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PRINCIPAL COMPONENT ANALYSIS APPROACH TO IDENTIFY GENETIC VARIATION IN SPRING MUNG BEAN UNDER THE FOOTHILL CONDITION OF MANIPUR INDIA

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ABSTRACT

Mung bean (*Vigna radiata* L. Wilczek) is the most cost effective and essential pulse crop. *Vigna* spp. is a diploid with 2n=2x=22 chromosomes that belongs to the subgenus Ceratotropis in the genus Vigna and has a genomic size of 579 Mb. Extensive research has been conducted on mung bean but relevant information remains dispersed across various sources. This study aimed to assess the genetic diversity among twenty-seven mung bean genotypes via principal component analysis (PCA). The experiment was conducted at the Central Agricultural University's Research Farm Andro, Imphal East, Manipur, during the spring of 2023. Eleven quantitative traits were evaluated, and PCA revealed that the first six principal components (PCs) accounted for 90.64% of the total variance. PC1 emerged as the most dominant component variance and highest eigenvalue, influencing yield and its associated traits. The biplot analysis identified genetically diverse genotypes, such as TCA DM-1, PUSA M 23-32, and TRM 230. These genotypes, with significant positive PC scores, hold potential for further breeding programs to develop improved mung bean cultivars. The findings of this study provide valuable insights into the genetic structure of the evaluated mung bean germplasm, facilitating the identification of superior genotypes for future breeding initiatives.

***Key words*:** Mungbean, PCA, Eigenvalue, Biplot, Genetic structure.

Introduction

Mung bean (*Vigna radiata* L. *Wilczek*) is the most cost effective and essential pulse crop. Vigna spp. is a diploid with 2n=2x=22 chromosomes that belongs to the subgenus Ceratotropis in the genus Vigna and has a genomic size of 579 Mb. It is also known as a green gram, golden gram or mung (1,2). While pulses play a crucial role as both a food sources and economic crop in the rice-based farming systems of South and Southeast Asia, their cultivation extends to other regions worldwide (IIPR, Kanpur annual report 2023). The 2022-23 financial year witnessed a total pulse production of 260.58 lakh tonnes, compared to the five-year average of 246.56 lakh tonnes. Mung bean, one of the most important chief edible legume crops with a global average yield of 721 kg per hectare, is cultivated on approximately 7.3 million hectares area worldwide. India and Myanmar are major producers, together accounting for 30% of the global production of 5.3 million tonnes (3). According to the report of the Directorate of Economics & Statistics, Government of India, Ministry of Agriculture & Farmer Welfare (DA & FW) mung bean covers an area of 0.005 lakh hectares in *kharif* 2021-22 in Manipur and produces 0.005 lakh tonnes with a yield of 959 kg per hectare. Mung bean are abundant in protein (20.97-31.32%) and have a well-balanced amino acid composition, and the digestibility of fiber, antioxidants, phytonutrients is greater than that of other vegetable proteins (4,5). The low productivity of

green gram is attributed to a combination of factors including abiotic and biotic stresses, suboptimal crop management practices, and the unavailability of quality seeds of improved cultivars (6, 7). Biotic factors include diseases, whereas abiotic stresses include waterlogging, salinity, heat, and drought (8, 9). The genetic diversity within cultivated mung bean germplasm is constrained by the narrow genetic base resulting from the limited genetic resources contributing to breeding programs. To address this limitation, efforts are needed to broaden the genetic base. The development of short-duration varieties has facilitated the integration of mung bean into diverse cropping systems, particularly rice-based systems/rice fallow systems, and has expanded its cultivation to new geographical regions such as South-Asia, Sub-Saharan Africa and South America (10, 11) Despite the development of numerous mung bean varieties, most exhibit a high degree of genetic similarity. To cultivate superior, high-yielding cultivars with diverse traits, crossing programs should incorporate genetically diverse genotypes. Principal component analysis (PCA), a multivariate statistical method with rooted in the work of (12,13) is utilized to reduce the dimensionality of a dataset while preserving the maximum amount of information. By identifying the principal components, which are linear combinations of the original variables, PCA enables the ranking of genotypes on the basis of PC scores. Principal component analysis (PCA) is a statistical technique that diminishes the dimensionality of a dataset by identifying a smaller set of uncorrelated variables, known as principal components, which capture the majority of the variance in the original data and can also be utilized to identify key phenotypic traits for germplasm characterization, visualize genetic relationships among individuals, and quantify their contribution to overall genetic diversity (14,15) This technique is predominantly useful for efficiently screening extensive genetic resources using a multitude of descriptive variables (16). Keeping the above facts in mind the present study revealed that the identified novel genotypes have the potential to serve as foundational material for future mung bean breeding initiatives. These genotypes may be directly selected through multilocation trials or integrated into hybridization programs to facilitate the development of improved cultivars.

