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Evaluating Agrobiodiversity and Viral Resistance in Soybean Genotypes to Mitigate Cowpea Mild Mottle Virus Using Disease Observation and RT-PCR

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ABSTRACT

Soybean is an important crop with high protein content but susceptible to various pests and diseases, including Cowpea mild mottle virus (CpMMV). This problem can be overcome by using CpMMV-resistant soybean plants. This study aimed to identify CpMMV-resistant soybean genotypes and their impact on plant productivity. A total of 21 soybean lines were tested. CpMMV detection was conducted using RT-PCR. The tested soybean genotypes showed variability in agronomic traits and disease scores (SCR). Overall, excluding seed size, 19 lines outperformed the check varieties Argomulyo and Dega 1 across agronomic traits. G18 showed the highest seed yield per plant (27.41 g) and plot (465 g), the highest number of productive nodes, and the highest number of filled pods. Disease scores ranged from 1 to 3, with the virus detected in all genotypes but having a limited effect on productivity. Seed yield per plant was associated with days to maturity, number of branches, number of productive nodes, and number of filled pods, with higher-yielding plants showing longer maturity and a greater number of filled pods. Disease score correlated with multiple agronomic traits, but no correlation was found between Cq value and these traits. Some genotypes showed better resistance and higher yields despite infection, supporting the potential for breeding CpMMV-resistant soybean lines as a sustainable approach to managing viral infections without sacrificing productivity. These promising genotypes can be used as parental materials in soybean breeding

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programs, while further evaluation under controlled inoculation and diverse growing environments is needed to validate their resistance and yield stability.

Keywords: Agrobiodiversity, agronomic traits, CpMMV, disease severity, productivity, RT-PCR, soybean, viral resistance

INTRODUCTION

Soybeans are one of the most important agricultural commodities worldwide. They are known as a source of vegetable protein containing around 36-40% protein, making them widely used as an alternative protein source in various foods and beverages for humans, livestock, and pets (Alaswad et al., 2021). Soybeans can also fix atmospheric nitrogen, which helps increase soil fertility and reduce the need for nitrogen fertilisers. Soybeans are widely used as effective companion plants to enhance crop rotation and reduce the risk of pest and disease attacks. Their numerous benefits have also led to their development as a primary source for producing soybean oil for food and non-food needs (Harsono et al., 2022).

Many factors can decrease soybean productivity, including virus attacks. Virus attacks are the most common factor in the field and cause systemic damage to soybean plants (Ali et al., 2024). Soybeans attacked by viruses generally exhibit morphological symptoms, such as leaves with yellow spots, wrinkling with rough mosaics, necrosis, and chlorosis, all of which disrupt the formation of quality soybean seeds (Cheruku et al., 2017). Soybean plants with these symptoms are often associated with *Cowpea Mild Mottle Virus* (CpMMV) infection. However, some soybeans infected with the virus do not show visible symptoms and are only marked by a decrease in yield (Krause-Sakate et al., 2020). Cultivar selection influenced the estimated yield losses, which fell within the range of 174 to 638 kg ha^{-1} (da Silva et al., 2020). CpMMV is a virulent virus that has been transmitted through the insect *Bemisia tabaci*, thus leading to extreme reductions in yield. This virus has a very diverse range of hosts, which mostly include members of the legume family. Also, *Bemisia tabaci* is known to infect soybeans, cowpeas, beans, and many more legumes (Gilbertson et al., 2015). Due to the molecular characteristics of the virus, CpMMV is most often diagnosed by RT-PCR techniques, which are able to detect viral RNA in infected plants. Other methods for the diagnosis of the virus include ELISA and Immuno Strip tests (Wang et al., 2022).

Although emphasised as a factor in causing reduced soybean productivity, controlling the spread of CpMMV with the use of chemical insecticides may pose larger future challenges. Continuous application of chemical insecticides or pesticides on soybean farms would immensely decrease the numbers of *Bemisia tabaci*. These creatures flourish in semidense habitats, and if they should become extinct, the balance in the ecosystem would be disrupted to the detriment of the food chain and biosphere. The significance of

the presence of *Bemisia tabaci* lies in the role it plays in the balance of an ecosystem. It feeds voraciously on food sources made available by predators and parasitoids (Moro et al., 2021). The extermination of these insects would deprive their associated net predators of food, leading to a decreased number of predators and a subsequent increase in that of other pests, again disrupting the whole ecological balance. Moreover, the continued absence of *Bemisia tabaci* may contribute to its unregulated growth on its host plants, which eventually overwhelms other components in the ecosystem. According to the theory of natural balance, all components of an ecosystem should be included in equilibrium even when it allows some species to dominate (Geary et al., 2020).

