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Discovering Bacterial Defense Systems within Mycobacteriophage Miryou

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This study explores the complex evolutionary dynamics of interspecies lateral gene transfer (LGT), focusing on cluster K5 Mycobacteriophage Miryou’s acquisition of bacterial restriction modification (R-M) systems and toxin-antitoxin (TA) systems. Using bioinformatics programs such as HHpred, BLASTP, Phamerator, and AlphaFold, our research indicates that mycobacteriophage Miryou contains genes with similarity to bacterial R-M systems and TA systems. Gene 38 bears a strong resemblance, from BLAST results, to proteins contained within R-M system operons in bacteria. Furthermore, the presence of R-M systems is supported by AlphaFold identifying two surface-accessible residues, Proline-136 and Cysteine-137 on a vicinal carbon, characteristic of a methyltransferase protein, with considerable alignment to gene 39. Moreover, genes 90 and 91, belonging to phamilies 4290 and 4157, are classified as BrnT-like toxins and BrnA-like antitoxins, respectively. Notably, a ribbon-helix-helix DNA binding domain, which is a domain commonly found in BrnA-like antitoxins, was discovered within phamily 4157, further supporting these classifications and the presence of a TA system. These findings highlight the dynamic nature of gene function annotation and comparative genomics, while enhance our understanding of phage-bacteria interactions.