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# Identification of yellow mosaic virus resistant mung bean genotypes through field screening and evaluation of agro-morphological traits

**Debadarshan Samal[1], Ravi Kant[2*], Madhuri Arya[3], V K Choudhary[4], Nilanjaya[1], Hem Chandra Chaudhary[5], C S Choudhary[6], Avinash Singh[1], Satish Chandra Narayan[2] & Piyush Kumar[7]**

[1]Department of Genetics and Plant Breeding, Post Graduate College of Agriculture, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur 848 125, Bihar, India

[2]Department of Genetics and Plant Breeding, Regional Research Station, Madhopur, Dr. Rajendra Prasad Central Agricultural University, Pusa, West Champaran 845 454, Bihar, India

[3]Department of Genetics and Plant Breeding, Tirhut College of Agriculture, Dr. Rajendra Prasad Central Agricultural University, Pusa, Dholi, Muzaffarpur 843 121, Bihar, India

[4]Department of Genetics and Plant Breeding, Directorate of Seed, Dr. Rajendra Prasad Central Agricultural University, Pusa, Dholi, Muzaffarpur 843 121, Bihar, India

[5]Department of Plant Pathology, Directorate of Seed, Dr. Rajendra Prasad Central Agricultural University, Pusa, Dholi, Muzaffarpur 843 121, Bihar, India

[6]Department of Plant Pathology, Tirhut College of Agriculture, Dr. Rajendra Prasad Central Agricultural University, Pusa, Dholi, Muzaffarpur 843 121, Bihar, India

[7]Division of Plant Pathology, Faculty of Agriculture, Wadura, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Wadura 193 201, Jammu & Kashmir, India

***Correspondence:** ravikant@rpcau.ac.in

## Abstract

Mung bean (*Vigna radiata* (L.) Wilczek) is an important pulse crop belongs to family Fabaceae, but its productivity is greatly affected by mung bean yellow mosaic virus (MYMV). This study evaluated 42 mung bean genotypes, including 2 checks, for genetic variability, yield, agro-morphological traits and MYMV resistance during the summer of 2024–25 at the Regional Research Centre, Madhopur, Bihar, using a randomised block design with 3 replications. Analysis of Variance revealed significant genotypic differences for days to maturity, number of pods per plant, 100-seed weight, seed yield per plant, MYMV incidence and whitefly population at vegetative, flowering and pod-formation stages, indicating substantial genetic variability for these traits. Seed yield per plant ranged from 2.02 to 6.91 g, with a mean of 4.46 g. TC-34 (6.91 g plant$^{-1}$) and TC-17 (6.82 g plant$^{-1}$) outperformed the best check, SML 668 (5.51 g plant$^{-1}$) and were identified as promising high-yielding genotypes. Mung bean yellow mosaic virus incidence ranged from 6.67 to 50.00 %, with TC-11 recording the lowest incidence (6.67 %), followed by TC-14 and TC-29 (10.00 % each). High phenotypic and genotypic coefficients of variation for MYMV incidence and whitefly population indicated considerable exploitable variability. High heritability coupled with high genetic advance for 100-seed weight, seed yield per plant and whitefly population suggested predominantly additive gene action and good prospects for selection. Seed yield showed significant positive correlations with number of pods per plant and 100-seed weight, whereas MYMV incidence and whitefly population were negatively associated with yield. Path analysis identified 100-seed weight as an important positive direct contributor to seed yield, while whitefly populations at vegetative and flowering stages showed negative direct effects. Mahalanobis' $D^2$ analysis grouped the genotypes into 3 clusters, with maximum divergence between Clusters II and III. Screening using the McKinney scale identified TC-11, TC-14 and TC-29 as resistant and 12 genotypes as moderately resistant. These genotypes offer valuable resources for developing high-yielding, MYMV-resistant mung bean cultivars.

**Keywords:** disease resistance; genetic divergence; mung bean yellow mosaic virus; seed yield; *Vigna radiata*; whitefly

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## Introduction

Mung bean (*Vigna radiata* (L.) Wilczek) is a widely grown grain legume across tropical and subtropical regions of Asia, Africa, Australia and the Americas. It is a diploid species with a chromosome number of 2n = 2x = 22 and believed to have originated from the wild species *Vigna radiata* var. *sublobata* (1). Because of its high protein content (20–25 %), easy digestibility and short growing season, mung bean is a key crop for food and nutritional security, especially in South and

Southeast Asia. According to Pulse Pod / Global Pulses Confederation, 2025, India is the largest producer (3.8 million tonnes) and consumer (2.7 million tonnes), contributing a substantial share of global area and output. Moong bean is cultivated across 1.55 to 2.0 lakh ha in Bihar, accounting for roughly 4 % of the national area and 5 % of total production. The summer season drives nearly 80 % of the state's total moong bean cultivation, yielding a seasonal productivity range of 680 kg/ha to 900 kg/ha depending on environmental conditions (2). Despite its importance, mung bean yields remain limited by multiple biotic and abiotic stresses. Among the various biotic stresses, the MYMV holds the prominent place, caused by most destructive diseases is mung bean yellow mosaic disease (MYMV), caused by begomoviruses in the family Geminiviridae. Whitefly (*Bemisia tabaci*) transmits MYMV mainly during early seedling stage, cause yield losses from 10 to 100 %, depending on the cultivar, infection timing and severity (3, 4). The disease is widespread in major mung bean-growing areas of notably India (5–7).

