

TITLE: GENOMIC ANALYSIS OF A BIOFILM INVOLVED IN CONCRETE DETERIORATION OF TUCURUÍ HYDROPOWER PLANT

AUTHORS: CUÓCO, C. M.^{1,3}; FURTADO, A. F.^{1,3}; MARQUES, J. M.²; COSTA, M. G.²; SILVA, A. L. C.²; GRAÇAS, D. A.²

INSTITUTION: **1** - Faculty of Biotechnology, Institute of Biological Science, Federal University of Pará (Augusto Corrêa St., 1 - Guamá, Belém – PA, CEP: 66075-110); **2** - Laboratory of Biological Engineering, Guamá Science and Technology Park (Perimetral Avenue, km 01 - Belém – PA: 66075-750); **3** - Center of Genomics and system Biology, Institute of Biological Science, Federal University of Pará (Augusto Corrêa St., 1 - Guamá, Belém – PA, CEP: 66075-110);

ABSTRACT:

It was believed that the concrete corrosion was purely caused by chemical reactions, however, later on, such degradation was discovered to have biological origin. This type of deterioration caused by microorganisms has a special importance when it harms the maintenance of buildings, in particular, those affected by other types of degradation, such as physical and chemical deterioration. To minimize this damage to buildings, it is necessary to evaluate the capacity of degradation this substrate by the resident organisms, which is the case of many the tunnels present in Tucuruí hydroelectric power plant (HPP). Biofilm samples from HPP tunnels were acquired using sterile tools and transported to the lab into STE buffer in controlled temperature . Total DNA extraction was performed using UltraClean®Microbial DNA Isolation Kit and sequenced by Ion Torrent PGM using Ion Chip 318 Kit v2, both following their respective manufacturer's protocol. Reads produced by the sequencing were submitted to MG-RAST for subsequent taxonomic (RefSeq) and functional analysis (KEGG) using the following parameters: e-value = 5; min. length = 15 pb; min. ident = 60%; and min. abundance = 1. The taxonomic analysis revealed 43 different phylums in the sample (31 bacteria, 3 archaeas and 14 eukaryotes). Regarding the 16s rRNA analysis, the sample showed the following major taxon distribution: Firmicutes (96,88%), Bacilli (95,10%), Bacillales (94,07%) e Bacillaceae (91,27%). At genus level, two taxons were present at abundant number: *Bacillus* (43,58%) and *Lysinibacillus* (42,59%). The functional analysis indicated the presence of proteins related to sulfur and nitrogen acquisition by those organism in the biofilm (K02045, K02047, K02046, K02049, K02050 e K02051), as well as the presence of metabolic pathways (ko00910 e ko00920) that produce compounds responsible for concrete degradation (HNO₃, H₂S e H₂CO₃). It is reported by literature that this genus, *Bacillus*, is known for its concrete degradation capacity; *Lysinibacillus*, being formerly part of *Bacillus* genus, has this same capacity. In addition to taxonomic results, the proteins identified in the sample indicates that there is, indeed, a potential for concrete biodeterioration. Therefore, this study can conclude that the biofilm collected in UTH tunnels probably is responsible for some concrete degradation in the local.

KEYWORDS: Biofilm, Metagenomics, Amazon.

DEVELOPMENT AGENCY: CNPq e Centrais Elétricas do Norte do Brasil