19-What prediction can be done from the consequences of an encounter between highly recombinogenic viruses

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Begomoviruses (Family Geminiviridae) have a circular single-stranded DNA genome (2.8 kb) and are transmitted by the whitefly *Bemisia tabaci* by the persistent modal. Tomato yellow leaf curl virus (TYLCV) is a begomovirus from the Middle East that has been disseminated in numerous regions of the world. This is the most invasive and damaging begomoviruses on tomato crop. In most regions where TYLCV was introduced, indigenous begomoviruses infecting tomato have been identified. The risk of emergence of recombinant forms of TYLCV is considered to be high as begomoviruses are known to be highly recombinogenic. The outcome of the meeting of TYLCV with Tomato yellow leaf curl Sardinia virus has been described in Spain (1) and Italy (2) and recombinant viruses with a wider host range and higher virulence than the parents were identified in field. The introduction of TYLCV in Reunion Island has created a dangerous situation because indigenous begomoviruses infecting tomato occurred in several islands of the South West Indian Ocean. The risk of the meeting of these indigenous begomoviruses with TYLCV species was estimated by testing recombinant generated artificial (3) or natural recombinants between TYLCV and Tomato leaf curl Mayotte virus (ToLCKMV). Considering their infectivity, relative accumulation and vector transmission, some recombinants genomes appeared to be serious candidates for the emergence.

1. **Monci *et al*., 2002**. A natural recombinant between the geminiviruses Tomato yellow leaf curl Sardinia virus and Tomato yellow leaf curl virus exhibits a novel pathogenic phenotype and is becoming prevalent in spanish populations. Virology 303, 317–326 (2002).
2. **Davino *et al*., 2012**. Recombination profiles between Tomato yellow leaf curl virus and Tomato yellow leaf curl Sardinia virus in laboratory and field conditions: evolutionary and taxonomic implications.JGV in Press. as doi:10.1099/vir.0.045773-0.
3. **Vuillaume *et al*., 2011**. Distribution of the Phenotypic Effects of Random homologous recombination between two virus species. PLoS Pathogens, 7 (5) : e 1002028 (10p.). [20110601].