Identification of Resistance to Geminivirus and Whitefly in Pepper

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Research Article

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Abstract

Pepper yellow leaf curl disease caused by geminivirus (Geminiviridae) is a major problem in chili pepper production. The availability of resistant varieties to geminivirus and whitefly Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae) as its vector has the potential to overcome this problem. The use of resistant varieties has various advantages, namely reducing pest control costs, producing no harmful chemical residues, and being acceptable and usable by farmers in the long term. This study aims to identify genotypes that are resistant to geminivirus and its vector. Nineteen chili pepper genotypes obtained from the Center for Tropical Horticulture Studies of IPB University were examined in this study by conducting field and laboratory tests. Based on the results, several chili pepper genotypes were found to be resistant to whiteflies and geminivirus. However, none of those genotypes had sufficient vector and virus resistance. This study also found that there was a significant correlation between the numbers of surviving imago and pupae with disease incidence, as well as between disease incidence and disease severity. Thus, the resistance to whitefly as a geminivirus vector can potentially reduce disease severity in chili pepper plants.

Introduction

One of the main problems of chili pepper cultivation in tropical countries is pest attack which causes a decrease in the yields. This is closely related to the unpredictable climate during the production cycle. The warm and wet climate in the major chili pepper producing areas highly contributes to the increase in this threat. One of the plant diseases that cause huge losses in this commodity is the one caused by geminivirus (Geminiviridae), commonly referred to as the yellow disease. Geminivirus is transmitted by a vector, namely *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) or whiteflies, which acquire the virus when they feed on infected plants. Whitefly infection on plants can also cause a decrease in plant metabolic processes due to damage to the leaves of the infected plants (Pollard 1995). The whitefly uses its stylet to navigate the cuticle, epidermis, and mesophyll of the leaf and builds feeding sites on the phloem. Whitefly nymphs feed on the phloem almost continuously for 21-30 days (Wang et al. 2017). As the vector of geminivirus, whitefly will directly and indirectly damage the infected plants.

Geminivirus infection will drastically reduce photosynthesis, growth, fruit growth, and fruit quality in host plants, although the effects depend on the number of infected plants and the age of the plant at the time of infection (Marwal et al. 2014). A previous study by Sukada et al. (2004) found that chili plants affected by geminivirus of the genus Begomovirus, or commonly referred to as the Pepper Yellow Leaf Curl Virus, can cause yield losses of up to 84.25%. Meanwhile, Nagata et al. (2016) stated that yield loss due to geminivirus infection on tomato plants with high intensity of whitefly attack reaches up to 100%. Plants infected with this yellow disease have also been shown to produce seeds that can carry the disease (Fadhilah et al. 2020), leading to the possibility of continuous production loss.

Various control efforts have been carried out, from the implementation of physical methods, such as spraying insecticides, to the production of resistant varieties by crossbreeding techniques and biotechnology. Several whitefly control efforts were done to reduce the incidence of diseases caused by geminivirus, e.g. by screening chili accessions (Jeevanandham et al. 2018), testing pure lines and crosses

(Costa et al. 2021), using natural enemies such as predators and parasitoids (Gerling et al. 2010; Tian et al. 2020), and conducting countermeasures by using certain types of insecticides (i.e. afidopyropen) (Zhang et al. 2021). Other attempts to control the disease include intervening resistance genes from wild relatives or resistant species (Neria et al. 2010) and using various biotechnological techniques such as gene silencing mechanisms or ribonucleic acid interference (RNAi) technology and genome editing with CRISPR/Cas to produce plants which are resistant to geminivirus (Teniente et al. 2015; Marwal et al. 2012; Schenke et al. 2020). In their study, Verdugo et al. (2001) argued that an alternative solution for controlling this disease is to use varieties that have high resistance or tolerance to the virus and its virus-carrying vectors. The use of resistant cultivars has various advantages; it reduces the pest control costs, produces no harmful chemical residues, and is acceptable and usable by farmers in the long term. Currently, especially in Indonesia, there are no studies that explain the combination of two resistance traits (the disease and the vector) in a chili pepper genotype. This study aims to obtain information on the resistance of several chili pepper genotypes to both geminivirus and its vector.

