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Dominance and complexity of *Begomovirus species* infection on eggplant in lowlands and highlands

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Abstract

Eggplant (*Solanum melongena L.*) is an important Indonesian crop increasingly threatened by begomoviruses that reduce yield and quality. Transmitted persistently by the whitefly *Bemisia tabaci*, these viruses are genetically diverse and often occur in mixed infections, intensifying disease severity and complicating control. This study aimed to identify begomovirus species infecting eggplant, determine their geographic distribution and dominance, and characterize the associated *B. tabaci* biotypes across major eggplant-producing regions of Java, Indonesia. Field surveys were conducted in five provinces—Banten, West Java, Central Java, Yogyakarta, and East Java—covering 30 lowland and 15 highland sites. From each site, 20 symptomatic plants were collected for molecular analysis, while disease incidence (DI) and severity (DS) were assessed from 200 plants. Across 45 sites, mean DI and DS reached 54.0% and 32.7% in lowlands and 34.8% and 26.8% in highlands, respectively. PCR amplification and sequencing confirmed three begomovirus species: Tomato yellow leaf curl *Kanchanaburi virus* (TYLCKaV), *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), and Tomato leaf curl New *Delhi virus* (ToLCNDV). TYLCKaV was the most prevalent, occurring alone or in combination with PepYLCIV, particularly in lowlands, while ToLCNDV occurred at low frequencies, mainly in mixed infections. Four *B. tabaci* biotypes (A, B, Q, and AN) were detected, with biotype A dominating in lowlands and Q prevailing in highlands. This study provides the first island-wide molecular mapping of begomovirus species and B. tabaci biotypes infecting eggplant in Indonesia and elucidates the complex virus–vector interactions that shape eggplant disease epidemiology in tropical Asia.

Keywords: *Bemisia tabaci,* begomovirus, disease incidence, severity, TYLCKaV

Introduction

Eggplant (*Solanum melongena L.*) is an important solanaceous crop cultivated widely across Asia, Africa, and Europe, and is believed to have originated in India. Beyond its role as a staple vegetable, eggplant is valued for its rich composition of bioactive compounds such as flavonoids, glycoalkaloids, and nasunin, which contribute to its nutritional, functional, and medicinal properties (Naeem and Ugur, 2019). In Indonesia, eggplant holds a significant place in both commercial and subsistence farming systems due to its short growing cycle and adaptability to a wide range of agroecological conditions. National production has shown an upward trend in recent years; however, a notable decline was recorded between 2022 and 2023, particularly in West and East Java (Central Bureau of Statistics of Indonesia, 2023). Among the major biotic constraints limiting eggplant productivity is yellow leaf curl disease caused by begomoviruses, which has emerged as a serious threat to solanaceous crop production in tropical regions.

Begomoviruses are single-stranded DNA (ssDNA) plant viruses with either monopartite or bipartite genomes, and they are primarily transmitted by the whitefly *Bemisia tabaci* in a persistent and circulative manner. Infected plants typically exhibit symptoms such as chlorosis, upward leaf curling, vein thickening, and growth stunting, often leading to substantial yield losses (Fiallo-Olivé and Navas-Castillo, 2023).

In Indonesia, Pepper yellow leaf curl Indonesia virus (PepYLCIV) was first reported infecting chili (Capsicum spp.) in 1999 and later Tomato leaf curl virus (TLCV) detected in pumpkin (Singh et al., 2001). Other begomovirus species, Tomato yellow leaf curl Kanchanaburi virus (TYLCKaV) detected in eggplant (Kintasari et al., 2013; (Subiastuti et al., 2019; Kandito et al., 2020) also Pepper yellow vein Mali virus have also

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been associated with eggplant infections in Mali (Soro et al., 2021). Similar infections have been reported in several crops in tropical and subtropical regions, such as India, China and Southeast Asia, suggesting the wide adaptability and host range of these viruses.

Whiteflies, particularly *B. tabaci*, serve as highly efficient and persistent vectors of begomoviruses. The *B. tabaci* species complex consists of multiple cryptic biotypes that vary in their geographic distribution, host preference, and resistance to insecticides (Fiallo-Olivé et al., 2020; Yao et al., 2017). On Java Island, *B. tabaci* populations display altitude- and crop-specific patterns: biotype B tends to dominate in chili, while biotype Q is more frequently found in tomato (Wahyono et al., 2023; Hermanto et al., 2024). These ecological patterns suggest that the distribution of vector biotypes may influence the epidemiology and severity of begomovirus infections across different agroecological zones.

Despite the economic and agronomic importance of eggplant, comprehensive studies on the diversity, distribution, and dominance of begomovirus species, along with their associated *B. tabaci* biotypes, remain limited in tropical region including Indonesia. Understanding these virus–vector dynamics is crucial for developing resistant cultivars and designing effective, region-specific management strategies. This work simultaneously analyzes virus diversity, vector biotypes, and altitudinal distribution in eggplant ecosystems, offering the first comprehensive molecular–ecological assessment in Indonesia. Therefore, this study aimed to (i) evaluate the incidence and severity of begomovirus infections in eggplant across lowland and highland regions of Java, (ii) identify the begomovirus species present and their geographic distribution, and (iii) characterize the *B. tabaci* biotypes associated with eggplant under different agroecological conditions.

