CONSIDER FOR TALK

2021 SEA Symposium Abstract

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Who’s Bigger than Rasputia?

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Bacteriophages have been investigated throughout history, however with their genetic variation and diversity, there is still undiscovered and uninvestigated information regarding these organisms. Rasputia, a *Microbacterium foliorum* bacteriophage, was retrieved from soil in Langhorne, PA, and isolated through direct isolation. The process was followed by a series of serial dilutions until there was enough pure lysate to extract DNA to be sent for sequencing. Once Rasputia was sequenced, PCR was used to identify the cluster the phage belonged to– in this case - it was determined to be the GC cluster. DNA master and other resources have been utilized to annotate Rasputia’s genome and its functions. Rasputia’s genome was then compared to other GC genomes that were annotated. Through the annotation process, information was gathered by using DNA master, starterator, Phamerator, NCBI Blast, and HHPred to assign start sites, and functions where applicable. One interesting discovery found in this genome was the RtcB-like RNA ligase function which is quite uncommon among phage genomes. It acts as a tRNA ligase and works with a polymerase to repair broken tRNAs in the genome. Peptidase was another function found in Rasputia’s genome, however this function, oddly enough, was found in an orpham. Peptidases break down peptides into amino acids and it may have originated from horizontal gene transfer from bacteria. Additionally, unlike most phage genomes, Rasputia’s tape measure protein is not the longest gene. Tape measure proteins form the core of the tail and directly corresponds to the tail length. The gene with the capsid maturation protease function had the longest length of any gene in the genome. This protease cleaves the scaffolding protein which controls the assembly of the head. Overall, Rasputia and the overall GC cluster is very unique, but as seen by some of these intriguing features, Rasputia has a genome that makes it very diverse from others.