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Screening 27 Genotypes of Eggplant (*Solanum melongena*) for Resistance to Three Species of *Begomovirus*

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Abstract

Three primary species of *Begomovirus*, *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV), *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), and *Tomato leaf curl New Delhi virus* (ToLCNDV), have significantly impacted eggplant production in Indonesia, with infections often involving multiple viruses causing severe symptoms. Utilizing resistant cultivars for these viruses is the most effective control method. This study aimed to identify resistant genotypes and evaluate the heritability of eggplant resistance to *Begomovirus*. In a controlled environment, 27 eggplant genotypes were inoculated with the single of three *Begomovirus* species separately (molecularly confirmed), using *Bemisia tabaci* as a vector. The plants were inoculated at the seedling growth stage and observed weekly until the disease progression stabilized. These assessments included monitoring symptoms, the number of symptomatic plants, and assigning disease severity scores to each individual. The data were analyzed using ANOVA and Tukey-HSD tests at $\alpha = 5\%$. The results indicated that EPA 21016 A genotype was resistant to TYLCKaV, with the lowest disease incidence (2.5%) and severity (1.25%), making it a promising parental line for breeding virus-resistant cultivars. However, all genotypes were susceptible to PepYLCIV and ToLCNDV, with a 100% disease incidence. High heritability for TYLCKaV resistance suggests its potential for early-generation selection, while low heritability for PepYLCIV and ToLCNDV indicates the need for enhanced genetic variability.

Keywords: heritability; PepYLCIV; resistance; ToLCNDV; TYLCKaV

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INTRODUCTION

Eggplant (*Solanum melongena*) is the fifth most economically significant vegetable crop within the Solanaceae family, following tomato (*Solanum lycopersicum*), potato (*Solanum tuberosum*), chili pepper (*Capsicum annuum*), and tobacco (*Nicotiana tabacum*) (Oladosu et al., 2021). According to the FAO (2023), Asia contributes to more than 90% of global eggplant production, with Indonesia ranking as the fifth-largest producer globally, following China, India, Egypt, and Turkey. In 2022, Indonesia's eggplant productivity was 13.74 tons ha^{-1} and increased by 2.77% to 14.12 tons ha^{-1} in 2023. Despite the consistent rise in production, Indonesia still accounts for only 1% of global demand, partly due to constraints such as pathogen attacks, particularly *Begomovirus*.

Begomovirus is the largest genus of the Geminiviridae family of plant viruses and causes devastating diseases in many economically

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important crops worldwide. *Begomovirus* mainly affects a wide range of dicotyledonous plants, including Cucurbitaceae, Euphorbiaceae, Solanaceae, Malvaceae, and Fabaceae (Zaidi et al., 2017). The common symptoms of *Begomovirus* infection include yellowing, leaf curling or rolling, stunting, and a decreased fruit yield per plant (Wahyono et al., 2023). Eggplant is one of the main hosts for the *Begomovirus* and is highly favored by the whitefly as a vector (Sudiono, 2001). Three primary species of *Begomovirus* have been identified as infecting eggplants in Indonesia: *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV), and *Tomato leaf curl New Delhi virus* (ToLCNDV) (Sidik, 2017).

Since 2013, TYLCKaV has been reported to damage eggplant plantations in West Java (Bogor and Bandung), Central Java (Pati and Blora), and the Special Region of Yogyakarta (Bantul) (Kintasari et al., 2013). TYLCKaV infection in eggplant induced chlorotic, yellowing, and mosaic symptoms. Other symptoms include leaf curling, malformed fruits, and stunting (Santoso, 2023). In contrast to the widely reported TYLCKaV infections, reports on PepYLCIV and ToLCNDV are still very limited. ToLCNDV was first reported on eggplant in India in 2011 and induced leaf curling, yellow mosaic, and mottling of leaves at a later stage of infection (Pratap et al., 2011). The first reported case of PepYLCIV in eggplants was in Kencong, where it was mixed with TYLCKaV and ToLCNDV (Sidik, 2017). Consequently, it became difficult to distinguish between symptoms caused by individual or multiple *Begomovirus* species, as all infected plants showed similar symptoms of leaf yellowing and mosaic.

Begomovirus is exclusively transmitted by the whitefly (*Bemisia tabaci*) (Shen et al., 2020). In practice, the method of preventing viruses from infecting the host is the control of virus vectors through appropriate physical barriers (traps and screens) and chemical agents (insecticides). Nevertheless, building effective physical barriers is not always feasible, and the application of chemical compounds can lead to the development of resistance against the compound by whiteflies. The disease incidence caused by *Begomovirus* remains challenging to manage due to the high viral genetic diversity, recombination among virus species, multiple infections, and a wide range of virus hosts, as well as *Bemisia tabaci* as the vector (Bhattacharyya et al., 2015).

Multiple infection is the presence of multiple viruses in a single plant, which leads to a variety of symptoms simultaneously and causes the severity of the disease to increase. It also has the potential to result in recombination between species (Singhal et al., 2021). Sidik (2017) reported that multiple *Begomovirus* species, specifically PepYLCIV, TYLCKaV, and ToLCNDV, infected Kencong's eggplants, highlighting the urgent need for effective management strategies. The use of resistant cultivars is a critical crop protection method to mitigate damage caused by these viruses while reducing the excessive use of insecticides (Shen et al., 2020). Resistant cultivars help decrease dependency on agrochemicals, lower production costs, and enhance resilience to biotic stress, especially in resource-limited developing countries, where sustainable practices are essential for food security and environmental conservation (Zhang et al., 2018).