Materials And Methods

Materials

Nineteen chili pepper genotypes consisting of two species of *Capsicum* (*Capsicum frutescens* and *Capsicum annum*) were examined in this study. The seeds of those genotypes were obtained from the Center for Tropical Horticulture Studies of IPB University. Those genotypes are Bonita, CR2, CR3, CR4, CR6, CR9, CR11, CR13, CR14, CR15, KD2, KD3, KD4, KD5, KD7, F3U3, JT1, and JT5.

The population of uninfected whitefly imago was acquired from a rearing facility of the Department of Plant Protection, Faculty of Agriculture, IPB University. The whiteflies were reared and maintained on cotton plants in cages. For the virus resistance test, the obtained whiteflies were transferred to geminivirus-infected chili pepper plants. The confirmation of geminivirus in leaves was carried out using universal primers for pepper yellow leaf curl disease, namely SPG1 (5'-CCCCKGTGCGWRAATCCAT-3') and SPG2 (5'-ATCCVAAYWTYCAGGGAGCT-3'). After three weeks, the imagoes harvested from the plants were used.

Whitefly resistance test

Resistance tests were conducted in insect-free greenhouses in two separate locations during the dry season in Indonesia (25-32°C, 80% RH). The experimental design used was a completely randomized design with three replications. For each replication, three plants in each genotype were taken as samples. Combined analyses of different location/greenhouse for the resistance tests were carried out.

The study began with sowing the chili pepper seeds. Four weeks afterwards, the seedlings were then transferred individually to cages containing 40x40 cm polybags filled with a mixture of soil, rice husk, and green manure (1:1:1 v/v/v). After 14 days, 10 sterile whitefly imagoes were introduced to each plant.

Observations were made on the numbers of surviving imago and offspring population, as well as the symptoms on plant leaves. The number of offspring population covers the numbers of all eggs, pupae, and

nymphs from 4 randomly selected leaves per plant under the microscope (Manwan et al. 2014). These observations were made 14 days after whitefly inoculation. Sample plants were harvested by placing them into plastics that had been soaked in 70% alcohol, and cut to the base of the root. Then, the plants were shaken to kill the imagoes so that they were easy to count.

The value of disease intensity (I) was calculated using the following formula (Manwan et al. 2014):

$$I = \frac{\Sigma (n \times v)}{N \times V} \times 100\ \%$$

Where I is the attack intensity, N is the total number of leaves, V is the highest score, n is the number of leaves in score category, and v is the score category.

The score categories are as follows: 0: plants are not infected with whitefly and show no symptoms of leaf curl or the appearance of sooty mold on the leaves; 1: plants are infected with whitefly and characterized by symptoms of leaf curl and/or the appearance of sooty mold on the leaves with an intensity of >0–25 %; 2: plants are infected with whitefly and characterized by leaf curling and/or the appearance of sooty mold on the leaves with an intensity of >25–50%; 3: plants are infected with whitefly and characterized by leaf curling and/or the appearance of sooty mold on the leaves with an intensity of >50–75%, and the fruits as well as the seeds did not develop properly (abnormal); and 4: plants are infected with whitefly and characterized by leaf curling and/or the appearance of sooty mold on the leaves with an intensity of >76%, and the fruits as well as the seeds did not develop properly (abnormal).

Geminivirus resistance test

Resistance tests were carried out in the field. The field test was conducted at three locations under a completely randomized design with three replicates for each location. Twelve plants from each genotype were subjected to geminivirus-infected whiteflies. The test began with sowing the chili pepper seeds. After four weeks, the seedlings were then transferred individually to the 40x40 cm polybags containing a mixture of soil, rice husk, and green manure (1:1:1 v/v/v). The geminivirus-infected whitefly and geminivirus inoculum were introduced between groups of plants at 10 days after transplanting. For each experimental unit, six plants from each genotype were taken as samples. Observations were made on disease incidence (DI) and disease severity value (DSV).

The calculation of DI was based on the following formula:

$$DI = \frac{n}{N}\ x\ 100\%$$

Where DI is disease incidence, n is the number of symptomatic plants, and N is the number of plants observed.

