



Principal Component Analysis of Quantitative and Qualitative Traits in Sixty Mung Bean (*Vigna radiata* L. Wilczek) Genotypes


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ABSTRACT

The present study was conducted at Genetics and Plant breeding plot, Central Agricultural University in July 2021–August 2022, sixty mung bean genotypes were evaluated for 28 morphological quantitative and qualitative traits planted in RBD with three replications. Among traits, 14 were yield and its attributing traits and other 14 were qualitative characters scored according to IBPGR guidelines of mung bean. Principal component analysis (PCA) was done to identify the significant characters and the variation of genotypes based on different traits. Principal Component Analysis revealed that out of 28, only first nine principal components exhibited more than 1.0 eigen value and showed about 71.22% total variability. PC1 showed 19.42% variability with eigen value 5.44, and was dominated by traits i.e., plant height (0.496), number of clusters plant⁻¹ (0.762), number of pods plant⁻¹ (0.868), number of seeds pod⁻¹ (0.409), number of seeds plant⁻¹ (0.933), biological yield (0.905) and seed yield plant⁻¹ (0.878), which concludes it as a yield attributing principal component. PC 1 and PC 9 accounts for yield contributing traits, PC 6 accounts for seed characters, PC 2 for duration and all the remaining PCs for different qualitative characters. Based on the PC scores in PC 1 and PC 9 which are yield attributing components the genotypes namely SML 1115(8.7), IPMD 1604(6.93), IPM 1103-1(9.58) PM 1624(8.08), RMG 1132(10.27), Virat (IPM 205-7) (7.42), IPM 1603-1(9.77) and MML 2568(7.77) were selected for high yield and its attributing traits.

KEYWORDS: Eigen, mung bean, scree plot, rotated matrix

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

India is the world's largest producer of mung bean (*Vigna radiata* L. Wilczek), accounting for roughly 65% of worldwide acreage and 54% of global production (Singh, 2011). Mung bean is India's third most significant pulse, accounting for 16% of the country's total pulse area. It is planted on around 3.58 mha, with an average productivity of 548 kg ha⁻¹ and accounting for 10% of total pulse production. According to the Government of India's first Advance estimates of production of food grains for 2022–2023, Mung bean production was 3.15 mt in 2021–2022 and estimated 1.75 mt in 2022–2023 for the *kharif* season (Anonymous, 2022). Mung bean is a legume that is grown throughout Asia for its edible seeds, sprouts, translucent noodles, starch extraction, and animal feed. The plant is an annual, upright or semi-erect, reaching a height of 0.15–1.25 m. It has a well-developed root system and is slightly hairy. In order to generate high yielding mung bean varieties using various breeding methods, cultivar selection is critical, and cultivars must be thoroughly examined for qualitative and quantitative features. Although many varieties of mung bean were developed most of them had similar genetic constitution, to have high yielding superior cultivars for various characters genotypes which are highly diverse should be taken in the crossing programs.

Principal component analysis (PCA) is a multivariate statistical tool which was pioneered by Pearson (1901) and was later developed independently by Hotelling (1933). The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972, Morrison, 1982) and also to rank genotypes on the basis of PC scores. PCA uses only a few components, each sample can be represented by relatively few numbers instead of by values for thousands of variables (Ringner, 2008). Principal Component Analysis is a statistical approach for categorizing many variables into primary uncorrelated variables. PCA can be employed to identify germplasm characterization features, visualize individuals' differences and relationships, and assess their contribution to total variation (Singh et al. (2016) and Martínez-Calvo et al. (2008)) and This method is particularly valuable for screening large number of genetic resources by a large number of descriptor variables (Beiragi et al. (2001) and Golbashy et al. (2010)). Considering the importance of PCA, an investigation was carried using 60 mung bean genotypes to dissect componential traits for yield and quality to obtain precise information and to select genotypes for this Twenty-eight quantitative and qualitative characteristics were used. PCA is an important tool to identify the important traits which have greater impact on the total variables and each coefficient of the

