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Exploring Variability in E-Cluster Phages: Insights from Comparative Genomics Research

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In 2018, Saint Leo University joined the SEA-PHAGES program 11th cohort. Students and faculty from Saint Leo have currently discovered 72 bacteriophages, with 15 of them having been sequenced and annotated so far; all belong within the E-cluster: 8 EE, 4 EB, 2 EK1, and 1 EF phage. Presented here is a comparison of the variability - or lack thereof - between the subclusters existing within the greater E-cluster. For example, the variability in the amount of homology between phage genomes in the same subcluster and the proximity of where they were isolated from. The genomes of the EE phages are notably well conserved, despite their distances. The main difference within these genomes is gene 13, which has been observed to have the highest variance amongst genes of the EE subcluster. In contrast, the genomes of phage in the EB subcluster show a much greater deviation in comparison, where substantial portions of their genome diverge in homology, although they were all discovered within the Saint Leo campus. With the exception of the EK1 phages, Wesak and BlueRugrat (podoviridae), all of the phage discovered by Saint Leo are siphoviridae, most of which contain programmed translational frameshifts. These frameshifts display the level of conservation found within the genomes of different subclusters. Saint Leo's EE phages all have frameshifts that code for extremely similar tail assembly chaperones, whereas the EB phages all have much greater variation in their frameshifts. Also discussed here is an analysis of an unusually large gene, greater than 13000 bp’s, that can be seen in both EK1 and EK2 genomes. These genes share no significant nucleotide homology, however, there is greater amino acid homology. According to BLASTs from the sites PhagesDB and NCBI, this gene does not have a known function associated with it.