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Relationships of Genome Length, Capsid Size, Tape Measure Protein, Tail Length and Functional Gene Calls Across Multiple Phage Clusters

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Genome sizes in actinobactrtiophages range from 14,270bp to 235,841bp. Actinobactrtiophages also have three different morphologies: siphoviridae, myoviridae, and podoviridae, all typically characterized by tail size. This research investigated several relationships: 1) genome size to capsid size; 2) tape measure protein size compared to tail size; 3) genome size to function gene calls; and 4) genome size compared to functional gene calls with structural proteins. Five clusters were utilized that varied in genome size: Cluster C (C1) (154,830 bp), Cluster J (110,185 bp), Cluster E (75,874 bp), Cluster AK (43,397 bp), and Cluster AN (15,547 bp), and 10 phages from each were evaluated. EM images were used to measure the diameter and volumes of the capsid and determine the length of the tail. The genes list was evaluated for function and classified as structural proteins, enzymes, or regulatory proteins. T tests were used to determine statistical significance between the different measurements and regression analysis used to determine correlations. The results show that there is a significant correlation between capsid size and genome volume/length. From the 50 phages evaluated, the phage, Dandelion from Cluster C (C1) has the largest genome with a capsid size of 100 nm compared to 25 nm for the phage, Toulouse (AN) with the smallest genome. The length of the measure protein also correlates to tail size. The phage, BAKA, found in Cluster J has the longest tape measure protein with a tail size of 240 nm, while Hunnie is one of the phages with the shortest tape measure protein with a tail size of 71 nm. When relating genome size to the percentage of called functions, there is only a relationship between certain clusters. Clusters C (C1), J, and E have an average percentage of called functions of 21%, 24%, and 22%, even though the genome sizes range from 75kbp to 154kbp. However, the percent of called genes is statistically significant when these clusters are compared to Cluster AK and Cluster AN due to an average percentage of called functions of 42% for Cluster AK and 61% for Cluster AN. The data also show that as the genome size increases, the percentage of called-functional genes with structural proteins decreases. For Cluster AN, the average percentage of called-functional genes with structural proteins is at 75% compared to about 35% in Cluster C (C1). This research supports an evolutionary relationship between genome size and the size of the capsid. Future research might explore whether there are also differences in the size of capsid proteins and how the capsid is assembled. The data show that the most compact genomes have a high number of called genes of which the majority encode structural proteins. This raises the question regarding why a phage would evolve with a genome that can be up to 10—times larger and what functions exist for the high percent of uncalled genes in one of these phage.