vectors indicate the degree of contribution of every original variable with which each principal component is associated Sanni et al. (2008). The first three principal components are stated to be most often the most important in revealing the variation patterns among the different genotypes and the characters associated in differentiating various genotypes (Clifford and Stephenson, 1975, Guei et al., 2005). Similarly, Tahir et al. (2020) evaluated 533 accessions of Mungbean for qualitative and quantitative traits and Khatun et al, (2022) analysed PCA for sixteen qualitative characters and seventeen quantitative characters. Whereas, Similar usage of PCA is done to understand the genetic diversity was earlier employed in various crops Jadhav et al. (2014) in finger millet; Naik et al. (2016) in cotton; Priya et al. (2017) in rice and Ayesha and Babu, 2018 in foxtail millet and Priya et al. (2019) in Mungbean. The objective of the present study is to identify the diversity among genotypes and variation based on different characters based on PCA of genotypes.

2. MATERIALS AND METHODS

The experiment was carried out using 60 genotypes of mung bean, at Genetics and Plant Breeding (GPB) Farm, College of Agriculture, Central Agricultural University, Imphal, Manipur during *kharif* (July–October) 2021, following Randomized Block Design with three replications. Each row was 4 m length with spacing of 30×10 cm² between and within rows. The geographical location of research farm is at 24.811°N and 93.891°E, at an elevation of 781.8 m above mean sea level. The crop duration was from July–October with average maximum temperature of 28.82°C, average minimum temperature of 19.5°C and average monthly rainfall of 110 mm (July–October) during the crop growth period. Twenty-eight quantitative and qualitative characteristics were used to characterize and assess the genetic diversity of mung bean genotypes as per guidelines given by IBPGR, Rome (Table 1). Ten plants were randomly chosen from each replication in each genotype for yield assessment and quality attributed traits. The observations were recorded as per the standard procedure and subjected to statistical analysis using mean values. The statistical analysis of data on individual characters was carried out using mean values of randomly selected plants from each genotype in each replication.

The different characters which were studied viz., Ten randomly selected plants from each genotype in each replication were taken and observed for several traits i.e., days to 50% flowering (number of days from sowing until 50% of plants in a genotype plot per replication had atleast one open flower), days to maturity (number of days was taken from sowing to 80% pods maturation on a plant), plant height (cm) (it was measured at maturity from



Table 1: Eigen values, percentage of variance and cumulative variance of 28 principal components of mung bean

Traits	Eigen value	Percentage of variance	Cumulative percentage of variance
Days to 50% flowering	5.44	19.42	19.42
Days to maturity	3.54	12.63	32.05
Plant height (cm)	2.04	7.30	39.35
No. of primary branches	1.83	6.55	45.89
Primary branch length (cm)	1.58	5.66	51.55
No. of clusters plant ⁻¹	1.54	5.49	57.04
No. of pods plant ⁻¹	1.44	5.15	62.19
Pod length (cm)	1.38	4.92	67.11
No. of seeds pod ⁻¹	1.15	4.12	71.22
No. of seeds plant ⁻¹	0.96	3.41	74.63
100 seed weight (g)	0.89	3.16	77.80
Biological yield (g)	0.87	3.10	80.90
Harvest index	0.86	3.06	83.97
Seed yield plant ⁻¹ (g)	0.73	2.60	86.57
Hypocotyl colour	0.65	2.33	88.90
Growth habit	0.58	2.07	90.98
Primary leaf shape	0.48	1.72	92.70
Terminal leaflet shape	0.42	1.49	94.19
Leaf pubescence	0.39	1.40	95.59
Petiole colour	0.31	1.12	96.71
Stem colour	0.27	0.98	97.69
Seed shape	0.20	0.72	98.40
Seed colour	0.15	0.52	98.92
Seed lustre	0.11	0.41	99.33
Pod pubescence	0.08	0.30	99.63
Raceme position	0.05	0.19	99.82
Calyx colour	0.04	0.14	99.96
Corolla colour	0.01	0.04	100.00

ground level to tip of the main axis), number of primary branches (number of branches emerging directly from the main shoot), primary branch length (cm), number of clusters per plant (number of pod bearing clusters in a plant was calculated), number of pods plant⁻¹, Pod length (cm) (it was measured at the time of maturity), number of seeds per pod, number of seeds per plant, 100 seed weight (g), biological yield (g) (weight of all the above ground