Infected plants typically show yellow patches on young leaves that may progress to a full mosaic pattern, reducing photosynthesis, impairing pod development and sharply lowering yields. The virus primarily targets phloem tissues (8) and because chemical control of its whitefly vector often gives inconsistent results, developing resistant cultivars is the most cost-effective and environmentally sound strategy. Despite the availability of mung bean germplasm with diverse agronomic characteristics, systematic evaluation of advanced breeding lines for combined resistance to Mung bean yellow mosaic virus (MYMV), whitefly infestation, yield potential and associated agro-morphological traits remains limited, particularly under the agro-ecological conditions of Bihar. Moreover, resistance to MYMV alone may not be sufficient for cultivar development unless it is accompanied by desirable plant architecture, early maturity and stable yield performance. Therefore, there is a need to identify genetically diverse and superior breeding lines that combine effective MYMV resistance with reduced whitefly population and favourable agronomic attributes. Such comprehensive characterisation would help bridge the gap between the identification of resistant material and its effective utilisation in mung bean improvement programmes. Hence, the present study was undertaken to systematically evaluate advanced breeding lines of mung bean available at the Department of Genetics and Plant Breeding, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, under natural field conditions, with the objective of identifying promising lines possessing resistance to MYMV and associated whitefly infestation together with superior yield and desirable agro-morphological traits. The identified lines could serve as valuable genetic resources and potential donor parents for developing high-yielding and MYMV-resistant mung bean cultivars.

## Materials and Methods

### Plant material and experimental site

A total of 42 mung bean (*Vigna radiata* (L.) Wilczek) genotypes, including the released cultivars SML 668 and HUM-16 as checks, procured from AICRP on kharif pulses (Mung) and were evaluated during the summer 2024–25 season at the Regional Research Centre, Madhopur, Dr. Rajendra Prasad Central Agricultural University (RPCAU), Bihar, India (26.75° N, 84.70° E; 84.26 m above msl). The site has sandy loam soil (pH 7.7–8.5) and assured irrigation.

### Experimental design and crop husbandry

The trial was laid out in a randomised complete block design (RCBD) with 3 replications. Each genotype was grown in 2 m² plots and managed according to recommended agronomic practices for mung bean (spacing : 25 cm row to row and 10 cm plant to plant); N : P : K:: 20 : 60 : 20). To allow natural infestation and disease development, no insecticides were applied during the crop season.

### Phenotypic evaluation

For each replication, 5 plants were selected at random and measured for plant height (cm), days to 50 % flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, pods per plant, 100-seed weight (g) and seed yield per plant (g).

### Screening for mung bean yellow mosaic disease

Genotypes were screened for MYMV under natural epiphytotic conditions and observation were recorded during flowering (30 DAS) and at pod maturity (60 DAS). Disease incidence was expressed as the percentage of infected plants within each genotype. Disease reactions were classified using The McKinney index or Disease severity index (DSI) (1923) (0–5 score) into highly resistant (HR), resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS).

### Whitefly population assessment

The principal vector, *Bemisia tabaci* Genn., was monitored at vegetative, flowering and pod development stages. Adult whiteflies on the abaxial surface of young leaves were counted in the morning and recorded as number of whiteflies per plant.

### Statistical analyses

Analysis of variance (ANOVA) were performed in R software version 4.6.1 to test genotypic effects. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability and genetic advance were estimated following standard procedure (9–11). Phenotypic and genotypic correlation coefficients were also calculated (12). Path coefficient analysis (13, 14) was used to partition direct and indirect contributions of component traits to seed yield. Genetic divergence was estimated using Mahalanobis' $D^2$ statistics (15) and clusters were formed by Tocher's method; intra- and inter-cluster distances were computed to identify genetically diverse parental combinations for future breeding.

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## Results

### Analysis of variance

Analysis of variance showed significant genotypic differences for days to maturity, number of pods per plant, 100-seed weight, seed yield per plant, MYMV incidence and whitefly counts at vegetative, flowering and pod-ormation stages (Table 1). The significant variation indicates substantial genetic variability for these traits and suggests good potential for selection to improve both disease resistance and yield.

### Mean performance of genotypes

Marked variation was observed across genotypes for agronomic traits, yield components and MYMV incidence. Seed yield per plant ranged from 2.02 to 6.91 g, with a mean of 4.46 g. Genotypes TC-34 (6.91 g plant$^{-1}$) and TC-17 (6.82 g plant$^{-1}$) outperformed the best check, SML 668 (5.51 g plant$^{-1}$), highlighting their promise as high-yielding breeding parents. Mung bean yellow mosaic virus incidence ranged from 6.67 % to 50.00 %, revealing wide diversity in disease response. TC-11 recorded the lowest incidence (6.67 %), followed by TC-14 and TC-29 (10.00 % each), identifying these lines as potential resistance donors (Fig. 1).

