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Mycobacteriophage Morphology as a Diagnostic for Cluster Assignment

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Abstract
Phages are viral bodies that infect bacterial hosts, and have shown promising applications as alternatives to antibiotics for the treatment of bacterial infections. This project examines the morphology of siphoviridae mycobacteriophage, which have long, flexible, non-contractile tails as well as the characteristic head, called a capsid. Using electron microscopy photos of sequenced phages, tail length and capsid diameter were measured and compared to further characterize morphological relationships between genetically distinct phages. The data presented has the potential to work as a diagnostic tool to classify unsequenced phages to genetically similar groupings, called clusters.

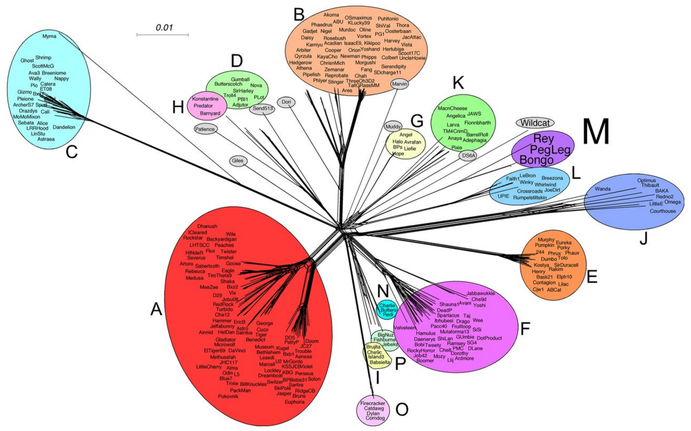

Figure 1. An evolutionary schematic of phage clusters (Pope et al.)

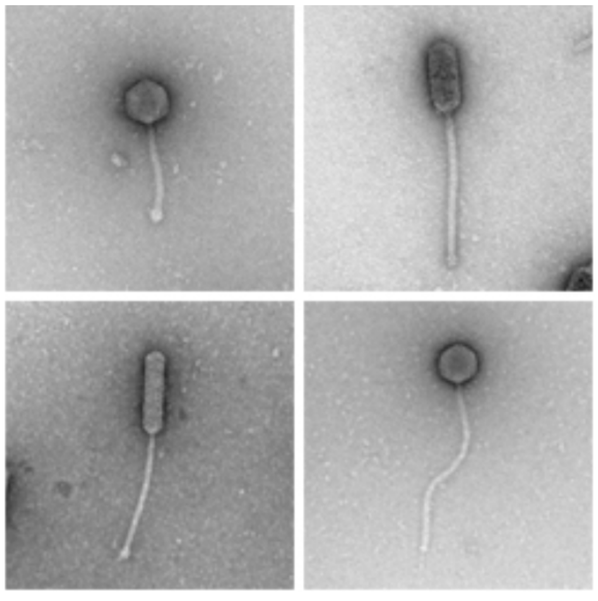

Figure 2. The diverse structures of siphoviridae phages (phagesdb.org)

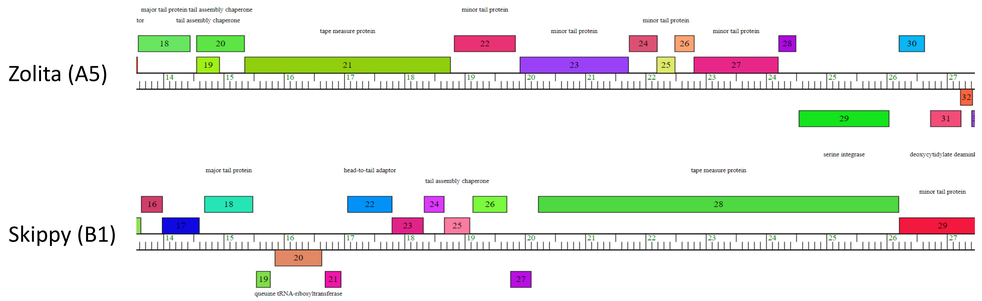

Figure 5. Tail length is directly proportional to the tape measure gene.

Methods

Microscopy photos were sourced from phagesdb.org, a phage database, and select images were sourced from Dr. Joe DiGiorgis of the Providence College Department of Biology. Microscopy photos were measured using ImageJ. Tail length was measured from the base of the tail to the visible terminus, with straight tails selected over curved ones for more accurate measurements. Capsid diameter was measured from the base of the tail and through the capsid center to the opposite end. An average of measurements was taken in samples with more than one high-quality specimen.

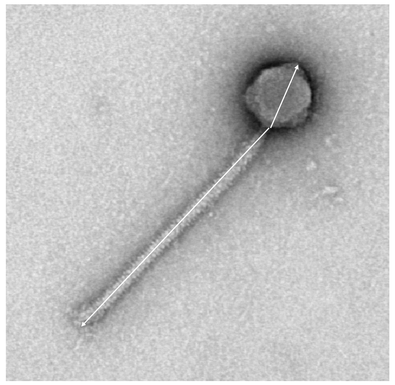

Figure 3. Method for measuring.