The infection of CpMMV takes place via vector insects that spread the virus and by seeds that were previously infected. It is thus obvious that resistance against CpMMV, not targeting this vector but appropriate yielding so that the ecosystem is not disturbed, will be the suitable approach. Healthy seeds that have gone through proper examination and found clear have also recorded better performance than the above-mentioned patterns according to Tsedaley (2015). Seed testing is usually carried out by RT-PCR and ELISA techniques before planting to make sure that seeds planted are not infected; otherwise, it will yield plants with imperfect growth from the CpMMV-infected seeds. While the development of soybean varieties resistant or tolerant to CpMMV has become the focus of recent research, fully resistant varieties have not yet been achieved.

MATERIALS AND METHODS

Materials

The lines used in this study came from crossing Panderman, Burangrang, and Argomulyo with the CpMMV-resistant lines of UM 7.6, UM 6.3, UM 6.2, UM 6.1, UM 4.1, and UM 3.4. The total number of lines used was 21 lines, including Argomulyo and Dega 1. Detailed descriptions of the lines can be seen in Table 1. Meanwhile, the materials used for virus detection and quantification were liquid nitrogen, Maxwell RSC Viral Total Nucleic Acid Multi-Pack Kit, primer pair CpMMV

Table 1
Soybean lines used in the experiment

Code	Soybean line
G1	Burangrang × UM 7.6-215-1
G2	UM 6.3 × Panderman-170-1
G3	UM 6.3 × Panderman-170-2
G4	UM 4.1 × Burangrang-242-1
G5	UM 4.1 × Burangrang-242-2
G6	UM 6.1 × Argomulyo-57-3
G7	UM 6.3 × Panderman-161-2
G8	UM 6.3 × Panderman-161-3
G9	UM 3.4 × Burangrang-241-1
G10	UM 4.1 × Argomulyo-24-1
G11	UM 4.1 × Argomulyo-24-2
G12	UM 4.1 × Argomulyo-24-3
G13	UM 4.1 × Argomulyo-24-4
G14	UM 4.1 × Argomulyo-24-5
G15	Burangrang × UM 4.1-182-1
G16	UM 6.2 × Panderman-155-1
G17	UM 6.2 × Panderman-155-2
G18	UM 6.2 × Panderman-155-3
G19	Panderman × UM 6.3-96-9
G20	Argomulyo
G21	Dega 1

F (5'-AATTAAGGATCCGAGTTGATTTAAATAAGT-3 ') and CpMMV (CP) R (5'-AATTAAGAATTCCTTGTGATTGAAATTGCG-3 '), with PCR products having a size of 820 bp, and iTaq universal SYBR Green Reaction mix.

Research Location

The planting process was carried out in Srigading Village, Tajinan District, Malang Regency, East Java, Indonesia. To provide optimal environmental conditions for soybean growth, all lines were planted with a spacing of approximately 40 cm between each row and 15 cm between plants, with two plants per hill. Each row was approximately 3 m long. The research location was situated at coordinates 8.05568°S, 112.66675°E, with an altitude of 478 meters above sea level. The leaves of the soybean plants were used as the objects for virus detection and quantification using Real-Time PCR, as they are the most impacted parts when infected by CpMMV.

Treatment during Planting Process

Before planting, the soil was plowed to improve aeration and enhance water drainage, ensuring a consistent water supply for the plants. In addition, herbicides were applied to eliminate weeds that could interfere with the seeding process.

Agronomic Observations

After passing the vegetative growth period, several agronomic parameters related to growth and productivity were observed, namely the 100-seed weight (SEW), the number of filled pods (POF), the number of unfilled pods (POU), the total number of productive nodes (NOD), the number of branches (BRC), plant height (HGT), days to maturity (DTM), days to flowering (DTF), seed yield per plant (YLDP), and seed yield per plot (YLD).

