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GENETIC VARIABILITY STUDIES ON YIELD AND YIELD RELATED TRAITS IN MUNGBEAN MINI-CORE

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ABSTRACT

Mungbean (*Vigna radiata* L. Wilczek) is a short-duration legume of major nutritional and agronomic importance, yet its productivity remains constrained by a narrow genetic base and susceptibility to biotic and abiotic stresses. The present study evaluated 230 genotypes from the mini-core collection under an alpha-lattice design to assess genetic variability, trait associations, and genetic divergence for six key traits: days to 50% flowering (DF), days to maturity (DM), pod length (PL), number of pods per plant (NPP), seeds per pod (SPP), and yield per plant (YPP). Descriptive statistics revealed substantial variation across all traits, with wide ranges and diverse distribution patterns. ANOVA confirmed highly significant genotypic differences, indicating ample exploitable variability, with PL, SPP, and DM emerging as traits under strong genetic control. Correlation and path analyses identified NPP as the most important determinant of yield, exerting the highest direct positive effect on YPP, underscoring its value as a selection criterion. Mahalanobis D^2 analysis grouped the genotypes into eight clusters, with maximum divergence observed between Clusters I and VIII, highlighting their potential for generating heterotic combinations. Overall, the findings provide a comprehensive framework for parental selection and breeding strategies aimed at improving mungbean productivity and adaptability.

***Key words*:** *Vigna radiata*, genetic variability, heritability, genetic advance, correlation, yield traits

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is a vital short-duration legume widely cultivated across Asia and parts of Africa. It contributes substantially to food and nutritional security, being a rich source of protein (20–25%), minerals, and vitamins (Nair *et al.*, 2019). In India, Myanmar, China, and Thailand, mungbean forms an integral part of traditional cropping systems, often cultivated as a catch crop or relay crop due to its short life cycle and adaptability (Pratap *et al.*, 2022). Globally, mungbean cultivation spans over 7 million hectares, yet productivity remains low (~0.7–0.9 t/ha) compared to its yield potential of 2.5–3.0 t/ha (FAO, 2023).

The productivity gap is largely attributed to a narrow genetic base, susceptibility to major pests and diseases such as yellow mosaic virus (YMV), powdery mildew, and bruchids, as well as abiotic stresses like drought and heat (Nair *et al.*, 2019). Additionally, limited investment in breeding programs and inadequate exploitation of genetic variability have constrained genetic gains. Given its significance, systematic efforts are needed to broaden the genetic base and identify stable, high-yielding cultivars suited to diverse environments.

Genetic variability studies are the foundation of crop improvement programs. Correlation analysis is another essential tool in breeding, as it quantifies relationships among yield and its component traits. However, correlations alone do not reveal whether the association is due to direct or indirect effects. Path coefficient analysis, introduced by Wright and later applied to plant

Table 1: Descriptive statistics for yield and yield related traits.

	Range	Min	Max	Mean	Std. Dev	Variance	Skewness	Kurtosis
DF	27.00	29.00	56.00	39.46	4.08	16.66	0.43	2.06
DM	83.00	0.00	83.00	64.13	9.31	86.60	-1.17	8.26
NPP	27.67	3.33	31.00	12.43	5.24	27.48	0.96	0.94
PL	7.33	3.25	10.58	6.78	1.08	1.18	0.03	1.03
SPP	10.67	2.00	12.67	8.54	2.40	5.78	-0.92	0.42
YPP	7.01	0.66	7.67	3.10	1.24	1.53	0.38	0.09

DFF- Days to fifty per cent flowering; DM – days to maturity; NPP- number of pods per plant; SPP- Number of seeds per pod; YPP- yield per plant

breeding by Deway & Lu (1959), partitions correlations into direct and indirect effects, providing deeper insights into trait interrelationships. This makes it invaluable for identifying the most effective selection criteria (Kumar *et al.*, 2020).

Assessment of genetic divergence using Mahalanobis D^2 statistics is equally important. It allows the grouping of genotypes into distinct clusters based on multivariate trait data, thereby guiding the selection of diverse parental combinations for hybridization. Tocher's method provides a systematic clustering approach, identifying genotypes with maximum inter-cluster divergence as potential candidates for heterosis breeding. Studies in mungbean and other legumes have demonstrated the utility of D^2 statistics in broadening genetic diversity (Singh *et al.*, 2018).

The present investigation was carried out on 230 mungbean genotypes to (i) assess the extent of genetic variability, (ii) study the correlation and path coefficients among traits to identify effective selection criteria, and (iii) evaluate genetic divergence using Mahalanobis D^2 statistics to identify divergent parental lines for hybridization. These findings aim to provide a comprehensive framework for mungbean improvement programs.