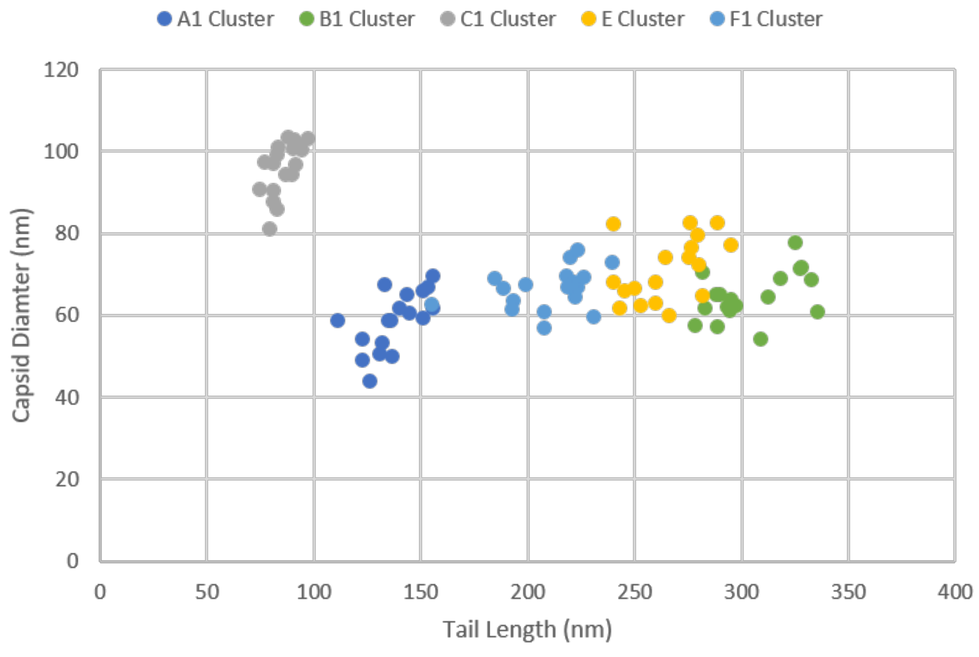

Figure 4. Comparing capsid diameter and tail length of A1,B1, C1, E, and F1 cluster phages reveals distinct groupings.

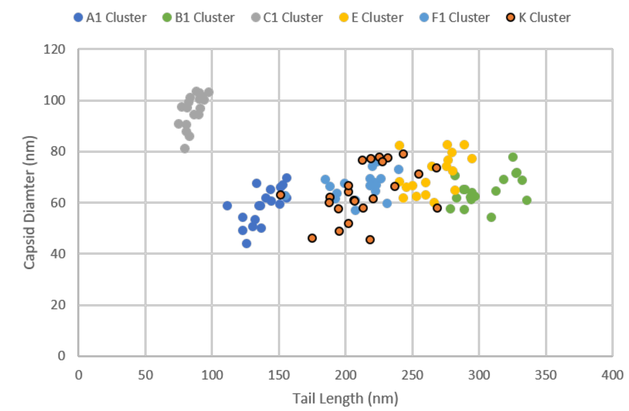

Figure 5. K Cluster phages do not show a distinct grouping in relation to other phage clusters.

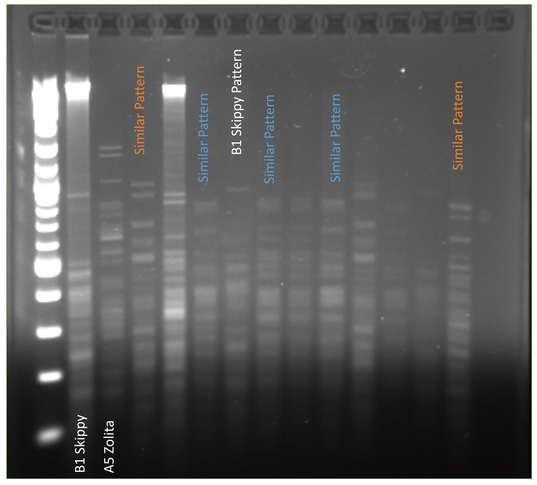

Figure 6. A DNA restriction digest gel demonstrates another method of classifying or grouping unsequened phages.

Conclusion

Clusters A1, B1, C1, E, and F1 have distinct structural characteristics. While this trend does not hold true for all mycobacteriophage clusters, such as K cluster phages, the distinct groupings shown here through the comparison of capsid diameter and tail length can be used as a diagnostic tool alongside PCR or a DNA restriction digest to classify unsequenced phages.

References

Pope, W.H., *et al*. (2014) Cluster M mycobacteriophages Bongo, Pegleg, and Rey with unusually large repertoires of tRNA isotypes *J Virol* **88(5)**, 2461-2480
The Actinobacteriophage database (phagesdb.org)