HOST RECOGNITION AND INTEGRATION OF FILAMENTOUS PHAGE ФRSM IN THE PHYTOPATHOGEN, RALSTONIA SOLANACEARUM

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Background: ФRSM1 is an Ff-type phage infecting the phytopathogenic bacterium Ralstonia solanacearum. The ФRSM1 genome is a ssDNA of 9,004 nt in size and contains 14 ORFs. Strains of R. solanacearum sometimes contain two different types of ФRSM1-related prophages. Two prophages, called ФRSM3 and ФRSM4, that are closely related to, but differ from, ФRSM1, have been detected in strains of the R. solanacearum species complex.

Objectives:
1. Characterization of different types of ФRSM phage.
2. Comparison of pIII sequence among ФRSM1-related phages.

Methods: PCR, genomic sequencing, Pili separation by SDS-PAGE.

Results: The prophage ФRSM3, found in host strain MAFF730139, could be converted to infectious phage by means of PCR and transfection. The nucleotide sequence of ФRSM3 is highly conserved relative to ФRSM1 except for open reading frame 2 (ORF2), encoding an unknown protein, and ORF9 encoding the presumed adsorption protein that determines host range. The two host ranges differ dramatically and correlate closely with different gel electrophoresis banding patterns for cell surface fimbriae. Database searches in the R. solanacearum strains of known genomic sequence revealed two inovirus prophages, one designated ФRSM4 that is homologous to ФRSM1 and ФRSM3, and one homologues to ФRSS1, in the genome of strain UW551.

Conclusion:
1. The host range determined by pIII-D2 domain may be exchangeable among phages by some specific mechanisms.
2. Infection by ФRSM1 and ФRSM3 reduces drastically the host virulence in tomato plants.

Reference: