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Analyzing the Product Variations of Minor Tail Protein within Subcluster A4 Bacteriophages

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Minor tail proteins (MTP) in bacteriophages assist in recognizing a host and allows attachment of the phage. This connects MTP to their main role in infection. During annotation, differences were found between the products of SenorClean MTP and other A4 bacteriophages. We used Phamerator to collect 3 MTPs from all 137 A4 bacteriophages in the 18 to 25 Kbp range, using only those with products over 150 amino acids. Draft A4s were removed, and the 3 products were combined from upstream to downstream, creating a single product averaging 1,678 amino acids in length. Muscle, a multiple sequence alignment tool from EMBL-EBI, was used to build a phylogenetic tree and subsequently identify representative phages from each node. Muscle alignment revealed amino acid residue differences: (1) single change at residue 178, (2) triple replacements at residues 248/250 in phage Stink, (3) deletions at residues 449/450 in phages Noelle and Cindaradix, and (4) insertions at residues 858/863 in multiple phages. Largest amino acid differences were observed in the third MTP, so it was folded using AlphaFold 3 to observe structural differences. Wet-lab experiments could then test if structural changes translate to a different host range.