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2023 SEA Symposium Abstract

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Discovery and Annotation of Microbacterium foliorum Actinobacteriophages and Statistical Analysis of the Percentage of Genes with No Known Function across the E Cluster.

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Three *Microbacterium foliorum* actinobacteriophages were discovered and annotated by Salem State University. BabyDaisy (EB), Erudite (EF) and Jemerald (EA6) genomes ranged from 41 kb to 56 kb in length and followed typical structure with capsid genes including a programmed translational frameshift in the tail assembly chaperone in the left arms and control genes in the right arms. All phages were lytic and their genomes circularly permuted. We were surprised at the high percentage of genes with no known function (NKF). A statistical approach was used to compare % NKF gene frequency to other E cluster phages. We found wide diversity across phages sampled which indicated the importance of the breadth of the SEA program and need for further research.