Materials and Methods

The experimental work was carried out at Central Agricultural University's Research Farm Andro in Imphal East, Manipur during the spring of 2023. A randomized block design (RBD) with three replications was used, with plots measuring 3×1.5 m² with a spacing of 30 cm × 10 cm between and within rows. The farm is located at 25°42 5.453 N, 94°82 423 E, at an elevation of 790m above mean sea level (MSL). A total of 27 genotypes were evaluated for the study and were obtained from AICRP on MULLaRP, CAU, Imphal Centre. The crop was sown in May 2023 and harvested in July 2023. Temperatures during the cropping season ranged from an average minimum of 21.19°C to an average maximum of 30.73°C. Total rainfall received during this period was 41.95 mm. Five plants were randomly selected from each plot and genotype within each replication for the quantitative assessment of the following traits: plant height (cm), number of primary branches, days to 50% flowering, days taken to maturity, number of clusters/plant, number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g), protein percentage (%), and seed yield/plant (g). Data were collected according to standard procedures and analyzed using mean values. Statistical analysis was performed on mean values calculated from randomly selected plants within each genotype and replication. To identify the major sources of variation, a correlation matrix was used to extract principal components. PCA was performed via the methodology described by (17,18). The analysis was implemented *via* R Studio 4.4.2.

Results and Discussion

Principal components of genetic variation

In this study, all the quantitative traits examined exhibited statistically significant ($P<0.05$) differences. Eleven quantitative characteristics were studied to assess their contribution to variability, Principal component analysis (PCA) revealed that the first six principal components (PCs) accounted for 90.64% of the total

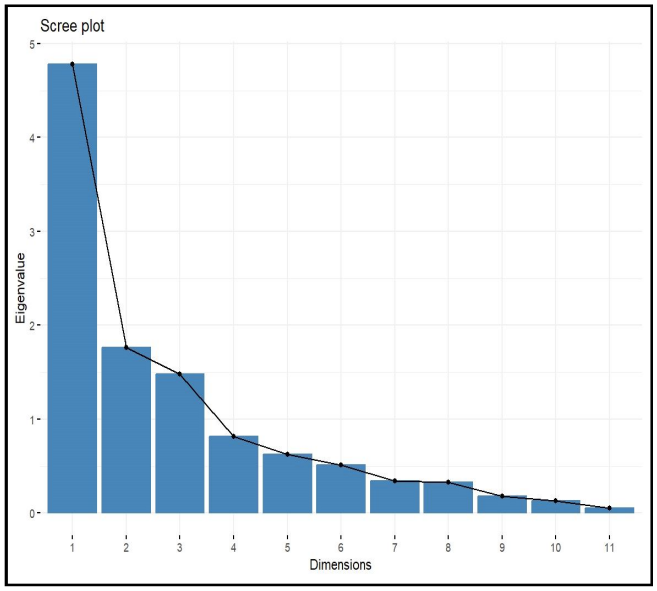

Fig. 1: Scree plot depicting the eigenvalue and number of principal components for mung bean genotypes.

Table 1: Eigen values, percentage of variance and cumulative percentage of variance of 11 principal components (PC) of mung bean.

Traits	Eigen value	% of vari-ance	Cumul-ative % of variance
Plant height (cm)	4.77	43.43	43.43
Number of primary branches	1.76	16.04	59.48
Days to 50% flowering	1.47	13.43	72.91
Days to maturity	0.81	7.38	80.30
Number of clusters per plant	0.62	5.66	85.96
Number of pods per plant	0.51	4.67	90.64
Pod length (cm)	0.34	3.13	93.78
100 seed weight (g)	0.32	2.98	96.77
Number of seeds per pod	0.17	1.60	98.37
Protein percentage	0.12	1.15	99.52
Seed yield per plant (g)	0.05	0.47	100.0

variance in the dataset. These three PCs each exhibited an eigenvalue greater than 1, indicating that they capture a substantial proportion of the underlying data structure. The remaining five PCs, with eigenvalues less than 1, were considered to contribute less significantly to the overall variability and were thus excluded from further analysis. PC1 emerged as the most dominant component, accounting for 43.43% of the variability with an eigenvalue of 4.77 eigen value, followed by PC2 (16.04%), PC3 (13.43%), PC4 (7.38%), PC5 (5.66%), PC6 (4.67%) and PC7 (3.13%). The eigenvalue distributions across these PCs are detailed in Table 1.

