Winston M.O. Thompson *Editor*

The Whitefly, *Bemisia tabaci* (Homoptera: Aleyrodidae) Interaction with Geminivirus-Infected Host Plants

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Dedicated to Iris and Christina

Preface

Whiteflies cause significant problems to agricultural production worldwide. There are various biotypes, but B-biotype is of particular importance because of its polyphagous feeding habit, high fecundity and resistance to a wide range of insecticides. It causes direct feeding damage such as the silverleaf condition in squash, but its efficacy in successfully transmitting several geminiviruses is responsible for a number of disease epidemics around the world. Examples include *Cotton leaf curl virus* (CLCuV) in Pakistan and India, *Tomato yellow leaf curl China virus* (TYLCCNV) in China and *Tomato yellow leaf curl virus* in various parts of the world. In Africa and India, the cassava biotypes pose similar problems. *East African cassava mosaic virus* and *African cassava mosaic virus* are effectively transmitted by the cassava biotype *B. tabaci.* In India, the *Indian cassava mosaic virus* is also transmitted by a cassava biotype that is genetically incompatible with the biotype transmitting *East African cassava mosaic virus* and *African cassava mosaic virus*.

The pathosystems involving B-biotype and crops such as cotton and tomatoes, and the respective geminiviruses: CLCuV, TYLCCNV present similar consequences as the pathosystems involving the cassava biotype, cassava and the geminiviruses affecting cassava. The interaction of vector, virus and host plant in some pathosystems, results in high population levels of the vector, which is responsible for several disease epidemics. In more complex situations, mixed infections and recombinant viruses involved in mixed infections contribute to the interplay of host plant, vector and viruses. Effects of infected host plants on population increase of the vector have been related to improved nutritional status of the host plant and/or suppressed plant defense mechanisms towards the vector. It is worthy to note that not all interactions are favorable to the vector, suggesting that pathosystems vary in the outcome of disease epidemics.

The objective of this E-Book is to introduce the different pathosystems along with the most recent findings and research endeavors. The various systems, each with its own challenge and complexity will unequivocally contribute to existing knowledge. With evolving geminiviruses and the appearance of new *B. tabaci* biotypes, new interaction events and disease epidemics can be anticipated. To this end, chapters are included to deal with emerging geminiviruses, and the distinction

between *B. tabaci* biotypes using advanced molecular techniques. This E-Book will be a good reference source, comprising related chapters devoted to an improved understanding of the intricacies underlying geminivirus disease epidemics in various parts of the world. Since the ultimate goal is to advance such understanding into sustainable management practices against *B. tabaci* and the geminiviruses they transmit, concluding chapters deal with management, and possible applications of Remote Sensing and Geographic Information Systems (GIS) technology.

This book will be of value to researchers in the biological and agricultural sciences, graduate students and corporations linked to the agricultural industry.

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Abbreviations

AISA	Airborne Imaging Spectroradiometer for Applications
ANOVA	Analysis of variance
AVIRIS	Airborne Visible/Infrared Imaging Spectrometer
BCIP	5-Bromo-4-chloro-3-indolyl phosphate
CASI	Compact Airborne Spectrographic Imager
CIR	Color Infrared
DNA	Deoxyribonucleic acid
dNTP	deoxyribonucleoside triphosphate
GIS	Geographic Information System
HYDICE	Hyperspectral Digital Imagery Collection Experiment
HyMap	Hyperspectral Mapper
IPM	Integrated Pest Management
IRM	Insecticide Resistance Management
ISEM	Immunosorbent Electron Microscopy
kDa	Kilodalton
NBT	Nitro blue tetrazolium
NCBI	National Center for Biotechnology Information
NIR	Near Infrared
ORF	Open Reading Frame
PCR	Polymerase Chain Reaction
PNPP	*p*-Nitrophenyl Phosphate
RAPD	Random Amplified Polymorphic DNA
RH	Relative Humidity
RNA	Ribonucleic acid
SDS-PAGE	Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis
TAS-ELISA	Triple Antibody Sandwich Enzyme Linked Immunosorbent Assay
TBS	Tris Buffered Saline
UV	Ultraviolet
WTGs	Whitefly Transmitted Geminiviruses