Resistant cultivars can be obtained by selecting existing germplasm and crossbreeding among selected parents. Genetic variability plays a crucial role in determining the success of such breeding programs. Studies have shown that certain genotypes, such as doubled haploid lines with Green Super Rice (GSR) characteristics, exhibit varying resistance levels, making them valuable resources for breeding programs (Nurhidayah et al., 2024). Several genotypes have been reported to be resistant to TYLCKaV, such as Hitavi (Mulyani et al., 2021) and Yuvita (Alhaddad et al., 2023). Currently, particularly in Indonesia, no genotype is resistant to PepYLCIV, ToLCNDV, or the multiple infections of these three viruses. This research aims to develop resistant genotypes to all three *Begomovirus* species–TYLCKaV, PepYLCIV, and ToLCNDV to serve as foundational material for resistance breeding. Furthermore, understanding the inheritance patterns of resistance traits is critical to efficiently use genetic sources of resistance to each *Begomovirus* species and determine optimal plant breeding strategies.

MATERIALS AND METHOD

The research was conducted in August-December 2023 in the Department of Horticulture Crop Research Development (Farm Kencong and Karangploso) and the Department of Biotechnology of PT BISI International Tbk. The research was arranged in a completely randomized design (CRD) consisting of two

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replications for each treatment, where the treatment involved different genotypes tested for resistance to *Begomovirus* species. For each replication, 20 plants in each genotype were taken as samples.

Plant materials

Twenty-seven eggplant genotypes were examined in this research. The seeds of 24 genotypes were obtained from PT BISI International Tbk, while three genotypes are commercialized eggplant varieties. Genotypes include: HTV 234-13-01, HTV 234-13-02, HTV 296-01-01, HTV 302-04-01, HTV 304-02-04, HTV 333-11-01, HK 280-11-02, HK 293-19, HK 319-10, HK 321-08, HK 331-05, YVT 339-06-04, YVT 339-06-10, YVT 339-06-12, YVT 339-06-14, EP 1011 A, EP 1011 B, EP 18178 B, EP 18014 A, EP 18014 B, EPA 21016 A, EPA 21016 B, Antaboga, New Prince, Hitavi, Yuvita, and Hijau Kuat. The selection of genotypes was based on an assessment of market preferences, including fruit color, length, shape, and size, aiming to identify resilient genotypes suitable for developing high-quality eggplant cultivars resistant to viruses.

Maintenance of the whitefly (*Bemisia tabaci*)

Non-viruliferous whiteflies were maintained on healthy cotton (*Gossypium hirsutum*) grown in muslin-covered cages at the Department of Biotechnology, PT BISI International Tbk. Whiteflies were reared on cotton plants for at least 20 to 25 days to complete their life cycle and to obtain enough adult whiteflies for the transmission experiments.

Maintenance of virus isolates

The inoculums of TYLCKaV, PepYLCIV, and ToLCNDV have been collected from pure culture maintained at the Department of Biotechnology, PT BISI International Tbk. TYLCKaV was maintained in eggplant (var. Antaboga), PepYLCIV was maintained in chili (var. Imola), and ToLCNDV was maintained in cucumber (var. BCU542). These host plant varieties were selected based on their susceptibility to *Begomovirus* while maintaining sufficient vigor to support virus propagation without collapsing (Ghosh et al., 2019). This research used a single inoculum that had been confirmed through PCR analysis (Figure 1). The total DNA was extracted from the inoculum using cetyltrimethylammonium bromide (CTAB) method with suitable modifications and subjected to PCR analysis using TYLCKaV F-R, PepYLCIV F-R, and ToLCNDV F-R for the confirmation of each species of *Begomovirus*. PCR was performed as described by Wahyono et al. (2023).

Seedlings eggplant germplasms

Healthy eggplant seedlings were used in this research. Forty seeds of each genotype were sown in seed trays filled with cocopeat and compost mixture in a 2:1 ratio and kept in the greenhouse.

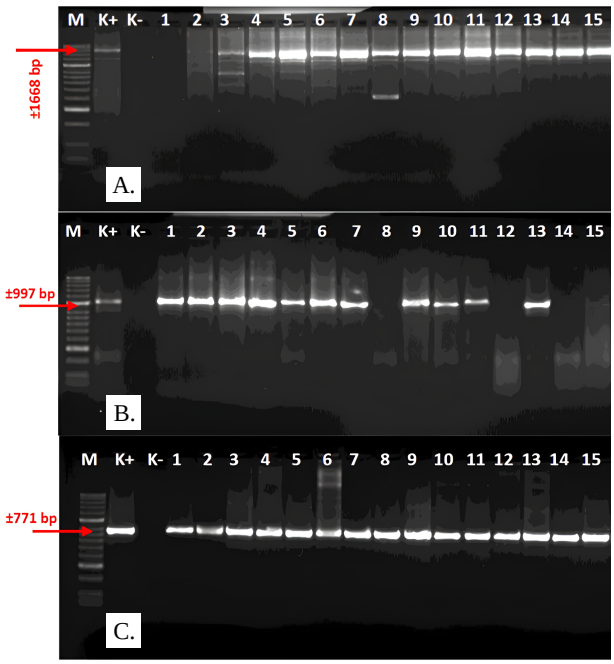

Figure 1. Visualization of PCR amplification results on an electrophoresis gel, (A) TYLCKaV, (B) PepYLCIV, (C) ToLCNDV isolates

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Acquisition

Non-viruliferous whiteflies were collected from cotton plants using an aspirator and then released on TYLCKaV, PepYLCIV, and ToLCNDV-infected plants separately for a 24-hour acquisition period (Marianah, 2020).

