POSTER - DNA AND GENOMICS

GENOMICS OF MARINE BACTERIA FROM EXTREME ENVIRONMENTS OF ANTARCTICA

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The Antarctic continent keeps several extreme environmental conditions and specific isolation from the effects of human society. In that place, the genetic material of the organisms is under constant aggression, with various agents that damage the DNA molecule, including the ultraviolet radiation (UV) from sunlight. Other environmental conditions can also challenge the maintenance of DNA stability, such as the very low temperatures, making Antarctica an interesting place to study how organisms maintain genome integrity. In this work, we have sequenced the genomes of three Antarctic marine bacteria, two isolated from sediment samples from a depth of 280 m and the third from 1500 m (samples obtained at the Bransfield Strait). The greater the depth conditions in the sea, the bacteria endure higher concentrations of CO2 under higher atmospheric pressure. The DNA from these isolates was extracted and sequenced by the

Illumina platform. De novo genome assembly was performed with SPAdes v3.15.4. Assembly metrics were assessed with QUAST v5.2.0 and genome completeness was analyzed by BUSCO v5.3.1. Additionally, annotation was conducted using the Prokaryotic Genome Annotation Pipeline (PGAP) and species identification was done based on 16S ribosomal RNA (rRNA) sequence and using the software GTDB-Tk 2.1.0. Functional annotation was assessed by eggNOG. Also, we have analyzed the presence of DNA repair genes of these organisms using tblastn. Species identification has revealed that the species are Bacillus siamensis, Rossellomorea vietnamensis, and Ralstonia pickettii. Preliminary results indicate that most of the protein functions of these bacteria are unknown. Moreover, we have found that most of the DNA repair genes are present in these bacteria, pointing out that there are many ways for them to deal with DNA damage. As a perspective, we intend to do a transcriptome of R. picketti, the 1500 m-bacteria, in two conditions: one with atmospheric pressure and no saturation of CO2 and other with 100 atm and 100% of CO2, to know which genes are more expressed in the last condition.