Meanwhile, the calculation of the disease severity value and its classification is done based on the formula proposed by Chiang et al. (2017) as follows:

$$DSV = \frac{\sum_{0}^{i}(ni \times zi)}{(N \times Z)} \times 100\%$$

Where DSV is disease severity value, ni is the number of symptomatic plants with a certain value, zi is symptom value, N is the total number of plants observed, and Z is the highest symptom value.

The criteria for symptoms of viral infection are as follows: 0: healthy plants; 1: yellowing; 2: yellowing and mild leaf curling; 3: yellowing and leaf curling up and/or down; 4: yellowing, leaf curling up and/or down, and stunted plants.

The disease severity value was then used to classify resilience with the criteria presented in Table 1 (Genefianti et al. 2017).

Observations were also made with a score of 0-4 on the symptoms that appeared on the leaves.

Molecular confirmation through viral DNA was performed at the Molecular Laboratory of the Center for Tropical Horticulture Studies of IPB University in February 2021 – June 2021. The confirmation process began with the isolation of genomic DNA from symptomatic plants, followed by the amplification of the target DNA on a PCR machine and the visualization of the PCR results on gel electrophoresis using a UV transilluminator machine with the amplicon target being 912 bp. The volume of the PCR reaction mixture was 12.5 L, consisting of 0.5 L DNA, 0.5 L forward primer, 0.5 L reverse primer, 4.75 L nuclease free water, and 6.25 L MY TaqTM HS RED Mix. The amplification reaction program was as follows: predenaturation at 94°C for 5 minutes, followed by 35 cycles with denaturation at 94°C for 1 minute, primer attachment at 50°C for 1 minute, DNA elongation/synthesis at 72°C for 1 minute, and final elongation at 72°C for 7 minutes. A total of 5 µl of the PCR product was then put into 1.2% agarose gel in TAE buffer and electrophoresed at 50 volts for 46 minutes. The staining process was done by immersing the gel electrophoretic into a solution of ethium bromide (0.5 mg L-1) for 10 minutes, then soaking it in water for 1 minute before being visualized using a UV Transilluminator.

Statistical Analysis

Statistical analysis was done by performing analysis of variance (ANOVA) with a significance level of 5% using R 4.0.5 software. For the results of the ANOVA analysis that show a significant difference, further tests were carried out using the Tukey Honest Significant Difference (Tukey HSD) test with a significance level of 5%. The correlation analysis applied the Pearson method with a significance level of 5% using R 4.0.5 software.

Results And Discussion

Results

Resistance to whitefly

The results of the analysis of variance at the 5% level indicate that the genotypes had a significant effect ($p<0.05$) on the number of eggs which had an F-Value of 2.2953 and a very significant effect ($p<0.01$) on

the percentage of imago survival rate, the number of nymphs, and the number of offspring population which had F values of 2.4345, 2.7591, and 2.4911, respectively. In addition, the genotypes possessed a highly significant effect ($p<0.001$) with an F value of 4.4296 on the whitefly attack intensity parameter, but had no significant effect on the number of pupae (See Table 2).

The results of the whitefly resistance tests on 19 chili pepper genotypes prove that several genotypes, namely Bonita, CR2, and JT1, can be categorized as resistant genotypes due to lower attack intensity values compared to the other genotypes. These genotypes had an attack intensity value of 0%. Meanwhile, the highest attack intensity values were found in CR3, CR4, and KD3 genotypes with values of 17.2%, 16.3%, and 17.9%, respectively. Therefore, the three genotypes can be categorized as susceptible to whitefly attacks (See Table 3).

The Honest Significant Difference (HSD) test at α= 5% level. SI = survival rate of imago (%). E = number of eggs. N = number of nymphs. P = number of pupae. OP = number of offspring population. I = whitefly attack intensity (%).

The number of whitefly offspring in each genotype also showed significant differences, where in Bonita, CR2, and JT1 genotypes there was a smaller average number of offspring, ranging from 2-5 per genotype. Genotypes with high attack intensity value also had a higher average number of offspring, around 31-50 per genotype. Table 3 indicates that in line with the value of pest attack intensity, Bonita, CR2, and JT1 genotypes also showed a lower percentage of imago survival, namely 10%, 20%, and 0%, respectively. Meanwhile, the surviving imago value for CR3, CR4, and KD3 genotypes are 70%, 100%, and 40%, respectively.