parts along with the roots was calculated after harvest), harvest index (%) (calculated by dividing total seed yield by biological yield plant⁻¹ which is expressed as percentage) and seed yield plant⁻¹ (g), the mean of all ten sampled plants from each genotype is drawn and used for further calculations, hypocotyl colour was recorded after 10 days after emergence as green, green-purple, purple and dark purple, growth habit was recorded when the first pod on plant changes colour as erect, semi-erect and spreading, primary leaf shape was recorded as ovate-lanceolate and lanceolate of the first leaf which emerges on stem, terminal leaflet shape recorded as deltate, ovate, ovate-lanceolate, rhombic and obovate, leaf pubescence was recorded as glabrous, very sparsely pubescent, puberulent, moderately pubescent and densely pubescent, petiole colour recorded as green, green with purple spots, greenish purple, purple and dark purple, stem colour was recorded as green, dark green, light purple and dark purple, seed shape recorded as globose, ovoid and drum shaped, seed colour was observed after harvest of mature seeds as light green, dark green, green-brown, brown and yellow, seed lustre was recorded as present (shiny) and absent (dull) by visual observation of the harvested seeds, pod pubescence was recorded when the first pod changed colour, as glabrous, puberulent, moderately pubescent and densely pubescent, raceme position was recorded when the first pod changes colour, as mostly above canopy, intermediate and no pods visible above canopy, calyx colour recorded as green, purple green and greenish purple and corolla colour of wing and standard of freshly opened flowers was recorded. In the present investigation correlation matrix was used to extract the principal components. PCA analysis was done using the methodology given by Massy (1965) and Jolliffe (1986) using R software.

3. RESULTS AND DISCUSSION

3.1. Genetic variability and principal component analysis

All the qualitative characters are scored for their conversion according to descriptors of mung bean given by the International board of plant genetic resources (IBPGR), Rome guidelines and scaling of all the 28 characters is done before the analysis. Out of twenty-eight principal components, first nine PCs exhibited more than 1 eigen value and showed about 71.22% of total variability. PC1 showed 19.42% followed by PC2 (12.63%), PC3 (7.3%), PC4 (6.55%), PC5 (5.66%), PC6 (5.49%), PC7 (5.15%), PC8 (4.92%) and PC9 (4.12%) of variability as shown in Table 1. According to Paliwal et al. (2022) PC1 showed maximum variability of 18.139% with eigen value of 2.177. Jadhav et al. (2021) evaluated 20 components where, components PC1 to PC7, with eigen values more than one which are extracted from the original data, contributed



76.70% of the total variation. Yoseph et al. (2021) evaluated 17 quantitative characters of mung bean and found that 7 principal components accounted for 80.1% of variation where PC1 with eigen value of 4.246. As per Desta et al. (2023) the first two principal components including component 1 (PC1) and component 2 (PC2) demonstrated 36.74 and 21.12% of the total variation, respectively. Based on the eigenvalue >1, a total of eight PCs were formed contributing total variance of 78.8% according to Sharma et al. (2023).

Scree plot graph depicted in Figure 1 explained the percentage of variance associated with each PCs obtained by drawing a graph between Eigen values and principal component numbers. PC1 showed 19.42% variability with Eigen value 5.44, which then declined gradually.

3.2. Rotated component matrix

The rotated component matrix is presented in Table 2 and 3 revealed that PC1 and PC9 accounted for yield and also its

attributing traits. The PC2, PC3, PC4, PC5, PC6, PC7 and PC8 accounted for quality and few yield attributing traits while, PC6 was dominated by seed characters. PC1 accounts

