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2022 SEA Symposium Abstract

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Annotation saturation: differences among phage genomes that are very similar to each other

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There is great diversity among bacteriophages, even those that infect a single host. The goal of SEA-PHAGES is to explore that diversity by culturing large numbers of bacteriophages and sequencing and annotating their genomes. However, the more phages we acquire, the more likely we are to find ones that are not substantively different from ones that have already been encountered. In the Fall of 2021, students in the Miami University Bacteriophage Biology class (MBI 223) sought bacteriophages that infect the host Microbacterium foliorum strain NRRL B-24224. DNA extracted from 12 phages was subjected to restriction digestion, and every sample had patterns consistent with cluster EE, which include the smallest actinobacteriophages, with genome sizes of only 16.9-17.5 kbp. Two of them, EdElric and KyriosFaba were selected for genome sequencing. Though not identical, both genomes had sizes of 17,362 bp, placing them within a subgroup of cluster EE phages, including 17 others at the time of abstract submission, whose genomes are in the narrow window of 17,360-17,368 bp, and all of which have nucleotide identities greater than 99%. This information suggests that these 19 bacteriophages, isolated from various locations spread all over the northern half of the 48 contiguous states of the US, are members of a single, highly successful species, harboring allelic variation, that might include other cluster EE phages as well. The students annotated the genomes of EdElric and KyriosFaba. To understand the nature of the differences among individual members of this group of 19 bacteriophages, the students used BioEdit to identify the sequence differences and to determine whether they were in coding regions or non-coding regions, and if the former, whether they resulted in synonymous or non-synonymous codons.