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10th Annual SEA Symposium Abstract

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Phighting bacteria entails: Comparative analysis of phage genomes and proteins

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Due to the alarming rates of bacterial antibiotic resistance, the field of phage therapy has recently garnered increased attention. The applications of this therapy are numerous and varied from dentistry all the way to agriculture. Bacteria and their phages have coevolved for so long that they respond quickly to adaptations, giving phage therapy a huge advantage over traditional “fixed” antibiotics. We used comparative genomics to better understand a collection of phage genomes and the whole genome as well as individual protein level.   
  
As part of the 2018 VCU Phage lab, students annotated the genomes of four bacteriophages, Kamfam, ALPS, OmnioDeoPrimus (ODP) and Kioshi. The phages were found using Bacillus thuringiensis bacteria. These phages belong to the family myoviridae, which are characterized by double-stranded DNA and a long contractile tail. The genomes of three of the phages were very similar in length, averaging around 161800 bp with terminal repeats between 2000 and 3000 bp. ODP and ALPS have 294 and 291 open reading frames, respectively, while Kamfam has 284 along with 7 tRNAs. In contrast, Kioshi is 165,676 bp long, has 260 open reading frames and 22 tRNAs. All four phages had a GC content of 38%. In the lab, we used bioinformatics tools to further analyze these phages and compare them to larger databases of known protein functions, such as Blastp, HHpred, and PDB. These databases, paired with Genemark predictions, allowed us to create a complete annotation of the phages in DNA Master. Subsequently, a more in depth analysis of the phages was performed using comparative genomics tools for phylogeny, protein content comparisons, and dot plot comparison. This poster will also highlight projects examining the conservation of capsid protein and horizontal gene transfer of a family of intron encoded endonucleases that helped us understand more about inheritance of genes. Ultimately, these approaches were employed to gain a better understanding of the evolutionary similarities and differences between phages that infect Bacillus.