



First report of *Strawberry crinkle virus* in Argentina

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Strawberry crinkle virus (SCV) is one of the most frequent viruses affecting strawberry worldwide, and responsible for important reductions in yield and fruit quality. Stunted dwarfed plants with distorted leaves were found in Lules (26°55'22"S 65°20'15"W), Tucumán province, Argentina, in 2010, suggesting the virus presence. Total nucleic acids were isolated from leaves of 26 strawberry plants (*Fragaria x ananassa* cv. Camarosa) showing symptoms using the modified cetyltrimethylammonium bromide method (CTAB) as performed by Chang *et al.* (2007). Healthy strawberry plants previously tested by grafting to indicator plants (*Fragaria virginiana* clone UC-12, *F. vesca* clone UC-6 and cv. Alpine) were used as negative controls.

The extracts were analysed by one-step nested RT-PCR (RT-PCR Kit, Qiagen) with specific primers (Posthuma *et al.*, 2002), which amplify a 573-bp genome fragment corresponding to a conserved region of the rhabdovirus polymerase (L) genes. Two PCR products were cloned into the pCR4-TOPO[®] vector (TOPO[®] TA Cloning Kit for Sequencing of Invitrogen Lab) and bi-directionally sequenced. In addition, new primers were designed based on the previously obtained sequences and others retrieved from the GenBank: Cito1/for: TCTATCAACCCTATGCAATATCCG; Cito1/rev: GTAGTATCTTCCAGCCACCTGATG (expected fragment size 744 nt) and Cito2/for: ATGGGACCTATGTACCGGACATC; Cito2/rev: GGAAATTGTCTCTCCCCATTG (687 nt) (Fig. 1). The PCR products obtained from each sample were cloned and bi-directionally sequenced. Sequences were assembled using the SeqMan program (Lasergene software, DNASTar ver. 5, 2001), and manual adjustment was done when necessary. The assembly of the three genomic fragments retrieved a consensus sequence (1897 nt), which was deposited in GenBank

(Accession No. KJ748457). BLAST analysis showed that the Argentinean isolate has 95% (AY250986.2 - cover 100%) to 89% (JN542482.1 - cover 15%) nucleotide identity with SCV sequences (15). Phylogenetic analysis performed with a 258 nt fragment of 14 SCV sequences downloaded from the GenBank generated a tree in which the Argentinian isolate was grouped in group II according to Klerks *et al.* (2004) (Fig. 2). Collectively, the data implicate the SCV as the etiological agent. To our knowledge, this is the first report of *Strawberry crinkle virus* infecting strawberry in Argentina. Additional studies to complete the characterisation are being carried out.

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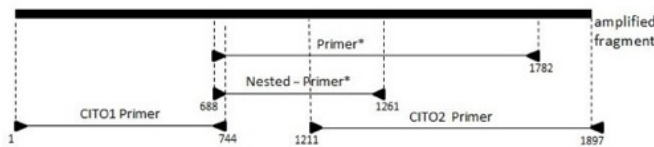


Figure 1

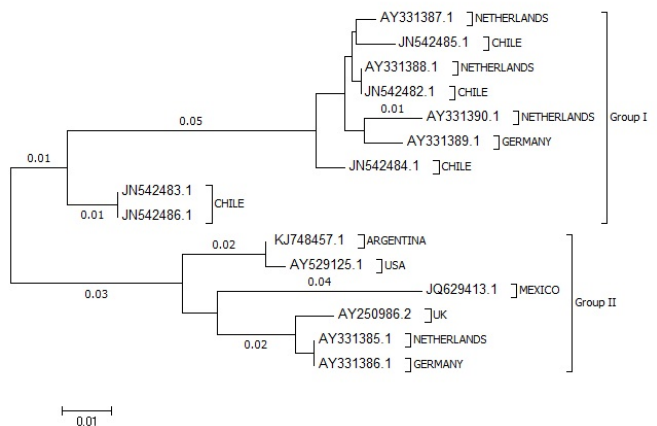


Figure 2

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