

Ralstonia solanacearum is a soil-borne gram-negative bacterium that causes bacterial wilt disease in many important crops. Bacteriophages are viruses infectious to bacteria, and some virulent bacteriophages can lyse bacteria. The use of virulent bacteriophages may have great potential for protecting plant from *R. solanacearum* infection. In this study, new bacteriophages infectious to *R. solanacearum* were isolated and characterized.

Three kinds of *R. solanacearum* bacteriophages, ϕ RS138, ϕ RS611, and ϕ RS603 were isolated from the soil of a tomato field, and the host specificity and growth curve of them were analyzed. Based on their morphology, ϕ RS138 was classified into the *Siphoviridae* family. ϕ RS611 and ϕ RS603 were characterized as an Ff-type phage belonging to the *Inoviridae* family. Further, the whole genome sequences of the three phages were determined.

The ϕ RS611 genome showed high similarity to those of *Ralstonia* phages RSS0 and RSS1 which have been reported by other group. However, approximately 900-nucleotide deletions were found, indicating that ϕ RS611 is a deletion mutant of them. The ϕ RS603 genome showed high similarity to those of *Ralstonia* phages ϕ RSM1 and ϕ RSM3 reported by Askora *et al.* However, ϕ RS603 genome was unique, because its genome lost some open reading frames (ORFs) including integrase of ϕ RSM3. In stead, ϕ RS603 had ORF 11 that was homologous to other *Ralstonia* phages ϕ RSS0 and ϕ RSS1, indicating that ϕ RS603 is an evolutionary intermediate between RSS phages and RSM phages. In order to reveal integration mechanism, integration site of ϕ RS603 genome in the genome of *R. solanacearum* was analyzed.

The ϕ RS138 genome was composed of 41,941 base pairs in lengths of double-stranded DNA with a G + C content of 65.1% and putative 56 ORFs. The ϕ RS138 genome could be divided into three regions homologous to prophage gene in *R. solanacearum* K60-1, *Pseudomonas aeruginosa* phages of the *Siphoviridae* family, and genomes of other *R. solanacearum* strains. This is the first report for the complete genome sequence of *R. solanacearum* phage

of *Siphoviridae* family.

The three phages isolated from the same soil of tomato field were different and unique, and may be useful for understanding molecular basis of infection to bacteria and as a biopesticide for controlling bacterial wilt disease.