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University of California, Los Angeles

Los Angeles CA

Corresponding Faculty Member: Amanda Freise (amandafreise@gmail.com)



Catherine S Beaudin



Lily Dines

Comparative Genomic Analysis of Streptomyces Bacteriophage Clusters BE, BK, BC, and BP

Catherine S Beaudin, Sophie Billings, Lily Dines, Sam Kelly, Ryan Ngo, Michelle Zorawik, Krisanavane Reddi, Ana Garcia Vedrenne, Amanda C Freise

Frequent exchange of genetic material between bacteriophages through processes like horizontal gene transfer (HGT) has led to extensive genetic diversity. Thus, phages are classified based on gene content similarity (GCS) into groups called clusters. While comparative studies have previously been conducted on *Gordonia*, *Staphylococci*, *Mycobacterium*, and *Arthrobacter* phages, a large-scale in-depth analysis examining the relationships of *Streptomyces* phages has yet to be completed. *Streptomyces* are infrequent pathogens but produce over two-thirds of the clinically useful antibiotics. To better understand the diversity among these bacteria and the phages capable of infecting them, this study investigates the overall trends and patterns between *Streptomyces* phage clusters BE, BK, BC, and BP. Bioinformatic tools such as Phamerator, GCS heat maps, and phylogenetic trees were used to comparatively analyze phages. Most notably, phages in clusters BE and BK share between 35% to 40% GCS and exhibit extensive pham conservation in genes associated with the tail. Similarly, phages in clusters BC and BP share between 43% to 50% GCS, where the pham of genes involved in DNA replication and processing are highly conserved. While the life cycle of cluster BP phages is currently unknown, it is hypothesized that cluster BP phages are temperate, given that a serine integrase gene was found in every phage currently classified in cluster BP. Furthermore, serine integrase genes in cluster BC and BP phages share the same pham. Additional findings potentially indicate HGT between certain *Streptomyces* and *Rhodococcus* phages. Overall, this study helps better understand the genetic diversity of *Streptomyces* phages.