DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

University of Maryland, Baltimore County

Baltimore MD

Corresponding Faculty Member: Steve Caruso (scaruso@umbc.edu)



Eni Adesola



Beryl Fuamazeh



Jariatu Kargbo



Dania Mahmood



Emmanuel O Okusanya



Jeshuwin D Prabakaran

Genomic and Comparative Analysis of Bacteriophage Riptide (Subcluster BE1) Highlights Iron-associated Proteins

Eni Adesola, Beryl Fuamazeh, Jariatu Kargbo, Dania Mahmood, Emmanuel O Okusanya, Jeshuwin D Prabakaran, Elana L Frazier, Steven M Caruso

*Streptomyces* is a genus of gram-positive bacteria that plays a significant role in the production of natural antibiotics. The mechanism of infection of host bacteria by many bacteriophages is known to occur by phages injecting their DNA into the host bacterium through their tails. The lytic bacteriophage Riptide is a siphovirus from subcluster BE1, isolated using the bacteria *Streptomyces mirabilis* obtained from a soil sample in Odenton, MD in 2024 by researchers at the University of Maryland, Baltimore County. Its 132,142 bp genome, featuring 10,690 bp direct terminal repeats and a GC content of 49.6%, was sequenced using Illumina technology at the Pittsburgh Bacteriophage Institute. Genomic annotation of Riptide identified 237 putative protein coding genes that encode two gene products that directly interact with iron: gene product 31 and 40. Gene product 31 is a DNA-binding protein with a defined iron-binding motif, suggesting that iron availability may regulate host interactions or influence genome injection efficiency. Gene product 40 is a ribonucleotide reductase—a well‐characterized enzyme that typically requires an iron center for the generation of a tyrosyl radical necessary for the reduction of ribonucleotides. Notably, ribonucleotide reductases are critical enzymes that allow phages to synthesize deoxyribonucleotides independently of host limitations, particularly under iron‐restricted conditions. Together, these findings not only underscore the dependence of phage Riptide on iron for essential enzymatic activities and structural stability, but also align with established phage strategies, such as the use of iron‐dependent enzymes to overcome host resource constraints. Discovery of iron‐utilizing proteins in Riptide supports the view that iron metabolism is integral to the replication and infection cycles of lytic phages.