Begomoviruses and Their Emerging Threats in South Korea: A Review

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Diseases caused by begomoviruses (family *Geminiviridae*, genus *Begomovirus*) constitute a serious constraint to tropical and sub-tropical agro-ecosystems worldwide. In recent years, they have also introduced in temperate regions of the world where they have great impact and are posing a serious threat to a variety of greenhouse crops. Begomoviral diseases can in extreme cases reduce yields to zero leading to catastrophic losses in agriculture. They are still evolving and pose a serious threat to sustainable agriculture across the world, particularly in tropics and sub-tropics. Till recently, there have been no records on the occurrence of begomoviral disease in South Korea, however, the etiology of other plant viral diseases are known since last century. The first begomovirus infected sample was collected from sweet potato plant in 2003 and since then there has been gradual increase in the begomoviral epidemics specially in tomato and sweet potato crops. So far, 48 begomovirus sequences originating from various plant species have been submitted in public sequence data base from different parts of the country. The rapid emergence of begomoviral epidemics might be with some of the factors like evolution of new variants of the viruses, appearance of efficient vectors, changing cropping systems, introduction of susceptible plant varieties, increase in global trade in agricultural products, intercontinental transportation networks, and changes in global climatic conditions. Another concern might be the emergence of a begomovirus complex and satellite DNA molecules. Thorough understanding of the pathosystems is needed for the designing of effective managements. Efforts should also be made towards the integration of the resistant genes for the development of transgenic plants specially tomato and sweet potato as they have been found to be widely infected in South Korea. There should be efficient surveillance for emergence or incursions of other begomoviruses and biotypes of whitefly. This review discusses the general characteristics of begomoviruses, transmission by their vector *B. tabaci* with an especial emphasis on the occurrence and distribution of begomoviruses in South Korea, and control measures that must

be addressed in order to develop more sustainable management strategies.

Keywords : *Begomovirus*, recombination, satellites, weed plants, whitefly biotype

They are the most numerous of the *B. tabaci* transmitted viruses and cause crop yield losses of between 20% to 100% (Picó et al., 1996; Polston and Anderson, 1997; Roye et al., 2007). In severe epidemics, the effect of the disease is near total loss of crops and annual damages range in the hundreds of millions of dollars (Brown and Idris, 2008; Morales and Anderson, 2001; Nakhla et al., 2005). Cassava, cotton, beans, cowpea, soybean, tobacco, tomatoes, peppers, okra, cucurbits, crucifers, melon, watermelon, lettuce, pea and papaya have been affected by one or more whitefly transmitted begomovirus diseases. However; tomatoes, peppers, beans and cassava have been cited as the most widespread and important. Symptoms include mosaic, leaf curling, leaf rolling, vein thickening, vein yellowing or more generalized leaf yellowing, and often accompanied by stunting of plant growth. Fauquet et al. (2008) listed whitefly transmitted *Begomovirus* species occurring worldwide. *African cassava mosaic virus* (ACMV), *Tomato leaf curl virus* (ToLCV), *Tomato yellow leaf curl virus* (TYLCV), *Cotton leaf curl Multan virus* (CoLCMV), *Papaya leaf curl virus* (PLCV), *Bhendi yellow vein mosaic virus* (BYVMV), *Mungbean yellow mosaic virus* (MYMV) and *Bean golden mosaic virus* (BGMV) are the major begomovirus causing destructive yield loss to related crops and other crop and non-crop species.

Genome organization of Begomoviruses

The circular single stranded DNA genomes of begomoviruses are mostly bipartite and both components (DNA-A and DNA-B) are approximately 2.5 to 2.8 kb in length and have protein coding sequences (genes) in the virion and complementary-sense strands (Bisaro et al., 1982; Hamilton et al., 1983). DNA-A has either one or two genes in the virion-sense strand [AV1/AR1-coat protein (CP) and AV2/AR2-pre coat protein] and four genes [AC1/AL1-replication

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initiator protein (Rep), AC2/AL2–transcription activator protein (TrAP), AC3/AL3–replication enhancer protein (REn), AC4/AL4 and AC5/AL5] in the complementary-sense strand (Fig. 1a; Hanley-Bowdoin et al., 1989; Lazarowitz, 1992; Rojas et al., 2005; Seal et al., 2006a). DNA-B encodes for two proteins; BV1–nuclear shuttle protein (NSP) on the virion-sense strand and BC1–movement protein (MP) on the complementary sense strand (Fig. 1a; Stanley et al., 2005; Seal et al., 2006a) and both are essential in efficient systemic spread and symptom expression within the plant (Revington et al., 1989; von Arnim and Stanley, 1992), host range and symptom modulation (Ingham et al., 1995; Barnabas et al., 2010; Carvalho and Lazarowitz, 2004; Hussain et al., 2005; Noueiry et al., 1994; Revington et al., 1989). Among both the genes of DNA-B, BC1 protein is reported as major symptom determinants inducing disease-like symptoms (Duan et al., 1997; Gafni and Epel, 2002; Hou et al., 2000) except a recent report where NSP of ToLCNDV has been found to be pathogenicity determinant (Hussain et al., 2005). The DNA-A and DNA-B components share little sequence similarity, except for ~200 nt of sequence in the intergenic region (IR), termed as common region (CR; Lazarowitz, 1992). The CR is present in the intergenic region between ORFs AV1 and AC1 in DNA A and between ORFs BV1 and BC1 in DNA-B (Fig. 1a & b; Hanley-Bowdoin et al., 1999). The CR sequence is different among different begomoviruses and is used to identify the A and B components of the same virus. The CR has many regulatory element including two TATA motifs, involved

