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Saratos: A Newly Isolated and Novel Microbacterium foliorum Bacteriophage

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*Microbacterium foliorum* is a soil-borne bacterium that we used to isolate bacteriophage Saratos. Saratos’ genome was sequenced at the University of Pittsburgh. We are reporting the annotation, interpretation of coding regions and possible gene functions. We used DNAMaster and coding potential was determined using Glimmer and GeneMark. The protein function of called genes were compared using HHPred, NCBI BLASTP, phagesdb.org, and Phamerator. We determined that Saratos is a EA2 subcluster bacteriophage. Phamerator was used to confirm and compare the identified gene functions of the genome with bacteriophages in the same subcluster. Saratos has a total of 40351 base pairs which contain a total of 63 open reading frames with 29 forward and 34 reverse ORFs, with significant coding potential. Saratos is closely related to and shares synteny with most other bacteriophages in the EA2 subcluster including Eleri, MCubed, Glamour, and ColaCorta with a 98.45% average nucleotide identity. Saratos has 7 comparatively rare ORFs that are found in less than ten other bacteriophages. Comparing open reading frame 14 with other EA2 cluster genomes shows that the tail assembly chaperone protein in the Saratos genome appears to have fewer amino acids. Our data show that Saratos has a novel genome and our analysis contributes to the information regarding cluster EA2 phages.