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Bemisia tabaci (Gennadius): From Complex Species to a Species-Complex

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Abstract
The whitefly, *Bemisia tabaci* (Gennadius), a cryptic species-complex, encompasses a number of morphologically indistinguishable species which differ genetically from each other. It probably represents the highest number of biotypes or genetic groups than any other species in the order Hemiptera. The pest is distributed over almost all regions of the world with high economic impact owing to its direct feeding effect as well as vector of many plant viruses. Since the emergence of its invasive B-biotype in 1980s, novel genetic groups are being reported from different regions of the world based on biochemical techniques and mitochondrial CO1 gene sequences. With only few biotypes identified in early 1990s, reports of new genetic species are increasing in recent years. Here, we present in this review, the progress made in the identification and classification of different genetic groups within this species-complex. Besides, its role as a plant virus-vector and management aspects are also discussed.

Keywords: Biotypes, Cryptic Species, Endosymbionts, Genetic Groups, Virus-Vector, Whitefly

Introduction
In 1889, a fly-like pest was observed devastating tobacco crop in Greece which was described by the then Inspector of Agriculture, Panayiotis Gennadius, as the tobacco whitefly, *Aleyrodes tabaci* Gennadius [1]. Since then, it was reported independently in different parts of the world with different names assigned [2,3]. All of these species were later brought under *Bemisia tabaci* (Gennadius) [4]. Among different morphologically indistinguishable populations under Bemisia, a number of biological and behavioral variations like host range, their adaptability, virus transmission efficiency, resistance to insecticides, degree of invasiveness, capability to produce phytotoxic effect were observed which led to the concept of biotype or host races [5]. Although, the term biotype was coined to differentiate among races, but the B-biotype with considerably broad host range, high invasiveness, biology, and efficient virus transmission, was reviewed as a separate species under the genus *Bemisia* [6]. Based on some morphological and allozymic characters, the B-biotype was described as a distinct species, the silverleaf whitefly, *Bemisia argentifolii* Bellows and Perring [7,8]. However, owing to the monophyly of biotypes under the genus *Bemisia*, as revealed by phylogenetic analysis and other experimental supports, the status of a distinct species was argued [9-12]. On the basis of plastic morphological differences, *B. argentifolii* could not be delineated as a species, but only as a member of *B. tabaci* species complex [10]. The taxonomy of whiteflies is mainly based on the morphological characters of 4th instar nymphs, also referred as puparium, which remains adhered to the leaf surface of the host plant [13]. Plasticity in morphological variations is common among the biotypes of *B. tabaci,* which can be accounted to host plants leaf surface characteristics or environmental conditions [14,15].

The impact of this pest was not so serious until 1980s when a highly invasive biotype started causing havoc, particularly in ornamental plants grown in greenhouse conditions in South Western America and some other parts of the New World. Onset of intensive agricultural practices, high use of nitrogenous fertilizers, and particularly wide-scale monoculture has intensified the insect-pest problems. The losses in United States alone due to B-biotype were estimated as half a billion dollars in 1991 which was extremely high as compared to the native A-bioytpe [16]. The B-biotype started dominating the A-biotypes and the *Trialeurodes vaporarium* in the new world. These biotypes of *B. tabaci* were used to be demarcated on the basis of distinct esterase banding pattern and some biological characteristics [17]. The B-biotype had highly invasive nature and was able to cause silverleaf symptoms in squash and some other plants like honeysuckle and nightshade [17,18]. In contrast, the A-biotype, (Arizona), native to the new world, was not able to produce any phytotoxic symptom [19]. The invasiveness and serious economic impact created by the B-biotype attracted many workers as a hotspot study area. This biotype, at present, is categorized under the Middle East Asia Minor (MEAM) genetic group which has been found with a number of genetic uniqueness related to insecticide resistance, detoxification and virus transmission. Individuals of genetic group MEAM1 have very high fecundity hence, these are highly invasive [20]. In addition, horizontally transferred genes from bacteria and fungus also enable it as a highly invasive and efficient vector of viruses [21]. Population of many genetic groups can also shoot up without having invasion of a new population or species into their region [22,23].