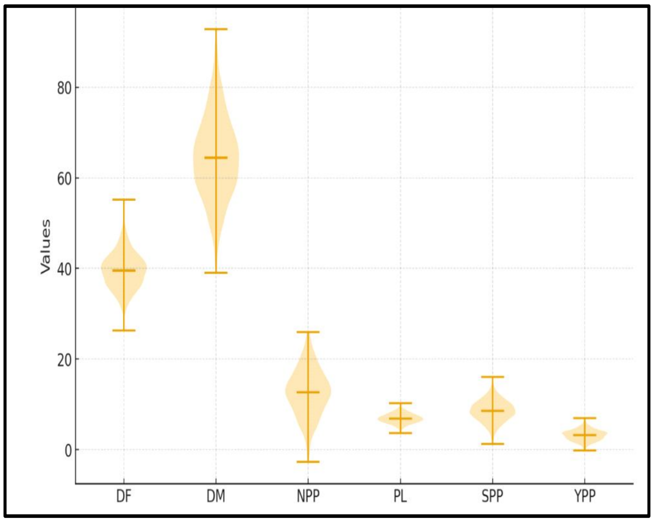

Fig. 1: Violin plot depicting the frequencies of different traits.

Material and Methods

The experimental material comprised 230 mungbean genotypes from the mini-core collection, evaluated during Summer 2024 at Patancheru, Hyderabad (17.53°N, 78.27°E, 545 m above mean sea level). The site has a semi-arid climate, with average summer temperatures ranging between 24°C and 42°C. The soil wasvertisols, low in organic matter but adequate in phosphorus and potassium. The crop was sown under irrigated conditions to minimize drought stress.

The experiment was laid out in an alpha-lattice design with two replications. Each plot consisted of two rows, 2 m in length, with spacing of 15 cm between rows and 10 cm between plants. Standard agronomic practices, including weeding, irrigation, and pest management, were followed to ensure uniform crop growth. Data were recorded on six quantitative traits: days to 50% flowering (DF), days to maturity (DM), pod length (PL), number of pods per plant (NPP), seeds per pod (SPP), and yield per plant (YPP).

Descriptive statistics, including mean, range, standard deviation, skewness, and kurtosis, were computed using SPSS v26. Analysis of variance (ANOVA) was carried out following standard procedures to test for significant differences among genotypes. Trait associations were studied using Pearson correlation coefficients. Path coefficient analysis was performed according to Deway & Lu (1959) to partition trait correlations into direct and indirect effects on yield per plant. Genetic divergence was assessed using Mahalanobis D^2 statistics (Mahalanobis, 1936), and clustering was performed using Tocher's method, grouping genotypes into distinct clusters based on inter-genotypic distances.

Results And Discussion

Descriptive statistics

Descriptive statistics were computed for six quantitative traits across all the genotypes (Table 1). Substantial variation was observed, as reflected by wide ranges, moderate to high standard deviations, and diverse skewness–kurtosis patterns.

Table 2: Analysis of variance for yield and its attributes.

Trait	Source	df	Sum of Squares	Mean Square	F Value
DF	Replication	1	11.27	11.27	0.708
	Genotype	229	4023	17.57	1.103*
	Block(Rep)	22	317	14.39	0.904
	Residual	207	3297	15.93	
DM	Replication	1	507.7	507.7	9.879
	Genotype	229	18857	82.3	1.603**
	Block(Rep)	22	1592	72.4	1.408*
	Residual	205	10534	51.4	
PL	Replication	1	0.74	0.74	1.489
	Genotype	229	428.2	1.87	3.754**
	Block(Rep)	22	8.2	0.37	0.748
	Residual	207	103.1	0.5	
NPP	Replication	1	72.14	72.14	2.914
	Genotype	229	6952	30.36	1.226**
	Block(Rep)	22	465	21.12	0.853
	Residual	207	5124	24.76	
SPP	Replication	1	0.68	0.68	0.147
	Genotype	229	1612.4	7.04	1.529**
	Block(Rep)	22	86.7	3.94	0.856
	Residual	207	953.4	4.61	
YPP	Replication	1	15.42	15.42	10.992
	Genotype	229	340.9	1.49	1.061*
	Block(Rep)	22	53.5	2.43	1.734
	Residual	207	290.3	1.4	
DFF- Days to fifty per cent flowering; DM–days to maturity; NPP- number of pods per plant; SPP- Number of seeds per pod; YPP- yield per plant					