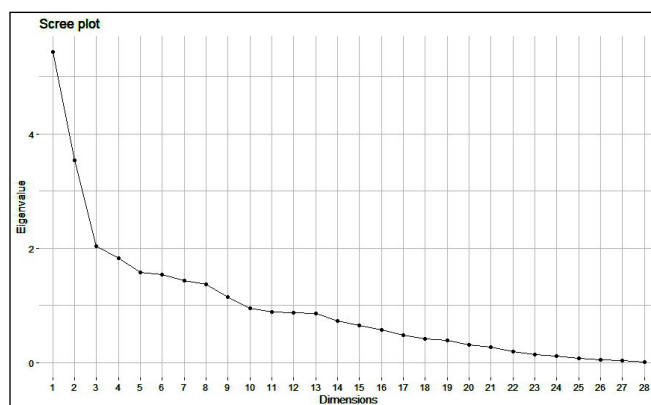


Figure 1: Scree plot of principal component analysis for mung bean genotypes between their Eigen value and the number of principal components

Table 2: Rotated matrix for different traits of mung bean

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
DF	0.250	0.817	0.149	0.099	0.201	-0.201	-0.023	0.013	-0.130
DM	0.006	0.855	0.182	0.043	0.206	-0.150	-0.011	0.060	-0.117
PH	0.496	0.171	0.457	0.208	-0.038	-0.250	0.020	0.230	0.015
PB	-0.221	0.075	-0.012	0.587	0.242	0.342	0.029	0.361	-0.026
PBL	0.189	0.156	0.495	0.224	0.352	-0.200	0.222	0.166	0.036
NC	0.762	0.050	0.298	0.180	-0.034	-0.292	0.142	0.024	0.116
NPP	0.868	-0.159	0.187	0.110	-0.007	-0.072	0.106	0.104	0.076
PLN	0.318	-0.010	0.114	-0.065	-0.256	-0.156	-0.112	0.082	0.754
SPP	0.409	-0.082	-0.013	-0.201	-0.726	0.035	-0.111	-0.020	0.215
SPPL	0.933	-0.013	-0.161	-0.104	0.069	-0.034	-0.040	0.034	0.061
TW	0.144	0.029	-0.061	0.103	0.028	0.116	0.003	-0.225	0.858
BY	0.905	0.039	0.057	0.049	-0.160	-0.014	-0.134	-0.067	0.101
HI	0.161	-0.053	-0.675	-0.074	0.344	0.013	0.065	0.300	0.302
SY	0.878	-0.007	-0.306	-0.032	0.085	0.009	-0.090	0.084	0.230
HC	-0.008	-0.206	-0.037	-0.160	0.086	-0.179	0.079	-0.751	-0.053
GH	-0.192	0.609	0.033	-0.054	0.028	0.225	0.040	0.165	0.132
PLS	-0.054	0.115	-0.299	0.144	-0.205	-0.128	0.721	0.063	-0.228
TLS	-0.067	0.574	-0.327	0.101	-0.219	-0.117	-0.128	0.109	-0.009
LP	0.289	0.107	-0.010	0.723	-0.078	0.061	-0.003	-0.168	0.058
PC	-0.203	-0.061	-0.091	0.235	-0.120	0.236	0.028	-0.716	0.136
St C	0.169	-0.250	0.176	-0.031	-0.006	-0.133	0.237	0.197	0.387
SS	0.072	0.320	0.180	-0.457	-0.058	0.348	0.026	-0.177	-0.506
SC	-0.043	-0.212	0.167	0.128	-0.010	0.620	-0.097	-0.019	-0.029
SL	-0.144	0.055	-0.139	0.005	-0.006	0.767	0.136	0.024	-0.053

Table 2: Continue...

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
PP	0.007	0.045	0.674	-0.152	0.040	0.093	-0.039	0.147	0.138
RP	-0.087	0.409	0.320	-0.085	0.454	0.144	0.252	0.067	-0.253
Ca C	0.010	0.129	-0.190	0.097	-0.051	-0.159	-0.693	0.169	-0.143
Co C	0.155	0.117	-0.083	-0.099	0.737	-0.009	-0.297	-0.024	0.048

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; PB: No. of primary branches; PBL: Primary branch length; NC: No. of clusters plant⁻¹; NPP: No. of pods plant⁻¹; PLN: Pod length; SPP: No. of seeds pod⁻¹; SPPL: No. of seeds plant⁻¹; TW: 100 seed weight; BY: Biological yield; HI: Harvest index; SY: Seed yield plant⁻¹; HC: Hypocotyl colour; GH: growth habit; PLS: Primary leaf shape