Genetic Groups Under *B. Tabaci* Species-Complex

With advancement in molecular technologies and phylogenetic analyses, the genetic variations among the biotypes of *B. tabaci* were being worked out with more clarity and have had increasing reports of distinct genetic groups. Molecular evidences, on the basis of mitochondrial 16S and COI sequences, revealed that the B-biotype originated in the old world and invaded new world through increased anthropogenic activities [24]. Cervera et al. grouped *B. tabaci* biotypes in four clusters using Amplified Fragment Length Polymorphism (AFLP) markers, (1) Near East and Indian subcontinent biotypes, (2) B and Q biotypes including a Nigerian population from cowpea, (3) New World A-biotype and, (4) S-biotype including a Nigerian population from cassava. Boykin et al. used the Bayesian technique of phylogenetic analysis of mtCO1 gene and listed 12 major genetic groups (Table 1) [25,26].

S. No.	Location of sample collection	Name of the biotypes/genetic groups reported	References	Remarks
1.	Arizona and Floida	(1) A biotype and (2) B biotype	[17]	Population distinguished in to A and B biotypes based on esterase banding pattern
2.	World-wide	(1) Benin (2) India (3) Sudan (4) Israel-Yemen, (5) New world type	[24]	1. First molecular evidence that B-biotype was introduced from Old world to New world 2. Provided MtCO1 sequences as a baseline set to which other sequences could be compared
3.	World-wide	(1) Type A from California (US) and a population from Culiacan, Mexico (2) *B. tabaci* (type B) and *B. argentifolii* (3) A single population from Benin, Africa.	[123]	
4.	India, Pakistan, Turkey, Arizona, Nigeria, Spain	(1) Near East and Indian subcontinent biotypes (2) B and Q biotypes including a Nigerian population from cowpea (3) New World A biotype and (4) S biotype and a Nigerian population from cassava	[25]	Used Amplified Fragment Length Polymorphism (AFLP) markers for assessing genetic variations
5.	World-wide	(1) Mediterranean/Asia Minor/ Africa invasive (B, B2 biotypes) (2) Mediterranean (MED) invasive (Q, J, L biotypes) (3) Indian Ocean (MS biotype) (4) Sub-Saharan Africa silverleafing (Q-related biotypes) (5) Asia I (M biotype), (6) Australia (AN biotype), (7) China (Non-B biotype), (8) Asia II (H, K, P biotypes), (9) Italy (T biotype), (10) New world (A, C, D, G, N, R biotypes), (11) Sub-Saharan Africa non-silverleafing (E, S biotypes), (12) Uganda Sweetpotato	[26]	Phylogenetic analysis was done first time through Bayesian technique using large scale world-wide sampling

