



Assessment of Genotype $\times$ Environment Interaction and Stability in MYMV-Resistant Greengram Genotypes using AMMI and GGE Biplot Analyses

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ABSTRACT

Background: Mungbean yellow mosaic virus (MYMV) is recognized as a major viral disease severely limiting greengram [*Vigna radiata* (L.) Wilczek] production resulting in severe yield reduction. Identification of resistant and consistently performing genotypes under varying environments is essential for improving productivity in MYMV-endemic regions.

Methods: Fifty MYMV-resistant greengram genotypes were assessed during *Kharif* 2024-25 across three locations-Mandya, GKVK and Chamarajanagar, using a randomized complete block design with two replications. AMMI and GGE biplot models were utilized to evaluate genotype $\times$ environment interactions and assess yield stability among the test genotypes.

Result: The pooled ANOVA indicated significant effects of genotypes, environments and their interactions, indicating substantial genetic variability and differential environmental responses. AMMI analysis resulted that IPCA1 and IPCA2 explained 84.5% and 15.5% of the $G \times E$ interaction, respectively. Genotypes G8, G9 and G10 were recognized as stable and high-yielding across environments, while G39, G40, G43 and G44 exhibited specific adaptation to favorable sites (E1 and E2). Genotypes G6, G5 and G25 performed well under E3 conditions. The identified stable and resistant genotypes can be productively used for MYMV-prone regions to enhance greengram yield stability and productivity. The integration of multi-environment evaluation with advanced statistical models further strengthens the identification of widely adaptable genotypes. Such approaches can significantly contribute to the development of resilient greengram varieties suited for diverse agro-climatic conditions.

Key words: AMMI, Genotype $\times$ environment interaction, GGE biplot, Greengram, MYMV, Stability.

INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek] is a short-duration, self-fertilizing diploid pulse crop ($2n = 2x = 22$) grown widely across tropical and subtropical Asia. It serves as an important source of protein, carbohydrates and micronutrients, contributing to nutritional security and sustainable farming. India is the largest producer and consumer, cultivating about 4.5 million hectares with an annual production of 3 million tonnes (Indiastat, 2023-24). However, productivity remains low compared to its potential due to susceptibility to biotic and abiotic stresses. Among the biotic stresses, mungbean yellow mosaic virus (MYMV), transmitted by whitefly (*Bemisia tabaci*), is the most destructive, causing yield losses up to 100% depending on infection stage and environment. MYMV also affects seed quality, posing severe economic challenges. Breeding for resistance remains the most effective strategy to stabilize productivity in endemic zones.

The yield performance of resistant genotypes often varies due to genotype $\times$ environment interaction (GEI), which complicates the identification of lines that are both resistant and high-yielding across environments. Hence, multi-environment evaluation combined with robust statistical tools is essential Sanasam *et al.* (2024). The additive main effects and multiplicative interaction (AMMI) and genotype plus genotype $\times$ environment interaction (GGE) biplot analyses provide reliable insights into

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GEI, stability and adaptability patterns. The present investigation aimed to evaluate fifty MYMV-resistant greengram genotypes screened under natural hotspot conditions using AMMI and GGE models to identify stable, high-yielding genotypes suited for MYMV-prone regions

and to support resistance breeding for sustainable yield improvement.

MATERIALS AND METHODS

The experimental material comprised fifty greengram genotypes derived from a cross between a susceptible parent ABL-449 (DGGV-2 × IPM-2-14) with yield 48.05 g/plot and a resistant parent ABL-265 (mutant of SM-17) with yield 40.36 g/plot. The trial was carried out during *Kharif* 2024 across three locations: (1) K-Block, GKVK, Bengaluru; (2) VC Farm, Mandya; and (3) KVK, Chamara Nagar. The design was randomized complete block (RCBD) with two replications, including standard checks 'Chinamung' and 'LM-1668'. The traits recorded were days to 50% flowering, plant height (cm), primary branches per plant, clusters per plant, pod length (cm), seed yield per plant (g) and seed index. Seeds from single plants were harvested individually. A combined ANOVA was performed to evaluate genotypic (G), environmental (E) and G × E interaction effects using a mixed linear model (R Software, Metan package). The AMMI model (Gauch and Zobel, 1988) and GGE biplot analysis (Yan *et al.*, 2000) were used to assess and visualize yield stability. Analyses were conducted in R version 4.2.0.