As seen in Figure 1, the whitefly-resistant genotypes showed no sign of significant damage, either on the upper or the lower surfaces of the leaves. Meanwhile, the susceptible genotypes exhibited signs of leaf damage, such as chlorosis spots on the upper leaf surfaces and sooty mold covering the lower leaf surfaces of the affected plants. The leaves of susceptible genotypes appeared to be more yellow, lacking nutrients, and wilted more than the leaves of whitefly-resistant genotypes.

Resistance to geminivirus

The results of the analysis of variance at the 5% level prove that the genotypes had a very significant effect ($p<0.01$) on the percentage of disease incidence and disease severity (Table 2).

Symptoms found in the field (Figure 2) due to geminivirus infection differed from one genotype to another. Several genotypes displayed symptoms such as the appearance of yellow mosaics on the leaves, the occurrence of ven clearing on young leaves, leaves curling up and/or down, curly and thickened leaves, yellow leaves, curled up and stunted top leaves, and stunted plants. In addition, sooty mold developed on the underside of the leaves. These symptoms appeared simultaneously in one genotype. However, several genotypes only presented one or two of these symptoms. Some other genotypes even appeared to grow normally without any symptoms of viral attack when the observations were made.

Based on the symptoms emerged, the resistance level of the chili pepper genotypes can be seen from the values of disease incidence and experienced disease severity. Based on the results of this study (Table 4), two genotypes were found to have a lower disease incidence value than the other genotypes, i.e. CR9 genotype with a value of 10.71% and JT5 genotype with a value of 19.23%. In addition, these two genotypes had low disease severity values; CR9 had a disease severity value of 7.14% and was included in the moderately resistant category, while JT5 had a disease severity value of 5.19% and fell under in the resistant category.

Genotypes with a high percentage of disease incidences were CR15, CR13, Bonita, and KD4 genotypes, whose values ranging from 80.00-92.86%. Based on the disease severity values, these four genotypes belonged to the medium and high categories. The highest disease severity value was found in CR15 genotype, which was 76.36%, meaning that this genotype fell under the very susceptible category. CR13 and KD4 genotypes were both included in the susceptible category with a disease severity value of 27.69% and 34.05%, respectively. Meanwhile, Bonita genotype was in the moderately susceptible category with a disease severity value of 18.86%. All tested genotypes, both those belonging to the resistant and susceptible categories based on the values listed in Table 4, confirmed the presence of the geminivirus strands in plants molecularly by PCR method.

Confirmation of the presence of geminivirus in plants was obtained 30 days after the inoculation. The PCR results indicate that viral DNA was present in all tested genotypes, both those included in the resistant and susceptible categories. Figure 3 signifies that all genotypes were infected by the virus although they showed phenotypic differences in symptoms and resistance responses.

The connection between plant resistance to vectors and the yellow disease can be seen through the correlation between observed characters as displayed in the following diagram (Figure 4).

The correlation diagram reveals that the number of whitefly pupae has a highly significant correlation value (64%) to the severity of the disease caused by geminivirus. The observed character which was also significantly related to disease severity is the number of imago, with a correlation value of 39%. The disease severity possessed a highly significant correlation with the incidence of disease in plants, with a correlation value of 49%. Furthermore, the intensity of vector attack on plants had a highly significant correlation with the number of surviving imago (74%), the number of offspring (82%), and the number of eggs (83%), and significantly related to the number of nymphs, with a correlation value of 52%. The number of nymphs and the pest attack intensity parameters also had a significant correlation with the percentage of disease incidence, with values of 44% and 43%, respectively.

