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RESEARCH ARTICLE

Deciphering Genetic Variability and Stability for Yield Improvement in Mungbean (*Vigna radiata*)

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Abstract

Mungbean [*Vigna radiata* (L.) R. Wilczek] is an important short-duration and widely adaptable pulse crop known for its nutritional and soil-ameliorative properties. However, its productivity still lags due to photo- and thermo-period sensitivity, the seasonal specificity of the available cultivars, and susceptibility to a wide range of biotic and abiotic factors. Therefore, breeding for developing stable elite cultivars is urgently required to improve productivity. A total of 55 genotypes of mungbean, including released varieties and elite lines, were tested over a period of three years to identify the stable elite lines for high yield. A wide range of variability was recorded for seed yield per plant (SYP) and its key component traits. Based on correlation coefficient analysis, PL and NSP were found to be key components. The significant interaction of genotype × year indicated the crucial role of the environment on SYP. The correlation coefficient analysis revealed that pod length (PL) and number of seeds per pod (NSP) were key yield contributing traits. GGE biplot analysis demonstrated that five genotypes, i.e. G42 (BMS 19-3), G17 (Shikha), G49 (ML 134), G18 (TRAM-18), and G27 (BMS 18-4), were found most stable and high-yielding genotypes over the year. Further, the molecular characterisation of these selected genotypes with SSR and functional markers opens the scope for their effective utilization in the mungbean breeding programme.

Keywords: Adaptability, DNA fingerprinting, Functional markers, Greengram, G × E interaction, Promising genotypes, Stability, SSR

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Introduction

Mungbean [*Vigna radiata* (L.) R. Wilczek] is an important short-duration grain legume that is cultivated over a wide range of environments (Singh *et al.,* 2022). It is rich in protein (25-28%) and several micronutrients (Pratap *et al.,* 2022; Zafar *et al.,* 2023). It improves the soil health by fixing the free atmospheric nitrogen into the soil and also improves the carbon content of the soil, which leads to yield improvement of the subsequent crop (Diatta *et al.,* 2020; Arya *et al.,* 2024). However, the productivity of mungbean is quite low due to several factors such as non-availability of quality seeds of improved varieties, abiotic and biotic stresses, poor crop management practices, low harvest index and post-harvest losses (Nair *et al.,* 2019; Pratap *et al.,* 2019).

Yield is a complex trait that always depends on its component traits and is determined by its genotype, environment and their interactions (Kumar *et al.,* 2023a; Kumar *et al.,* 2023b). Hence, consideration of environmental effect is necessary as many factors overshadow the genetic potential of the genotype and lead to their low performance (Parihar *et al.,* 2022; Bomma *et al.,* 2024; Sadaiah *et al.,* 2026; Irfan *et al.,* 2026). The significant gap between the observed yield and the potential yield of any cultivar occurs due to its variable

performance in different environments and the major reason behind this is the lack of performance stability.

Genotype by environment interaction (GEI) provides opportunities to select genotypes that interact positively with a specific environment (specific adaptation) or record outstanding performance in a wider range of environments (general adaptation). Further, it helps the breeders for a robust evaluation and appropriate selection of genotypes for yield stability over the environments or adaptability in the target environment (Abou-Khater *et al.,* 2022; Rao *et al.,* 2023; Wodebo *et al.,* 2023; Shobeiri *et al.,* 2024; Jafarullakhan *et al.,* 2024; Mohammadi *et al.,* 2024; Ortiz *et al.,* 2024; Kona *et al.,* 2024; Torres-Ordoñez *et al.,* 2024; Ma *et al.,* 2024). The characterization of identified genotypes for breeding programmes also needs attention for their effective utilization in further breeding programmes. Molecular markers have evolved as a unique tool for assessing genetic variability under the influence of the environment. Nowadays, various marker systems are available (Kyu *et al.,* 2024; Kohli *et al.,* 2024; Sao *et al.,* 2025; Ghallab *et al.,* 2025). Previous workers also gave emphasis on various types of omics approaches for characterizing the *Vigna* species for crop improvement (Raizada *et al.,* 2019; Altaf *et al.,* 2026; Pookhamsak *et al.,* 2026). Chugh *et al.,* (2022) also focused on molecular tools for improving the oilseeds and legumes. Keeping the above in view, the present study was undertaken with 55 genotypes of mungbean to evaluate the influence of G × E interaction on seed yield and its component traits; and identify the high yielding stable mungbean genotype for cultivation.