Materials and methods

Field Survey and Sample Collection

Field surveys were conducted from 2022 to 2023 across five provinces of Java—Banten, West Java, Central Java, Yogyakarta, and East Java—covering a total of 45 locations (30 lowland (400 m asl) and 15 highland sites (700 masl)). From each site, 20 symptomatic leaf samples were collected for molecular analysis. Disease incidence (DI) and disease severity (DS) were assessed on 200 plants per site, with symptom severity evaluated using a 0–4 scale as described by Romero-Masegosa et al. (2020).

The levels of DI and DS were determined through visual observation of 200 plants at each sampling location. Disease incidence was calculated as the percentage of plants showing typical begomovirus symptoms relative to the total number of plants observed (200 plants). Disease severity was calculated using the Townsend and Heuberger formula (Lavenia and Kuswanto, 2021):

$$DS = \sum \frac{(n.v)}{(N.V)} \times 100\%$$

with n, the number of plants showing symptoms with a certain score; v, symptom score; N, total number of plants observed per replication; V, highest disease symptom score.

DNA Extraction and Identification of Begomovirus Species and Bemisia tabaci Biotypes

Twenty leaf samples were collected from each location, resulting in a total of 900 samples analyzed to identify begomovirus species. Molecular identification was performed at the Molecular Laboratory of PT. BISI International Tbk, following protocols similar to those previously used for chili (Wahyono et al., 2023) and tomato (Hermanto et al., 2024). Total DNA was isolated from leaf tissues using the method described by Lukman et al. (2019). DNA extraction from whitefly samples was conducted using the Geneaid Genomic DNA Mini Kit (Tissue) according to the manufacturer's protocol (https://geneaid.com/data/files/1605685391109197921.pdf).

The PCR reaction mixture for begomovirus identification had a final volume of 10 µL, consisting of 20 ng of DNA template, 1× DreamTaq Buffer (containing 1.5 mM $MgCl_2$), 0.2 mM dNTP mix, 0.25 µM of each forward and reverse primer, and 1 U of DreamTaq DNA Polymerase (Thermo Fisher Scientific, USA). The amplification was performed with an initial denaturation at 94 °C for 4 minutes, followed by 35 cycles of denaturation at 94 °C for 30 seconds, primer annealing at the appropriate temperature for 1 minute, extension at 72 °C for 1.5 minutes, and a final extension at 72 °C for 7 minutes.

For *Bemisia tabaci* biotype identification, PCR reactions were carried out in a total volume of 12.5 µL containing 20 ng of DNA template and 1× MyTaq HS Red Mix (2×). The thermal cycling program consisted of an initial denaturation at 94 °C for 5 minutes, followed by 35 cycles of denaturation at 94 °C for 1 minute, annealing at the primer-specific temperature for 1 minute, extension at 72 °C for 1 minute, and a final extension at 72 °C for 5 minutes.

All amplifications were performed using a SimpliAmp Thermal Cycler (Applied Biosystems, Thermo Fisher Scientific, USA) with primer sets listed in **Table 1**. PCR products were separated by electrophoresis on 1.5%

Table 1. Primers for detecting Begomovirus species and *Bemisia tabaci* biotypes

No.	Nama Primer	Virus/vectors targeted	DNA targeted (bp)
1	rrn5/rrn18-1	*Internal positive control primer*	± 273
2	PepYLCIV F-R	*Pepper yellow leaf curl Indonesia virus*	± 997
3	TYLCKaV F-R	*Tomato yellow leaf curl Kanchanaburi virus*	± 1668
4	ToLCNDV F-R	*Tomato leaf curl New Delhi virus*	± 771
1	LepF1/LepR1	*Internal positive control primer*	±648
2	BaAF/BaAR	Biotipe A	± 812
3	BaBF/L2-N-3014R	Biotipe B	± 661
4	BaANF/L2-N-3014R	Biotipe AN	± 665
5	BaQF/BaQR	Biotipe Q	±892, 700, 400
6	BaNaF//L2-N-3014R	Biotipe Nauru	±578
7	BaSF/L2-N-3014R	Biotipe S	±613

agarose gels, stained with FluoroVue™ Nucleic Acid Gel Stain (Smobio), and visualized using a Gel Doc system (Kodak 139 MI, USA) to confirm the presence of specific amplicons for begomoviruses and *B. tabaci* biotypes (Wahyono et al., 2023; Hermanto et al., 2024).

Statistical Analysis

All data were analyzed using Minitab 19. Statistical tests included t-tests, stepwise regression.

Results and discussion

Distribution, symptom, disease incidence and disease severity of Begomovirus infection

The survey was conducted at 45 eggplant production sites located in both lowland and highland areas across the island of Java, covering the provinces of Banten, West Java, Central Java, Yogyakarta (D.I. Yogyakarta), and East Java (**Figure 1**). The results indicated that begomovirus infections were present in nearly all surveyed locations across these provinces.

Begomovirus infections were detected in nearly all surveyed sites. The overall disease incidence was higher in lowland areas (54.03%) than in highland areas (34.77%), although disease severity did not differ significantly between the two regions (32.65% vs. 26.83%). Symptom severity varied among eggplant varieties: resistant cultivars such as Hitavi, Kenari, and Ungu exhibited less than 10% severity, whereas the susceptible variety Prince 07 exhibited high infection intensity (DI > 80%) levels, exceeding 50% in highland areas and reaching up to 80% in lowlands.