Chapter 1
Introduction: Whiteflies, Geminiviruses and Recent Events

Winston M.O. Thompson

Abstract The first part of this chapter introduces the whitefly as an important economic pest affecting agricultural crops worldwide. It deals with whitefly development and classification, whitefly biotypes and whiteflies as important vectors of plant viruses. Among such viruses are the geminiviruses which are discussed in terms of genetic constitution, host plants and insect vector, of which the whitefly *Bemisia tabaci* is among the most destructive of the vectors. The developments over the past two decades as these relate to *B. tabaci* and transmitted geminiviruses are highlighted. The second part of the chapter introduces the forthcoming chapters of the book.

1.1 The Whitefly

Whiteflies (Homoptera/Hemiptera: Aleyrodidae) are insect pests of significant economic importance affecting agricultural crops such as tomatoes, cotton, cassava and beans, as well as ornamentals. Of importance is the fact that they have worldwide distribution and as such are commonly known insect pests and vectors to entomologists, virologists, agriculturists and growers. They are about 2–3 mm in length, and wings are present in the adult stage of both sexes. The wings are generally opaque and covered with a whitish powder or wax. Abdomen lacks cornicles (tubular structures located dorsally towards the posterior end of the abdomen), and the hind wings are nearly as long as the forewings (Borror et al. 1989).

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Unlike many Homopterans that undergo paurometabolous development (gradual metamorphosis), the metamorphosis of whiteflies is different showing a pattern more towards complete metamorphosis (holometabolous development). Borror et al. (1989) describes the metamorphosis as "Intermediate". There are five instars including the adult. The first instar is active, while the following three are inactive or sessile. During metamorphosis wing development is internal and the wing pads are everted at the end of the third instar, appearing in the fourth instar which resembles a pupa.

Most whitefly species are oligophagous, but most whitefly pest species are polyphagous. There are however some oligophagous whitefly pest species such as *Aleurocybotus* spp. and *Aleurolobus* spp. that affect plants in the Family: Gramineae, and *Asterochiton* spp. affecting plants of *Acer* spp. (Byrne et al. 1990).

Many whitefly pest species are multivoltine, producing several generations a year. They also tend to develop resistance rather quickly to a large number of pesticides (Byrne et al. 1990). As vectors of pathogens, although bacteria and fungi can be transmitted by whiteflies (Costa 1976) whitefly pest species are of greater economic importance as vectors of plant viruses. Some Geminiviruses, Carlaviruses, Nepoviruses, Potyviruses and Closteroviruses can be transmitted by this group of insects (Byrne et al. 1990).

Brown (1994) reported 1,100 species of whiteflies worldwide, and only three are recognised as vectors of plant viruses. Of this number *Bemisia tabaci* (Gennadius) is considered the most important of the whitefly vectors of plant viruses, and the only whitefly species transmitting geminiviruses (Duffus 1987; Harrison 1985). Additionally, *B. tabaci* can also cause direct damage through sucking phloem sap and secretion of honeydew, which in particular, has caused serious problems in the cotton industry (Pollard 1955).

The Indian subcontinent is the suspected centre of origin of *B. tabaci* based on the presence of a large number of its natural enemies in that region. It has been suggested that the spread of the species probably occurred from the Indian subcontinent to Africa, Europe and the Americas, through the movement of plant material by man (Cock 1986).

Under favourable conditions *B. tabaci* can undergo 11–15 generations a year (Avidov 1956), and a female can lay between 100 and 300 eggs in her lifetime, which varies from 3 to 6 weeks (Azab et al. 1971; Bethke et al. 1991).

