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2025 SEA Symposium Abstract

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Isolating and Understanding the Genomic Characterization of Bacteriophages in the Rio Grande Valley

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To further contribute to the discovering of new phages, a field where there is still much to be discovered, we went bacteriophage hunting with the HHMI SEA-PHAGES program. Due to the limited research on bacteriophage hunting in the Rio Grande Valley (RGV), we chose to contribute to this field of study by isolating the genome of a local bacteriophage. Our research began with isolating bacteriophage from a local soil sample of Mission, TX. Thereafter, some of our lab procedures included serial dilutions, plaque assay, amplification, DNA extraction, and gel electrophoresis. The host bacteria used for our experiments was Microbacterium foliorum. Our bacteriophage, “Violeta” achieved a DNA concentration of 53.3 ng/uL, and was fortunately high enough to be sent for sequencing. After sequencing, we found that “Violeta” consisted of 68 genes and belongs to the cluster GA. We cross analyzed the genes of our phage against some of the world’s largest DNA databases. By comparing previously studied genes that were alike to the genes of our phage, we were able to predict the function of the genes in our phage. The databases consulted included DNA Master (a bioinformatics software), as well as Phages DB, (an Actinobacteriophage database associated with SEAPHAGES), and the database of The National Center for Biotechnology Information (a division of the NIH and PubMed).