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Comparative Analysis of Cluster A Bacteriophage Tape Measure and Minor Tail Protein Phamilies

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Bacteriophages are extremely host specific and usually only infect a single bacterial species. During infection, bacteriophage DNA goes through the tail into the host cell cytoplasm. The tape measure protein (TMP) determines phage tail length. By controlling tail length, TMPs ensure that phages can effectively recognize and infect suitable hosts. Bacteriophage minor tail proteins (MTP) assist in phage tail assembly, adsorption, host cell wall penetration, and DNA ejection. Therefore, bacteriophage MTPs and TMPs could serve as reliable tools for bacteriophage phylogenetics, bacterial pathogen identification, host range determination, and host infection dynamics studies. To further knowledge of bacteriophage evolution, host range and host infection dynamics, it is necessary to investigate the sequence and structural diversity of MTPs and TMPs. Five phages were analyzed per subcluster (A1, A2, A3, A4, A5, A6, A7), together with phage Chargerpower, the sole non-subclustered cluster A member. The TMP and one MTP were analyzed per phage, giving a total of 36 TMPs and 36 MTPs analyzed. Phamerator was used to do pairwise sequence comparisons, assort the protein-coding genes into phamilies, and provide a color-coded visual display of the comparative analysis of the phage genomes, genes, gene products, and gene relationships. MEGA11 was used to construct maximum likelihood phylogenetic trees using the TMPs and MTPs. For MTPs, phages in subclusters A1, A3, A4, A5, and A6 grouped in their own distinct clades, but this was not the case for A, A2 and A7 members in which some of their members were scattered across clades. Specifically, cluster A grouped in the same clade with two subcluster A2 phages and fell between the A3 and A4 clades. Two subcluster A7 members grouped in their own clade, falling between A2 and A5. The other subcluster A2 and A7 members grouped in a larger clade having a common ancestor with the subcluster A6 members. For TMPs, phages in subclusters A3, A5, A6, and A7 grouped in their own clades while cluster A fell between some members of A1 and A2. Subcluster A4 partially grouped into its own clade, with one A4 member grouping in a different clade with one A1 member. One member of subcluster A2 was more closely related to the subcluster A6 members, falling between the A6 and A7 clades. Another subcluster A2 member fell between A1 and A5, while the other members clustered between A and A4. Using the SWISS-MODEL, three-dimensional protein folding models were constructed. Overall, DNA sequence and protein structural diversity was observed even within clades. Further studies are warranted to investigate MTP and TMP diversity and structural conservation across all cluster A members in relation to host infection dynamics, host range, bacterial pathogen identification, bacteriophage evolution, and phylogenetics.