Discussion

Variation of the resistance to whitefly and geminivirus in pepper

This study finds that there is considerable variation of chili pepper genotypes for their resistance to whitefly and geminivirus. The values of the intensity and the number of whitefly population in the observed genotypes reflect the resistance level of the genotypes to whitefly attacks. Chiang and Talekar (1980)

argued that the higher the whitefly population on a plant, the lower the resistance of the plant to whitefly. Plant resistance to whitefly can also be seen from the ability of the imago to survive (as shown in the imago survival rate) in the plant (Firdaus et al. 2011). The high value of attack intensity based on the symptoms that appear on the surface of the leaves, as well as the high population of whitefly imagoes, eggs, nymphs, and pupae, indicate the low level of resistance of the plant to whitefly attacks. This signifies that the genotype has characteristics favored by whiteflies as a place to live and breed as well as a source of food. There are several factors that influence the attraction of whiteflies to host plants, namely leaf morphological characteristics such as leaf thickness, leaf color, and trichome density (Hasanuzzaman et al. 2016), as well as the content of compounds in these plants (Darshanee et al. 2017).

The difference between resistant and susceptible genotypes to whitefly attack can also be seen from the appearance of plant phenotypes (Figure 1). Plants that are attacked by whiteflies appear to be more wilted and experience symptoms of nutrient deficiency. The macroscopic effects caused by whiteflies on plants include the presence of chlorotic spots due to feeding activity of the whiteflies, resulting in a decrease in the amount of chlorophyll and starch in the leaves and the presence of sooty mold covering the leaf surface and thereby inhibiting the rate of photosynthesis (Pollard 1995). Another impact of whitefly attacks on chili plants is a decline in plant dry weight due to loss of nutrients in plants caused by the whiteflies that feed on leaf phloem (Jeevanandham et al. 2018). This generates physiological disturbances in plants due to the loss of nutrients as well as the closure of the leaf lamina on account of the excretion of sooty mold. The sooty mold that covers the leaf surface gradually develops into a fungus with a blackish color, thus disrupting the photosynthesis process of the plants.

Plants infected with geminivirus will show phenotypic symptoms in response. This is the impact of the virus attack as well as the plant's defense efforts against it. Interactions between viruses, plants, and the environment are characterized by the appearance of phenotypic symptoms as a sign of infection (Bennet and Agbandje 2017). As seen in the field, the common symptoms of Begomovirus attack on chili peppers are discoloration of leaves, distortion, curling, mosaics, and yellowing of leaves, yellowing and purpling of leaf veins, and decreasing crop yields (Bennet and Agbandje 2020; Genefianti et al. 2017). The incidence of diseases in plants marked by these symptoms indicates the high and low level of plant sensitivity to virus attacks. In addition to the indicated symptom score, the percentage of disease incidence also affects the severity of disease experienced by the plants (Ayu et al. 2021). Among all genotypes, JT5 genotype did not display any symptoms of geminivirus infection at the time of observation, despite the molecular confirmation of geminivirus DNA (PepYLCV) in plant DNA. Meanwhile, the other genotypes showed symptoms of viral infection even before the time of observation. Resistant genotypes are thought to have a protein-based resistance mechanism or certain genes that inhibit or even block the expression of viral genes (Lin et al. 2007; Venderschuren et al. 2006).

Disease severity signifies how severe the phenotypic effect of the yellow disease on the plants due to virus attack is. The high activity of viruses in plants can interfere with plant physiological processes by decreasing plant metabolism which can inhibit plant growth. The symptoms, such as the appearance of yellow mosaics and the clearance of leaf veins due to the induction of certain proteins from viral DNA, damage plant chloroplasts and interfere with photosynthesis (Bhattacharyya et al. 2015). Furthermore,

disruption of plant physiological mechanisms causes inhibition of plant growth and development, thus affecting its yield.

Resistance to whitefly as a geminivirus vector can potentially reduce disease severity in chili peppers

This study find out that whitefly resistance has the potential to be a useful effort to control geminivirus in chili pepper plants since it can reduce the severity of the disease. The high severity and incidence of the yellow disease in chili pepper plants are suspected to be caused by the large whitefly population and the intensity of their attacks. According to Bennet and Agbandje (2017), vectors play an important role in transporting viral genes to the plant nucleus through the plant phloem, which is a source of food for whiteflies. In addition, the results of this study signify that the number of imagoes was positively correlated with attack intensity, total population, and disease incidence. Furthermore, the number of nymphs also has a significant positive correlation with disease incidence. The correlation diagram shows that a large whitefly population may increase disease severity in chili plants due to the increasing attack intensity. In other words, the large whitefly population is suspected to increase the disease severity in chili plants due to the huge virus load invested by whitefly. A study by Plotnikov et al. (2020) stated that there was a significant relationship between the magnitude of the virus load and the level of manifestation of the cucumber green mottle mosaic virus (CGMMV) infection on cucumber leaves. A similar result has been previously identified in thrips-virus relation by Maris et al. (2003) who found that thrips resistance had a significant positive effect in reducing virus spread in both virus-susceptible accessions, resulting in a low number of infected plants, and virus-resistant accessions, resulting in less cosmetic damage.

