## Identifying Keystone Bacterial Species In Recalcitrant Terrestrial Organic Matter Transformation Within Marine Environments

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The microbial transformation of terrestrial organic matter, particularly recalcitrant lignin and hemicellulose, is a significant but poorly understood phenomenon within the deep ocean. 16S rRNA gene amplicon sequencing and metagenomic sequencing are relatively inexpensive molecular tools to quickly assess microbial diversity and functional genes in response to different carbon sources. Using sequencing, we aim to elucidate the diversity and metabolic potential of bacterial communities subsisting on lignin and hemicellulose in laboratory cultures. Seawater and sediments from the Eastern Mediterranean were incubated with an added concentration of purified lignin or xylan. CO<sub>2</sub> respirometry and enzyme assays showed high microbial activity on both substrates compared to Dissolved organic matter unamended controls. characterization using FTIR spectroscopy and UV-Vis fluorescence showed changes during incubation. Samples were sequenced for 16S rRNA gene amplicons and metagenomics using the Illumina MiSeq. Qiime and MG-Rast annotated data was compared in detail using phyloseq, vegan, and DESeq2 in R. Several species belonging to phylum of Proteobacteria, Flavobacteria, and Firmicutes significantly increased in abundance when lignin or hemicellulose was added. Groups of functional genes related to carbohydrates and aromatic catabolism significantly increased in abundance. Our methods may uncover important species that have been previously overlooked for terrestrial organics degradation.