Inoculation

The single-inoculation method was used to ensure precise control over virus transmission and minimize cross-contamination. After the acquisition period, viruliferous whiteflies were transferred to feed on three weeks of eggplant seedlings using an aspirator at the rate of 10 whiteflies per plant (Yan et al., 2021). After 48-hour inoculation period, the whiteflies were eliminated by spraying insecticide Winder 100 EC and Samite 125 EC (PT BISI International Tbk). Inoculated eggplant seedlings were transplanted into 30 cm x 30 cm polybags filled with soil and compost mixture in a 1:1 ratio and kept in the screenhouse.

Screening process

Evaluation of TYLCKaV, PepYLCIV, and ToLCNDV symptoms in each plant was conducted 7 days after inoculation (DAI) until the disease progression stabilized. TYLCKaV, PepYLCIV, and ToLCNDV were evaluated over the periods of 49, 56, and 63 days, respectively. These assessments included monitoring symptom variations, counting symptomatic plants, and assigning disease severity scores to each individual.

Disease incidence

Disease incidence was calculated based on the proportion of affected plants within the population using Equation 1 (Agrios, 2005).

$$DI = \frac{n}{N} \times 100\% \quad (1)$$

Where, DI is disease incidence, n is the number of diseased plants, and N is the total number of plants examined.

Table 1. Criteria for plant resistance to *Begomovirus* infection (Dolores, 1996)

DS (%)	Response
0	Highly resistant
DS ≤ 10	Resistant
10 < DS ≤ 20	Moderately resistant
20 < DS ≤ 30	Moderately susceptible
30 < DS ≤ 50	Susceptible
DS > 50	Highly susceptible

Note: DS = Disease severity

Disease severity

Disease severity was determined by scoring the number of plants that showed symptoms every week, using Equation 2 (Campbell and Madden, 1990).

$$DS = \frac{\Sigma (ni \times vi)}{N \times V} \times 100\% \quad (2)$$

Where, DS is disease severity, ni is the number of infected plants in the same category, vi is the severity score, N is the total number of plants observed, and V is the maximum rating score.

The criteria for evaluating symptoms of viral infection were based on the method described by Romero-Masegosa et al. (2020), including 0 (no visible symptoms and normal growth), 1 (slight yellowing on leaves and normal growth), 2 (yellowing and slight mosaic on leaves, normal plant growth), 3 (curling, yellowing, mosaic on leaves, and stunted growth), and 4 (pronounced yellowing and mosaic of all leaves on the whole plant and stunted growth). The disease severity was used to classify resilience with the criteria presented in Table 1 (Dolores, 1996).

Area under the disease progress curve (AUDPC)

The AUDPC was calculated based on the disease severity using Equation 3 (Wolf and Verreet, 2009).

$$AUDPC = \sum_{i=1}^{n=1} \frac{(X_i + X_{i+1})}{2} \times (t_{i+1} - t_i) \quad (3)$$

Where, X_i is disease level at time t_i, $t_{(i+1)}$-t_i is the time between two disease scores, and n is the number of dates at which symptoms were recorded. AUDPC was assessed based on the category scale outlined in Table 2 (Sinaga, 2003).

Statistical analysis

The data of disease incidence and severity were statistically analyzed using analysis of variance (ANOVA), and further tests were carried out using the Tukey-HSD test with a significance

Table 2. Criteria for plant resistance to *Begomovirus* based on AUDPC (Sinaga, 2003)

AUDPC	Response
0 < x ≤ 50	Highly resistant
50 < x ≤ 100	Resistant
100 < x ≤ 250	Moderately resistant
x > 250	Susceptible

Note: AUDPC = Area under the disease progress curve

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level of 5%. Broad-sense heritability was calculated using Equation 4 (Hill et al., 1978).

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} \quad (4)$$

Where, h^2_{bs} is broad-sense heritability, σ^2_g is genotypic variance, σ^2_p is phenotypic variance.

According to Stansfield (1991), broad-sense heritability $h^2_{bs} > 0.5$ was considered high, meanwhile $0.2 \leq h^2_{bs} \leq 0.5$ were considered medium, and $h^2_{bs} < 0.2$ were considered low.

RESULTS AND DISCUSSION

The evaluation of 27 eggplant genotypes for resistance to TYLCKaV indicated a diverse range of disease incidences, from 2.5 to 100% (Figure 2). Although the virus can successfully infect plants, not all plants display infected symptoms. The virus strain and environmental conditions like temperature influence the presence of symptoms, impacting the virus's infection, replication, and spread within the plant (Honjo et al., 2020). In contrast, the evaluation for resistance to PepYLCIV and ToLCNDV showed that all plants of each genotype exhibited disease symptoms, resulting in a 100% incidence rate (Figure 2). Responses or symptoms in all evaluated plants may be due to the genotype's susceptibility to the virus, particularly if the infection occurs before the generative period, resulting in more severe and varied symptoms. The high disease incidence may also be attributed to the effective transmission of the virus within the plant. The transmission method employed was individual transmission, which is regarded as the most effective approach to reduce the risk of escape or unintended spread.

