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Isolation and Annotation of Cluster EB Bacteriophage IndyLu

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With the growing concern surrounding antibiotic resistance, there is increased interest in bacteriophage-based therapies as an alternative treatment strategy. Bacteriophage IndyLu was directly isolated from a soil sample taken from a dry area near a horse barn in Stephenville, Texas, and incubated in host *Microbacterium foliorum* NRRL-24224 SEA. Following two rounds of serial dilutions and plaque assays with a soft agar overlay, IndyLu formed small, defined lytic plaques less than 1cm in diameter. Negative-staining transmission electron microscopy revealed *Siphoviridae* morphology with an approximate tail length of 140 nm and capsid diameter of 60 nm. Phage DNA was extracted with a modified zinc chloride precipitation method and sequenced to 1156-fold genome coverage by the Pittsburgh Bacteriophage Institute using Illumina Next Generation Sequencing. A double-stranded DNA genome of 41,958 base-pairs with a 10 base 3’ sticky overhang (ACTCCCGACA) was determined, making IndyLu the sixth largest member of cluster EB, with an average G+C content of 66.2% for the cluster, and most closely related to Microbacterium phages Didgeridoo (96% coverage) and Lahqtemish (95%). Whole-genome sequence analysis using PECAAN, PhagesDB, NCBI BLASTn and BLASTp, HHPRED, and TmHmm revealed 72 protein-coding genes transcribed rightwards (94.5% of genome) and leftwards (5.6% of genome). Putative genes include structural proteins, a HNH endonuclease, Holliday junction resolvase, and Cas4 family exonuclease have already been identified.