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Codon Usage Bias: What do Subcluster M1 Mycobacteriophages Glaske16 and Dimiminus Contribute to the Story?

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Codon usage bias (CUB) is the phenomenon where specific codons are used more often than other synonymous codons during translation of genes, and this bias may vary within and among species. Since codon usage bias can impact gene expression and cellular function, it is important to investigate whether the non-random use of synonymous codons is observed in bacteriophages. Subcluster M1 Mycobacteriophages Glaske16 and Diminimus were selected for codon usage bias analysis using DNA Master’s Bias Table function. The Bias Table included all genes and tRNAs within within the Glaske16 and Diminimus genomes. Percentages were calculated for each codon and compared with previously examined codon bias in phylum Actinomycetes. Similarities were observed between both phages and their isolation host *Mycobacterium smegmatis* mc2 155. In phage Glaske16, the top three codon usage bias percentages from the highest to the lowest were: Lysin codon AAG (96%), Phenyalanine codon UUC (91%), Tyrosine codon UAC (89.5%). In phage Diminimus, the top three CUB percentages from the highest to the lowest were: Lysin codon AAG (95.3%), Phenyalanine codon UUC (89.7%), and Tyrosine codon UAC (83%). This indicates that both phages have similar codon usage bias. Whereas our data show codon usage bias in Glaske16 and Diminimus, this was limited to only these two subcluster M1 phages. Future work should be expanded to compare all phages within the M1 subcluster, and among phages across clusters and subclusters to determine if there is an overall codon bias pattern for each bacteriophage cluster and subcluster. Such comparisons could reveal whether there is an overall codon bias pattern, and possibly lead to the uncovering of novel codon bias patterns.