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GENOME SEQUENCING OF A *Marinobacter nauticus* STRAIN WITH POTENTIAL FOR BILGE WASTE TREATMENT THROUGH HYDROCARBON DEGRADATION AND DEMULSIFIER PRODUCTION

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Bilge waste is a liquid residue produced by ships that contains high amounts of water with emulsified hydrocarbons. We have previously reported the isolation a strain from bilge waste with the ability to degrade hydrocarbons and produce a demulsifying compound for hydrocarbon-in-water emulsions, including bilge waste emulsions. Given the high potential of this strain in the treatment of such wastes, we proceeded with its genome sequencing. Genomic DNA of the strain was extracted, purified and sequenced on a 350bp genome library on an Illumina NovaSeq 6000 platform for 150 cycles in paired-end sequencing, obtaining 1.7Gb of information in a total of 11.557.956 reads. Reads were submitted to the comprehensive genome analysis service at PATRIC. There were 157 contigs with an average coverage of 389-fold per base, an estimated genome length of 4,327,601 bp, and an average G+C content of 57.19%. The genome was annotated using RAST tool kit (RASTtk) showing 4,186 protein coding sequences (CDS), 46 transfer RNA (tRNA) genes, and 2 ribosomal RNA (rRNA) genes. The annotation included 1,230 hypothetical proteins and 2,956 proteins with functional assignments. The taxonomic assignment indicated that it belongs to the species *Marinobacter nauticus*. Among specially interesting genes, there are 32 genes for resistance to a wide variety of antibiotics, 10 transporters and the complete genetic pathway for polyhydroxyalkanoate production. Concerning to hydrocarbon degradation, only alkane degradation route was found, including 3 alkane 1-monooxygenase genes. The biodemulsifier produced by this strain has not yet been characterized, so we have not yet been able to associate genes with this compound. This analysis could include identifying metabolic pathways associated with the production of molecules, such as lipoproteins, glycolipids and some lipases that are involved in demulsification processes in other species. Given that few *Marinobacter* strains have been sequenced, these results are highly relevant for future studies. The information obtained can facilitate the

development of effective strategies for the treatment of bilge waste with this strain, both through the production of demulsifiers and its ability to degrade hydrocarbons.

Palabras clave: Bilge waste - *Marinobacter nauticus* - genome - hydrocarbons