TITLE: CHANGES IN BACTERIAL BIODIVERSITY IN THE TRANSITION FROM PLANKTONIC TO BIOFILM POPULATIONS ALLOW ADAPTATION TO EXTREME ENVIRONMENTS

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ABSTRACT:

Bacterial biofilms have been studied on Medical Sciences, and just recently it has received more attention to Environmental Microbiology. By this recent point of view, the biofilm can be composed by organisms from different kingdoms and capable to integrate metabolisms. These organisms will show interactions, such as competition or cooperation, by the secretion of components regulated by quorum sensing, which will determine the local diversity. This research aimed to evaluate the response system of bacteria exposed to stressful environments, as high temperature, acidity and chemical toxicity, considering the diversity and richness of bacterial families isolated from six different ecological niches, using artificial metagenomic. The tested environment was water used to wash more than 30 different agrochemicals, with liberation of F⁻ and Cl⁻, submitted to higher temperatures to evaporate and decrease the water volume to be transported. We obtained samples of planktonic and biofilm bacteria, from which DNA was extracted for sequencing and artificial metagenomic analysis. The pre- and post-heating planktonic niches presented a higher homogeneity of families, mainly Rhodospirillaceae and Burkholderiaceae, with variations of richness. The mainly components of pre- and post- heating biofilm were respectively Pseudomonadaceae and Enterobacteriaceae. These microorganisms are well known by their capacity to form capsules and biofilm, possibly providing tolerance to unfavorable conditions at the studied environments. The more richness genera that were established on biofilm post heating were Enterobacter and Acinetobacter, which were not present on the planktonic environment, probably being contaminants that have presented a better adaptability to the found conditions, such as the ability of forming biofilms and metabolic cooperation. The obtained data on artificial metagenomic analysis have shown that the genes related to cellular, environmental and metabolic processes have an important correlation with the identified sequences from the two prominent genera on biofilm, and being likely related to the adaptive response systems from the bacteria found on these extreme conditions.

Keywords: Biofilm, metagenomics, adaptation, stress.

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