

## Abstract:

The goal of this research was to isolate, purify, and characterize bacteriophages found in Northern Nevada soils. In conjunction with the Howard Hughes Medical Institute's Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program, this research expands our understanding of the diversity of bacteriophages in this region. This study focused on three different bacteriophages; two Mycobacteriophages, Topgun and ScoobyBlue, and one Gordoniophage, TinaLin. Topgun and ScoobyBlue were isolated on the host *Mycobacterium smegmatis mc2155*. Phage TinaLin was isolated on the host *Gordonia terrae NRRL B-16283*. Topgun and TinaLin were found in 2019 and ScoobyBlue was discovered in 2017. Each phage was isolated and purified by the plaque purification method until uniform plaques were obtained. Phage DNA was extracted from each lysate and sent for sequencing at the Pittsburg Bacteriophage Institute, followed by annotation using PECAAN and Phamerator. TopGun is in the mycobacteriophage A1 subcluster with a 63.9% GC content and a genome length of 50,977 base pairs with 91 genes and no tRNAs. ScoobyBlue is a subcluster A3 mycobacteriophage with a GC content of 63.9% and a genome length of 49,638 base pairs with 88 genes and two tRNAs. TinaLin is a subcluster CU1 Gordoniophage with a 65.4% GC content and a genome length of 43,366 base pairs with 75 genes and one tRNA. TinaLin shows 82.71% and 82.71% sequence similarity to CU1 phages Splinter and Vendetta, respectively. TopGun shows 99.74% sequence similarities to A1 phages Wilkins and CactusRose, respectively. ScoobyBlue shows 99.11% and 98.87% sequence similarity

to A3 phages HelDan and Fred313. The genome arrangement of ScoobyBlue is unlike any other A3 mycobacteriophage, making it unique among its genomic cluster which is an area of interest for future research. ScoobyBlue can cross infect a non-pathogenic strain of *Mycobacterium tuberculosis* H37Ra. TinaLin also is a point of interest due to it being one of the few Gordoniaphage that TMCC has discovered. Future research could include host range analysis on these three phages to explore the differences between the phage captured at TMCC to other phages in the same cluster to find genomic differences.