CONSIDER FOR TALK

2021 SEA Symposium Abstract

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Isolation and Characterization of Two (Semi-)Novel Mycobacteriophages, Calamitous and MadMen

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In the fall semester of 2020, the William and Mary SEAPHAGES program conducted an in-person phage discovery class with 25 freshmen eager to conduct authentic research. Using *Mycobacteria smegmatis* as the host, each and every student got their own phage and was able to carry it through to purification, DNA isolation, and electron microscopy, and not a single student (or instructor) got SARS-CoV-2! We considered this feat to be one of the greatest successes of our 13 years in the SEAPHAGES consortium. At the end of fall semester, we held our masked, socially-distanced Phall PhagePhest, with take-away goodie bags instead of the usual feast, to discuss and democratically vote on which phages should be selected for sequencing. Based on some intriguing characteristics observed in plaque morphology and in the electron micrographs, MadMen and Calamitous were chosen for further analysis. MadMen has 57,759 base pairs with 115 genes and is a temperate phage in the F1 subcluster. Calamitous has 67,371 base pairs and 93 genes and is a lytic phage in the B2 subcluster. Both are siphoviridae. We are currently annotating both phages, with special attention to potential intergenic regions, and conducting comparative genomics of the F1 and B2 subclusters.