

Research Paper

Resistance of Eight Premium Melon Varieties to Viral Diseases in a Commercial Greenhouse in Central Kalimantan

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Abstract

Melon (Cucumis melo L.) is one of the most important horticultural commodities in Indonesia, especially premium varieties with high market value. However, viral diseases such as Cucumber mosaic virus (CMV), Zucchini yellow mosaic virus (ZYMV), Papaya ringspot virus (PRSV), and Watermelon mosaic virus (WMV) remain a significant constraint, causing mosaic, chlorosis, deformation, and yield reduction. This study aimed to evaluate the resistance of eight premium melon varieties against viral diseases under commercial greenhouse conditions in Palangka Raya, Central Kalimantan. The experiment was conducted in a hydroponic production system under natural infection pressure without artificial inoculation. Disease incidence was visually assessed at both vegetative and reproductive stages, and disease progression was quantified using the Area Under the Disease Progress Curve (AUDPC). Results showed apparent variation among varieties in their response to viral infection. Inthanon exhibited the highest disease incidence (up to 45%) and the highest AUDPC value (12.36), indicating high susceptibility. Kirin and Sweet D25 also displayed relatively high incidence and AUDPC values (7.6-7.7). Conversely, Alisha and Meldo UPNVY No. 1 consistently showed the lowest incidence (<15% and <5%, respectively) and the lowest AUDPC values (0.83 and 3.24), demonstrating strong resistance. The remaining varieties (Apollo, Sweet D25, Meldo UPNVY No. 2, and Sweet Hami) showed intermediate resistance. These findings underscore the significance of varietal selection in the integrated management of viral diseases in melon. Resistant varieties such as Alisha and Meldo UPNVY No. 1 may serve as promising candidates for commercial production and future breeding programs to reduce yield losses and minimize reliance on chemical or vector control strategies.

Keywords melon, viral disease, resistance, AUDPC, greenhouse

INTRODUCTION

Melon (Cucumis melo L.) is one of the most important commercial horticultural crops in Indonesia, particularly premium varieties that have high market value due to their sweetness, aroma, fruit color, and size. Greenhouse cultivation offers the potential for stable yields and fruit quality; however, production still faces significant challenges from viral diseases, which cause mosaic, yellowing, stunted growth, leaf deformation, fruit malformation, and overall yield reduction. Infections by viruses such as Cucumber mosaic virus (CMV), Zucchini yellow mosaic virus (ZYMV), and Papaya ringspot virus (PRSV) have been reported as among the most significant constraints in melon production worldwide.

Previous studies in Indonesia and abroad have evaluated the resistance of melon lines against several viruses under experimental or research greenhouse conditions. For example, Study by Monica et al. (2022) evaluated Madurese melon lines against Cucumber mosaic virus in greenhouse trials. The study found that some lines exhibited higher levels of resistance compared to susceptible checks. Daryono and Fitriyah (2016) studied the inheritance of resistance in the

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melon cultivar Melodi Gama 3 against Kyuri green mottle mosaic virus and reported that MG3 displayed tolerance under greenhouse conditions.

While such experimental studies are valuable for understanding genetic resistance and host-pathogen interactions, evaluating melon varieties in commercial production greenhouses is equally important. Trials under real production conditions provide a more practical representation of natural disease pressure, environmental interactions, and actual farming practices. Thus, the results are directly relevant for farmers, breeders, and stakeholders in the horticultural sector.

The objective of this study was to evaluate the resistance of eight premium melon varieties to viral diseases under commercial greenhouse production in Palangka Raya, Central Kalimantan. The findings are expected to identify superior resistant varieties that can support sustainable melon cultivation and reduce reliance on intensive chemical or vector management practices.

LITERATURE REVIEW

Despite these advances, several significant challenges remain in breeding for virus resistance. Viruses evolve rapidly, often generating new strains that can overcome existing resistance mechanisms. Additionally, introgression from wild relatives can alter the genetic background, thereby affecting the stability of resistance. The genetic basis of resistance is often complex; for example, CMV resistance is controlled by multiple recessive genes, and to date, no commercial CMV-resistant melon cultivars have been available in Western production regions. Another challenge is maintaining a balance between resistance and desirable agronomic traits such as fruit sweetness (Brix), flesh color, shape, and shelf life. Combining resistance to multiple viruses without compromising fruit quality remains difficult. Furthermore, breeding success must consider economic feasibility, since traditional methods are often ineffective under high infection pressure, making it essential to integrate advanced breeding technologies with practical production needs (Tian et al., 2024).

