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Comparative Genomics of the Tail Region in Cluster AO Phages

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Bacteriophages are viruses that are the subject of growing interest in microbial research due to their ability to infect specific bacteria. The bacteriophage tail is responsible for host detection and interaction. However, some tail proteins require further investigation to determine their potential role in host infection. Studying the host-specificity of *Arthrobacter* bacteriophages may yield potential candidates for biocontrol and other agricultural applications. By exploring the tail region in cluster AO phages, this study aims to build upon current knowledge on the conservation of tail genes among phages infecting different bacterial hosts. Bioinformatic tools such as Phamerator, SplitsTree, Gepard, and Clinker were used to analyze cluster AO phages on whole-genome, amino acid, and nucleotide levels. Within cluster AO, phages have been isolated on two different *Arthrobacter* species: *A. sp.* and *A. globiformis*. Based on bioinformatic analysis alone, no individual tail gene could be identified as responsible for host specificity. Instead, all cluster AO phages from both hosts displayed strong amino acid conservation in tail proteins of interest. Furthermore, *A. sp* phages shared higher nucleotide and amino acid content in the tail region than *A. globiformis* phages. These findings enhance our current knowledge of the AO cluster, and further in vitro analysis of these tail proteins may reveal their specific functions in host infection. Discovering host-specific patterns within and across phage clusters could provide insight into selective mutagenesis to expand the host range of phages and enable broader application of phage therapies.