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The Genomic Investigation and Analysis of Squint, a Novel J Cluster Mycobacteriophage

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Presenter Information

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Poster Presentation P9

**THE GENOMIC INVESTIGATION AND ANALYSIS OF SQUINT,
A NOVEL J CLUSTER MYCOBACTERIOPHAGE**

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The SEA-PHAGES program expands the knowledge of bacteriophages through extensive research completed by students isolating and annotating unique bacteriophages. During the fall of 2016, a J cluster bacteriophage, Squint, was isolated, purified and sequenced. The J cluster bacteriophages are characterized by their average genome size of 110,848 base pairs and average gene number, 235. The J cluster contains thirty-five members, which is relatively small in comparison with other mycobacteriophage clusters. DNA isolated from Squint was sequenced at the University of Pittsburgh, and annotated at Illinois Wesleyan University. Squint was discovered by Alecia Beagles in the Fall of 2016 from a soil sample collected in El Paso, Illinois. Using a variety of bioinformatics tools and databases such as DNA Master, HHpred, BlastP (of Phagesdb.org), Glimmer and Genemark, the genome of Squint was successfully annotated. One aspect of annotation is to search for predicted protein functions. HHpred and BlastP were utilized in the search for similar proteins. Protein functions identified were noted in the Squint DNA Master file, along with each gene's length (DNA Master), coding potential (Genemark and Glimmer), relation to genomically similar phages (BLAST), and Shine-Dalgarno site information (DNA Master). Based on our annotations, Squint contains a 110,240 bp long genome, 244 open reading frames (ORFs), and one tRNA. Through the annotation of Squint's genome, we discovered the unique organization of a new bacteriophage. The completed annotation of Squint will be sent to GenBank, where it will be added to an enormous database of annotated phage genomes