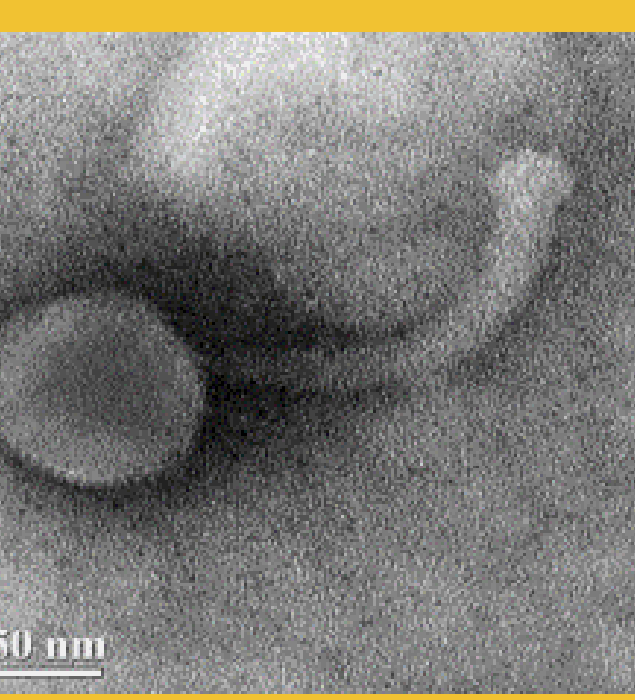


A Comparative Study of Bacillus Phage Phireball's Genomics to Other *Bacillus* Phage Genomes

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Goal:

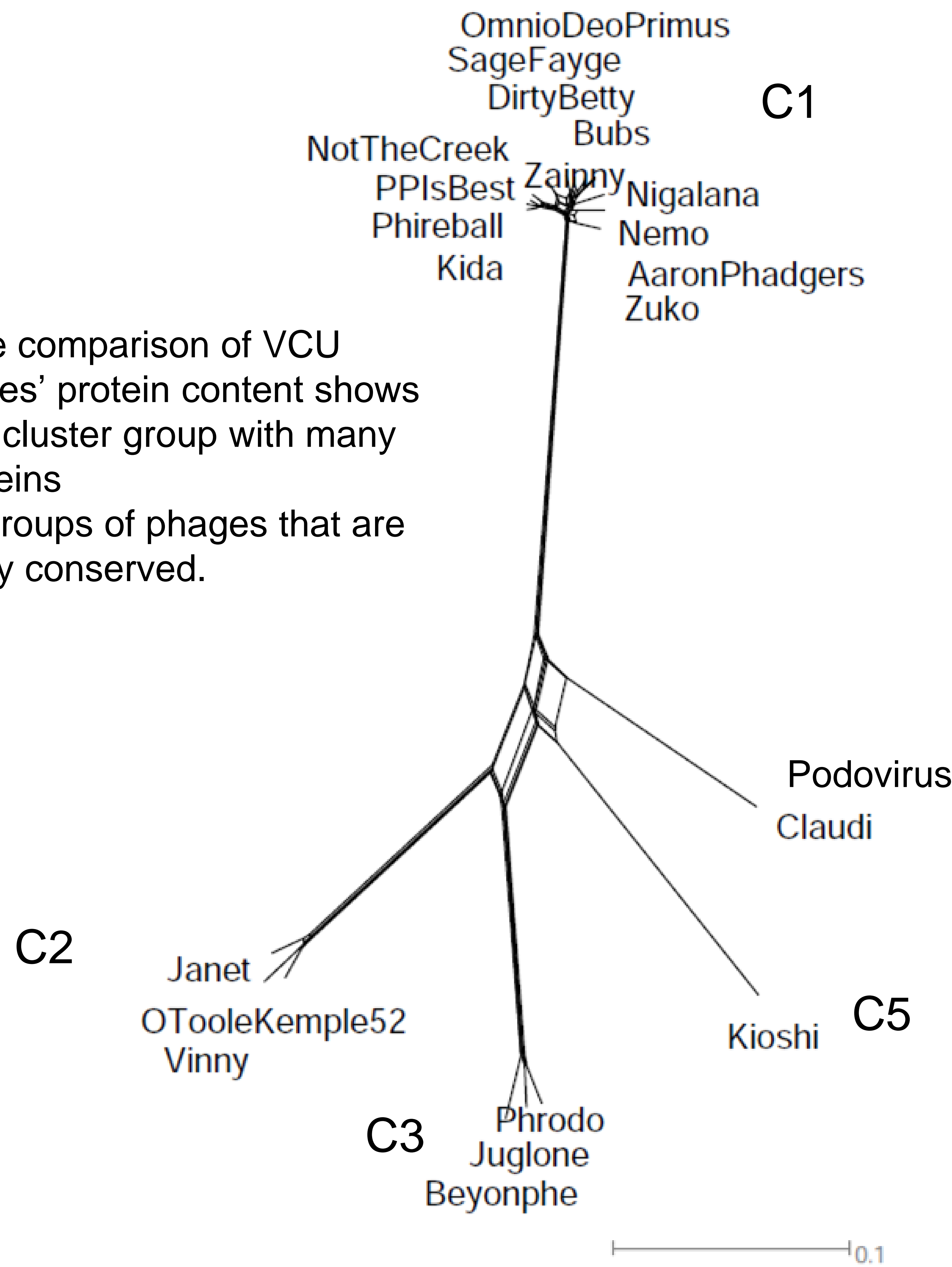
Our goal over the past semester has been to understand and contribute to the phage community by discovering and characterizing bacteriophages. We seek to diversify the tools researchers can use to find treatments of illness that antibiotics don't affect by submitting our phage to databases in anticipation that our phage will hold unique characteristics that will help researchers understand the world of bacterium and how to use viruses as a treatment.

