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Non-Conserved Regions in the Cluster E Phages Genome Reveal Relationship with Cluster J

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Bacteriophages are diverse viruses that infect bacteria and are the most abundant entities on Earth. They can be organized into clusters based on degrees of genetic similarity, though they exhibit a continuum of diversity and can share genes between clusters. Not all phage clusters are extensively characterized, including Cluster E wherein phage genomes exhibit high levels of intra-cluster similarity but also contain four understudied non-conserved genomic regions. Apart from associations with non-conserved regions of Cluster J phages, little is known about the inter-cluster diversity of Cluster E. In order to address this lack of understanding, we performed comparative genomic analyses between Cluster E and Cluster J phages. They revealed that both Clusters E and J phages share the D-ala-D-ala carboxypeptidase gene, a critical gene in infecting bacteria, in one of the non-conserved regions. Phylogenetic analysis revealed genes from different clusters branching together, supported by amino acid analyses. ​A methylase gene was also identified to be shared between clusters, containing two different versions of the gene. This was consistent with previous knowledge of the shared genes between Clusters E and J. The phylogenetic tree results suggest horizontal gene transfer of this gene between clusters. Exploring the relationship between these clusters provided insight into their complex evolutionary histories, and this method can also be applied to phages in other clusters. This sheds light on the continuum of diversity in bacteriophages and their relationships between bacteriophages, and host bacteria.