

Inside the Human Microbiome: A Microcosm For Bacteriophage Evolution

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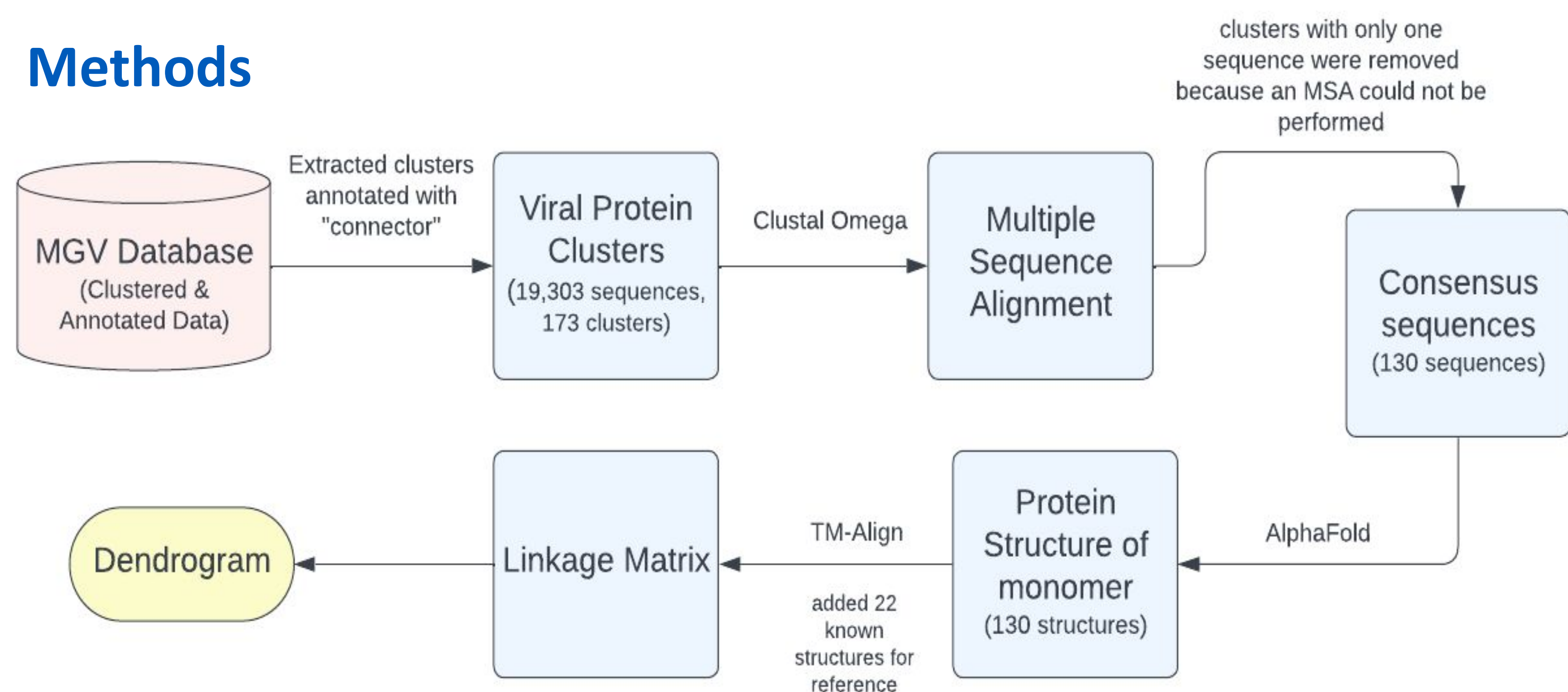
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Introduction

