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2023 SEA Symposium Abstract

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Microbacterium Cluster EE Phages Are Highly Conserved with Widespread Geographic Distribution

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During Chatham University's first year participating in the SEA-PHAGES program, 107 students worked to isolate, annotate, and evaluate different phages discovered around Chatham’s campus. The phages were all isolated using the same host bacterium, *Microbacterium foliorum*, using the enrichment technique with room temperature incuabtions. Thirty-eight new, unique phages were collected. Of these, nine were sequenced: Chatham, Danimal, Dooby, Douggie, Goobery, Horacetta, LionelHutz, Picnic, and Rhogar, All nine sequenced phages are members of the EE cluster, with an average genome length of 17,418. These phages are closely related, with percent identity ranging from 99% to 95%. The phages can be separated into two groups based on differences found in gene 12 (tape measure protein) and 13 (minor tail protein). Interestingly, some of the Chatham phages, Chatham and Goobery, are more closely related to phages Aztec and TeddyBoy (isolated in 2019 and 2018 by Gonzaga University and Virginia State University, respectively) than to each other, suggesting that our phages are independent isolates, and that the genome sequences of EE phages as a whole are highly conserved across time and geographic distribution.