Studies mapping the distribution of begomoviruses and their whitefly vector biotypes in eggplant production areas of Indonesia remain limited. Such mapping is a strategic approach to identify the dominant virus species, the complexity of mixed infections, and the distribution of vector biotypes under field conditions. Knowledge of the predominant virus species provides an essential foundation for developing resistant lines and breeding virus-resistant varieties.

Symptom variations of begomovirus infection observed across 45 locations in lowland and highland regions included mosaic patterns, leaf curling, yellowing, bleaching, leaf size reduction, and stunted growth (**Figure 2**). These findings are consistent with Navas-Castillo et al. (2021), who reported that begomoviruses commonly induce similar symptoms—such as leaf curling, crumpling, deformation, stunting, golden-yellow mosaic or mottle, and veinal or interveinal chlorosis—often resulting in

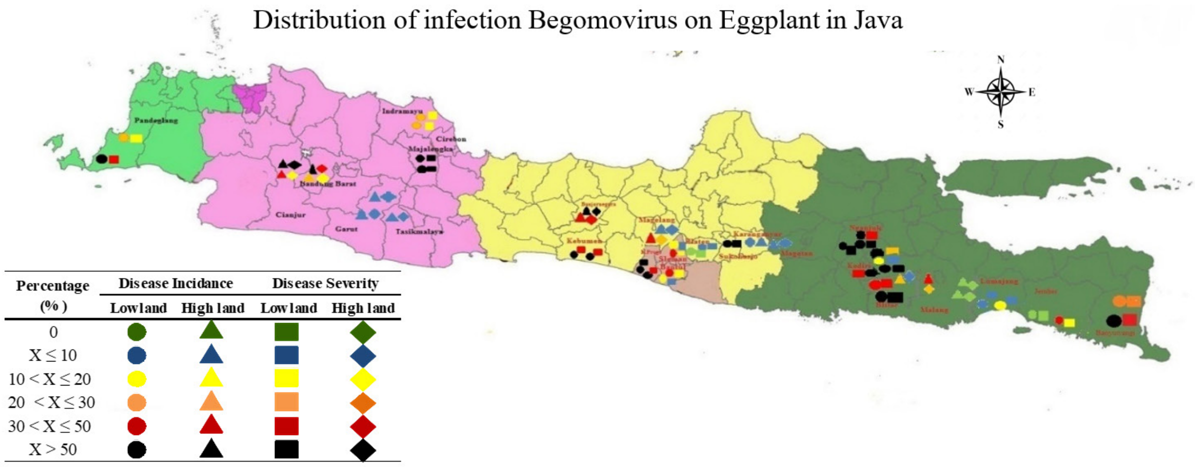

Figure 1. Distribution of begomovirus infection in 45 locations of eggplant production center on Java island