The symptoms of a TYLCKaV infection were leaf yellowing and mosaic, leaf curling, leaf rolling, leaf malformation, and shortened internodes or branches, which led to clustered leaf growth resembling a rosette and stunted plant growth (Figure 3). Variations in the symptoms of eggplant infected with PepYLCIV included leaf curling, leaf rolling, leaf upward or downward cupping, petiole twisting or bending, leaf malformation, reduced leaf size, imperfect flower or branch development, rosette, and stunted plant growth (Figure 4). PepYLCIV infection induces petioles to bend upwards, creating the appearance of upright leaves. In some cases, nearly all petioles stand erect, resembling a witches' broom (Figure 4J). The symptoms of ToLCNDV infection were leaf curling, leaf rolling, leaf upward or downward cupping, leaf malformation, erect leaves, reduced leaf size, shortened flower stalks, twisted petioles, vein banding, rosette, and plant stunting (Figure 5). Many things in the environment can cause different symptoms in different host-virus combinations. These include temperature, the host plant's genetics, the pathogen's traits, and the interactions between the host and the pathogen.

Disease severity is the proportion of plant area affected by pathogens relative to the total plant area (Herliyana et al., 2020). Based on the evaluation for resistance to TYLCKaV, all genotypes exhibited disease symptoms by the

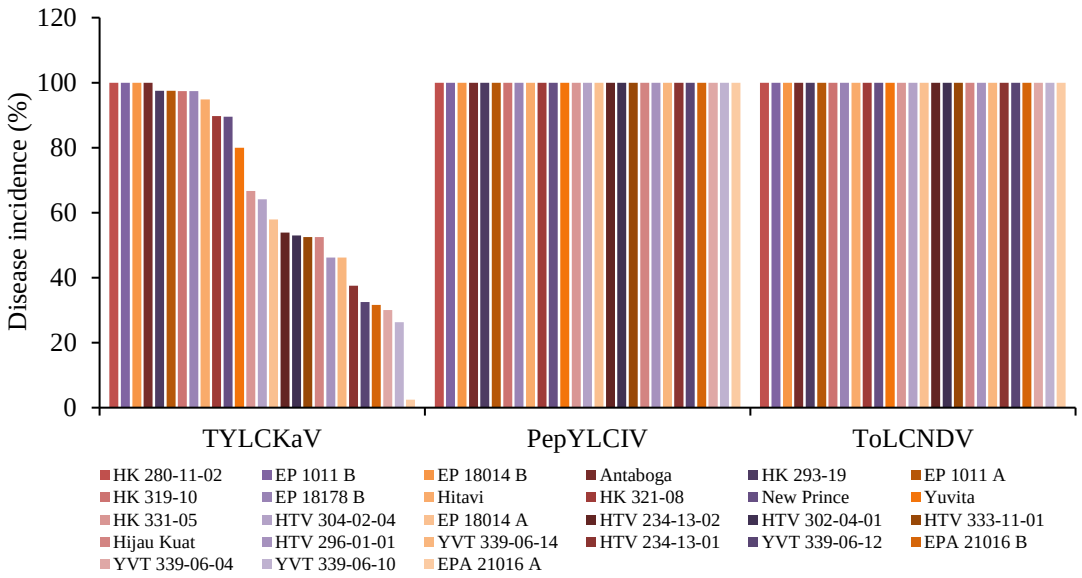

Figure 2. Disease incidence caused by TYLCKaV, PepYLCIV, and ToLCNDV

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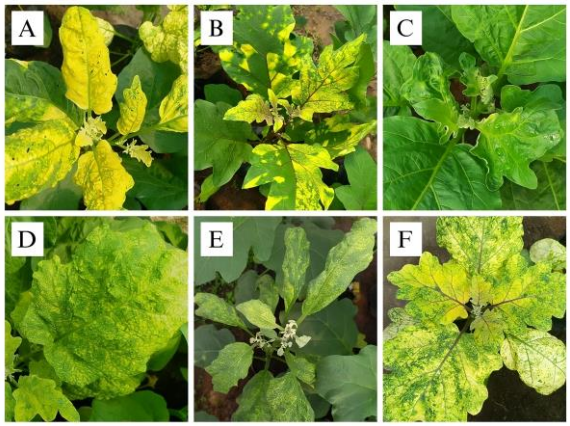

Figure 3. Variations in the symptoms of eggplants infected by TYLCKaV, (a) leaf yellowing, (b) leaf mosaic, (c) leaf malformation, (d) leaf curling, (e) leaf rolling, and (f) rosette and stunting

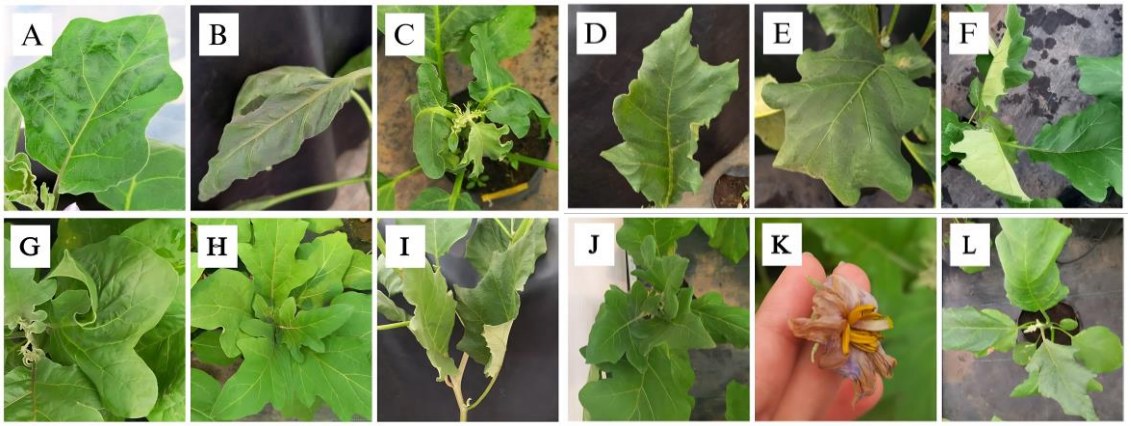

Figure 4. Variations in the symptoms of eggplants infected by PepYLCIV, (a) leaf curling, (b) leaf rolling, (c) petiole bending, (d) leaf upward cupping, (e) leaf downward cupping, (f) twisted petiole, (g) leaf malformation, (h) rosette, (i) erect leaves, (j) witches' broom, (k) imperfect flower development, and (l) stunting

