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2021 SEA Symposium Abstract

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Annotation and Analysis of Two Cluster AU1 Phage, CastorTray and DevitoJr

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Students at The Ohio State University have been participating in the course-based undergraduate research experience, SEA-PHAGES, since 2011. To date, they have isolated 180 phages using the hosts *Mycobacterium smegmatis*, *Arthrobacter sp.* and *Gordonia terrae*. 55 genomes have been sequenced and 47 have been annotated and uploaded to GeneBank. This semester, students have annotated two phage genomes belonging to Cluster AU1 which currently has 16 members, 10 of which were isolated at OSU. The genomes of CastorTray and DevitoJr are 58,377bp and 58,044bp, respectively compared to the cluster average of 58,137bp. CastorTray has 94 predicted open reading frames to DevitoJr’s 89 and both have a GC content of 50.0%. While working on the annotations, students recognized several features that they wished to investigate further, including potential promoters and gaps with little to no coding potential. Since checking for transmembrane domains is a relatively new addition to the annotation protocol, students decided to look through the older AU1 genomes to see if any potential membrane proteins were missed during the original analysis.