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Characterization of curtobacteriophage Giorgio and other cluster AZ5 actinobacteriophages for biocontrol of Curtobacterium flaccumfaciens

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Curtobacterium flaccumfaciens is a pathogen of legume crops and a growing threat to agricultural industries worldwide. The European and Mediterranean Plant Protection Organization (EPPO) ranked C. flaccumfaciens on the A2 list of pests recommended for regulation as quarantine pests, highlighting the industry's need for an efficient strategy for disease control. One emerging alternative is bacteriophage, highly host-specific viruses, as biocontrol for Curtobacterium infections in crops. This study aims to isolate and characterize six Curtobacteriophages Giorgio, Sabourin, Beaupre, Stuu, RockScotty, and GumPizza. Phages were isolated from soil using an enrichment method with the bacterial host C. flaccumfaciens NRRL B-59340. All six phages belong to cluster AZ5 and have genomes 39,983-40,128 bp in length, GC contents of ~71%, and encode 64-6965 protein-coding genes and one tRNA gene. Giorgio’s synteny was conserved within the AZ5 subcluster and demonstrated little mosaicism, indicating minimal genetic change. The left arm in Giorgio and other AZ5 genomes contains structural genes, while the right arm contains early lytic and replication genes. AZ5 phages, such as Sabourin and Rockscotty, can form stable lysogens, although lysogens of Giorgio were unable to be isolated. All AZ5 genomes encode a serine integrase on the right arm suggesting Giorgio is most likely a temperate phage. These results suggest that Giorgio could be a potential biocontrol agent for Curtobacterium flaccumfaciens, as future research could determine its effectiveness in agriculture.