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Comparative metagenomics of terrestrial organic matter degradation in the Western Arctic

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The Arctic Ocean receives more terrestrial dissolved organic matter (tDOM) on a per volume basis than any other ocean, resulting in Arctic coastal waters harboring the highest concentration of tDOM among the world's oceans. Due to climate change induced intensification of the hydrological cycle, permafrost thaw, and coastal erosion, tDOM input into Arctic coastal waters has been steadily increasing. Nguyen et al. (2022) have speculated that the increasing presence of tDOM in the Arctic Ocean is causing a shift in the local microbiological communities. This may significantly affect CO₂ fluxes and food web dynamics in the ocean. Despite recent incubation experiments reporting substantial biodegradation of tDOM in Arctic coastal waters, very few studies have attempted to examine the genetic capacity of Arctic marine microorganisms to process lignocellulose and other recalcitrant aromatic compounds of terrestrial origin. In this study, we perform comparative metagenomics in order to assess the diversity and distribution of microbial genes responsible for tDOM degradation in the Western Arctic. We searched 361 seawater metagenomes from the Bering Shelf, Bering Strait, and Chukchi Shelf for orthologs responsible for ring-opening reactions associated with degradation of tDOM (Grevesse et al., 2022). Like others, we identified Rhodobacterales as important contributors to microbial communities encoding the ring-opening reactions required for degradation of aromatic compounds such as tDOM and petroleum products, including members of the Roseobacteraceae (*Sulfitobacter*, *Roseomonas*) and Rhodobacteraceae (*Planktomarina*, *Asciadiaceihabitans*, and uncultured taxa). We found the presence of degradation genes to be widely distributed across temperature-, salinity-, depth-, and latitudinal gradients, with no clear patterns in the richness of genes. Future work will investigate the relative abundance of these functional genes among metagenome assembled genomes derived from these samples. Doing so, we hope to elucidate the environmental factors supporting the presence of tDOM degrading microorganisms. This study will contribute to the accumulating knowledge on adaptability of marine microorganisms to inputs of recalcitrant organic compounds.