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Annotation and characterization of Gordonia bacteriophage Sedona

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Gordonia bacteriophage Sedona belongs to cluster DE, sub-cluster DE1, which is made up of 36 members with average genome length of 58,733 base pairs and an average G+C content of 67.6% (https://phagesdb.org/subclusters/DE1/). Sedona was originally isolated from an unenriched soil sample by the University of Pittsburg team in 2019. The phage was grown on Gordonia terrae 3612 isolation host and sequencing information shows approximate shotgun coverage of 1264X. It has circularly permuted ends, a G+C content of 67.4%, and a genome length of 59,571 base pairs (https://phagesdb.org/phages/Sedona/). Like other members of the sub-cluster DE1, Sedona exhibits a lytic cycle, evidenced by the presence of lytic proteins Lysin A and B. NCBI-BLASTn (https://blast.ncbi.nlm.nih.gov/Blast.cgi) whole-genome sequence alignment revealed considerable nucleotide similarities between Sedona and other sub-cluster DE1 members, with the closest relative being phage Bibwit (https://www.ncbi.nlm.nih.gov/nuccore/MH976508). The overall nucleotide similarity is revealed on the generated Phamerator and BLAST Ring Image Generator (BRIG) maps.  
Auto-annotation carried out using Glimmer and GeneMark predictors on DNA Master predicted 84 protein-coding features, which was also confirmed by auto-annotation created on RAST server (https://rast.nmpdr.org/). Manual inspection and start site refinement using conserved start site predictions from Starterator index (http://phages.wustl.edu/starterator/), gene synteny on Phamerator, and six-frame translation inspection on DNA Master and Artemis resulted in the deletion of gene 47, a reverse transcribed gene with very poor supporting information. Ninety-nine percent of the predicted protein-coding features are forward transcribed genes, with a single exception of gene 36 (33689 to 34162 bp), which codes for an HNH-Endonuclease. Putative functional assignment carried out on NCBI BLASTp, Uniprot, and HHPred successfully assigned putative functions to Forty-two percent of the predicted gene features. Some of the predicted protein functions include Helix-turn Helix DNA Binding protein, HNH Endonuclease, RNA Ligase, Terminase, Portal protein, and Tape Measure protein.