**Group 3: Abstract Rough Draft**

General Feedback from Dr. Clase:

The abstract should have 1-2 introductory sentences that provide a broad overview and introduction to the topic, include context of wet lab activities from last semester, include background information from the phage you are working on -----data that was gathered during the wet lab and noted on the Purdue phage page, describe current activities including genome annotation, comparative genome analysis with the other sequenced phages, tools that you are using to conduct the in silico analysis, summary of current findings which should include the functional annotation and also next steps for research.

* This research aims to produce an annotated genome of a mycobacteriophage associated with the SEA-PHAGES project.
* Mycobacteriophage are virions that infect mycobacterial cells for the purpose of utilizing the bacteria’s ability to reproduce genetic material.
* The SEA-PHAGES project is an international effort of undergraduate students to log genomes of mycobacteriophage found in environmental samples in order to discover new genes and their functions to further the field of genetics.
* Last semester, various species of mycobacteriophage were discovered and isolated using wet lab techniques, and this semester the project was continued after the Purdue Genomics Core Facility sequenced the genome of the mycobacteriophage.
* Using programs such as DNA Master, GeneMark, BLAST, Starterator, and Phamerator, the genes of this mycobacteriophage were systematically annotated to determine which features were genes and the likely functions of these genes.
* The predictions from these programs and databases are heavily reliant on historical data from other related mycobacteriophage.
* After determining start and stop codons of potential genes, BLAST assists in comparing that DNA sequence to known amino acids in order to decide upon the most likely position at which the gene should be called.
* This annotated genome can now be submitted to the GenBank database where it will be validated through wet lab testing to determine the type and function of the projected proteins.
* Following validation, the genome can be compared with others from the same cluster to analyze the adaptations and evolution of the phamily. This research ultimately contributes to the knowledge of mycobacteriophages and the mycobacteria they infect and their potential applications in medical and environmental fields.

The SEA-PHAGES project is an international effort furthering the field of genetics by discovering and determining the function of novel genes from mycobacteriophage - virions that infect mycobacterial cells to reproduce. As a part of the SEA-PHAGES project, this research aims to produce an annotated genome of two mycobacteriophage to add to the growing database. During Fall 2016, various species of mycobacteriophage were extracted from environmental samples and isolated in petri dishes using aseptic technique. The Purdue Genomics Core Facility sequenced the genomes of the mycobacteriophages. The annotation of this genome as well as the associated function predictions was supported by programs such as DNA Master, GeneMark, BLAST, Phamerator, and HHpred. These programs primarily rely on databases composed of previously cataloged genomes of related bacteriophages. Annotation skills were first practiced on a portion of the genome of the bacteriophage JewelBug as an effort to annotate the genome along with other research groups. This annotated genome can now be submitted to the GenBank database where it will be validated through wet lab testing to confirm the type and function of the projected proteins. Following validation, the genome can be compared with others from the same cluster to analyze the adaptations and evolution of the phamily. The group has begun work on a second annotation in order to complete characterization of a bacteriophage that was found Fall 2016. This research ultimately contributes to an understanding of genetics of infectious diseases with potential application in fighting antibacterial resistance and genetic engineering.

MODEL:

Mycobacteriophages are a diverse group of phages, encompassing roughly thirty distinct types that share genome level similarity (Hatfull, 2014). Many have been identified using Mycobacterium Smegmatis to screen environmental samples for mycobacteriophages which were subsequently isolated and sequenced. The novel mycobacteriophage Cosmolli16 was isolated from the West Lafayette, Indiana area in the Fall of 2015 by Giulia Olivieri and Jennifer Nance. After purification and sequencing the annotated genome was then annotated for gene function and function analyzed in respect to its location within the genome. A better understanding of the structure of mycobacteriophage genomes may answer questions of the evolution and future restructuring. Identification and characterization of the genomes and proteomes of mycobacteriophages may lead to use in the treatment of disease, namely 2016 Undergraduate Research & Poster Symposium – Abstracts 111 tuberculosis (McNerney, 2005). Future uses of mycobacteriophages may include better disease identification, genetic engineering and treatment of bacterial infections.