

AGROECOLOGICAL AND EVOLUTIONARY FACTORS DRIVING THE SUCCESS EMERGENCE OF A NON-CANONICAL TOMATO YELLOW LEAF CURL VIRUS RECOMBINANT

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BACKGROUND and OBJECTIVES

Recombination is one of the driving forces for viral evolution, and particularly for the Tomato yellow leaf curl (Tylc) associated begomoviruses (family *Geminiviridae*). TYLCV-IS76 (IS76) is a peculiar recombinant from Morocco generated between representatives of the Israel strain of *Tomato yellow leaf curl virus* (TYLCV-IL) and the Spanish strain of *Tomato yellow leaf curl Sardinia virus* (TYLCSV-ES). Unlike the previously reported TYLCV/TYLCSV recombinants, IS76 has a non-canonical recombination profile and has entirely displaced its parental viruses, possibly because of its positive selection by tomato cultivars bearing the *Ty-1* tolerant gene (see the sister communication of Belabess et al.⁽¹⁾). This prediction was tested by comparing the fitness of IS76 to those of representatives of parental viruses, in tomato plants harboring or not the *Ty-1* gene. As the fitness results were consistent with the selective hypothesis, a second question had to be addressed: as all the Mediterranean used tomato cultivar tolerant to Tylc associated viruses are bearing the *Ty-1* gene, why has such recombinant not been reported elsewhere?

MATERIAL and METHODS

The fitness of IS76 was estimated in a *Ty-1* tolerant cultivar, and in a susceptible nearly isogenic line, in single or mixed infections with parental viruses TYLCV-IL and TYLCSV-ES. Viral DNA intra plant accumulation was measured with real time PCR (qPCR) and used as a proxy of fitness. An artificial TYLCV-IS76 recombinant (IS76') was constructed by site-directed mutagenesis to analyze the molecular determinant of the potential fitness advantage. The probability of emergence of IS76 type recombinants was estimated in 10 *Ty-1* tolerant and 10 nearly isogenic susceptible plants co-infected with parental viruses, by monitoring the generated recombination patterns over time up to 240 days post inoculation (dpi).

RESULTS

IS76 DNA accumulation was significantly higher than that of TYLCV-IL and TYLCSV-ES in the tolerant cultivar, both in single or mixed infections. The fitness advantage of IS76 in the tolerant plants did not pay any accumulation cost in the susceptible plants in which IS76 accumulation was similar or higher than that of both parental viruses. Interestingly the IS76 selective advantage was associated with a dramatic negative impact on TYLCV-IL accumulation, which was shown to be determined by the recombination nature of IS76. Indeed, the TYLCV-IL parent dropped below the qPCR detection level at 120 dpi and the whitefly transmissibility level from 60 dpi. Recombinants exhibiting the typical IS76 recombination breakpoint were generated in plants of both cultivars co-inoculated with the parental viruses but very unexpectedly they remained at an extremely low frequency even up to one year after infection.

CONCLUSIONS

Our results support the positive selection of IS76 by the *Ty-1* gene and validate the selective hypothesis to explain its emergence and the entire displacement of its parents in the Souss. It is expected that the fitness advantage of IS76 may involve gene silencing because the *Ty-1* gene codes for an RdRp⁽²⁾ and because the short TYLCSV derived region of IS76 is located in a region which has been reported for two begomoviruses to be one of the favored target of siRNA and methylation⁽³⁾. The fact that IS76 type recombinants did not dominate in co-inoculated plants in which they were generated may suggest that their emergence may need a highly improbable combination of circumstance which may have occurred by chance in the Souss.

REFERENCES

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Programme and Abstracts