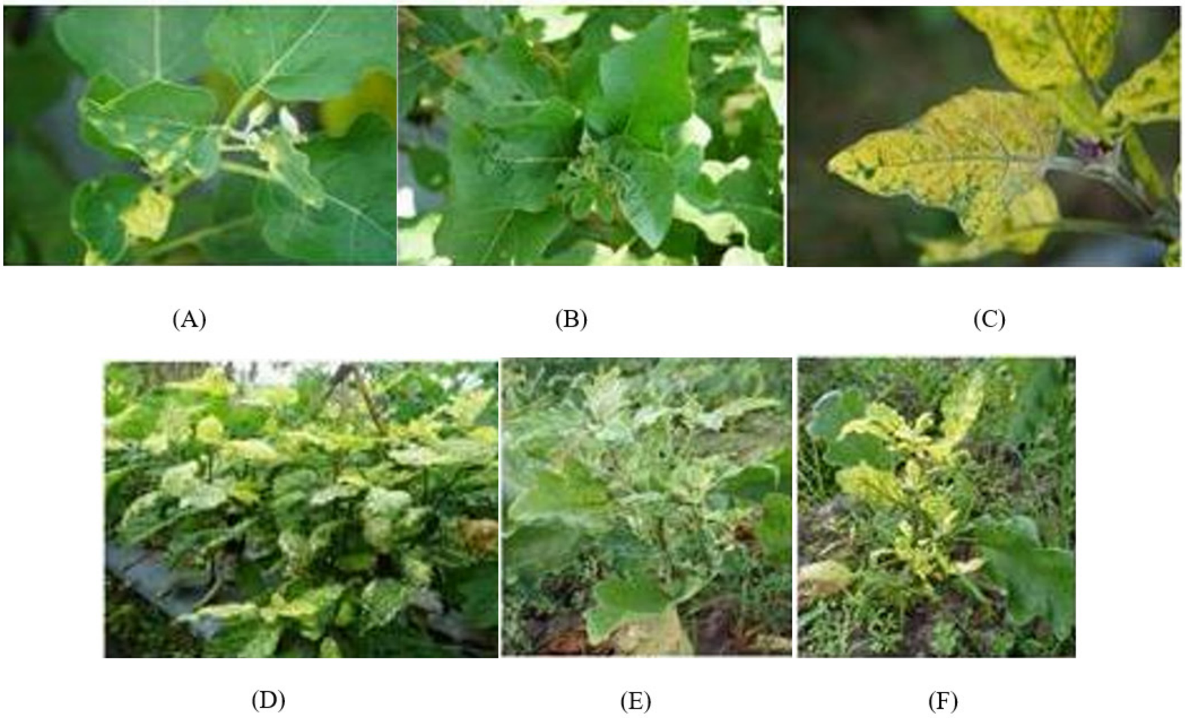

Figure 2. Variation symptoms of begomovirus infection. (A) Mosaic in Pandeglang, Banten; (B) Leaf curling in Sleman, D.I Yogyakarta; (C) Yellowing in Bandung Barat, West Java; (D) Leaf bleaching in Kediri, East Java; (E) Reduce leaf size in Bantul, D.I.Yogyakarta; (F) Stunted in Bantul, D.I. Yogyakarta

substantial yield losses.

The incidence and severity of begomovirus infection varied widely across surveyed sites. In the lowlands of Java, disease incidence ranged from 0 to 100% and severity from 0 to 92.71%, whereas in the highlands, incidence ranged from 0 to 96.05% and severity from 0 to 86.83%. Among lowland provinces (LL), Yogyakarta exhibited the lowest disease incidence and severity, while Central Java recorded the highest levels (**Figure 3**a, 3b). Similarly, in the highlands (HL), the lowest incidence and severity were found in East Java, with the highest again observed in Central Java.

This variation may be attributed to differences in cultivar susceptibility and the diversity of begomovirus species present in each location. Field observations revealed the coexistence of both susceptible and resistant eggplant varieties. Overall, begomovirus incidence was higher in lowlands (54.03%) than in highlands (34.77%), while disease severity was also relatively higher in lowlands (32.65%) than in highlands (26.83%), although the difference was not statistically significant.

Begomovirus infection in different eggplant varieties at the surveyed sites produced symptoms ranging from mild to severe, characterized by uniform yellowing of leaves, curling, and plant stunting. The varietal response to infection, expressed as disease incidence and severity, varied considerably among genotypes (**Figures 4**a and 4b). These variations reflect the relative level of resistance

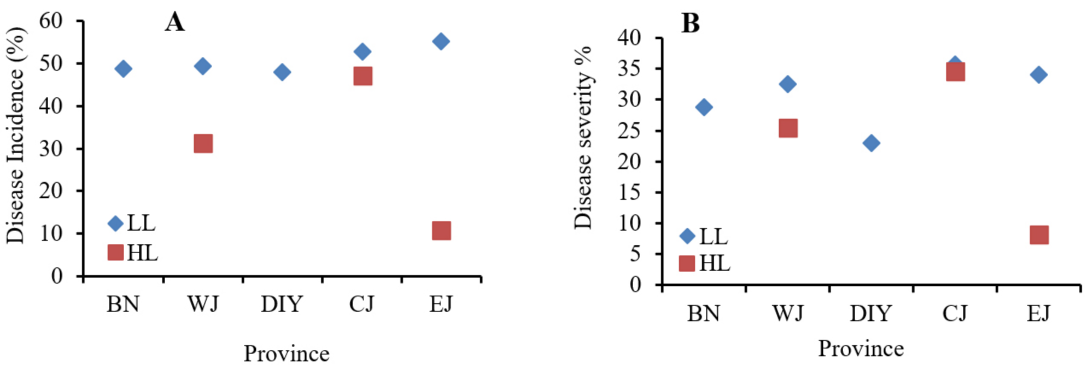

Figure 3. Disease incidence (3A) and Disease severity (3B) that infected by begomovirus in lowland (LL) and highland area (HL) in Java. Province name: BN=Banten, WJ=West Java, DIY= D.I.Yogyakarta, CJ= Central Java, EJ=East Java.

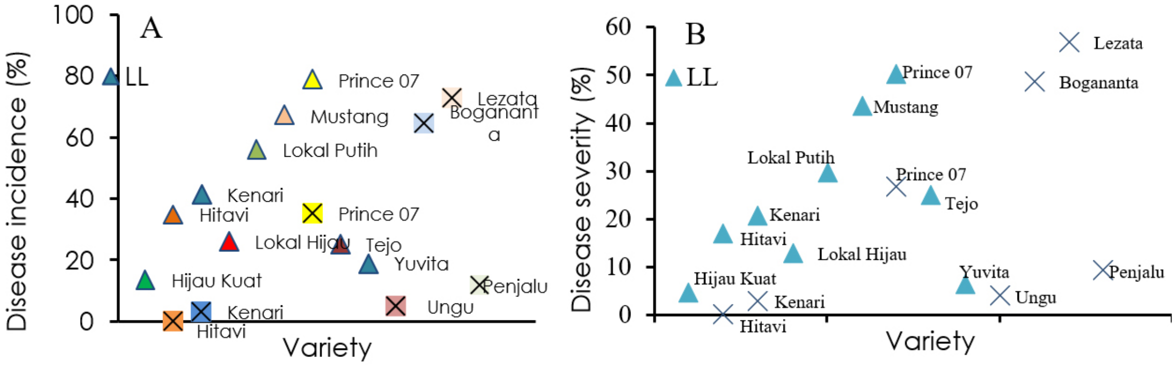

Figure 4. Disease incidence (4A) and severity (4B) of variety that infected by begomovirus in lowland (LL) and highland (HL)

of each variety to begomovirus infection. Resistant varieties exhibited lower disease incidence and severity compared to susceptible ones.