RESULTS AND DISCUSSION

Data obtained from individual F_2 plants were utilized to compute descriptive statistics, including first-order measures such as mean, absolute range (AR) and standardized range (SR), as well as second-order parameters like phenotypic variance (σ^2_p), phenotypic standard deviation (σ_p) and usefulness index based on the relevant formulae. All statistical analyses were carried out using R software (Version 4.4.0; R Core Team, 2024). Additionally, the distribution pattern of the F_2 population was visualized through graphical plots generated in R.

In recent years, greengram cultivation in major regions has been challenged by MYMV and climatic variability. Changes in temperature, humidity and rainfall favor whitefly (*Bemisia tabaci*) multiplication, intensifying MYMV incidence and influencing yield and seed quality. Thus, identifying genotypes with resistance and stability across environments is critical.

Analysis of variance

The pooled ANOVA (Table 1) revealed significant variation among genotypes, locations and their interactions, confirming that yield expression was influenced by both genetics and environment. Location effects contributed 5.43% of total variation, genotypes 23.85% and G × E 16.71%, with minimal replication effects (0.41%), validating experimental precision.

The AMMI analysis partitioned G × E, where IPCA1 and IPCA2 explained 98.5% and 18.09% of the interaction, respectively, with only 1.2% residual variation. This indicated a robust model and strong genotypic differentiation across sites.

The ANOVA (Table 2) across three environments indicated significant differences among genotypes, environments and their interactions for grain yield in MYMV-resistant greengram. The environmental effect was highly significant ($F = 13.22$, $p = 0.032$) and contributed the largest share of the variation (69.5%), underscoring the strong influence of location-specific factors on yield expression. Genotypic effects were also highly significant ($F = 7.26$, $p < 0.001$), explaining 20.3% of the total variance and reflecting sufficient genetic variability for effective selection.

The genotype × environment (G × E) interaction was significant ($F = 1.58$, $p = 0.0058$) and accounted for 5.6% of the total variation, confirming that genotypes responded differently across environments. Replications within environments were non-significant, contributing only 0.2%,

Table 1: Pooled ANOVA for stability (AMMI) for grain yield.

Source of variation	Yield plant ⁻¹			
	DF	MSS	F val	% variation
Replications	3	0.136	0.181	0.408
Genotypes	49	8.65	7.26	23.85
Locations	3	1.811	13.22	5.433
Genotypes × locations	98	1.191	1.58	16.71
IPCA 1	50	1.97	2.62	98.5
IPCA 2	48	0.377	0.5	18.09
Residuals	147	0.752	0.32	1.2

Table 2: ANOVA for stability (AMMI) for grain yield.

Source	Df	Sum Sq.	Mean Sq.	F value	Pr (>F)
ENV	2	3.622193	1.81109633	13.22451	0.032514
REP (ENV)	3	0.41085	0.13695	0.181906	0.908551
GEN	49	424.0712	8.65451519	7.265075	6.11E-17
GEN: ENV	98	116.7424	1.19124928	1.582298	0.00582
Residuals	147	110.6704833	0.752860431		

indicating good experimental precision. The residual variance explained 4.4% of the total, suggesting minimal unexplained variation. Similar findings were also reported by Arunar *et al.* (2024) in mungbean and Sharma *et al.* (2022) in blackgram, where significant genotype, environment and $G \times E$ interaction effects were noted for yield traits, highlighting the importance of multi-environment testing for stable genotype identification. Sheeba *et al.* (2024) further emphasized that environmental variance contributes the major portion of total variability in yield performance of MYMV-resistant greengram genotypes, reaffirming the present results and Dang *et al.* (2024).

Overall, the results emphasize that while environmental factors exerted the greatest influence on yield, both genetic effects and $G \times E$ interactions played a key role in determining the performance of MYMV-resistant greengram genotypes under hotspot conditions.