The characteristic manifestations of melon yellow spot disease (MYSV) include leaf curling, mosaic patterns, chlorotic spotting, fruit discoloration, and surface cracking, which are frequently observed in melon greenhouses throughout Indonesia. RT-PCR assays targeting the N gene confirmed that all tested samples were infected with MYSV (Hartono et al., 2025).

Melon plants in Indonesia often exhibit curling and yellowing symptoms during early growth stages, the causal agent of which has not been fully identified. A study conducted in seven regencies of Bali identified three viruses infecting melon: Squash leaf curl virus (SLCuV), Squash leaf curl COVID-19 (SLCCNV), and Squash leaf curl Philippines virus (SLCuPV). SLCCNV was the most widespread, detected in all surveyed regencies, while SLCuV was present in six regencies and SLCuPV was restricted to Denpasar, Badung, and Buleleng. Sequence analysis revealed high homology between Bali isolates and their regional counterparts: SLCuV with East Timor (98.4–99.0%), SLCCNV with Malaysia (98.8–99.8%), and SLCuPV with Taiwan (98.8–99.5%). Importantly, SLCuPV was reported for the first time infecting Cucurbitaceae in Indonesia, highlighting a new threat to melon production and contributing to regional knowledge of Begomovirus diversity (Temaja et al., 2025).

Cucurbit Aphid-Borne Yellows Polerovirus (CABYV) was initially reported infecting cucumber in Java. Melon isolates from Nganjuk showed the highest similarity to cucumber CABYV isolates from Nganjuk and Tulungagung. In contrast, bitter gourd isolates clustered more closely with melon isolates from France and squash isolates from Spain. This study constitutes the first report of CABYV infection in melon and bitter gourd in Java, indicating a rapid expansion of its host range within the Cucurbitaceae family (Damayanti et al., 2021).

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The findings are expected to identify superior resistant varieties that can support sustainable melon cultivation and reduce reliance on intensive chemical or vector management practices.

RESEARCH METHOD

The study was conducted in a commercial production greenhouse located in Palangka Raya, Central Kalimantan, Indonesia, at the following coordinates: Latitude: -1.965796 (\approx approximately 1° 57′ 57″ South), Longitude: 113.729738 (\approx approximately 113° 43′ 47″ East). The greenhouse was managed according to standard commercial practices, including fertigation, pruning, and training systems typical of premium melon cultivation.

Eight premium melon (Cucumis melo L.) varieties were evaluated in this study (Alisha, Apollo, Inthanon, Kirin, Sweet D25, Sweet Hami, Meldo UPNVY No. 1, Meldo UPNVY No. 2). These varieties were selected based on their popularity in the Indonesian market and availability for commercial production. Each variety was planted using a hydroponic system with solid growing medium.

The evaluation was carried out under natural infection pressure within the production greenhouse. No artificial inoculation of viruses was performed. Each variety is planted in a mixed manner in the greenhouse, taking into account considerations for production activities (Figure 1). Disease assessment focused on viral symptoms. Data were collected during two observation periods: the vegetative stage (11-19 days after transplanting) and the reproductive stage (40–54 days after transplanting). All plants in the production house were used as samples. Each variety has a different number of population, Alisha (206 plants), Apollo (384 plants), Inthanon (84 plants), Kirin (283 plants), Sweet D25 (227 plants), Sweet Hami (351 plants), Meldo UPNVY No. 1 227 plants), Meldo UPNVY No. 2 (288 plants). There is no replication in this study.

Disease incidence was observed at 19, 28, 41, and 48 days after transplanting. Disease incidence (DI) was calculated as follows:

Disease incidence =
$$\frac{\text{Total number of infected plants in production greenhouse}}{\text{Total plants in production greenhouse}} \times 100\%$$

Disease incidence was compared with The area Under the Disease Progress Curve (AUDPC), following the formula below:

$$AUDPC = \sum_{i=1}^{n-1} \frac{(yi + yi + 1)}{2} x(ti + 1 - ti)$$

yi: disease incidence or severity (%) at the i-th observation

ti: time (days after transplanting or inoculation) at the i-th observation

n: total number of observations

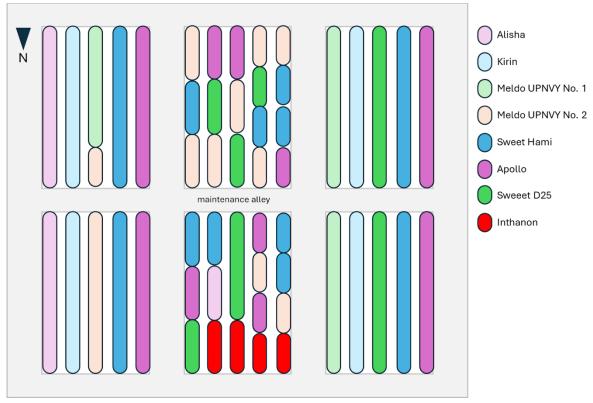


Figure 1. Planting Layout of Eight Melon Variety in a Mixed Manner in the Greenhouse Following Production Activity Considerations