The commercial varieties Hitavi, Kenari, and Ungu—previously released as resistant cultivars—showed less than 10% disease incidence and severity in highland areas. In contrast, the susceptible variety Prince 07 exhibited higher levels of infection, with approximately 30% incidence in highlands and up to 80% incidence and 50% severity in lowland areas. These results indicate that altitude influences the response of both resistant and susceptible cultivars to begomovirus infection, possibly through environmental effects on virus replication and vector activity.

According to Legarrea et al. (2015), virus accumulation is generally lower in resistant genotypes than in susceptible ones at 3, 6, and 12 weeks post-inoculation. Moreover, behavioral assays revealed that non-viruliferous whiteflies preferentially settled on virus-infected plants, whereas viruliferous whiteflies were more attracted to healthy plants. This vector behavior suggests a mechanism that facilitates virus dissemination—where increased vector abundance enhances the spread and intensity of begomovirus infections across eggplant populations.

Molecular detection using species-specific primers confirmed the presence of three begomovirus species (**Figure 5**): *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV), *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), and *Tomato leaf curl New Delhi virus* (ToLCNDV).

Similar begomovirus species were detected in both lowland and highland regions, including PepYLCIV, TYLCKaV, and ToLCNDV. These viruses occurred either as single infections or in mixed combinations. The distribution pattern of begomovirus species infecting eggplant across Java varied considerably in terms of infection type and frequency. In lowland areas, TYLCKaV showed the highest infection rate, followed by mixed infections of TYLCKaV and PepYLCIV, and then single infections of PepYLCIV. In contrast, in highland areas, single infections of TYLCKaV were most prevalent, followed by PepYLCIV single infections and mixed infections involving TYLCKaV and PepYLCIV.

TYLCKaV was the dominant virus species overall, consistent with previous reports by Kintasari et al. (2013), Sidik et al. (2017), and Lukman et al. (2019). Single ToLCNDV infections were relatively rare, detected in only four lowland sites (Yogyakarta, Central Java, and East Java) and one highland site in West Java, each with low infection frequencies (approximately 5%). Triple infections involving TYLCKaV, PepYLCIV, and ToLCNDV were also uncommon, detected in one site each in West Java, Yogyakarta, and Central Java, and in three sites in East Java, with frequencies ranging from 5% to 10%.

These results indicate that ToLCNDV, whether occurring alone or in combination with other begomoviruses, had a limited distribution compared to the more widespread single or mixed infections involving TYLCKaV and PepYLCIV.

Dominancy of Begomovirus species

Molecular analysis revealed the presence of three begomovirus species: *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV), *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), and *Tomato leaf curl New Delhi virus* (ToLCNDV). Among these, TYLCKaV was the most prevalent, particularly in lowland regions, followed by PepYLCIV. ToLCNDV was detected at a low frequency (≤5%), primarily in mixed infections. Triple infections involving TYLCKaV, PepYLCIV, and ToLCNDV were rare, occurring in less than 10% of the samples.

A notable finding in this study was the recent expansion of *Pepper yellow leaf curl Indonesia virus* (PepYLCIV) across Java, including the emergence of cases involving single infections. In lowland regions,

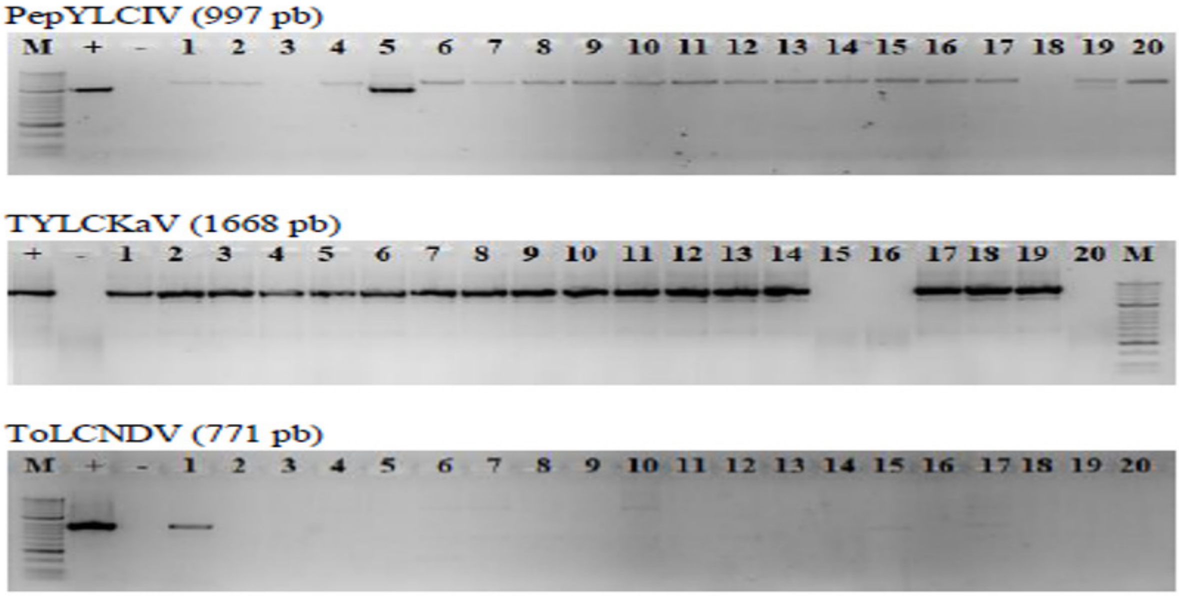

Figure 5. Begomovirus species that detected on samples from survey location, PepYLCIV (997 pb), TYLCKaV (1608 pb) and ToLCNDV (771 pb)