Early taxonomic separation of whitefly species was for the most part dependent on morphological characteristics of the pupal case (Gill 1992; Mound and Halsey 1978). This approach however, had some weaknesses because morphological characteristics can be altered based on species adaptation to a specific host. For example Russel (1958) reported that the early literature identified several genera and species of whiteflies that are now grouped under the single species, *B. tabaci;* some 18 previously described *Bemisia* species are now classified as *B. tabaci.* International collections of *B. tabaci* were shown to be genetically variable (Costa et al. 1993; Brown 1994). Wool et al. (1993) reported that such populations differed in the ability to utilise specific host plants for feeding and reproductive purposes. These populations also showed differences in virus transmission characteristics (Bedford et al. 1992, 1994). Although these differences occurred, the morphological characteristics of the pupal case were indistinguishable (Mound and Halsey 1978; Russel 1958).

From these earlier studies, it was recognized that a more reliable classification system depended on genetic and biochemical properties, and host plant adaptation, in addition to the morphological characteristics. Subsequently, the application of molecular techniques such as Polymerase Chain Reaction (PCR) and the use of DNA probes, as well as biochemical tools utilised for determining esterase banding patterns, had made possible the identification of different biotypes of *B. tabaci.*

Through the application of DNA sequencing, Fauquet et al. (1998) were able to identify a distinctive population of *B. tabaci* suspected as the driving factor for the cassava mosaic disease (CMD) epidemic in Uganda. In addition, a general esterase marker had been developed for identification of the B-biotype of *B. tabaci* (Brown et al. 1992; Bedford et al. 1992).

Characteristics of the B-biotype of *B. tabaci* include: Their highly polyphagous nature, feeding on a wide range of host plants of distinctive Families (Bedford et al. 1994); their high resistance to a wide range of insecticides including DDT, endosulfan and methyl parathion (Byrne and Devonshire 1993; Perrings et al. 1993); their ability to induce physiological disorders in several plant species within Cucurbita and Brassica, and *Solanum lycopersicum* L. (Bedford et al. 1992; Schuster et al. 1990). Some of these symptoms include the "silverleaf" condition in squash, tomato irregular ripening and broccoli light stalk (Toscano et al. 1994).

Some authorities were of the opinion that the B-biotype had sufficient distinguishing characteristics to warrant its placement under a new species. As a result the new species name, *Bemisia argentifolii* Perrings and Bellows, was sometimes seen in the literature. However, experimental findings of Byrne et al. (1998) questioned the species status of *B. argentifolii* since they reported interbreeding between the B-biotype and other biotypes of *B. tabaci*. In their work, they observed two insensitive forms of acetylcholinesterase (AchE) in the species responsible for resistance against carbamates and organophosphorus insecticides. According to their findings, AchE transcended the biotype boundaries established by the esterase binding pattern, and individuals of different biotypes showed the heterozygous form of AchE. They concluded that this was evidence of interbreeding having occurred. Thus, at that time, against a background of varying taxonomic opinion in relation to this particular group of whiteflies, it was not surprising that it was referred to in the literature as *B. argentifolii* or B biotype *B. tabaci.* Interestingly, with the appearance of other biotypes the more recent question has been whether *B. tabaci* is a species of many biotypes or rather a cryptic species complex.

While the effects of B biotype were seen from the mid1980s, another whitefly of great significance, *B. tabaci* Q biotype emerged on the scene *c.*10 years later. The Q biotype was observed in the Mediterranean basin (Guirao et al. 1997). It showed some of the early traits of B-biotype; exhibiting resistance to many insecticides, high fecundity and the capability to displace its competitors. In Spain during 2001–2002 B-biotype was displaced by the indigenous Q-biotype (Brown 2007). The Q biotype is closely monitored by researchers because of its potential to cause significant crop damage and losses through its ability to rapidly expand its population, transmit geminiviruses and overcome the effects of insecticides.

1.2 Geminiviruses

Geminiviruses are plant viruses with one or two single stranded circular DNA molecules. The single genome is *c*. 2.5–3.0 kb (Bisaro 1996; Gutierrez 2000). The capsid consists of two icosahedral particles of 18–30 nm in size (Gutierrez 1999).

