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Conservation of Recombination Directionality Factor and Lysogenic Genes within Temperate AZ4 Actinobacteriophages

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Temperate bacteriophages can switch to a lysogenic life cycle in which their genome is integrated into the host genome, replicating with the host until conditions change to favor a switch to the lytic cycle. This process is mediated by an integration cassette containing genes for excise, integrase, and immunity repressor proteins, often found in the center of the bacteriophage genome. Isolation of phage LadyAstra revealed halo plaque morphology, characterizing it as a temperate bacteriophage. TEM imaging further classified LadyAstra as a Siphoviridae. While temperate bacteriophages are not readily used for therapeutic purposes due to limited understanding of their effects on the human microbiota, sequencing, annotation, and structural analysis of LadyAstra were performed to understand its genome. These analyses confirmed the presence of genes associated with the integration cassette. Annotation revealed the Recombination Directionality Factor (RDF) gene, which aids integrase in the excision of the prophage during the switch to the lytic life cycle, and DNA binding proteins (DBPs), which can maintain the lysogenic state by acting as repressors for lytic genes. Conservation of RDF and DBP protein sequences within LadyAstra’s subcluster AZ4 and subcluster AZ1 was confirmed through bioinformatic analysis and phylogenetic tree analysis. Gene conservation indicates their importance to bacteriophage survival. Further analysis of protein structures suggests independent functions for DBPs, each containing unique DNA-binding motifs and DNA-binding potentials. Understanding lysogenic bacteriophages can contribute to their use in vaccine development or as adjuncts for antibiotics.