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2022 SEA Symposium Abstract

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Discovery of 42 novel Microbacterium phages

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This year students at Drexel University discovered 42 novel bacteriophages using Microbacterium foliorum NRRL B-24224 as a host. These phages were isolated and purified from soil samples collected largely near Drexel’s campus in Philadelphia, but also included samples from rural Pennsylvania and New Jersey. Five of these novel Microbacterium phages were sequenced by the Pittsburgh Bacteriophage Institute: two from the EA1 subcluster (Phireproof and PhredFlintston), two from the EC cluster (CrazyRich and Phorgeous), and one from the EE cluster (BinkBonk). All five produced lytic plaques and are expected to exhibit siphoviridae morphology. Bioinformatics analysis of these five genomes revealed high similarity to previously characterized phages in their respective clusters, with no distinguishing features identified to-date. Each of our four student sections annotated two genomes: one unique to their section, and one that was subsequently annotated by all four sections. BinkBonk was annotated by all four sections and was the object of our second annual “Phage Cup” competition, where each section competes with one another to produce the most accurate annotation. Students are guided and mentored through the bioinformatics process for their section’s first genome, after which they apply the skills they have practiced, and self-organize to direct their section’s efforts during the Phage Cup. Student demonstrated a remarkable increase in both efficiency and accuracy in genome annotating during the Phage Cup, due, perhaps, to their practice, motivation, and self-organized quality-control activities. Students have now submitted research proposals for their Spring projects to further characterize the five sequenced genomes discovered this year. These projects will test the impact of a wide range of experimental factors on phage life cycle and lytic efficiency. These factors include various antibiotics, UV light, pH, pressure, temperature, nutrient composition, salinity, bacterial cell wall precursors, toxins, mutagens, tail length, host density, fertilizer components, directed evolution, location, organic origins, and ethanol. Our students’ Spring projects will generate significant insight into the nature and behavior of the phages we discovered this year, and perhaps—due to the high degree of genome similarity—other EA1, EC, and EE cluster phages.