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Annotation and Characterization of EA1 Microbacterium foliorum bacteriophage ShaiHulud

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ShaiHulud is a lytic bacteriophage currently assigned to subcluster EA1 that infects *Microbacterium foliorum* that was isolated by students from Northwest Indian College in Ferndale, WA in 2022. The genome is currently being annotated at Stevenson University in Owings Mills, MD. ShaiHulud’s genome is 41812 base pairs (bps) long, tightly packed with 64 predicted genes and no evidence of tRNAs. The EA1 subcluster contains 128 other phages that all exhibit a high degree of synteny. Notably, all EA1 phage genomes have a similar structure in that the first half of the genome contains genes in the forward direction, the second half contains genes in the reverse direction, and the final 1-3 genes are in the forward direction.

Two areas of ShaiHulud’s genome are being investigated, one being gp 41 (bp 29558-29674) which is located in the second half genome and is the only gene on the forward strand in this region. This violates one of the guiding principles of annotation. Of the nine draft genomes within the EA1 subcluster, this gene was predicted in five, but interestingly did not appear in any of the annotated genomes. Despite the presence of coding potential, the small size of the gene (less than 120 bps) and lack of BLAST matches suggest that this may not be a gene after all. The other area being investigated is the last 1500 bp of the genome. EA1 phages typically have 1-3 genes in this region, but ShaiHulud is predicted to have just 1 gene here. However, there is a ~500 bp gap between the final 2 genes in ShaiHulud that will be investigated for coding potential and homology to other sequences in NCBI.