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AAA to the Rescue: Characterization of Novel A1 Phages Hermia, QTRlifeCrisis, and LilBib

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Non-tuberculosis mycobacteria (NTMs) are pathogens that are dangerous to the elderly, infants, and the immunocompromised. NTM infections are rapidly increasing in the US, and are difficult to treat due to multi- or total-drug resistance. Mycobacteriophages (phages), viruses that can infect and kill mycobacteria, have been successfully used as an alternative treatment to drug-resistant infections. We isolated 3 novel, temperate, cluster A1 mycobacteriophages—Hermia, QTRlifeCrisis, and LilBib—using the non-pathogenic host Mycobacterium smegmatis MC2155. LilBib and QTRlifeCrisis are only able to infect M. smegmatis, while Hermia can also infect strains of M. abscessus, M. chelonae, and M. salmoniphilum. All three phages have Siphoviridae morphology. Hermia has a genome length of 49,670 bps, and a GC content of 63.9%; LilBib has a genome length of 50,325 bps, and a GC content of 63.8%; QTRlifeCrisis has a genome length of 49,633 bps, and a GC content of 63.7%. The genomes of Hermia, LilBib and QTRlifeCrisis encode 83, 80 and 85 protein-coding genes and no tRNAs. The cluster A1 genomes vary significantly in the minor tail protein region immediately upstream of the integrase. Hermia gp39 and QTRlifeCrisis gp39 are putative minor tail proteins that belong to different phams but share glycine-rich repeats, whereas LilBib gp37 shares no sequence identity with Hermia and QTRlifeCrisis gp39. The plating efficiency of Hermia will be confirmed in future host range assays and potential escape mutants will be isolated.