considering the potential biotechnological application of these enzymes, this work aims at the selection and characterization of novel lipases genes from metagenomic library from soil from savannah-like vegetation.