Genomic and Phenotypic Characterization of Novel Bacteriophages Infecting Rhizobia

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Bacteriophages that are collectively known as ‘rhizobiophages’ can play a vital role in the Rhizobium-legume symbiosis by altering the population dynamics of the rhizobia present in the rhizosphere. They have frequently been isolated from legume soils associated with their susceptible Rhizobium host. Despite their diversity and abundance in the rhizosphere, rhizobiophages are understudied, and the precise role of rhizobiophage in an ecological context is poorly understood. Given their significance in influencing the population dynamics and evolution of rhizobia in rhizosphere, fundamental characterization of rhizobiophage diversity and studying of rhizobiophage biology is desirable.

The Hynes lab has a collection of rhizobiophages that has been isolated from soil samples with history of legume growth in western Canada. This collection includes phages infecting different rhizobial hosts such as R. leguminosarum, R. gallicum and Mesorhizobium loti. All the phage isolates were screened to assess their spectrum of host specificity with an array of rhizobial hosts. Transmission electron microscopy of selected phages revealed that they were tailed phages belonging to families Siphoviridae, Myoviridae and Podoviridae. These phages were further subjected to genomic and proteomic characterization. Phage genome sizes were approximated using pulsed-field gel electrophoresis, and sub-clone generation of phage DNA for Sanger sequencing was carried out to prepare scaffolds for assembling the genomes of selected phages. Sanger sequences combined with sequence data obtained through high throughput sequencing methods such as 454-pyrosequencing and Ion-Torrent were used in assembling and completing the genomes of three rhizobiophages. Phage vB_RgaS_P106B, a phage that infects R. gallicum, has a genome of 56 kb whereas R. leguminosarum bv. viciae 3841 phage vB_RlvS_L338C contains a 109 kb genome. The vB_RlvM_PPF1 is a temperate phage that can lysogenize R. leguminosarum strain F1 and has a genome of 54 kb. These three genomes have been annotated and the putative functions assigned for the predicted ORFs indicated the presence of genes involved in DNA packaging, phage morphogenesis, and DNA replication and recombination functions.