Detection of genotype and environment interaction (GEI)

$G \times E$ interaction (GEI) poses a substantial challenge in plant breeding, genetics and agronomy, particularly during crop performance evaluations. The inconsistent performance of genotypes across different environments weakens the relationship between observed phenotypes and underlying genotypes, leading to biased estimations of gene effects and combining abilities, especially for traits greatly influenced by environmental factors. This makes selection for such traits considerably more difficult. To effectively address this challenge and improve the accuracy of genotype selection, a combined assessment of both yield potential and environmental stability is crucial for achieving a more precise and efficient selection process.

AMMI biplots provide a powerful visual tool for understanding genotype-by-environment interaction (GEI) in agricultural trials. By analyzing grain yield, its components and grain quality traits, these biplots offer a detailed representation of the AMMI model's results. Two main types exist: AMMI1 biplots, displaying genotype and environment means alongside the first principal component of the interaction (IPCA1) and AMMI2 biplots, plotting the first two principal components of the interaction (IPCA1 and IPCA2). Typically, the x-axis represents the main effects (genotype and environment mean), while the y-axis represents the IPCA1 scores. Interpretation centers on the relationship between main effects and IPCA scores: scores near zero indicate minimal GEI; matching signs on the IPCA axis suggest a positive interaction, while opposing signs indicate a negative interaction (Anandan *et al.*, 2009 and Naresh *et al.*, 2025). This visual approach facilitates the identification of genotypes performing exceptionally well or poorly in specific environments, ultimately enhancing the selection of superior and stable genotypes (Esan *et al.*, 2023; Kona *et al.*, 2024).

The AMMI1 biplot (Fig 1) for grain yield of fifty MYMV-resistant greengram genotypes across three environments revealed that the main effects (genotypes and

environments) explained a substantial proportion of the total variation, as also reported by Rahmati *et al.* (2024) while the first interaction principal component (IPCA1) captured 84.5% of the genotype $\times$ environment ($G \times E$) interaction. Environments E1 and E2, positioned close to the origin with relatively higher yield means, indicated that genotypes such as G11, G39, G40, G43 and G44 performed well under these conditions. In contrast, E3, located on the lower side of the biplot, was associated with genotypes like G6, G20, G24 and G50, suggesting their better adaptation to this environment. Genotypes clustered around the origin (e.g., G2, G10, G8 and G25) were relatively stable with average performance across environments. Similar results were announced by Rani *et al.* (2020) and Singh *et al.* (2022), who observed that a large portion of $G \times E$ interaction in greengram yield was captured by the first IPCA component, indicating that a few principal axes can effectively explain the interaction pattern, which is in line with Rajalakshmi *et al.* (2024).

The AMMI2 biplot (Fig 2), which jointly explains 84.5% of the interaction through PC1 and 15.5% through PC2, provided further insights into $G \times E$ relationships. Environment E2 showed strong interactions with genotypes G11, G17, G35 and G39, while E1 was more closely related with G40 and G44. In contrast, E3 exhibited distinct interaction patterns and favored genotypes such as G1, G6 and G25. Genotypes located near the origin (e.g., G8, G9 and G10) displayed broad adaptability with minimal interaction, suggesting stability across environments.

Overall, the AMMI analysis identified G39, G42, G43 and G44 as high-yielding and specifically adapted to favorable environments (E1 and E2), whereas G6, G2 and G25 were better suited for E3. Several genotypes near the origin demonstrated stable performance, making them potential candidates for broad adaptation under MYMV hotspot conditions. Comparable results were also noticed by Naresh *et al.* (2025) and Anandan *et al.* (2009), who

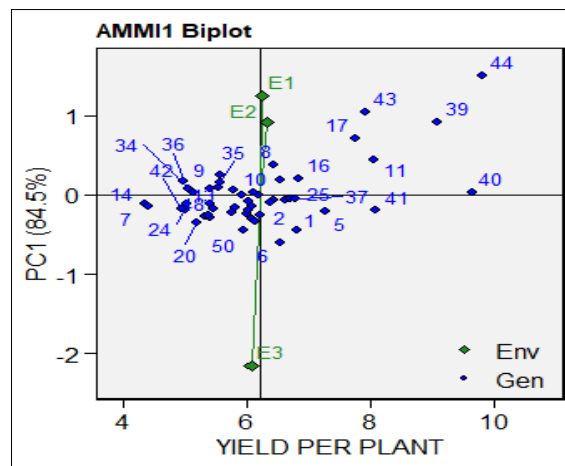


Fig 1: AMMI1 biplot showing genotype $\times$ environment interaction for seed yield per plant in greengram.

observed that AMMI2 biplots effectively discriminate genotype adaptation patterns and environmental interactions in greengram and other legumes.

