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Codon Usage in Actinobacteriophage Zooman (Cluster GD) Versus its Host Microbacterium foliorum

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The goal of this project was to look at the codon usage of Phage Zooman (cluster GD) and compare it to the host organism, *Microbacterium foliorum*. Zooman has an unusually large number of tRNA coding sequences (46) in its genome. We looked at the tRNA sequences via PECAAN and calculated codon usage with the cusp program (part of the emboss package). A Wilcoxon Signed-Rank test did not reveal significant differences in codon usage between Zooman and M. foliorum. Using the codons and frequencies we compared the codon differences. Zooman more frequently uses codons that are A and T rich; whereas M. foliorum uses codons that are C and G rich. This bias is also reflected in the frequencies of amino acids that use codons with an A in the center of the codon (Y, Q, K). A total of 16 out of the 64 codons showed a difference in the percent frequencies that were 1% or greater. The codon that had the largest difference between the phage and host organism was GCG. GCG was more present in M. foliorum than in Zooman. We did not find significant differences in codon usage for codons for which Zooman encodes a tRNA. However, in general, the codon usage in the phage was less biased than in the host, reflected in a smaller variance for the codon frequencies in the phage (the host had a more extreme codon usage). We divided the codon frequencies into two sets, one for codons that contained two or three Gs of Cs, the other for codons containing two or three As. For both of these sets, the Fligner-Killeen test of homogeneity of variances found that the distribution of usage in the phage and the host was significantly different. The Fligner-Killeen test is less sensitive to deviations from normality than the F-Test comparing the variances. We will try continuing to investigate the role of phage-encoded tRNAs and other factors impacting codon usage through literature research. Conclusion: We did not detect significant differences in codon usage between codons for which Zooman encodes its own tRNA and those for which it does not. However, comparison of codon usage between Zooman and its host revealed that the host’s usage is biased towards codons that contain two or three Gs and C, whereas the phage’s usage is biased towards codons that contain two or three As and Ts.