CONSIDER FOR TALK

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Evolutionary and Syntenic Comparison of Tail Proteins in Roary to Other A8 Phages

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Bacteriophages are specific to bacterial host species; however, the molecular mechanism that drives the virus/host specificity remains elusive. The analysis of tail proteins from mycobacterial phages could begin to uncover more details about the relationship between the virus and the host it infects. We tested the hypothesis that variability in amino acid sequences in major and minor tail proteins among phages could potentially reflect the binding site that allows the phage to specifically attach to the surface of the bacterial host. In this study, the synteny variation among phages was also analyzed in particular in those related structural tail proteins in comparison with the rest of the phage genome. The comparison of protein sequences was conducted within cluster A8; which is the sub-cluster where our newly isolated phage belong, Roary. From the alignment and phylogenetic analyses, the level of amino acid differences varied depending on the protein analyzed and it ranged between 0 and 1.3% amino acid differences. These results are discussed within the context of potential bacterial host binding site. From the synteny analyses, very few changes of gene order was documented among most of the structural tail proteins found on half of the genome that had the same transcriptional orientation. However, and very interestingly, the number of gene order changes in the other half of the genome with opposite transcriptional orientation was much higher. Further research is needed to determine if the difference in tail protein sequence detected in this study mirrors the specific area of attachment of the virus on the bacterial host. This will help the field of phage biology to understand the role of tail proteins on modulating the specificity of virus/host interactions.