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Genome Annotation of Cluster CP Phage DonTron

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DonTron belongs to the cluster CP, of only 8 members to date. It has a genome size of 58,182 bp. Programs used for annotation include DNA Master, NCBI BLAST, Phamerator, Starterator, GeneMark, Gene Content Similarity Tool, and HHPred. On auto-annotation, DNA Master called 89 genes with no tRNAs while Phagesdb and Phamerator called 90 genes with no tRNAs also. After manual annotation, 88 genes were called.   
  
All of the 89 ORFs in this phage were forward genes; no reverse genes were found. 72.7% of the start codons were ATG and the others were GTG. Gene 19 was deleted and no gene was added. The longest gene in DonTron encodes the tape measure protein (5190 bp) while the shortest gene, gene 21, is 114 bp long with a hypothetical protein. Out of the 89 ORFs, 34 genes have known functions and 55 genes have no known function. Among the identified functional genes, several categories were observed: structural proteins, including the portal protein, capsid maturation protease, major tail protein, tape measure protein, and minor tail protein; DNA processing and replication proteins, such as DNAQ-like DNA polymerase, DNA binding protein, helix-turn-helix DNA binding protein, SSB protein, and ParB-like nuclease domain protein; host lysis proteins, including endolysin and holin; and enzymes involved in genome packaging and modification, such as terminase and HNH endonuclease.  
  
DonTron exhibits strong genetic similarity to other members of its cluster, with the highest gene content similarity observed in the unannotated phage Jollymon (95.6%), followed by Sting (94.4%). Additional cluster members show varying degrees of similarity, including Soos (93.8%), Amo99, Coldsoup, and KingstonB (92.9%), while Clawz has the lowest similarity at 86.04%. In terms of shared phams, DonTron shares 86 phams with Jollymon, 85 with Sting, and 77 with Clawz.  
  
DonTron is the first Cluster CP phage being annotated by Unilag. A comparative analysis using the GCS tool revealed minimal similarity between DonTron and the previously annotated phages phages Arcanine (A1), Kenmech (A1), Big3 (A1), and Ringer (A1) (0% similarity), while Peterson (A1), McGee (C1), and Rockne (F1) exhibited 1.1%, 0.8%, and 1.0% similarity, respectively. The low or negligible similarity is expected, as these phages belong to different clusters and more importantly, DonTron is a Gordonia phage.