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Role of a short non coding viral sequence in bypassing crossprotection in tomato infecting begomoviruses

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TYLCV-IS76 (IS76) is a natural recombinant of Tomato Yellow Curl Virus (TYLCV, *Begomovirus, Geminiviridae*) in which 76 nucleotides (nts) of the intergenic region (S76) have been replaced by the homologous sequence from Tomato Yellow Curl Sardinia Virus (TYLCSaV). We monitored the emergence of IS76 in Morocco and showed, in controlled conditions, that its intra-plant accumulation was significantly higher than those of parental viruses in resistant cultivars carrying the *Ty-1* resistance gene. This gene is known to code for a γ-clade RNA-dependent RNA polymerase that prevents symptoms and reduces viral load. The competitive advantage of IS76 is detected irrespective of co-infection conditions, simultaneously with parents or 1 or 4 months after parents, which questioned the existence of crossprotection with TYLCV and more generally with begomoviruses.
Using TYLCV variants differing by 8 or 30 nts within the S76 region and qPCR monitoring of viral DNA accumulations, we proved the existence of a crossprotection phenomenon with the TYLCV parent, in Ty-1-resistant and susceptible tomato plants, and in turn that IS76 escapes this mechanism. Although crossprotection mechanisms with TYLCV are not yet known, we studied the genetic determinism of the crossprotection-escape and more specifically whether it is determined only by the S76 region. It this is true, the escape would be observed with the TYLCSaV parent, the donor of S76, and also with any other begomovirus that inherit S76 by recombination. A TYLCSaV mutant and a recombinant Tomato leaf curl Comoros virus (ToLCKMV) carrying S76 were engineered to test this hypothesis. Results will be discussed in relation with the emergence of IS76 and more generally with the crossprotection phenomenon in begomoviruses and its potential application in their management.

Mots clés : Premunition - Viral accumulation - Emergence - TYLCSaV.

Références :

1. Jammes et al., 2023, Virology, (578), pp. 71-80.
2. Belabess et al., 2016, J. Gen. Virol., (97), pp. 3433-3445.

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