single infections caused by PepYLCIV were less frequent than mixed infections involving both *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV) and PepYLCIV. This suggests that the presence of TYLCKaV in mixed infections may enhance the infection rate or symptom severity compared to PepYLCIV alone (**Figures 6** and **7**).

The increasing prevalence of PepYLCIV has also been reported in several other countries, including Mali (Soro et al., 2021). Similarly, *Tomato leaf curl New Delhi virus* (ToLCNDV) has been identified as a major pathogen infecting eggplant in India (Pratap et al., 2011; Singh et al., 2015; Venkataravanappa et al., 2023). The widespread occurrence of PepYLCIV in combination with the already dominant TYLCKaV appears to exacerbate symptom expression and overall disease impact in eggplant.

In addition, ToLCNDV has recently been detected infecting eggplant in Java. This virus, which is known to primarily affect members of the *Cucurbitaceae* family, has previously been reported in multiple hosts worldwide (Singh et al., 2001; Shtayeh et al., 2010; Moriones et al., 2017), indicating its expanding host range and potential threat to solanaceous crops.

The influence of different begomovirus species on disease incidence and severity in eggplant was described by the regression models presented in Equations (1) and (2). Disease incidence (Equation 1) was significantly affected by the presence of *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), *Tomato yellow*

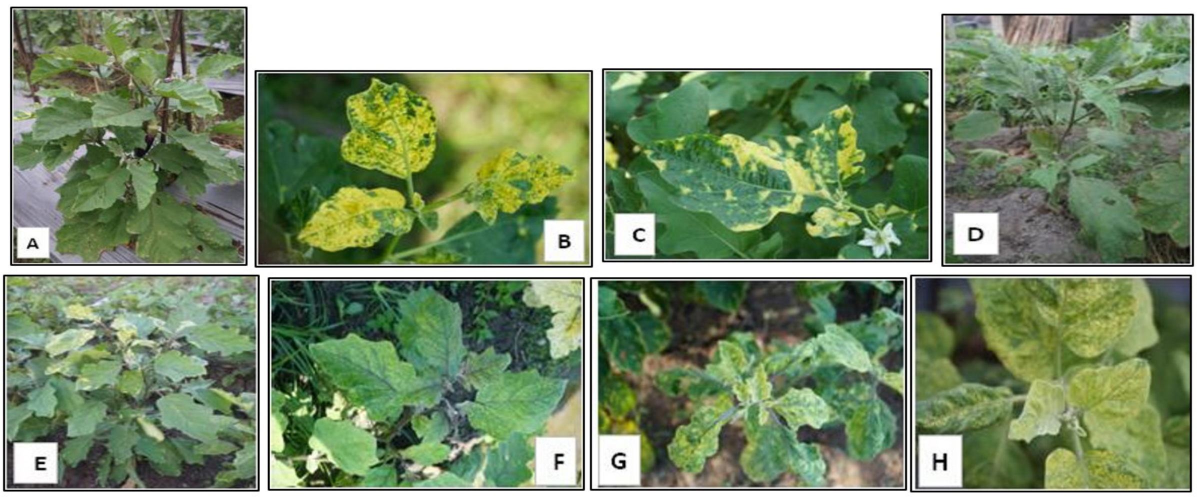

Figure 6. Begomovirus **spesies** that infected in lowlands. (A) Normal plant in Ngaglik, Sleman D.I.Yogyakarta; (B) PepYLCIV in Majasari, Pandeglang, Banten; (C) TYLCKaV in Pagelaran, Pandeglang Banten; (D) ToLCNDV in Wedomartani, Sleman, D.I.Yogyakarta; (E) PepYLCIV_TYLCKaV in Sliyeg 1, Indramayu, West Java; (F). PepYLCIV_ToLCNDV in Polokarto, Sukoharjo, Central Java; (G) TYLCKaV_ ToLCNDV in Sliyeg 2, Indramayu, West Java; (H) PepYLCIV_TYLCKaV_ToLCNDV in Penataran, Blitar, East Java.

leaf curl Kanchanaburi virus (TYLCKaV), and their mixed infections, as well as by co-infection between TYLCKaV and *Tomato leaf curl New Delhi virus* (ToLCNDV). In contrast, disease severity (Equation 2) was primarily influenced by TYLCKaV alone and by the mixed infection of TYLCKaV and PepYLCIV.

