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2025 SEA Symposium Abstract

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Garden to Genome: Annotation of Bacteriophage Coriander

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A novel bacteriophage, Coriander, was isolated from a soil sample collected in Pittsburgh, Pennsylvania, as part of the SEA-PHAGES (Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science) discovery course using bacterial host *Gordonia terrae* 3612. The name Coriander was inspired by its founding location, in the soil next to a garden bed of beautiful flowers. It is a temperate phage assigned within Cluster DB, and its genome has been fully sequenced at the Pittsburgh Bacteriophage Institute (Illumina MiSeq platform). The genome is 44,192 base pairs, has a GC content of 66.8%, and predicts 66 protein-coding genes. The small genome and well-established bioinformatic tools provide a coherent annotation workflow. Utilizing DNA Master, Starterator, Phamerator, and Phage Evidence Collection And Annotation Network (PECAAN) collectively with resources from the Actinobacteriophage Database, we conduct a comprehensive genome characterization: no tRNA was identified by DNA Master or PECAAN and confirmed with ARAGORN and tRNAscan-SE. Currently, Cluster DB comprises 20 members, all of which exhibit a high degree of conservation within the gene functions.