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SHORT COMMUNICATION

The complete genome sequence of Citrus vein enation virus from China

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Abstract

The complete nucleotide sequence of an isolate of Citrus vein enation virus (CVEV-XZG) from China has been determined for the first time. The genome consisted of 5 983 nucleotides, coding for five open reading frames (ORFs), had a similar genomic organization features with *Pea enation mosaic virus* (PEMV). Nucleotide and deduced amino acid sequence identity of the five ORFs compared to isolate CVEV VE-1 range from 97.1 to 99.0% and 97.4 to 100.0%, these values compared to isolate PEMV-1 range from 45.2 to 51.6% and 31.1 to 45.2%. Phylogenetic analysis based on the complete genome sequence showed that the isolate CVEV-XZG had close relationship with *Pea enation mosaic virus*. The results supports CVEV may be a new member of genus *Enamovirus*. The full sequence of CVEV-XZG presented here may serve as a basis for future study of CVEV in China.

Keywords: Citrus vein enation virus (CVEV), genome sequence, *Enamovirus*

1. Introduction

Citrus vein enation disease was first reported by Wallace and Drake in 1953, the symptom was described as small papillae grew from veins on leaf under sides of sour orange. After that the disease was proved to be graft-transmitted and insect-transmitted by at least one species of aphis, so causal agent was concluded be a new virus (Wallance and Deake 1953). In 1960, Fraser (1960) found woody galls disease on rough lemon stock and speculated it might be induced by a viroid. Later, it was shown that the two diseases were induced by the same virus (Wallace and Deake 1960), and the virus was proposed to be named Citrus vein enation virus (CVEV). In 1986, virus-like particles were observed by electronic microscope in infected rough lemon. Also some results indicated that CVEV was a persistently transmitted virus, with a latent period of 2–3 days (Maharaj and da Graca 1988). Furthermore, four weak dsRNA bands with molecular weight of 3.6, 2.6, 1.9 and 0.5×10^6, respectively, were detected in bark extracts from the infected plants (da Graça and Maharaj 1991). These characteristics suggested CVEV might belong to the *Luteovirus* group. Recently, the genome sequences of CVEV VE-1 were obtained by deep sequencing, which showed closed phylogenetic relationship with *Pea enation mosaic virus* (PEMV-1) compared by amino acid signatures probably be a new member of genus *Enamovirus* (Vives *et al.* 2013). The genus *Enamovirus* is one of three genera in the family *Luteoviridae* and currently has only one member, *Pea cnation mosaic virus*.

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So far, the CVEV was reported in many citrus production areas, including the United States, Australia, Brazil and Spain (Wallance and Deake 1953; da Graça and Maharaj 1991; Jacomino and Salibe 1993). However, it caused generally low economic losses, except in Peru (de Segura *et al.* 1969). In China, this disease was first reported on six local commercialized citrus varieties in Huangyan District of Zhejiang Province in 1992 (Chen *et al.* 1992), except that, limited studies were focused on this virus. In this study, the complete nucleotide sequence of CVEV from China has been determined, which provides more evidence for the virus taxonomic status.

2. Results

The genome of CVEV-XZG consisted of 5 983 nucleotides (nt), compared to the published VE-1 isolate, the identity of nt sequence was 97.2%. It contained five open reading frames (ORFs) and two untranslated regions (UTR) of 207 and 198 nt at the 5′ and 3′ termini, respectively. The ORF 0 consisted of 1 065 nt that potentially encoded a polypeptide of 39 kDa. The cognate product of PEMV is a strong locally-acting suppressor, and the suppressor acts as a F-box-like protein (Fusaro *et al.* 2012). The four landmark amino acids (LPxx(L/I)x$^{10–13}$P) of a putative F-box-like motif was identified in ORF 0 of the CVEV. ORF 1 contained 2 709 nt and encoded a protein of 100 kDa, and in this region also kept active-site residues of the serin proteinase domain. ORF 2 translated *via* frame shift and produced a putative fusion protein of 148 kDa. The required two signals of frameshifting (Giedroc and Cornish 2009), a heptanucleotide and a very stable RNA