6.	Japan	(1) *JpL*, (2) Asia I, (3) Asia II (4) China, (5) MED/Asia Minor/Africa	[27]	*JpL* genetic group was reported distinct from rest of the groups
7.	Guatemala	(1) New World, (2) B-biotype, (3) Q-biotype	[124]	First report of *Q*-biotype in Guatemala
8.	World-wide	(1) Asia I (H, M, NA biotypes), (2) Australia/Indonesia, (3) Australia (AN biotype), (4) China 1 (ZHJ3 biotype), (5) China 2, (6) Asia II 1 (K, P, ZHJ2 biotypes), (7) Asia II 3, (8) Asia II 4, (9) Asia II 2 (ZHJ1 biotype), (10) Asia II 5 (G biotype), (11) Asia II 6, (12) Asia II 7 (Cv bioytpe), (13) Asia II 8, (14) Italy (T biotype), (15) Sub-Saharan Africa 1 (SabSahAf1), (16) SubSahAf2 (S biotype), (17) SubSahAf3, (18) SubSahAf4, (19) Uganda, (20) New world (A, C, D, F, Jat, N, R, Sida biotypes), (21) Mediterranean (MED) (Q, J, L, SubSaharan Africa Silverleaf biotypes), (22) Middle East-Asia Minor (MEAM) 1 (B, B2 biotypes), (23) MEAM 2, (24) Indian Ocean (IO) (MS biotype)	[28]	1. Defined *B. tabaci* as a species complex of 11 groups containing 24 distinct genetic species 2. Generated new consensus sequences which was followed for new species identification
9.	China	(1) Asia I, (2) Asia II 1, (3) Asia II 2, (4) Asia II 3, (5) Asia II 4, (6) Asia II 6, (7) Asia II 7, (8) Asia II 9, (9) Asia II 10, (10) Asia III, (11) China 1, (12) China 2, (13) China 3, (14) MEAM 1, (15) MED	[30]	Four genetic groups viz., *Asia II 9*, *Asia II 10*, *China 3*, and *Asia III* were reported for the first time
10.	Argentina	Two distinct genetic species	[31]	One indigenous group from Argentina found as a separate species (*New World 2*)
11.	India, Indonesia, Thailand and China	(1) Asia I, (2) Asia IV, (3) Asia III, (4) Australia, (5) Australia/Indonesia, (6) China 1, (7) China 2, (8) China 3, (9) Japan 1, (10) Asia II 1, (11) Asia II 7, (12) Asia II 5, (13) Asia II 6, (14) Asia II 2, (15) Asia II 3, (16) Asia II 4, (17) Asia II 9, (18) Asia II 10, (19) Asia II 12, (20) Asia II 8, (21) Asia II 11, (22) Africa, (23) Italy, (24) MEAM 1, (25) MEAM 2, (26) MED, (27) IO, (28) New world, (29) New world 2, (30) SubSahAf1, (31) SubSahAf5, (32) SubSahAf2, (33) SubSahAf3, (34) SubSahAf4, (35) Japan 2, (36) Uganda	[33]	Seven new genetic groups viz., *Asia IV*, *Japan 1*, *Asia II 12*, *Asia II 11*, *Africa*, *SubSahAf5* and *Japan 2* were added to the list
12.	India	(1) Asia I, (2) Asia II 5, (3) Asia II 7, (4) Asia II 8, (5) MEAM 1, (6) Asia 1-India	[32]	*Asia I-India* was reported for the first time
13.	Italy	(1) Q-biotype, (2) B-biotype, (3) Ru biotype	[34]	*Ru* genetic group was reported for the first time
14.	North America, Bermuda, Canada, Mexico	(1) New world, (2) B-biotypes, and (3) Q biotypes	[125]	*Q*-biotype detected for the first time in Canada and Bermuda
15.	East Africa (Kenya, Tanzania, and Uganda)	(1) Sub-Saharan Africa 1 (SSA1), comprising of two sub-clades (I and II), and a (2) South West Indian Ocean Islands (SWIO)	[126]	*SSA1* sub-clade I found widely distributed in East Africa

