CONSIDER FOR TALK

2021 SEA Symposium Abstract

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Four Mycobacterium Phages: Leviathan (A2), Miculucigas (A2), Thresher (E), and Wiggen (E).

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All phages were isolated from enriched soil samples on Mycobacterium smegmatis mc2155. Annotations were done in PECAAN. Phages were compared to sub-clusters and to closest relatives in order to identify common and unique features.

Leviathan and Miculucigas are cluster A2 Mycobacteriophages that exhibit large 4 mm turbid plaques, some with clear centers. Genome lengths are 53,239 and 52,760 bp respectively. They each contain 94 and 97 protein coding genes, with 1 and 0 tRNAs respectively. They have Siphoviridae morphotypes with 48 and 42 nm diameter heads and with 120 and 120 nm long tails respectively. Even though they both belong to the same sub-cluster, they are less related to each other and most closely related to Jerm and Flare16 respectively.

Thresher and Wiggin are cluster E Mycobacteriophages that exhibited large 3 mm, turbid plaques with clearer centers. Genome lengths are 76,192 and 74,903 bp respectively. They contain 143 and 144 protein coding genes respectively and 2 tRNAs each. They have Siphoviridae morphotypes with 55 and 66 nm diameter heads with 205 and 260 nm long tails respectively. Mycobacteriophages Thresher and Wiggin are generally organized the same way. However, Cjw1 is the closest relative to Thresher and Adnama is the closest relative to Wiggin.