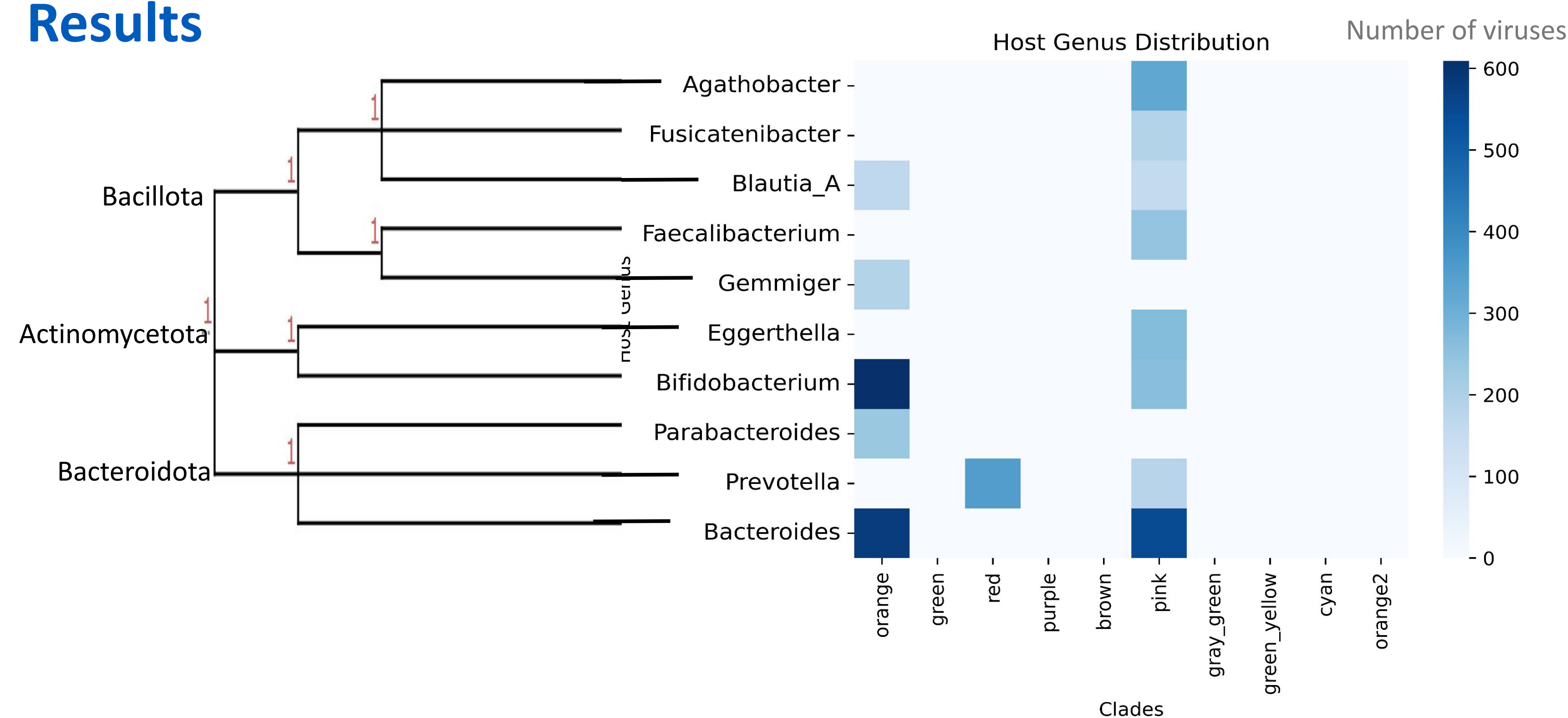
- The human microbiome is linked to many aspects of human health ¹
- In addition to the bacteria in the microbiome, there is a rich ecosystem of roughly 200,000 bacteriophages living in tandem with these bacteria and their are not yet well understood ²
- Because viruses evolve so quickly, deriving their phylogenetic tree based on sequence can be difficult BUT structure is known to be more conserved than sequence, and so we propose using structure to determine bacteriophage evolution ³

Goal: Determine evolutionary relationships of phages in the microbiome based on structural similarities of the connector protein

