

Abstract

Mesorhizobium phage vB_MloS_Cp1R7A-A1 was isolated from soil cultivated to chickpea in Saskatchewan and is dissimilar in sequence and morphology to previously described rhizobiophages. It is a B3 morphotype virus with a distinct prolate capsid and belongs to the tailed phage family *Siphoviridae*. Its genome has a GC content of 60.3% and 238 predicted genes. Putative functions were predicted for 57 genes, which include 27 tRNA genes with anticodons corresponding to 18 amino acids. This represents the highest number of tRNA genes yet reported in a rhizobiophage. The gene arrangement shows a partially modular organization. Most of the structural genes are found in one module, whereas tRNA genes are in another. Genes for replication, recombination and nucleotide metabolism form the third module. The arrangement of the replication module resembles the replication module of Enterobacteria phage T5, raising the possibility that it uses a recombination-based replication mechanism. Phage termini appear to be long direct repeats of length just over 12 kb. Phylogenetic analysis revealed that Cp1R7A-A1 is more closely related to phiCbK-like *Caulobacter* phages and other B3 morphotype phages than to other rhizobiophages sequenced thus far.

Key words

Rhizobiophage, *Mesorhizobium loti*, *Mesorhizobium japonicum*, *Siphoviridae*, Prolate capsid, Genome sequence, bacteriophage