CONSIDER FOR TALK

2022 SEA Symposium Abstract

Neumann University

Aston PA

Corresponding Faculty Member: Matthew Mastropaolo (mastropm@neumann.edu)

Host Range Experiments and In silico Analysis of Possible DNA Modification Enzymes on Sequenced Microbacterium Phage at Neumann University

Davia Campbell, Kho Tuang, Patricia Fallest-Strobl, Matthew D Mastropaolo

Bacteriophages are abundant life on the planet that have a very complex life cycle and genetic structure. Our main questions are 1) Why do some bacteriophages have a broad range of host species in the same genus, while others have a narrower host range in the same genus? and 2) What types of DNA modification enzymes are being utilized to protect phage DNA from host restriction systems? Senior students at Neumann University worked on different aspects of phage host ranges and DNA Modifications to gain a better understanding of how these bacteriophages infect different species of organisms. Data has shown that several of our bacteriophage infect multiple hosts within the *Microbacterium* genus, one isolate in particular from cluster EA9 infects 6 of 8 hosts tested, except at a lower infectivity rate. Students are further investigating this by examining similarities and differences between minor tail proteins found in different clusters of bacteriophage: EA9, EB, EC, EE, EF, EK1, and EK2. In addition, students are investigating the effects of DNA modification enzymes on digestion of phage DNA using HaeIII, NspI, and SacII by comparing DNA gel electrophoresis profiles from agarose gels of our sequenced phages with that of a virtual digested DNA samples using REBites.