CpMMV Inoculation and Disease Observations

CpMMV inoculation on plants was carried out to ensure that all plants had a chance of being infected by the disease caused by CpMMV. In this treatment, *Bemisia tabaci*, an insect carrying the CpMMV virus, was propagated for one season. The insect population was allowed to live around the plants that were the objects of the study. The insect population was applied per plot, rather than per individual plant. In addition, to support the propagation of the *Bemisia tabaci* population, during the planting process until harvesting, pesticides that could kill *Bemisia tabaci* were not applied so that their numbers would continue to increase until the harvesting process. With this treatment, all plants in the place would have a high risk of being infected with CpMMV, following the objectives of this study. Furthermore, disease score (SCR) evaluation was carried out 30 days after planting to determine the

effect of CpMMV infection on soybean plants. The disease score was followed using our previous method (Zubaidah & Kuswantoro, 2016).

Detection and Quantification of CpMMV Using Real-Time PCR

The process of detecting and quantifying the presence of the CpMMV virus in soybean leaf samples was carried out using the Real-Time PCR method. The extraction process began with the leaf. After obtaining the RNA extract, Real-Time PCR was carried out to determine the estimated number of viruses in the leaf sample.

Data Analysis

Data analysis was performed to integrate all datasets into mutually supportive information, enabling comprehensive interpretation. MS Excel served the purpose for histogram and correlation analysis, whereas R (version 4.3.1) was used to generate heatmaps. Disease severity evaluation formed the basis for assessing disease impact. In contrast, virus detection and quantification by Real-Time PCR were performed to confirm that all the planted lines were infected by the CpMMV virus, as determined by their Cq (Cycle Quantification) values.

RESULTS AND DISCUSSIONS

The flowering days ranged between 29 and 42 DAP, while maturity days varied between 78 and 87 DAP (Figure 1). Out of the 19 soybean lines and two check varieties, the shortest days to flowering and maturity belonged to Dega 1, whose flowering was at 29 DAP and maturity at 78 DAP. The longest flowering period, on the other hand, was

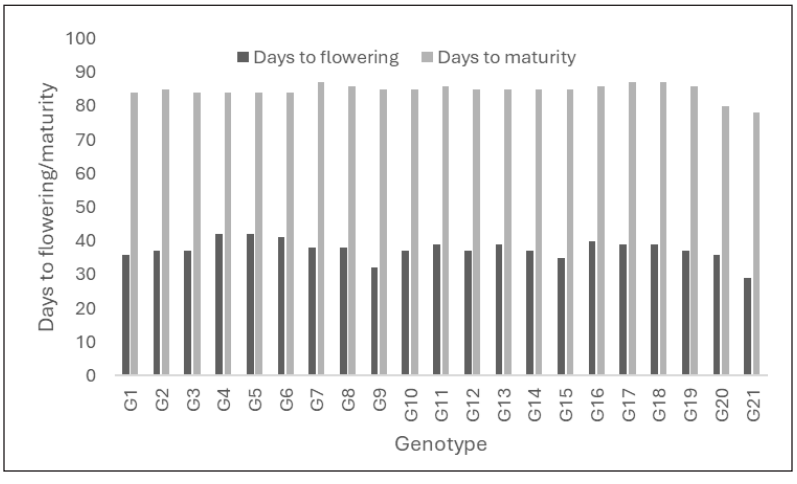


Figure 1. Phenological traits of 21 soybean lines

recorded at 42 DAP in G4 and G5, whereas from those same varieties, the longest days to maturity, 87 DAP, were achieved by G7, G17, and G18. The early flowering was not necessarily coupled with early maturity in every genotype since photoperiod sensitivity of the soybeans determines days to flowering and days to maturity, which are critical factors for their adaptability under diverse environments and productivity (Zhang et al., 2015). Flowering days and maturity days varied among the tested soybean lines (Figure 1), reflecting the variation in their genetic composition. Such duration of flowering and maturity was under the influence of genetics, the environment, and their interaction; some genes have been identified to play crucial roles in controlling flowering and maturity in soybean (Hou et al., 2022; Kou et al., 2021; Liu et al., 2020).