Disease Incidence = 0.007 + 0.984 PepYLCIV + 0.591 TYLCKaV + 0.371PepYLCIV_TYLCKaV + 0.702 TYLCKaV_ToLCNDV (1)

Disease Severity = 0.1574 + 0.216 TYLCKaV+ 0.355 PepYLCIV_TYLCKaV (2)

The regression models indicated that *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV) was the primary determinant of both disease incidence (DI) and disease severity (DS), either as a single infection or in mixed infections. Mixed infections involving TYLCKaV and *Pepper yellow leaf curl Indonesia virus* (PepYLCIV) resulted in increased symptom severity, suggesting a possible synergistic interaction between the two viruses. This finding is consistent with the report of Annisaa et al. (2021), who observed that dual infections of PepYLCIV and TYLCKaV in chili and eggplant could facilitate recombination events, potentially leading to the emergence of new begomovirus strains.

Indentified Bemisia tabaci biotypes

Four *Bemisia tabaci* biotypes—A, B, Q, and AN—were detected across the surveyed sites. Biotype A predominated in lowland regions, whereas biotype Q was more prevalent in highland areas (**Figure 8**). All identified biotypes were capable of transmitting begomoviruses. The overall distribution of *B. tabaci* biotypes did not differ significantly between lowland and highland locations, as nearly all biotypes (A, B, AN, and Q) were present across most sampling sites. However, biotype A was the dominant form in lowlands, while biotype Q was predominant in highlands.

Between 2017 and 2021, Indonesia ranked fifth in global eggplant production after China, India, Egypt, and Turkey, with an average annual growth rate of 5.8% (FAOSTAT, 2021; Ministry of Agriculture, 2022). Despite this growth, eggplant productivity remains constrained by begomovirus infections, which have become increasingly prevalent in tropical Asia. Similar reports of begomovirus outbreaks in *Solanum* crops have emerged from India (Singh et al., 2001; Pratap et al., 2011; Singh et al., 2015; Venkataravanappa et al., 2023), China and Japan (Van Brunschot et al., 2010), and several Southeast Asian countries, including Laos, Vietnam, and Cambodia (Ha et al., 2008; Tang et al., 2014; Bagewadi et al., 2015), confirming the transboundary nature and rapid adaptability of these viruses.

This represents the first molecular–ecological survey mapping *Begomovirus* diversity and *B. tabaci* biotypes infecting eggplant across multiple altitudinal zones in Indonesia. In Indonesia, the present study revealed that begomovirus incidence was substantially higher in lowland regions than in highlands, while disease severity remained relatively similar across both zones. This elevation-dependent pattern mirrors earlier observations in chili (*Capsicum* spp.) and tomato (*Solanum lycopersicum*) (Wahyono et al., 2023; Hermanto et al., 2024), and is strongly linked to the population dynamics of the whitefly vector *Bemisia tabaci*. Warmer, drier lowland climates favor rapid whitefly reproduction and extended feeding activity, whereas cooler and more humid highland environments reduce vector fecundity and mobility. The frequent intercropping of solanaceous crops—such as eggplant, tomato, and chili—further facilitates cross-host transmission and maintains continuous virus–vector

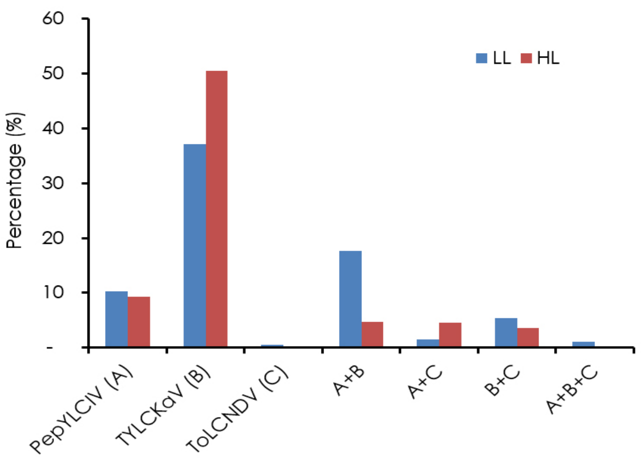

Figure 7. Begomovirus species infected in lowlands (LL) and highlands (HL)

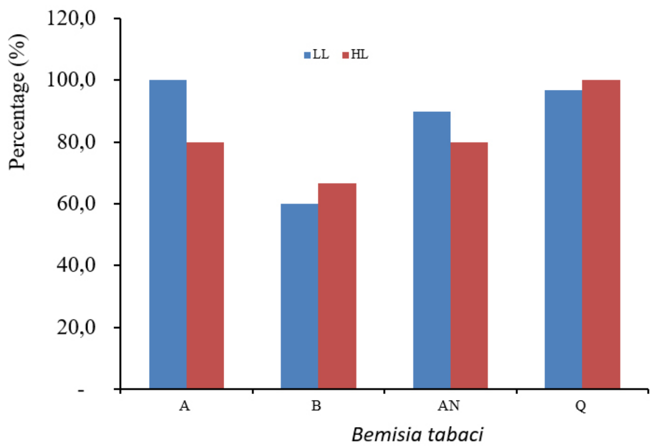

Figure 8. Percentage of Biotypes of *Bemisia tabaci* in lowland (LL) and highland (HL)

circulation within the landscape.