Substantial variability was evident across all six traits studied in mungbean, reflecting the genetic diversity within the mini-core collection. Days to 50% flowering (29–56 days; mean 39.46) showed moderate variation, with positive skewness indicating a predominance of early-flowering lines that could be targeted for short-duration cropping systems. Days to maturity displayed the widest range (45–83 days; mean 64.13), with high variance and a leptokurtic distribution pointing to strong clustering around late-maturing genotypes. Such diversity provides scope to select both early and late types suited to contrasting environments. Yield components also exhibited broad variation: number of pods per plant (3.33–31; mean 12.43) had high variance and positive skewness, suggesting many low- to moderate-podded lines with a few high-podded types, while pod length (3.25–10.58 cm; mean 6.78) was relatively stable with limited extremes.

Seeds per pod (2–12.67; mean 8.54) showed moderate variation, with negative skewness reflecting a predominance of higher-seeded genotypes. Yield per plant ranged widely (0.66–7.67 g; mean 3.10), with positive skewness indicating a majority of low-yielding lines but with some high-performing entries offering promise for improvement. Overall, traits such as days to maturity, pods per plant, and yield per plant exhibited the broadest variability, confirming their importance as key differentiating factors among genotypes. The mixture of normal and skewed trait distributions underscores the complexity of yield determination in mungbean.

The descriptive statistics highlight ample exploitable variability in the studied genotypes, with yield potential strongly linked to pod number and maturity duration. Early-flowering lines, high-pod genotypes, and high-seeded types represent particularly valuable targets for selection.

Analysis of Variance

The ANOVA results revealed significant genotypic differences for all the traits studied.For DF and DM, genotypic variation was significant, with additional replication and block effects observed for DM. This indicates that while maturity duration is largely genetically controlled, it is also influenced by micro-environmental heterogeneity, underscoring the importance of proper experimental design and replication in evaluating this trait. Pod length and seeds per pod exhibited strong genetic control, as indicated by highly significant genotypic effects and negligible environmental influence. These traits, being directly associated with yield components, offer reliable targets for selection. An investigation done by Reddy *et al.*, (2011) revealed that genotypes differed significantly for all the characters studied. These results were confirmed with the experiment conducted by Patel *et al.*, (2012) and Hemavathy *et al.*, (2015). Contradictory results were shown by Khan *et al.*, (2004) in which highly significant genetic differences were observed for days to fifty per cent flowering.

NPP also showed significant genotypic differences with minimal environmental influence, highlighting its

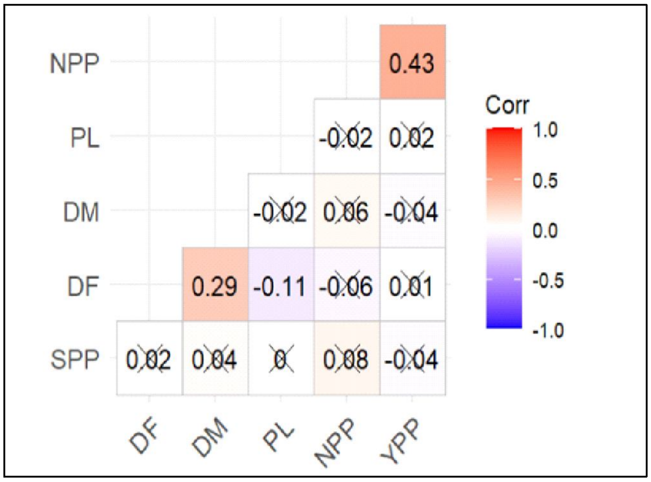

Fig. 2: Heat map indicating the correlations between yield and yield related traits.

Table 3: Path coefficient analysis of yield and yield attributing traits.

Trait	Direct Effect on YPP	Total Indirect Effect	Correlation with YPP	Via DF	Via DM	Via PL	Via NPP	Via SPP
NPP	0.446	-0.015	0.431	0	-0.023	-0.004	-0.027	-0.002
DF	0.062	-0.056	0.006	0.018	0	-0.001	0.029	-0.003
PL	0.035	-0.016	0.018	-0.007	0.002	0	-0.011	0
SPP	-0.07	0.034	-0.036	-0.004	-0.005	-0.001	0	-0.005
DM	-0.079	0.043	-0.035	0.001	-0.003	0	0.035	0

potential as a dependable selection criterion for yield improvement. Yield per plant displayed significant genotypic variation; however, it was also affected by block and replication effects, suggesting that yield expression is more sensitive to environmental fluctuations than its component traits. This emphasizes the need for multi-location and multi-season evaluation to identify stable, high-yielding genotypes.

