INTERNATIONAL WORKSHOP

SURVEILLANCE AND CONTROL OF CASSAVA DISEASES IN AFRICA

PÔLE DE PROTECTION DES PLANTES (3P) SAINT-PIERRE, LA RÉUNION ISLAND

JUNE 10-13, 2014





















A POPULATION GENETIC APPROACH ON WHITEFLIES VECTORS OF CMGs AND CBSVs

Hélène DELATTE Entomologist, population geneticist Cirad, Reunion Island

MGs that cause CMD are transmitted by the whitefly *Bemisia tabaci* Gennadius (Homoptera: Aleyrodidae). *B. tabaci* is a complex of cryptic species comprising genetically variable but morphologically indistinguishable populations. These cryptic populations vary in host range, fecundity, insecticide resistance, and virus transmission competency (among others). Within this species complex, several species are associated with cassava. Some might be better vectors or the most prevalent vectors of these viruses. Virus transmission was shown to be relatively efficient, indicating that even a small number of whiteflies is enough to transmit the virus and cause disease outbreaks.

In Africa, *B. tabaci*-colonizing cassava have been shown to be different from non-cassava-colonizing species. Those cassava-associated genotypes were raised at species rank and recently renamed as sub-Saharan Africa high-level genetic group (non-silverleafing). During the past decades, outbreaks of *B. tabaci* in many parts of sub-Saharan Africa have become more and more frequent. This whitefly is not only the vector of CMGs. It has also been conclusively proven as the vector of CBSVs. At present, *B. tabaci* is driving the dual pandemic of CMD and CBSD in several East and Central African countries and causing tremendous yield loss every year. Whitefly species diversity on cassava thus still needs more attention as few populations were studied from few African countries.

To fill this knowledge gap, two PhD students (Lensa Sefera Tajebe and Brice Kette Tocko-Marabena) have made recent studies in Tanzania and countries around CAR. Those studies focus on determining whitefly species on cassava plants, together with their associated endosymbionts, and more specific studies on some of those species at a population level. Our knowledge of biology, population genetic, and endosymbionts studies on *B. tabaci* in the Indian Ocean area will contribute to an understanding of the overall scheme of these whitefly upsurges observed together with CMD/CBSD pandemics.