Methods

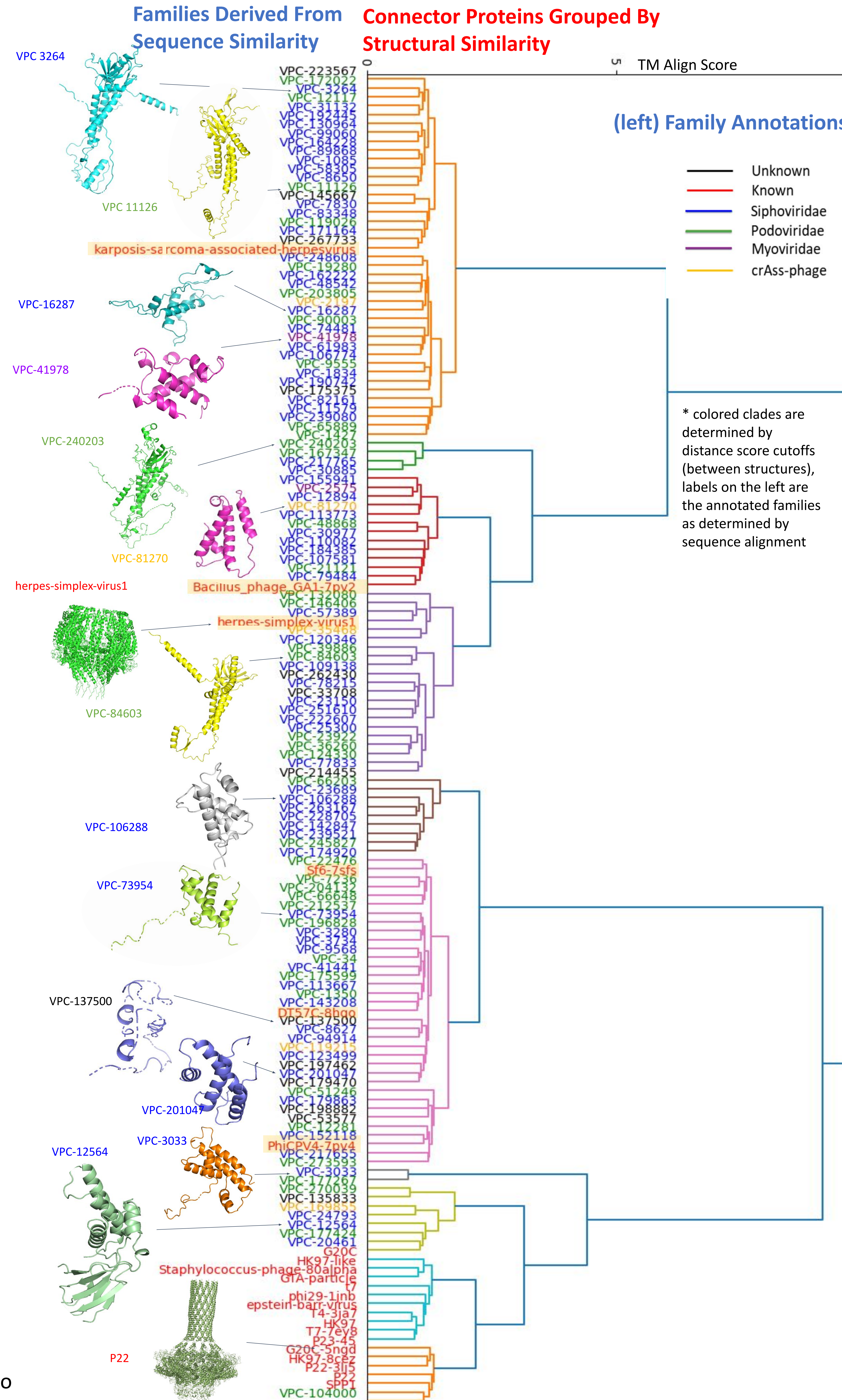
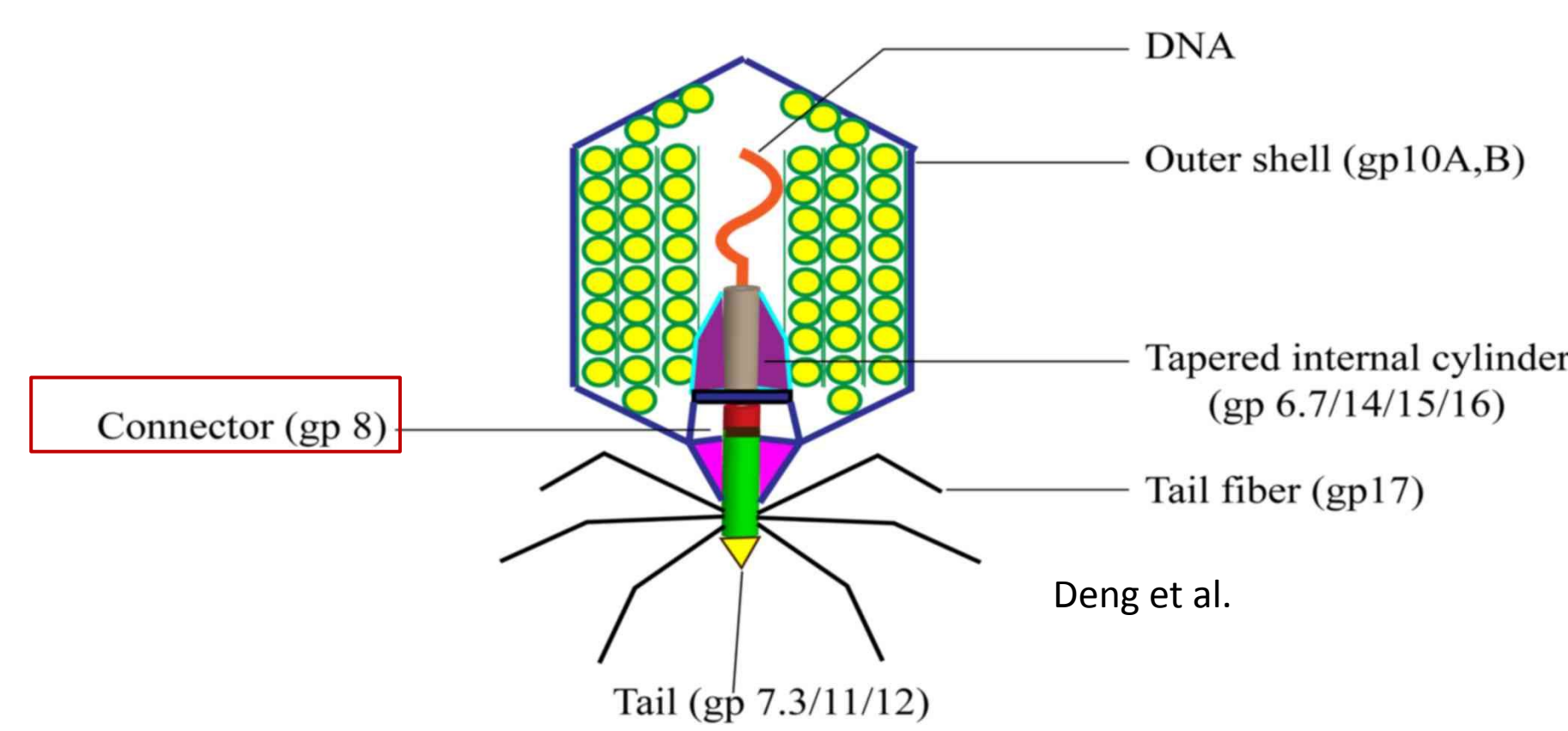


