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Investigation of C1 cluster mycobacteriophage Izajani

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Bacteriophage (phage) are the most abundant organisms on earth, yet only a fraction have been annotated and added to the phage database. The annotation of bacteriophage will continue to enhance the scientific database and aid in new phage therapy techniques.  
  
Izajani is a phage that was discovered in 2018 in West Lafayette, IN. It is in the C1 cluster and Myoviridae family. Here we report the annotation of mycobacteriophage Izajani, which was annotated using the software PECAAN. The programs Phamerator, Starterator, GeneMark, NCBI, and HHPred were used to further support annotations. Within Izajani, genes in the base pair range of 16,241 to 55,644 were annotated. A total of eight unique functions were identified, the most common functions being Helix-turn-helix DNA binding domain protein and membrane protein.  
  
In addition to gene annotations, the proteins nucleotidyltransferase, Thyx-like thymidylate synthase, and tape measure in Izajani were visualized through Splitstree and Phyre2. Specifically, Splitstree is used to interpret phylogenetic trees across multiple clusters including C1, and Phyre2 analyzes protein structures. Together, these programs were used to identify the similarity of individual gene functions across clusters. Finally, a Python program was used to identify and compare mutations across similar genomes. Ultimately, the annotations from PECAAN and the conclusions drawn regarding Izajani’s gene sequences will contribute to a greater understanding of Izajani and similar C1 cluster phages in the scientific database.