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The Purpose of the Gene Functions in Mycobacteriophage Xavia

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Mycobacteriophage Xavia (GenBank MH230879) was isolated from a soil-water sample in Atlanta, Georgia, using *Mycobacterium smegmatis* as the host. Xavia is a Cluster P3 phage that is 49,808bp long. The purpose of our research was to finalize the draft annotation of this phage by manually confirming potential genes and identifying gene functions. Utilizing the annotation program, DNA Master, and guided by heuristic GeneMark output we determined the most likely open reading frames to identify each gene in this genome. Starterator reports were used to help identify the most conserved starts in each pham, and BLASTp searches and HHPred searches were used to identify the function of more than half of the genes in this genome. Comparisons between the Phamerator maps showed remarkable similarity in both nucleotide sequences and protein products early in each genome. Synteny in the Cluster P phages is very strong in the first half of each genome, but differences between the Cluster P phages is observed in the second half of the genomes and after ORF 28 in our phage. In our completed annotation, there are a total of 71 genes in Xavia and no tRNA or tmRNA sequences. The functions of 38 of the 71 genes were identified. A total of 19 genes have virion structure and assembly functions, one is a phage DNA replication gene, 3 are life cycle regulation genes, 3 are lysis genes, and 12 are other well-characterized genes. As seen in other members of Cluster P such as Bartholomew (P1) and Tortellini (P2), Xavia has a programmed translational frame shift in the tail assembly chaperone genes just upstream of the tape measure protein. The presence of integrase (Y-int), and immunity repressor genes suggest that Xavia is capable of lysogeny.