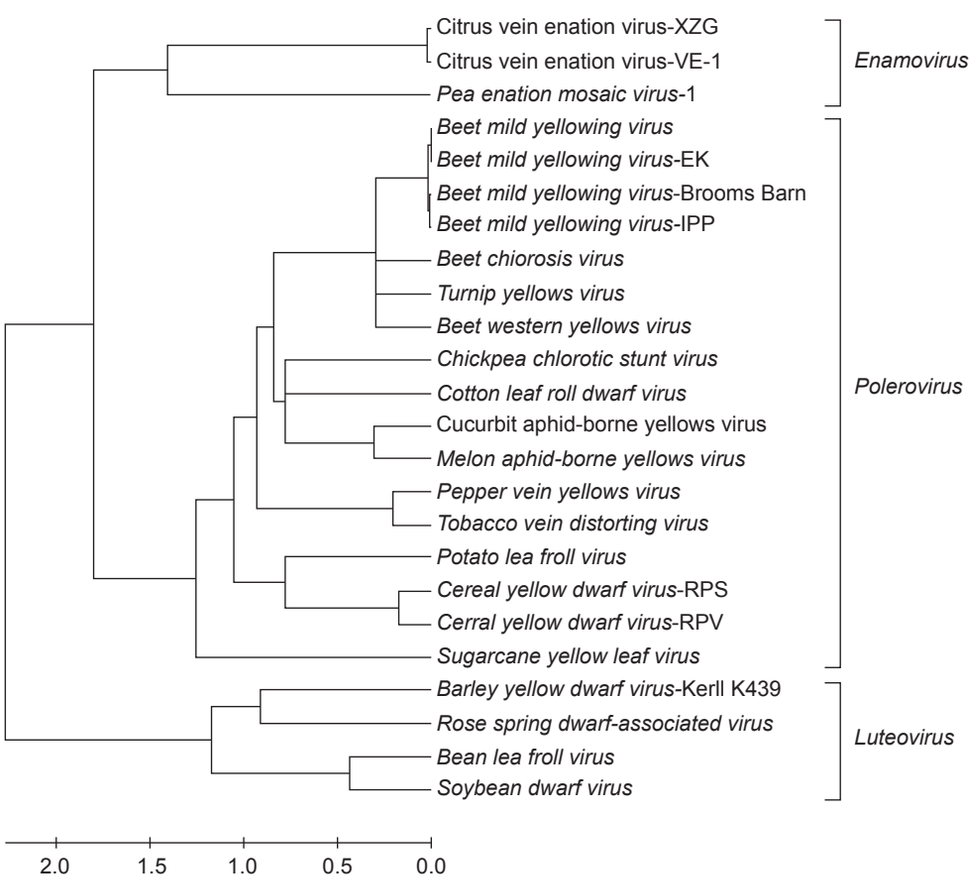

Fig. 1 Phylogenetic analysis of CVEV-XZG and other members of family *Luteoviridae* based on complete genome sequences. The virus names and GenBank accession numbers are as follows: Citrus vein enation virus (HF679486), *Pea enation mosaic vius*-1 (NC_003629), *Beet mild yellowing virus* (NC_004756), *Beet mild yellowing virus*-EK (KC121026), *Beet mild yellowing virus*-Broom Bam (EF107543), *Beet mild yellowing virus*-IPP (DQ132996), *Beet chlorosis virus* (NC_002766), *Turnip yellows virus* (NC_003743), *Beet western yellows virus* (NC_004756), *Chickpea chlorotic stunt virus* (NC_008249), *Cotton leaf roll dwarf virus* (NC_014545), Cucurbit aphid-borne yellows virus (NC_003688), *Melon aphid-borne yellows virus* (NC_010809), *Pepper vine yellows virus* (NC_015050), *Tobacco vein distorting virus* (NC_010732), *Potato leaf roll virus* (NC_001747), *Cereal yellow dwarf virus*-RPS (NC_002198), *Cereal yellow dwarf virus*-RPV (NC_004751), *Sugarcane yellow leaf virus* (NC_000874), *Barley yellow dwarf virus*-Kerll K439 (NC_021481), *Rose spring dwarf-associated virus* (NC_010806), *Bean leaf roll virus* (NC_003369), *Soybean dwarf virus* (NC_003056).