

Metagenomic characterization of anaerobic hydrocarbon degradation in benthic marine sediment core from the Antarctic Peninsula

KATIE HOWLAND¹, HANNAH NYGAARD¹, ANDREW STEEN² AND DERIC LEARMAN¹

¹Central Michigan University

²University of Tennessee

Presenting Author: howl1ke@cmich.edu

The unique environment of Antarctica has amassed attention from scientists and, more recently, tourists, resulting in anthropogenic activities polluting the once-untouched environment. The remote location and extreme climate require large quantities of diesel fuel to support human activity. Consequently, anthropogenic activity on and around the ice-covered continent has led to hydrocarbon pollution. In benthic marine environments, bioremediation is a preferred removal method in the event of hydrocarbon exposure. While bioremediation in marine sediments is widely studied, there is a knowledge gap on the metabolic capabilities of anaerobic microorganisms, especially those in cold polar environments. This study seeks to investigate the genetic potential of microbes to anaerobically degrade hydrocarbons throughout sediment cores (12 cm in depth), which were collected along the Antarctic Peninsula at two sites in the Weddell Sea. Shotgun metagenomics was utilized to examine the anaerobic metabolic capabilities of the microbial communities at 3 cm depth intervals. Analyses of metagenome assembled genomes (MAGs) reveal five sulfate-reducing MAGs from the phylum Desulfobacterota, MAG-4506-123 (3-6 cmbsf), MAG-5809-30 (6-9 cmbsf), and MAGs 4512-123, 4512-32, 5812-130 (9-12 cmbsf), containing an abundance of alkane, MAH, and PAH hydrocarbon degradation genes. The genetic potential of Desulfobacterota MAGs 4506-123, 4512-32, 4512-123, 5809-30, and 5812-130, suggests they are hydrocarbon generalists. These results indicate sediment communities possess the microbial genetic potential to degrade hydrocarbons in anoxic sediments.