

Studying begomovirus recombination in controlled and natural conditions

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Recombination is an important driving force in plant virus evolution. Tomato yellow leaf curl virus (TYLCV, Begomovirus) is a relevant model for studying recombination in controlled and natural conditions because of the following reasons: (i) begomoviruses are recombination-prone, (ii) the small size of their genomes is adapted for identifying genome-wide recombination profiles and creating libraries of randomly generated recombinants by genome-wide gene-shuffling [5], (iii) the straightforward determination of recombinant phenotypes using an original system allowing direct cloning of infectious genomes [5], (iv) the spread of TYLCV from the Middle East to the World with the risk of naturally emerging inter-species recombinants.

TYLCV has spread to Réunion Island where it is close but not in contact with the indigenous viruses of the South West Indian Ocean Islands, like Tomato leaf curl Comoros virus (ToLCKMV), because none of them was reported from Réunion. TYLCV has also spread to Western Mediterranean countries where it is in contact with the indigenous Tomato yellow leaf curl Sardinia virus (TYLCSV). Whereas recombinants isolated from tomato plants co-inoculated with TYLCV and TYLCSV exhibit a “monomorphic pattern” [1, 2], the TYLCV/ToLCKMV recombinants were highly variable within and between the co-inoculated plants [3, 4]. Consistently, all the 47 TYLCV /ToLCKMV recombinants randomly selected from a library of random recombinants were found to be infectious and their within-host accumulation was similar or intermediate to that of the parental clones [5]. The contrasting recombinant composition between plants co-infected with TYLCV and ToLCKMV was associated with stochastic effects including continuous random generation of a large range of recombinants and the relatively narrow population bottleneck determined here for the first time for a geminivirus. However, four recombinants were obviously selected for because they were detected from distinct plants [4].

Interestingly, the most frequent of these four recombinants — detected in 6 of 13 co-inoculated plants— exhibited the same recombination pattern as an emerging TYLCV/TYLCSV recombinant detected on tomato in Morocco (IS76). The non-TYLCV derived fragment of these recombinants was limited to a ~100 nt region located at the origin of replication which contrasts with the previously reported TYLCV/TYLCSV recombinants where the non-TYLCV fragment was at least 800 nts [1, 2]. Moreover, unlike the previously reported TYLCV/TYLCSV recombinants which were mostly detected with potentially parental viruses, IS76 was mostly detected without them.

References:

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