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9th Annual SEA-PHAGES Symposium Abstract

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Isolation and Genome Annotation of mycobacteriophage "ArcusAngelus", a Siphoviridae Group F Cluster F1 from Austin Community College

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It was the first year for submissions of mycobacteriophages to the SEA PHAGE program from the Central Texas area. We were able to discover a novel phage ‘ArcusAngelus’ isolated from the host bacteria Mycobacterium smegmatis, mc2155. The isolation method was enrichment. The plaques produced were small and clear. Electron microscopy was performed by the facility at the Universiti of North Dallas. The electron micrographs showed that the virus morphology was consistent with the Siphoviridae. The genome of ‘ArcusAngelus’ was sequenced by the Pittsburgh Bacteriophage Institute using Illumina Sequencing. The genome was annotated using bioinformatics software including DNA Master, NCBI's Blastp,Phamerator and Starterator. The genome had 113 predicted genes. We found protein functions that match functions for bacteriophages in the national database as well as unknown function proteins by comparing the phage ‘ArcusAngelus’ with other phages isolated from the same host.