GGE-biplot analysis

The GGE biplot (Fig 3) provided a comprehensive view of both genotype main effects (G) and genotype $\times$ environment interactions (GE), explaining 85.73% of the variation through PC1 and 11.22% through PC2, together accounting for 96.95% of the total G+GE variation. This high explanatory power indicates the reliability of the biplot in capturing the essential pattern of genotype performance across environments Rao *et al.* (2023).

Environments E1 and E2 were positioned close to each other, indicating similar discriminating ability and representativeness, whereas E3, located distantly, exhibited a unique interaction pattern, suggesting it as a distinct environment influencing genotype performance differently. Genotypes G39, G11, G43 and G44 were plotted in proximity to E1 and E2, confirming their superior and specific performance under favorable conditions, as observed in the AMMI analysis. In contrast, G6, G1 and G40 aligned closely with E3, indicating their adaptation to less favorable or stress-prone environments.

Genotypes G8, G9 and G10, clustered near the origin, showed minimal interaction with environmental vectors and were therefore identified as stable and widely adaptable, corroborating the AMMI-based stability interpretation. The “which-won-where” pattern of the GGE biplot clearly delineated mega-environment groupings, with E1 and E2 forming one favorable cluster and E3 representing a separate environment.

Discriminating ability and representativeness of environments for seed yield

The primary goal of test-environment evaluation is to identify environments that effectively differentiate superior genotypes within a larger, more heterogeneous region (mega-environment). A well-chosen test environment should possess both high discriminatory power and strong representativeness of the mega-environment. Discriminatory power refers to the environment's ability to distinguish between genotypes, identifying the superior ones; representativeness reflects how well the test environment reflects the conditions and variability present within the broader mega-environment (Yan *et al.*, 2007), as also emphasized by Sulthana *et al.* (2025). In a GGE biplot, these characteristics are assessed using the environment vectors. The length of each environment vector, approximately equal to the standard deviation of the data within that environment, represents its discriminatory power: longer vectors indicate greater discriminatory ability. The angle between each environment vector and the average environment coordinate (AEC) reflects its representativeness, which is in agreement with Sood *et al.* (2025).

The discriminatory power of a test environment is directly related to the length of its vector in a GGE biplot. Shorter vectors indicate lower discriminatory ability, meaning the environment is less effective at distinguishing between genotypes. Conversely, longer vectors signify higher discriminatory ability, indicating the environment's effectiveness in differentiating superior genotypes from others. The discriminativeness vs. representativeness biplot (Fig 3) revealed clear differences among the three test environments (E1: Mandya, E2: GKVK and E3: Chamarajanagar) in their ability to discriminate among genotypes for grain yield. The vector length of each environment indicated its discriminating power, while the angle with the Average Environment Coordinate (AEC) represented its similarity to the overall mean environment.

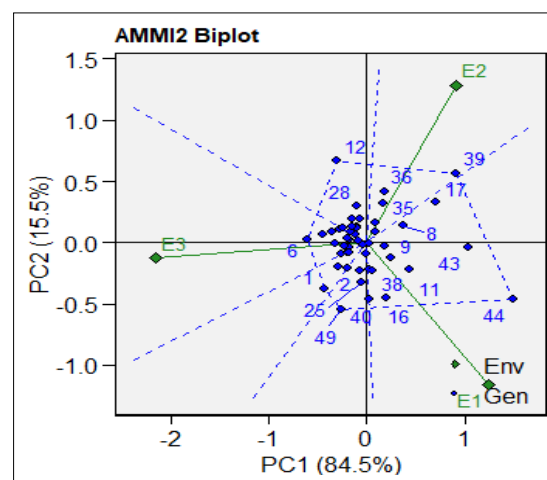


Fig 2: AMMI 2 biplot illustrating genotype $\times$ environment interaction for seed yield per plant in greengram.

