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Alyxandracam: A Newly Isolated and Annotated Microbacteriophage from Oklahoma Soil

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Bacteriophages are viruses which selectively invade bacterial host cells, taking control of the enzymatic machinery associated with replication and subsequently multiplying within the host. Throughout this project, our goals were to isolate a microbacteriophage from Oklahoma soil, characterize it, sequence and annotate its genome. The microbacteriophage Alyxandracam was isolated from reddish-brown clay soil located in a field near a residential area. We used the direct isolation method for isolating the phage and did three rounds of plaque purifications to obtain a pure phage. We used webbed plates for obtaining a 2.3 x 1010 pfu/mL high titer concentration, and transmission electron microscopy revealed a siphoviridae morphology. Phage DNA was extracted using the PCI method and was sequenced via Illumina sequencing technology. These methods enabled us to isolate, characterize and sequence a microbacteriophage from Oklahoma soil successfully. Bioinformatics tools were used to annotate Alyxandracam’s genome. Our phage has a circularly-permuted, 41,770 bp genome with 63.4% GC content. Alyxandracam belongs to cluster EA and subcluster EA1, and appears to enact a lytic viral cycle. Alyxandracam has 63 genes, 25 of which appear to have known protein function based on BlastP and HHPred comparison. No tRNAs were found, and there did not appear to be a translational frameshift within the tail assembly chaperone genes.