Declarations

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Competing Interest

The authors declare that they have no financial interests.

Author Contribution

All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Yuke Mareta Ariesta Sandra, Awang Maharijaya and Sobir. The first draft of the manuscript was written by Yuke Mareta Ariesta Sandra and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Data Availability

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

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Tables

Table 1. Criteria for plant resistance to begomovirus infection

Response	Disease severity value (DSV)
Resistant	0%<DSV ≤5%
Moderately Resistant	5%<DSV ≤10%
Moderately Susceptible	10%<DSV ≤20%
Susceptible	20%<DSV ≤40
Very Susceptible	DSV>40%

Table 2. Results of the combined analysis of variance for the observed characters in 19 chili genotypes

	SI*	E*	N*	P*	OP*	I*	DI*	DSV*
degree of freedom	18	18	18	18	18	18	18	18
sum square	35.691	25.414	13.0018	7.8113	13.291	28.174	29.573	273.908
mean square	1.98282	1.41191	0.72232	0.43396	0.73837	1.5652	1.6429	15.27
F Value	2.4345**	2.2953*	2.7591**	1.5174	2.4911**	4.4296***	2.52**	1.99**

SI = number of surviving imago (%), E = number of eggs, N = number of nymphs, P = number of pupae, OP = number of offspring population, I = whitefly attack intensity (%), DI = disease incidence (%), DSV = disease severity value (%). = significantly different at α=5%, ** = significantly different at α=1%, *** = significantly different at α=0.1%

Table 3. Number of surviving imago, eggs, nymphs, pupae, offspring population, and disease intensity on 19 chili pepper genotypes with standard error

Genotype	SI*	E*	N*	P*	OP*	I* (%)
Baja	10 ± 0.83 ab	0 ± 0.56 a	12 ± 0.26 abc	4	16 ± 0.28 ab	0.5 ± 0.32 abc
Bonita	10 ± 0.83 ab	0 ± 0.56 a	2 ± 0.26 c	2	2 ± 0.28 b	0 ± 0.32 c
CR11	80 ± 0.83 ab	2 ± 0.56 a	6 ± 0.26 abc	2	10 ± 0.28 ab	13.3 ± 0.32 abc
CR13	60 ± 0.83 ab	0 ± 0.56 a	1 ± 0.26 abc	2	3 ± 0.28 ab	1.6 ± 0.32 abc
CR14	70 ± 0.83 ab	9 ± 0.56 a	4 ± 0.26 abc	10	23 ± 0.28 ab	12 ± 0.32 abc
CR15	10 ± 0.83 ab	1 ± 0.56 a	4 ± 0.26 abc	7	12 ± 0.28 ab	2.5 ± 0.32 abc
CR2	20 ± 0.83 ab	0 ± 0.56 a	4 ± 0.26 abc	1	5 ± 0.28 ab	0 ± 0.32 c
CR3	70 ± 0.83 ab	14 ± 0.56 a	13 ± 0.26 abc	4	31 ± 0.28 ab	17.2 ± 0.32 ab
CR4	100 ± 0.83 a	13 ± 0.56 a	19 ± 0.26 a	5	37 ± 0.28 a	16.3 ± 0.32 a
CR6	50 ± 0.83 ab	1 ± 0.56 a	2 ± 0.26 abc	4	7 ± 0.28 ab	1.1 ± 0.32 abc
CR9	60 ± 0.83 ab	8 ± 0.56 a	14 ± 0.26 ab	2	24 ± 0.28 ab	2.4 ± 0.32 abc
F3U3	80 ± 0.83 ab	0 ± 0.56 a	17 ± 0.26 abc	9	26 ± 0.28 b	9.3 ± 0.32 ab
JT1	0 ± 0.83 b	0 ± 0.56 a	1 ± 0.26 bc	0	1 ± 0.28 b	0 ± 0.32 c
JT5	30 ± 0.83 ab	6 ± 0.56 a	4 ± 0.26 abc	3	13 ± 0.28 ab	1.8 ± 0.32 abc
KD2	10 ± 0.83 ab	1 ± 0.56 a	2 ± 0.26 abc	2	5 ± 0.28 ab	0.2 ± 0.32 bc
KD3	40 ± 0.83 ab	42 ± 0.56 a	5 ± 0.26 abc	3	50 ± 0.28 ab	17.9 ± 0.32 ab
KD4	20 ± 0.83 ab	4 ± 0.56 a	5 ± 0.26 abc	3	12 ± 0.28 ab	0.6 ± 0.32 abc
KD5	30 ± 0.83 ab	10 ± 0.56 a	2 ± 0.26 bc	2	14 ± 0.28 ab	1.8 ± 0.32 abc
KD7	20 ± 0.83 ab	7 ± 0.56 a	2 ± 0.26 abc	2	11 ± 0.28 ab	2 ± 0.32 abc

