Genetic diversity analysis of Papaya leaf-distortion mosaic virus isolates infecting transgenic papaya 'Huanong No. 1' in South China

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Abstract

Abstract: The commercialised genetically modified papaya 'Huanong No. 1' has been utilised to successfully control the destructive virus-Papaya ringspot virus (PRSV) in South China since 2006. However, another new emerging virus, Papaya leaf-distortion mosaic virus (PLDMV), was found in some PRSV-resistant transgenic plants in Guangdong and Hainan provinces through a field investigation from 2012 to 2019. The genetic diversity of the isolates is not clear. In the present study, 20 representative isolates were selected to inoculate 'Huanong No. 1', and all of the inoculated plants showed obvious disease symptoms similar to those in the field, indicating that PLDMV is a new threat to widely cultivated transgenic papaya in South China. Phylogenetic analysis of the Coat protein genes of 111 PLDMV isolates from Guangdong and Hainan showed that PLDMV can be divided into two groups. The Japan and Taiwan isolates belong to group I, whereas the Guangdong and Hainan isolates belong to group II and can be further divided into two subgroups. The Guangdong and Hainan isolates were far from the isolates of Japan and Taiwan and belong to a new lineage. Further analysis showed that the Guangdong and Hainan isolates had a high degree of genetic differentiation, and no recombination was found. These isolates deviated from neutral evolution and experienced population expansion events in the past, which might still be unstable. The results of this study provide a theoretical basis for clarifying the evolutionary mechanism and population genetics of the virus and for preventing and controlling the viral disease.

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