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Unraveling Uncommon Traits: Annotating Aikyam and Raqqa, Distinct AY Phages

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Bacteriophages are viruses that infect, replicate and lyse bacterial cells. Due to the increasing prevalence of antibiotic resistance, phages are emerging as a promising alternative to traditional antibiotics to combat bacterial infections. Our study aims to gain a deeper understanding of AY phages, which infect *Arthrobacter globiformis* bacteria, by studying the annotated genome of Raqqa and Aikyam bacteriophages. *Arthrobacter globiformis* is a gram-positive bacterium that grows using glycine as a sole energy source. Aikyam and Raqqa genomes have an average of 53000 base pair length, and 62.7% GC content. Their genes were annotated using various computational tools including PECAAN, HHPRED, Starterator, DeepTMHMM, Phamerator, and BLASTp followed by a detailed quality control of the annotations.

In cases of genes with no known function, we used AlphaFold structure predictions to identify structural patterns in the proteins encoded by these genes. Genes that did have a clear function were compared to other AY phages to determine any unique features requiring further elucidation. A gene of note that was discovered was a tRNA-encoding gene identified in the Aikyam and Raqqa phage genomes, which was rarely called in other AY phages, although there is a high degree of similarity in the nucleotide sequence in this region in all AY phages. .

Also notable was a tyrosine integrase gene identified in phage Aikyam responsible for carrying out the recombination between the bacterial and phage genomes required for lysogeny. We have isolated lysogens of both Raqqa and Aikyam, and are in the process of purifying them, confirming they are stable, and testing whether they confer super-infection immunity against themselves, and other *Arthrobacter globiformis* phages we have isolated in the laboratory.
We have also utilized comparative genomics to compare Aikyam and Raqqa to all other AY phages using dot plots. The analysis revealed a high degree of genomic similarity with other AY phages, except minor differences such as the annotation of the tRNA.

In conclusion, our study provides a comprehensive overview through multiple approaches including computational predictions, gene annotations, wet lab experiments, and comparative genomics.