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Corresponding Faculty Member: Jordan Parker (jordan.p.parker@kp.org)

Cluster H: Inter and Intra-cluster Relationships

Divya Adem, Stephanie Bottomley, Lesli Gutierrez, Andrew Kapinos, Canela Torres, Amanda C Freise, Jordan Moberg Parker

Bacteriophages represent a class of viruses that infect, replicate in, and kill bacteria. They are placed into clusters based on similar genomes and other criteria. Phage genomes exist on a continuum of diversity due to frequent horizontal gene transfer (HGT), making phage and cluster relationships incredibly complex. Due to pervasive mosaicism within phage genomes, clusters are not discrete and are subject to constant change. In particular, there appears to be great diversity within cluster H despite its small size. This being said, current published literature exploring cluster H is limited and outdated. The cluster’s intriguing situation warrants deeper exploration in scientific research. Here, we examine the intra and inter cluster relationships of cluster H phages. Comparative genomic tools such as BLASTn, Phamerator maps, genome content similarity (GCS) heatmaps, nucleotide dot plots, OrthoANI heat maps, and Phylogenetic trees were used to characterize the cluster. These tools all indicated synonymous levels of genomic similarity among analyzed clusters. Intra cluster relationships were more prominent and had higher GCS values while inter cluster relationships were not as apparent. However, several previously unknown inter cluster relationships were identified as well as evidence of potential HGT in cluster H. The starting framework of the evolutionary relationships that this project provides will serve as a jumping off point for a deeper investigation into cluster H, as a major update is overdue. In order to harness the power of phages for use in medicine and agriculture, the scientific community must first understand them.