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2021 SEA Symposium Abstract

University of Colorado Boulder

Boulder CO

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An Entomopathogenic Bacteria-Like Insecticidal Toxin With ADP-Ribosyltransferase Activity Characterized In A2 Mycobacteriophage BengiVuitton

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Bacteriophage are viruses that infect bacteria and are now, more than ever, widely studied due to their potential to be used therapeutically against the increasing threat of antibiotic resistance bacteria (ARB). While all bacteriophages can cycle through the lytic life cycle, infecting, replicating, and lysing out of cells, other bacteriophages can choose an alternative lifecycle. Temperate bacteriophages can immediately integrate their DNA into a host’s chromosome, becoming a prophage. Excising out of the host chromosome and entering the lytic life cycle allows for potential recombination and horizontal gene transfer between bacteriophage and bacterial hosts. Current research suggests that both gene recombination and horizontal gene transfer have contributed to various evolutionary differences between organisms’ genomes. Entomopathogenic bacteria like Bacillus thuringiensis encode insecticidal Cry proteins most commonly referred to as VIP1, VIP2, and VIP3. Recent genome analysis revealed various A15 and A2 cluster mycobacteriophages like BengiVuitton, known for infecting Mycobacteria smegmatis (M. smeg), encode a VIP2-like toxin with ADP-ribosyltransferase activity, commonly found in various pathogenic bacteria. This gene is highly conserved among the A2 sub-cluster to which BengiVuitton belongs and warrants further investigation into the acquisition of this gene and the potential evolutionary relationship between AT mycobacteriophage and Bacillus thuringiensis.