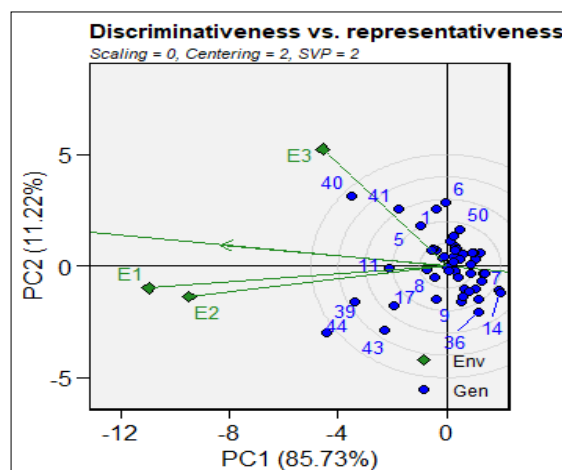


Fig 3: GGE biplot showing discriminativeness and representativeness of test environments for seed yield per plant in greengram.

Among the three sites, Chamarajanagar (E3) exhibited the longest vector, indicating the highest discriminating ability for grain yield per plant. This suggests that E3 was the most informative environment for identifying genotypic differences. Conversely, Mandya (E1) and GKVK (E2) displayed shorter vectors, signifying lower discriminating power.

In terms of representativeness, the smaller angle of Mandya (E1) with the AEC axis suggested that it was the most representative environment, providing yield performance patterns close to the overall mean. In contrast, Chamarajanagar (E3), with a wider angle from the AEC, was less representative but highly discriminative.

Overall, Mandya (E1) can be considered a suitable test site for selecting genotypes with broad adaptability, while Chamarajanagar (E3) is ideal for identifying specifically adapted genotypes. GKVK (E2), being moderately discriminative and representative, serves as a balanced testing environment for evaluating stable yield performance under MYMV hotspot conditions.

Which-won-where' patterns for seed yield per plant

GGE biplots offer a unique "which-won-where" visualization, displayed as a polygon, that effectively illustrates the interaction patterns between genotypes and environments. This feature is valuable in identifying crossover interactions-situations where the ranking of genotypes changes across environments and helps determine the existence of distinct mega-environments (Yan, 2007). Understanding this "which-won-where" pattern is crucial for identifying different mega-environments within a target region and for tailoring genotype recommendations to specific environmental conditions.

In a GGE biplot, if all environment markers fall within a single sector, it suggests that a single genotype consistently outperforms others across all environments. Conversely, if environment markers are distributed across multiple sectors, it indicates that different genotypes perform best in different environments, implying the presence of distinct mega-environments. This is a key characteristic of GGE biplots, stemming from the biplot's inherent inner product properties. Conversely, a genotype located at a sector vertex without any environment markers suggests consistently poor performance across all tested environments.

The "which-won-where" GGE biplot (Fig 4) for grain yield per plant in MYMV-resistant greengram genotypes illustrated clear patterns of genotype performance across the three test environments. The polygon was formed by connecting the outermost genotypes, which represent those with the highest performance in one or more environments. In the present study, G40, G44, G7, G14, G43 and G6 occupied the vertices of the polygon, signifying that these genotypes showed superior yield potential in at least one environment.

Among them, G40 was identified as the winning genotype for Chamarajanagar (E3), which corresponded to the sector containing E3. Similarly, G44 and G39, positioned in the sector associated with Mandya (E1) and GKVK (E2),

were the highest-yielding genotypes in these locations, respectively. The remaining genotypes that fell within the polygon but close to the origin (e.g., G5, G10, G27, G16, G37 and G20) were relatively stable and less sensitive to environmental fluctuations, indicating broad adaptability.

This biplot effectively delineated the presence of three distinct mega-environments, each represented by one of the testing sites (E1, E2 and E3). Genotypes G40, G44 and G39 emerged as potential candidates for specific adaptation, while genotypes near the biplot origin exhibited general adaptability across diverse MYMV hotspot conditions.

