Bacterial Lifestyles Influence Mobile Genetic Elements in Aquatic Ecosystems

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Mobile genetic elements (MGEs) such as plasmids and bacteriophages are significant drivers of horizontal gene transfer (HGT) within microbial communities. However, the role of MGEs in the environment are not well understood. Aquatic bacteria can be categorized into three lifestyles: truly free-living (FL), particle-associated (PA) that form microbial cohorts on particles, or bacteria that alternate between these two lifestyles, known as generalists. Given that particles serve as hotspots of microbial activity and help to facilitate direct cell-to-cell contact, we hypothesized that PA and generalist microbes have enhanced opportunities to engage in HGT and will have higher rates of MGEs. We investigated microbial metagenomes from a freshwater estuary—Muskegon Lake, Michigan. From sixteen samples we first looked at the assembly-level view of assembled short read contigs. Then, we binned the assembled contigs and generated 346 metagenome assembled genomes (MAGs) to identify MGEs using geNomad within these three lifestyles. At the assembly-level, we find the same distribution of conjugation genes, which facilitates the dissemination of plasmids. Additionally, the FL fraction had a significantly higher number of phage-encoded genes. At the MAG-level, the generalist species had the greatest number of conjugation genes, phage-encoded genes, and phage diversity. At both assembly and MAG levels, these results reveal more complex community interactions than originally expected which further highlight the importance of microbial lifestyles. By studying MGEs in aquatic environments, we will be better able to understand the ecology and microbial community dynamics of bacterial lifestyles including the dissemination and maintenance of antibiotic resistance genes.