



WORLD MICROBE FORUM
20-24 JUNE 2021 | ONLINE WORLDWIDE
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Session AESP127 - AES11 Genetic and Metabolic Functions in Environmental Microbes

Neutral Lipid Biosynthetic Potential in Sediment Microbial Communities from Subantarctic Environments

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Disclosures

F. Pascutti: None. **V. Galván:** None. **N. Sandoval:** None. **M. Lanfranconi:** None. **M. Lozada:** None. **A. Arabolaza:** None. **W. Mac Cormack:** None. **H. Álvarez:** None. **H. Gramajo:** None. **H. Dionisi:** None.

Abstract

Bacteria from a limited number of taxa are known to accumulate wax esters (WE) and triacylglycerol (TAG) as an adaptation response to stressful environmental conditions, although this capability is poorly understood at the microbial community level. The goal of this work was to uncover the prevalence and diversity of bacteria with the potential to synthesize neutral lipids in coastal sediments of Subantarctic and Antarctic environments, and to characterize the gene clusters related to this process. More than 48,000 sequences containing the PF03007 domain (specific of the key enzyme wax ester synthase/acyl-CoA:diacylglycerol acyltransferase, WS/DGAT) were retrieved from 13 metagenomes, including subtidal and intertidal sediments of Ushuaia Bay, Argentina (54° 48' S, 68° 17' W), and subtidal sediments of Potter Cove, 25 de Mayo Island, Antarctica (62° 13' S, 58° 39' W). Abundance of putative WS/DGAT sequences in the sediment metagenomes was 1.23 ± 0.42 times relative to 12 single-copy genes encoding ribosomal proteins, much higher than in seawater (0.13 ± 0.31 times in 338 metagenomes). In an ordination analysis, the metagenomes were grouped by geographic location, although closely related sequences were present in both environments despite a 1,000 km distance and the potential barrier of the Antarctic Circumpolar Current. Most sequences were binned to the Proteobacteria or the Actinobacteria phyla. Phylogenetic analysis revealed that the majority of the identified sequences were most closely related to sequences from genomes assembled from metagenomes, from environmental samples

including seawater, marine sediments, groundwater, freshwater and biological wastewater treatment plants. The genomic context of putative WS/DGAT sequences included genes encoding putative Type-2 PAPs and HAD-type hydrolases, glycerol- and acylglycerol- phosphate O-acyltransferases, some of them potentially responsible for specific steps in WE and TAG biosynthesis. In addition, some scaffolds contained genes of related pathways such as fatty-acids metabolism, suggesting carbon recycling might drive the flux to neutral lipid synthesis. These results indicate the presence of abundant and diverse bacterial populations with the potential to synthesize lipid storage compounds. This information increases our understanding on the mechanisms used by bacteria from extreme environments to adapt to environmental stressors. FP and VG contributed equally

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