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

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
PH		DF	PBL	PB	HI	PC	PLS	Ca C	PLN
NC		DM	PP	LP	RP	SS			TW
NPP		GH			Co C	SL			St C
SPP		TLS			HC	SC			
SPPL									
BY									
SY									

for most of the yield and its attributing traits namely plant height, number of clusters plant⁻¹, number of pods plant⁻¹, number of seeds plant⁻¹, number of seeds plant⁻¹, biological yield and seed yield. PC2 was dominated by days to 50% flowering, days to maturity, growth habit and terminal leaflet shape. PC3 contributed for primary branch length and pod pubescence. PC4 was accounted for number of primary branches and leaf pubescence. PC5 was contributed by harvest index, raceme position, hypocotyl colour and corolla colour. PC6 was dominated by seed characteristics viz., seed shape, seed colour, seed lustre and petiole colour. PC7 and PC8 were contributed by single trait each i.e., primary leaf shape and calyx colour respectively. PC9 was contributed by pod length, 100 seed weight and stem colour. Mohan et al. (2021) revealed that PC1 was associated with seed yield plant⁻¹, number of pods plant⁻¹ and number of clusters plant⁻¹. Popoola et al. (2017) found similar results for days to maturity and days to 50% flowering. Shyamalee et al. (2016) the yield-related characteristics are close together when the second principal component is related to days to flowering and days to maturity. According to Jadhav et al. (2021) PC1 contributed maximum variability of yield associated traits, In the biplot (Figure 2) and the loading plot (Figure 3), the traits found near to the origin such as calyx colour, harvest index, primary leaf shape, leaf pubescence, pod pubescence, terminal leaflet shape, seed colour, corolla colour, hypocotyl colour, seed lustre, seed shape, number of primary branches, growth habit and stem colour have smaller loading effects and also had little influence. Traits like days to 50% flowering,

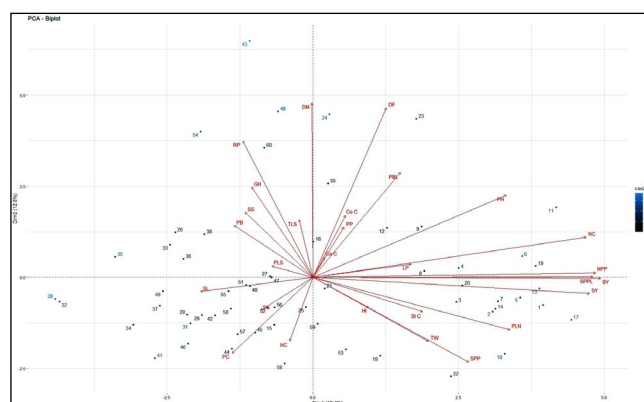


Figure 2: Biplot showing the distribution of genotypes and contribution of all the characters in first two principal components (*DF: Days to 50% flowering; DM: days to maturity; PH: Plant height; PB: No. of primary branches; PBL: Primary branch length, NC: No. of clusters plant⁻¹, NPP: Number of pods plant⁻¹, PLN: Pod length, SPP: No. of seeds pod⁻¹, SPPL: No. of seeds plant⁻¹; TW: 100 seed weight; BY: Biological yield; HI: Harvest index; SY: Seed yield plant⁻¹; HC: Hypocotyl colour; GH: Growth habit; PLS: Primary leaf shape; TLS: Terminal leaflet shape; LP: Leaf pubescence; PC: Petiole colour; St C: Stem colour; SS: Seed shape; SC: Seed colour; SL: Seed lustre; PP: Pod pubescence; RP: Raceme position; Ca C: Calyx colour; Co C: Corolla colour).

days to maturity, raceme position, number of pods plant⁻¹, biological yield, seed yield plant⁻¹, number of seeds plant⁻¹, number of clusters plant⁻¹, 100 seed weight, petiole colour, primary branch length, plant height, pod length and number of seeds pod⁻¹ are far from the origin and had higher loading