in initiation of transcription of AV1 and/ or AV2 and AC1 and/ or AC4, respectively, and a putative stem loop structure containing the highly conserved nonanucleotide (TAATATTAC) that functions in the initiation of rolling circle replication, and conserved iterated sequences (iterons) required for specific recognition and binding by AC1 during replication (Arguello-Astorga et al., 1994; Chatterji et al., 1999; Hanley-Bowdoin et al., 1999).

Old World and New World Begomoviruses

Begomoviruses are broadly divided into two groups, the Old World (OW) viruses (eastern hemisphere; Europe, Africa, Asia) and the New World (NW) viruses (western hemisphere; the Americas) (Paximadis et al., 1999; Rybicki, 1994). Begomovirus genomes have a number of characteristics that distinguish OW and NW viruses. All NW begomoviruses are bipartite, whereas both bipartite and monopartite begomoviruses are present in the OW (Duffy and Holmes, 2007; Ha et al., 2006). In the OW bipartite begomoviruses (Harrison and Robinson, 1999), and an additional gene AV2 in the viral sense strand and AC4 on the complementary strand are found (Hanley-Bowdoin et al., 1999). In OW begomoviruses lacking the DNA-B component only the DNA-A component is required to infect plants systemically and symptomatically (Guo et al., 2009; Navot et al., 1991). In contrast there are also few reports that in few cases of bipartite begomoviruses the DNA-B is not required for systemic infection. Galvão et al. (2003) demonstrated that a naturally occurring recombinant DNA-A of a typical bipartite begomovirus does not require the cognate DNA-B to infect systemically, however, such infections also reported tend to be non-symptomatic (Briddon and Markham, 2001). The monopartite begomoviruses may acquire the DNA-B from bipartite begomoviruses (Saunders et al., 2002; Shafiq et al., 2010). Recently, a proposed evolution of bipartite begomoviruses suggested that they originated as monopartite begomovirus and acquired a genomic DNA-B from ancestor (Nawaz-ul-Rehman and Fauquet, 2009). Interestingly, Briddon et al. (2010) analyzed the hypothesis that DNA-B originated as a satellite that was captured by the monopartite progenitor of all extant bipartite begomoviruses and subsequently evolved to become the essential genomic component of the begomoviruses. The DNA-B components show a much wider range of molecular diversity than the DNA-A components. The DNA-A component is capable of autonomous replication in plant cells, whereas the DNA-B component is required in the synthesis of proteins necessary for intracellular, intercellular and systemic movement and for nucleo-cytoplasmic export of virus DNA (Noueiry et al., 1994; Thommes et al., 1993).

Fig. 1. Genome organization of begomoviruses.

Satellites associated with Begomoviruses

In recent years betasatellites (formerly DNA- β) molecule approximately half the size of begomovirus DNA has been found to be associated with majority of the OW monopartite begomoviruses including few bi-partite begomoviruses (Fig. 1c; Briddon et al., 2001; Kon et al., 2007; Lee et al., 2011; Reddy et al., 2005; Seal et al., 2006a; Xie et al., 2010; Zhou et al., 2003). However, none has yet been reported from the NW (Briddon, et al., 2003).

Recent studies have elucidated the role of betasatellite in viral pathogenicity. They have been investigated to be involved in systemic infection, and as symptoms modulating agents in development of typical phenotypic symptoms of the diseases (Briddon et al., 2001; Guo et al., 2009; Ito et al., 2009; Ogawa et al., 2008; Saeed et al., 2005; Saunders et al., 2004). A less virulent species and/or strains become more virulent with the association of beta satellites resulting in the occurrence of new epidemics in new crops in environment. They are easily adopted with the begomoviruses during mixed infections which prevalence nowadays is very common due to the wide distribution of begomoviruses in the agro-ecosystems. The betasatellite components require the helper begomovirus for replication in cells of host plants, systemic infection and trans-encapsulation in virus particles, but share no significant sequence similarity (Mansoor et al., 2003). All betasatellite molecules encode a conserved open reading frame (ORF) and termed as β CI. The betasatellite shows negligible sequence identity either to DNA-A or to DNA-B components associated with begomoviruses except from the sequence TAATATTAC which is common in all geminiviruses which also contain the initiation site of rolling circle replication (Briddon et al., 2003). The betasatellites could also substitute for DNA-B of a bipartite begomovirus in providing the movement function for systemic infection but with a low DNA accumulation in host cells (Saunders et al., 2002; Saeed, 2006).