As pathogens of significant economic importance, geminiviruses were responsible for tremendous yield losses. *Tomato yellow leaf curl virus* (TYLCV) in some fields caused up to 100% crop loss in the Dominican Republic and losses were estimated at more than US $10 million (Gilbertson et al. 2007). *Cotton leaf curl virus* has affected 50% of the crop in Pakistan (Ali et al. 1993) and severe cassava mosaic disease had caused a famine situation in parts of Uganda (Otim-Nape et al. 1994).

In an earlier classification in the 1980s, the family *Geminiviridae* showed four subgroups of geminiviruses transmitted by Homopterous insects. Subgroups I and II were transmitted by leafhoppers and planthoppers, whereas subgroups III and IV contain viruses transmitted by the whitefly, *B. tabaci* (Brown 1994).

Geminiviruses of subgroups I and II contain two icosahedrons (subunits) fused together giving a twin-like appearance, with a single circular DNA strand holding the units together (Goodman 1981; Goodman et al. 1980; Stanley and Davies 1985). In subgroup III two circular DNA strands are present, each in a separate coat protein (capsid). Members of subgroup IV are monopartite and contain a single DNA strand (Brown 1994).

A more recent classification, place geminiviruses into three genera: monogeminiviruses, hybrigeminiviruses and bigeminiviruses. Hybrigeminiviruses and monogeminiviruses are transmitted by different species of planthoppers and leafhoppers, and bigeminiviruses are transmitted by whiteflies (Gray and Banerjee 1999).

The two component geminiviruses show a conserved 200 nucleotide (nt) noncoding intergenic region (Matthews 1991). This region is capable of forming a hairpin loop and within this loop is a conserved sequence: TAATATTAC, seen in all geminiviruses (Lazarowitz 1987; Bisaro 1996).

Both DNA A and DNA B are required for infectivity of *African cassava mosaic virus* (ACMV) (Stanley 1983) as well as for *Tomato golden mosaic virus* (TGMV) and *Bean golden mosaic virus* (BGMV) (Morinaga et al. 1988). Sequences of the two DNAs are different except for the 200 nt conserved region (Matthews 1991). Comparisons of sequences of ACMV (Matthews 1991) with sequences of TGMV (Hamilton et al. 1984) and BGMV (Howarth et al. 1985) reveal that six of the open reading frames (ORFs) are conserved. The two ORFs in DNA B of ACMV are required for infectivity (Etessami et al. 1988).

In ACMV the coat protein gene is located in DNA A (Townsend et al. 1985). This is also the case for TGMV (Kallender et al. 1988). Based on the findings of Briddon et al. (1990), coat protein was observed to be a function of vector specificity. Coat protein is not essential for infectivity of ACMV (Etessami et al. 1989) or TGMV (Gardiner et al. 1988).

Bipartite whitefly transmissible geminiviruses can occur in mixtures within the host especially in Solanaceous plants (Garzon-Tiznado et al. 1993) and in Cucurbits

(Lazarowitz 1992) thereby allowing for genetic recombination and transencapsulation between viruses (Brown 1994). Padidam et al. (1999) have identified up to 420 significant recombinant fragments, and recombination events could occur both within and between genera suggesting the high versatility or plasticity of this group of viruses.

1.2.1 Genera of Geminiviruses

In the most recent classification, Geminiviruses belong to the Family: *Geminiviridae*. The genera within this family of viruses are described by several researchers (Lazarowitz 1992; Bisaro 1996; Fauquet et al. 2000; Briddon and Markham 2001).

Mastrevirus of which *Maize streak virus* is the type species, is the oldest and most diverse group. The viruses in this group are monopartite, transmitted by leafhoppers and they infect mainly monocotyledonous plants. These viruses encode the movement protein (MP) and the capsid protein (CP) on the virus sense strand. The complementary strand encodes the Rep protein and the Rep A protein; that is exclusive to Mastreviruses.

