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Molecular Differentiation of Mild and Severe 
*Citrus tristeza virus* Isolates in Mexico

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ABSTRACT. *Citrus tristeza virus* (CTV) is the most important viral disease of citrus world-
wide. In the last 20 yr it has caused the death of more than 100 million trees in South America, 
California, Florida, Israel and Spain. CTV is transmitted by the aphid *Toxoptera citricida* and in 
infected propagating material. The presence of both the virus and the aphid in Mexico are of great 
concern, since most of the commercial plants are grafted on sour orange rootstocks that are sus-
ceptible to CTV. The molecular characterization of different CTV strains, including the complete 
sequence of the virus genome has opened the door to studies with the goal of diminishing the 
damage caused by this viral complex. The objectives of this study were to develop a method to dif-
ferentiate CTV strains based on the molecular characterization of the p25 coat protein gene. The 
sequence of this gene was amplified, and RFLP polymorphisms were examined with restriction 
enzymes that allowed the differentiation of mild strains from severe ones. The results showed 
that digestion with the enzyme *Hae* III made it possible to accomplish this. In addition, the use of 
the enzyme *Kpn* I discriminated between the strains that cause stem pitting from those that 
induce tree decline. These results were also observed by in *silico* digestion, with the same 
enzymes, of several coat protein gene sequences deposited in Genbank. The derived dendograms 
of the multiple alignments of the amino acids sequences of p25 gene showed the separation of the 
weak strains from the severe ones. The analysis of the nucleotide sequence of gene p25 at posi-
tions 49, 63 and 124 showed that the amino acids glycine, threonine and phenylalanine are con-
served in severe strains.

*Citrus tristeza virus* (CTV) has worldwide distribution, and its 
strains vary in symptoms in differ-
ent hosts, as well as in their trans-
missibility by aphids (16). CTV 
strains have been found that cause 
tree decline and death in orange, 
grapefruit and mandarin, grafted 
onto sour orange rootstock, while 
others cause stem pitting in various 
species. There are also isolates that 
do not cause any visible effects on 
the infected host (7).

This virus is disseminated in a 
semi-persistent way by several spe-
cies of aphids; the most efficient vec-
tor being *Toxoptera citricida* 
(Kirkaldy). CTV is transmitted by 
the vector without a period of latency 
and it looses its efficacy of transmis-
sion 48 hr after acquisition (8, 15).

Most CTV isolates are complex 
populations containing mixtures of 
different viral genotypes (2). These 
mixtures include genetic variants, 
defective RNAs (dRNAs) and chi-
merical genomes that are possibly 
generated as consequence of recom-
bination events. Recombination dur-
ing transcription is considered one 
of the main factors that determine 
the evolution of positive sense RNA 
viruses.

It has been postulated that at 
least four species are the progeni-
tors of current citrus varieties, and 
that the different strains of CTV 
evolved in the native citrus of Asia, 
and were dispersed around the 
world through infected buds (1). Strains considered mild, for exam-
ple T-30, are genetically related to 
Asian strains, as well as other iso-
lates from Colombia and California 
isolates B272 and B354, respec-
tively, of the USDA exotic CTV col-
lecion, Beltsville, MD, USA), and are related to isolate T385 from Spain, which is also considered mild. Phylogenetic analysis showed that T30 was introduced to Florida more than 200 yr ago and that its genetic changes are mostly related to the movement of the citrus throughout the world (16).

At present, the main detection method for CTV is an enzyme linked immunosorbent assay (ELISA). The monoclonal antibodies 3DF1 and 3CA5 are able to detect most of the known isolates of this virus (18). However, other antibodies such as MCA13 are specific for severe strains. The methods previously used to differentiate CTV strains include different monoclonal antibodies (13), the analysis of dsRNAs in infected plants, and molecular hybridization with probes of complementary DNA (cDNA) (11). The ability to differentiate strains based on single strand conformational polymorphism (SSCP) and restriction fragment length polymorphisms (RFLP) is due to a nucleotide change resulting in the DNA acquiring a different conformation. This allows the DNAs to migrate at different rates when analyzed in polyacrylamide gels.