Results

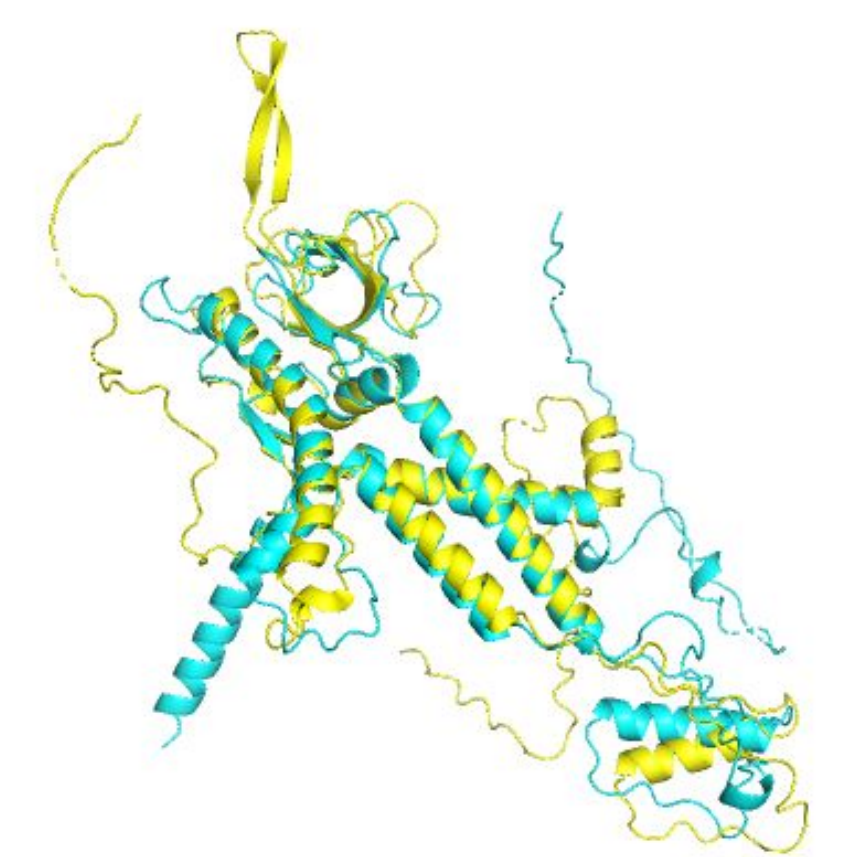


- Clades (x axis) correspond to clades shown on tree (right)
- Hosts (y axis) are labeled with their phylogenetic tree
 - labels (Bacillota, Actinomycetota, and Bacteroidota) are their phylum

Results: While we are not able to make any conclusive findings, we are seeing a connection between host and connector protein structure. And so, we believe that further studies using structural phylogenetic trees and host annotation could allow us to see what specific structures are co-evolving in phages due to selection by host defenses.



Data Analysis



VPC 3264(cyan, orange clade) aligned with VPC 11126 (yellow, orange clade)

- RMSD = 1.389



VPC 3264 (cyan, orange clade) aligned with VPC 73954 (lime, pink clade)

- RMSD = 19.404

Future Directions

- Local Similarities:
 - finds more conserved residues which may be more informative of evolutionary relationships as conservation often implies function and would not be influenced as much by genetic drift
 - An interesting software package is [DALI](#) which was not used for various reasons
- Include more structures
 - More data is always good.
- Model the complex
 - more biologically accurate

Acknowledgements

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