CONSIDER FOR TALK

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It's About Damn Time to make a Phylogenetic Tree for the Lizzo Phage

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Bacteriophage are known to infect and kill bacteria that can harbor diseases in humans. They are split into different groups depending on DNA similarity and the bacteria hosts they are found on. Phages are split even further into different subgroups based on higher percentages of DNA similarity. Subgroup CS2 infects the bacterium Gordonia Terrae, which causes pulmonary disease, skin infections,etc. The lack of information in the subgroup led to our interest in annotating the phage Lizzo. Throughout our research, we want to find out if the similarities between Lizzo and other phages in the CS2 subgroup can help find treatments for these conditions. A phylogenetic tree was the best approach to test this hypothesis as it shows the evolutionary process in organisms while also showing which species are most closely related to one another. Using fasta files, clustal omega, and phagesdb.org, we were able to create a phylogenetic tree. We found that Flakey was most closely related to Lizzo. To support the phylogenetic tree further, Phamerator was used to compare the closely related phages found by the tree to see how similar each were. By adding to the database of phage knowledge, we hope to aid in medical advancement in relation to treating various diseases correlated with Gordonia Terrae.