CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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The Isolation and Annotation of Prolate-Head Bacteriophage Satis and Three Other Highly Novel Streptomyces Bacteriophage

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The Washington University in St. Louis SEA-PHAGES program isolated and annotated four novel *Streptomyces* (*lividans* and *viridochromogenes*) bacteriophages Mildred21, BillNye, Bing, and Satis. Three out of four of the studied phages have genomes larger than 125,000bp and of all Streptomyces phages listed in Phagesdb, Satis has the largest genome at 186,702 bp, approximately 20,000 bp longer than the next largest phage, *Mycobacteria* phage Myrna. Satis, a Singleton phage, displays many novel features and thus was chosen for in-depth study. Satis was isolated from a direct environmental sample collected from outside Danforth House on the Washington University in St. Louis campus. Satis infects bacterial species *Streptomyces lividans* producing pinpoint, cloudy plaques less than 1mm in diameter. Electron microscope data show rare, atypical physical features. Rather than the common octahedral capsid shape, Satis has a prolate head, the first of its morphology to be isolated in *Streptomyces* hosts. Its head measures, on average, 285nm by 47nm, longer than its flexible tail measuring 268nm. The genome is also quite novel in sequence, as its closest published genetic match, bacteriophage Chymera, is similar across only 15.9% of the genome (using EMBOSS Global Alignment). Satis’ genome contains 324 annotated protein coding genes and 13 tRNAs. All but 33 of the proteins are orphams, leaving 291 proteins completely novel. Putative functions were called for 47 of the 324 genes, representing 14.5%. Curiously, another Streptomyces phage JustBecause, with almost identical prolate head morphology, was isolated in Fall 2016 concurrently with phage Satis. JustBecause has a genome length of 184,281bp and the draft DNAMaster annotation of JustBecause calls 340 protein coding genes, displaying very similar characteristics to Satis and its genome. Curiously, no tRNAs are found in JustBecause. Comparative genomic analysis between the two phages shows that 266 of their protein coding genes are considered orthologs as judged by DNAMaster, representing about 78.5% of each’s called genes. Surprisingly, comparison of the two genomes showed an ANI (average nucleotide identity) of only 74.4%, far less than predicted considering their protein, morphological, and genomic similarities. Based on the relatively high level of protein similarity yet low level of DNA identity, the two phage appear to have diverged long ago, implicating the existence of an ancient family of *Streptomyces* phage with prolate morphology. *emphasized text*