Understanding Mobile Genetic Elements and Bacterial Lifestyles

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Mobile genetic elements (MGEs) such as plasmids and bacteriophages are significant drivers of horizontal gene transfer (HGT) within microbial communities. Pelagic bacteria can be categorized as free-living (FL) or particle-attached (PA) via size filtration, yet bacteria within these fractions alternate between these two lifestyles (generalists). Given that particles serve as hotspots of microbial activity and facilitate direct cell-to-cell contact, we hypothesize PA and generalist microbes have enhanced opportunities to engage in HGT and will have higher rates of MGEs. We investigated microbial communities from Muskegon Lake, Michigan employing metagenomic analyses. From sixteen samples we assembled and annotated contigs at the whole community level and generated 346 metagenome assembled genomes (MAGs) to identify MGEs within these lifestyles. To understand the conjugation machinery facilitating the dissemination of plasmids, at the whole community level view we find the same distribution of conjugation genes but at the MAG level the generalist species have the greatest number of conjugation genes. Additionally to understand phage-microbe interactions, we find at the assembly level view there is a greater amount of phage-encoded genes in the FL fraction but at the MAG level the generalist fraction has the greatest amount of phage-encoded genes as well as phage diversity. Furthermore, we find that plasmid-encoded and conjugation genes exhibit a strong dependency on phylogenetic relationships whereas phage-encoded genes have a relatively low phylogenetic signal. By studying MGEs in aquatic environments, we will be better able to understand microbial community dynamics, including the dissemination of antibiotic resistance genes.