

TITLE: *IN SILICO* TRANSCRIPTOME ANALYSIS: LACCASE PSEUDOGENE FROM THE MARINE-DERIVED FUNGUS *Peniophora* sp. CBMAI 1063

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ABSTRACT:

Most of the laccase genes emerge from duplication events. A new gene may encode a new isoenzyme with different features (e.g. higher or lower oxidoreduction potential) and cellular function. However, some mutations may turn the new gene into a pseudogene, which is incapable to codify a functional protein. Representatives of the basidiomycetes usually have more than one gene for laccase, and a previous study demonstrated that *Peniophora* sp. CBMAI 1063 exhibit at least 2 putative laccase genes. The present study aimed to identify possible laccase pseudogenes among the new putative laccase genes expressed by the marine-derived fungus *Peniophora* sp. CBMAI 1063. Laccase isoforms were obtained from transcriptome annotation performed by Blast2GO. All sequences assigned with EC 1.10.3.2 (laccase EC) were selected. Peptide chain prediction was performed using GeneRunner (version 5.0.66e). A search of multicopper oxidase domains was performed in Conserved Domains - online database (NCBI) after performed a Blastp. The alignment with others laccase genes were performed in order to recognize the genomic laccase signature using ClustalW (BioEdit - version 7.0.0). One isoform, Comp14944_c0_seq1, with 1404 bp and peptide chain with 468 aa, showed 57% of similarity with laccase 2 from *Trametes versicolor*, and presented the second domain of multicopper oxidases. The sequence Comp14944_c0_seq1 showed three complete conserved regions for laccase (L1, L2 and L3), however the region L4 exhibited a deletion of seven residues, among them a histidine and a variable residue (alanine/phenylalanine/methionine), which binds copper type 1 in fungal laccases. Furthermore, the sequence do not exhibit a stop codon and may represents a processed laccase pseudogene (without introns). The study of pseudogenes can help in the understanding of gene regulations. Nowadays it is known that transcribed pseudogenes may act as siRNAs, which are involved with regulation of the parental genes. In this context, Comp14944_c0_seq1 as an expressed pseudogene might be related to the regulation of the expression of other laccase genes in the marine-derived fungus *Peniophora* sp. CBMAI 1063.

Keywords: Basidiomycete; Bioinformatics; Ligninolytic Enzyme; Marine-derived Fungus; Transcriptome.

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