

Emergence of a recombinant *Tomato yellow leaf curl virus* and displacement of parental-type viruses in Morocco

Zineb Belabess^{1,2,3}, Cica Urbino¹, Sylvie Dallot¹, Martine Granier¹, Abdelali Blenzar³, Abdessalem Tahiri² and Michel Peterschmitt¹

¹ CIRAD-INRA-SupAgro, UMR BGPI, CIRAD TA A - 54 / K, 34398 Montpellier, France

² Ecole Nationale d'Agriculture BPS 40, Meknès, Morocco

³ Faculté des Sciences de Meknès BP 11201, Avenue Zitoune, Meknès, Morocco

Genetic recombination is a major mechanism of virus evolution and it is sometimes associated with serious epidemics especially within the *Geminiviridae* family. *Tomato yellow leaf curl virus* (TYLCV) and *Tomato yellow leaf curl Sardinia virus* (TYLCSV) are two geminiviruses of the genus *Begomovirus* which severely affect tomato crops in the Mediterranean basin. In Morocco, the epidemics caused by these two viruses have been successfully managed by controlling the insect vector, *Bemisia tabaci*, and by the use of symptomless tomato plants of cultivars bearing the resistant gene Ty1. As virus multiplication is only reduced but not completely abolished in those plants, it was expected that viruses may evolve under the selection pressure exerted by Ty1.

In 2010, TYLCV/TYLCSV recombinants were detected in symptomatic Ty1 tolerant cultivars. Further surveys carried out since 2012 evidenced that one of them, IS76, was widespread and had virtually displaced parental-type viruses in the Souss, the region with the highest tomato production of Morocco. As IS76 was not detected in old samples collected before 2003, we hypothesized that its emergence might be associated with the increasing use of tolerant cultivars in the years 2000. Using Bayesian inference with a temporally structured TYLCV and IS76 sequence dataset, the approximate date of occurrence of the recombination event leading to IS76 was determined and found to be consistent with such hypothesis.

To further support this hypothesis, the fitness of IS76 was compared with that of potential parental viruses of TYLCV and TYLCSV in controlled conditions. Taking viral DNA accumulation as a proxy for fitness, IS76 and parental viruses were compared in a susceptible and a tolerant Ty1 bearing cultivar. IS76 accumulated significantly more than its parental viruses in co-infected tolerant plants. This advantage did not pay any cost on coinfecting susceptible cultivars in which the accumulation of IS76 was similar to those of the parental viruses. Further studies are needed to understand the genetic determinism of the fitness advantage of IS76.

Mots-clés : Resistance breaking, Ty1 gene, viral fitness, Bayesian inference.