Novel Biosurfactant Derived From a Metagenomic Library

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Microorganisms show high genetic diversity and are present throughout the biosphere, however it is estimated that only 1% of the species can be cultivated by standard laboratory techniques, while 99% of the remaining diversity represents a huge genetic and biological pool to be explored. The metagenomics made possible direct access to microbial genomes derived from environmental samples. This approach allows to obtain functional information about genes and the identification of biotechnological products, including new solutions for environmental impacts. Oil-contaminated areas are characterized by a large accumulation of hydrocarbons and surfactants are used as adjuncts in bioremediation. In this work, the metagenomic approach was used to select genes involved in the degradation and oil emulsification process. In a previous research, the environmental DNA (eDNA) was extracted from a soil collected in a saline river of Rio Grande do Norte (Brazil) and a metagenomic library was built and functionally analyzed. The selected clones capable of degrading the oil were evaluated for the ability to synthesize biosurfactant. The positive clone 3C6, has an ORF with 897 bp coding for a hypothetical protein with 298 amino acids and a molecular weight around to 32 kDa, similar to protein of representatives of Halobacteriaceae family. The ORF of interest was amplified by PCR and subcloned into pHIS-parallel1 vector for expression of the recombinant protein and further purification by affinity chromatography. The emulsification test to confirm the activity was positive, using different sources of hydrocarbons. The biosurfactant was purified by acid precipitation, also showing emulsifying activity. This study was the first to report a possible protein with biosurfactant activity obtained from a metagenomic approach.

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