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GENOME ANALYSIS OF ANOXYBACILLUS STRAINS FROM AN ANTARCTIC POLAR VOLCANO HIGHLIGHTS POTENTIAL FEATURES FOR ASTROBIOLOGY

Abstract

Antarctica is a mosaic of extremes and harbors different analogue sites mimicking extraterrestrial environmental settings, such as Deception Island, a polar volcano located at Maritime Antarctica. Deception is notable for presenting Antarctic environmental stressors and also an extreme steep temperature gradient, with fumaroles and glaciers. This represents an opportunity to recover different culturable extremophiles that may provide insights regarding their adaptations, response/survival strategies to multiple environmental stressors, and possibility to study them as candidates for growth in analogue conditions for Mars, Enceladus's cryovolcanoes, exoplanets and the icy moons. Thus, the objective of this work was to access the putative biological functions trough genome analysis for the potential application in astrobiology. From 159 bacterial strains isolated in Deception Island's fumaroles, 7 isolates were previously identified as belonging to the *Anoxybacillus* genus by 16S rRNA gene sequencing. For the whole genome sequencing, an amount of 5 μg/μl of gDNA was considered for the construction of paired-end sequencing libraries (2150 bp) using NEBNext® and sequenced on the Illumina HiSeq 2500 platform. Genome assembly were performed using Edena and SPAdes after check the read's quality through FastQC. CD-HIT was used to remove the redundant contigs and assembly quality was checked in QUAST. The bacterial genomes were annotated with Prokka, RAST and FASTER. *Anoxybacillus* strains presented an average genome size of 3 Mb with a G+C content of 42%. The pairwise ANI of *Anoxybacillus* species showed that our strains grouped between them with the highest ANI of 98-99%, and 94% with the closest species of *Anoxybacillus flavithermus* WK1. RAST annotation revealed the involvement of 25 to 31 genes for stress responses, including osmotic stress, oxidative stress, detoxification, general stress response and a few for periplasmic stress response. Dormancy and sporulation genes were predominantly associated with the strain LAT_36, with 150 genes annotated. Several of secondary metabolite regions were identified, highlighting the presence of ectoine synthesis, which could contribute to its osmotic and salt stress tolerance. Different prophage regions were identified among the genomes, including phages from *Geobacillus, Salmonella, Thermus* and *Brevibacillus*, suggesting that HGT might be one of the adaptation strategies employed by this bacterial genus. Although some previous studies have isolated thermophiles from cold ecosystems, the information about genus *Anoxybacillus* are scarse, mainly with a potential focus on astrobiology. Our data on genomic analyzes can provide insights into thermophilic spore-forming bacteria with possible implications to astrobiology research.