In addition, one more small (approx. 1350 nucleotides) ssDNA molecule (termed alphasatellites, formerly DNA1) is usually found in association with OW begomovirus-betasatellite complexes (Mansoor et al., 1999, 2000a; Nawaz-ul-Rehman and Fauquet, 2009; Saunders and Stanley, 1999) but very recently, it has also been investigated to be associated with few NW begomovirus (Paprotka et al., 2010; Romay et al., 2010). In an extensive survey, Xie et al. (2010) found that all samples those contain alphasatellites also contain betasatellites, but only few samples that contain betasatellites contain alphasatellites. In some cases, alphasatellites have been found to suppress viral symptoms (Nawaz-ul-Rehman and Fauquet, 2009).

Moreover, two novel subviral DNAs (referred to as

satDNA-II and satDNA-III) have recently been isolated from cassava infected with bipartite cassava mosaic begomoviruses in Tanzania (Briddon and Stanley, 2006). They are relatively small (approximately 1000 and 1200 nucleotides) and contain a GC-rich region. They are 77% distinct from each other (only 23% nucleotide identity) and from all geminiviruses and other subviral components. Nothing is yet known about their replication and gene expression strategies. Infectivity studies showed that both the subviral DNAs increase the symptoms severity in cassava caused by *African cassava mosaic virus*, *East African cassava mosaic virus* and *East African cassava mosaic Cameroon virus*, and also allow these begomoviruses to produce symptomatic infections in resistant cassava landrace (Briddon and Stanley, 2006).

Recombination of Begomoviruses

Recombination and pseudo-recombination among begomoviruses is very frequent due to mixed infection and resulting in the genetic diversification of begomoviruses in nature (Bull et al., 2007; Fazeli et al., 2009; Matsuda et al., 2008; Monci et al., 2002; Saunders and Stanley, 1999; Sanz et al., 2000) and is known for the emergence of more virulent variants/strains, severe disease phenotypes and novel crop diseases (Matsuda et al., 2008; Moriones and Nvas-Castillo, 2008; Pita et al., 2001; Zhang and Zhou, 2010). Both the recombination and pseudo-recombination may occur in between variants of same virus, between virus species and even between genera which result the fast development of new forms (Briddon et al., 1996; Graham et al., 2010; Kitamura et al., 2004; Kon et al., 2007; Morilla et al., 2004; Saunders et al., 2002; Sawangjit et al., 2005). This phenomenon has resulted in severe epidemiological emergence of isolates capable of overcoming host resistance or isolates with a host range wider than the original one (García-Andrés et al., 2006; Monci et al., 2002; Ndunguru et al., 2005). Intergenic region (IR) is the hot spot of recombination of begomoviruses (Seal et al., 2006b; Tsai et al., 2011).

Recombination is also known to occur in between the helper begomovirus genomes and their betasatellites. In a study Saunders et al. (2001) demonstrated that the yellow vein phenotype of *Ageratum conyzoides* can also be produced by co-inoculating with *Ageratum yellow vein virus* DNA-A (AYVV DNA-A) and recDNA-Abeta17, a naturally occurring recombinant of approximately the same size as DNA- β that contains sequences from both DNA-A and DNA- β . They suggested that such recombination events are likely to occur frequently with this type of disease complex in the field. Lately, recombinant DNA- β molecules (RecDNA-A β) comprising parts of DNA-A and DNA- β

associated with *Tomato yellow leaf curl China virus* (TYLCCNV) have been identified in a 5 naturally infected tobacco plants. All were found approximately half the size of TYLCCNV genomic DNA, and all contained the $\beta C1$ gene and the A-rich region from TYLCCNV DNA- β as well as intergenic region sequences and the 5' terminus of the *AC1* gene from TYLCCNV DNA-A. Co-inoculation of TYLCCNV DNA-A and RecDNA-A β induced symptoms indistinguishable from those induced by TYLCCNV DNA-A and DNA- β in several test plants (Tao and Zhou, 2008).

The vector and the population changes

Whitefly (*Bemisia tabaci*) is the only known vector of begomoviruses. This is most important pests worldwide in tropical and sub-tropical agriculture as well as in greenhouse production systems. Currently, *B. tabaci* is the most difficult pest to manage on greenhouse crops in many countries. Under suitable conditions, *B. tabaci* may develop 10 to 15 generations in one year. Females may lay 100–500 eggs over a period of 3 to 6 weeks. About 1300 whitefly species in over 120 genera have been described (Anonymous, 2001; Mound and Halsey, 1978). Such distinct populations have been termed 'biotypes' A to T (Demichelis et al., 2005; Perring, 2001). The sweet potato whitefly (*B. tabaci* Gennadius, biotype A) and silver leaf whitefly (*B. tabaci*, biotype B or *B. argentifolli* Bellows and Perring; Bellows et al., 1994; Brown et al., 1995) and Biotype Q are the three main pests of several economically important crop plants. But very recently, a new investigation (De Barro et al., 2011) suggested that *B. tabaci* (different biotypes) is actually a complex of 24 morphologically indistinguishable species rather than biotypes. This will most likely change the way we refer to *B. tabaci* (and its biotypes) in the future.