Plant height ranged from 34.1 to 92.6 cm, with a mean height of 75.3 cm (Figure 2a). The tallest plant height was recorded for G12 (92.6 cm), while G5 and G7 followed with 91.0 and 90.2 cm, respectively. Dega 1 was observed to have 34.1 cm plant height,

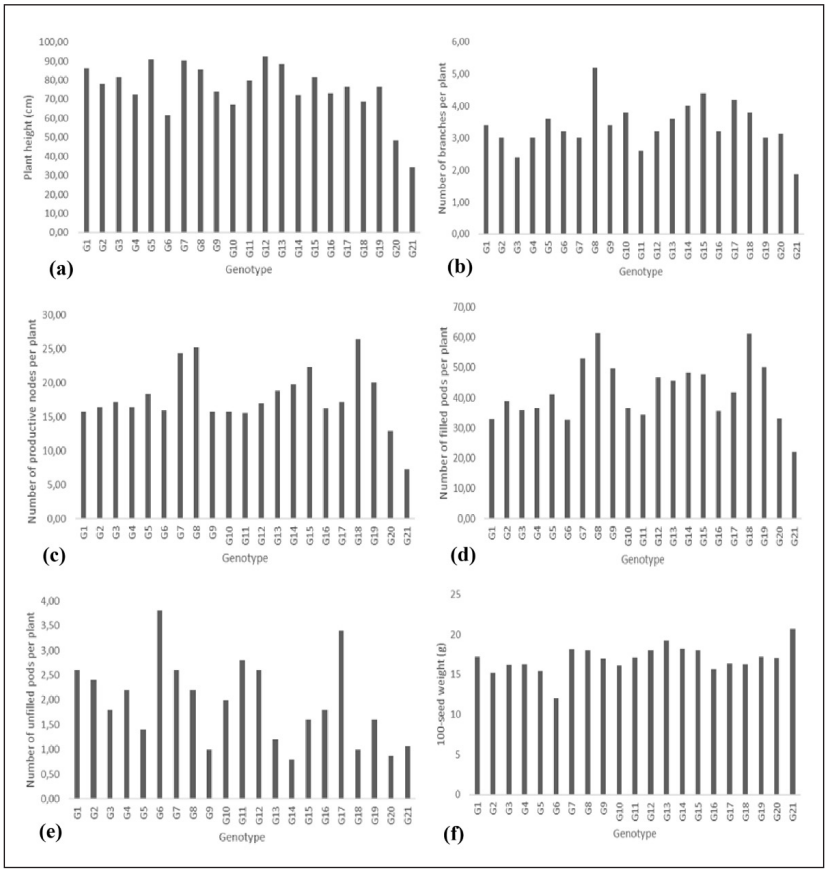


Figure 2. The yield components of 21 soybean lines: (a) plant height, (b) number of branches per plant, (c) number of productive nodes per plant, (d) number of filled pods per plant, (e) number of unfilled pods per plant, (f) 100-seed weight

whereas Argomulyo recorded 48.5 cm (Figure 2a). The shortest cross-bred line was G6 at a height of 61.6 cm. Most lines fell in a middle range around 70 to 90 cm. The lines showed variation in height even when they derived from similar parentage. For instance, the lines from Panderman × UM 6.3 ranged from 78.0 cm (G2) to 90.2 cm (G7), thus showing the genetic diversity even among closely related groups. Plant height is an important trait for growth, and its productivity is affected by both genetic and environmental conditions (Yang et al., 2021). Differences in plant height were found amongst the soybean genotypes tested, ranging from 34.1 to 92.6 cm (Figure 2a). The difference in plant height is caused by differences in genetic background. Argomulyo, one of the crossing parents, was shorter than its six offspring. Therefore, the other parents played a more significant role than Argomulyo in the performance of plant height. The height of the plants is uniform from the perspective of crop improvement. Two relevant agronomic traits when considering their direct impact on soybean yield are flowering time and plant height (Chen et al., 2020). The majority of lines studied here would be considered medium height, with an average height ranging from 70 to 90 cm (Figure 2a). This range is thought to be the ideal height for soybean cultivation in subtropical regions (Yang et al., 2021).

Across the 21 genotypes, the average number of branches per plant was 3.4, with the least branching observed for Dega 1 and G3 at 1.87 and 2.4 branches, respectively. On the contrary, G8 had the highest branching, averaging 5.2 (Figure 2b). Several lines polled above-average branching compared to these two check varieties. G15 and G17 were proportional in mean branches at 4.4 and 4.2, respectively, demonstrating strong branching character. Thus, the average branch number in this study was 3.4 per plant, with the maximum recorded for G8 at 5.20 per plant (Figure 2b). It is higher than that of Zubaidah et al. (2023), who reported an average of 3 branches in the CpMMV-resistant genotype and 1 branch per plant in the CpMMV-sensitive genotype. Badiaraja et al. (2021) also revealed that no maternal effect controlled the number of branches. Genetic factors are not the only ones that affect the number of branches; ecological factors like plant density can also have a significant impact. Soybean plants at low density tend to put out more branches and pods, thereby contributing to yield per plant. Since it is branches that are playing a more integral part in yield at lower density with wider spacing (Werner et al., 2021). Soybean varieties with high branching plasticity can sustain stable yields when the number of main stem nodes per unit area is low (Yoshihira et al., 2020).

