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Host Specificity in Arthrobacter Phages: A Comparative Genomic Study of Minor Tail Proteins in Select Phages Infecting Arthrobacter sp. and Arthrobacter sulfureus

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Bacteriophages play a crucial role in ecosystem dynamics and microbial evolution, yet their genetic determinants of host specificity remain largely unexplored. This study examines the role of minor tail proteins (MTPs) in phage-host interactions, using select phages infecting *Arthrobacter sp.* and *Arthrobacter sulfureus*. Given the role of phage tails in host receptor recognition and attachment, specific MTPs with a potential role in host-specificity are expected to be shared among phages infecting the same host. A comparative genomic analysis was conducted using Phamerator maps, nucleotide dotplots, and phylogenetic evaluation with SplitsTree to evaluate MTP conservation among phages from each host group and the findings indicated that MTPs are not universally conserved across phages infecting the same host. However, select phages infecting *Arthrobacter sp.* exhibited shared MTPs, with a lack of nucleotide similarity outside of the MTP encoding region, suggesting a possible role in host specificity and potential horizontal gene transfer events. Despite notable cases of genomic similarity between phages infecting *Arthrobacter sp.* and *Arthrobacter sulfureus*, no MTPs were shared between host groups, reinforcing the hypothesis that MTPs may contribute to host specificity. These results support the view that while some MTPs may play a role in host recognition in phages, they are not the sole determinants of specificity. This study contributes to the current body of knowledge on phage-host interactions and further investigations, including functional assays and large-scale bioinformatics studies, could further these findings and inform the development of bioengineered phages for therapeutic applications.