

TITLE: CARBOHYDRATE-ACTIVE ENZYMES IN THE MICROBIOME ALONG A TRANSECT IN ANTARCTIC SOILS

AUTHORS: DUARTE, A.W.F.^{1,4}, SILVA, L.J.²; ROSA, L.H.³, CENTURION, V.B.⁴; LACERDA-JÚNIOR, G.V.⁴; NORONHA, M.F.⁴; OLIVEIRA, V.M.⁴

INSTITUTION: 1. UFAL/*Campus* Arapiraca – Universidade Federal de Alagoas (Av. Manoel Severino Barbosa, S/N, Arapiraca/AL, CEP 57309005); 2. EMBRAPA/CNPMA – Empresa Brasileira de Pesquisa Agropecuária (Rod. SP 340, Km 127,5, Tanquinho Velho, Jaguariúna/SP, CEP 13820-000); 3. UFMG – Universidade Federal de Minas Gerais (Av. Antônio Carlos, nº 6627, Pampulha, CEP 31270-901) 4. UNICAMP/CPQBA – Universidade Estadual de Campinas (Av. Alexandre Cazelatto, Betel, Paulínia/SP, CEP 13148218);

ABSTRACT:

Deception island is an environment with restrictive features such as low temperatures and geothermal activity. In this island, seasonal small lakes derived from the melting of glaciers are formed during the Antarctic summer, offering an interesting environment for microbial diversity functional studies. The aim of this study was to evaluate the profile of carbohydrate active enzymes (CAZymes) in soil samples from Deception Island. Samples were collected from four sites along a 30 m-transect in a biofilm formed on the surface of one of these seasonal lakes, in Whalers Bay, Deception Island, during 2014-2015. Samples were submitted to community DNA extraction using the MoBio PowerSoil™ kit (MOBIO) and further shotgun metagenome sequencing on the Illumina HiSeq platform. Reads were analyzed using the Metagenomics RAST Server (MG-RAST), as well as used for contig assembly using the SPADES (version 3.8.1). Open Reading Frames (ORFs) were predicted using the FragGeneScan 1.30; contigs length ranged from 347 to 406 pb and the number of ORFs predicted was between 504,699 to 864,571. After normalization, sequences were submitted to CAZymes analysis. A total of 298 families of the 425 CAZymes available in the database were annotated and the most abundant families were: glycoside hydrolase – GH (116 families), glycosyltransferase – GT (83), carbohydrate binding module – CBM (53), polysaccharide liase – PL (19), carbohydrate esterase – CE (16), and auxiliary activity (16). In addition, the majority of genes were related with complex carbohydrates, such as chitin and peptideoglycan (GH23, CE4, CBM44 and CBM50). Regarding the taxonomic affiliation of GH23, a higher frequency of genes related to the phylum Proteobacteria was observed, followed by Bacteroidetes and Actinobacteria. At the genus level, most of the GH23 were related to *Psychrobacter* at site P1 (below the ice and at 1.0 °C), whereas at the other sites the genes related to GH23 family were mainly assigned to the genera *Polaromonas* and *Flavobacterium*. Almost 50% of the ORFs annotated as CBM belonged to the CBM50, related to the metabolism of chitin and peptideoglycan and mainly assigned to the Deinococcus-Thermus and Firmicutes phyla. Contrarily to some studies that suggest the Antarctic environment as a place with low or limited metabolic diversity, results gathered in this work reveal a diverse wealthy of annotated CAZymes families, suggesting high metabolic potential for carbon cycling in Antarctic soils.

Keywords: CAZymes, Antarctica, Metagenomics, Deception Island

Development Agency: FAEPEX – UNICAMP, FAPESP (2016/05640-6)