The mean number of productive nodes was 17.9, with Dega 1 characterised by the lowest node number of 7.3. In contrast, the highest counts were noted in G8 and G7 at 25.2 and 24.4 nodes, respectively (Figure 2c). The fewer productive nodes at Dega 1 were attributed to shorter plant heights. The productive nodes of the tested soybeans were highly variable, ranging from 7.3 to 24.4 nodes. Dega 1 had the fewest productive nodes, while G8 had the largest number (Figure 2c). Number of productive nodes is influenced

by genetic factors, where the heritability is high (Gastl Filho et al., 2022; Kuswantoro et al., 2022). The most promising characteristic for increasing grain output and the number of soybean pods is increased node number (Chen et al., 2020). The number of productive nodes is significantly correlated with days to maturity, plant height, and number of branches (Table 3). The development of productive nodes increases with increasing maturity because productive nodes are related to generative organs that appear at the nodes. Tall plants allow the formation of many stem nodes (Yang et al., 2021).

The number of filled pods averaged 42.2 (Figure 2d). The highest number of filled pods was achieved by G8 (61.4 pods) and G18 (61.2 pods), while the lowest number of filled pods was achieved by Dega 1 (22.1 pods) and G1 (32.6 pods). The highest number of unfilled pods was reached by G6 and G17, with unfilled pods of 3.8 and 3.4, respectively (Figure 2e). The lowest number of unfilled pods was reached by G14 and Argomulyo, with unfilled pods of 0.80 and 0.87, respectively. The study found that cross-breed soybean lines consistently produced more filled pods than Dega 1. G8 and G18 had the highest filled pods (Figure 2d). Argomulyo and Dega 1 had low unfilled pods. G6 had the highest unfilled pods (Figure 2e). Zubaidah et al. (2023) reported more filled pods on the CpMMV-resistant genotype and the same number of unfilled pods. There was no correlation between filled and unfilled pods (Table 3). Filled pods contain fully developed seeds, so the more filled pods, the more soybean seeds are produced, while unfilled pods are pods that do not contain seeds or only contain seeds that are not fully developed. Disease attacks can cause a decrease in filled pods and an increase in unfilled pods (Rao et al., 2023). Plants with virus disease symptoms produce fewer pods (Sandra et al., 2020). Although it was never observed that the virus produced symptoms of proliferation, virus infection in soybeans was thought to have a major impact on pod development (Zamharir et al., 2022). The number of pods also affects the yield of soybean seeds because pods can also carry out photosynthesis (Burgess & Degen, 2023).

The average 100-seed weight was 16.93 g. The highest weight of 100 seeds was reached by Dega 1 (20.68 g) and G13 (19.21 g), while the lowest weight of 100 seeds was achieved by G6 with a weight of 12.01 g. Seed size in 19 tested lines followed the large-seeded parent except G6 (Figure 2f). The 100-seed weight was a crucial characteristic in soybean cultivation, often indicative of seed size and potentially influencing overall yield and seed quality. The average seed weight was 16.93 g, with Dega 1 and G13 having the highest and lowest weights, with seed size following the large-seeded parent (Figure 2f). Seed size is genetically controlled. Nine candidate large-seed genes have been identified in soybean (Zhang et al., 2024). However, soybean seed size is also affected by disease attacks that cause seed quality degradation (Liu et al., 2019). According to Usovsky et al. (2022), viral diseases can reduce the size of soybean seeds. Seed-pod abortion occurred in symptomatic soybean shoots due to infection by healthy soybean plants (Zamharir et al., 2022).

