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8th Annual SEA-PHAGES Symposium Abstract

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Lorie C Leyva

Isolation and Characterization of the Novel Actinobacteriophage ‘Draco’ and Annotation of the Actinobacteriophage ‘Oogway’

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Bacterial resistance to antibiotics has become a global epidemic that is steadily increasing. Research on what causes resistance and ways to stop it are in high demand. Actinobacteriophages (phages) are viruses that are being studied to help combat antibiotic resistant bacteria because they are target-specific, can lyse the bacteria, and can be used to produce treatments for bacterial infections. The ability to find a phage that is able to infect and then destroy target bacteria that are nonpathogenic to humans would be of great importance in the biomedical field. We were able to discover a novel phage ‘Draco’ isolated from the host bacteria *Mycobacterium smegmatis*, mc2155, and we studied the genes of phage ‘Oogway’ using bioinformatics software. By comparing the phage ‘Draco’ with other phages isolated from the same host, such as ‘Oogway,’ we may be able to find genes that have similar functions. By comparing phage genomes, we are able to probe the function of the individual genes that have been studied, sequenced and tested. Of particular interest was gene 32 in the phage ‘Oogway,’ which codes for a putative D-alanyl-D-alanine carboxypeptidase, that may have originated from lateral gene transfer from its host. Carboxypeptidase enzymes are known for penicillin-binding proteins and may serve as possible binding sites to lyse bacterial strains that have become antibiotic resistant. We hypothesize that with future research it may be possible to show similar antimicrobial gene products in the phage ‘Draco.’