The scree plot in Fig. 1 shows the eigenvalue spectrum of the principal component analysis (PCA). Each point on the plot represents an eigenvalue, corresponding to the amount of variance explained by a particular PC. By examining the rate of decline in the eigenvalues, the optimal number of PCs can be determined. The scree plot in Fig. 1 reveales that PC1 captured the largest proportion of variance (43.43%),

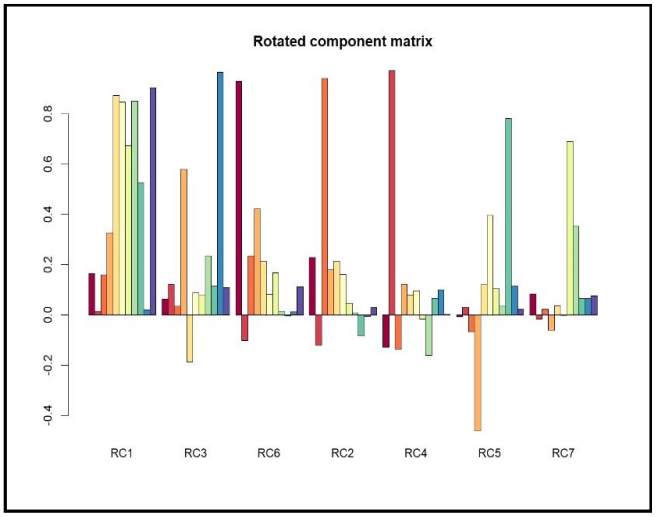

Fig. 2: Rotation matrix of seven principal components.

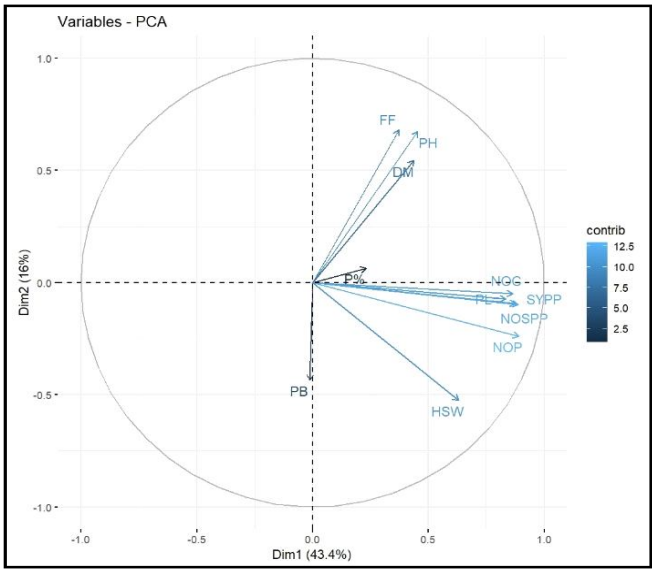

Fig. 3: Plot of the variable loadings on the first two principal components.

corresponding to an eigenvalue of 4.77. A discernible pattern of diminishing returns was observed for subsequent PCs, as indicated by the decreasing magnitude of their eigenvalues.

Table 2. Rotated matrix for different quantitative characteristics of mung bean genotypes.

Traits	RC1	RC2	RC3	RC4	RC5	RC6	RC7
Plant height (cm)	0.170	0.230	0.06	-0.130	-0.010	0.930	0.080
Number of primary branches	0.010	-0.120	0.12	0.970	0.030	-0.100	-0.020
Days to 50% flowering	0.160	0.940	0.03	-0.140	-0.070	0.230	0.020
Days to maturity	0.330	0.180	0.58	0.120	-0.460	0.420	-0.060
Number of clusters per plant	0.870	0.210	-0.19	0.080	0.120	0.220	0.040
Number of pods per plant	0.850	0.160	0.09	0.100	0.400	0.080	0.000
Pod length (cm)	0.670	0.050	0.08	-0.020	0.100	0.170	0.690
100 seed weight (g)	0.850	0.010	0.23	-0.160	0.040	0.010	0.350
Number of seeds per pod	0.530	-0.080	0.11	0.060	0.780	0.000	0.070
Protein percentage	0.020	-0.010	0.97	0.100	0.110	0.010	0.060
Seed yield per plant (g)	0.900	0.030	0.11	0.000	0.020	0.110	0.080

Table 3: Interpretation of the rotated component matrix for the traits having the highest value in each PCs.