Among the detected species, *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV) emerged as the predominant begomovirus infecting eggplant in Java, corroborating earlier findings by Kintasari et al. (2013) and Lukman et al. (2019). The high prevalence of TYLCKaV in lowlands reflects its strong ecological compatibility with *B. tabaci* populations, which are temperature-dependent vectors. Molecular evidence indicates that Indonesian isolates share high sequence identity with TYLCKaV strains from Thailand, underscoring a regional epidemiological link and suggesting cross-border dispersal through whitefly migration or seedling trade (Kikkawa et al., 2023). The observed dominance of *TYLCKaV* highlights the need for incorporating *Ty*-like resistance genes from wild type into eggplant through interspecific hybridization or marker-assisted backcrossing.

*The detection of Pepper yellow leaf curl Indonesia virus (PepYLCIV) in eggplant mark*s an important epidemiological shift. Originally regarded as chili-specific, PepYLCIV has now expanded its host range to eggplant, where it commonly co-occurs with TYLCKaV. Such mixed infections often exacerbate symptom expression and may accelerate recombination events that give rise to novel begomovirus variants with enhanced virulence or altered host specificity (Annisaa et al., 2021). Although *Tomato leaf curl New Delhi virus* (ToLCNDV) was detected only sporadically, its presence signals a potential future expansion of host range, consistent with its aggressive spread in India and other parts of Asia (Singh et al., 2015; Venkataravanappa et al., 2023). The coexistence of multiple begomovirus species thus creates a genomic “melting pot,” heightening the risk of recombination-driven evolution and underscoring the need for multi-gene resistance breeding programs targeting durable and broad-spectrum protection.

Begomoviruses are transmitted persistently and circulatively by *B. tabaci*. Once acquired, the virus resides within the insect’s midgut and hemolymph, allowing long-term transmission efficiency even in the absence of continuous virus acquisition (Putri et al., 2023). This study identified four *B. tabaci* biotypes A, B, Q, and AN with distinct ecological distributions: biotype A dominated in lowlands, while biotype Q prevailed in highlands. The dominance of biotype Q, known for its high insecticide resistance and competitive displacement capacity, suggests an adaptive advantage under cooler highland conditions and possibly reduced chemical selection pressure. Similar patterns were reported in tomato fields on Java (Hermanto et al., 2024) and in Fujian, China, where biotype Q replaced B within a decade due to its superior adaptability and resistance traits (Yao et al., 2017).

The occurrence of multiple biotypes highlights the ecological plasticity of *B. tabaci* and its capacity to maintain begomovirus transmission across environmental gradients. The rough, pubescent surface of eggplant leaves offers a favorable microhabitat for whitefly colonization compared with the smoother surfaces of chili (Rahayuwati et al., 2020). This morphological advantage, coupled with year-round host availability, sustains whitefly populations and perpetuates virus transmission even in marginal conditions. Notably, the predominance of biotypes A and Q rather than the typically aggressive biotype B found in chili may partly explain the lower overall disease severity in eggplant relative to chili.

Taken together, these findings elucidate the intricate ecological interplay among begomovirus species, whitefly biotypes, and environmental factors in shaping eggplant disease epidemiology in Indonesia. They also demonstrate that the begomovirus complex infecting eggplant in Java is part of a larger transnational virus network in Southeast Asia. Understanding these patterns is essential for designing predictive disease models, strengthening phytosanitary measures, and guiding the development of eggplant cultivars carrying pyramided resistance genes against multiple begomovirus species.

The findings of this study also raise important biosecurity concerns, particularly regarding the potential cross-border spread of begomoviruses through the movement of infected seedlings, transplants, or ornamental solanaceous plants. In regions with active trade of vegetable seedlings and ornamentals such as *Solanum*, *Capsicum*, and *Petunia*, asymptomatic carriers can serve as hidden reservoirs for begomoviruses and their whitefly vectors. Given the persistent–circulative transmission mode of *Bemisia tabaci*, even a small number of viruliferous insects introduced through nursery materials can trigger new outbreaks in previously uninfected areas. Moreover, the increasing regional connectivity among Southeast Asian countries facilitates the rapid dissemination of viral genotypes, as seen with the spread of *Tomato yellow leaf curl Kanchanaburi virus* from Thailand to Indonesia. Strengthening phytosanitary surveillance, regulating the transboundary movement of planting materials, and implementing virus-free certification programs for nurseries are therefore critical components of an integrated biosecurity framework to prevent the establishment and reintroduction of exotic begomovirus strains.

Conclusions

The incidence of begomovirus infection in eggplant was consistently higher in lowland regions than in highlands, whereas disease severity remained relatively similar across both agroecological zones. *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV) was identified as the predominant species, frequently occurring alone or in mixed infections with *Pepper yellow leaf curl Indonesia virus* (PepYLCIV). In contrast, *Tomato leaf curl New Delhi virus* (ToLCNDV) was detected at low frequencies but may pose an emerging threat to eggplant cultivation in Indonesia. Four *Bemisia tabaci* biotypes were identified, with biotype A predominating in lowlands and biotype Q in highlands, reflecting ecological adaptation to altitude and temperature differences. This study provides the first island-wide molecular mapping of begomovirus species and their associated *B. tabaci* biotypes infecting eggplant in Indonesia, offering a foundational understanding of virus–vector interactions across contrasting agroecological zones. These findings underscore the importance of developing cultivars with pyramided resistance genes and implementing region-specific integrated management strategies to ensure sustainable control of begomovirus-associated diseases.

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