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2021 SEA Symposium Abstract

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Isolation and annotation of Xitlalli, a cluster EK phage

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The phage Xitlalli, was isolated from a soil sample collected near the Buffalo Bayou which runs through the University of Houston-Downtown campus. The phage was isolated by the soil enrichment method using the host, Microbacterium foliarum NRRL B-24224. After purification, and amplification, genomic DNA was isolated and sequenced at the Pittsburgh Bacteriophage Institute. Genome sequencing identified the phage belonging to Cluster EK with a genome size of approximately 54 kb and 60.2% GC content. Electron microscopy identified Xitlalli to have a podoviridae morphotype. Annotation was carried out mainly using DNA master, Phamerator, and PECAAN. Of the 52 predicted ORFs, 1-29 genes were in the reverse orientation, and genes 30-52 were in the forward orientation. Gene 29 was added because of the large gap between gene 28 and 30. The genes with known functions included those for Cas 4 exonuclease, lysin A, DNA helicase, primase. In the central region of the genome, a 13 kb ORF was present with no known function and this was found in all Cluster EK phages that have been sequenced.