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COMPARATIVE FUNCTIONAL ANNOTATION OF MOOSE SWISS CHEESE, ROHR, AND BIG MAU

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Mentor: Chris Shaffer

This experiment was a part of a larger movement to annotate and explore phages and their diversity using a consortium of students and resources. Soil samples were collected around Washington University's campus, from which phages were subsequently isolated and purified; these phages genomes were sequenced, and eventually annotated. We report here on the annotation of phage Moose, Swiss Cheese, Rohr, and Big Mau all belonging to the A1 subcluster. They are all lysogenic as evidenced by the presence of an Integrase and the presence of small, cloudy plaques. The length for all four genomes are 52,695 bp, 51,439 bp, 53,483 bp, and 52,632 bp, respectively. All four have similar number of protein coding genes (95, 95, 93, and 94, respectively). Functional annotations based on similarity at either the primary or secondary amino acid structure were assigned to some but not all genes in these phages. Each phage also has interesting functional annotations that are not commonly found in other phages, including Transposase, RNA sigma factor, Recombination directionality factor, and Immunity Repressor. Comparison within the four phages revealed that Moose and Swiss Cheese are more similar to one another, as are Rohr and Big Mau for both the numbers of genes, their functional annotations, and the number of tRNA present for each phage. Due to low numbers of tRNA in their respective genomes, all four can be considered to be not very virulent.