Materials and Methods

Plant materials, field experimentations and data recording

The present experiment was conducted with 55 genotypes of mungbean, including released varieties, breeding lines and checks (Supplementary Table 1). The experiments were conducted at the Research Farm of Banda University of Agriculture and Technology, Banda (25.5°N, 80.3°E and 113 MSL), India. The experiments were laid out in randomized block design (RBD) with three replications during *kharif* 2020-22. Each entry was grown in four rows of 2m length with 45 cm × 10 cm plant geometry. All the cultural operations were carried out as per the standard package and practices recommended for raising a good crop in the region. Harvesting of the crop was done twice, first through pod picking when >75% pods were mature and final harvesting was done after 10 days of the first picking. The observations were recorded on six important yield traits and their contributing traits, such as days to maturity (DM), number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), seed index (SI) and seed yield per plant (SYP). All the traits except DM were recorded on five random plants and averaged in each entry in each replication, whereas DM was calculated on a plot basis.

Statistical analysis

The data analysis for two-way ANOVA, genetic parameters and correlation coefficient were done by using R-Statistical software version 4.0 (package "Metan"). The GGE biplot analysis for SYP was done by estimating each element of the matrix using GEA-R software.

DNA extraction and fingerprinting of selected promising genotypes

Six mungbean genotypes, including two elite lines such as G42 (BMS 19-3), G27 (BMS 18-4); three released varieties, i.e. G17 (Shikha), G49 (ML 134), G18 (TRAM-18), and one check variety (IPM 02-3), were subjected to DNA fingerprinting. The 200 mg tiny leaves of selected genotypes were frozen in liquid nitrogen and homogenized using tissuelyser-II (Qiagen). The homogenized samples were further subjected to DNA extraction using Qiagen's DNeasy® Plant Mini Kit as per the manufacturer's protocol. After extraction, the quality of extracted DNA was examined on 0.8% agarose gel and quantified using Nano Drop (Qiagen QIAxpert). Further, the set of 12 markers (10 functional and 2 SSR) were used for the fingerprinting of genotypes through polymerase chain reaction (Supplementary Table 2). The 20 µL PCR reaction mix, 10 µL of PCR master mix (Thermo Scientific), 1 µL of each forward and reverse primer, and 6 µL nuclease-free water were mixed with 2 µL genomic DNA. The polymerase chain reaction (PCR) amplification was carried out in a thermo-cycler (Veriti, Applied Biosystems) with the programming: initial denaturation at 95℃for 3 min, followed by 35 cycles of denaturation at 95℃for 30 sec, annealing (52-58°C) for 30 sec, extension at 72°C for 30 sec, and the final extension for 7 min at 72°C. Thereafter, the amplified PCR product was resolved through electrophoresis in 3% (w/v) agarose gel containing 0.5 µg/mL ethidium bromide. A 1kb DNA ladder (Thermo Scientific) was utilized in gel electrophoresis to determine the size of the amplicons. The gels were visualized under a gel documentation unit (Vilber E-box).

Results

Genetic variability assessment

The two-way ANOVA showed significant differences (P<0.05) among the yield and yield components for all traits under study (Table 1). The effect of year was also found to be significant for all the traits, except PL. In contrast, the genotype × year interaction was non-significant for most of the traits, except for SYP.

The boxplots (Fig. 1) illustrate the distribution of six traits under study, i.e. DM, NPP, PL, NSP, SI and SYP, across three years. Two traits, such as DM and PL, did not differ significantly across the years and were found to be relatively stable. In NPP, Year 1 showed the highest median value, Year 3 the lowest median value, while Year 2 was found intermediate. For NSP, Years 1 and 2 were statistically similar and superior to Year 3. The SI exhibited a significant decline from Year 1 and Year 2 to Year 3, showing that environmental conditions in Year 3 negatively affected this trait. The most pronounced difference was observed for SYP, where Year 1 recorded the highest yield, followed by Year 2 and then Year 3, with

Table 1: Pooled analysis of variance for different traits in mungbean during *kharif* 2020-22

	DF	DM	NPP	NSP	PL	SI	SYP
Genotype	54	280.07**	443.67**	4.531**	7.95**	3.40**	21.47**
Year	2	57.69**	569.71**	27.45**	0.16	12.61**	417.91**
Gen × Year	108	2.89	9.96	0.093	0.06	0.07	1.004**
Residuals	324	3.30	8.32	0.14	0.081	0.06	0.500
Mean	-	63.68	20.92	10.34	7.72	3.62	8.43
CV (%)	-	2.71	9.55	13.67	18.31	27.60	11.85