Curtovirus of which *Beet curly top virus* is the type species. The viruses in this group are transmitted by leafhoppers and infect dicotyledonous plants. These viruses are also monopartite and are thought to have originated from an ancient recombination event between a *Mastrevirus* and a *Begomovirus* (Rybicki 1994). The virus sense strand encodes the MP, CP and a V2 protein. The complementary strand has four open reading frames (ORFs) namely; Rep, C2, REn and C4.

Begomovirus of which *Bean golden mosaic virus* is the type species. These are transmitted only by whiteflies of the species *B. tabaci*. They include a large group of economically important viruses affecting dicotyledonous plants. Members in this group are mainly bipartite.

In genome A there are four ORFs on the complementary strand: AC1 (Rep), AC2 (TrAP), AC3 (REn) and AC4. The virus sense strand encodes the CP. On the B genome, two proteins encoded on the ORFs: BV1 and BC1 are involved in movement.

Topocuvirus of which *Tomato pseudo-curly top virus* is the type species. These are thought to have originated from Begomoviruses interacting with another virus. These viruses are transmitted by tree hoppers and they affect dicotyledonous plants (Gray and Banerjee 1999).

1.3 Significant Events over the Last Two Decades

The first evidence in the displacement of Biotype A by Biotype B in the USA was seen in 1990 when Arizona fields showed respectively compositions of 70% and 30% for the B and A biotypes (Brown 2007). Not surprisingly this newer more abundant biotype was found to be resistant to several insecticides. This

'abundance' characteristic of a *B. tabaci* biotype, in later years became an important driving force in geminivirus disease epidemics. The early 1990s were quite eventful with severe cassava mosaic virus disease seriously affecting cassava in Uganda (Otim-Nape et al. 1994; Gibson et al. 1996), Tomato yellow leaf curl being introduced into the Dominican Republic (Salati et al. 2002) and Cotton leaf curl disease from Pakistan spreading rapidly, moving into Northern India (Varma et al. 1993). Incidentally during the 1990s farmers and researchers in Indonesia observed symptoms of pepper yellow leaf curl on chilli peppers, but at that time the disease was not as yet causing serious problems. There was a complete different scenario however at the turn of the century when a condition referred to as Penyakit Kuning was of serious concern to chili pepper farmers in Indonesia (Chap. 9).

In 1991–1992, host associated biotypes were described on cassava and Okra (Burban et al. 1992) and Legg et al. (1994) reported cassava and non-cassava (sweet potato) biotypes in Uganda. There were also reports on the biological characterization of *B. tabaci* biotypes from various locations (Brown et al. 1992; Bedford et al. 1994). During this time B-biotype was rapidly spreading in Latin America and the Caribbean (Costa et al. 1993; Brown 1994) and had also moved into Brazil (Lourencao and Nagai 1994). The Silverleaf condition on squash was observed in the Southwestern USA (Liu et al. 1992; Cohen et al. 1992). This period had also seen the introduction of TYLCV into the USA (Polston et al. 1994) and the Caribbean region (Rojas and Gilbertson 2008). In 1994 B-Biotype was introduced into Australia (Gunning et al. 1997). Between 1994 and 1996, B-biotype displaced the Jatropha and Sida biotypes in Puerto Rico (Brown 2007). In 1996, Q-biotype was recognized as an important native pest in the Mediterranean basin (Guirao et al. 1997). At this time recombination of geminiviruses was observed (Zhou et al. 1997). In the late 1990s, displacement did not only occur among the vectors but among the viruses as well. In Spain, *Tomato yellow leaf curl Sardinia virus* (TYLCSV) was displaced by TYLCV (Sanchez-Campos et al. 1999). There was also the first report of TYLCV in Japan (Kato et al. 1998) and TYLCV had also spread into Puerto Rico (Bird et al. 2001). Interestingly B-biotype was not always the predominant biotype for competitive space and resources. In the period 2001–2002, B-biotype was displaced by the indigenous Q-biotype in Spain (Brown 2007). Around this time B biotype was first reported in Argentina (Viscarret et al. 2003). In the period 2003–2005, it was found that the silverleaf condition was also produced by a non-B biotype from Uganda (Sseruwagi et al. 2005), and that some *B. tabaci* populations infesting cassava could infest other host plants (Thompson 2003; Sseruwagi et al. 2006). Silverleaf condition was also induced by the Ms biotype of *B. tabaci*, indigenous to the Islands Southwest of the Indian Ocean. This latter biotype was found to be closely related to biotypes B and Q (Delatte et al. 2005). Years 2005–2006 had seen the introduction of Q-biotype into the USA, China, Japan and Mexico (Dennehy et al. 2005; Dong et al. 2006; Ueda and Brown 2006; Martinez-Carrillo and Brown 2007). In the 2005–2006 period severe cassava mosaic virus disease continued to spread and evidence indicated the involvement of an invasive biotype (Legg et al. 2002). In the USA, the Q biotype was found to be restricted to greenhouse