B and Q biotypes rapidly displace the native *B. tabaci* (biotype A). It is believed that B biotype originated in Sahel region of Africa, and its surroundings first jumped to Middle East, and later spread all over the world through ornamentals trade. In USA, B biotype first emerged in the late 1980s and soon it spread like wildfire across the country, nearly wiping out the vegetables and cotton industries, and ornamental crops in many of the states. The most recently discovered Q biotype is thought to have originated from the Mediterranean region and has been associated with whitefly control problems in greenhouses in Spain where it escaped from pesticide (as it is extremely resistant to several pesticides) which wiped out the B biotype. Biotype Q has since wide spread through the ornamental industry in various parts of the world. In US where it was first introduced during December 2004 in Arizona, but as of January 2008, 25 states have been reported to have occurrences of Q-biotype ([\[wiki.bugwood.org/Bemisia_tabaci_biotype_Q\]\(http://wiki.bugwood.org/Bemisia_tabaci_biotype_Q\)\).](http://</p>
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The increase on the incidence of begomoviruses is specifically associated with the explosion of *Bemisia* population especially the spread of the more fecund B-biotype (Castillo-Urquiza et al., 2008; Hanssen et al., 2010; Perring, 2001; Polston and Anderson, 1997; Seal et al., 2006b; Varma and Malathi, 2003). Populations of *B. tabaci* in the Imperial Valley of California increased 300-fold from the mid-1970s to the mid-1980s, and 1600-fold from the mid-1970s to the mid-1990s (Wisler et al., 1998). In Israel, *Tomato yellow leaf curl virus* (TYLCV-Is) has emerged as a major constraint due to the introduction of biotype B. Over the last three decades in tropical and sub-tropical Americas, begomovirus epidemics has increased several folds due to the introduction and wide dissemination of biotype B (Ambrozevicius et al., 2002; Ribeiro et al., 2003). Ribeiro et al. (2003) described the emergence of some tomato infecting begomoviruses in Brazil due to the introduction of biotype B whitefly. In Jamaica due to the introducing of B biotype, a sharp increase in begomoviral diseases resulting in severe yield losses in several economic crops have been reported (Roye et al., 2003). In south India till early 1990s, tomato was not favoured as a host by indigenous *B. tabaci* populations but due to the introduction of B-biotype, *B. tabaci* numbers on tomato increased by approximately 1,000-fold at the last of the century (Banks et al., 2001).

Hurricanes and/or prevailing winds are known to move viruliferous whiteflies long distances over water resulting in the spread of begomoviruses (Blair et al., 1995; Loebenstein and Thottappilly, 2009; McGlashan et al., 1994; Polston et al., 1998; Polston and Anderson 1997; Varma and Malathi, 2003). But trade route (transportation) of seedlings, flowers and ornamentals, seems to be the major means of spread over long distances (Brown et al., 2001; Ha et al., 2006; Lyttle and Guy, 2004) especially to lead to an introduction of the B and Q biotypes (Ha et al., 2006; Ma et al., 2007). Recently, the rapid dispersal of biotype Q in China (Zhang et al., 2005) and in New Zealand (Drayton et al., 2009) was found to be directly associated with the ornamental trades from other countries.

The relationship with weed plants

Weed plants are well known reservoir of begomoviruses and their role in epidemiology of begomoviral disease have been reported time to time across the world (Delatte et al., 2005). They play important role in the perpetuations and transmissions of begomoviruses as well as whiteflies resulting in the outbreak of the disease round the year. They work as a green bridge for begomoviruses and whiteflies to the succeeding crops. Many severe epidemics have been reported time to time from various parts of the world.