**P<0.01 level of significance.

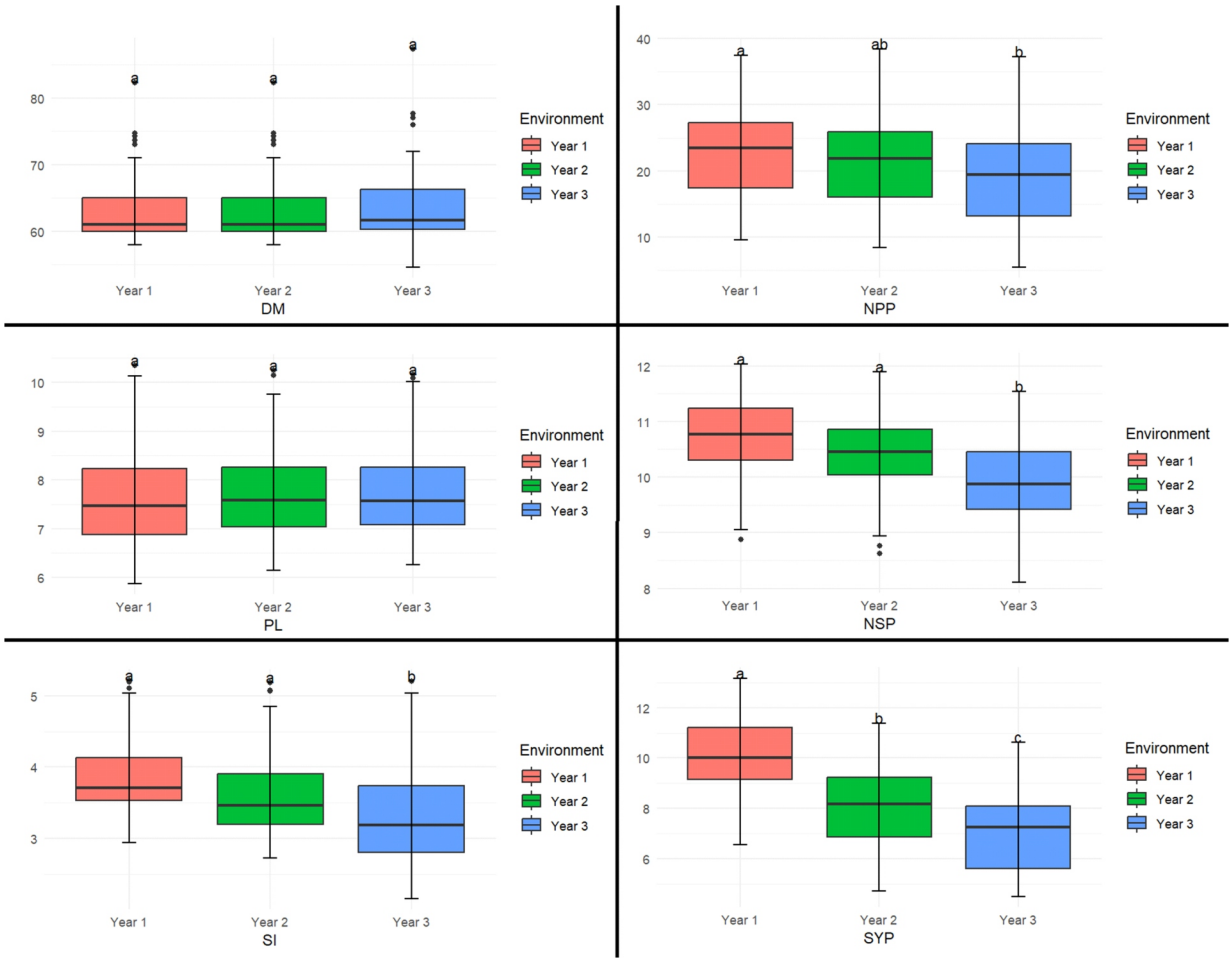

Fig. 1: Box plot analysis of 55 mungbean genotypes across the three years.

all years differing significantly from each other. Overall, the results indicate that environmental variation had little influence on DM and PL, whereas NPP, NSP, SI, and especially SYP were substantially affected by year-to-year changes, resulting in reduced performance under the conditions prevailing in Year 3.

Trait association analysis

Correlation analysis showed a strong, significant association between SYP and PL (r = 0.74, P<0.001) (Fig. 2). NSP exhibited a positive and significant correlation with PL (r = 0.61, P<0.001) and SYP (r = 0.61, P<0.001), indicating that these qualities contribute considerably to yield enhancement. SYP showed strong positive associations with DM (r = 0.29, P<0.05) and PL (r = 0.35, P<0.01), but non-significant with NSP (r = 0.23). The SI had a substantial positive correlation with DM (r = 0.40, P<0.01).

