

## Is it possible to be “better” than wild type TYLCV?

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### ABSTRACT

Begomoviruses (Family Geminiviridae) are highly recombinogenic ssDNA viruses which are transmitted by the whitefly *Bemisia tabaci*. Consistently, potential recombination breakpoints were frequently detected on begomovirus genomes and natural recombinants were isolated in areas where different begomoviruses infect the same host species (Seal, 2006). The emergence of recombinants in natural conditions suggests that their fitness is high enough to compete with parental viruses but there are presently very few experimental data to support this suggestion. Tomato yellow leaf curl virus (TYLCV) is the most damaging and invasive begomovirus of tomato. Due to its spread to new areas, TYLCV does presently coexist with other begomoviruses isolated from tomato. Emergence of TYLCV recombinants was reported but their relative fitness and virulence compared to TYLCV were never tested. We have monitored how such recombinants emerge in tomato plants co-inoculated with TYLCV and a begomovirus isolated from tomato in an Indian Ocean island, Tomato leaf curl Mayotte virus (ToLCKMV), and have tested the fitness of a frequently isolated recombinant.

Recombinants were isolated as early as 30 days post inoculation (dpi) at a frequency of 1%. At 150 and 330 dpi more than 40% of the isolated genomes were recombinants. Unexpectedly, TYLCV tend to be displaced at 330dpi. Some recombinant patterns increased in frequency at 150 dpi and at 330 dpi in individual plants, and some of them were detected in parallel in distinct plants suggesting a positive selection. The most frequently isolated recombinant genome (R4) was prepared as an infectious clone which happened to be more virulent than its parents. Its fitness was tested in coinfection with both parental viruses. At 30 dpi, its infectivity (% of infected plants) was significantly higher than that of ToLCKMV, the parent with the lowest infectivity, but similar to TYLCV. Viral DNA accumulation of R4 was equivalent to that of TYLCV, the parent which accumulated the most. However, R4 is as poorly vector transmitted as ToLCKMV, the parent with the lowest transmission efficiency. The most “promising” recombinant of our experiment was finally not “better” than TYLCV, which is consistent with the previous results obtained with randomly generated TYLCV/ToLCKMV recombinants (Vuillaume et al., 2011) which were not fitter than both parental viruses.

It is proposed that complex competition and complementation interactions between several recombinants and the parental viruses may eliminate TYLCV at late stage of co-infection but possibly none of them may individually be “better”.

### References

Seal S.E. et al., 2006. *Critical Reviews in Plant Sciences*, **25**:23–46.

Vuillaume F et al., 2011. *PLoS Pathogens*, **7**(5): p. e1002028.