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Characterization of Novel Cluster JA Phage Sweetclover and its Intergenic Region Repeat Sequences

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Actinobacteriophages are viruses that infect bacterial hosts and are highly diverse and abundant. Actinobacteriophages targeting Curtobacterium flaccumfaciens, a plant pathogen, represent a possible treatment strategy for pea and soybean plants, which are vital global protein sources. Only 54 Curtobacteriophages have been isolated and described. Sweetclover is a novel Curtobacteriophage isolated on Curtobacterium flaccumfaciens NRRL B-729 from an enriched soil sample collected in Unity, Maine. Sweetclover has a Siphoviridae particle morphology and belongs to cluster JA. It forms 0.5-1-mm turbid plaques on a lawn of C. flaccumfaciens. Its genome is 54,115 bp long, encodes 83 protein-coding genes, and has a GC content of 60.3%. Sweetclover has an unusual genome organization beginning with an endolysin and minor tail protein on the left arm, followed by the structural and assembly genes which includes two major tail proteins. There are no obvious genes related to lysogeny. Immediately after the lysis cassette there is a ~2,500-bp region that encodes short genes (gp 29 - gp34) each with intergenic regions that contain four sequences that are repeated in variation. A 19-bp repeat overlaps the Shine Dalgarno sequences and start codons of three genes. The three other repeats are 36-41 bp in length, overlap putative promoters and often occur in tandem in varying combinations. How these repeat sequences potentially play a role in genomic regulation and their presence in bacterial genomes will be the focus of future research.