CONSIDER FOR TALK

2022 SEA Symposium Abstract

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Isolation and characterization of phages: Rumi, ParvusTarda, Phepper and HappinessHere we describe four novel bacteriophages, Happiness, Phepper, Rumi and ParvusTarda

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Here we describe four novel bacteriophages, Happiness, Phepper, Rumi and ParvusTarda. All four phages were isolated in Northern Virginia via the enrichment method using either *Gordonia rubripertincta* NRRL B-16540 (Rumi, Phepper and ParvusTarda) or *Mycobacterium smegmatis MC2155* (Happiness) as the host. All four genomes were sequenced using Illumina sequencing at the Pittsburgh Bacteriophage Institute.  
  
Both Rumi and ParvusTarda are cluster DV Gordonia phages. Rumi, named for a Persian poet, was found on the George Mason University campus and ParvusTarda (little and late) was found in Annandale, VA. Both phages presented with small turbid plaques. We will present an analysis of the evolutionary relationship between these two phages. The Rumi genome is 64,869 bp in length and has a GC content of 57.7%. There are ~94 predicted gene products for phage Rumi. The ParvusTarda genome is 67.279 in length and has a GC content of 58.3%. There are ~97 predicted gene products for phage ParvusTarda.  
  
Phepper, isolated from a hot pepper garden, is a cluster DJ Gordonia phage that was isolated in Springfield, VA. Phepper forms tiny clear plaques and is likely a lytic phage as it lacks an integrase gene and other genes associated with lysogeny. The genome is 60,626 bp long and has GC content of 51.6%. Phepper has ~91 predicted gene products. Phylogenetic analysis of cluster DJ and related phages will be presented and underscores the remarkable diversity found in the Gordonia phages.  
  
Happiness, named for a smiley face plaque pattern on a plate, is a cluster A4 Mycobacteriophage that was isolated from a soil sample from the George Mason University campus. Happiness forms large plaques with clear centers and a turbid halo and is a temperate phage as it’s genome contains an integrase gene and other genes associated with lysogeny. The genome is 51.398 bp long and has GC content of 63.9%. Happiness has ~84 predicted gene products.