Alternate sources of *Tomato yellow leaf curl virus* (TYLCV), that cause most devastating epidemics in tomato agriculture (Czosnek and Laterrot, 1997; Picó et al., 1996) have been found in many weed hosts. Dalmon and Marchoux (2000) reported that *Solanum nigrum*, *Datura stramonium* and *Malva* sp. could serve as reservoirs of TYLCV in France. In Spain numerous weed species viz. *Chenopodium murale*, *Datura stramonium*, *Malva parviflora*, *Solanum nigrum*, *Convolvulus* sp. and *Cuscuta* sp. were recorded to be the reservoirs of TYLCV (Bedford et al., 1998; Jorda et al., 2001). In southern Spain, Sánchez-Campos et al. (2000) found *Datura stramonium*, *Mercurialis ambigua*, *Solanum nigrum*, and *S. luteum* as an alternate host of TYLCV and concluded that these may all be involved in epidemics in other countries affected by TYLCV because these species frequently grow in many temperate regions worldwide. Recently, in Iran Fazeli et al. (2009) found two very distinct weed species viz. *Chrozophora hierosolymitana* and *Herniaria* sp. as a reservoir of TYLCV and concluded that these weed plants might be playing important role in the spreading of TYLCV to tomato and other commercial crops. *Tomato leaf curl New Delhi virus* (ToLCNDV), a devastating species in Indian sub-continent has been reported on two commonly growing weeds viz. *Croton bonplandianum* and *Eclipta prostrata* in India and Pakistan, respectively (Haider et al., 2006; Reddy et al., 2005). Hang and Zhou (2006) surveyed weeds to identify the alternate host of *Papaya leaf curl China virus* (PaLCuCNV) recently causing a severe leaf curl disease on papaya in southern China, and found that *Corchoropsis timentosa* is the alternate host of the PaLCuCNV and play an important role in papaya leaf curl disease epidemiology.

Recent reports of Begomoviruses in Korea

In the past century, there has been no report on the occurrence of begomovirus disease in South Korea. Until recently (2005), the Q biotype of *B. tabaci* occurring in South Korea were found to be non-viruliferous (Lee et al., 2010). The first occurrence of begomovirus in Korea seems to be on sweet potato (Acc. No. FJ560719) which was collected from Yeosu, Gyeonggi in 2003, and since then there has been sharp increase in the outbreak of the disease in several crop species. So far, 48 DNA-A sequences belonging to 4 distinct monopartite begomovirus species viz. *Honeysuckle yellow vein virus* (HSYVV), *Tobacco leaf curl Japan virus* (TobLCV), *Tomato yellow leaf curl virus* (TYLCV) and *Sweet potato leaf curl virus* (SPLCV) originating from different plant species have been submitted in public sequence data base across the country. Till date, the occurrence, distribution and host plants of begomoviruses are summarized in Table 1 and illustrated in Fig. 2. Very recently,

four begomovirus research articles have appeared (Kim et al., 2011; Lee et al., 2010; Lee et al., 2011; Wang et al., 2011). In a phylogenetic analysis of complete nucleotide sequences (genome) as well as individual ORFs of Korean TYLCV isolates with Far East Asian begomoviruses and also across the world, all the Korean TYLCV isolates showed highest sequence identity and clustered with the Japan TYLCV isolates. The phylogenetic analysis of Korean *B. tabaci* based on 16S rRNA and mitochondria cytochrome oxidase I (MtCOI) sequences clustered with Iranian and Nigerian *B. tabaci*. On the basis of these data Lee et al. (2010) described that the TYLCV has very recently (2008) introduced to Korea from Japan via unknown route and then subsequently transmitted across the country by native *B. tabaci*. In these literatures, the outbreak of begomoviral disease have considerably been reported in tomato and sweet potato, the chief and staple crops of South Korea; however, severity, incidence, and yield loss have not been estimated. Kim et al. (2011) also detected the presence of begomovirus infection in pumpkin, eggplant and the vector *B. tabaci* in open field samples, strongly suggests the occurrence and prevalence of begomoviruses in open field conditions.

Lee et al. (2010) described that the first TYLCV infected tomato sample was isolated from Tongyeong in 2008 which very rapidly spread to other regions like Gyeongsang-Do, Jeolla-Do, and Jeju-Do within one year. Busan located in the south east of the Korean peninsula is the largest port city in South Korea and the fifth largest port in the world might be playing important role in the disseminations of begomovirus and its vector whitefly in the southern part which is chief agricultural region of the country. The Fig. 2 clearly shows the wide distribution of the begomovirus in the country especially in southern region. On the other hand, the gradual increase in the temperature of the Korean peninsula (particularly Jeju Island) making it to be a subtropical country, might also be favoring the adaptation and perpetuations of whitefly in greenhouse and open field crops. Overall, the climate of Jeju Island is warmer to the rest peninsular part of the Korea. It is most likely that begomoviruses as well as whiteflies might be spreading from Jeju to other geographical parts of the country, mainly through viral reservoir germplasms (seedlings). Being an entry port, from where obviously the domestic transportation is very common throughout the country, Jeju Island might be considered towards the dissemination of begomovirus and its vector whitefly.

