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A Comparison of Three Subcluster BE1 Phage

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Annotation of three subcluster BE1 genomes, Evy, Daubenski, and Braelyn, will lead to a better understanding of genome structure in *Streptomyces* phage. Genomes were annotated using PECAAN and functions were assigned using PhagesDB BLASTp, NCBI BLASTp, and HHpred. tRNA and tmRNA were identified and trimmed using Aragorn 1.2.38 and tRNAscanSE. Genome size in these phage ranged from 131,234 to 133,090 bp and annotations identified between 218 and 226 genes. Gene order, genome size, number of genes, and tRNA number and position match other subcluster BE1 phage. The three genomes also contain the large terminal repeats of about 10,000bp that are characteristic of subcluster BE1 genomes. Putative RIIA and RIIB-like genes were identified in all three genomes and this function was supported by NCBI BLASTp and HHpred comparisons.