Thus, ANOVA confirmed substantial genetic diversity across all traits, with pod length, seeds per pod, and days to maturity emerging as the most strongly governed by genetic factors. These traits, along with pods per plant, represent key targets for effective selection. Although yield per plant is genetically variable, its environmental sensitivity necessitates broader testing to ensure stability. This variability is consistent with earlier reports in mungbean and other legumes (Raturi*et al.,* 2012; Das *et al.,* 2025). The results underline that both yield and its contributing traits can be exploited in breeding programs to develop improved genotypes with enhanced productivity and adaptability.

Correlation Studies

A Pearson correlation analysis was conducted to examine the relationships between various agro-morphological traits: Days to Flowering (DF), Days to Maturity (DM), Pod Length (PL), Number of Pods per Plant (NPP), Seeds per Pod (SPP), and Yield per Plant (YPP). The analysis revealed several key associations that can inform breeding strategies for crop improvement.

There was a moderate, positive, and statistically significant correlation between the Number of Pods per Plant (NPP) and Yield per Plant (YPP), with a correlation coefficient of r=0.43. This was the strongest positive association observed, suggesting that NPP is a primary yield-contributing trait. Therefore, selecting for an increased number of pods per plant appears to be a direct and effective strategy for enhancing crop yield.

A weak but significant positive correlation was found between Days to Flowering (DF) and Days to Maturity (DM) (r=0.29). This is biologically logical, indicating that plants that take longer to initiate their reproductive phase (flowering) also tend to have a longer overall lifecycle leading to maturity. Conversely, a very weak negative correlation was observed between Days to Flowering (DF) and Pod Length (PL) (r = –0.11). These results align with the conclusions of Kaur *et al.,* (2024) that multi-trait selection strategies, based on genetic parameters and correlations, can accelerate mungbean yield improvement. The previous studies on mungbean by Manivelan *et al.,* (2019), Divya *et al.,* (2018), Azam *et al.,* (2018), Bhutia *et al.,* (2016) also reported a significant and positive association with different parameters in mungbean.

Path analysis

Path coefficient analysis was undertaken to partition the correlation of component traits with grain yield per plant (YPP) into their direct and indirect effects. Among the yield components, number of pods per plant (NPP) exerted the highest direct positive effect (0.446) on YPP, followed by days to flowering (DF; 0.062) and pod length (PL; 0.035). In contrast, days to maturity (DM; –0.079) and seeds per pod (SPP; –0.070) registered direct negative effects on yield. The indirect pathways revealed notable contributions. DM exhibited the highest positive indirect effect (0.043), mediated primarily through NPP, whereas SPP contributed indirectly to YPP via NPP (0.035). DF, despite its small positive direct effect, exerted a negative total indirect effect (–0.056), mainly through

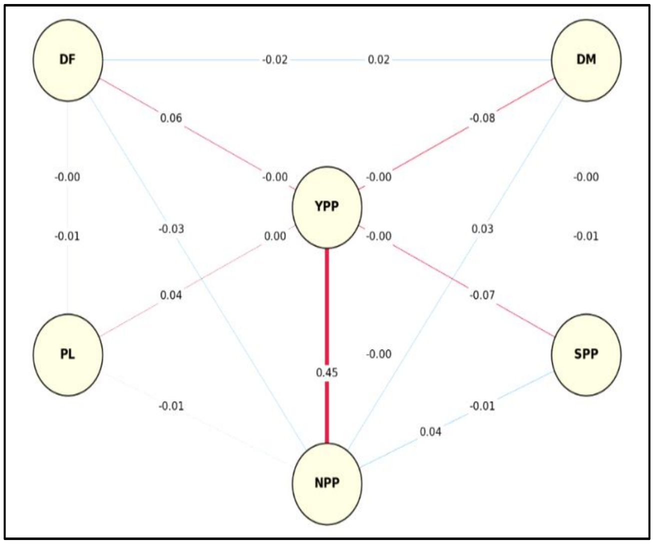

Fig. 3: Scatter plot depicting the partitioning of correlation.

Table 4: Average Intra and inter-cluster Mahalanobis D^2 distances among 8 clusters.

