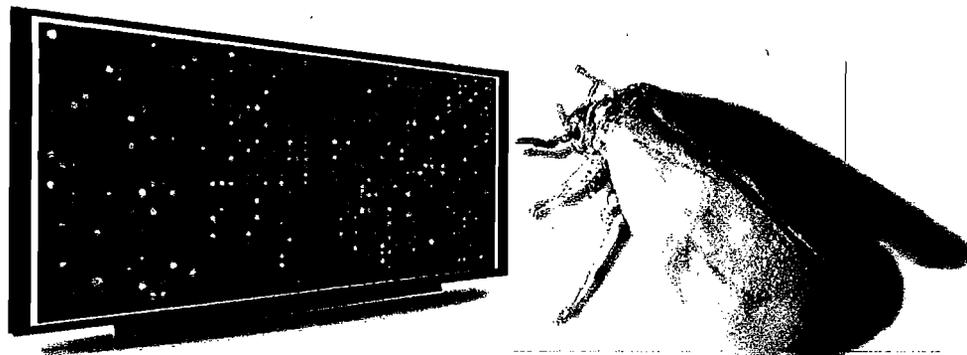




Genomics of Insect Pests to Agriculture

Program



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Multiple genetic and ecological outcomes following contacts between invading and indigenous populations of *Bemisia tabaci*

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The whitefly *Bemisia tabaci* is a pest of vegetable, ornamental and field crops. It is also the vector of several economically important plant viruses as Tomato yellow leaf curl virus. The comparison of cytochrome oxidase 1 sequences of a global collection of *B. tabaci* has revealed 12 well resolved genetic groups with a strong geographic structure. Based on the considerable genetic diversity together with distinct biological parameters and particularly varying abilities to interbreed, it was proposed that *B. tabaci* represent a cryptic species complex. Due to human activities, a genetic group, believed to be originating from the sahel-like regions of Middle Eastern Mediterranean/ North Africa/ Asia Minor, was very largely dispersed outside its geographic origin. This group, mainly consisting of individuals inducing physiological disorders on infested plants, is commonly referred to as the biotype B. As *B. tabaci* is a worldwide pest, the dispersed biotype B was often introduced into agroecosystems containing indigenous populations of *B. tabaci*. The objective of this study was to analyze the genetic and ecological outcomes of such contacts between the invading biotype B and indigenous populations in different regions of the world. In the Caribbean islands we have observed the almost complete displacement of the indigenous populations. In Reunion Island, we have detected the introgression of genetic material from the indigenous populations into biotype B. In Morocco, we have observed the coexistence of the indigenous populations and biotype B without any clear evidence of gene flow.

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