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James Madison University

Harrisonburg VA

Corresponding Faculty Member: Steven Cresawn (cresawsg@jmu.edu)



Frances Thiry

Exploring the Role of tRNA Genes in Mycobacteriophages

Frances Thiry, Sofiya Biryukova, Georgia Coose, Luca Dooley, Timothy Edelman, Anna Grove, Alison Hauck, Jonathan Miller, Alend Rostem, Abdelmoneim Sidahmed, Rafe Smith, Ryan Starling, Haden Walker, Ryan Granché, Madison G Bendele, Steven G Cresawn

The role of tRNA genes in bacteriophage genomes remains an enduring mystery despite years of study. The number of tRNA genes annotated in the genomes of phages that infect members of the Actinobacterium varies substantially. The largest number annotated in a single genome thus far is 48, however, most phage genomes encode no tRNAs, implying that tRNA genes are non-essential for many bacteriophages. For those phages that encode tRNA genes, it may be that they compensate for differences in codon bias between host- and phage-encoded proteins in such a way as to improve the efficiency of phage protein translation relative to that of the host. To learn more about the role of tRNA genes in bacteriophage genomes, we used Phamerator.org and its underlying database to assess tRNA distribution in phage genomes and clusters as well as their potential role in phage protein translation. In addition, we looked for spatial correlations between tRNA genes and protein phamilies. The role of phage-encoded tRNA genes has long been an enigma, but the development of robust computational approaches to its study is likely to shed some light on this interesting phenomenon.