Bacillus Phage Phireball was discovered and sequenced in Fall 2018. Spring 2019 VCU Phage Lab students:

- Annotated each gene in the genome
- Completed comparative genomics projects exploring genome features.

Genome wide comparison of VCU Bacillus phages' protein content shows

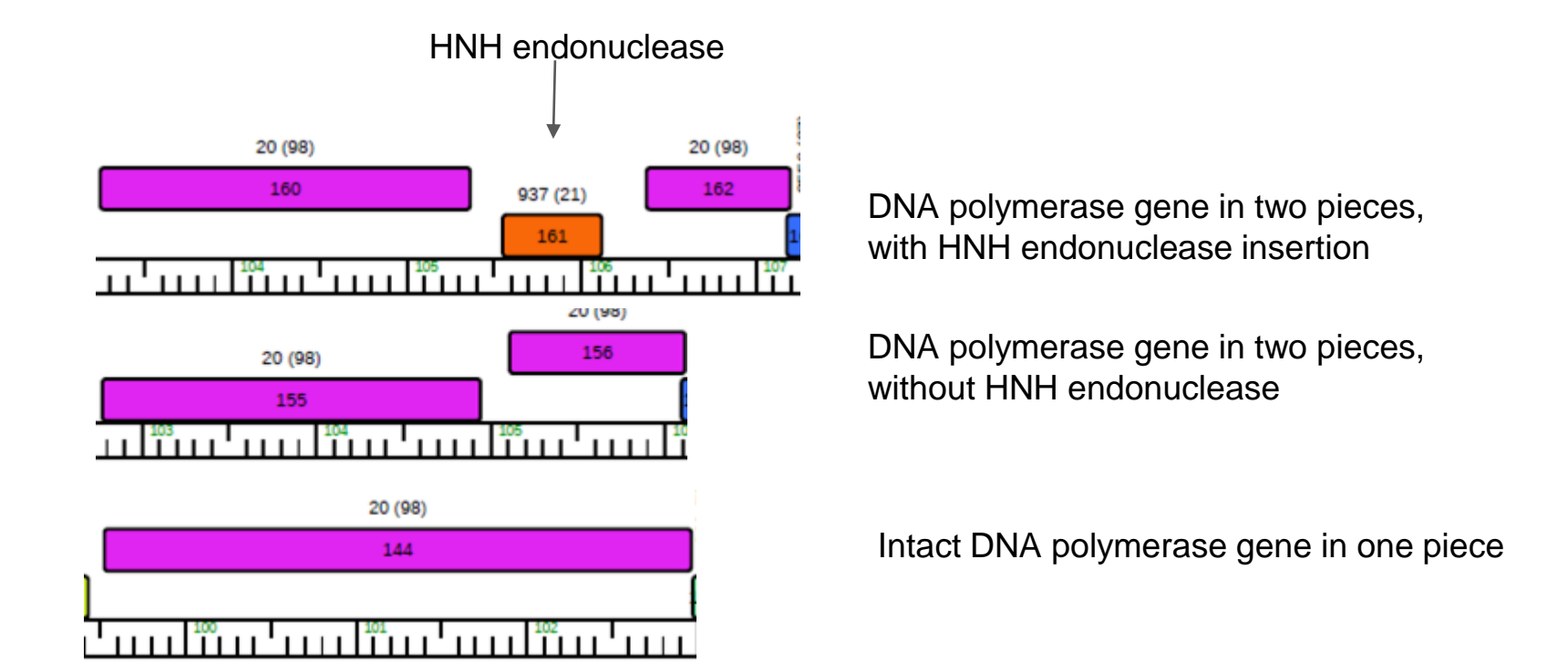
- a large C1 cluster group with many shared proteins
- four other groups of phages that are not as highly conserved.