### Genetic variability, heritability and genetic advance

High PCV (37.42) and GCV (36.54) values for MYMV incidence and whitefly populations indicate ample exploitable variation for these traits (Table 2). The relatively small differences between PCV and GCV for 100-seed weight, seed yield and whitefly counts suggest a limited environmental influence on their expression (Fig. 2). High heritability coupled with high genetic advance for 100-seed weight, seed yield per plant and whitefly population implies predominantly additive gene action and predicts a favourable response to direct selection.

Traits with high heritability coupled with high genetic advance-100-seed weight, seed yield per plant and whitefly population-point to predominately additive gene action and predict good response to direct selection. By contrast, days to 50 % flowering and MYMV incidence showed low heritability, indicating a larger environmental component and the need for multi-environment evaluation or indirect selection strategies.

### Associations among traits

Correlation analysis showed seed yield per plant was positively and significantly correlated with number of pods per plant (r = 0.212) and 100-seed weight (r = 0.228), indicating that selection for these components should raise yield. Mung bean yellow mosaic virus incidence was significantly negatively correlated with seed yield (r = -0.182), confirming that disease pressure reduces productivity (Fig. 3). Whitefly populations at vegetative, flowering and pod-formation stages were also negatively associated with yield, underscoring the importance of reducing vector abundance to protect yield potential. A strong positive correlation between whitefly density and MYMV incidence confirmed *Bemisia tabaci* as the principal driver of disease spread under these field conditions.

### Path coefficient analysis

Path analysis identified 100-seed weight (0.187) as having the largest positive direct effect on seed yield, followed by the direct effects of MYMV incidence (0.074) and whitefly population at pod formation (0.089) as presented in Fig. 3, Table 3. The prominent direct contribution of seed weight supports its use as an effective selection criterion for improving yield. Negative direct effects were largest for whitefly populations during flowering (-0.310) and vegetative stages (-0.171), indicating that high vector loads directly reduce yield. These results suggest that breeding for high seed weight combined with strategies to limit whitefly infestation can improve mung bean productivity.

### Genetic divergence

Mahalanobis' $D^2$ clustering grouped the 42 genotypes into three clusters, reflecting substantial genetic diversity (Fig. 4). Cluster I contained the majority of genotypes, while Clusters II and III comprised fewer but distinct genotypes. The greatest inter-cluster distance occurred between Clusters II and III, implying that crosses between genotypes from these clusters are likely to produce maximum heterosis and broader segregating populations for selection.

### Screening for MYMV resistance

Using the McKinney scale, 3 genotypes (TC-11, TC-14, TC-29) were classified as resistant and 12 as moderately resistant; none qualified as highly resistant (Fig. 5). The resistant genotypes consistently showed lower whitefly counts and reduced disease incidence relative to susceptible entries. Among them, TC-11 combined the lowest MYMV incidence (6.67 %) with comparatively high seed yield, making it a strong donor for resistance breeding.

TC-14 and TC-29 also paired low disease incidence with acceptable agronomic performance and therefore represent useful genetic resources for developing MYMV-resistant cultivars. TC-11, TC-14 and TC-29 emerged as promising sources of MYMV resistance, while TC-17 and TC-34 stood out as superior high-yielding genotypes. These lines can be used in crossing programmes to combine resistance and productivity and crosses between genotypes from divergent clusters (especially Clusters II and III) may maximise genetic gain in segregating generations.

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**Table 1.** Anova for 10 traits of mung bean genotypes

| Sl. No. | Source | Mean sum of squares (MSS) | | |
|---|---|---|---|---|
| | Degree of freedom | Replications | Treatments | Error |
| | | 02 | 41 | 82 |
| 1 | Plant Height (cm) | 34.03 | 63.00 | 2.79 |
| 2 | Days to 50 % flowering | 54.02 | 27.07 | 19.25 |
| 3 | Days to maturity | 20.00 | 54.27** | 12.49 |
| 4 | Number of primary branches | 0.40 | 0.24 | 0.04 |
| 5 | Number of secondary branches | 0.90 | 4.36 | 0.02 |
| 6 | Number of Pods per plant | 5.66 | 16.19** | 8.68 |
| 7 | 100 Seed weight (g) | 0.002 | 0.60** | 0.007 |
| 8 | Seed yield per plant (g) | 0.18 | 2.28** | 0.15 |
| 9 | Infection % of MYMV | 551.79 | 353.37** | 185.73 |
| 10 | (i) No. of white fly vector per plant (Vegetative stage) | 0.13 | 7.09** | 0.11 |
| | (ii) No. of white fly vector per plant (Flowering stage) | 0.02 | 1.80** | 0.03 |
| | (iii) No. of white fly vector per plant (Pod formation stage) | 0.008 | 0.45** | 0.007 |

