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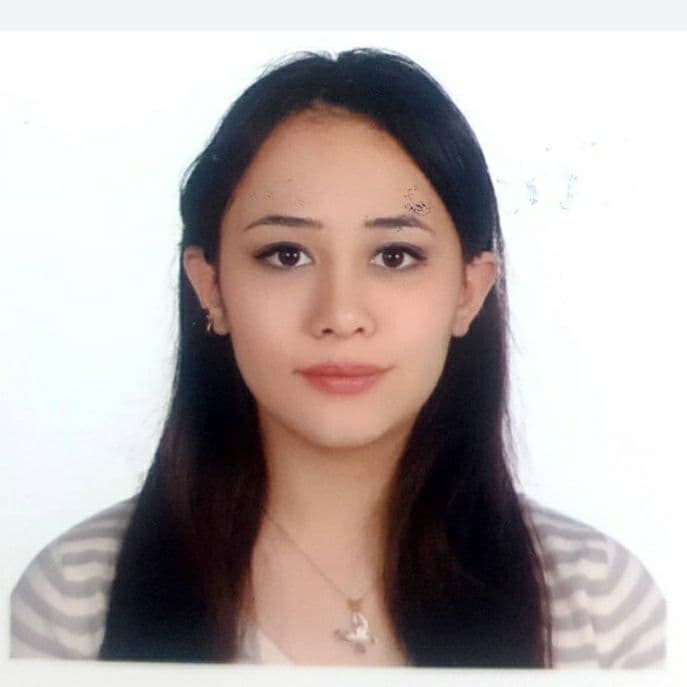
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Comparative Genomic Analysis of Cluster FH Arthrobacter Phages

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Phages infecting *Arthrobacter globiformis*, a Gram-positive, aerobic soil bacterium responsible for creating usable nitrogen products for plants, are of great ecological importance. They drive soil microbial evolution by facilitating horizontal gene transfer between various strains of *A. globiformis* and potentially other soil bacteria. Despite their importance, literature on these phages is sparse and revolves around intercluster comparisons or characterizations of individual phages, resulting in a lack of intracluster genomic analyses. Studies of transcriptional regulation in these phages can shed light on how phages exploit host transcriptional machinery and provide a clearer picture of phage-host interactions. Hence, a study of intracluster genomic relationships and transcriptional regulation was performed on cluster FH, a small group of five recently discovered *A. globiformis* phages, with the goal of observing their unique characteristics and understanding their diversity. To accomplish this goal, we used various bioinformatic tools to perform genome-wide comparisons, identify variable regions, and pinpoint transcriptional regulatory sequences. These analyses showed that most cluster FH phages have a 3kb region containing unique, potentially recombinant tail proteins, suggesting differing host ranges across these phages and a genetic insertion event. We note that phage Bumble is different from other cluster FH phages and contains a lysin potentially derived from a co-infection event with another phage. Finally, a novel putative transcriptional regulatory element and three putative operons, two of which may be responsible for DNA-editing, were discovered. These findings highlight intracluster diversity in viral attachment proteins and elucidate mechanisms of transcriptional regulation in *A. globiformis* phages.