



# Molecular Identification of *Cactus virus X* Infecting *Hylocereus polyrhizus* (Cactaceae) in Hainan Island, China

C. Peng, N. T. Yu, Z. W. Luo, H. Y. Fan, F. He, X. H. Li, Z. L. Zhang, and Z. X. Liu

Affiliations

## Authors and Affiliations

C. Peng, Institute of Tropical Fruit Trees, Hainan Academy of Agricultural Sciences, Haikou, Hainan 571100, P.R. China

N. T. Yu, Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agricultural Sciences, Haikou, Hainan 571101, P.R. China

Z. W. Luo

H. Y. Fan

F. He

X. H. Li

Z. L. Zhang, Institute of Tropical Fruit Trees, Hainan Academy of Agricultural Sciences / Investigation Station of Tropical Fruit Trees, Ministry of Agriculture, Haikou, Hainan 571100, P.R. China

Z. X. Liu, Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agricultural Sciences, Haikou, Hainan 571101, P.R. China.



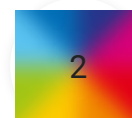
Vol. 100, No. 9  
September 2016

Subscribe

ISSN: 0191-2917  
e-ISSN: 1943-7692

## Metrics

Downloaded 541 times



2 Total citations

2 Recent citations

0.59 Field Citation Ratio

n/a Relative Citation Ratio

## Article History

*Hylocereus polyrhizus* Britt. & Rose (Cactaceae), commonly known as pitaya or dragon fruit, is widely cultured in tropical and subtropical regions of China and has become an increasingly important fruit in recent years. In October 2014, in a survey of diseases on pitaya, approximately 44% of field plants showing virus-like symptoms including chlorotic halos and small chlorotic spots on stems were observed in Qionghai, Hainan Island, China. Flexuous filamentous virus particles of about 600 nm in length were observed from stem-sap preparation of four symptomatic plants with a transmission electron microscope (TEM). To further ascertain the presence of *Cactus virus X* (CVX), stems from 20 symptomatic samples (including four samples found positive by TEM) and 20 healthy samples were collected from different fields for RT-PCR. Total RNAs were extracted and reverse transcribed using random primers according to the manufacturer's instructions for the RevertAid first strand cDNA synthesis kit (Thermo Scientific). The cDNA of each sample was then used in PCR using the CVX-specific forward (5'-CCCTCTATGTTTCTTACCTATTTG-3') and reverse (5'-CTACTGCGGGAGCCTTGTTTC-3') primers designed based on a conserved sequence spanning the triple gene block protein 3 (TGB-3) and coat protein (CP) genes (Accession No. AF308158). A fragment of approximately 900 bp was amplified from each symptomatic sample. No amplification was observed when cDNA from healthy plant samples was used as a template. The PCR products were cloned into the pMD18-T vector (Takara, Dalian, China) and sequenced at ThermoFisher Scientific in Shanghai, China. The sequences were deposited in GenBank (Accession Nos. KU497493 and KU497494, respectively). Both nucleotide sequences were analyzed by

BLASTn and found to share 97% identity with a Taiwan isolate (KM365479) that was reported from *Hylocereus undatus* Britt. & Rose (Liou et al. 2001). The amino acid sequences of the coat protein showed 97.1 and 99.1% identity with a South Korean isolate (BAO73885) by BLASTp. Phylogenetic analysis of the CP amino acid sequences using MEGA6.0 (Tamura et al. 2013) showed that Hainan isolates and all other CVX isolates formed a high-confidence subclade, except AFJ00097 (Taiwan-NTU). To our knowledge, this is the first report of CVX on *H. polyrhizus* Britt. & Rose in Hainan Island, China. The presence of this destructive virus on pitaya could represent a serious threat to this fruit, and therefore further surveys are needed from more tropical and subtropical areas of China in order to determine its prevalence and yield losses on pitaya.



**The American Phytopathological Society**

**(APS)**

📍 3340 Pilot Knob Road, St. Paul, MN 55121 USA

☎ +1.651.454.7250

**FAX** +1.651.454.0766

 APS