16.	World-wide	(1) MED, (2) MEAM 1, (3) MEAM 2, (4) IO, (5) New World, (6) New World 2, (7) Asia II 5, (8) Asia I-India (9) Asia II 6, (10) Asia II 1, (11) Asia II 2, (12) Asia II 7, (13) Asia II 3, (14) Asia II 4, (15) Asia II 9, (16) Asia II 10, (17) Asia II 8, (18) Asia I, (19) Asia III, (20) Australia/Indonesia, (21) Australia, (22) China 1, (23) China 2, (24) China 3, (25) Italy, (26) Sub Saharan Africa 1 (SSA1), (27) SSA2, (28) SSA3, (29) SSA4, (30) Uganda, (31) JpL	[35]	Proposed minimum genetic divergence should be 4% to demarcate genetic groups
17.	Yunnan, China	(1) MEAM1, (2) MED (3) China 2, (4) China 3, (5) China 4, (6) Asia I, (7) Asia II 1, (8) Asia II 6	[30]	*China 4* genetic group was reported for the first time
18.	Karnataka, India	(1) Asia-I, (2) Asia-II-7, (3) Asia-II-8, (4) MEAM-1, (5) MEAM-K	[37]	*MEAM-K* was reported for the first time
19.	India	(1) Asia I, (2) Asia I India, (3) Asia II 1, (4) Asia II 5, (5) Asia II 7, (6) Asia II 8, (7) Asia II 11, (8) China 3, (9) MEAM 1	[38]	*China 3* recorded for first time in India
20.	South West China	(1) Asia II 1-12, (13) China 1-5, (18) Asia III, (19) Asia IV, (20) Asia V, (21) Asia I	[39]	*China 5* and *Asia V*; two new genetic groups were reported for the first time
21.	Pakistan	(1) Asia II-1, (2) Asia II-5, (3) Asia II-7, (4) Asia II-8, and (5) MEAM-1	[127]	*Asia II 1* found prevalent all over the country
22.	Uganda	(1) SSA1, (2) SSA2, (3) SSA6 (4) SSA9, (5) SSA10, (6) SSA11, (7) SSA12, (8) SSA13, (9) MEAM 1, (10) MEAM 2, (11) MED, (12) IO	[40]	*SSA 9-13* were discovered in this study
23.	Israel	(1) MED, (2) MEAM 1	[41]	1. A total of 44 distinct genetic group was reported in the study based on 2903 sequences selected world-wide, out of which two genetic groups, *Asia II 13* and *Spain 1* were discovered for the first time
24.	Samples represented major geographical regions	(1) SSA (Uganda, Tanzania, and Democratic Republic of The Congo), (2) NAF–MED–ME ("B" reference genome and Sudan), (3) ASIA (India), (4) AS–PAC–AU (China), and (5) AM-TROP (Arizona, Puerto Rico, Ecuador) (Grouping done into major clades (Brown, 2010) rather than numerous genetic species)	[44]	This grouping was done through Automatic Barcode Gap Discovery (ABGD) analyses based on Nuclear Orthologs and CO1 data
25.	South Sudan	(1) MED, (2) IO, (3) Uganda, (4) Sub-Saharan Africa 1 sub-group 1 (SSA1-SG1), (5) SSA1-SG3, and (6) SSA2	[128]	
26.	Ecuador	(1) AM-TROP, (2) NAF-MED-ME	[129]	Grouping done in to major clades (Brown, 2010; de Moya et al, 2019)
27.	Uganda and Tanzania	(1) SSA1 (SSA1-SG1, SSA1-SG2, SSA1-SG3), and (2) SSA2	[130]	
28.	Uganda	(1) SSA1, (2) SSA2, (3) SSA6, (4) SSA9, (5) SSA10, (6) SSA11, (7) SSA12, (8) SSA13, (9) SSA14, (10) SSA15, (11) SSA16, (12) MED, (13) MEAM 1, (14) MEAM 2, (15) IO, (16) EA1	[131]	*SSA14*, *SSA 15* and *SSA 16* were discovered in this study
29.	North east region of India	(1) Asia I, (2) Asia II 1, (3) Asia II 5, (4) Asia II 7 and (5) China 7	[132]	China 7 was reported for the first time

Table 1: Biotypes/Genetic Groups Under *B. Tabaci* Species-Complex, as Reported from Different Studies