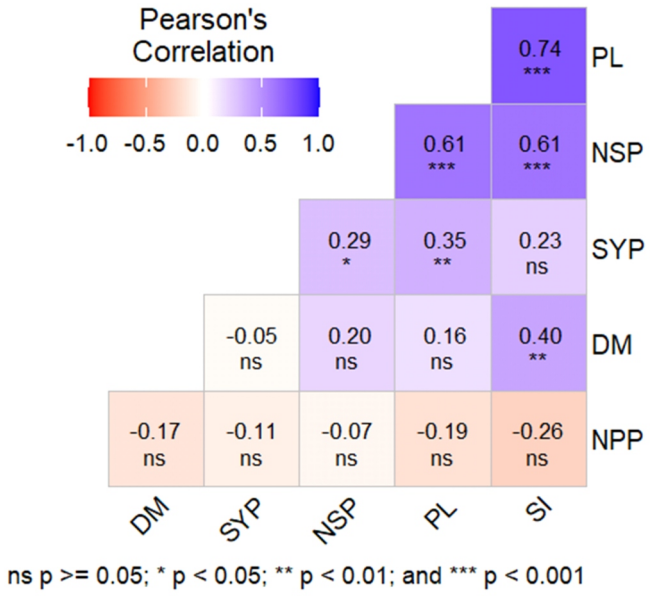

Fig. 2: Pearson's correlation matrix depicting relationships among yield and its component traits. DM, Days to maturity; NPP, Number of pods per plant; PL, Pod length; NSP, Number of seeds per pod; SI, Seed index; SYP, Seed yield per plant; ns, non-significant.

Genetic parameters

The result revealed that the PCV was slightly higher than the corresponding GCV for all the traits (Table 2). Out of six traits studied, only NPP exhibited high GCV and PCV estimates, whereas three traits, such as PL, SI and SYP, exhibited moderate GCV and PCV estimates. The traits, i.e. DM and NSP, showed low GCV and PCV estimates. In terms of heritability, all the traits showed high heritability. The high GCV, PCV, and heritability coupled with high GAM were recorded for NPP, PL, SI and SYP, whereas the traits such as DM and NSP showed high heritability coupled with moderate GAM, but the extent of GCV and PCV was low to moderate.

GGE biplot analysis

The GGE biplot is an effective approach to identify the ideal genotypes for the target trait under the specific or macro environments correctly. The ideal genotype should have superiority for the target trait in terms of mean performance, in addition to the minimum interactions with the environment. The biplot view ranked the genotypes based on the average yield of test entries over the three years. PC 1 explained about 55.36% variability, whereas PC 2 explained 42.93% of the total variations of the year, which indicated the cumulative variation of 98.29% (Fig. 3A). Each genotype positioned along the AEC axis illustrated its average performance across the environments, while the length of the perpendicular projection from the AEC axis denoted the stability of genotypes. In this study, G27, G48, G25, G47, G5, G50, G22 and G26 had superior mean performance and the most stable genotypes across the environments. The proximity of these genotypes to the ideal genotype position further validated their superior adaptability and reliable performance across the environments. These genotypes thus signify interesting prospects for extensive trials and prospective application in future breeding projects focused on enhancing adaptation and performance stability. The

Table 2: Analysis of genetic parameters of different traits in promising genotypes of mungbean

	DM	NPP	PL	NSP	SI	SYP
Maximum	87.33	38.43	10.35	12.03	5.21	13.17
Minimum	54.67	5.47	5.88	8.11	2.16	4.49
Mean	63.68	20.92	7.72	10.34	3.62	8.43
CD 5%	1.58	2.93	0.25	0.30	0.24	1.00
GCV (%)	8.56	32.60	11.90	6.68	16.51	17.38
PCV (%)	8.70	33.72	12.07	6.91	17.03	18.86
Heritability (bs) (%)	97.00	93.00	97.00	93.00	94.00	85.00
GA % of mean (GAM)	17.36	64.91	24.17	13.29	32.98	33.00

environment plays an important role in the projection of the phenotype in the case of quantitative traits. Therefore, screening of genotypes under multiple environments would be more effective to tag the potential genotypes. Discrimination and representativeness are based on the ability to discriminate the test genotypes, the ability to represent the mega environment and their joint response. In the GGE biplot, the lengths the vectors demonstrated the discrimination ability, while the angle between the environmental vectors and the AEC abscissa shows the representativeness of the testing location. Among the three test environments, E3 had the longest environmental vectors, indicating the most "discriminating year" followed by E2 and E1 (Fig. 3B). However, E2 followed by E1 showed a minimum angle with the average environment, which indicated that these were the most ideal testing years, accounting for both discrimination ability and representativeness. The results demonstrated the polygon view with six genotypes, namely G27, G42, G2, G32, G44 and G6 at the vertices (Fig. 3C). All three test years were scattered in two sectors within the biplot, which indicated that these environments could be divided into two mega environments (MEs). The ME-I was represented by E1 and E2, whereas ME-II was represented by E3. All three years within the MEs exhibited <90° angle with each other. Most of the mungbean genotypes were placed near the origin, indicating their consistency in terms of yield performance. The genotypes, viz. G42, G17, G49, G18, G27 were found to be the most stable and high yielding over the environments (Fig. 3D).