Cluster	1	2	3	4	5	6	7	8
1	8	13.51	15.09	19.18	17.13	14.94	15.98	24.06
2	13.51	7.12	12.43	11.97	12.98	11.78	16.3	13.19
3	15.09	12.43	6.52	12.66	12.9	10.78	14.05	11.99
4	19.18	11.97	12.66	8.76	14.79	13.3	17.36	17.33
5	17.13	12.98	12.9	14.79	9.08	10.95	16.11	15.44
6	14.94	11.78	10.78	13.3	10.95	6.49	13.04	12.19
7	15.98	16.3	14.05	17.36	16.11	13.04	3.47	13.84
8	24.06	13.19	11.99	17.33	15.44	12.19	13.84	6.55

DM and NPP. Similarly, PL and SPP, although having direct negative or weak positive contributions, influenced yield indirectly through other characters.

Overall, the correlation coefficients of component traits with YPP reflected the balance between their direct and indirect effects. NPP had the strongest positive correlation with YPP (0.431), while DF and DM showed negligible or negative correlations despite some indirect contributions. The results indicate that NPP is the most important determinant of yield per plant, given its strong positive direct effect as well as its substantial positive correlation with yield. Thus, NPP can be considered the most reliable selection criterion for enhancing yield potential. These findings are in agreement with earlier reports in pulses and cereals where NPP was identified as the key driver of yield by Divya *et al.,* (2018) and Marawar *et al.,* (2020).

On the other hand, DF and DM, though agronomically important, displayed low or negative associations with yield. The negative direct effect of DM suggests that prolonged crop duration may not favour yield under the studied environments, possibly due to stress conditions or reduced efficiency of assimilate partitioning. PL and SPP had relatively smaller direct effects, yet their indirect contributions through NPP highlight their complementary role in influencing yield. This suggests that while longer pods and higher seed counts per pod are desirable, their ultimate impact on yield is largely mediated via their contribution to NPP.

Mahalnobis D^2 Analysis

Mahalanobis D^2 statistics revealed the presence of eight distinct clusters among the evaluated genotypes, indicating considerable genetic divergence. The distribution of genotypes across clusters was highly uneven, with Cluster VI accommodating the largest number of genotypes (61), followed by Cluster V (49) and Cluster III (40). In contrast, Cluster VII contained the least number of genotypes (8), suggesting the presence of rare or unique lines with specific characteristics. The clustering pattern indicates broad genetic variability among the material studied, which is essential for effective selection and crop improvement.

Intra-cluster divergence

The intra-cluster D^2 values (diagonal elements) ranged from 3.47 (Cluster VII) to 9.08 (Cluster V). Cluster VII exhibited the lowest intra-cluster distance, signifying close genetic relatedness among its genotypes. In contrast, Cluster V showed the highest intra-cluster distance, suggesting greater heterogeneity within its members. This indicates that genotypes from Cluster V may offer scope for within-cluster selection, while Cluster VII genotypes may be more uniform.

Inter-cluster divergence

The inter-cluster distances varied widely, with the minimum observed between Cluster III and VI (10.78), followed by Cluster VI and V (10.95). This suggests that these clusters share a relatively narrow genetic base, possibly due to common ancestry or similar selection pressures. Conversely, the maximum inter-cluster distance was recorded between Cluster I and VIII (24.06), followed by Cluster IV and VII (17.36) and Cluster IV and VIII (17.33), indicating substantial genetic divergence. Hybridization involving genotypes from these widely separated clusters could generate high heterotic combinations and broad variability in segregating generations.

The identification of divergent clusters is crucial for the selection of parental lines in breeding programs. Genotypes from Cluster I and VIII, owing to their wide divergence, can be exploited in hybridization to maximize heterosis and transgressive segregation. Meanwhile, clusters with moderate to low divergence (e.g., III vs. VI, V vs. VI) may contribute to incremental improvement of specific traits. The presence of both large heterogeneous clusters (e.g., VI, V, III) and small homogeneous clusters (e.g., VII, I) provides a rich source of genetic diversity that can be strategically utilized in crop improvement programs targeting yield, resilience, and quality traits.

The I × VIII cross emerged as the most divergent combination, followed by IV × VII and IV × VIII. These cluster pairs represent ideal candidates for hybridization to harness heterosis and broaden the genetic base. At the same time, crosses among clusters with moderate divergence (e.g., III × VI, V × VI) may contribute to incremental improvements with relatively stable performance.

Conclusion

The mungbean mini-core evaluated in this study exhibited substantial genetic variability for yield-related traits, with high heritability across all traits. SPP and NPP, in particular, offer excellent prospects for improvement through direct selection. The strong association between SYP and NPP indicates potential for simultaneous enhancement. The identified promising traits can be effectively utilized in breeding programs to develop high-yielding mungbean varieties.

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