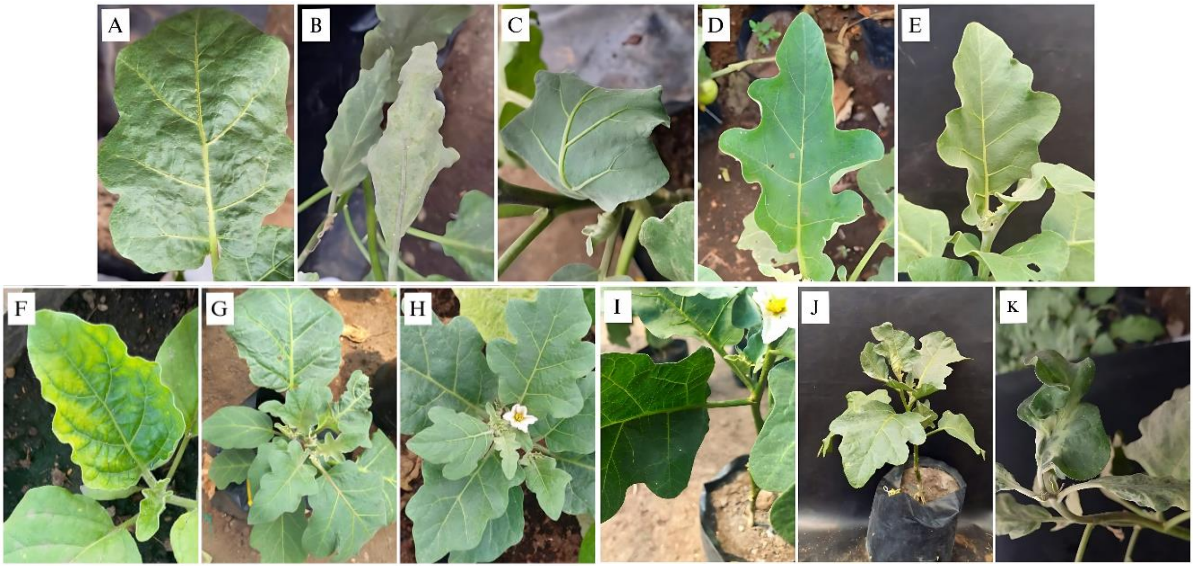

Figure 5. Variations in the symptoms of eggplants infected by ToLCNDV, (a) leaf curling, (b) leaf rolling, (c) leaf downward cupping, (d) leaf upward cupping, (e) erect leaves, (f) vein banding, (g) rosette, (h) shortened flower stalks, (i) twisted petiole, (j) stunting, and (k) leaf malformation

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third week after inoculation. Almost all tested genotypes showed an increase in disease severity as the plants aged (Figure 6). Genotype EPA 21016 A had the lowest disease severity by the final observation week at 1.25%. The low disease severity could be attributed to the plant's ability to inhibit virus replication and localize it within infected cells, thereby preventing viral spread to other plant parts. Genetically, resistance traits are governed by multiple genes on chromosomes, known as resistance genes, which regulate toxin production and metabolism to suppress disease development (Muis et al., 2015).

In assessing PepYLCIV resistance, all genotypes showed disease symptoms by the second week after inoculation (Figure 7). Generally, nearly all genotypes displayed increasing disease severity with plant age, although some experienced reduced severity in weeks 4, 5, 7, and 8 (Figure 7). Symptom reduction may indicate plant recovery, characterized by initial severe symptoms followed by gradual attenuation or asymptomatic phases on new leaves (Bengyella et al., 2015). Notably, genotype HTV 304-02-04 exhibited prominent recovery phenomena in this study (Figure 9). Regarding resistance to ToLCNDV, all genotypes exhibited disease symptoms by the second-week post-inoculation (Figure 8). Generally, disease severity increased with plant age, although some genotypes showed reduced severity in week 7 (Figure 8). By the final observation week, nearly

