

Research Article

Diversified *Citrus tristeza virus* Causing Decline Disease in Khasi Mandarin in Manipur State of North-East India

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Abstract

A survey was conducted in the khasi mandarin (*Citrus reticulata*) orchards in three districts of Manipur (Churachandpur, Tamenglong and Chandel) which belongs to the rich Indo-Burma biodiversity hotspot region of the world. The combined diagnosis results of DAC-ELISA and RT-PCR showed that the CTV incidence in different citrus growing districts of Manipur was 53.3-70 per cent. Three CTV isolates, Mnp1 (Churachandpur), Mnp2 (Tamenglong) and Mnp3 (Chandel) of Manipur were characterized, for the first time, based on sequencing of three genomic regions, complete CP (ORF7, 672nt), suppressor p23 (ORF11, 630 nt) genes and 404 nt fragment of 5'ORF1a (L Pro domain) (5' ORF1a). These isolates showed 90-98 per cent identity for 5'ORF1a, 94-98 per cent for CP gene and 93-97 per cent for p23 gene. Two phylogenetic groups among the Manipur CTV isolates were generated for each of the three genomic regions but placement of these isolates in the phylogenetic tree for all the three genomic regions was inconsistent, indicating high genetic diversity among the present CTV isolates. In Tajima's tests both the CP and p23 genes showed negative D values, -0.202 and -0.187, respectively indicating purifying selection due to low frequencies of polymorphism. The dN/dS value of CP gene was lower (0.069) than that of p23 gene (0.162), indicating CP gene to be under high selection pressure compared to p23 gene. Recombination analysis detected that CP gene of isolate Mnp2 and p23 gene of Mnp3 were strong recombinant. The present study concluded that CTV isolates in Manipur state pertain to citrus decline inducing strains of CTV.

Key words: *Citrus tristeza virus*, citrus decline, disease incidence, genetic diversity, Manipur state, phylogeny, recombination

Citation: Palchoudhury S , Sharma S K, Biswas M K and Biswas K K. 2015. Diversified *Citrus tristeza virus* causing decline disease in khasi mandarin in Manipur state of North-East India. *J Mycol Pl Pathol* 45(4): 317-323.