The emergence of begomoviral disease in Korea is a matter of great concern. It has been noted that high incidence of the begomovirus disease is directly proportional to the large population of whitefly *B. tabaci*. Expansion of its geographic distribution, together with the appearance of

Table 1. Distribution of Begomoviruses, host species, and locations in South Korea

Accession No.	Name of virus*	Host plant	Location/Place	Sample collection date/ Data submission Date	Length of Genome	ORFs in the Genome	Reference
GQ477135	HSYVV	Lonicera japonica	Daegu/Chungnam	Oct-2005/13-AUG-2009	2763	Lee et al., 2011	6
HQ189431	HSYVV	honeysuckle	Dangjin/Chungnam	23-Aug-2009/27-AUG-2010	2764	Wang et al., 2011	6
HM164547	TobLCV	Tomato	Kwangju/Honam	Dec-2007/29-APR-2010	2762	-- [#]	6
AB613209	TYLCV	Tomato	Nonsan/Chungnam	01-Nov-2010/08-FEB-2011	2781	--	6
AB613208	TYLCV	Tomato	Iksan/Jeonbuk	01-Aug-2010/08-FEB-2011	2781	--	6
GU325634	TYLCV	Tomato	Boseong/Jeollanam-do	13-Oct-2009/16-DEC-2009	2774	Kim et al., 2011	6
GU325633	TYLCV	Tomato	Jeju/Island	15-Jul-2009/16-DEC-2009	2781	Kim et al., 2011	6
GU126513	TYLCV	Tomato	Hwaseong/Gyeonggi	11-May-2009/21-OCT-2009	2775	Kim et al., 2011	6
GU325632	TYLCV	Tomato	Jeju/Island	14-Sep-2009/16-Dec-2009	2781	Kim et al., 2011	6
GQ141873	TYLCV	Tomato	Busan/Gyeongnam	23-Jan-2009/10-May-2009	2774	Kim et al., 2011	6
HM856919	TYLCV	--	Uiseong/Gyeonbuk--	--/ 26-Jul-2010	2774	--	6
HM856918	TYLCV	--	Nonsan/Chungnam	--/ 26-Jul-2010	2781	--	6
HM856917	TYLCV	--	Jangheung/Jeonnam	--/ 26-Jul-2010	2774	--	6
HM856916	TYLCV	--	Iksan/Jeonbuk	--/ 26-Jul-2010	2781	6	--
HM856915	TYLCV	--	Gyeongju/Gyeongbuk	--/ 26-Jul-2010	2774	6	--
HM856914	TYLCV	--	Gwangyang/Jeonnam	--/ 26-Jul-2010	2774	6	--
HM856913	TYLCV	--	Gwangju/Honam	--/ 26-Jul-2010	2774	6	--
HM856912	TYLCV	--	Gunwi/Gyeonbuk	--/ 26-Jul-2010	2774	6	--
HM856911	TYLCV	--	Goseong/Gyeongnam	--/ 26-Jul-2010	2774	6	--
HM856910	TYLCV	--	Buyeo/Cheonnam	--/ 26-Jul-2010	2781	6	--
HM856909	TYLCV	--	Busan/Gyeongnam	--/ 26-Jul-2010	2774	6	--
HQ260984	TYLCV	--	Chang won/Gyeongnam	--/ 14-Sep-2010	2772	6	--
HM754641	SPLCV	--	Haenam/Cheonnam	--/13-Jul-2010	2828	6	--
HM754640	SPLCV	--	Haenam/Cheonnam	--/13-Jul-2010	2829	6	--
HM754639	SPLCV	--	Haenam/Cheonnam	--/13-Jul-2010	2829	6	--
HM754638	SPLCV	--	Haenam/Cheonnam	--/13-Jul-2010	2829	6	--
HM754637	SPLCV	--	Yeoju/Gyeonggi	--/13-Jul-2010	2828	6	--
HM754636	SPLCV	--	Nonsan/Chungnam	--/13-Jul-2010	2829	6	--
HM754635	SPLCV	--	Yeoju/Gyeonggi	--/13-Jul-2010	2829	6	--
HM754634	SPLCV	--	Chungju/Chungbuk	--/13-Jul-2010	2829	6	--
FJ434943	ToBLCV	Tomato	Jeju-si/Jeju	00-Jul-2007/03-Nov-2008	2763	6	Wang et al., 2011
HM856873	TYLCV	Tomato	Samcheonpo/Gyeongnam	28-Nov-2008/26-Jul-2010	2786	6	--
NC_014482	TobLCV	Tomato	Iksan/Jeonbuk	Sep-2008/ 02-Sep-2010	2763	6	--
HM164549	TobLCV	Tomato	Samcheok/Gangwon	Dec-2007/ 29-Apr-2010	2763	6	--
HM164545	TobLCV	Tomato	Jeju/jeju	Sep-2008/ 29-Apr-2010	2766		--
HM164541	TobLCV	Tomato	Iksan/Jeonbuk	Sep-2008 /29-Apr-2010	2763		--
HM130914	TYLCV	Tomato	Jeju/Jeju	23-Dec-2008/13-Apr-2010	2781		Lee et al., 2010
HM130913	TYLCV	Tomato	Jeonju/Jeonbuk	23-Dec-2008/13-Apr-2010/	2781	6	Lee et al., 2010
HM130912	TYLCV	Tomato	Masan/Gyeongnam	23-Dec-2008/ 13-Apr-2010/	2774	6	Lee et al., 2010
FJ560719	SPLCV	Sweet potato	Yeoju/Gyeonggi	30-Sep-2003/17-Dec-2008	2828	6	--
AB669434	TYLCV		Iksan/Jeonbuk	01-Aug-2011/ 07-Sep-2011	2781	6	--
JN680149	TYLCV	Tomato	Goseong/Ganwon	2008/14-Sep-2011	2774	6	--
JN680150	TYLCV	Tomato	Haenam/Jeonnam	2008/14-Sep-2011	2774	6	--
AB636264	TYLCV	Tomato	Yesan/Chungnam	01-Jan-2011/31-May-2011	2781	6	--
AB636409	TYLCV	Tomato	Gangju/Jeonnam	Mar-2011/02-Jun-2011	2774	6	--
AB636410	TYLCV	Tomato	Jeju city/Jeju	Feb-2011/02-Jun-2011	2781	6	--
AB636411	TYLCV	Tomato	Jeju city/Jeju	Feb-2011/02-Jun-2011	2774	6	
AB636412	TYLCV	Tomato	Jeju city/Jeju	Feb-2011/02-Jun-2011	2781	6	

