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2022 SEA Symposium Abstract

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Exploring the Essence of Phage Malisha

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Our research combines the genomic characterization and host range testing of the phage Malisha, a novel bacteriophage of the DN cluster, discovered in the fall of 2021 by one of our teammates. We aim to test if Malisha can infect different species of the actinobacterium *Gordonia*. We plan to present the isolation and characterization of phage Malisha as well as our findings regarding Malisha’s gene functions and the host range experiments we are currently performing. So far, we have used many programs such as Starterator, HHpred, and Phamerator to learn more about the specific genes in this phage’s genome. Our group was tasked with characterizing a string of genes located in the left arm and in the middle of the genome and we have seen these Malisha genes are either very supportive of a specific protein function or they are very vague regarding protein function or evidence of a gene. This could be due to the lack of research on the DN cluster or maybe even new processes specific to phage Malisha. Moving forward in the semester, our group plans to explore the genes with vague protein function designation. We plan on using our participation in the symposium to find other researchers similarly vague genomes to gain a better understanding. We hope that our findings with Malisha’s host range will help provide more information about the overall diversity of phages and their evolution and throughout the process, maybe discover something the SEA-PHAGES community hasn’t seen before!