grown plants (Brown 2007). In 2007, *B. tabaci* Q biotype was observed in Syria (Fujiie et al. 2009). During this period it was once again displacing the B biotype in the Shandong Province of China (Chu et al. 2010).

The last two decades of events that occurred simultaneously or in tandem project a pattern of new emerging *B. tabaci* biotypes, movement of biotypes into other geographic locations, spread of begomoviruses into other areas, and in some cases displacement of one biotype by another. The displacement mechanism has also been seen among the begomoviruses, but the biological phenomenon quite common with begomoviruses is their propensity to undergo recombination; the consequences of which have presented challenges not only in terms of management but in the development and application of a robust dependable classification system. The classification of geminiviruses has been revised on a number of occasions (Fauquet et al. 2000, 2003), and some of the difficulties were related to the appropriate placement of new geminiviruses and/or recombinant viruses that were incongruous with the existing system. Although there is presently a more updated classification system of the geminiviruses even at levels below the species taxon (Fauquet et al. 2008), it is anticipated that further updates will become necessary as more geminiviruses begin to emerge.

1.4 Objectives and Outline

The objectives of this book is to present the different pathosystems to examine the consequences of the interaction of *B. tabaci* with begomoviruses: *East African cassava mosaic virus*-Uganda (EACMV-UG), *East African cassava mosaic virus* (EACMV), TYLCV and *Cotton leaf curl virus* (CLCuV). Also since geminiviruses continue to evolve and new *B. tabaci* biotypes emerge frequently, it is important to devote attention to whitefly biotypes, and evolving geminiviruses. The ultimate objective is to explore and present ecologically sound management practices for *B. tabaci* whiteflies and the geminiviruses they transmit.

The following chapter by Morales, presents a comprehensive handling of the subject on geminiviruses affecting Latin America and the Caribbean. It identifies problems of *B. tabaci* being associated with intensive cultivation, abusive use of pesticides, favorable conditions for the vector and disturbed ecosystems. The introduction of B-biotype, its adaptation to indigenous and exotic spp. and its efficacy in transmitting geminiviruses are also addressed. Mention is made of the original wild type plant spp. of *B. tabaci*, the appearance of *Bean golden mosaic virus* and *Bean golden yellow mosaic virus* and the distinction between these. One of the highlights of this chapter is the historical naming of Tomato yellow vein streak virus (Syn: Potato deforming mosaic virus) and the scientific debate regarding one name versus the other.

Chapter 3 by Czosnek and Ghanim, deals with TYLCV, vector transmission characteristics of this virus and in detail, outlines the intriguing events of virus travel through the vector's body. The important role of the GroEL homologue is emphasized along with the interaction of virus with vector proteins. The chapter

also reports on the inimical effects of the virus on the vector and introduces the whitefly functional genomics project and its benefits in elucidating for example, cellular determinants involved in transmission and the interactions involved during translocation of the virus within the vector.

