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Metagenome Assembled Genomes (MAGs): Extreme Habitat of Deception Island

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Deception Island is an active volcano area in the southern Antarctic and forms a very unique ecological niche for extremophilic organisms, especially microbes, that survive and thrive in such habitat. A total of 7 samples were collected in an expedition in 2022 at sites of Fumarole Bay, Kronar Lake, Whaler's Bay, Pendulum Cove, Crater 70, Telephone Bay, and Obisidiana. Multiple extractions were performed for gDNA and the final 7 pooled gDNA samples were processed for metagenome library and sequencing using Rapid barcoding SQK-RBK114.24 kit from Oxford Nanopore. The sequencing generated 3.84 GB of raw data with N50 of 1.5 Kb. All the reads were processed for quality trimming using super-quality parameters using Guppy v6.7.0. Taxonomic analysis of reads using the NCBI-nr database resulted in 62 bacterial genera from all the samples. Sample MetaFum recovered only 1 read and was identified as Sulfitobacter. Sample MetaKronr recovered 2 reads and both were identified as Photobacterium leiognathi. Sample MetaPenCor also obtained 2 reads, and identified as Pseudomonas aeruginosa and as Photobacterium leiognathi. Sample MetaWhalbay, obtained 58 reads and found similarity with 27 bacterial genera where Streptomyces was predominant. Sample Meta-Crat70 achieved a metagenome assembly of 20 contigs, where 10 contigs were identified as Photobacterium leiognathi, 6 as chloroplast from Orchophyta and 4 contigs did not find any match in the database. Sample MetaTelBay obtained 1204 reads reads were identified as Photobacterium leiognathi, followed by Salmonella, and Salmonella. We also have found a few reads matched with viruses such as uncultured marine virus and bacteriophage Pelagibacter phage Skadi-8. Sample MetaObis, obtained only 623 reads and got similarity with Photobacterium leiognathi, Olleya sp. Mesoflavibacter sp., Uncultured flavobacterium, Flaviramulus, Kineobactrum salinum, Sulfuriminas autotrophica, Polaribacter, Lutibacter, Pseuoalteromonas artica, and Mesorhizobium terrae. These results indicate that Photobacterium followed by Streptomyces and Salmonella are the dominant genera present in Deception Island but there were other unique genera present that could be novel for taxonomy and contribute novel metabolic functions as well. This study is brief and preliminary and warrants a more detailed sampling and metagenome sequencing for MAGs assembly and analysis to unveil the microbial treasure of Deception Island.

Keywords: Deception Island, Extreme environments, Long-read sequencing, Metagenome, Metagenome Assembled Genomes

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