(*significance at 5 % level, **significance at 1 % level)

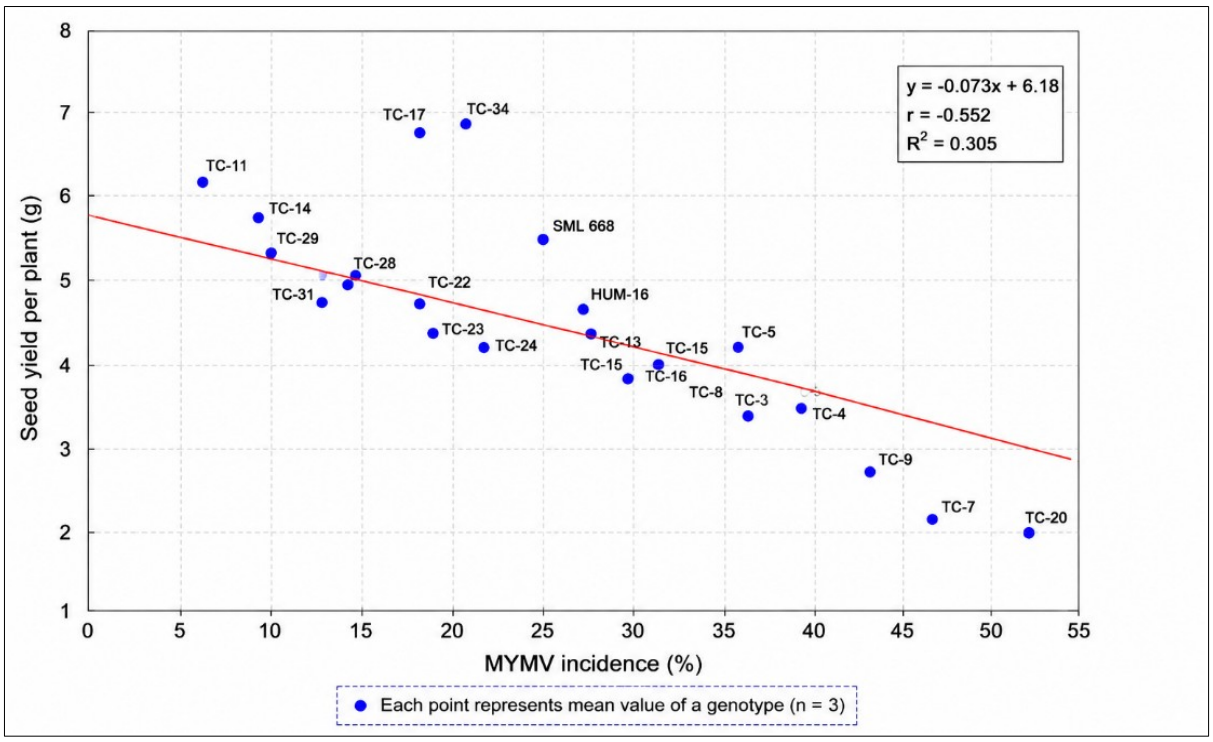



**Fig. 1.** Scatter plot showing relationship between MYMV incidence (%) and seed yield per plant (g).

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**Table 2.** Estimates of genetic variability parameters (GCV, PCV, heritability and genetic advance) for quantitative traits

| Sl. No. | Traits | (σ2g) | (σ2p) | GCV (%) | PCV (%) | H (%) | GA | GAM |
|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | 20.07 | 22.86 | 10.93 | 11.67 | 87.70 | 8.64 | 21.10 |
| 2 | Days to 50 % flowering | 2.89 | 21.50 | 4.26 | 11.63 | 13.45 | 1.28 | 3.22 |
| 3 | Days to maturity | 13.92 | 26.42 | 6.10 | 8.40 | 52.71 | 0.57 | 39.81 |
| 4 | Number of primary branches | 0.08 | 0.11 | 19.70 | 20.09 | 92.13 | 0.01 | 0.75 |
| 5 | Number of secondary branches | 0.84 | 0.97 | 20.54 | 22.13 | 86.13 | 1.70 | 39.27 |
| 6 | Number of pods per plant | 2.50 | 11.18 | 9.61 | 20.32 | 22 | 1.54 | 9.37 |
| 7 | 100 Seed weight (g) | 0.19 | 0.20 | 11.40 | 11.61 | 96 | 0.89 | 23.05 |
| 8 | Seed yield per plant (g) | 0.84 | 0.97 | 20.54 | 22.13 | 86 | 1.75 | 39.24 |
| 9 | Infection % of MYMV | 50.17 | 252.82 | 26.96 | 60.52 | 19 | 6.50 | 24.74 |
| 10 | (i) No. of white fly vector per plant (Vegetative stage) | 2.32 | 2.44 | 35.20 | 36.15 | 95 | 3.06 | 70.84 |
| | (ii) No. of white fly vector per plant (Flowering stage) | 0.58 | 0.62 | 33.29 | 34.23 | 94 | 1.53 | 66.69 |
| | (iii) No. of white fly vector per plant (Pod formation stage) | 0.14 | 0.15 | 36.54 | 37.42 | 95 | 0.77 | 73.53 |

