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Comparative Analysis of Cluster M Actinobacteriophage Minor Tail Protein Phamilies

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Actinobacteriophages are viruses that use bacteria in phylum Actinobacteria as their hosts. The bacteriophage (or phage) tail, a necessary tool needed by the viruses to breach the cell envelope to inject their genome into bacteria and establish infection, is a complex, multiprotein structure. The tail facilitates adsorption, penetration of the cell wall, and genome ejection. Bacteriophage minor tail proteins (MTPs) play an important role in phage tail assembly and are essential for phage adsorption. Because phages are very host species-specific and typically only infect a single bacterial species or strain, MTPs could serve as reliable tools for bacterial pathogen identification. For host infection and host range to be better understood, it is necessary to investigate the sequence and structural diversity of MTPs. Previous research focused on cluster F phages. The current research is focused on cluster M phages. Gene products of the two MTP phams downstream the tape measure, closest to the lysin A gene where most diversity was observed based on Phamerator color codes were comparatively analyzed. Seventy-seven MTPs were observed in the 15 currently fully annotated phages within cluster M, two of which were analyzed per phage, giving a total of 30 MTPs compared across subclusters M1, M2, and M3. The two amino acid sequences of each phage were convocated. Clustal Omega and MEGA11 were used to construct maximum likelihood cladograms. Phages in subclusters M1 and M2 grouped in their own clades, with M3 coming in between. Differences in sister taxa were observed, due to differences in MTP primary structure within the clades. The clustering in the cladograms was consistent with that which is based on whole genome sequence analysis, indicating that MTPs could be useful in bacteriophage phylogenetic studies. Three-dimensional protein folding models were also constructed using SWISS-MODEL, and structural differences were observed. Further studies should expand this investigation to understand MTP diversity and structural conservation across a wider range of clusters in relation to host range. The potential for using phage minor tail proteins for pathogenic bacterial identification to replace the time-consuming culture methods should also be investigated.