*HSYVV = *Honeysuckle yellow vein virus*, TobLCV = *Tobacco leaf curl virus*, TYLCV = *Tomato yellow leaf curl virus*, SPLCV = *Sweet potato leaf curl virus*

[#]= Denotes the unavailability of the data.

Fig. 2. The geographical map for the area in South Korea from where Begomovirus infected samples have been collected.

several distinct biotypes, has increased the worldwide importance of *B. tabaci* as a vector of plant viruses. Wind speed and direction play a significant role in dispersal of whiteflies, but transportation (trade routes) on specially ornamentals is the major means of spread over long distances. However, there is insufficient information to determine whether the presence of TYLCV and SPLCV in Korea is a result of a recent introduction from Japan and or China or whether these species was already present in Korea. But it is intriguingly be speculated that the virus and/or the viruliferous whitefly vectors were introduced from Japan and or China into Korea carried by strong winds/hurricanes or on imported plant materials where these had been endemic since last two decades (Kato et al., 1998; Ogawa et al., 2008; Wu et al., 2006; Yin et al., 2001).

Effect of Begomoviruses movement on disease dynamics

Previous reports indicated that the local disease dynamics of established begomoviruses can be disturbed by exotic begomoviruses. For example, *Tomato yellow leaf curl virus* from Israel has spread to become the dominant tomato-infecting begomovirus in many countries including the

Dominican Republic, Spain, Sicily, Italy and islands of the Indian Ocean (Davino et al., 2006; Delatte et al., 2007; Gilbertson et al., 2007; Polston and Anderson, 1997; Sanchez-Campos et al., 1999). In Sicily, *Tomato yellow leaf curl Sardinia virus* (TYLCSV) was causing severe crop losses since 1989 but recently in 2002, *Tomato yellow leaf curl virus* (TYLCV) introduced from Italy get spread in most of the tomato growing areas, and firstly resulted in the occurrence of mixed infection with TYLCSV. But very shortly in 2003–2004, it considerably displaced the incidence of TYLCSV with alone infecting the tomato crop by 18–35% with the prevalence of 8–28% by TYLCSV alone and 41–69% of both the viruses mixed infections (Davino et al., 2006).

Similarly, *Tomato leaf curl New Delhi virus* (ToLCNDV) was first time recorded in north India in 1995 (Srivastava et al., 1995) and subsequently reported across the country (Khan et al., 2006; Padidam et al., 1995; Raj et al., 2005; Sohrab et al., 2003; Usharani et al., 2004). Later on, the virus has been reported from other neighboring countries like Pakistan (Haider et al., 2006; Hussain et al., 2004; Hussain et al., 2005; Mansoor et al., 1997; Mansoor et al., 2000b; Tahir and Haider, 2005), Bangladesh (Maruthi et al., 2005), Thailand (Ito et al., 2008) and Indonesia (Mizutani et al., 2011) where it has great concern in the association of various commercial crop diseases.

Tomato yellow leaf curl Thailand virus (TYLCTHV) was for the first time reported from Thailand in 1994 (Blawid et al., 2008; Knierim and Maiss, 2007; Rochester et al., 1994; Sawangjit et al., 2005) and then subsequently it spread to Myanmar (Green et al., 2001), south China (Guo et al., 2009; Li et al., 2004) and recently it introduced in Taiwan in 2005 (Jan et al., 2007) where it has changed the dynamics of pre tomato existing begomoviruses as itself a leading tomato-infecting begomovirus; and is causing extensive damage to tomato production in Taiwan (Shih et al., 2010; Tsai et al., 2011). It seems likely that TYLCTHV is more virulent and aggressive with a wider host range (Shih et al., 2010) and outcompetes and replaces *Tomato yellow leaf curl Taiwan virus* (ToLCTWV), which might be due to more efficient transmission by either indigenous or introduced biotypes of whitefly (Tsai et al., 2011). The introduction of ToLCTWV in China has also considerable effect on tomato production. De Barro et al. (2000) demonstrated that the epidemic of pepper yellow leaf curl disease spreading through the Indonesian islands of Sumatra then Java and Bali was the result of the introduction of the begomovirus and a more efficient vectoring biotype of *B. tabaci* from Thailand. The ornamental honeysuckle often found affected with yellow-vein disease, which originates in eastern Asia, has become naturalized in Europe and North America (Mansoor et al., 2003).

