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Characterization of the Cluster FE lytic bacteriophage Utopia

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Viruses are infectious agents that infect hosts such as humans, animals, plants, and microorganisms. In our research laboratory, we focus on phages, viruses that replicate inside bacteria. Phages have two main infection cycles: the lytic cycle, in which the phage lyses the host cells, and the temperate cycle, in which the phage integrates into the host chromosome. This study focuses on Utopia, a phage isolated using the soil bacterial host Arthrobacter globiformis B-2880. Prior research determined that Utopia's viral structure is most similar to Siphoviruses, which typically have isometric capsids and flexible tails. Utopia infects A. globiformis B-2880 effectively at lower temperatures, such as 22°C and 30°C, with fewer plaques observed at 37°C. In addition to its temperature sensitivity, Utopia exhibits a narrow host range; it is unable to infect other Arthrobacter species and strains, including A. sulfureus, A. atrocyaneus, and A. globiformis B-2979. During infection. Utopia consistently forms 1 mm clear plaques, leading us to hypothesize that it follows the lytic cycle. To investigate this further, we sequenced and analyzed its genome using bioinformatics and annotation programs. Utopia’s genome was assigned to Arthrobacter Cluster FE, and shares the highest similarity with Yavru (91%), Piku (90%), and Whytu (90%). The genome is 25,899 base pairs long and contains 23 predicted open reading frames (ORFs). Genes associated with host cell lysis, including endolysin and holin, were identified, supporting our hypothesis of a lytic infection cycle. Future work will include comparative genome analysis and phage infection studies, particularly in comparison with phage Piku, due to their differing infection profiles.