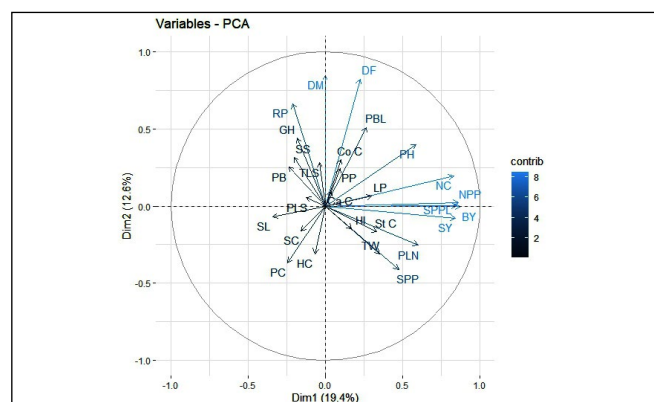


Figure 3: Loading plot showing contribution of variables towards the first two PCs

and great influence on the variation. Therefore, the loading plot reflecting the contributions of the characters to PC1 and PC2. Genotypes closer to each other and overlapping on the biplot had similar characteristics whereas; those genotypes far apart from each other and those found distantly far from the origin are genetically diverse. According to Table 2, the component loadings for PC1 to PC6, PC1 has highest component loading for number of seeds per plant (0.933), biological yield (0.905), number of pods plant⁻¹ (0.868) and

number of clusters plant⁻¹ (0.762), PC2 for days to flowering (0.817) and days to maturity (0.855), while PC3 has highest loading for primary branch length (0.425), PC4 for leaf pubescence (0.723), PC5 has corolla colour (0.737), PC6 has for seed lustre (0.767) and seed colour (0.620), where PC7 for primary leaf shape (0.721) and negative loading in PC8 for hypocotyl colour (-0.751). Finally, PC9 contain highest positive loading for pod length (0.754).

Most of the genotypes were concentrated in the third and fourth quadrant and few genotypes in the first and second quadrant. The genotypes PM 1624, IPM 1603-1, Pusa M 2132, IPM 604-1-2, MI 750-1 and LGG 600 were realized to have diverged greatly from the other genotypes.

Based on PC scores presented in table 4, the genotypes under research were chosen. With the use of these scores, it is possible to suggest exact selection indices, the strength of which can be determined by the variability each principal component can explain. High values for the variables in a particular genotype are indicated by a high PC score for that genotype in that component (Singh and Chaudhary, 1977). Based on the top PC scores of positive values >1.5 in each PC for all the mung bean genotypes were selected in each of the 9 principal components. Similarly, Mahadev Prasad

Table 4: PC scores of 60 mung bean genotypes in each PC

Sl. No.	Genotype	Seed yield	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
1.	SML 1115	8.70	1.87	-0.56	0.18	1.72	-0.40	1.01	-0.47	-0.03	0.11
2.	RMG 1166	5.93	1.43	-0.52	0.18	0.64	-0.42	-0.31	0.75	-0.98	-0.12
3.	TBMB 117-5	3.97	0.74	-0.41	0.71	0.51	-0.07	-1.00	1.35	-1.22	0.64
4.	MH 1830	6.07	1.13	-0.09	0.16	0.08	0.21	-0.79	0.23	-0.66	-0.24
5.	Pusa M 2131	5.87	0.78	-0.38	1.35	-0.73	-0.51	-0.42	-1.58	0.83	1.41
6.	IPMD 1604	6.93	1.60	-0.53	0.54	0.79	0.53	-1.02	1.22	-0.51	-0.40
7.	IPM 99-125	5.11	0.74	-1.66	1.47	0.69	0.36	-0.69	2.17	1.17	1.03
8.	TBMB 17-2	6.27	0.30	0.44	-0.13	-1.74	-0.71	-0.24	0.28	2.13	1.23
9.	MML 2568	7.77	0.10	3.25	-1.58	-0.87	-1.10	-0.34	-0.34	0.33	2.46
10.	IPM 1103-1	9.58	1.53	-0.76	-1.49	-1.07	0.41	-0.17	0.48	-0.04	0.71
11.	PM 1624	8.08	1.88	1.92	-0.34	0.81	-1.19	-0.21	-0.30	-0.33	-0.08
12.	Pusa BM 16	4.91	0.80	1.10	0.19	0.13	-0.92	-0.24	-1.98	-0.59	-1.09
13.	RMG 1132	10.27	2.03	-0.37	-1.32	1.20	0.54	-0.52	0.06	-0.45	-0.57
14.	Virat (IPM 205-7)	7.42	1.78	-1.00	0.01	-0.81	-0.65	-0.35	0.72	0.23	-1.18
15.	IPM 1610-1	3.23	0.03	-0.79	0.42	0.17	-1.01	0.12	-0.77	-0.81	-1.21
16.	PM 504-20-27	3.87	-0.17	1.91	1.87	-0.80	-0.43	1.39	-0.77	-2.21	1.66
17.	IPM 1603-1	9.77	1.96	-0.26	-0.51	-1.26	-1.04	0.02	0.49	0.84	0.33
18.	MHBC 20-7	6.73	0.69	-1.30	0.28	-0.70	0.01	0.89	0.46	-0.24	0.33
19.	PM 1605	6.40	1.44	-0.49	1.53	0.67	-0.08	1.13	-0.63	1.11	0.80
20.	TCADM 20-5	8.47	1.35	0.16	-1.70	-0.01	0.09	-0.01	0.16	0.70	-0.06

