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Investigating the Genetic Diversity of Arthrobacter Bacteriophages of the Myoviridae Family

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Bacteriophages are highly abundant in the ecosystem. As more phages are added to the diversity of phages in PhagesDB, it is necessary that information is accurate to prevent confusion in future phage research. Phages are classified into three families, *Podoviridae*, *Myoviridae*, and *Siphoviridae*, based on tail morphology determined by electron microscopy and bioinformatically. After identifying *Myoviridae* phages from clusters AO, AR, and FH that were potentially misclassified as *Siphoviridae*, the research question became: Should these *Siphoviridae* phages be reclassified to *Myoviridae*? More broadly, it was asked: how are the *Arthrobacter*-infecting *Myoviridae* phages of clusters AO, AR, FH, and FL genetically related? Answering these questions can further contribute to understanding phage diversity and improve the accuracy of the expanding phage database. In order to investigate the genetic similarities between phages from the selected clusters, annotated genomes and multiple bioinformatic tools were utilized to assess nucleotide and gene content similarity, synteny, and evolutionary relationships. High intercluster nucleotide sequence similarity, synteny and gene content similarity were observed between phages of these clusters. Surprisingly, gene content similarity between clusters FH and AO exceeded the clustering threshold of 35%. These genetic similarities suggest there is a vertical evolutionary relationship between phages of these clusters. Due to the high genetic similarity between these erroneously classified *Siphoviridae* phages and their *Myoviridae* phage counterparts, these phages should be considered for reclassification to *Myoviridae*. Our findings demonstrate the need for peer review in the phage classification process, which will improve access to accurate phage information.