Microbial generalists have greater genetic mobility

1Sophia Aredas; 1Marian Schmidt, Ph.D.

1Department of Microbiology, Cornell University, Ithaca, NY 14853

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: true plankton or free-living (FL), particle-associated (PA) that form microbial cohorts in or 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 hypothesize 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 assembled and annotated contigs at the assembly-level and generated 346 metagenome assembled genomes (MAGs) for a MAG-level analysis to identify MGEs using XXX within these three lifestyles. We found the same distribution of conjugation genes, which facilitates the dissemination of plasmids, across lifestyles at the assembly-level. However, at the MAG-level the generalist species had the greatest number of conjugation genes. At the assembly-level, there was a greater amount of phage-encoded genes in the FL fraction while phage-encoded genes and phage diversity were highest in the generalist fraction at the MAG-level. Further, Plasmid-encoded and conjugation genes exhibit a strong phylogenetic relationship whereas phage-encoded genes have a relatively low phylogenetic signal. [*Insert a sentence on interpreting the results.*] By studying MGEs in aquatic environments, we will be better able to understand the ecology and microbial community dynamics of \_\_\_, including the dissemination of antibiotic resistance genes.