

A field survey, phylogenetic analysis and infectious clone construction of papaya leaf-distortion mosaic virus taiwan stra

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ABSTRACT

Papaya ringspot virus (PRSV) causes the most economy loss in papaya production of Taiwan. Recently, the Papaya leaf-distortion mosaic virus (PLDMV) was also found. The infection rate of both viruses on papaya are uncertain. In this study, we investigated the PRSV and PLDMV distribution in Taiwan. Total 768 samples of papaya were collected from net-houses and field in papaya growth area, including MiaoLi, Changhua, Yunlin, Nantou, Chia-yi, Tainan, Kaohsiung, Pingtung, Taitung, and Hualien. According to Enzyme-Linked Immunosorbent Assay (ELISA), 53% of samples were only infected with PRSV, 4% were only infected with PLDMV, 17% were co-infected with PRSV and PLDMV, and 30% were undetectable. Multiplex RT-PCR for the specific detection of PRSV and PLDMV was used to identify the ELISA uncertain samples. The amplified DNA fragments of 378 bp and 564 bp indicated the infection of PRSV and PLDMV, respectively. The coat protein genes of 15 PLDMV samples that amplified by RT-PCR were further cloned. Sequence analysis of these CP genes showed 97.7 to 99.7% of nucleotide identities with each other, and 94.9-99% identity with other Taiwan isolates (TW-KS, TW-DL, and TW-TD. Moreover, these CP genes showed 93.7-95.2% identity with Japan strain (J56P and J179P) and much lower sequence identity (85.1-86.4%) with J199C strain which only infected cucurbit specie. Phylogenetic tree of 15 PLDMV CP gene is shown in differen clade of TW-TD、TW-KS and Japan isolates. To determine if the PLDMV-P Taiwan isolates could infect cucumber plants, two PLDMV isolates were inoculated into *Cucumis metuliferus* Acc.2459 and *Cucumis sativus* and the infectivity of the virus was detected by ELISA and western blotting analysis. Only 8.8% of symptomless *C. metuliferus* showed PLDMV infection. In previous study, the full-length PLDMV DL sequence was complete except for the nucleotides near the 5' end. 5'RACE was performed to obtain the 5'end sequence. Comparison of the full-length sequence of DL isolate with PLDMV TW-KS and J56P showed 94.5% and 94.6% of nucleotide identity, respectively. When comparing with the 5'UTR region, the identity to PLDMV TW-KS and J56P was 87.4% and 84.4%, respectively. With the PLDMV-DL complete sequence, an infectious transcript can be constructed. Seven PLDMV clones, including p35S-5'426, pPL5'-2764, pPL2680NarI-4361, pPL4247-6604, pPL5761-8298, pPL8150-9810, and pPL9528-3'NotI, with overlapping DNA fragments to each other were obtained by RT-PCR. These PLDMV DNA fragments were used to replace the sequence in 35S-PRSV infectious clone. A plasmid p35SPL2711-HA-9779NotI was obtained that contained the 35S promoter sequence followed by the 5'end of PLDMV nt 1 to 2711 and the 3'end of nt 9779 to the poly(A) tail. Finally, by introducing the PLDMV DNA fragment of nt 2680 to 9810 into p35SPL2711-HA-9779NotI, the full-length genomic sequence of PLDMV will be complete.

Keywords : Papaya leaf-distortion mosaic virus (PLDMV)、infectious transcript、ELISA、multiplex RT-PCR

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