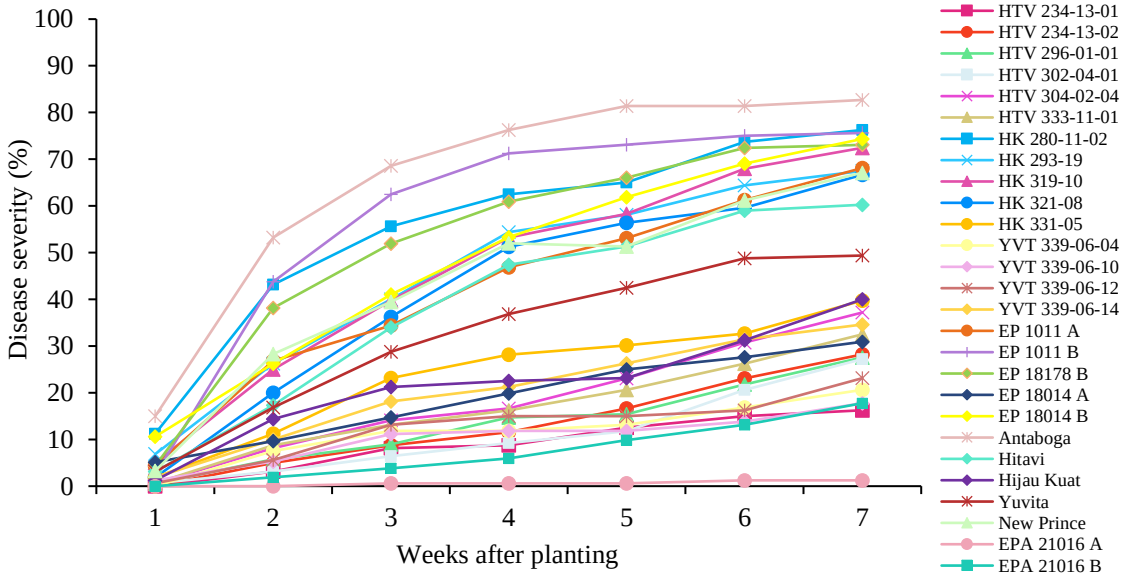

Figure 6. Disease severity progression caused by TYLCKaV

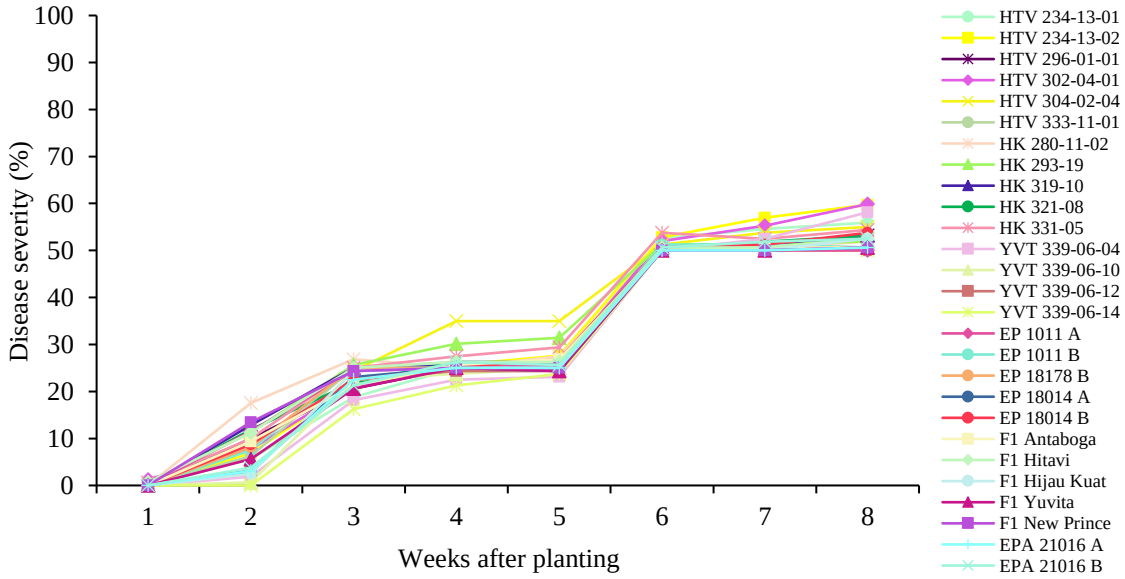

Figure 7. Disease severity progression caused by PepYLCIV

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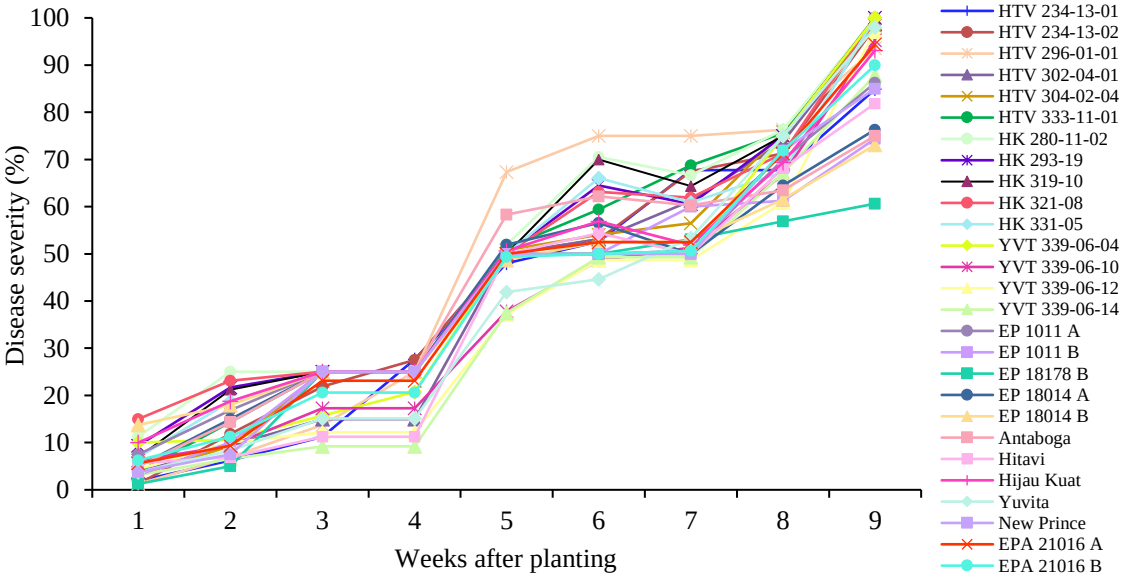

