Title: MICROBIAL FUNCTIONS AND INTERACTIONS IN A BIOFILM FROM ANTARCTIC SEDIMENT AND ITS POTENTIAL FOR PROSPECTING GENES INVOLVED IN CHITIN DEGRADATION

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ABSTRACT:
In an environment with restrictive features such as the Antarctic continent, the biogeochemical cycles and food webs often happen to be formed exclusively by microorganisms. The aim of this study was to evaluate the phylogenetic and functional diversity of microbial communities in a sediment biofilm from the volcanic Deception Island (maritime Antarctica), in addition to exploring gene clusters involved in chitin degradation. Samples were collected along a transect in a sediment biofilm (four sites, P1-P4) in Deception Island during the summer 2014-2015 by the research team of MycoAntar Project. The samples were submitted community DNA extraction using the MoBio PowerSoil™ kit (MOBIO, 12888-100) and subsequent metagenome sequencing on the Illumina Hiseq platform. Physicochemical parameters of samples were analyzed, named total carbon, total N, NO_{3-}, NH_{4+}, and metals (Cr, Cu, Co, Cd, Fe, Ni and Zn). Reads were analyzed using the Metagenomics RAST Server (MG-RAST) and Statistical Analyses of Metagenomic Profiles (STAMP). The similarity among the four samples (P1 to P4) was evaluated using the Principal Coordinates Analysis (PCoA) and Heatmap multivariate analysis based on microbial functions. The number of sequences ranged from 11.843.020 to 7.451.335 among the samples and reads showed GC content from 44 ± 12% to 58 ± 10%. The most abundant phylum in the different samples was Proteobacteria followed by Bacteroidetes, Actinobacteria, Firmicutes, Cyanobacteria, Planctomycetes, and others. Functional annotation using SEED showed that about 3.5% of the sequences in each metagenome were related to the stress response. From this total, cold-shock proteins, cold-shock DEAD-box protein A, cold shock protein CspA, cold shock protein CspG, trehalose synthetase and cold-shock family of protein showed the highest relative frequencies. Sequences showing high similarity with genes coding for conserved protein domains (EC 3.2.1.14) involved in the degradation of chitin were found in different biofilm samples. This study will contribute to the understanding of microbial functions and interactions responsible for maintaining life in biofilm from Antarctic sediment as well as enable the discovery of new chitinase genes with biotechnological potential.

Keywords: Cold-adapted chitinase, Bioprospecting, Antarctic microbiome, cold-shock proteins, psychrophilic microorganisms.

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