A year later, a distinct group (referred as JpL) was claimed in Honshu, Japan related to the B-bioytpe but still not considered widely as a member under the *B. tabaci* [27]. Dinsdale et al. grouped the *B. tabaci* species complex in to 24 genetic groups under 11 major groups using 3.5 % genetic divergence, however, recently, Brown et al. have proposed 1% nuclear divergence as a better threshold for drawing a phylo-biogeographical species boundary [28,29]. Subsequent to Dinsdale work, four new genetic groups (Asia II 9, Asia II 10, Asia III, and China 3) were added to the list by Hu et al. while studying diversity in China [30]. A year later, an indigenous biotype from Argentina was found as a distinct genetic species (New World 2) under *B. tabaci* species complex [31]. Concurrently, a new genetic group, Asia I-India, was reported from India, seven new (Asia IV, Japan 1, Asia II 12, Asia II 11, Africa, SubSahAf5 and Japan 2) were discovered while investigating populations from India, Indonesia, Thailand and China and a distinct one (Ru) was found in Italy [32-34]. These all genetic groups were reported based on the threshold of 3.5 % genetic divergence. Owing to large genetic variation observed amongst different genetic species within *B. tabaci* species complex, this threshold was not found realistic and a higher threshold of 4 % was used with report of 31 distinct genetic species [35]. Hu et al. reported 8 species from Yunnan, China, out of which China 4 was found distinct from all of previously known groups [36]. Survey made in Karnataka, India, revealed a diversity of 5 different genetic groups including MEAM-K which was reported for the first time [37]. In a country-wide sample survey made, a diversity of 9 genetic groups were found with China 3 reported for the first time in India [38]. Later on, China 5, Asia V, SSA 9-13, Asia II 13, Spain I were added to the list of genetic groups under *B. tabaci* species-complex [39-41]. Naga et al. recorded Asia II 5 in the major potato growing areas of India [42].

In contrast of numerous genetic groups, Brown had mentioned only 7 major phylogeographic clades i.e. (1) Sub-Saharan Africa I, (2) Sub-Saharan Africa II, (3) North Africa-Mediterranean-Middle East region (NAF-MED-ME), (4) Asia I & Australia-Pacific, (5) Asia II, (6) American Tropics (AM-TROP): North & Central/Carribean, and (7) AM-TROP: South America. As new reports of genetic groups were being added to an already numerous lists, the validity and usefulness of vast number of genetic species was doubted [43]. Large number of genetic groups might be the result of higher divergences in mitochondrial CO1 gene, so consideration of nuclear genes with lower divergence is needed [44]. Unlike genetic groups, populations representing major geographical regions of the world were grouped in to 5 major clades, (1) Sub-Saharan Africa (SSA), (2) North Africa-Mediterranean-Middle East (NAF-MED-ME), (3) Asia, (4) Asia-Pacific-Australia (AS-PAC-AU), and (5) American Tropics (AM-TROP), through Automatic Barcode Gap Discovery (ABGD) analyses based on Nuclear Orthologs and CO1 sequences [44].

Life-Cycle and Biology

B. tabaci, taxonomically positioned under the family Aleyrodidae of the superfamily Aleyrodoidea (Sternorrhyncha group) in the order Hemiptera of the class Insecta, is presently distributed widely over the globe (particularly in tropical and subtropical regions) owing to swift trade and transportation facilities. The life cycle consists of six stages; eggs, four nymphal stages and adults. An adult female, in its short life-span of about 4 weeks, can lay about 300 to 400 eggs [45]. The eggs are spindle shaped, yellowish-white in colour, laid in circular fashion or scattered singly attached mostly on the abaxial surface of the leaf. These are attached to the leaf surface through pedicels. The variation in period of life cycle mainly depends on temperature, relative humidity and host plants [46-49]. The hatching period varies from 2 to 9 days depending upon temperature conditions and host plants [50-55]. The first stage nymphs are oval in shape and whitish yellow in colour [50,52,56,57]. These nymphs crawl on the surface of the leaf for few hours to find a suitable feeding place. Once a suitable place is achieved, it settles where it continues to grow through second, third and fourth nymphal stages. The fourth instar nymphs are seen as a pupal stage of this insect. This stage is important in taxonomical identifications as it exhibit some morphological variations which can be used to separate *Bemisia* from other genus [13,58]. The adults are white in colour with yellowish wings and emerge from an inverted T- shape slit on the dorsal surface of the puparium. Ghelani et al. reported an average incubation period for eggs of *B. tabaci* as 7.04±0.52 days, hatching per cent of 65.11 ± 7.31, total nymphal period of 13.22 ± 1.1 days, adult longevity of 3.41± 0.37 days (male); 5.74± 0.49 days (female) and total life cycle of 25.16±1.26 days (male) and 27.48± 1.30 days (female) on tomato [55]. The mean total life cycle on cotton was reported as 25 days (female) and 23 days (male) on the variety H-1117 while on the Hybrid (RCH 134 BG II), it was observed as 23.9 days (female) and 22 days (male) [50]. Fekrat and Shishehbor reported total life cycle of *B. tabaci* as 14.9, 20 and 14.2 days, on eggplant, tomato and potato, respectively [48].

