IDENTIFICATION AND ANNOTATION OF THE MULTICOPPER OXIDASES CODING GENES IN THE GENOME OF THE FUNGUS TRICHODERMA KONINGIOPSIS POS7

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RESUMO

Introduction: Laccase-like multicopper oxidases belong to a group of oxidoreductases that is distributed across bacteria, fungi, and plants. The low substrate specificity of these enzymes makes them interesting for many biotechnological purposes. However, the slow growth rate and poor enzyme secretion for some microorganisms under natural conditions limits the technological use of fungi that produce them. In this regard, different strategies such as heterologous enzyme production or modulation of the protein-coding genes in the fungal isolates may improve the obtaining of these enzymes and their technological use. The *Trichoderma koningiopsis* POS7 isolate secretes a wide variety of enzymes and is therefore a promising candidate as source of multicopper oxidases. However, the *T. koningiopsis* genes encoding multicopper oxidases have not been well explored. Objective: The aim of this work was to find and annotate the multicopper oxidases coding genes in the genome of the fungus *T. koningiopsis* POS7. Methods: Genomic DNA library construction was performed by Macrogen using the Illumina MiSeq system. These sequences were assembled *de novo* using the SPAdes software. To predict genes the ab initio gene predictor, AUGUSTUS and FgenesH, were used. A database with the nucleotide sequences of genes that code for multicopper oxidases in other species of Trichoderma and related fungi was made. These sequences were blasted in the NCBI database in order to determine their identity (ie, regions containing sequences of the genes encoding multicopper oxidases). In addition, Integrative Genomics Viewer and Geneious software were used to determine the complete structural regions of each gene of interest. Results: The genome of *T. koningiopsis* POS7 carried two genes encoding multicopper oxidases and one gene encoding for transportator multicopper. One of the multicopper oxidases gen was located in the minus strand and had 1.764 bp with two exons, the other multicopper oxidase gene was located in the plus strand and had 1.847 bp with one exon. Particularly the transportator multicopper gene was located in the plus strand and has 2.184 bp with five exons. This information will contribute to study of the *in vitro* secretion of multicopper oxidases by *T. koningiopsis* POS7 and their modulation under specific culture condiotions. Conclusions: The omics technologies allowed us to increase the potencial use of *T. koningiopsis* POS7 for multicopper oxidases production.

PALAVRAS-CHAVE: annotated genes – genome - laccase-like multicopper oxidases - omics technology

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