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The Isolation, Purification, and Characterization of Fourteen Mycobacterium Smegmatis Bacteriophages

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Presenter and Advisor Information	
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Poster Presentation P1

THE ISOLATION, PURIFICATION, AND CHARACTERIZATION OF FOURTEEN MYCOBACTERIUM SMEGMATIS BACTERIOPHAGES

Marissa Alcala, Alecia Beagles, Caroline Marchi, Samantha Ziomek and Richard Alvey* and David Bollivar* Biology Department, Illinois Wesleyan University

The overall goal of the SEA-PHAGES program is to utilize microbiology and bioinformatic techniques to study the characteristics of discovered bacteriophages. The collected data will contribute to the growing database of phage genomic information. Since bacteriophages are estimated to be the most numerous biological entities on earth, understanding the diversity of these entities is of significant biological interest. Bacteriophages from gathered soil samples were isolated utilizing the host Mycobacterium smegmatis, mc2155, through direct and enrichment procedures. During the Fall of 2016, fourteen M. smegmatis bacteriophages were isolated and streaked for purification. The fourteen phages were initially characterized by their plaque size and clarity, and their ability to form a lysogen. True lysogens were formed from nine of the fourteen isolated bacteriophages. Further analysis through electron microscopy lead to the determination of tail length and capsid size. Tail lengths ranged from 73 nm to 344 nm, and capsid diameters ranged from 60 nm to 95 nm. Electron microscopic analysis also allowed for the categorization of the fourteen bacteriophages into three classes: siphoviridae, myoviridae, and podoviridae. Twelve of the fourteen phages were classified as siphoviridae and two were classified as myoviridae. Specific phages, Squint, isolated by Alecia Beagles, and Tesla, isolated by Colin Page, were further analyzed because of their unique qualities highlighted during the isolation and characterization processes. The discovery of these fourteen novel bacteriophages is a step towards a greater understanding of phage diversity.