Virus Transmission, Damage and Economic Impact

The whitefly, *B. tabaci* has been known to infest more than 600 species of plant mostly from families Asteraceae, Euphorbeaceae, Malvaceae, Soalanaceae and Fabacae [3,59,60]. It is specially a phloem sap feeder and affects the plant in many ways. In direct feeding damage, it directly sucks the sap nutrient which debilitates the plant it infests. The infestation can result in chlorotic spots on the leaf, curling, drooping, and wilting which ultimately ceases the normal growth of a plant. Another way, in the process of feeding, it may induce some physiological disorder like silverleaf in squash (seen in case of B-biotypes), uneven ripening of tomato [61]. The honey dew secreted by these insects invites sooty mould which affects the process of photosynthesis and diminishes the appearance and marketability of the product. It causes stickiness in cotton which affects its processing. The most damaging way is it acts as a vector of some serious plant viral diseases. Of all the known viruses, nearly 75 % of them are transmitted by insect vectors, majority of them belong to the order Hemiptera [62].

Most of viruses which are transmitted by *B. tabaci*, belong to the genus *Begomovirus* under family Geminiviridae

and about 300 viruses from this genus are transmitted by *B. tabaci* [63]. These viruses are mostly transmitted in a persistent circulative manner. Acquisition of virus from the diseased plant by the insect vector and its inoculation back to a healthy one occurs through the stylet while feeding on plant sap. In some cases, while feeding on sap, virus is retained only up to the stylet and lost after few minutes or hours (non-persistent) beyond which the vector cannot inoculate it to other plants. In other cases, virus can enter and is retained in foregut of the insect, enhances the chances of inoculation to hours and days (semi-persistent). In case of Begomoviruses vectored by whitefly, it enters in to the midgut through the stylet, then to the haemolymph from where it reaches the salivary gland of the insect (persistent-circulative).

Also, there are instances where virus does replicates within the haemolymph or other tissues of the insect by virtue of which the inoculation capacity persists for whole life of the insect (persistent-propagative). An insect vector, when totally free of virus, needs a particular time period to acquire the virus and enable itself to transmit it to a healthy plant. This time period is known as Acquisition Access Period (AAP). The rate of virus transmission increases with the AAP [64]. Mehta et al. achieved the transmission of Tomato Yellow Leaf Curl Virus (TYLCV) through the vector, *B. tabaci* with a minimum Acquisition Access Period of 15 minutes and observed an increasing rate of transmission with higher AAP and a maximum transmission rate was achieved after 24 h of AAP [65]. Similarly, minimum Inoculation Access Period (IAP) (the exposure period required by the vector transmitting the virus into a healthy plant) was 15 minutes and the rate of transmission was observed increasing with higher IAP and a maximum after 12 h of IAP. After acquisition, the virus circulates or in some cases, propagates within the body of the vector which is referred as the Latent Period (LP). Maximum efficiency was achieved with 20 adults of *B. tabaci* in transmitting Mungbean Yellow Mosaic Virus with an AAP of 48 h and IAP of 24 h in greengram plants [66].

The whitefly, *B. tabaci* can transmit plant viruses in both persistent and semi-persistent manner, depending on the virus [67]. Cucumber Vein Yellowing Virus (Ipomovirus) is transmitted in a semi-persistent mode where it cannot retain infecting ability more than 5 h after acquisition [68]. Others viruses in the genus Ipomovirus like Cassava Brown Streak Virus (CBSV), Squash Vein Yellowing Virus (SqVYV), and Sweet potato mild mottle virus (SPMMV) are also vectored by whitefly in a semi-persistent manner [69]. Criniviruses like Tomato Chlorosis Virus (ToCV) and Tomato Infectious Chlorosis Virus (TICV), Carlaviruses like Cowpea Mild Mottle Virus (CpMMV) and Melon Yellowing-associated Virus (MYaV) are also vectored in a semi-persistent manner by *B. tabaci* [70-72].

