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Diverse intracluster and intercluster relationships between novel cluster AZ and EH bacteriophages

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Bacteriophages are highly abundant, bacteria-infecting microorganisms that vastly improve microbial diversity. Phages themselves display a vast spectrum of diversity which led to their categorization through clustering and subclustering. Phage cluster comparisons and intracluster studies lead to uncovering more about microbial diversity and the impact phages have on bacteria. Since phages are constantly found and classified into new subclusters and the parameters for subclustering phages are not absolute, this study investigated the novel AZ subclusters and their genetic relatedness to cluster EH in order to strengthen the pre-existing genomic relationship between the two clusters. Nucleotide, amino acid, and gene content comparisons were conducted through phage isolation, DNA extraction and sequencing, and comparative genomic tools. It was found that new AZ phages retained the genomic relationship previously identified with Cluster EH phages. By comparing the functionality and sequences of proteins shared between the AZ and EH phages such as the unique protease-toxin fusion protein, capsid maturation protease and VIP2-like ADP-ribosyltransferase toxin, more gene similarities between the two clusters were uncovered, again strengthening their genomic relationship. This comparison also revealed the spectrum of relatedness and diversity within the AZ subclusters as well as the EH cluster. These findings expanded on the current understanding of AZ-EH intercluster dynamics and uncovered the intracluster diversity within AZ and EH. As phages continue to be discovered, the diversity between phages of the same and different clusters will reveal more about the overarching diversity present in the microbial world.