CONSIDER FOR TALK

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There’s no such thing as overpacking: do phages compensate for GC content mismatch by bringing their own tRNAs?

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The *Streptomyces* bacteriophage TunaTartare is a member of the cluster BK. The phage’s genome, and that of other cluster BK phages, is quite different from other *Streptomyces* infecting bacteriophages. TunaTartare’s genome varied enough that host-based GeneMark program predictions did not prove useful for our annotations. Instead, a GeneMarkS self-trained model of TunaTartare was used. A likely explanation for this is the low GC content of these phages compared to their hosts, which alters their codon usage patterns. The GC content may vary from the host because of a possible recent jump from a different host with a lower GC content. However, it was also noted that the phage encodes its own tRNAs and could therefore potentially use a different set of codons from that of its host. This would enable the phage to infect a broader range of bacteria, and might also explain a sustained difference in GC content. Cluster BK phages have roughly ten times as many tRNA genes as phages in other *Streptomyces* infecting clusters surveyed in PhagesDB (clusters BA-BR and two additional singletons). Of note, cluster BE phages, which have a similarly low GC content, also encode a high number of tRNAs. Cluster BE phages encode 43-46 tRNAs, similar to cluster BK phages, which have 33-38 tRNA genes. This supports the second hypothesis, that the low GC content may be evidence of a broad host range made possible by the large amount of tRNAs. Surveyed *Streptomyces* phages average approximately 67% GC, similar to *Streptomyces* species, which range from 69-78%. Clusters BK and BE have GC contents well below *Streptomyces* species, with 48.3% and 49.5%, respectively. Phamerator will be used to analyze similarities and differences in genome architecture between the BK and BE clusters, and the rest of *Streptomyces*-infecting clusters. We hope to investigate the similarities between these two clusters, the relevance of their variation in GC content from their host, and the high number of tRNA encoding genes in their genomes.