



Occurrence of the Israel strain of *Tomato yellow leaf curl virus* and the whitefly *Bemisia tabaci* MEAM1 species in French Polynesia

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In 2014, severe symptoms of leaf curling and yellowing resembling those of tomato yellow leaf curl disease were observed for the first time on tomato (*Solanum lycopersicum*) plants with a 100% incidence in affected greenhouses in Tahiti (Fig. 1). Tomato samples with leaf curling and yellowing symptoms, and whiteflies were collected in Tahitian greenhouses from August 2015 to January 2016 (Table 1). Other whiteflies were collected from tomato and melon plants in Huahine and Tubuai islands.

Fourteen tomato samples were tested for the presence of begomoviruses using PCR assays with two sets of degenerate primers designed to amplify the coat protein gene of the Old World begomovirus DNA-A component (FD-CP-382/RD-CP-1038, Lett *et al.*, 2009; Clust4CP-F342/Clust4CP-R1032, Seka *et al.*, 2016). PCR products of the expected size were obtained from all the samples, suggesting the presence of an Old World begomovirus. Direct sequencing of the PCR amplicons (669 bp) and initial sequence similarity searches using BLAST indicated that the samples were infected by *Tomato yellow leaf curl virus* (TYLCV, genus *Begomovirus*, family *Geminiviridae*).

To confirm the molecular identification of the begomovirus, full-length viral genomes from two PCR-positive samples (Table 1) were amplified by rolling-circle amplification, cloned using *NcoI* restriction enzyme and sequenced. The two genome sequences were 2,781 nucleotides in length (GenBank Accession Nos. KY656825 and KY656826) and showed the highest pairwise sequence identity, 99.3%, (SDT; Muhire *et al.*, 2016) with isolates of the Israel strain of TYLCV (TYLCV-IL) from Australia ([AU:Bun2:06], GU178819) and China ([CN:Sha:SH2:06], AM282874). A maximum-likelihood phylogenetic tree constructed with publicly available TYLCV sequences (MEGA6; Tamura *et al.*, 2013), confirmed the genetic relationship of the French Polynesian isolates of TYLCV-IL with isolates from the Asia-Pacific region (Fig. 2). In parallel, total DNA was extracted from 96 female whiteflies (6 to 10 per greenhouse), sampled from different locations on each island (Table 1), to identify their species. The core region of the mitochondrial cytochrome oxidase I gene was amplified and sequenced (Thierry *et al.*, 2011). Sequences of 598 bp were obtained for 92 samples. A single haplotype was retrieved from all three islands and showed 100% pairwise sequence identity (BLAST) with the Middle East-Asia Minor 1 (MEAM1, KM821540) *B. tabaci* species.

To our knowledge, this is the first report of Old World TYLCV-IL implicated in yellow leaf curl disease on tomato in Tahiti. The occurrence of *B. tabaci* MEAM1 species was reported in 1996-97 in Tahiti (De Barro

et al., 1998), but never on the neighbouring islands of Huahine and Tubuai. This description confirms the invasion and the dissemination of both TYLCV-IL and *B. tabaci* MEAM1 species in the Asia-Pacific region. This report is of prime importance for the regional management of emerging diseases in these crops and for phytosanitary regulation.

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Figure 1



Figure 2

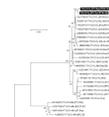


Figure 3

Figure 4

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