Lozano (9) used RFLPs, digesting the amplified products of the reverse-transcription polymerase chain reaction (RT-PCR) with the restriction enzyme *Hinf* I and found that it was useful to characterize the adenovirus family. Studies carried out by Gillings (5) analyzing the p25 CTV coat protein gene digested with the same restriction enzyme *Hinf* I, generating a dendrogram of the similarity of different isolates which correlated with their biological characterization, allowing prediction as to whether these were mild or severe strains. This approach allowed differentiation of isolates of CTV without having to clone and sequence the p25 gene (4).

This study was conducted to develop a molecular method based on RT-PCR jointly with the use of RFLP using the coat protein gene and the virulence of CTV isolates to differentiate severe from mild strains.

**MATERIALS AND METHODS**

**Virus isolates.** CTV isolates were obtained from sweet orange field trees in northeast Mexico. Isolates NL1, NL2, V1 and H33 showed typical CTV symptoms of either stem pitting or tree decline, and consequently were considered severe. But, isolates NL3-7, T2 and V2 did not show any CTV symptoms and were thus considered mild isolates. Biological characteristics of Mexican CTV isolates were also evaluated in sweet orange, Mexican lime and grapefruit plants. Sequences of the coat protein gene from mild strains T30 and T385, and severe strains SY568 and T36 were also included as reference CTV strains.

**CTV reverse transcription, PCR and cloning.** Primers R731-7
(5’-cggagaacgagatcaacg-3’) and R731-6 (5’-attatggacgacgaaacaaa-3’) were designed for performing RT-PCR of the coat protein, producing an expected product of 688 base pairs (bp) (8). Viral dsRNA was purified from young bark tissue by a Trizol method and was used as templates for RT-PCR. Reverse transcription using dsRNAs was performed at 70°C for 5 min in a 15 µl reaction volume containing 2 µl (2 mg) of dsRNA, 0.5 mM of reverse primer, followed by incubation at 42°C for 50 min in a 25 ml reaction containing 1× M-MLV buffer, 0.5 mM dNTPs, 15.6 units of Rnasin, 200 units of M-MLV reverse transcriptase. PCR was performed in 25 µl reactions containing 2.5 ml of the RT solution, 1× Taq buffer, 1.5 mM MgCl₂, 0.5 mM each primer 0.2 mM dNTPs and 1.25 units of Taq polymerase. The samples were incubated first at 94°C for 5 min, followed by PCR for 30 cycles of 94°C (30 sec), 50°C (30 sec), 72°C (1 min) followed by a final 7 min extension at 72°C. RT-PCR products were directly cloned using pCR® 2.1
(Invitrogen) as described by the manufacturer. RT-PCR and PCR products were detected by electrophoresis in a 2% agarose gel.

**RFLP analysis of the coat protein gene.** PCR products were digested with restriction endonucleases *Hae* III and *Kpn* I at 37°C for at least 2 h according to manufacturers’ instructions (Gibco BRL). The digests were resolved by electrophoresis with 2% agarose gels in Tris-borate-EDTA buffer at 5V/cm for 2 h. The reference severe strain was H33 from Texas (6). The RFLP migration pattern of p25 was observed and photographed under a UV transilluminator.

**Nucleotide sequences and computational analysis.** The cloned cDNAs were sequenced using Sequi Therm Excel II DNA sequencing in a Li-Cor sequencer (LI-COR, Inc., Nebraska, USA). Sequences were analyzed by a BLAST program at Gen Bank (www.ncbi.nlm.nih.gov). The multiple sequence alignment program Clustal W (version 1.6) (17) was used to obtain an optimal nucleotide or amino acid sequence alignment file. Phylogenies constructed using phylogenies created by DNA STRIDER software (10) with 20 different restriction enzymes. This analysis showed that the CTV strains designated as mild strains did not contain the *Hae* III and *Kpn* I.

**RESULTS AND DISCUSSION**

**Coat protein RT-PCR.** Fig. 1 shows the 688 bp fragments amplified by RT-PCR, corresponding to the coat protein gene of several CTV isolates from Nuevo Leon (NL), Tamaulipas (T) and Veracruz (V). The last lane corresponds to CTV H33, a severe virus strain from Texas used as a reference. One sample, NL1, yielded poor amplification, in spite of an increase in the total RNA concentration and modification of several PCR reaction conditions, such as the annealing temperature. It may have been due to low virus concentration affecting the quantity of the RNA template. Similar results were reported by Bar-Joseph, (3) where they showed that low concentrations of viral RNA cause defective amplification.