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
	NOC	FF	DM	PB	HSW	PH	PL
	NOP		P%				
	NOSPP						
	SYPP						

Pattern matrix of rotated components

The rotated component matrix, presented in Tables 2 & 3 and visualized in Fig. 1, revealed that PC1 and PC7 were the primary factors influencing yield and its attributing traits. PC2, PC4, PC5, PC6, and PC8 were associated with a subset of yield-related characteristics. PC1 was the dominant factor influencing yield and its constituent traits, including the number of clusters/plants, pod number/plant, pod length, seed number/pod, 100-seed weight, and seed yield/plant. PC2 was influenced primarily by the time required for to 50% flowering. PC3 was predominantly associated with days taken to maturity and protein percentage. PC4 was driven primarily by the number of primary branches. PC5 was dominated by

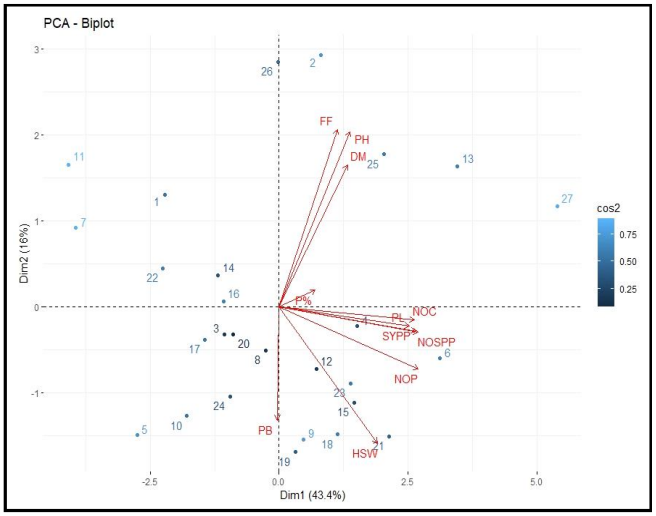

Fig. 4: Biplot showing the genotype distribution and trait contributions on PC1 and PC2 (PH: plant height, PB: number of primary branches, FF: days to 50 % flowering, DM: days to maturity, NOC: number of clusters per plant, NOP: number of pods per plant, PL: pod length, HSW: 100 seed weight, NOSPP: number of seeds per pod, P%: protein percentage, SYPP: seed yield per plant).

Table 4: PC score of the studied genotypes in each PCs.

Genotypes	Seed yield/ plant (gm)	PC1	PC2	PC3	PC4	PC5	PC6	PC7
IPM 1707-1	1.33	2.18	-1.28	-1.61	-0.60	-1.09	0.13	1.04
TCA DM-1	1.71	-0.79	-2.87	-1.33	-0.97	-0.78	0.00	0.16
BCM 20-45	1.61	1.04	0.31	-1.66	0.83	-0.37	1.04	-0.21
JLPM 818-8	1.92	-1.49	0.22	-0.72	-1.43	0.14	-1.04	-0.04
BCM 20-1	1.55	2.70	1.46	0.51	-1.63	0.64	0.12	0.32
TRM 230	2.15	-3.06	0.58	-0.31	-0.30	-1.51	0.21	-1.38
SML 1115 (Check)	1.28	3.87	-0.90	0.10	-0.34	-0.28	-1.05	-0.61
SML 2108	1.77	0.25	0.50	-0.06	-0.26	0.04	0.38	-0.18
JLPM 707-27	1.78	-0.46	1.51	-0.28	-0.48	0.22	0.29	0.27
TRM 146	1.68	1.75	1.25	-1.21	0.68	1.31	0.37	-0.03
RMG 1148	1.38	4.01	-1.62	0.64	0.35	-0.04	-0.12	-0.11
SVM 66	1.80	-0.71	0.71	-1.46	0.53	0.14	1.06	0.61
PM 1711	2.56	-3.39	-1.61	-1.40	0.28	2.39	-0.27	-1.10
MH 18-100	1.51	1.16	-0.36	-0.05	-1.03	0.48	-0.95	0.05
GM 6 (Check)	1.77	-1.43	1.09	2.27	-0.82	0.33	0.40	0.50
Pusa M 23-31	1.61	1.06	-0.06	-0.62	0.07	0.25	-0.06	-0.22
SVM 88	1.56	1.41	0.37	-0.22	0.23	0.71	0.81	0.39
IPM 1604-1	2.10	-1.11	1.46	-0.09	-0.32	-1.07	-0.16	-0.62
PMS 9	1.93	-0.31	1.66	1.74	0.69	-0.32	-0.26	-0.15
BCM 20-50	1.68	0.88	0.31	1.94	2.23	0.23	-0.67	0.06
MML 2552	1.84	-2.09	1.48	-1.65	1.36	-0.69	-1.18	1.15
RMG 1196	1.41	2.21	-0.44	-0.47	1.38	-0.39	0.31	-0.69
Virat (IPM 205-7) (Check)	2.01	-1.36	0.88	0.57	0.01	-0.78	-0.42	-0.47
PMS 13	1.78	0.93	1.02	1.25	-1.22	0.39	0.35	-0.09
Pusa M 2231	1.73	-1.99	-1.74	1.07	0.50	0.35	-1.44	0.73
PM 1803	1.46	0.02	-2.79	2.36	0.32	-0.48	1.23	0.06
PUSA M 23-32	2.94	-5.29	-1.14	0.69	-0.08	0.18	0.92	0.55

