

## **Título: DRAFT GENOME SEQUENCE DETERMINATION OF MORITELLA SP. STRAIN JT01 AND PROSPECTION FOR BIOTECHNOLOGICALLY RELEVANT GENES**

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### **Resumo:**

Deep-sea bacteria are responsible for the production of a wide plethora of enzymes with biotechnological relevance. This can be attributed to the adaptations of those organisms to the deep ocean, aphotic environment of high pressures and low temperatures. Considering this, we have determined the genome of the polymer-degrading bacteria *Moritella* sp. JT01. This isolate was obtained from sediment samples from the Japan Trench (6,957m, 40°01.61'N 144°12.88'E) by researchers of Japan Agency for Marine-Earth Science and Technology (JAMSTEC). Raw data obtained from an Illumina HiSeq2000 system (12,132,184 paired-end reads with 101bp average length from 400bp libraries) was trimmed based on quality scores (minimum Phred of Q20) using the CLC Genomics Workbench. The trimmed data was sorted into 42 contigs with a total length of 4,836,424 bp through *de novo* assembly (made with the same software). The Rapid Annotation using Subsystem Technology service (RAST) performed automatic annotation of the genome, with a total of 4,439 coding sequences and 101 RNAs predicted. Additional annotation based on predicted secondary structures of proteins that have not been characterized by RAST was made possible by the Protein Homology/analogY Recognition Engine (PHYRE). Gene products with biotechnological relevance, such as lipases and esterases (that may be related to polymer degradation), phospholipases, lysophospholipases, chitinases, proteases and glycoside hydrolases were found. Features in RAST's subsystems related to stress response, presumably relevant to the survival in deep-sea environments, such as cold shock proteins were also annotated. The Antibiotics and Secondary Metabolite Analysis Shell (antiSMASH) identified nonribosomal peptide synthetase, polyunsaturated fatty acid and bacteriocin clusters in the bacteria's genome.

**Palavras-chaves:** sequencing, bioprospection, marine bacteria

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