Mean performance vs. stability patterns for seed yield per plant

The mean vs. stability biplot (Fig 5) for grain yield per plant revealed distinct differences among the genotypes in both mean performance and stability across the three test environments. The average environment coordination

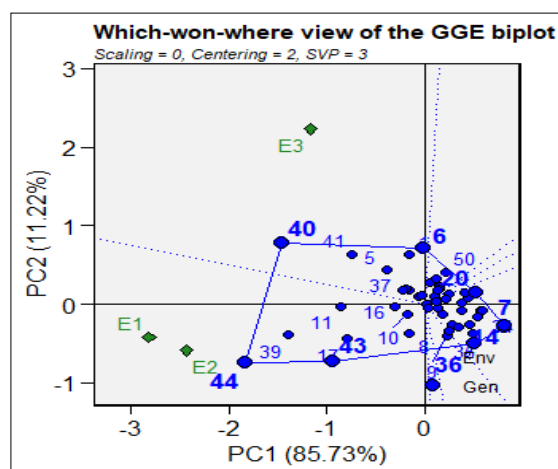


Fig 4: GGE biplot showing "which-won-where" pattern for seed yield per plant in greengram across environments.

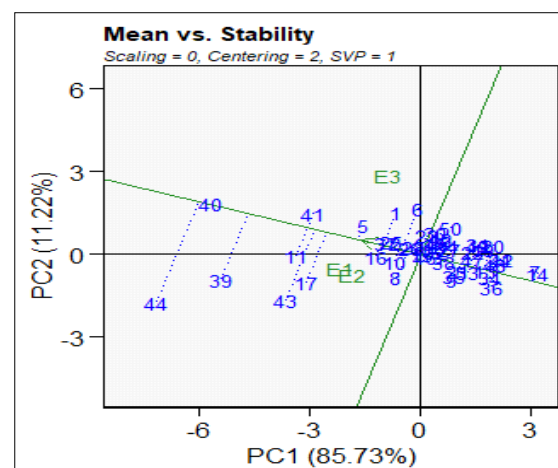


Fig 5: GGE biplot showing mean performance and stability of greengram genotypes for seed yield per plant.

(AEC) abscissa represents the mean yield performance, while the AEC ordinate indicates the stability of each genotype.

Genotypes G40, G41 and G39 were located toward the positive end of the AEC abscissa, indicating above-average yield performance across environments. Among them, G41 appeared closest to the AEC abscissa and exhibited a shorter projection onto the AEC ordinate, suggesting that it was both high-yielding and stable across environments. Similarly, G40 and G39 also demonstrated relatively good stability and consistent performance under varying environmental conditions.

In contrast, G44 and G43 showed larger projections onto the AEC ordinate, implying greater interaction with environments and hence, lower stability, although they possessed moderately high yield potential. Most other genotypes clustered near the origin, indicating average performance with moderate stability across all testing sites. Genotypes such as G40, G41 and G39 demonstrated superior mean performance coupled with high stability, suggesting their adaptability across all test locations. In contrast, G44 and G43 exhibited specific adaptation to particular environments but showed reduced stability. The clustering of several genotypes around the origin of the biplot indicated moderate yield performance and adaptability.

Overall, the integration of multi-environment trials and biplot analyses proved effective in identifying stable and MYMV-resistant genotypes suitable for breeding and large-scale cultivation. Among the evaluated materials, G40 emerged as the most desirable and stable performer across environments, making it a promising candidate for advancement in greengram improvement programs targeting both yield potential and MYMV resistance.

CONCLUSION

The study revealed significant genotype $\times$ environment interaction for seed yield among MYMV-resistant greengram genotypes. AMMI and GGE biplot analyses identified G8, G9, and G10 as stable and widely adaptable across environments. Genotypes G39, G40, G43 and G44 showed better performance under favorable conditions, indicating specific adaptation. The results confirmed the usefulness of AMMI and GGE models in identifying stable and high-yielding genotypes under MYMV hotspot conditions. These promising genotypes can be effectively utilized in future greengram improvement and resistance breeding programs.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

The authors declare that they have no conflict of interests or personal relationships that could have appeared to influence the work reported in this paper.

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