FINDINGS AND DISCUSSION

Figure 2 below presents symptomatic melon leaves showing characteristic features of viral infection. The most prominent symptoms include chlorotic mottle, vein clearing, mosaic patterns, and leaf deformation. Several leaves exhibit mild interveinal yellowing with irregular chlorotic patches, while others show more severe mosaic patterns with alternating green and yellow sectors. Leaf rugosity (wrinkling) and distortion are also visible in some samples, indicating differential host response to viral infection.

Such variability in symptom expression is common in viral diseases of cucurbits and may depend on factors including viral strain, host genotype, plant age, and environmental conditions. According to previous studies, typical viral diseases in melon such as, Cucumber mosaic virus (CMV), Zucchini yellow mosaic virus (ZYMV), Papaya ringspot virus (PRSV), and Watermelon mosaic virus (WMV) can induce similar symptoms, including mosaic, blistering, vein banding, and leaf malformation (Provvidenti et al., 1984; Lecoq & Desbiez, 2012).

The observed differences in symptom severity across leaves in the figure are consistent with reports that susceptible varieties often develop strong mosaic and deformation, while resistant or tolerant varieties may show milder chlorosis or faint mottling (Ali et al., 2016; Katis et al., 2017). Such variability underscores the importance of combining visual symptom evaluation with molecular diagnostics to confirm the causal virus and to quantify resistance levels among different melon genotypes.



Figure 2. Symptom Expression of Viral Disease in Melon Leaves

Further Figure 3 below illustrates the progression of viral disease incidence among eight melon varieties: Alisha, Apollo, Inthanon, Kirin, Sweet D25, Sweet Hami, Meldo UPNVY No. 1, and Meldo UPNVY No. 2 under greenhouse cultivation in Palangka Raya, West Kalimantan. At the first observation, 19 days after Transplanting (DAT), disease incidence was relatively low across all varieties, ranging from 2% (Sweet Hami and Meldo UPNVY No. 1) to 18% (Apollo). Inthanon displayed the highest initial incidence and consistently maintained a high level throughout the observation period. By 29 DAT, most varieties showed a slight to moderate increase in incidence, with Inthanon reaching the highest level, while Apollo, Kirin, Sweet D25, and Meldo UPNVY No. 2 remained below 15%. A sharp increase in incidence was observed at the third evaluation (41 days after treatment, DAT), particularly in Inthanon and Kirin, followed by Sweet D25, Meldo UPNVY No. 2, and Apollo. In contrast, Alisha and Meldo UPNVY No. 1 exhibited the lowest incidence levels (<12%), suggesting stronger resistance to the viral pathogen. By the final observation (48 DAT), Inthanon remained the most susceptible variety, while Kirin and Sweet D25 stabilized around 28–30%. Apollo, Sweet Hami, and Meldo UPNVY No. 2 showed moderate incidence (22–25%). Notably,

Alisha and Meldo UPNVY No. 1 consistently demonstrated the lowest incidence (<15% and <5%, respectively), indicating their potential resistance to the viral disease.

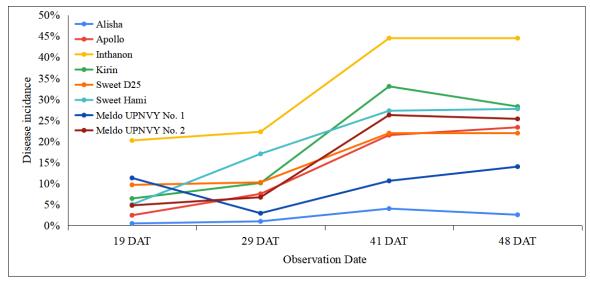


Figure 3. Disease Incidence of Viral Infection Across Eight Melon Varieties at Four Observation Time

