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Tony Li

Using Maximum Likelihood Phylogenetic Trees to Assess Horizontal Gene Transfer in Bacteriophages and Archaeal Viruses

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Bacteriophage evolutionary biology has always been difficult to study because of the recombination and exchanging of genes. Using data from PhagesDB, maximum likelihood phylogenetic trees of the major capsid protein and a non-structural protein, the viral DNA polymerase, were constructed and compared. With multiple well supported clades, one specific clade's movement indicates a possible horizontal gene transfer event while the rest show no sign of gene transfer.

During the annotation of our phage genomes, we found multiple surprising BLAST results matching a dsDNA phage with Haloviruses, which prompted an investigation of gene transfer between the dsDNA bacteriophages and Haloviruses. Their trees, though not as strongly supported, indicated much more movement within families of phages with homologous proteins than would be expected by horizontal gene transfer.