Chapter 4 by Mann, reports the complex etiology of Cotton Leaf curl disease and the implicated begomoviruses. Details are provided on whitefly morphometrics, development and feeding behavior. This chapter deals with the factors influencing transmission, from acquisition to inoculation, and provides evidence of the non-mutualistic or pathogenic consequences resulting from the interaction of *B. tabaci* with *Cotton leaf curl virus*-infected plants.

Chapter 5 by Thompson addresses the severe cassava mosaic disease in Africa. The components of the pandemic and the driving ecological factors are considered. In this chapter the disease is also discussed along physiological and biochemical perspectives with the view of enhancing an understanding of the disease dynamics. Chapter 5 progresses into Chap. 6 that examines the consequences of the interaction between the vector and one of the parents of the causative agent responsible for the Uganda pandemic, *East African cassava mosaic virus* (EACMV). It deals with the important research question regarding the effects on the vector caused by the virus as a non-recombinant as opposed to it in recombinant form.

Chapter 7 by Palaniswami and Henneberry presents the interaction of *Indian cassava mosaic virus* (ICMV) with its vector at different trophic levels with detection of the virus within the vector and infected plants through molecular tools and serology. The characteristics of ICMV transmission is explored using various acquisition and inoculation feeding schedules and a distinction is made between the cassava and sweet potato biotypes based on biological assays and isozyme banding pattern. The influence of infected plants on *B. tabaci* population development is highlighted along with the effects of insect infestation on plant pathogenesis proteins within plants.

Chapter 8 by Thompson examines the role of amino acids in the interaction of *B. tabaci* with host plants, either infected or uninfected. The chapter also sheds light on the probable involvement of other factors that may be beneficial or detrimental to the vector during its association with the host plant.

Chapter 9 by De Barro, emphasizes the importance of a standardized system in whitefly identification and classification. It provides details on the various molecular tools utilized in whitefly identification with guidelines on the appropriate application of these. It points out the shortcomings that could result from failure to judiciously and meticulously apply the technology. The capacity of *B. tabaci* biotypes to invade other territories and become established is discussed along with the contributing factors. One of the highlights of this chapter is the author's discussion of the contradictory findings of two different groups of researchers on the question of the Uganda pandemic and the involvement of an invasive biotype.

Chapter 10 by Varma et al. is a comprehensive handling of the emerging geminiviruses around the world. This chapter deals with the associated WTGs of cassava, cucurbits, legumes, Malvaceae and solanaceous crops. Spread dynamics of these

are presented along with propelling factors for geminivirus evolution. The versatility and adaptation of geminiviruses are clearly underscored with cassava WTGs now infecting legumes and Jatropha, and non-leguminous WTGs affecting legumes. With emerging geminiviruses, new challenges and research endeavors can be expected.

Chapter 11 by Horowitz et al., covers management of whiteflies and outlines the principles of ecologically sound control practices. The main areas of management: chemical, biological, physical and cultural are discussed. The newer insecticides are introduced and the prospects of these for implementation are illuminated. The significant argument is that chemical control is not the panacea to insect pest and disease problems. Successful control is more based on Integrated Pest Management approaches.

In Chap. 12 by Gilbertson et al.: IPM strategies for WTGs, a schematic outlay of the strategy is presented. The approach is versatile and pragmatic, it hinges on a combination of practices employed from pre to post cultivation, and it emphasizes the need for regional coordination. The strategy is demonstrated with case studies on two crops (one annual and one perennial). Importantly, the authors deliberated on considerations of logistics; which is consistent with the general success of such approaches.

Remote Sensing technologies by Yang and Everitt, are presented in Chap. 13. The application of Remote Sensing along with GPS and GIS for detecting and mapping whiteflies is illustrated and the merits and importance of these approaches could be appreciated for forecasting purposes that impinge on strategies for both whitefly and geminivirus management.

Chapters are self-contained. As such coverage of common ground in some instances is inevitable, and construed as a way of allowing the contributors to fully express and emphasize the essential core principles. This book is made possible through the collaborative work of some of the leading researchers in the field.

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