DO NOT CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

Virginia State University

Petersburg VA

Corresponding Faculty Member: Andrea (Andy) Beyer (abeyer@rbc.edu)



Sarah M Peebles

Discovery and Comparison of E Cluster Phages Infecting Microbacterium foliorum

Sarah M Peebles, Kathryn H Shows, Brian L Sayre, Andrea R Beyer

Bacteriophage are the most abundant microbes on earth, at an estimated population of 1031 particles. However, their genomes are grossly underrepresented in sequence databases, and a large portion of their genes are of unknown function. In order to gain a better understanding of phage diversity, novel viruses were isolated and characterized from soil using an Actinobacter host. *Microbacterium foliorum* is a Gram-positive, rod-shaped bacterium commonly found in soil and grass. Multiple bacteriophage were isolated from samples originating at various locations on the campus of Virginia State University and from additional sites in Virginia and North Carolina. Phage were isolated using both direct and enriched procedures, resulting in the discovery of 10 phage which were further characterized by transmission electron microscopy. Eight samples were successfully imaged; 5 were found to be the siphoviridae morphology, and 3 were podoviridae. Of these, DNA was extracted from phage TeddyBoy, Owens, and SansAfet, and submitted for sequencing. The genomes were subsequently annotated using PECAAN, DNA Master, HHPred, Phamerator, and Starterator. Though TeddyBoy and Owens were found in distinct locations in Virginia, they are both in the same phage cluster (EE), share similar genome sizes, and have a significant amount of overall sequence homology and shared synteny to one another. They also bore a strong resemblance to EE draft phage BurtonThePup, isolated from Maryland. Interestingly, TeddyBoy and SansAfet, which were isolated from different areas on the same farm in Gloucester, VA, were found to be very distinct from one another. SansAfet was placed in cluster EB, and it possessed a much larger and more complex genome, with multiple genes of unknown function. The results of this study underline the remarkable diversity of phage within geographically similar locations, as well as the intriguing similarities of phage isolated from spatially distant sites.