There was a significant difference in seed yield between the check varieties, Argomulyo and Dega 1, which exhibited lower productivity. The mean seed yield per plot varied from 100 to 465 g, with the highest-yielding lines being G18 and G13. The lowest-yielding lines were G16 and Dega 1 (Figure 3b). This variation indicates that certain combinations of genes greatly affect yield potential in a positive or detrimental way. Different genetic backgrounds allow for variability in yield performance per plant. Soybean seed yield is regulated by several complex genes (Tayade et al., 2023). Photosynthesis produces sugars, such as sucrose, which is later converted to energy and stored as starch (Fang et al., 2021). The longer the DTM, the greater the accumulation of photosynthates. Significant genotypic differences exist in grain-filling rate and length (Yang et al., 2008). A short growing season restricted splash growth, development, and maturity (Zhang et al., 2016). High BRC will elevate NOD and POF, which will, in turn, increase YLDP (Faot et al., 2019; Xu et al., 2021). In many cases, plants with high YLDP do not also supply high YLD. This can be ascribed to the existence of different alleles that further enhance plant cooperation and productivity (Wuest et al., 2022).

The average disease score for 21 lines was 2, with symptoms noted on leaves that were wrinkled with yellow spots. Nine lines recorded the worst disease score of 3 at 30 DAP, while two lines, Dega 1 and Argomulyo, scored only 1. The remaining 10 lines had a disease score of 2 (Figure 4). Based on the evaluation of the severity of disease, the maximum score attained was 3 out of a possible 5. This score reflected symptoms of slight mosaic wrinkling and yellow spots on the leaves. Even with a severity score of 3, however, none of the lines showed any significant reduction in productivity. These results verify that an increase in severity of infection did not significantly affect productivity. The disease score exhibited a positive correlation with days to maturity, plant height, number of branches, nodes, and filled pods. This positive correlation seems to be because the soybean lines have a tolerance mechanism as opposed to a rejection mechanism. This indicates that the virus had a limited effect on these plants in relation to growth and development. Agronomic traits of most

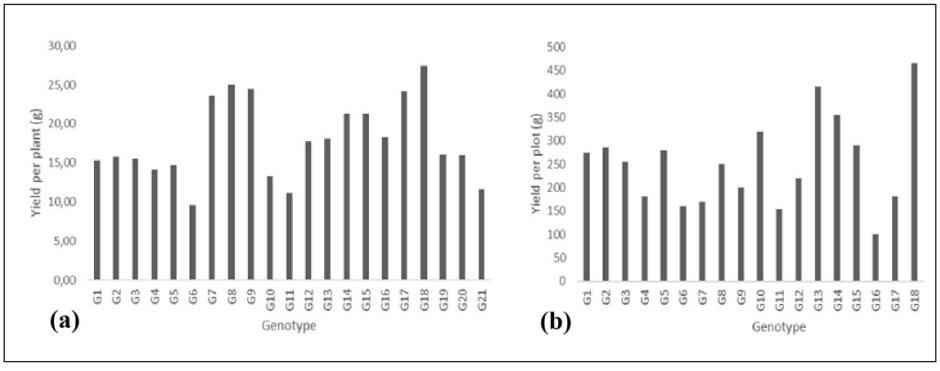


Figure 3. The seed yield per plant (a) and seed yield per plot (b) of 21 soybean lines

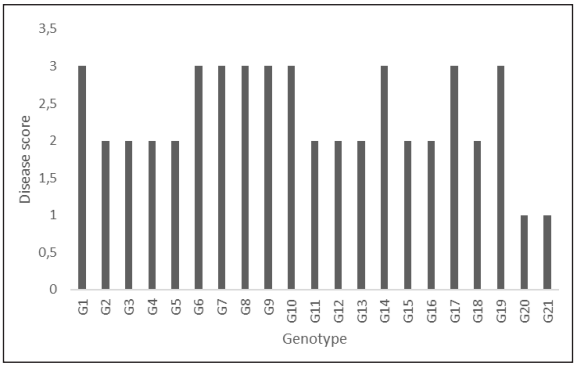


Figure 4. Disease score of 21 soybean genotypes

lines remained unscathed by CpMMV infection conditions later into the planting schedule. Resistant or tolerant plant genotypes, when faced with viruses, sometimes outgrow the infections as they age (Zubaidah & Kuswantoro, 2016). As the plant becomes mature, the immune system might become stronger and could ward off or reduce the trophic effect of viral infection. The multilayer immune response of plants to viral infection varies with genotype and environmental factors, conferring resistance, sensitivity or tolerance mechanisms (Baebler et al., 2020). The multilayer response will consequently determine at what level the plant is able to balance virus presence without losing much of its health. Where resistance is not attained, tolerance will be the strategy bearing the least cost to the virus and its host for continued existence in mutuality (Paudel & Sanfaçon, 2018).

