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Isolation and Characterization of Mycobacterium phage Jackal

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Bacteriophages are bacterial viruses, also called phages. Phage isolation and characterization is important for multiple reasons: phages have served as model organisms in genetics and molecular biology, are used to treat antibiotic-resistant bacterial infections, and have been used as vectors for genetic engineering. Our team isolated *Mycobacterium* Phage Jackal during Fall 2023 from a soil sample obtained at 32.46324° N, 94.72627° W at LeTourneau University, in Longview, Texas. The enriched isolation method was used, using *Mycobacterium smegmatis* mc2 155 as the bacterial host. The sample was tested for phages with a spot test, with the bacterial lawn divided into three sections which were inoculated with 5 µl, 10 µl, and 100 µl of our 0.22 µm-filtered enriched sample. Plaques were seen in all three inoculated spots. Purification, amplification, DNA extraction, and TEM followed the SEA-PHAGES Phage Discovery Guide. After aseptically picking a plaque from the spot plate, Jackal went through 3 rounds of purification, each time picking a plaque with was at least 1.59 cm away from its nearest neighbor. Jackal had clear, circular plaques with average diameter 0.89 mm (range 0.5 to 1.2 mm; n = 14). Jackal’s titer was 6.7 x 10ˆ10 PFU/mL, and TEM showed that it has siphovirus morphotype, an isometric capsid with an average diameter of 68 nm (range 60.6 - 72.9 nm; n = 6) and a long, flexible, noncontractile tail with an average length of 213 nm (range 200 - 233 nm; n = 6). Jackal’s genomic DNA and a sample of its lysate are archived at the University of Pittsburg. Its genome awaits sequencing. Jackal’s genomic and biological information may be useful in future research, genetic engineering, and therapeutic applications.