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Tarleton State University

Stephensville TX

Corresponding Faculty Member: Dustin Edwards (dcedwards@tarleton.edu)

Isolation and Annotation of Cluster EB Bacteriophage Softsoap

Mia Lombardo, Kendall Brown, Hannah McNab, Fathya Bashi, Grace Bransom, Evelyn Chacon, Priscilla Doucette, Shannon Dycus, Levi Jackson, Brittney Moser, Elizabeth Ronck, Gustave Allen, Dustin Edwards

Members of the genus Microbacterium infect fish, humans, and plants and are a potential target for phage therapy. *Microbacterium paraoxydans* outbreaks in farmed Nile tilapia (*Oreochromis niloticus*) contribute to a 40-100% mortality rate in isolated cases. Bacteriophage Softsoap was directly isolated from a soil sample under a Live oak tree (Quercus virginiana) in Salado, Texas, and incubated in a related host, *Microbacterium foliorum* NRRL-24224 SEA. Following two rounds of serial dilutions and plaque assays with a soft agar overlay, Softsoap formed small, defined lytic plaques. Negative-staining transmission electron microscopy revealed *Siphoviridae* morphology with an approximate tail length of 155 nm and capsid diameter of 60 nm. Phage DNA was extracted with a modified zinc chloride precipitation method and sequenced to 906-fold genome coverage by the Pittsburgh Bacteriophage Institute using Illumina Next Generation Sequencing. A double-stranded DNA genome of 41,652 base-pairs with a 10 base 3’ sticky overhang (TCTCCCGGCA) was determined, making Softsoap the 42nd largest member of cluster EB, with an average G+C content of 66.5% for the cluster, and most closely related to Microbacterium phages BubbaBear (96.06% coverage) and Albedo (93.98%). Whole-genome sequence analysis using PECAAN, PhagesDB, NCBI BLASTn and BLASTp, HHPRED, and TmHmm revealed 71 protein-coding genes transcribed rightwards (94.4%) and leftwards (5.6%). Putative genes include structural proteins, an HNH endonuclease, Holliday junction resolvase, and Cas4 family exonuclease have been identified.