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Complete genome annotation of new bacteriophage Lewando: Navigating challenges with cluster-specific features

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As one of the most diverse and abundant clades on Earth, bacteriophages are complex viruses that have greatly adapted to surviving in a bacterial world. As such, bacteriophage genomes demonstrate various adaptations that accommodate their unique life cycles. Examples include reduced sequence redundancies, the inclusion of select tRNA-encoding genes and minimal non-coding regions. Annotation of a bacteriophage genome can provide insight into the structural characterization and behaviour of a bacteriophage. As a part of the SEA-PHAGES program, the new bacteriophage Lewando was isolated from a soil sample collected in Montreal, Canada. Following its characterization through transmission electron microscopy, Lewando’s genome was sequenced by the University of Pittsburgh and annotated by a cohort of students at McGill University. As a Siphovirdae virus, Lewando has a long, non-contractile tail. Lewando belongs to the AU6 subcluster and has a genome of 55075 bp with a 51.2% GC content. Tools such as DNA Master, BLASTp, Starterator, HHPred and Deep TmHmm were utilised to annotate 89 genes, none of which were reverse genes nor tRNA-encoding genes. Interestingly, despite being a tailed bacteriophage, no conventional tail fibre assembly chaperone was found. However, it is hypothesised that the predicted gp26 is phage tail collar protein that assists in assembling the tail fibre. The existence of a conserved phage tail collar protein would partially explain the lack of a phage tail fibre assembly chaperone protein across all AU6 subcluster members. Furthermore, the predicted protein that follows gp26 appeared to possess great structural similarity to known bacteriophage tail fibre assembly chaperones. Hence, it is proposed that gp26 and gp27 can guide tail fibre assembly together. Additional annotations unique to the AU6 subcluster include two major tail proteins and an HFH motif instead of the classic HNH motif in its HNH endonucleases.