DNA fingerprinting of selected promising genotypes

DNA fingerprinting of six selected genotypes of mungbean, i.e. G18 (TRAM-18), G42 (BMS 19-3), G49(ML 134), IPM 02-3, G27 (BMS 18-4), and G17 (Shikha) was done by employing twelve markers. Out of these 12

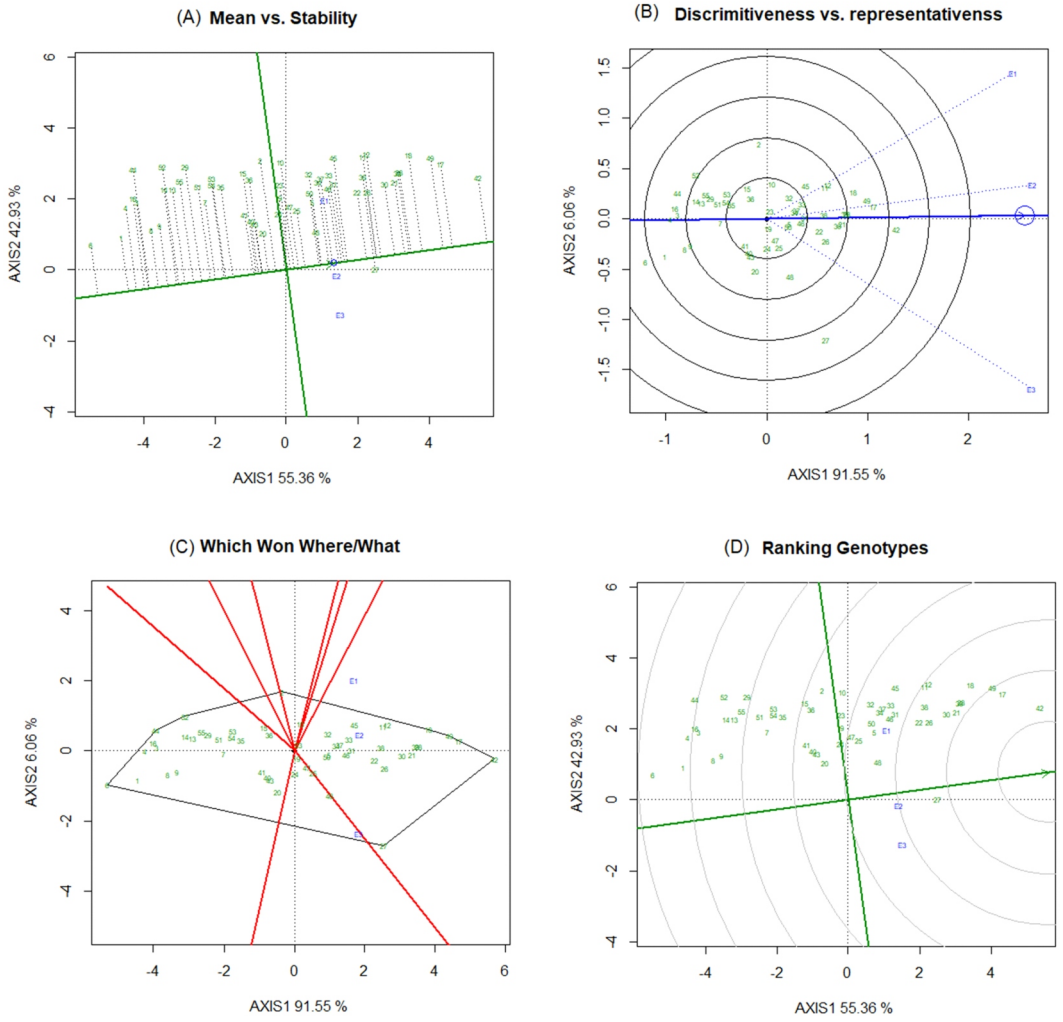

Fig. 3: GGE biplot of 55 mungbean genotypes for seed yield over the years. 2020 (E1); 2021 (E2), 2022 (E3).
(A) Mean vs stability biplot; (B) Discriminativeness *vs* representativeness biplot; (C) Which-Won-Where biplot; (D) Genotype ranking biplot.

markers, only six markers showed polymorphism (Fig. 4). *VrSnRK2.6c* exhibited a range of 460-475 bp in the test genotypes, the amplicons remained within the size of 180-200 bp and 140-160 bp for *VrSnRK2.1* and *VrHSfA6a*, respectively. Likewise, low polymorphism was exhibited by *VrHSfA6b,* Mchr3-76 and HAAS-VR-1437.

