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Annotation of Mycobacteriophage Nairb

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Mycobacteriophage Nairb was isolated from a soil sample in Atlanta, Georgia, using *Mycobacterium smegmatis* as the host. Nairb is a Cluster T phage that is 42,393bp 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. In our completed annotation, there are a total of 59 genes in Nairb and no tRNA or tmRNA sequences. The functions of 35 of the 59 genes were identified. We were particularly interested in the similarities and differences between this phage and other four phages in Cluster T. Synteny is very clear in all these phages in the first half of each genome. The two previously annotated Cluster T phages (Bernal13 and Ron RayGun) and Nairb have a programmed translational frame shift in the tail chaperone genes just upstream of the tape measure gene. The presence of integrase (Y-int), immunity repressor, and excise genes suggest that Nairb is capable of lysogeny. Comparisons between the Phamerator maps showed remarkable similarity in both nucleotide sequences and protein products early in each genome. Most of the differences between the five Cluster T phages is observed in the second half of the genomes.