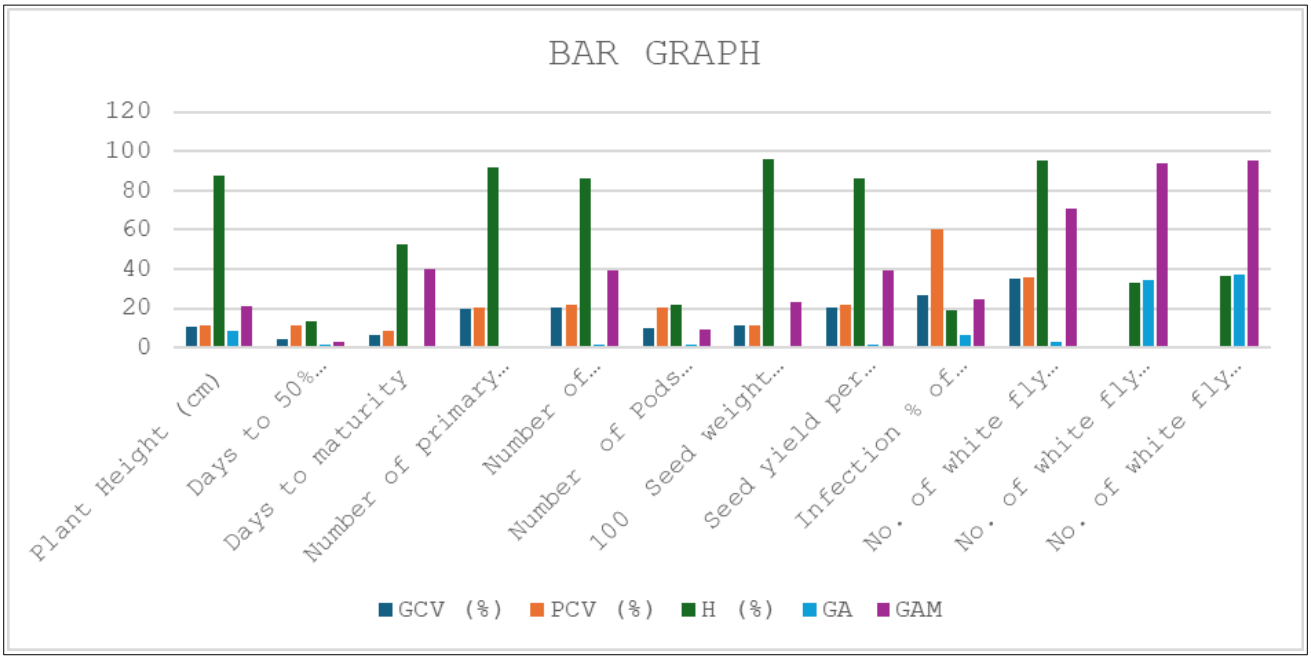



**Fig. 2.** Comparative bar graph of GCV, PCV and heritability estimates for studied traits.

## Discussion

### Genetic variability and performance of mung bean genotypes

The significant differences observed among the mung bean genotypes for days to maturity, number of pods per plant, 100-seed weight, seed yield per plant, MYMV incidence and whitefly population indicate the presence of substantial genetic variability within the experimental material. Such variability is essential for effective selection and crop improvement because it provides opportunities for identifying superior genotypes with desirable agronomic and disease resistance traits. These results align with previous reports of substantial genetic variation across mung bean genotypes, emphasising that genetic diversity is essential for the development of superior cultivars (16, 17). The wide range observed for seed yield, MYMV incidence and whitefly population further demonstrated the existence of exploitable variability. Genotypes TC-17 and TC-34 exhibited superior seed yield compared with the check variety SML 668, whereas TC-11, TC-14 and TC-29 showed lower MYMV incidence and were classified as resistant. These genotypes may therefore serve as

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valuable parental sources in future breeding programmes aimed at combining high productivity with disease resistance.

### Genetic parameters and breeding implications

The magnitude of genotypic and phenotypic coefficients of variation revealed considerable variability for MYMV incidence and whitefly population traits. The relatively small differences between PCV and GCV estimates for seed weight, seed yield and whitefly population indicate limited environmental influence on these characters and suggest that phenotypic selection would be effective.

This close correspondence between GCV and PCV further indicates a strong genetic contribution to the observed phenotypic variation, suggesting that selection based on phenotypic performance could be effective for improving these traits. Comparable findings have also been reported by earlier workers (18, 19). High heritability coupled with high genetic advance was observed for plant height, number of secondary branches, 100-seed weight, seed yield per plant and whitefly population at different growth stages. Such a combination generally indicates the predominance of additive gene action and suggests that substantial genetic improvement can be achieved through direct selection. Similar findings were reported by earlier workers (20), who emphasised the importance of these traits as reliable selection criteria in mung bean improvement programmes. In contrast, days to 50 % flowering and MYMV incidence exhibited relatively lower heritability estimates, indicating a stronger environmental influence on trait expression. Therefore, improvement of these traits may require multi-environment testing and the incorporation of resistant donor lines in breeding programmes.

