



Occurrence of the Israel strain of *Tomato yellow leaf curl virus* in New Caledonia and Loyalty Islands

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In 2007, severe symptoms of leaf curling and yellowing resembling those of tomato yellow leaf curl disease were observed for the first time on tomato plants (*Solanum lycopersicum*) with a high incidence in fields and greenhouses in the south western region (Nouméa) of the Pacific island of New Caledonia. Tomato samples with leaf curling and yellowing symptoms were collected in the south west and west of New Caledonia and also Ouvéa (Loyalty Islands), respectively, in November and December 2010 (Table 1). Samples were tested for the presence of begomoviruses using a polymerase chain reaction (PCR) assay with a set of degenerate primers designed to amplify genomic regions of the Old World begomovirus DNA-A component (Delatte *et al.*, 2005). PCR products of the expected sizes were obtained for all the five samples from New Caledonia and for four of the six samples from Ouvéa suggesting the presence of an Old World monopartite begomovirus.

PCR positive samples were processed further and full-length viral genomes were successfully amplified from six samples (Table 1) by rolling-circle amplification, cloned using *XmnI* restriction enzyme and sequenced (Shepherd *et al.*, 2008). The complete DNA-A genome sequences obtained (EMBL-GenBank-DDBJ Accession Nos. HE603241-HE603246), showed the highest pairwise sequence identity of 97.6 to 99.4% (BLAST, NCBI) with isolates of the Israel strain of *Tomato yellow leaf curl virus* (TYLCV-IL) from Spain ([SP:Alm], AJ489258) and Reunion ([RE:SGi:RE4:04], AM409201). The new sequences were aligned with representative sequences of TYLCV strains using MUSCLE (using default settings) in MEGA5 (Tamura *et al.*, 2011). A maximum-likelihood (ML) phylogenetic tree (Fig. 1) was constructed from the full alignment using PHYML with GTR+G4 selected as the best model of sequence evolution by RDP3 (Martin *et al.*, 2010).

The ML phylogenetic tree confirmed the relationship of New Caledonia and Ouvéa isolates of TYLCV-IL with the isolates of Spain [SP:Alm] and Reunion [RE:SGi:RE4:04] (Fig. 1). Surprisingly despite the proximity of New Caledonia and Ouvéa to Australia, the New Caledonian TYLCV isolates seem to have a different origin/source of introduction to those recently described from Australia [AU:Bri1:06] and [AU:Bun1:06] (Van Brunshot *et al.*, 2010). This divergence suggests that the epidemic of TYLCD in New Caledonia and Loyalty Islands seems not directly associated with the introduction of TYLCV-IL in Australia where the first symptoms of TYLCD were described in 2006. To our knowledge, this is the first report of the Old World TYLCV implicated in yellow leaf curl disease on tomato in New Caledonia and Loyalty Islands. This description confirms the invasion and the dissemination of the Israel strain, also called "severe" strain, of TYLCV in the Pacific region, and represents a new

record of first importance for the regional management of emerging crop diseases and regulatory institutions.

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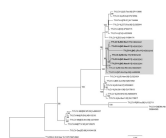


Figure 1

Table 1. Geographical origin of tomato samples and description of the Israel strain of *Tomato yellow leaf curl virus* (TYLCV-IL) isolates.

Accession No.	Region	Island of origin	Village	GPS coordinates	Host plant	TYLCV-IL genome sequence	EMBL accession No.
HE603241	New Caledonia	Nouméa	La Courbe	22°23'02" S 153°08'02" E	6	NC:New110	HE603241
HE603242	New Caledonia	Nouméa	La Courbe	22°23'02" S 153°08'02" E	6	NC:New110	HE603242
HE603243	New Caledonia	Nouméa	La Courbe	22°23'02" S 153°08'02" E	7	NC:New110	HE603243
HE603244	New Caledonia	Nouméa	La Courbe	22°23'02" S 153°08'02" E	11	NC:New110	HE603244
HE603245	New Caledonia	La Feu	Foua	21°15'00" S 153°07'02" E	20	NC:La110	HE603245
HE603246	Loyalty Islands	Ouvéa	Beau	20°48'00" S 153°00'02" E	6	NC:Ou110	HE603246

*From samples deposited in a public leafy stem collection.

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