Figure 4 presents the comparative Area Under the Disease Progress Curve (AUDPC) values for disease incidence in eight melon varieties: Alisha, Meldo UPNVY No. 1, Apollo, Sweet D25, Meldo UPNVY No. 2, Sweet Hami, Kirin, and Inthanon. AUDPC is a cumulative measure that integrates disease incidence over time, providing a robust indicator of varietal resistance or susceptibility. Among the tested varieties, Alisha and Meldo UPNVY No. 1 displayed the lowest AUDPC values (0.83 and 3.24, respectively), confirming their superior resistance to viral disease progression. Apollo, Sweet D25, and Meldo UPNVY No. 2 exhibited moderate AUDPC values (5–6), indicating intermediate levels of resistance. Sweet Hami and Kirin recorded higher values (7.60-7.70), reflecting greater susceptibility. The highest AUDPC value was observed in Inthanon (12.36), corroborating its role as the most susceptible variety, with consistent and severe disease development throughout the observation period.

Virus management in melon relies primarily on preventive strategies aimed at reducing vector transmission and minimizing inoculum sources, since aphid-borne viruses such as ZYMV, WMV, CMV, PRSV, and CABYV remain widely distributed and cause severe yield and quality losses. The use of resistant or tolerant cultivars is the most effective approach, supported by advances in marker-assisted selection, CRISPR/Cas9 genome editing, and the identification of resistance genes such as vat. Additional measures include the use of virus-free seeds through certification programs, as well as cultural practices such as weed removal, crop rotation, trap crops, and physical barriers (row covers, mulches, greenhouse netting, and sticky traps), all of which help reduce vector abundance and virus spread. Vector management is crucial, though pesticide use is often less effective against non-persistently transmitted viruses and faces limitations due to aphid resistance and environmental concerns. Novel approaches, such as nanotechnology-based treatments, mineral oils, and cross-protection strategies, have shown potential but remain under evaluation. Given the rapid evolution of viruses, the adaptability of aphid vectors, and changing agroecological conditions, integrated management combining host resistance, cultural practices, vector control, and innovative technologies is essential for sustainable melon production (Moya-Ruiz et al., 2023).

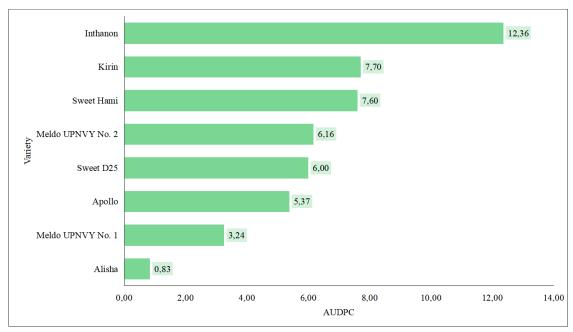


Figure 4. Area Under the Disease Progress Curve (AUDPC) of Viral Disease Incidence Across Eight Melon Varieties Under Greenhouse Cultivation in Palangka Raya, West Kalimantan

CONCLUSIONS

The evaluation of eight premium melon varieties under commercial greenhouse conditions in Palangka Raya revealed differences in their resistance to viral diseases. Inthanon was identified as the most susceptible, with the highest disease incidence and AUDPC values, indicating low resistance to the disease. Kirin and Sweet D25 also exhibited relatively high levels of susceptibility. Conversely, Alisha and Meldo UPNVY No. 1 consistently demonstrated the lowest disease incidence and AUDPC values across all observation periods, confirming their high and stable resistance under natural viral infection.

These findings emphasize that varietal resistance plays a crucial role in managing viral diseases in melon production systems. The adoption of resistant varieties such as Alisha and Meldo UPNVY No. 1 could substantially reduce yield losses, minimize dependence on chemical pesticides and vector control, and contribute to more sustainable and environmentally friendly melon cultivation practices. Moreover, identifying resistant genotypes under real production environments strengthens the relevance of this research to commercial-scale farming and breeding programs.

This study provides a practical reference for melon growers, breeders, and policymakers in selecting and promoting resistant varieties as a cornerstone of integrated viral disease management in Indonesia's horticultural sector.

LIMITATIONS & FURTHER RESEARCH

This study was conducted under natural infection conditions in a single commercial greenhouse without artificial inoculation or replication. Disease pressure and viral strain diversity may not have been uniformly distributed across the plots, which could have influenced the observed incidence levels. The lack of molecular identification of the infecting viruses also limits the precision of resistance characterization, as multiple virus species or mixed infections could be involved.

Further research should include molecular characterization of resistance, identification of the specific causal viruses, and evaluation across multiple environments to strengthen the selection of resilient varieties for commercial cultivation and breeding programs.

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