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2022 SEA Symposium Abstract

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Complete Genome of Actinobacteriophage NathanVaag

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The University of Hawai’i at Mānoa SEA PHAGES bioinformatics cohort of Spring 2022 annotated NathanVaag, a bacteriophage belonging to the AO1 subcluster. NathanVaag was discovered in El Paso, TX and was isolated at the University of Texas, at El Paso. NathanVaag is a lytic Actinobacteriophage that infects Arthrobacter sp. ATCC 21022. The genome size is 49,645bp in length with a GC content of 63.6%. The genome contains 73 genes, including gene 40 which is classified as an orpham. Gene 40 has been assigned the function of a RusA-like resolvase which codes for an endonuclease enzyme. There is no tRNA present in NathanVaag, and approximately 52% of genes have function assignments, while the other 48% have been assigned with “no known function” or “hypothetical protein.” The majority of the unassigned genes occur in the second half of the genome, while the first half of the genome tends to code for structural proteins. The first 67 genes are forward transcribed, with the remaining 6 being reverse transcribed. NathanVaag exhibits significant similarities between other AO1 phages, such as Piccoletto and Beans. Further examination and annotation will provide background on phage evolutionary relationships, protein functions and potential application usage.