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2023 SEA Symposium Abstract

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Wybie with the Phages: A characterization of Arthrobacteriophage Wyborn

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As bacteria are becoming more resistant to antimicrobials, phage therapy has provided an alternative to antibiotics. Bacteriophage are viruses that infect and kill bacterial cells. Our class, BIOL123 Biological Investigations I, is a part of a nationwide research program called SEA-PHAGES that investigates bacteriophage discovered from soil and water samples. During the 2022-2023 school year at Virginia State University, the class went through the processes of collecting environmental samples, then isolating, purifying, amplifying, and extracting bacteriophage using the SEA-PHAGES “Phage Discovery Guide.” After these processes, the class sequenced and annotated two bacteriophages including the phage Wyborn. Wyborn produces small plaques that are clear with a cloudy halo around them when plated on its host, *Arthrobacter globiformis*. Based on its DNA sequence, Wyborn was classified in the lytic subcluster AO2, along with 15 other phage. However, Wyborn is truly unique, as it is the first Myoviridae morphotype discovered by Virginia State University students. Additionally, it has 3 possible orphams, which are genes that no other annotated genome has. The Wyborn genome has 49,985 base pairs with a GC content of 63.7%. Wyborn has been analyzed in Phamerator and BLAST analyses and is currently being annotated using PECAAN as the primary tool to access PhagesDB, NCBI BLAST, HHPRED, and Conserved Domain Database data. Early annotation drafts using these tools suggest that Wyborn has approximately 79 genes. Further analysis will be performed to compare Wyborn with other sequenced phage to determine how phage like Wyborn might be useful in phage therapy studies.