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Comparative Genomic Analysis of the Singleton BaileyBlu and Clusters AZ & EH Phages Focusing on Genome Architecture and Pham Composition

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Singletons, phages below the clustering threshold of 35% gene similarity, are of interest due to their unique genomes, potential to form novel clusters, and evolutionary conservation mechanisms. Despite this, genome architecture and pham composition relationships between certain singletons and clustered phages remain unexplored. Comparative genomics can reveal unexpected similarities in unusual genome structure that singletons have with clustered phages that highlight their unique evolutionary pasts. It can provide insight into phage genome mosaicism and organization as a result of various processes such as horizontal gene transfer (HGT). One understudied singleton, BaileyBlu, was found to share significant gene content similarity (GCS) with cluster AZ phages. Since previous research showed that clusters AZ and EH exhibit high GCS, their relationship to BaileyBlu was questioned. Bioinformatic analyses through Phamerator, GCS, nucleotide dotplots, and single-gene phylogenetic trees demonstrated that BaileyBlu was most similar to cluster AZ, with an unusual genome architecture, as BaileyBlu’s first half exhibited genomic mosaicism and its latter half showed pham conservation and synteny to the compared phages in the phams of non-structural functions. This contradicts previous findings that most tailed phages tend to have the majority of their similarity located in the first half of their genomes via structural genes. Thus, BaileyBlu was found to have highly unique genetic relatedness with clusters AZ and EH that highlights its unusual, chimeric, evolutionary history with horizontal gene transfer shaping the first half of its genome and vertical transfer shaping the second half. These findings give insight into alternative patterns of phage evolution.