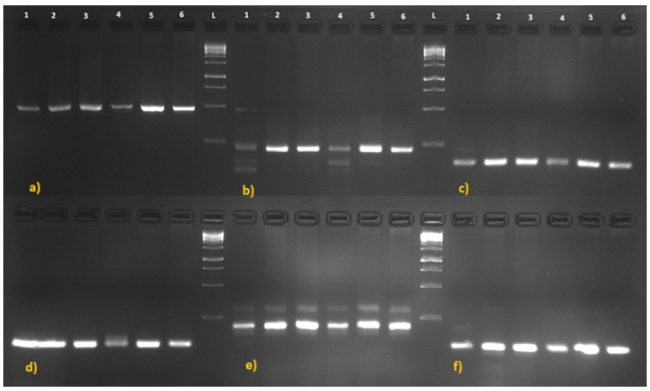

Fig. 4: DNA fingerprinting of promising genotypes of mungbean using markers.
L. Ladder (1kb); 1-6**,** mungbean genotypes (1. G18 (TRAM-18); 2. G42 (BMS 19-3); 3. G49 (ML 134); 4. IPM 02-3; 5. G27 (BMS 18-4); 6. G17 (Shikha).

Discussion

Evaluation and characterization of the breeding materials followed by assessment of their genetic variations, are the most important activities for crop improvement (Mahajan *et al.,* 2023; Singh & Collins, 2024; Ikram *et al.,* 2024). These help in the effective utilization of trait-specific promising genotypes in breeding programmes. In most of the crops, the genetic variation has been narrowed down significantly due to the repeated and frequent utilization of the common parents in breeding programmes (Singh *et al.,* 2023a; Singh *et al.,* 2023b). Similarly, in mungbean also, many of the modern varieties have been developed by deploying only a narrow spectrum of the existing variability due to frequent use of common parents in the breeding programme (Schreinemachers *et al.,* 2019). Therefore, identification of trait-specific diverse parental lines, which can help in broadening the genetic base of the cultivated lines, should be our prime objective in developing new varieties (Tripathi *et al.,* 2023a; Ogiso-Tanaka *et al.,* 2023; Mahalingam *et al.,* 2023). The present study showed a considerable amount of genetic variability for key agro-morphological traits in the panel of promising mungbean genotypes. The extent and magnitude of genetic variation, along with its usefulness, can be understood by the genetic parameters. In general, estimates of PCV were higher than the corresponding GCV in the present study, as the PCV includes the variability explained by the environment in addition to the GCV. However, the traits like DM, NPP, PL, NSP, and SI had small differences in their GCV and PCV estimates, which indicated that these traits are mostly governed by genetic factors, and the environment has a little role to play. Similarly, high h^2bs coupled with high GAM also indicated the preponderance of additive gene action in most of the traits under study. Earlier, breeding methods based on heritability and GAM were also advocated by some of the workers; however, considering the high estimates of GCV, PCV, heritability and GAM, strong association could be exhibited for these traits; therefore, indirect selection by simple plant selection methods would be more effective (Singh *et al.,* 2015). On the other hand, promising accessions for traits showing low or moderate heritability and genetic advance could be improved through hybridization programme.

The results also indicated that the traits like PL, NSP, and SI were strongly associated with SYP, suggesting their strength as selection criteria for improving the SYP of mungbean. Therefore, these traits may be chosen as selection criteria for improving SYP. Similar findings on the strong association of component traits with SYP have also been reported by (Tran and Truong 2023; Bhardwaj *et al.,* 2024; Chauhan *et al.,* 2024).

The performance of the genotypes is always influenced by the environmental conditions where they are grown. SYP is a dependent variable and is an outcome of the cumulative effect of its component traits. Therefore, tagging the key traits with stable performance is more important than the single-environment evaluation. GGE biplot serves a major role in selecting these traits under multiple environments. Therefore, the present investigation was undertaken to identify high-yielding and stable mungbean promising varieties or genotypes over the three years using GGE biplot analysis. Employing the GGE biplot approach to understand GEI is considered to be a systematic approach for isolating the best performing genotypes in accordance with the environment through ranking of phenotypic performance of genotypes and test environments (Yan & Tinker 2006; Arshadi *et al.,* 2018; Oral 2018; Kendal *et al.,* 2019). The discrimination ability of an environment is revealed by the length of environmental vectors, where E3 indicated the most "discriminating year", whereas E2 followed by E1, showed the minimum angle with the average environment, indicating that these were the most ideal testing environments. The mean vs stability analysis shortlisted the 39 varieties/ promising genotypes over the years and also exhibited superior performance than the check variety IPM 02-3. 'Which-Won-Where' analysis is the most efficient way of delineating the GEI of

genotypes through plotting the multi-year or multi-environment data in a polygon view of a GGE biplot (Yan and Kang, 2002). The genotypes, i.e. G42 (BMS 19-3), G17 (Shikha), G49 (ML 134), G18 (TRAM-18), G27 (BMS 18-4), were found to be most stable and high yielding over the years. Singh *et al.,* (2020) also employed a similar approach to select the potential mungbean genotypes. Likewise, Iqbal *et al.,* (2021) also adopted a similar approach of GGE biplot analysis to identify the stable and potential heat-tolerant mungbean lines.