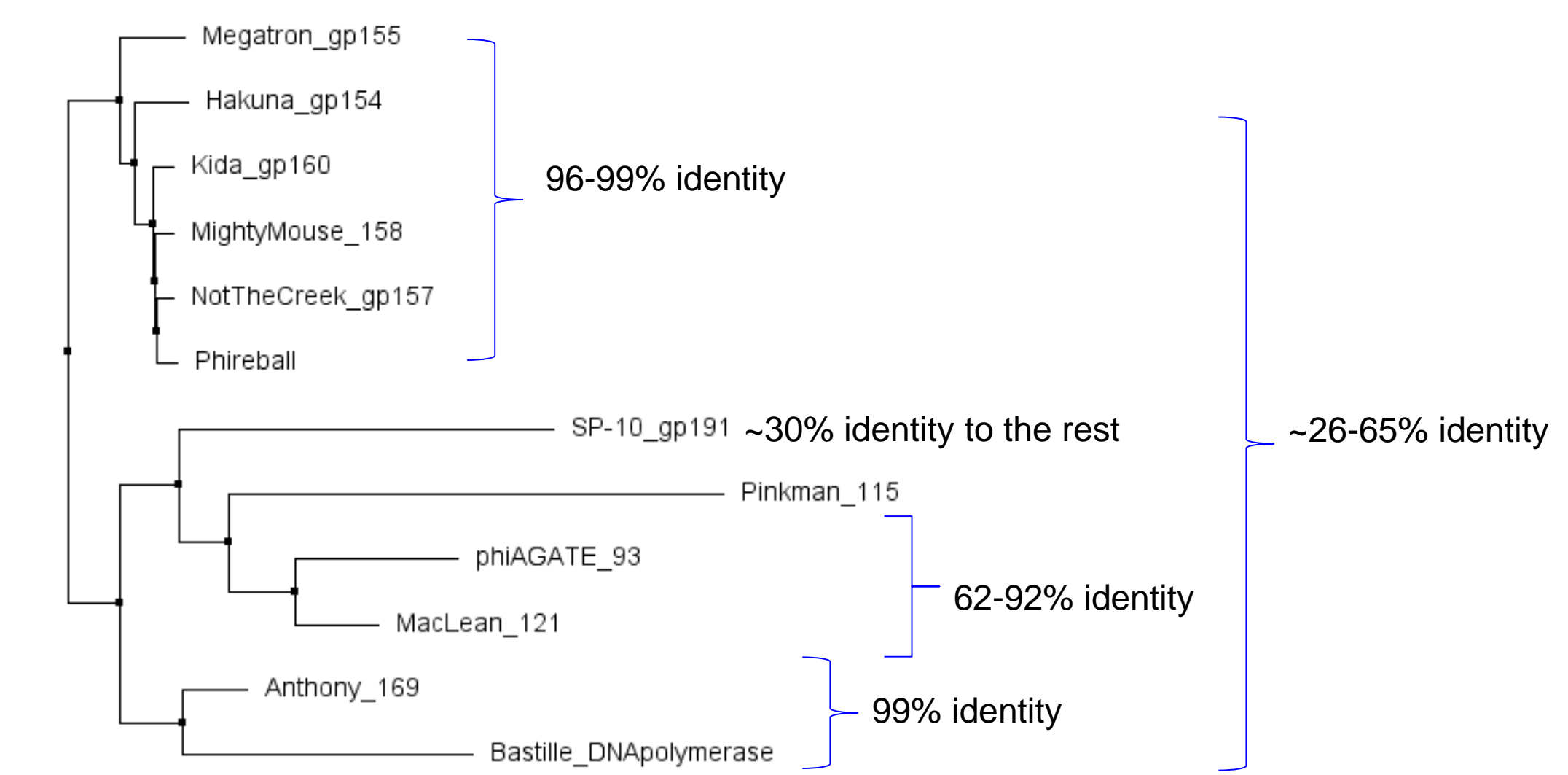
Comparison of Genome Characteristics of VCU Phages against Phireball					
Cluster	Genome Length (bps)	ORF	G/C Content (%)	% Identity	Length Of Terminal Repeats
Phireball	173720	293	38.7	100	2592
C1	162060	301	38.71	94.04	2749
C2	161792	298	38	81	2511
C3	164070	291	37.7	78.47	2367
C5	165676	275	0.395	79.72	7604
Podovirus	26504	46	30.3	85.71	N/A