Strategies for the control of Begomoviruses

Employing few necessary steps, the spread of the begomoviruses most likely be minimized viz. the greenhouses for transplant production should be isolated from field sources of Begomoviruses. Weeds should be eradicated from around greenhouses and infected plants should be discarded. In field production, weeds (especially perennials) that harbor whiteflies and or viruses should be removed when possible. Distancing tomato fields to chilli and other solanaceous crop production areas might be best way to limit begomovirus infection. Transplants should be produced free of virus and plants must be free of the whitefly vector. Another important control strategy may prove to be helpful is the reduction and elimination of whitefly populations. Tomato and other solanaceous crops residues should be removed promptly and destroyed at the end of their seasons.

The other alternate method is the genetic engineering in susceptible crops for the development of inbuilt resistance by mobilizing the viral gene(s) (CP, MP, Rep, and their fusion; Hong and Stanley, 1996; Kunik et al., 1994; Raj et al., 2005; Varma et al., 2002). Broad spectrum resistance against cassava-infecting begomoviruses has been developed based on the transgene-specific siRNAs (short interfering RNAs) (Chellappan et al., 2004). In recent years, a growing number of post-transcriptional gene silencing has been found quite effective against TYLCV (Abhary et al., 2006; Noris et al., 2004; Yang et al., 2004). Very interestingly recently, another approach known as artificial microRNAs (amiRs) is being practiced to develop resistant and have been found successful against few viruses (Qu et al., 2007). Thus, the genetic engineering based development of resistant transgenic plants (especially tomato and sweet potato cultivars of South Korea at earliest) might be started for the control of begomoviral epidemics. For more detailed information readers are referred to the review of Seal et al. (2006b).

Conclusion

Begomoviruses are a major constraint to agricultural productivity in all tropical and sub-tropical regions of the world (De Barro et al., 2008; Morales and Anderson, 2001; Nakhla et al., 2005). Recently, they have spread into more temperate regions because of changes in agricultural practices and ecological conditions, as well as the global trade in agricultural products, which all encourage dissemination of the insect vectors (Mansoor et al., 2003). The propensity of begomoviruses to undergo recombination and the global movement of both infected germplasms and *B. tabaci*, have undoubtedly encouraged the dissemination, diversification, and host adaptation of begomoviral disease complexes

(Briddon and Stanley, 2006). The other concern might be the emergence of begomovirus complex and satellite DNA molecules (Bull et al., 2004; Saunders et al., 2001; Varma and Malathi, 2003).

The frequency with which begomoviruses are evolving on various economically important crop species across the country is dreadful and a staggering news which calls for immediate steps to design the sustainable and efficient disease control strategy to prevent the further movement of one localized begomovirus to other locations. Intensive inspection of overseas plant materials via quarantines and other appropriate means might be a great concern to prevent further entry of any infested and infected plant materials. Moreover, extensive survey across the country is needed in order to know the current occurrence, incidence, severity, and epidemiology of begomovirus diseases in different geographical locations of the country. This will assist to understand the genetic diversity and variability of begomoviruses and will facilitate in working out how the new virulent strains of begomoviruses are emerging and pose the serious threat to other crops. This will also clear the current scenario of the begomoviruses distribution, dissemination (mono and/or bi-partite nature and associated satellite molecules), and mixed infection in South Korea and indeed help in the development of management strategies. Consequently, it is also important to manage the whitefly populations by implementing multiple management tactics such as cultural, physical, biological, and chemical controls.

The world wide reports strongly indicate, it is most likely be assumed to see new begomoviruses infection in cucurbits (squash, zucchini, pumpkin, cucumbers, melons), legumes (soybeans, green beans, cowpea), solanaceous crops (pepper, potato, tobacco), and *Malvaceae* (cotton, hibiscus, okra) and a wide range of ornamental species.

In consideration of the alarming rate with which new bogomoviruses are emerging in tomato, sweet potato, and other crops, there is an urgent need to develop economically and environmentally sound approaches (promoting quarantine procedures) for the successful management of these viruses. In conclusion, conventional control practices alone are far from providing adequate control of begomovirus. However, the integration of several of these practices following recommendations based on an appreciation of the epidemiology of the disease may facilitate management of begomovirus epidemics. Over all, the current scenario indicates that begomovirus problems are going to increase in near future.

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