According to the analysis of CpMMV detection and quantitation by Real-Time PCR, the Cq values ranged from 20 to 30 among the 21 lines tested (Table 2), indicating that they fall into the moderate category. This suggests that there is sufficient target gene present but not in very high concentrations. The lowest Cq value of 20.46, evidenced by the line G15, indicates

Table 2
Cq value of 21 soybean lines originated from some crossing

Code	Cq value	Category
G1	26.77	Middle
G2	25.09	Middle
G3	26.00	Middle
G4	23.25	Middle
G5	24.29	Middle
G6	25.54	Middle
G7	28.69	Middle
G8	27.29	Middle
G9	24.29	Middle
G10	23.25	Middle
G11	24.94	Middle
G12	23.51	Middle
G13	23.91	Middle
G14	23.97	Middle
G15	20.46	Middle
G16	22.17	Middle
G17	24.11	Middle
G18	26.42	Middle
G19	29.69	Middle
G20	24.23	Middle
G21	26.02	Middle

that this line holds the highest viral load among the lines under study. In contrast, the highest Cq value, 29.69, was observed in G19, signifying it had the lowest viral count. This result is similar to Lacerda et al. (2015), who reported that Cq values varied between 21 and 28, predominantly between 24 and 27, and Wu et al. (2014) reported that the Cq values were less than 30. G15 had the lowest Cq value among the soybean lines, and it had the lowest disease score. A lower Cq value indicates a greater number of viruses. However, in this study, the disease score of G15 was also low. The tolerance mechanism took place in this soybean line, where the number of viruses in plants was high; the plants did not show more severe symptoms of the disease. A quantitative trait controls disease tolerance (Lin et al., 2020). Through the use of the RNA silencing mechanism, small RNAs are crucial for plant immunity (Huang et al., 2016). The highest Cq value was achieved by G19 and G8, indicating that the number of viruses in these lines was lower than in other genotypes.

In the correlation analysis, a comparative analysis of the relationship between each trait observed was also carried out, whether synergistic or contradictory. The number of days to flowering had a substantial positive association with both the number of days to maturity and plant height (Table 3). Zhang et al. (2015) stated that plant height and days to flowering are the key factors for soybean production and adaptability. The positive correlation between the number of branches and days to flowering means that late-maturing soybeans show greater branching plasticity than early-maturing varieties (Yoshihira et al., 2020). Days to maturity had a significant positive correlation with the number of branches and productive nodes. The number of productive nodes and the number of filled pods are important components of the outcome. The number of productive nodes was correlated with days to maturity, plant height, and number of branches. Meanwhile, the number of filled pods was correlated with plant height, number of branches, and number of productive nodes. Other yield components influence seed yield. In this study, seed yield per plant correlated with days to maturity, number of branches, number of productive nodes, and number of filled pods. The 100-seed weight negatively correlated with days to flowering and unfilled pods number (Table 3). A negative correlation with days to flowering occurred because the longer the days to flowering, the shorter the seed filling duration, making the seeds smaller. A negative correlation with unfilled pods occurred because lines with large seeds tended to have a small number of pods. Hence, the number of unfilled pods was also small. Nair et al. (2023) also obtained a negative correlation between DTF and SEW.

There were two large groups of genotypes, each of which had two more groups, so there were four relatively large groups (Figure 5). The first group consisted of two genotypes, namely G20 and G21, which were the check varieties of Argomulyo and Dega 1. This is likely because they share a common genetic background, as they are derived from the same cross, UM 4.1 × Argomulyo. Their genetic similarity may contribute to comparable agronomic and disease trait performance. For example, these lines might exhibit similar

Table 3
Correlation among agronomic and disease traits

	DTM	**HGT**	**BRC**	**NOD**	**POF**	**POU**	**SEW**	**YLDP**	**YLD**	**SCR**	**Cq**
DTF	0.517*	0.457*	0.250	0.398	0.163	0.406	-0.597**	-0.066	-0.027	0.192	-0.077
DTM		0.718**	0.493*	0.753**	0.68	0.343	-0.257	0.534**	-0.002	0.647**	0.088
HGT			0.379	0.600**	0.518*	0.276	-0.047	0.313	0.382	0.433*	0.034
BRC				0.644**	0.653**	0.016	-0.038	0.619**	0.326	0.476*	-0.212
NOD					0.903**	0.001	-0.037	0.701**	0.057	0.440*	0.226
POF						-0.174	0.134	0.828**	0.058	0.429*	0.236
POU							-0.491*	-0.244	-0.181	0.406*	0.118
SEW								0.257	0.226	-0.260	0.077
YLDP									0.352	0.308	0.062
YLD										0.191	-0.228
SCR											0.313

