

 **P.23 - Searching for wide spectrum resistance to begomovirus disease in tomato in Réunion Island**

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The emergence of *Tomato yellow leaf curl virus* (TYLCV) and other begomoviruses from past decades in many countries was demonstrated to be coupled with the invasion of biotype B of the whitefly *Bemisia tabaci*. The vector is difficult to control with insecticides because of its feeding habit and its ability to develop resistance to most insecticides. Host plant resistance provides the best alternative means of managing the disease. Nevertheless, faced with the worldwide critical situation and the threat of mixed infections involving TYLCV and other begomoviruses, breeders now have to develop broad-spectrum genetic resistance for a more sustainable control of begomovirus diseases. As a close environment and a new ecological niche recently colonized by TYLCV, Réunion Island is an outstanding place to study and to analyze the evolution of the virus as well as the colonisation process of invasive biotype B of *B. tabaci* in tomato fields. It also offers experimental facilities in the tropics for diversifying resistance sources and building new strategies for durability in the face of the genetic plasticity of begomoviruses and their vectors. Resistances to both monopartite and bipartite begomoviruses were found from *S. chilense* and *S. pimpinellifolium* accessions. We also started to explore the whitefly resistance and its potential to provide additional scope for genetic resistance that could be efficient against diverse related begomoviruses. Another alternative for breeding resistance could be to search for recessive genes that are more likely to be constitutive components of cellular activity, providing other angles of attack on target viruses. Recently, we observed a high level of such a resistance in an accession of *S. pimpinellifolium*. In a preliminary study, this resistance appeared to be recessive with two genes involved. Novel recessive alleles of resistance could be obtained empirically from the mining of natural germplasm, but also from reverse genetic approaches such as targeting induced local lesions in genomes (TILLING). This technology does not rely on transgenics, is available for tomato, and has already demonstrated its capacity to create and identify novel alleles in other plants.