CONSIDER FOR TALK

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Genomic and proteomic analysis of Mycobacteriophage Kersh, an F1 cluster phage

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Students in the Phage Genomics Research Initiative course at UCSD isolated and characterized 27 Mycobacterium smegmatis bacteriophage from collection sites in San Diego, CA in the Fall quarter of 2014. All of the isolated phage were members of the family Siphoviridae. One of the phages, Kersh, appeared to be a temperate phage based on plaque morphology and was selected to be further characterized. The genome of Kersh was sequenced and assembled by the Pittsburg Bacteriophage Institute using Illumina sequencing technology; the Kersh genome is 60190 baseparis in length bp in length and has defined ends. Using NCBI BLASTn, it was found that Kersh is a member of the F1 cluster. Students annotated the Kersh genome using the computer program DNA Master, and together with maps of predicted coding potential, found 107 putative protein coding genes, all of which but 9 were transcribed in the same direction. Comparisons of the predicted proteins with NCBI BLASTp and Phamerator provided tentative functional assignments for many of the gene products, including several structural proteins and proteins involved in in cell lysis. An integrase as well as a putative repressor and antirepressor were also tentatively identified. Kersh appeared to contain several bacteria-derived genes including a gene for a lipase that is a member of a pham with only one other member. Tandem mass spectrometry of phage lysates is currently being used to increase the accuracy of the annotation by identifying the production of gene products and by confirming the predicted start site for some of the proteins.