Molecular breeding is one of the tools for characterization, assessing genetic variations without any environmental interruptions. Molecular breeding is now sounder after the decoding of whole genome sequence of mungbean (Kang *et al.,* 2014). Many of the *Vigna* germplasm had been characterized through different types of molecular markers (Pratap *et al.,* 2021; Singh *et al.,* 2021; Sahu *et al.,* 2023; Tripathi *et al.,* 2023b; Kumar *et al.,* 2024). These molecular markers are also used in gene discovery (Purwar *et al.,* 2023; Singh *et al.,* 2023; Sen Gupta *et al.,* 2025), QTL mapping (Subhashree *et al.,* 2024; Reddappa *et al.,* 2025) and marker-assisted breeding (Chugh *et al.,* 2022; Singh *et al.,* 2025). Functional markers are one of them, which can be effectively utilized in assessing genetic variations, tagging genomic regions and also for gene introgression (Salgotra and Stewart 2022; Xue *et al.,* 2024). In the present study, SSRs and functional markers have been used for DNA fingerprinting, and results indicated the significant variations among the promising mungbean genotypes for selected markers. The comprehensive fingerprinting with a large set of markers will help in accelerating the effective utilization of these genotypes in the breeding programme for yield improvement.

Conclusion

The study revealed that PL, NPP and SI were observed to be the key traits over the years, hence may be chosen as the selection criteria for improving the yield. Based on GGE biplot analysis, five genotypes, i.e. G42 (BMS 19-3), G17 (Shikha), G49 (ML 134), G18 (TRAM-18), and G27 (BMS 18-4) were found to be the most stable and high-yielding ones over the years. These genotypes should be used as the potential parents for mungbean improvement. Further, BMS 18-4 and BMS 19-3 are new promising entries and could be evaluated further in varietal yield trials for their potential as new varieties.

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Supplementary Table1: Performance of mungbean promising lines for yield and yield component traits over the three years

Genotype	Source	Days to maturity	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Seed index (g)	Seed yield per plant (g)
PDM 139	IIPR, Kanpur	59.56	24.07	6.72	10.40	3.48	5.85
PDM 54	IIPR, Kanpur	71.22	26.48	6.72	10.41	3.42	8.23
PDM 178	IIPR, Kanpur	65.11	33.96	6.87	10.61	3.70	6.18
IPM 2-14	IIPR, Kanpur	59.78	12.28	6.14	9.20	2.71	5.99
IPM 06-5	IIPR, Kanpur	60.11	22.95	8.39	11.23	4.27	8.99
IPM 409-4	IIPR, Kanpur	65.33	22.33	7.76	10.40	3.14	5.36
IPM 312-43K	IIPR, Kanpur	59.78	21.75	7.29	10.38	3.03	7.27
IPM 03-1	IIPR, Kanpur	60.44	24.01	8.10	10.32	3.24	6.35
IPM 03-3	IIPR, Kanpur	60.89	34.47	6.77	10.50	3.34	6.49
IPM 2-17	IIPR, Kanpur	60.78	37.74	7.96	10.18	3.29	8.56
IPM 02-3-2	IIPR, Kanpur	58.78	25.64	6.80	10.15	3.23	9.90
IPM 2-19	IIPR, Kanpur	60.44	21.80	6.65	9.67	3.09	9.97
IPM 05-3-22	IIPR, Kanpur	64.56	18.57	7.59	10.68	3.65	6.77
IPM 306-6	IIPR, Kanpur	62.34	23.07	7.00	10.01	3.27	6.64
Yellow Selection	IIPR, Kanpur	64.45	20.62	6.82	10.98	3.19	7.93
ML 1257	IIPR, Kanpur	74.78	25.09	6.91	9.67	3.70	6.12
Shikha	IIPR, Kanpur	59.11	25.15	7.83	10.51	3.24	11.14
TARAM 18	BARC, Mumbai	61.44	28.23	7.22	10.18	2.94	10.65
TMB 37	BARC, Mumbai	60.22	22.77	7.46	9.70	2.61	8.46
SPS-5	IIPR, Kanpur	69.67	10.84	9.01	11.35	4.23	8.13
SM 48	IIPR, Kanpur	59.56	13.15	8.44	11.39	4.17	10.36
PM-4	IIPR, Kanpur	59.78	17.35	8.34	11.41	3.74	9.74
UPM 98-1	IIPR, Kanpur	59.33	14.78	8.21	8.64	3.15	8.50
UPM02-17	IIPR, Kanpur	60.78	26.48	8.63	11.06	3.20	8.42
HUM 12	BHU, Varansi	67.78	16.84	6.96	9.94	3.59	8.74
BMS 18-3	BUAT, Banda	74.00	26.40	9.83	11.38	5.11	9.91
BMS 18-4	BUAT, Banda	75.45	15.48	8.29	11.09	4.73	9.87
EC 391178(y)	IIPR, Kanpur	66.66	15.08	7.51	9.86	3.43	10.46
BMS 18-5	BUAT, Banda	84.00	12.94	7.25	10.68	3.91	7.04
EC 520034	IIPR, Kanpur	68.22	12.06	8.32	10.02	3.70	10.20
GM 4	GAU, Gujrat	59.22	8.98	7.28	9.57	3.61	9.38
HW 421	IIPR, Kanpur	59.33	7.92	8.09	10.88	4.16	9.00
V1133	AVRDC, Hyderabad	61.33	22.43	7.44	10.56	4.10	9.33
China Mung 2	IIPR, Kanpur	61.11	10.76	7.86	10.33	3.85	9.13
IPOI 539	IIPR, Kanpur	60.66	22.43	6.77	9.50	3.08	7.55
F8(MXU) Extra Early	IIPR, Kanpur	60.11	20.96	7.61	10.14	3.76	8.02
MS 03-18	--	59.56	8.43	7.34	10.68	3.07	9.19
MH 805	CCSHAU, Hissar	60.22	28.55	8.36	11.03	4.14	9.86
SML 1815	PAU, Ludhiana	61.11	14.83	8.23	10.40	3.38	10.43
AKM/NP/8/9	PDKV, Akola	59.22	21.08	8.17	10.91	3.14	7.97
IPM 312-19	IIPR, Kanpur	58.22	27.46	7.34	8.62	3.08	7.89
BMS 19-3	BUAT, Banda	75.44	12.65	10.12	11.82	4.87	11.71
DGGV-2	UAS, Dharwad	63.78	16.69	9.37	11.39	5.16	8.02
BMS 18-17	BUAT, Banda	62.89	15.59	9.47	10.35	4.59	6.20
IC 296672	IIPR, Kanpur	62.78	26.56	6.20	8.85	3.09	9.43

