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2025 SEA Symposium Abstract

Benedictine University

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Corresponding Faculty Member: Tiara Perez Morales (tperezmorales@ben.edu)

Characterization of Cluster FL Arthrobacter globiformis B-2979 phage Hirko

Hajira Choudry, Tiara Perez Morales

Bacteriophages are viruses which specifically infect bacteria and have recently gained interest as potential therapeutics due to their host specificity. Bacteriophages can lyse host cells through the lytic cycle or integrate in the host chromosome through the temperate cycle. In this study, we characterized phage Hirko, which was isolated in 2022 at Benedictine University using the soil bacterial host Arthrobacter globiformis B-2979. Structurally, Hirko belongs to the Myoviridae family as it possesses a long, contractile tail. During infection, Hirko forms 1.5 mm plaques that have large cloudy halos. Preliminary data indicated that Hirko’s infection rate was influenced by temperature and was concentration-dependent at 22°C and 30°C. Based on these observations, we hypothesized Hirko was a temperate phage, and we selected it for genome sequencing. Its genome is 48,792 bp long and it is most similar to Cluster FL phages GoldDust (91%), Vibaki (91%) and Vitus (84%). Although we identified lytic genes (endolysin) we could not identify a known integrase required for the temperate cycle, labeling it as unknown similar to the phages present in this Cluster. The goal of this work was to determine if a Hirko lysogen could be generated and studied. We were successful in isolating one lysogen at 30℃ and corroborated using phage release assays. Our future work will focus on immunity studies using the Hirko lysogen against a collection of phages with known clusters. Our findings provide new insights into a small but diverse group of phages with unknown infection cycles.