Table 4: Continue...

Sl. No.	Genotype	Seed yield	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
21.	GM 6	4.47	-0.15	1.14	-1.42	1.61	-1.45	-0.84	-0.76	-0.66	0.02
22.	Pusa M 2132	4.45	-0.50	-1.19	1.65	0.28	-0.49	0.02	-1.50	0.90	3.45
23.	IPMD 101-2	7.97	1.18	0.89	-0.63	-0.76	5.61	-0.07	-2.27	-0.18	0.36
24.	VGG 15-013	4.37	0.67	1.99	0.62	-0.10	-0.55	0.02	-0.35	0.89	-2.00
25.	RVSM 18-1	2.81	-0.42	-0.26	0.40	2.44	-0.30	-0.63	0.86	-1.56	0.46
26.	VGG 17-049	3.72	0.13	0.17	-0.20	-0.46	0.34	2.64	1.47	0.94	-1.47
27.	RMG-1139	3.37	-0.43	0.05	0.07	1.33	-1.28	-0.07	-0.72	0.60	-0.65
28.	KM 2419	3.57	-0.98	-0.54	-1.09	1.19	0.16	0.48	-0.46	0.78	0.06
29.	PM 1609	3.50	-0.58	0.31	-1.37	1.74	-0.52	1.96	-0.16	0.32	0.38
30.	MLS	4.25	-0.54	0.30	1.29	2.90	1.58	0.26	1.29	1.04	1.38
31.	Pusa BM6	3.57	-0.70	-0.24	-0.57	1.10	-0.33	0.08	-0.57	-1.41	-0.58
32.	IPM 604-1-2	0.93	-1.49	-1.72	0.39	0.61	-0.10	0.54	-0.89	1.24	-2.05
33.	PM 1603	3.87	-0.98	0.81	-0.96	1.49	0.48	-0.36	-0.40	-0.81	-0.41
34.	BCM 18	2.27	-1.12	0.20	-0.92	-0.24	0.24	1.65	1.41	-0.40	0.98
35.	KM 2241	1.78	-1.33	0.23	0.16	0.25	0.78	-0.28	1.26	-1.31	-0.32
36.	IIPM 20-1	3.57	-1.16	0.46	-0.95	-0.14	-0.03	-0.35	-0.45	1.23	-0.01
37.	Pusa M 2071	3.57	-1.08	-1.12	0.38	-0.12	1.02	0.88	-0.62	0.51	0.05
38.	MGG 453	2.88	-0.92	0.87	0.30	-0.05	-0.18	0.29	0.77	0.34	0.28
39.	MI 750-1	1.59	-1.23	0.20	-0.15	-0.21	-0.28	2.58	0.79	-0.29	-0.32
40.	MI 181-1	6.58	0.52	-0.25	-0.47	-0.18	0.51	3.17	-1.29	0.66	-0.73
41.	MH 1772	2.50	-1.26	-0.61	-0.30	-0.31	-0.10	-0.38	-0.51	-1.60	0.18
42.	Pusa 0672	4.23	-0.71	-0.64	-1.51	-0.50	-0.38	-0.55	-0.28	1.54	-0.69
43.	LGG 600	2.10	-0.33	2.67	1.89	-0.28	0.41	-0.35	1.16	0.94	-1.14
44.	IIPM 20-2	3.33	-1.27	-0.71	-1.48	-0.56	-0.13	-1.14	0.73	1.41	1.12
45.	OBGG 109	3.50	-0.75	-0.20	0.13	-0.86	0.10	-0.50	1.03	-1.32	1.12
46.	MH 1468	2.97	-1.05	-0.19	-0.76	-1.13	0.19	-0.71	0.99	-1.45	0.64
47.	COGG 16-10	2.25	-0.67	-0.91	1.29	-0.64	-0.88	-0.66	-0.33	1.68	-0.57
48.	IGKM 06-18-3	2.00	-0.38	1.44	2.33	-0.88	-0.11	-0.99	0.37	0.89	-1.10
49.	SML 2015	1.85	-1.08	0.06	0.41	-1.36	-0.75	-0.17	0.63	-0.21	-0.36
50.	BCM 18-2	3.23	-0.53	-0.08	-0.61	-0.92	-0.38	-0.76	-0.12	-0.61	-0.49
51.	Pusa 1371	4.80	0.15	-0.28	-0.19	-1.12	1.04	0.88	1.26	-0.85	-0.42
52.	SML 1839	3.45	-0.43	-0.34	-0.07	-0.67	-0.46	-0.82	-1.73	-0.27	-0.55
53.	IPM 1604-1	6.33	0.01	-0.76	-0.51	-0.83	0.64	-0.15	-1.42	-0.45	0.97
54.	Pant M6	2.97	-0.36	0.80	1.16	-0.89	1.92	-0.77	0.62	-0.36	-1.61
55.	DGGV-91	3.27	-0.29	0.35	0.62	-0.57	-0.39	1.68	0.21	-0.81	0.21
56.	Pusa M 2072	3.27	-0.61	-1.04	1.45	0.11	0.24	-0.71	-1.65	-0.89	-0.10
57.	CAU-GG-1	2.30	-0.65	-1.08	0.38	-0.53	-0.27	-1.16	-1.74	-0.94	-0.83
58.	SKNM 1705	5.05	-0.02	-1.00	-1.67	-1.09	-0.02	-0.68	0.87	-0.12	-0.28
59.	RMG 1154	4.60	0.34	-0.45	-0.11	-0.69	-0.74	-0.11	0.67	-0.85	-0.65
60.	SKNM 1514	3.23	-1.01	1.00	-0.79	1.63	1.23	-2.20	0.28	2.14	-0.13