Pulses such as Green gram, Black gram, Cowpea, Dolichos, Velvet bean, Rhynchosia sp., Kudzu, Chickpea, Lentil, Mothbean, Horsegram, Pigeonpea, Common bean and Peas are prone to number of viral diseases. The most common viral disease of pulse crops is Yellow Mosaic Disease (YMD) which is transmitted by whiteflies in persistent-circulative manner. This disease is caused by a number of different species of Begomoviruses (individually or mixed) such as Mungbean Yellow Mosaic Virus, Mungbean Yellow Mosaic India Virus, Horsegram Yellow Mosaic Virus, Dolichos Yellow Mosaic Virus, Rhynchosia Yellow Mosaic Virus, Rhynchosia Yellow Mosaic India Virus, Velvetbean Severe Mosaic Virus, Kudzu Mosaic Virus, Bean Golden Mosaic Virus, Bean Golden Yellow Mosaic Virus, Calopogonium Golden Mosaic Virus, Cowpea Golden Mosaic Virus, Lima Bean Golden Yellow Mosaic Virus, Rhynchosia Golden Mosaic Virus, Tomato Leaf Curl Gujarat Virus, Tomato Leaf Curl New Delhi Virus, Frenchbean Leaf Curl Virus and Tomato Yellow Leaf Curl Virus. Transmitted by whiteflies, the Cowpea Mild Mottle Virus is an example of virus other than Begomoviruses causing disease in several pulse crops [73-83].

Tomato Yellow Leaf Curl Virus (TYLCV) is widespread in many parts of the world and is responsible for severe yield loss [83-85]. This virus is vectored by the whitefly, *B. tabaci* in a persistent circulative manner, but whether in a propagative fashion, is still controversial. Some researchers had supported its replication in the body of whitefly while others did not [86,87]. Li et al. demonstrated transmission of tomato yellow leaf curl Thailand virus (TYLCTHV) by *B. tabaci* in a persistent circulative mode but not propagative [88]. However, replication of TYLCV was reported in the salivary glands of the whitefly [89]. The high quantity of viral DNA observed in the body of the vector might be the result of efficient accumulation rather than its degradation [90]. Acquisition of virus may also alter the gene expression in the whitefly [91].

Cassava is an important food crop of many countries of African continent. Vectored by whitefly, the African Cassava Mosaic Virus (ACMV) is yet another example which raised serious concern in the production of this crop in many regions of Africa [92,93]. With emergence and spread of an infectious biotype as a serious pest, this viral disease also geared up in its formidable form during 1990s which devastated a large area and caused a million-dollar loss. Recently, Leiva et al. found the two cryptic species (Asia II 1 and Asia II 6) throughout the Lao PDR as a vector of Sri Lankan cassava mosaic virus (SLCMV) causing Cassava Mosaic Disease (CMD) [94]. Mungbean Yellow Mosaic Virus (MYMV), transmitted by the whitefly in a persistent but non-propagative manner, had severely impacted the crops like greengram, blackgram and soybean with an annual economic loss of over US$ 300 million [95]. A population density of one whitefly per trifoliate can reduce an approximate grain yield of Soybean by 31 kg per ha [96]. Besides quantitative losses, the pest also degrades qualities like length, strength, fineness and maturity in cotton [97].

Apart from this, genetic groups have their own weightage in determining the specificity of the viruses to be associated with, as well efficiency of transmission [98]. Gautam et al. observed *B. tabaci* MEAM1 as a better vector, (compared to MED) for the New World Begomoviruses like Cucurbit leaf crumple virus (CuLCrV) and Sida golden mosaic virus

(SiGMV) [99]. In case of Tomato Yellow Leaf Curl Virus (TYLCV), Sánchez-Campos et al. reported higher specificity of Begomovirus transmission by 'MED' as compared to 'MEAM1' whereas Wei et al. reported equal specificity [100,101].

