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2025 SEA Symposium Abstract

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The Isolation and Genomic analysis of the Bacteriophage Invectra

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Bacteriophages are bacteria-infecting viruses that are used in agriculture as an important bio-control tool. A newly discovered bacteriophage from the Siphoviridae family, named Invectra, was isolated using the bacterial host *Gordonia rubripertincta*. Through multiple series of indirect and direct isolations that utilized plaque assays, Invectra was isolated and purified. Following this isolation process, Invectra was genomically sequenced, then the genome was analyzed using DNA master. Auto annotation was completed using DNA master and start and stop sites were verified using BLAST, Phamerator, Starterator, and coding potential. Some of the start sites for genes were adjusted due to supporting evidence, or to better match the guiding principles for phage annotation. In cases where the start was more ambiguous, the numeric value of a genes start site would only be altered if there was substantial evidence indicating that the original value was incorrect. This process of checking and altering a gene was repeated for all 80 Genes within Invectra’s genome to get an accurate analysis of the genome structure. This genomic analysis will deepen the understanding of phage biology, host interactions, and potential applications within the scientific community.