METAGENOMIC ANALYSIS OF DIRECT CULTIVATED SOIL AND NATIVE FOREST FOR THE ANTIMICROBIAL PEPTIDES IDENTIFICATION

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Abstract

An interesting alternative to conventional antibiotics, which are increasingly less effective, is the prospection of antimicrobial peptides (AMPs). These peptides are molecules produced by most living organisms, like microorganisms, plants and animals, as a part of the defense against pathogens. They are main classified according with their biological activities, although there are others classifications. This study aims to identify antimicrobial peptides in the metagenome of two soils: one direct cultivated and other of native forest. Embrapa Agropecuaria Oeste (CPAO), located in Dourados-MS, collected the soil samples. For DNA extraction, we used the DNA spin kit (Mobio, USA), according to the manufacturer's instructions. The extracted DNA had its quality and quantity tested in Nanodrop and Quibit equipment. The DNA was sequenced with Illumina Hiseq 2000 equipment at UNESP Jaboticabal-SP. We verified the quality of the sequence using the FastQC program. The assembly of the sequences were performed using the UD-IDBA algorithm. We identified the ORFs using the software FragGeneScan. We used local alignment with the BLASTp by blastall script between the soil DNA and the bank of non-redundant peptides data provided by Dover Analyser. The alignment results were organized and analyzed using MySQL database tool. The annotation was performed seeking additional information in secondary banks UniProt and CAMP. The results after all the annotation process were as follows: the cultivated soil had 148 aligned sequences with 144 annotate sequences; the native forest soil had 190 aligned sequences with 179 annotate sequences. Peptides that most stood out in each soil were peptides with the following biological activities: antibacterial, antiviral, antifungal, bacteriocins and fungicides.

Keywords: microorganisms, bioinformatics, databases.

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