Critical Role of Endosymbionts

B. tabaci is associated with a primary endosymbiont, *Portiera aleyrodidarum* and besides this, several secondary symbionts including *Hamiltonella, Arsenophonus, Cardinium, Rickettsia, Wolbachia* and *Fritschea* are found in this insect [102,103]. These endosymbionts influence variation in their virus transmission capabilities [104]. *Hamiltonella* and *Arsenophonus* have been known to interact with the viral coat protein thus, affecting the viral transmission [105,106]. Endosymbionts have also been associated with one or the other genetic group, for example *Arsenophonus* and *Wolbachia* had been shown to be associated with MED, whereas, *Hamiltonella* had been reported to be found in MEAM1 [107]. Therefore, identification of these endosymbionts is essential for a better understanding of the bio-ecology of the insect [108].

Formulating Suitable Management Strategies

Relying on a single method of pest management has never yielded a sustainable and fruitful result. Successful pest management strategies always involved a combination of compatible and location specific management methods [109]. Large scale use of synthetic pesticides has led to the development of multifold resistance against many classes of insecticides. Proper insecticide resistance management strategies in combination with suitable cultural and biological control tactics may slowdown the resistance development and could yield effective control of the whitefly [110,111]. Cultural practices like allowing crop free periods, proper disposal of crop residue, adjusting planting dates, high crop barrier, intercropping and behavioral manipulations have successfully demonstrated in many places and have the potential to be adopted at wide scale [112,113]. Use of entomopathogenic fungi (EPF) is one of the eco-friendly management tools, where species of hypomycetes fungi are well known and popularly used [49,114-116]. Apart from these, there is enormous scope in the exploration of potential biocontrol agents. Parasitoids and predators can be used against *B. tabaci* through proper conservation and augmentation techniques [117]. Breaking the virus-vector relationship may help significantly in minimizing the economic losses occurring due to the highly infective and widespread nature of viral diseases in many crops. Viral coat proteins as well as insect (vector) proteins play an important role in the retention, circulation and transmission of plant viruses. GroEL is a protein belongs to Chaperonin family produced by many bacteria [118]. This protein interacts with the coat protein of virus, which is critical in its transmissibility [119]. Breaking the interaction between viral protein and vector (endosymbiont) protein may help in overcoming the virus transmissibility and controlling the diseases. Expression of these proteins in the host plant may also confer resistance against infecting viruses [120]. In whitefly, GroEL protein is attained by their endosymbionts. Different populations of whitefly may attain GroEL by different bacteria [105,106]. Another protein, *B. tabaci* Cyclophilin B (CypB) has significant role in transmission of TYLCV [121]. Understanding the genetic makeup and recognizing the specific target proteins could be a novel tool for controlling this pest, and in turn, could manage high infectivity of some widespread plant viral diseases [122].

Conclusion

The whitefly, *B. tabaci*, is a complex of morphologically indistinguishable but genetically differed species infesting a wide range of agricultural, horticultural and protected cultivation crops with considerable economic impact. It affects the crops by directly sucking up the sap nutrients, induce phytotoxic effects, impede photosynthesis by secreting honey-dew, (thereby attracting sooty mold), and most importantly by acting as a vector of a number of viruses, particularly the Begomoviruses. As of now, over 45 cryptic species under *B. tabaci* species-complex have been reported by authors from different parts of the world. Most of the categorization is based on partial mitochondrial CO1 sequence containing high genetic diversity, leading to a large number of genetic groups under the *B. tabaci* species-complex. Understanding the genetic mechanism and protein-protein interactions involved in virus-vector relationship could pave the way in opening new avenues for the management of wide-spread plant viral diseases. Insecticide resistance management along with ecological, cultural and biological control methods would be helpful in formulating management strategies against this pest [123-132].

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Conflict of Interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

- **Data Availability:** Not Applicable
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Authors' Contributions

All the authors have made contribution in drafting the work and revised it critically for important intellectual content. Authors have approved the version to be published.

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