

**TITLE:** Microbiome structure in biofilms from a volcanic island in Maritime Antarctica investigated by genome-centric metagenomics and metatranscriptomics

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**Abstract:**

Antarctica is the coldest and driest continent on Earth, characterized by polyextreme environmental conditions, where species adapted form complex networks of interactions. Microbial communities growing in these harsh environments can form biofilms that help the associated species to survive and thrive. A rich body of knowledge describes environmental biofilm communities; however, most studies have focused on dominant community members rather than functional complexity and metabolic potential. To overcome these limitations, the present study used genome-centric metagenomics to describe two biofilm samples subjected to different stress factors collected in Deception Island, Maritime Antarctica. The results unraveled a complex biofilm microbiome represented by 180 metagenome-assembled genomes, and demonstrated for the first time the occurrence of the autotrophic *Flavobacterium* genus and *Akkermansia* in Antarctic samples. The microbiomes of the two samples were highly divergent according to temperature, nitrogen and Pb concentrations, and position along a transect of Whalers Bay sediments. The potential metabolic interactions were investigated using metabolic flux balance analysis and revealed that purple bacteria (Alphaproteobacteria, Betaproteobacteria, and Gemmatimonadetes) are the community members with the highest correlations with other bacteria. Due to their predicted mixotrophic behavior, they may play a crucial role in the microbiome, likely supporting the heterotrophic species in biofilms. Metatranscriptomics results revealed that the chaperone system and proteins counteracting ROS and toxic compounds have a major role in maintaining bacterial cell homeostasis in sediments of volcanic origin.

**Keywords:** genome-centric metagenomics, Whalers Bay, Correlation Network, Purple Bacteria, Stress response

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