Brazil	Exotic collection	61.22	17.88	8.84	10.90	5.10	9.29
MGG-353	ARS, Mandira	60.22	20.34	7.20	10.38	3.37	8.63
EC 520022	IIPR, Kanpur	64.11	28.05	10.25	10.67	4.53	8.99
ML 134	PAU, Ludhiana	60.11	34.35	7.91	10.86	3.31	10.99
ML 1299	PAU, Ludhiana	64.56	31.36	7.01	10.42	3.09	8.97
HUM 16	BHU, varansi	63.22	24.06	7.54	10.09	3.27	7.19
VIRAT	IIPR, Kanpur	56.89	21.74	6.61	9.28	3.06	6.66
IPM 2-3	IIPR, Kanpur	71.00	15.10	7.22	9.91	3.70	7.43
SML 668	PAU, Ludhiana	71.33	17.21	7.53	9.96	3.79	7.41
IPM 99-125	IIPR, Kanpur	70.44	23.01	7.06	9.38	3.42	6.91

Supplementary Table 2: List of primers used in DNA fingerprinting

S. No.	Primers	Type of marker	Forward	Reverse	Annealing Temperature (°C)
a)	VrSnRK2.6c	Functional	GGTGTGAACGAGGATGTCGTA	CTCCTTCAGAGTCTCGTATCGT	56
b)	VrSnRK2.1	Functional	GTGAGGATGAGGCACGCTT	AACGAGGAGCTGGACTACCA	56
c)	VrHSfA6a	Functional	GCTTGCTATGAACATGGAGGA	TCATTATCATCATTTTCCAATGC	56
d)	VrHSfA6b	Functional	GAGCAAATTGGAAGCCAGAA	AGTTGCCGAGCCAATACATC	54
e)	Mchr3-76	SSR	GAAATAAGCCTAAAGACCAG	GAACTGCATCTGTCTATCCC	53
f)	HAAS-VR-1437	SSR	CCCCAGAATCAAGAAATCCA	GCTCTCGTTACTGGAGGCAC	56
g)	VrDREB5	Functional	CAATGCCACCATTCCCCCAT	TCCGAAGGAGAATAGGCCGT	57
h)	VrDREB12	Functional	TCACTTCTGTCACCTCCTCCA	AACGCCTCCAAGTCATACCA	57
i)	VrDREB13	Functional	ATTCGTCACCCTTTGCTGAAG	TTGTCTTGGCATTTCGACCA	55
j)	VrDREB22	Functional	CCAATCCATTTGCCTCTGCC	CCACGCTAACCCAATTCCCT	57
k)	VrDREB30	Functional	TCAACTTTCCCGACGAGGTG	ACTGCCATCCGCTTTCATCA	56
l)	SKPI	Functional	TGGCTGCCAACTACCTGAACA	ACATGTTCACCGACACCACCT	59