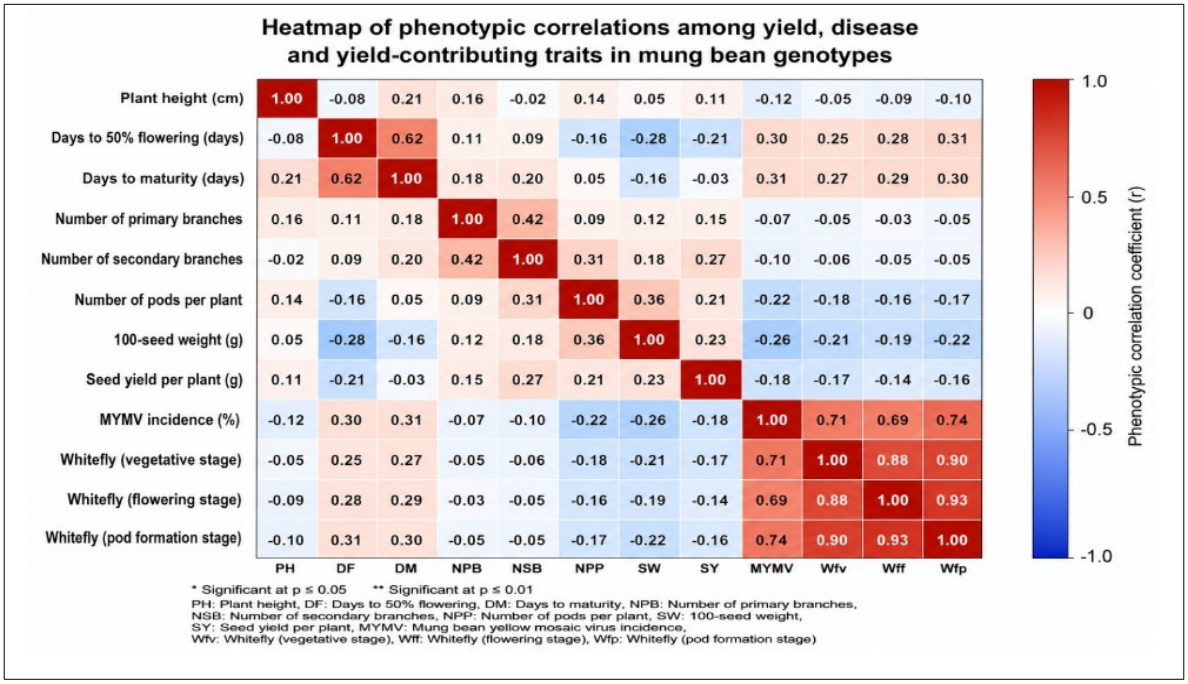



**Fig. 3.** Heatmap of phenotypic correlations among yield, disease and yield-contributing traits.

**Table 3.** Estimates of phenotypic path coefficient analysis of seed yield/plant (g) with its component traits in mung bean genotypes

| Traits | DM | NPP | SW | IP (%) | NWFV | NWFF | NWFP | SY |
|---|---|---|---|---|---|---|---|---|
| DM | -0.021 | -0.001 | 0.012 | -0.007 | 0.013 | 0.051 | -0.021 | 0.043 |
| NPP | 0.001 | 0.007 | 0.040 | -0.011 | 0.044 | 0.040 | -0.001 | 0.212* |
| SW | -0.001 | 0.001 | 0.187 | -0.002 | 0.001 | 0.065 | 0.003 | 0.228* |
| IP (%) | -0.002 | -0.001 | -0.005 | 0.074 | -0.089 | -0.101 | 0.018 | -0.182* |
| NWFV | -0.001 | -0.002 | 0.001 | 0.038 | -0.171 | -0.194 | 0.036 | -0.233** |
| NWFF | -0.003 | -0.001 | -0.039 | 0.024 | -0.107 | -0.310 | 0.063 | -0.340** |
| NWFP | -0.005 | -0.001 | 0.007 | 0.015 | -0.069 | -0.219 | 0.089 | -0.176* |

