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3 Biotech. 2019 Sep;9(9):348. doi: 10.1007/s13205-019-1876-4. Epub 2019 Aug 30.

Genome Characterization of Citrus Yellow Vein-Clearing Virus: Limited Heterogeneity of Viral Genomes in *Mandarivirus*-Infecting Different Citrus Species

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Abstract

Citrus yellow vein-clearing virus (CYVCV) is a mandarivirus infecting citrus producing yellow vein-clearing symptoms. The leaf samples collected during surveys of different citrus-growing areas in India exhibited diverse symptoms and 40% of the plants were positive for CYVCV in RT-PCR, indicating the wide distribution of the virus in India. It was reported for first time that CYVCV infects kinnow mandarin and sweet oranges and produces chlorotic ringspots symptoms identical to Indian citrus ringspot virus (ICRSV). The complete genome sequences of CYVCV infecting four citrus cultivars have been deciphered through overlapping primers. All the four genomes comprise of 7531 nucleotides excluding the 3' poly (A) tail. The sequence identity of genomes of four CYVCV isolates in

the present study ranged from 95.2 to 99.8% with genome sequences of 31 CYVCV isolates available in public domain and the mean genomic diversity was 0.017, indicating low level of heterogeneity. The phylogenetic analysis revealed that CYVCV isolates from India, Pakistan, and Turkey were clustered in the same clad apart from China isolates. The least normalized dN/dS mean value (0.092) indicated that RdRP region evolved under relatively stronger selection constraints than the other five coding regions of CYVCV. The four intragenic putative recombination events detected in RDP4 program occurred naturally in CYVCV genome, indicating the evolutionary progress of the virus. Tajima's and Fu and Li's D parameters were performed using genomic sequences in DnaSP v5 program and the retrieved negative values indicated the presence of limited genetic variability in CYVCV genomes. To the best of our knowledge, this is the first comprehensive report on molecular characterization of CYVCV from India. It will be helpful in understanding the evolutionary relationship of CYVCV and ICRSV.

Keywords: Citrus yellow vein-clearing virus; Detection; Genetic heterogeneity; Mandarivirus; Recombination.

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