*Values followed by the same letter in the same column are not significantly different based on the Honest Significant Difference (HSD) test at α= 5% level. SI = survival rate of imago (%). E = number of eggs. N = number of nymphs. P = number of pupae. OP = number of offspring population. I = whitefly attack intensity (%).

Table 4. Number of disease incidence, disease severity value, resistance criteria, and DNA virus confirmation in plant

No	Genotype	DI*	DSV*	Resistance Criteria	Virus DNA
1	Baja	47.83 ± 0.65 a	27.78 ± 7.65 a	Susceptible	Present
2	Bonita	88.89 ± 0.65 b	18.86 ± 7.65 ab	Moderately Susceptible	Present
3	CR11	77.27 ± 0.65 a	64.79 ± 7.65 ab	Very Susceptible	Present
4	CR13	84.62 ± 0.65 ab	27.69 ± 7.65 ab	Susceptible	Present
5	CR14	68.18 ± 0.65 ab	53.03 ± 7.65 b	Very Susceptible	Present
6	CR15	92.86 ± 0.65 ab	76.36 ± 7.65 ab	Very Susceptible	Present
7	CR2	62.50 ± 0.65 b	39.29 ± 7.65 ab	Susceptible	Present
8	CR3	65.38 ± 0.65 a	16.28 ± 7.65 ab	Moderately Susceptible	Present
9	CR4	62.50 ± 0.65 ab	62.50 ± 7.65 ab	Very Susceptible	Present
10	CR6	66.67 ± 0.65 a	45.36 ± 7.65 ab	Very Susceptible	Present
11	CR9	10.71 ± 0.65 ab	7.14 ± 7.65 ab	Moderately Resistant	Present
12	F3U3	66.67 ± 0.65 a	88.15 ± 7.65 ab	Very Susceptible	Present
13	JT1	68.42 ± 0.65 ab	31.58 ± 7.65 b	Susceptible	Present
14	JT5	19.23 ± 0.65 ab	5.19 ± 7.65 ab	Resistant	Present
15	KD2	47.06 ± 0.65 ab	24.71 ± 7.65 ab	Susceptible	Present
16	KD3	68.00 ± 0.65 ab	26.37 ± 7.65 ab	Susceptible	Present
17	KD4	80.00 ± 0.65 a	34.05±0.65 ab	Susceptible	Present
18	KD5	56.52 ± 0.65 ab	21.30±0.65 ab	Susceptible	Present
19	KD7	75. 00 ± 0.65 ab	24.19±0.65 ab	Susceptible	Present

*Values followed by the same letter in the same column are not significantly different based on the Honest Significant Difference (HSD) test at α=5%. DI = disease incidence (%). DSV = disease severity value (%)

