064 - STUDY OF GENE EXPRESSION OF EXTRACELLULAR LIPASE THE FILAMENTOUS FUNGUS *ASPERGILLUS JAPONICUS* IN DIFFERENT VEGETABLE OILS FOR BIODIESEL PRODUCTION

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ABSTRACT

The need for renewal of the global energy matrix, seeking cleaner energy sources and renewable have led researchers to explore the use of lipases, mainly, of microbial origin as biocatalysts in the production of biodiesel through transesterification reactions using vegetable oils. This study aimed to identify the best period of production of extracellular lipase synthesized by the filamentous fungus *Aspergillus japonicus*, enabling the future applicability of this enzyme, as biocatalyst, in the production of biodiesel from vegetable oils from soybean, olive, corn and sunflower.

Aspergillus Japonicus (106 spores) were cultivated in Czapec liquid culture medium without sugars, separately containing vegetable oils soybean, olive, sunflower and corn as the unique carbon source and maintained at a temperature of 28 oC, under orbital agitation of 140 rpm for 7 days. At the end of each 24 hours, the means containing different vegetable oils were subjected to potentiometric titration for analysis of fatty acids production. By daily potentiometric analysis (24 hours), it was observed that over seven days, an increase in the number of moles of fatty acids coupled to the four types of vegetable oils, however, this increase was more significant in the medium containing oil sunflower. Thus, the fungus *Aspergillus japonicus* when subjected to a liquid culture medium (free sugars), containing triglycerides as unique carbon source, apparently gradually increases the synthesis of extracellular lipases. This increase can be related to concentration of linoleic acid, the major component in the sunflower.

KEYWORDS: extracellular lipases, potentiometric titration, gene expression and biodiesel.

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065 - BRAZILIAN COWPEA TRANSCRIPTOME PROJECT: OVER 20 MILLION EXPRESSED SEQUENCE TAGS TO UNDERSTAND SALINITY AND VIRUS RESISTANCE

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The Brazilian Cowpea Genome Project was able to generate one of the most extensive expression panels considering legume crops around the world. This crop is the most important protein source for Brazilian and African semi-arid regions, where biotic and abiotic stresses have been seriously affecting the productivity, despite of the existing phenotypic and genetic variability in Brazilian germplasm. Considering biotic stress main concerns regard virus disease that may affect up to 80% of the productivity during the wet season. Aiming to change this situation, the NordEST network (http://www.vigna.ufpe.br/) was established, including 12 Laboratories, to generate genomic data useful for cowpea breeding and biotechnology programs. Efforts included generation of over five million transcripts, with 12 EST libraries for biotic (severe mosaic virus) and abiotic (salinity) stresses; with nine SuperSAGE libraries for salinity and severe mosaic virus and two LongSAGE libraries for potyvirus. The actual EST data bank includes 182.300 ESTs and 20.480.000 SuperSAGE tags (a superior technology as compared with the traditional SAGE – Serial Analysis of Gene Expression – method). In the scope of the project also a transformation protocol was developed, with stable transgenic plants in the generation T2 available. Two narrow crosses (400 inbred lines F7-F8) have been developed for mapping purposes, and markers (including gene markers, CAPs, dCAPs, DAF, SSR, AFLP, ISSR and RGAs) were developed in order to fine map regions responsible for both above mentioned virus resistance, as well as abiotic stresses and other features (including QTLs) as productivity under drought and salinity conditions, seed color and form as well as plant architecture. Physical chromosome maps are being developed, including microsatellites, rDNA and Phaseolus vulgaris BAC probes and shall also integrate marker bulks from important regions of the genetic map, allowing the rapid transference of data among both crops for breeding purposes. The consortium generated 21 articles in international journals, 17 in Brazilian periodicals, 19 book chapters, two divulgation articles, 70 complete works or expanded abstracts in events and more than 100 abstracts in events. The generated data reveals that the main features that collaborate to abiotic and biotic resistance are active in the first hours after stress begin, bringing important clues for breeding purposes.

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066 - A LIPID TRANSFER PROTEIN OF BLACK PEPPER: ISOLATION AND CHARACTERIZATION OF ITS CDNA SEQUENCE

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Black pepper *(Piper nigrum L.)* is one of the most widely used spices in the world belonging to the Piperaceae family which comprises about 1400 species distributed mainly in the American tropics and Southern Asia, where this crop originated. Black pepper was introduced in Brazil in the 17th century and has been a nationally important crop since 1933. The Pará State is the main Brazilian producer of black pepper; however, the spice's production has been damaged by the root rot disease caused by *Fusarium solani* f. sp. *piperis*. Previous studies reported by our group revealed the identification of some partial cDNA sequences differentially expressed during compatible black pepper - *F. solani* f. sp. piperis interaction. Among them, a putative Lipid transfer protein (LTP), which is know to play important roles in plant defense against insects and pathogens. Therefore, the aim of this work was to isolate the full-length cDNA sequence coding for LTP of black pepper using the SMARTer Race cDNA Amplification Kit (Clontech Laboratories). RNA samples were isolated from roots of black pepper infected by *F. solani* f. sp. *piperis*. The primers used here were designed according to the previously isolated partial cDNA sequence. The amplified fragments were cloned into bacterial vector and sequenced in an automated sequencer. Nucleotide sequences were