

TITLE: METAGENOME-ASSEMBLED GENOMES RECOVERED FROM EXTREME TEMPERATURE GRADIENTS IN DECEPTION ISLAND VOLCANO, ANTARCTICA

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ABSTRACT:

Active volcanoes in Antarctica contrast with their predominantly cold surroundings, resulting in environmental conditions capable of selecting for versatile and extremely diverse microbial communities. This is especially true on Deception Island (DI), where geothermal, marine, and polar environments combine to create an extraordinary range of environmental conditions. Due to these characteristics, DI is a peculiar “open-air” laboratory to elucidate central questions regarding molecular adaptability, microbial evolution, and biogeography of extremophiles in polar regions. Our goal in this study was to recover metagenomic-assembled genomes (MAGs) from DI glaciers and fumaroles, where environmental temperatures range from 0 to 98°C. Reads were assembled with IDBA-ud, and genomic binning was performed using MaxBin. Quality of bins were checked through CheckM and taxonomic classification based on marker genes was carried out using GTDB-Tk. High-medium-quality bins were annotated using prokka. More binning tools are being tested, as CONCOCT and MetaBat, and all bins will be further manual refined through anvio pipeline. By using MaxBin for metagenomic binning, a total of 187 bins was recovered, in which 110 exhibited >50% of completeness and 58 bins >70% of completeness. A total of 4 bins was considered as high-quality drafts with >90% completeness and <10% contamination, which were classified as *Calditrichia* class, Xanthomonadales order and 2 as Flavobacteriaceae family. We obtained 14 archaeal medium-quality drafts (~70% of completeness), 5 assigned within hyperthermophilic order Desulfurococcales (3 classified as Pyrodictiaceae family), and 9 assigned as Woesearchaeia class within Nanoarchaeota phylum. Bacterial bins were classified as Flavobacteriaceae (43 bins, 2 assigned as *Maribacter* and 2 as *Flavobacterium*), Alteromonadaceae (19 bins), Chitinophagaceae (8 bins), *Calditrichia* (8 bins), Anaerolineae (5 bins, 1 classified as *Caldilineaceae*), Xanthomonadales (3 bins), Thermonemataceae (1 bin), *Sulfurimonas* (1 bin), Dojkabacteria (1 bin), *Marinosulfonomonas* (1 bin), *Roseovarius* (1 bin) and Thiotrichaceae (1 bin). Through metabolic reconstruction of high-quality drafts we found genes associated to Wood-Ljungdahl pathway in FBB2_bin_12 (*Calditrichaeota*), assimilatory sulfate reduction in FBA2_bin_01 (*Desulfurococcales*) and to assimilatory nitrate reduction and nitrogen fixation in WBA1_bin_04 (*Nanoarchaeota*). Further exploration of these results have the potential to bring new insights about ecophysiology, molecular adaptation strategies and evolutionary process of yet-uncultivated lineages of extremophiles in polar ecosystems.

Keywords: metagenomics, extremophiles, marine volcano, extreme gradients, Antarctica

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