Residual effect: 0.828

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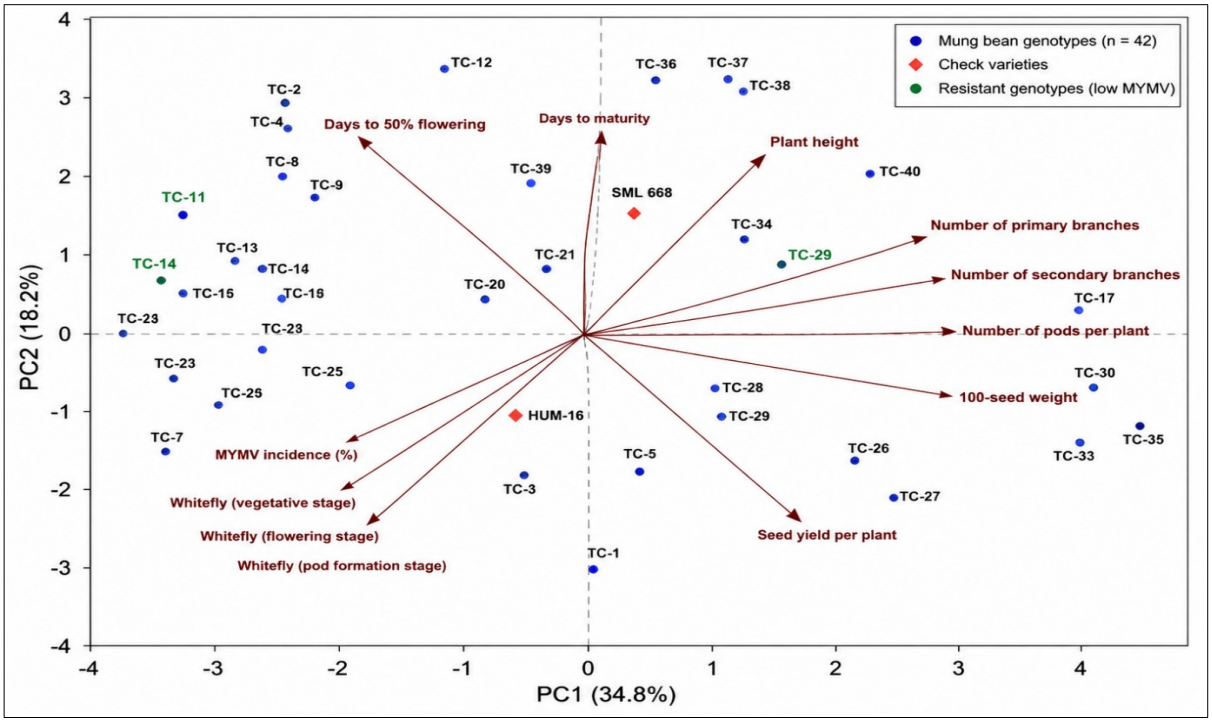



**Fig. 4.** Principal component analysis (PCA) biplot showing diversity among genotypes.

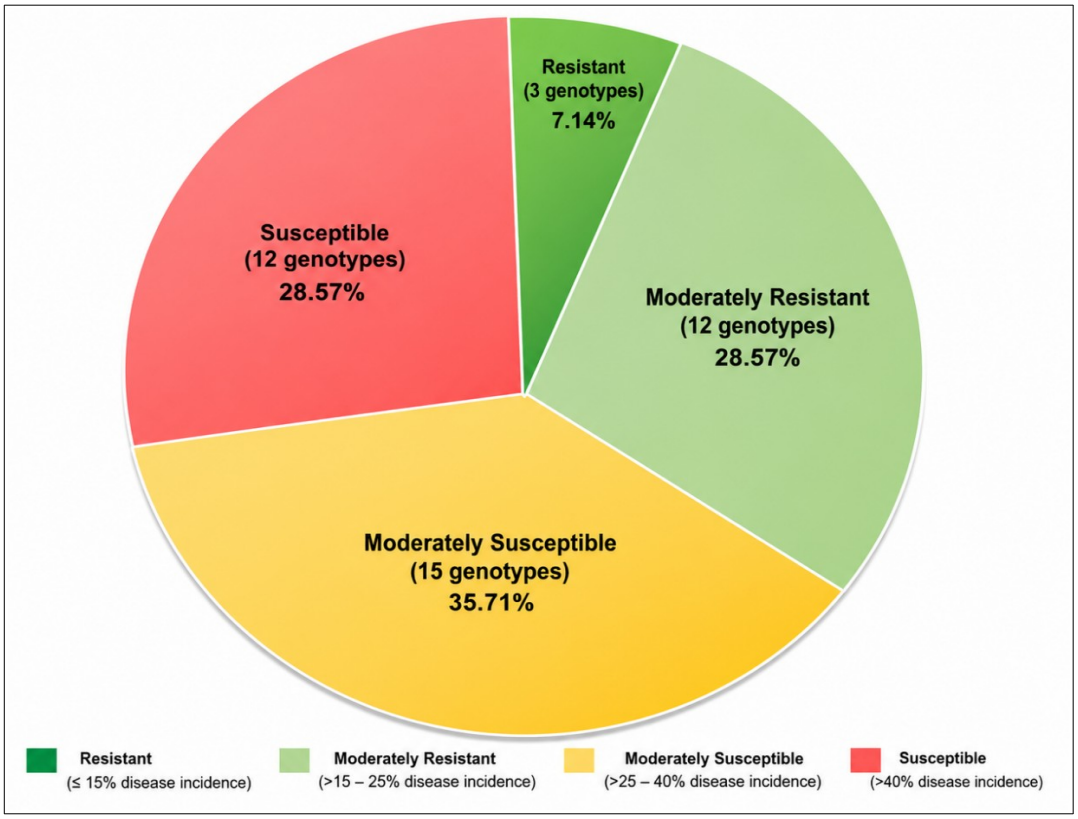



**Fig. 5.** Distribution of mung bean genotypes among resistance categories.

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### Association among yield, mung bean yellow mosaic virus incidence and whitefly population