Figure 8. Disease severity progression caused by ToLCNDV

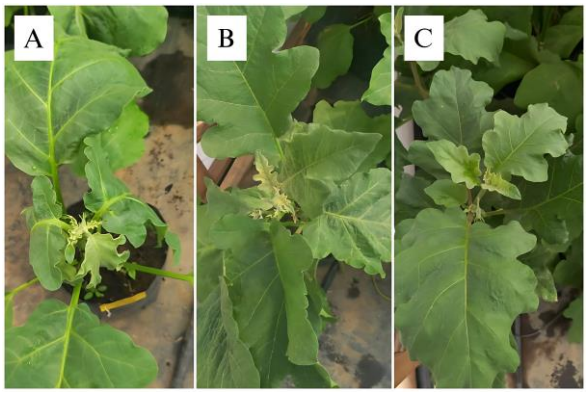

Figure 9. The recovery phenomenon in genotype HTV-304-02-04: at the (a) 4th, (b) 5th, (c) 6th week

all eggplant genotypes demonstrated high disease severity, reaching up to 100%. This observation likely reflects widespread severe symptoms, such as plant stunting, significantly affecting plant productivity. Virus infections disrupt plant metabolism by diverting photosynthate resources for virus replication and particle synthesis, limiting vegetative and reproductive growth resources (Ertunç, 2020).

Based on the screening resistance for TYLCKaV, one genotype was identified as resistant, EPA 21016 A, with disease severity of 1.25% (Table 3). Resistant genotypes are presumed to possess robust resistance mechanisms, including genetic factors that effectively suppress virus replication compared to susceptible genotypes. Genotypic responses to resistance are influenced by specific plant genetic factors (Santoso, 2023). Hence, EPA 21016 A, identified as resistant to TYLCKaV, holds potential as a source of resistance genes for the development of virus-resistant eggplant cultivars. In the screening for PepYLCIV and ToLCNDV resistance, nearly all tested genotypes were categorized as highly susceptible. This could be attributed to the absence of resistance genes (Ty-1 to Ty-6), which are known to confer resistance to various *Begomoviruses* in other crops. Without these genes, the genotypes lack the genetic mechanisms necessary to suppress viral replication or mitigate the severity of infections (Kaushal, 2020). However, YVT 339-06-12, YVT 339-06-14, and EP 1011 A showed some tolerance to PepYLCIV, with disease severity at 50%, and were considered susceptible (Table 3). Similarly, genotype EP 18178 B demonstrated better tolerance for ToLCNDV than other genotypes due to the least impact on growth and the mildest disease severity (60.63%) (Table 3). Plant resistance responses are influenced by their ability to suppress virus replication. Tolerance in plants refers to their capacity to endure

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Table 3. Number of disease severity and resistance criteria for TYLCKaV, PepYLCIV, and ToLCNDV

Genotype	TYLCKaV		PepYLCIV		ToLCNDV	
	DS (%)	Criteria	DS (%)	Criteria	DS (%)	Criteria*
HTV 234-13-01	16.25	MR	55.92	HS	84.87	HS
HTV 234-13-02	28.21	MS	59.72	HS	98.13	HS
HTV 296-01-01	27.56	MS	53.21	HS	93.59	HS
HTV 302-04-01	27.21	MS	59.87	HS	98.75	HS
HTV 304-02-04	37.18	S	55.00	HS	98.39	HS
HTV 333-11-01	32.50	S	53.13	HS	100.00	HS
HK 280-11-02	76.25	HS	51.88	HS	100.00	HS
HK 293-19	67.50	HS	51.92	HS	100.00	HS
HK 319-10	72.44	HS	53.21	HS	100.00	HS
HK 321-08	66.67	HS	53.13	HS	100.00	HS
HK 331-05	39.74	S	54.38	HS	100.00	HS
YVT 339-06-04	20.63	MS	58.13	HS	100.00	HS
YVT 339-06-10	17.76	MR	50.66	HS	95.27	HS
YVT 339-06-12	23.13	MS	50.00	S	97.14	HS
YVT 339-06-14	34.62	S	50.00	S	87.86	HS
EP 1011 A	68.13	HS	50.00	S	86.25	HS
EP 1011 B	75.63	HS	50.63	HS	74.38	HS
EP 18178 B	73.08	HS	50.63	HS	60.63	HS
EP 18014 A	30.92	S	50.64	HS	76.32	HS
EP 18014 B	74.34	HS	53.75	HS	73.08	HS
EPA 21016 A	1.25	R	50.63	HS	94.38	HS
EPA 21016 B	17.76	MR	52.50	HS	90.00	HS
Antaboga	82.69	HS	50.63	HS	75.00	HS
Hitavi	60.26	HS	52.50	HS	81.88	HS
Hijau Kuat	40.00	S	52.56	HS	93.13	HS
Yuvita	49.38	S	50.63	HS	97.97	HS
New Prince	67.11	HS	50.64	HS	85.00	HS

Note: DS = Disease severity, R = Resistant, MR = Moderately resistant, MS = Moderately susceptible, S = Susceptible, HS = Highly susceptible (*Resistance criteria according to Dolores, 1996)

virus infection, leading to a gradual reduction or disappearance of disease symptoms and minimizing yield losses (Calil and Fontes, 2017).

