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2022 SEA Symposium Abstract

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Birds of a pheather phlock together: Comparative analyses of two new F1 phages Beakin and Phalconet

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Twelve new mycobacteriophages were isolated from soil samples collected around the state of Michigan and parts of the United States. All phages were capable of infecting Mycobacterium smegmatis and were isolated via enrichment at 37°C or direct plating at 35°C. A variety of plaque morphologies were observed based on size, shape, and clarity. The mycobacteriophages Beakin and Phalconet were chosen for complete genome sequencing and comparative genomic analyses. Both appear to be new members of cluster F, subcluster F1. Based on BlastP analysis performed on the phagesdb website, Beakin is most similar to the F1 phage Tootsieroll. It has a genome size of 54,926 bp and contains 99 protein-encoding genes, one an ORPHam gene of unknown function. Phalconet appears most similar to the F1 phage CaptainTrips. It has a genome size of 57,648 bp, and may contain up to 110 protein-encoding genes. Neither phage appears to encode tRNA or tmRNA genes and both are predicted to execute a +1 programmed translational frameshift in the tail assembly chaperone genes. Beakin contains a predicted toxin/antitoxin gene pair (genes 46-47) not found in Phalconet while Phalconet contains 2 predicted immunity repressor genes. Both phages also have tyrosine-type integrases. A stable lysogen of Beakin was produced and found immune to infection by Phalconet and other known F1 mycobacteriophages. Direct comparison shows Beakin and Phalconet have 94.70% average nucleotide identity but only share about 65% of Phams. Beakin and Phalconet have multiple interesting genomic features that we are investigating over the remainder of the semester, including the following: 1) the presence of 2 possible attP sites in both phages targeting different M. smegmatis genomic locations, 2) the presence of 2 immunity repressor genes in Phalconet, and 3) the presence of a toxin/antitoxin gene pair in Beakin.