

## Epidemiology, coexistence, diversity and evolution through recombination of emergent begomoviruses

Pierre Lefeuve<sup>1</sup>, Frédéric Péréfarres<sup>1</sup>, Gaël Thébaud<sup>2</sup>, Darren Martin<sup>3</sup>, Jean-Michel Lett<sup>1</sup>

<sup>1</sup>CIRAD, UMR PVBMT, Pôle de Protection des Plantes, Ile de La Réunion, 97410 Saint-Pierre, France

<sup>2</sup>INRA, UMR BGPI, F-34398 Montpellier cedex 5, France.

<sup>3</sup>IIDMM, University of Cape Town, Observatory 7925, Cape Town, South Africa

Among the plant viruses transmitted by insect vectors, the genus *Begomovirus* is responsible for many emerging diseases of major economic importance on various crops. Tomato yellow leaf curl disease (TYLCD) is one of the most devastating viral diseases affecting tomato crops in warm and temperate regions of the world and is associated to a complex of begomoviruses (TYLCV-like viruses). After the first epidemic of TYLCD in Reunion in 1997, we have described the successive invasion of two strains of TYLCV (TYLCV-Mld and TYLCV-IL). During a 7-year field survey, we observed a partial displacement of the resident TYLCV-Mld by the newcomer TYLCV-IL (Péréfarres et al, 2014). The better ecological aptitude of TYLCV-IL in single infections was demonstrated experimentally, which explains its rapid spread. However, we demonstrate that the relative fitness of virus strains can drastically change between single infections and co-infections. An epidemiological model parameterized with our experimental data predicts that the two strains will coexist in the long run through unilateral assistance by the fitter strain. Using a phylogeographic analysis based on Bayesian inference, we have reconstructed a plausible history of TYLCV diversification and movements throughout the world, and demonstrated that the Mediterranean basin represent the main launch-pad of global TYLCV movements (Lefeuve et al, 2010).

In the South-west Indian Ocean (SWIO) Islands, the study of the genetic diversity of begomoviruses has revealed the existence of an extraordinary diversity of indigenous viruses (Lefeuve et al, 2007a). Phylogenetic analyses of these sequences revealed a polyphyletic origin and a close relationship with the Mediterranean and African cluster of monopartite and bipartite begomoviruses. Moreover, we present evidence that detectable recombination events amongst African, Mediterranean and SWIO begomoviruses, while significantly contributing to their diversity, have not occurred randomly throughout their genomes. Based on detailed analysis of unique recombination events, we have demonstrated the existence and conservation of recombination hot- and cold-spots in the begomovirus genomes, and the obviously non-random patterns of sequence exchange (Lefeuve et al, 2007b). To go one step further in the analysis of factors influencing recombination patterns we performed experiments of co-infection of tomato plants to study the viral progeny of a worldwide emerging virus (TYLCV) and an SWIO indigenous begomovirus (Martin et al, 2011). Patterns of sequence exchange between these viruses appeared to be extraordinarily complex and variable. The analysis of the distribution of breakpoints confirms the existence of recombination hot- and cold-spots, already observed *in natura*, and proved the existence of deterministic phenomena involved in the evolution of viral populations.

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Martin *et al* (2011). Complex recombination patterns arising during geminivirus coinfections both preserve and demarcate biologically important intra-genome interaction networks. *PLoS Pathogens*, 7(9): e1002203.

Péréfarres *et al* (2014). Frequency-dependent assistance as a way out of competitive exclusion between two strains of an emerging virus. *Proc Biol Sci* 281, 20133374.

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