et al. (2022) got both positive and negative PC scores and used them as selection indices. Mallikarjuna et al. (2022) found in black gram that the PCA analysis thus identified hypocotyl coloration and plant growth as the maximum contributing traits towards the total variability. Zeba et al. (2022) used PCA analysis to find out diversity among soybean accessions.

The genotypes such as SML 1115, IPMD 1604, IPM 1103-1, PM 1624, RMG 1132, Virat (IPM 205-7), IPM 1603-1, MML 2568, PM 504-20-27 and Pusa M 2132, fell in yield and its attributing traits associated PCs with high PC scores, these genotypes had high values for yield and its attributing traits. The characters with the most variability is highlighted by PC analysis. Therefore, rigorous selection techniques can be designed to quickly increase yield and quality defining characters.

4. CONCLUSION

The genotypes were varied for most of the characters studied where PC1 showed 19.42% variation and first nine principal components showed eigen value more than one, the yield attributing characters had shown more variability. Based on the PC scores in PC 1 and PC 9 which are yield attributing components the genotypes namely SML 1115, IPMD 1604, IPM 1103-1, PM 1624, RMG 1132, Virat (IPM 205-7), IPM 1603-1, MML 2568, PM 504-20-27 and Pusa M 2132 are selected for high yield and its attributing traits.

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