Seeing Horizontal Gene Transfer Through Phylogenetic Trees

A unique mechanism of horizontal gene transfer is observed in some Bacillus phages containing an HNH endonuclease that inserts itself into the gene for a DNA polymerase.

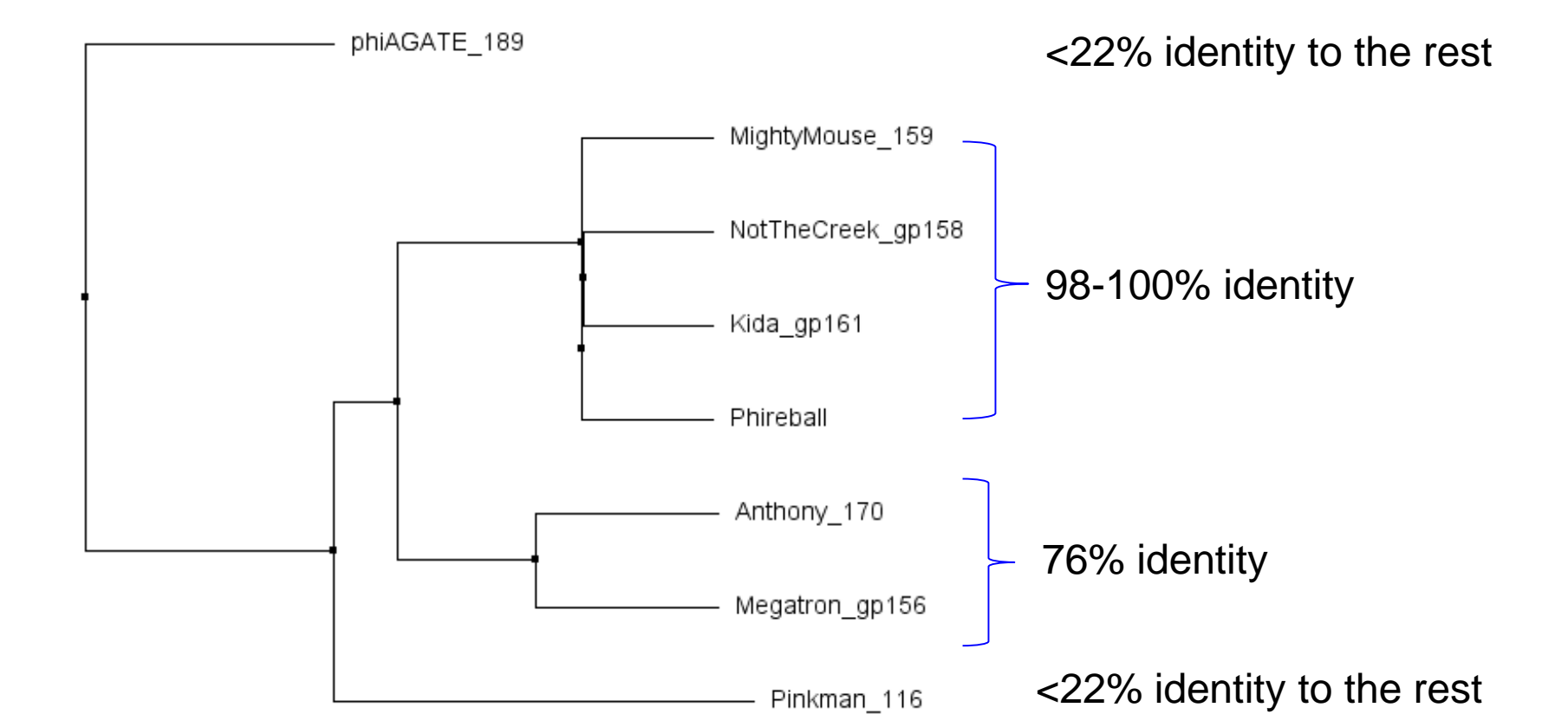


DNA Polymerase



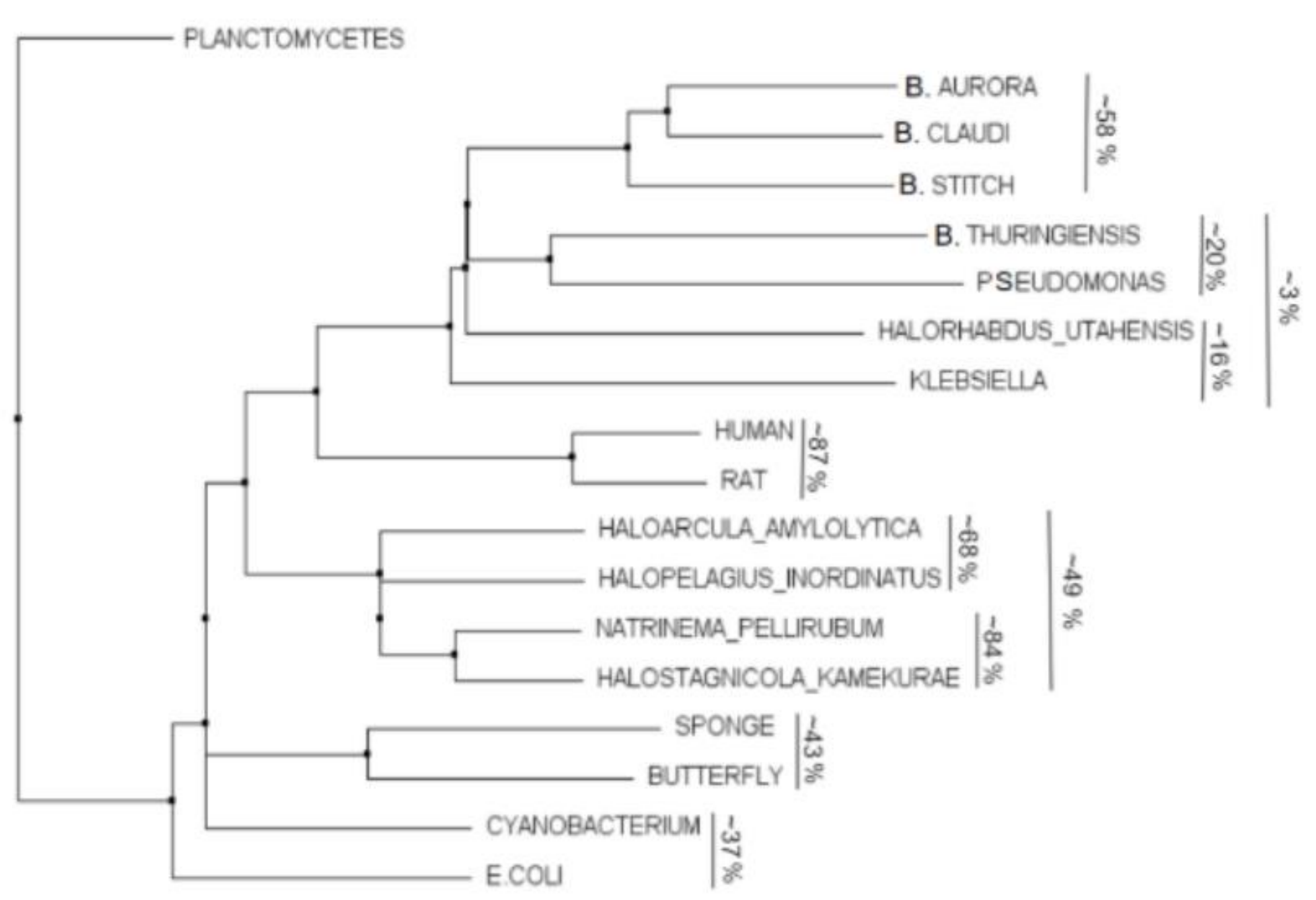
- DNA polymerase proteins are predicted to have the same function, and can vary in sequence between groups.
- Bastille and SP-10 DNA Polymerase proteins are not interrupted by HNH Endonuclease

HNH Endonuclease



- HNH Endonuclease protein sequences can be highly conserved, along with their DNA Polymerase 'host'.
- Some HNH Endonuclease sequences have low homology to the group.
- PhiAgate is an outlier in terms of sequence conservation

Percent Identity of Glutaredoxin Across Various Organisms



Some proteins are highly conserved across domains of life. Glutaredoxin homologs are present in bacteria, viruses, eukaryotes and archae.



Detailed Cluster Tables

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