Correlation analysis revealed that seed yield per plant was positively associated with number of pods per plant and 100-seed weight, suggesting that these traits contribute directly to productivity and can be utilised as indirect selection criteria for yield improvement. Similar associations between yield and its component traits have been reported previously (21). Conversely, MYMV incidence and whitefly population exhibited significant negative associations with seed yield. These findings confirm the detrimental effect of disease infection and vector abundance on crop productivity. The positive association between MYMV incidence and whitefly population further validates the role of *B. tabaci* as the principal vector responsible for disease transmission under field conditions. Consequently, breeding efforts should focus on the simultaneous improvement of yield potential and resistance to MYMV and its vector. The integration of host plant resistance with vector management strategies could substantially reduce disease pressure and improve yield stability under endemic conditions.

### Path coefficient analysis

Correlation analysis alone does not distinguish between direct and indirect effects of component traits on yield. Therefore, path coefficient analysis was performed to identify traits with the greatest direct contribution to productivity. The analysis revealed that 100-seed weight exerted the highest positive direct effect on seed yield, followed by number of pods per plant. These results indicate that improvement in these traits would directly enhance productivity and therefore should receive priority during selection. Similar findings were also reported earlier (22), were identified seed weight and pod number as major determinants of yield in mung bean. Whitefly population during flowering and vegetative stages exerted substantial negative direct effects on seed yield, indicating that vector infestation directly contributes to yield reduction. The observed negative indirect effects through MYMV incidence further support the importance of breeding for vector resistance and disease tolerance.

### Genetic divergence and parent selection

Genetic divergence analysis grouped the 42 genotypes into 3 distinct clusters, indicating the presence of measurable diversity among the evaluated germplasm. The highest inter-cluster distance was observed between Clusters II (895.27) and III (6038.33), suggesting that genotypes belonging to these clusters are genetically divergent and may produce greater heterosis and wider segregation when used in hybridisation programmes. The predominance of genotypes within Cluster I indicates relatively narrow diversity among a large proportion of the germplasm. Similar clustering patterns in mung bean were also reported earlier workers (23, 24). Selection of parents from genetically distant clusters is expected to increase the probability of recovering superior transgressive segregants in subsequent generations.

### Screening for resistance to Mung bean yellow mosaic virus

The screening of mung bean genotypes under natural epiphytotic conditions revealed substantial variation in disease response. Among the 42 genotypes evaluated, TC-11, TC-14 and TC-29 were classified as resistant, whereas 12 genotypes exhibited moderate resistance. No genotype was identified as highly resistant, indicating the scarcity of strong resistance sources within the evaluated material. The resistant genotypes consistently recorded lower MYMV incidence and comparatively reduced whitefly populations, suggesting that resistance may be associated with reduced vector preference and/or enhanced host tolerance mechanisms. Similar observations agreed with earlier findings (25–27), who identified significant variability in MYMV resistance among mung bean germplasm. The identified resistant genotypes represent valuable genetic resources for developing MYMV-resistant cultivars. Furthermore, combining resistance with superior yield performance, as observed in genotypes such as TC-17 and TC-34, could accelerate the development of high-yielding and disease-resistant mung bean varieties suitable for cultivation in MYMV-prone regions.

## Conclusion

The study revealed considerable genetic variability among mung bean genotypes for yield, yield-contributing attributes, MYMV incidence and whitefly population, indicating strong potential for crop improvement. High heritability and genetic advance for key traits suggest the effectiveness of direct selection. Number of pods per plant and 100-seed weight were identified as major contributors to seed yield. Genotypes TC-11, TC-14 and TC-29 showed promising MYMV resistance, while TC-17 and TC-34 recorded superior yield performance. These genotypes can be utilised as a valuable genetic resource for developing high-yielding, MYMV-resistant mung bean cultivars adapted to diverse agro-ecological conditions.

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## Authors' contributions

DS carried out the experiment, took observations and analysed the data. RK guided the research by formulating the research concept and MA approved the final manuscript. VKC, N participated in the design of the study and performed the statistical analysis reviewed the HCC, CSC contributed by imposing the

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experiment and helped edit, summarise and revise the manuscript. PK helped summarise and revise the manuscript. AS, SCN and all other authors read and approved the final manuscript.

## Compliance with ethical standards

### Conflict of interest

Authors do not have any conflict of interests to declare.

### Ethical issues

None

### Declaration of generative AI and AI-assisted technologies in the writing process

ChatGPT was used in limited portions of this manuscript solely for checking and improving grammatical accuracy and language clarity. No other artificial intelligence (AI) tools were used in the preparation, analysis, interpretation, or writing of this manuscript. The authors take full responsibility for the content, accuracy and originality of the manuscript.

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