100-seed weight. PC6 was strongly associated with plant height. PC7 was significantly correlated with pod length. (19[A]) recorded that PC1 is associated with the number of clusters per plant, the number of seeds per pod, and the seed yield per plant. (20) demonstrated that PC1 was the primary driver of variation in seed yield and its associated components, including seed yield/plant, pod number/plant, and cluster number/plant. (21) reported that PC1 explained the highest proportion of variance in yield-related traits.

A loading plot was employed to examine the contributions of individual characteristics to the first two principal components (PC1 and PC2). Genotypes clustered closely on the biplot were considered genetically similar, whereas those positioned farther apart or distant from the origin were deemed genetically diverse. Traits positioned closer to the origin in the biplot (Fig. 4) and loading plot (Fig. 3), including protein percentage, presented lower factor loadings and consequently had a limited impact on the total variance explained by the principal components. Traits positioned further away from the origin in the biplot (Fig. 2) and loading plot (Fig. 3), including plant height, primary branch number, days to 50% flowering, days to maturity, cluster number/plant, pod number/plant, pod length, seed number/pod, 100-seed weight, and seed yield/plant, presented greater larger factor loadings. These traits, therefore, contributed more significantly to the total variance explained by the principal components. Table 2 reveals that highest PC1 was primarily influenced by the number of seeds yield per plant (0.90), followed by the number of clusters per plant (0.87), the number of pods/plant (0.85), the number of seeds/pod (0.85) and the pod length (0.67), whereas PC2 included days to 50% flowering (0.94). PC3 had the highest loading for protein percentage (0.97). PC4 included the in number of primary branches (0.97). PC5 represent 100 seed weight. PC6 for plant height (0.93) and PC7 included pod length (0.69).

A preponderance of genotypes was observed in the third and fourth quadrants of the biplot (Fig. 2), with fewer genotypes occupying the first and second quadrants. A high degree of genetic distance (based on the biplot (Fig. 2) was observed between the genotypes TCA DM-1, PUSA M 23-32, TRM 230, MML 2552, BCM 20-1, and RMG 1148 and the rest of the genotypes.

Genotypes were selected for further study based on the basis of their principal component (PC) scores, as detailed in Table 3. PC analysis is a statistical technique used to reduce the dimensionality of complex datasets, identifying underlying patterns and relationships among variables. In this case, the PC scores represent the contribution of each genotype to the overall genetic variation. Genotypes exhibiting significant positive loadings on each of the seven principal components, as indicated by scores greater than the 1.5 PC score, can be used for further studies. These results are consistent with those of studies by (19[B]) who reported both positive and negative PC scores values, (22) also recorded positive and negative values (23) investigated 18 characteristics of diverse rice landraces, and calculating positive and negative PC values to identify distinct groups within their germplasm collection, (24) studied 16 characteristics of bread wheat and reported 8 PCs with positive and negative values for different genotypes.

Conclusion

PCA revealed significant genetic diversity among 27 mung bean genotypes. PCA revealed that the first six principal components accounted for 90.64% of the total variance. PC1 emerged as the most dominant component, explaining 43.43% of the variability, and was primarily associated with yield-related traits such as number of clusters/plants, pod number/plant, pod length, seed number/pod, 100-seed weight, and seed yield/plant. The biplot analysis revealed significant genetic diversity among the evaluated genotypes. Genotypes with high PC scores, particularly for PC1, were identified as potential candidates for future breeding programs. The findings of this study provide valuable insights into the genetic diversity of mung bean germplasm in Manipur and can guide future breeding efforts towards the development of high-yielding and resilient cultivars.

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Authors' contributions

This work was a collaborative effort, with all authors contributing Mukesh, Priyashree Laishram, Sonika Yumnam were responsible for the conception, design, editing, data analysis, finalization, and submission of the manuscript. conducted the literature survey, while SL contributed to the revision and redrafting of the manuscript. All authors contributed to this work and have approved the final manuscript.

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