Molecular characterization of *Enterococcus spp.* non-clinical isolates from pristine sites in Puerto Rico

Viruses are the most abundant biological entities; however little is known about their role in the environment, specifically in bacterial evolution. We hypothesize that Enterococci spp. prophage regions may play a significant role in genome architecture resulting in the acquisition of traits and genome diversity. We are focused on determining the host-range of induced lysogenic phages from Enterococci spp. environmental isolates and the characterization of prophage regions found in isolates from pristine sites in Puerto Rico. Our lab current research consists in the characterization of Enterococcus spp. using Whole Genome Sequencing (WGS) and PCR. Si far we found sequences coding for genes for antimicrobial resistance as well as virulence factors; a surprise given these are environmental isolates from pristine sites. Induction of these prophage regions to confirm the broad hostrange in several Enterococcus type strains host revealed that these phages can infect the following: 52.90% E. faecalis, 52.90% E. faecium, 17.70% E. hirae, 13.72% E. durans, 9.80% E. dispar, 3.92% E. pseudoavium and 3.92% E. gallinarum. The infection of induced temperate phages revealed the ability to infect several hosts within the same genus. At the genomic level, abundant prophage region sequences were observed; unexpectedly our results showed the presence of phages usually reported as infecting other genera. CRISPR sequences were detected in all our genomes, however more studies are needed to determine immunity sequences. The presence of these lysogens, as well as their apparent broad range hosts supports the hypothesis that phages may be key in the resulting genomic heterogenicity in genome architecture, at least amongst members of the same genus. Our data clearly demonstrate that lysogenic enterophages have a wide host range and being promiscuous may lead to a favorable gene exchange in the environment.