Figures

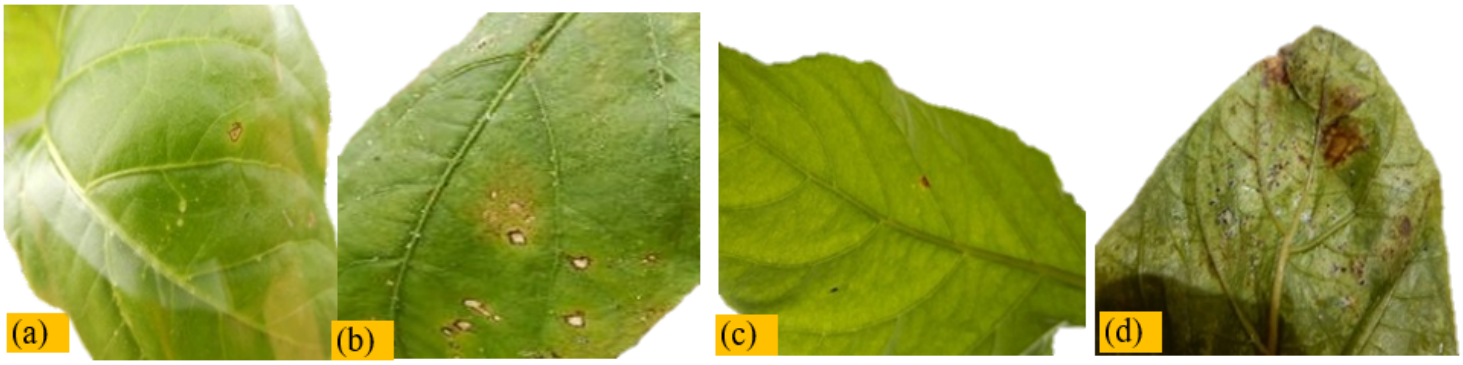

Figure 1

Genotype appearance after whitefly inoculation. (a) upper leaf surface of resistant genotype, (b) upper leaf surface of susceptible genotype, (c) lower leaf surface of resistant genotype, (d) lower leaf surface of susceptible genotype

Figure 2

Appearance of very susceptible chili genotype CR15 (a), moderately resistant genotype CR9 (b), and resistant genotype JT5 (c) to geminivirus

Figure 3

Visualization of amplified PYLCV DNA using universal primers SPG1/SPG2. M, DNA marker (1kb ladder); No. 1 to 19 are chili samples CR2, CR3, CR4, CR6, CR9, CR11, CR13, CR14, CR15, KD2, KD3, KD4, KD5, KD7, F3U3, Bonita, Baja, JT1, and JT5 consecutively

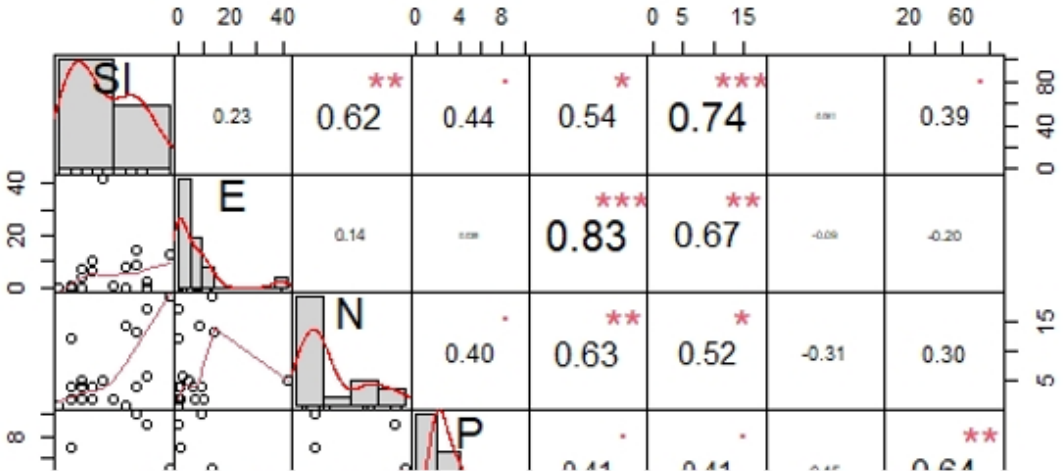

Figure 4

Correlation diagram between observed parameters of vector and disease resistance. SI = number of survival imago; E = number of egg; N = number of nymph; P = number of pupae, OP = number of offspring population; I = disease intensity; DI = disease incidence; DSV = disease severity value.