Based on the AUDPC analysis, one genotype, EPA 21016 A, was identified as highly resistant to TYLCKaV, with an AUDPC value of 26 (Table 4). The resistance response in virus-infected plants can be influenced by resistance genes. Upon viral infection, the resistance gene triggers a hypersensitive response (HR) characterized by programmed cell death, rapidly eliminating infected cells and restricting viral spread within the plant (Akhter et al., 2021). Additionally, the activity of resistance genes is linked to biochemical processes, such as the activation and expression of salicylic acid (SA), jasmonic acid (JA), pathogenesis-related (PR) proteins, like peroxidase, and the deposition of callose in the plasmodesmata, which limits viral movement from cell to cell. Currently, six resistance genes against TYLCV have been identified: Ty-1, Ty-2, Ty-3, Ty-4, Ty-5, and Ty-6. (Kalloo and Banerjee, 1990; Pilowsky and Cohen, 1990; Zamir et al., 1994; Ji et al., 2007; 2009; Scott et al., 2015). According to the AUDPC analysis, all genotypes were susceptible to PepYLCIV and ToLCNDV, with AUDPC values ranging from 1,304 to 3,564 (Table 4). The resistance classification based on AUDPC values is influenced by disease severity progression. Several factors influence the disease's severity, including the plant's age at the time of infection, environmental conditions favorable to viral proliferation, and the virulence of the virus. Viruses with high virulence can replicate rapidly within plant cells, resulting in more severe disease symptoms (Agrios, 2005).

Estimates of broad-sense trait heritability are useful to evaluate the amount of genetic variation in a breeding population and the influence of genotype × environment interaction in the expression of a characteristic, thus allowing us

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Table 4. Resistance criteria for TYLCKaV, PepYLCIV, and ToLCNDV based on AUDPC values

Genotype	TYLCKaV		PepYLCIV		ToLCNDV	
	AUDPC	Criteria	AUDPC	Criteria	AUDPC	Criteria*
HTV 234-13-01	389	S	1,485	S	2,922	S
HTV 234-13-02	554	S	1,547	S	3,175	S
HTV 296-01-01	565	S	1,460	S	3,480	S
HTV 302-04-01	455	S	1,534	S	2,959	S
HTV 304-02-04	781	S	1,606	S	3,124	S
HTV 333-11-01	711	S	1,477	S	3,341	S
HK 280-11-02	2,406	S	1,564	S	3,564	S
HK 293-19	1,962	S	1,591	S	3,388	S
HK 319-10	1,981	S	1,528	S	3,457	S
HK 321-08	1,805	S	1,507	S	3,392	S
HK 331-05	1,023	S	1,579	S	3,298	S
YVT 339-06-04	501	S	1,380	S	2,943	S
YVT 339-06-10	444	S	1,389	S	2,695	S
YVT 339-06-12	538	S	1,396	S	2,526	S
YVT 339-06-14	877	S	1,304	S	2,463	S
EP 1011 A	1,811	S	1,481	S	3,009	S
EP 1011 B	2,553	S	1,472	S	2,880	S
EP 18178 B	2,297	S	1,468	S	2,663	S
EP 18014 A	804	S	1,406	S	2,958	S
EP 18014 B	2,058	S	1,483	S	2,941	S
EPA 21016 A	26	HR	1,407	S	2,987	S
EPA 21016 B	305	S	1,439	S	2,903	S
Antaboga	2,868	S	1,463	S	3,137	S
Hitavi	1,685	S	1,516	S	2,658	S
Hijau Kuat	932	S	1,422	S	3,142	S
Yuvita	1,400	S	1,407	S	2,739	S
New Prince	1,872	S	1,492	S	2,914	S

Note: HR = Highly resistant, S = Susceptible (*Resistance criteria according Sinaga, 2003)

Table 5. Variance components and heritability of resistance traits against *Begomovirus*

Resistance traits	TYLCKaV				PepYLCIV	ToLCNDV
	σ^2_G	σ^2_E	σ^2_F	h^2_{bs}	h^2_{bs}	h^2_{bs}
Disease severity	1.85	0.19	2.05	0.91	0.00	0.00
Disease incidence	4.38	0.49	4.87	0.90	0.00	0.00

Note: σ^2_G = Genotypic variance, σ^2_F = Phenotypic variance, σ^2_E = Environmental variance, h^2_{bs} = Broad-sense heritability

to predict the potential improvements that can be obtained through selection (Ortiz et al., 2021). In this study, researchers found high heritability for resistance to TYLCKaV ($h^2_{bs} > 0.5$) and low heritability for resistance to PepYLCIV and ToLCNDV ($h^2_{bs} \leq 0.2$) (Table 5). Heritability estimates are influenced by genotypic variance, environmental variance, and genetic × environment interaction variance (Jameela et al., 2014). Environmental variance and the interaction between genetic and environmental variances negatively impact heritability estimates. The more significant the environmental influence and genetic × environment interaction, the lower the heritability estimate. High heritability suggests that genotypic factors are more dominant than environmental factors, indicating the trait has the potential to be consistently inherited, and selection can be conducted in early generations (Clement et al., 2015). To determine the genotype's potential as a parent for breeding pathogen-resistance cultivars, it is essential to monitor the progression of disease severity to ensure the observed resistance is stable and consistent. Genotypes with high heritability and consistent resistance possess a greater potential

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to develop resistant cultivars. In contrast, low to moderate heritability suggests that environmental factors are more dominant than genotypic factors, and therefore, selection is often postponed until the lines become more homozygous in later generations (Clement et al., 2015).

CONCLUSIONS

EPA 21016 A was resistant to TYLCKaV, as indicated by its low disease severity (1.25%) and low AUDPC value (26), and all genotypes were classified as susceptible to PepYLCIV and ToLCNDV. The high heritability for TYLCKaV resistance suggests effective selection in early generations, whereas low heritability for PepYLCIV and ToLCNDV indicates the need for further improvement. EPA 21016 A is recommended for further evaluation across diverse environments and as parental material in breeding programs. Future research should focus on uncovering the genetic mechanisms behind this resistance and exploring broader germplasm for resistance to PepYLCIV and ToLCNDV.

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