

TITLE: RESISTOME OF THE VULCANIC ISLAND DECEPTION IN MARINE ANTARCTICA

AUTHORS: CENTURION, V.B.¹; DUARTE, A.W.F.^{1,2}; LACERDA JUNIOR, G.V.¹; SILVA, L. J.³; BELLINI, G.B.¹; ROSA, L. H.⁴; OLIVEIRA, V.M¹

INSTITUTION: 1. MICROBIAL RESOURCES DIVISION, RESEARCH CENTER FOR CHEMISTRY, BIOLOGY, AND AGRICULTURE (CPQBA), CAMPINAS UNIVERSITY - UNICAMP, PAULÍNIA, SP, CEP 13081-970; 2. FEDERAL UNIVERSITY OF ALAGOAS, CAMPUS ARAPIRACA, ARAPIRACA, AL, CEP 57309-005; 3. BRAZILIAN AGRICULTURAL RESEARCH CORPORATION – EMBRAPA, JAGUARIÚNA, SP, CEP 13820-000; 4. FEDERAL UNIVERSITY OF MINAS GERAIS, BELO HORIZONTE, MG, CEP 31270-901.

ABSTRACT:

Deception Island in the Antarctic Maritime poses peculiar characteristics since it is an active volcano flooded by seawater. Due to the limited extent in space and time of research stations, it is quite preserved, with minimal anthropic impact. Thus, the Deception volcanic island is an excellent model to investigate the microbial resistance since the resistance of inhospitable environments may help to understand mechanisms related to antibiotic resistance. Therefore, the aim of this work was to perform resistance analysis along a biofilm on the volcanic island Deception using metagenomics approaches. Samples were collected in a biofilm in Deception Island by the research team of MycoAntar Project during the summer 2014-2015. The total DNA extraction of four samples was performed in duplicates of biofilm sediment using the MoBio PowerSoil™ kit (MOBIO, 12888-100), followed by its sequencing by the Illumina HiSeq platform. Sequences were stored at the MG-RAST server for quality control analysis, gene calling and annotation. The ORFs were then aligned locally against the ARDB (Antibiotic Resistance Genes Database) database, with a cutoff of 80% identity and e-value of 1×10^{-5} . Antibacterial resistance genes (ARGs) were found to be 18 to 22, with *baca*, *acrB*, *macB*, *mexB* and *amrB* being the most abundant types. A study of ARGs in Nova Bay, southeast Antarctica showed a high abundance of the *mexF* gene, from the same *mexB* complex. Functionally, these ARGs belong to the inherent mechanism of membrane protection, multidrug resistance efflux pump, and inactivation enzymes. 13 to 21 antibiotics were associated to these detected ARGs, with Bacitracin, Aminoglycoside, Macrolide, Acriflavine, Beta-lactams and Fluoroquinolone as the most abundant. About 0.010 - 0.021% of the total sequences are identified as ARGs, corroborating with previous studies of the literature. The genus *Psychrobacter*, *Polaromonas*, and *Pseudomonas* of the Proteobacteria phylum dominated the microbial community in all the samples, with about 50% of the sequences. With this, the current study support the view that even in isolated places of human civilization, we can find a wide diversity of resistance to antibiotics.

Keywords: ARGs, Antibiotic, Metagenomic, Deception Island, Antarctic Microbiome

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