**RFLP analysis of the coat protein gene.** The RFLPs of the amplified CP genes digested with the restriction enzyme *Alu* I showed that it was not possible to differentiate the isolates according to their RFLP patterns. (Data not shown) Furthermore, when the profiles were grouped, based on the pattern of bands, the dendrogram showed similar results with no evident relationship among CTV isolates. The severe strain H33 was grouped with the mild isolates V2 and NL1 (data not shown).

However, we found that restriction enzymes *Hae* III and *Kpn* I allowed the separation of severe strains from mild by analyzing the coat protein gene (data not shown). Over 25 sequences of the p25 gene from mild and severe strains were deposited in GeneBank and these were analyzed by DNA STRIDER software (10) with 20 different restriction enzymes. This analysis showed that the CTV strains designated as mild strains did not contain the *Hae* III and *Kpn* I.
restriction sites. On the other hand, the severe strains that cause tree decline had only the Hae III restriction site, but not the Kpn I site. An interesting point is that virus strains that induce stem pitting present both restriction sites Hae III and Kpn I. However it would be necessary to confirm this observation with larger numbers of biologically-characterized CTV isolates.

Isolates NL1, V1 and NL2 and reference strain H33 have the Hae III and Kpn I restriction sites, and isolates T2 and V2 do not (Fig. 2). Gillings (5) found that RFLPs generated by digesting the p25 gene with the restriction enzyme Hinf I proved useful separating strains of CTV. Seven groups were defined, some of which included isolates with similar biological characteristics. In our case, Hae III was useful for discriminating the mild from severe strains. We consider that the protocol developed in this work offers advantages to those previously reported, because a single digest could discriminate between mild and severe strains. A method to differentiate mild or severe strains based on monoclonal antibodies (11) has already been superseded by new molecular techniques. For such a reason, we consider that our method could help because is straightforward and less expensive.

**Sequence analysis of the p25 gene.** The amino acid sequences of isolates NL1, V1, NL2, V2 and T2 showed an 85% homology to one another. Pappu (12) found similar results when they analyzed the relationship between the virulence of different CTV isolates and the p25 gene sequences. The isolates NL1, NL2 and V1 showed 96% similarity with the severe CTV strain H33. Isolates T2 and V2 showed 99% of identity with strain T30 (characterized as mild).

The multiple alignment of CP amino acid sequences of strains T30, T385, SY568 and T36 showed that severe strains have conserved residues at positions 49, 63 and 124 corresponding to glycine (G), threonine (T) and phenylalanine (F) respectively, while strains considered as mild had serine (S), alanine (A) and a tyrosine (Y), respectively at the same positions (Fig. 3). The first two amino acid changes have not been reported in the literature before. However, Pappu (12) stated that severe strains have conserved phenylalanine (F), while the mild strains have conserved tyrosine (Y) at the same position, with this being the only distinguishing characteristic among the previously reported severe and mild strains. We believe that these residues could play an important role in the CTV pathogenesis that would be worthwhile to study in the future.

Isolates V2 and T2 do not possess the restriction sites Hae III and Kpn I, reported from mild strains. However, severe strains such as T36 that cause tree decline, have only the restriction site Hae III, while severe strains such as SY568 that also induce stem pitting, have both the Hae III and Kpn I restriction sites. Isolates NL1, NL2 and V1 have both these sites. From the multiple alignments of
our sequences, and with those already reported and biologically characterized, T36 (decline), SY568 (stem pitting), T30 and T385 (mild) (12), a dendrogram of similarity was generated with Protodist and Phylip software. Isolates NL1, NL2, V1 and T2 formed one group closely related to the severe isolate T36/SY568 cluster (all possessing the HaeIII and KpnI sites), while isolate V2, formed a cluster with the mild isolates T30. Isolates V2 and T30 were related with a genetic distance of 0, as was the cluster formed by the severe strains SY568 and T36. Isolate CBG-T2 showed a greater phylogenetic distance compared to other isolates where distances between 1.4 and 1.6 were observed (Fig. 4).

The RFLP analysis of the coat protein gene after digestion with Hae III and Kpn I restriction enzymes has the potential to differentiate mild strains from severe, but
more characterized isolates need to be evaluated to determine if this pattern holds.

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