



## New Disease Reports

**First report of Tomato leaf curl Sinaloa virus infecting tomato crops in Panama**J.A. Herrera-Vásquez<sup>1\*</sup>, D. Ortega<sup>2</sup>, A.B. Romero<sup>1</sup>, S. Davino<sup>3,4</sup>, L.C. Mejía<sup>5,6</sup>, S. Panno<sup>4</sup> and M. Davino<sup>7</sup>

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In April 2011 and September 2012, virus-like symptoms were observed in open field- and greenhouse-grown tomato crops (*Solanum lycopersicum*) in Chiriquí, the westernmost province of Panama. Samples from symptom-bearing plants (127 in all) were collected and tested for the presence of begomoviruses by polymerase chain reaction (PCR) assays with sets of degenerated primers designed to amplify parts of the DNA-A and DNA-B components (Rojas *et al.*, 1993; Table 1). Products of the expected sizes, obtained with both DNA-A- and DNA-B-specific primers for 49 samples, suggested infection with New World bipartite begomoviruses. This corresponds to an incidence of 26% (8 plants) in open field, and 43% (41 plants) in greenhouse crops. Primers specific for ten tomato-infecting begomoviruses found in Central America (Engel *et al.*, 1998; Nakhla *et al.*, 2005; Table 1) were used to typify the PCR-positive samples.

This analysis revealed *Potato yellow mosaic Panama virus* (PYMPV) or *Tomato leaf curl Sinaloa virus* (ToLCSiV) in 44 (90%) or 40 (82%) of the samples, respectively. All contained at least one virus, the majority (i.e. 35) indeed both, with no indication of the other viruses tested. BLAST analysis of two PCR products' sequences of the distinct viruses (GenBank Accession Nos. KP313717 for PYMPV and KP318651 for ToLCSiV, respectively) revealed that KP313717 shared 99% DNA sequence identity with PYMPV - [Panama:Divisa:Tomato:1996] (PYMPV-[PA:Div:Tom:96], (Y15034) (Engel *et al.*, 1998), and KP318651 99% identity with ToLCSiV - [Nicaragua:Santa Lucia] (ToLCSiV-[NI:SL], (AJ608286) (Rojas *et al.*, 2005) and three other ToLCSiV sequences: [Nicaragua:Santa Lucia] (AJ508779), [Nicaragua:Sebaco] (AJ508780) (Rojas *et al.*, 2005), and [Costa Rica:Alajuela] (AF131213); as well as 98% identity with ToLCSiV-[Nicaragua:Condega] (AJ508778) (Rojas *et al.*, 2005).

Differences in symptom expression were in some cases observed between plants infected with both viruses (Fig. 1A), or with PYMPV (Fig. 1B) or ToLCSiV (Fig. 1C) alone. Begomovirus-free plants (Fig. 1D) also showed virus-like symptoms resembling those induced by other viruses, especially in the *Potyviridae* and *Tobamoviridae* (Polston & Anderson, 1997). Due to the high capacity of recombination between different begomoviruses (Davino *et al.*, 2012), the existence or development of novel recombinant molecules cannot be excluded, which could lead to the emergence of new begomoviruses with different biological properties compared to the

ancestral parental viruses in the future. To our knowledge, this is not only the first detection of ToLCSiV in Panama, but also the first report of PYMPV in Panama's western highlands, and the first ever report of PYMPV/ToLCSiV mixed infection. Additional studies on incidence and distribution of these viruses in Panama are in progress.

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Figure 1

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