Note. ** = significant at $\alpha_{0.05}$; YLD = seed yield per plot, YLDP = weight of seeds per plant, SEW = weight of 100 seeds, NOD = number of productive nodes, POF = number of filled pods, POU = number of unfilled pods, BRC = number of branches, HGT = plant height, DTM = days to maturity, DTF = days to flowering, SCR = disease score, Cq = cycle quantification value

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yields (YLD) and seed size (SEW). The second group contained five genotypes. This group consisted of four types of crosses. There were two genotypes derived from one cross, namely G13 and G14. The third group consisted of one genotype, G6. G6 is the only genotype with UM 6.1 as the male parent. It is believed that the male parent has a more significant influence than the female parent, Argomulyo. The fourth group consisted of 13 genotypes. This group contained genotypes from various crosses (Figure 5). The grouping was formed by agronomic and disease traits. Each trait had a different influence on genotype performance, thus forming a certain grouping. In the first group containing Argomulyo and Dega 1, the impact of most observed traits was generally low, except for seed size. Thus, the first group was more influenced by seed size. In the second group, the largest influence was BRC and YLD, followed by YLDP, NOD, and POF, which suggests that this group was influenced by yield and yield components. The third group, filled by G6, was influenced by POU, which suggests that G6 had its group because its POU was the highest compared to other genotypes. In the fourth group, the influence of traits was almost evenly distributed but higher than in the first group (Figure 5).

CONCLUSION

The performance of the tested soybean genotypes varied, as indicated by the diversity of agronomic traits and disease scores. The 19 tested lines generally had higher agronomic traits than the check varieties Argomulyo and Dega 1, except for seed size. Of the 21 soybean genotypes, G18 had the highest seed yield per plant at 27.41 g and per plot at 465 g.

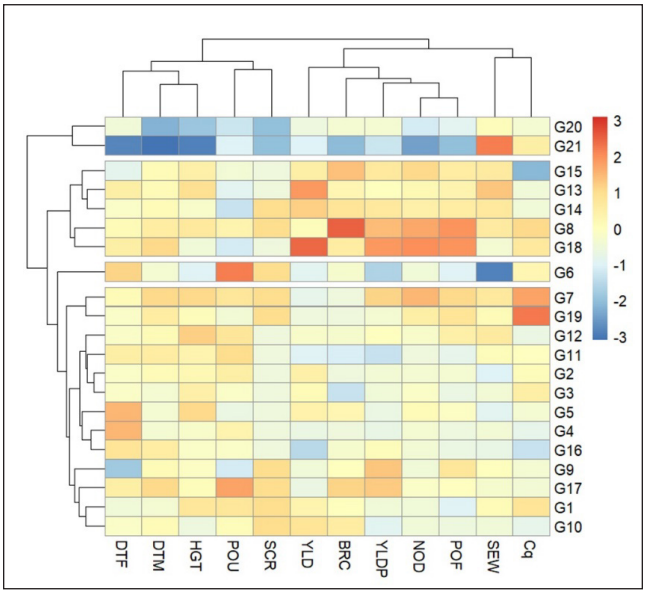


Figure 5. Heatmap of 21 soybean genotypes

G18 also had the highest number of productive nodes per plant and the most filled pods per plant. The observed disease score ranged from 1 to 3, with a Cq value in the middle category. Hence, the virus was detected in all genotypes, but the impact on productivity was relatively limited. Seed yield per plant was associated with days to maturity, number of branches per plant, number of productive nodes per plant, and number of filled pods per plant, indicating that higher-yielding plants were characterised by longer days to maturity, a greater number of branches, more productive nodes, and a higher number of filled pods. Disease score showed a positive correlation with days to maturity, plant height, number of branches, number of productive nodes, number of filled pods, and number of unfilled pods per plant. No correlation existed between Cq value and other agronomic characteristics. The soybean lines ranged widely in resistance levels, with some genotypes being less severely diseased while still producing better yields. This study opens up avenues for breeding CpMMV-resistant genotypes in soybean, with partial resistance lessening CpMMV's deleterious effects but not lowering productivity. These genotypes offer potential genetic resources for soybean breeding, although their resistance and yield stability need to be further validated through controlled inoculation experiments and multi-environment trials.

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