*R*ESEARCH *P*APER

Principal component analyses in mungbean genotypes under summer season

Priya Tiwari* **and** Stuti Sharma
Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) India
(E mail: tpriya725@gmail.com)

Abstract : Yield is a complex trait subjective to several components and environmental factors. Therefore, it becomes necessary to apply such technique which can identify and prioritize the key traits to lessen the number of traits for valuable selection and genetic gain. Principal component analysis is primarily a renowned data reduction technique which identifies the least number of components and explain maximum variability, it also rank genotypes on the basis of PC scores. PCA was calculated using Ingebriston and Lyon (1985) method. In present study, PCA performed for phenological and yield component traits presented that out of thirteen, only five principal components (PCs) exhibited more than 1.00 eigen value, and showed about 80.28 per cent of total variability among the traits. Scree plot explained the percentage of variance associated with each principal component obtained by illustrating a graph between eigen values and principal component numbers. PC1 showed 26.12 per cent variability with eigen value 3.40. Graph depicted that the maximum variation was observed in PC1 in contrast to other four PCs. The PC1 was further associated with the phenological and yield attributing traits viz., number of nodes per plant, number of pod cluster per plant, number of pod per plant. PC2 exhibited positive effect for harvest index. The PC3 was more related to yield related traits i.e., number of seeds per pod, number of seeds per plant and biological yield per plant, whereas PC4 was more loaded with phenological traits. PC5 was further related to yield and yield contributing traits i.e. number of primary branches per plant, seed yield per plant and 100 seed weight. A high value of PC score of a particular genotype in a particular PC denotes high value for those variables falling under that specific principal component. Pusa Vishal found in PC 2, in PC 3, PC 4 and PC 5, can be considered as an ideal breeding material for selection and for further deployment in defined breeding programme.

Key Words : Eigen values, Mungbean, Principal component analysis, Summer

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] is commonly known as green gram, golden gram, oregon pea, chickasano pea, which is self-pollinated diploid plant species having chromosome number 2n = 2x = 22 and a genome size of 579 Mb (Parida *et al.,* 1990). The crop is assumed to have been originated from Indian-subcontinent (Vavilov,1926) prevails through India and Burma, South and East Asia, Africa, West Indies and dry areas of Southern Europe and United States. Mungbean is a major edible pulse crop in Asia and is also consumed in Southern Europe and in the Southern USA. It ranks 3rd position in acreage among the pulse

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* **Author for correspondence :**

crops in our country. Low yield as well as poor stability remains one of the most important constraints in its expansion. Yield, being a quantitative trait is a complex character in any crop. Various morphological and physiological plant characters contribute to yield. These yield contributing components are interconnected with each other presenting a complex series of association and also immensely subjective to the environmental conditions in mungbean as factual as in other crops. Due to lack of knowledge concerning relative importance and usefulness of variables, the researcher tries to take in account all the possible variables and makes the data matrix clearly huge, complicated and beyond comprehension. Therefore, the researcher needs a method for systematic reduction and summarization of data sets. Principal component analysis, chiefly a well known data reduction technique identifies 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.

MATERIAL AND METHODS

The present investigation was carried out at the College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur during the *summer* 2020. The experimental material comprised of 36 genotypes of mungbean grown in three replications. Observations were recorded randomly on five competitive plants selected from each line and each replication. The observed characters were days to flowering initiation, days to maturity, number of primary branches per plant, number

of nodes per plant, number of pod cluster per plant, number of pod per plant, number of seeds per pod, number of seeds per plant, pod length (cm), biological yield per plant (g), 100 seed weight (g), harvest index (HI) (%), seed yield per plant (g). Principal component analysis (PCA) is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. It was calculated using Ingebriston and Lyon (1985) method.

RESULTS AND DISCUSSION

PCA performed for phenological and yield component traits in promising lines of mungbean revealed that out of thirteen, only five principal components (PCs) exhibited more than 1.00 eigen value and showed about 80.28 per cent total variability among the traits studied. So, these five PCs were given due importance for further explanation (Table 1).

Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 26.12 per cent variability with eigen value 3.40 which then declined gradually. Semi curve line is obtained which after fifth PC tended to show decrease in slope of curve with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other four PCs, which is selected for explaination here. So, selection of lines from this PC will be useful (Fig. 1).

Rotated component matrix (Fig. 2) revealed that

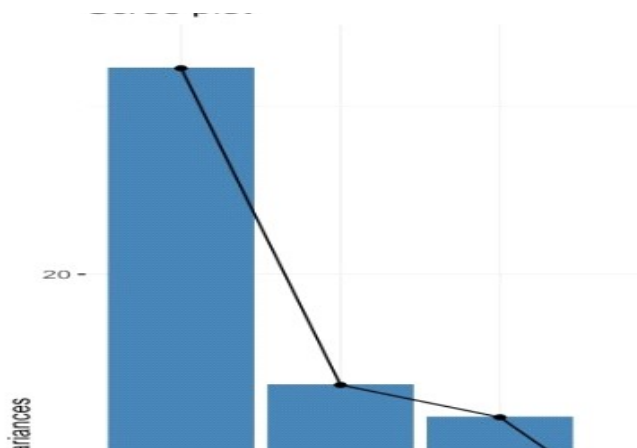| Table 1 : Eigen values, % variance and cumulative % values of promising lines of mungbean				
Traits	Principal component	Eigen values	Variability %	Cumulative %
Days to flowering initiation	PC1	3.396	26.123	26.123
Days to maturity	PC2	2.173	16.714	42.837
No. of primary branches per plant	PC3	2.048	15.754	58.591
No. of nodes per plant	PC4	1.621	12.467	71.058
No. of pod cluster per plant	PC5	1.199	9.223	80.281
No. of pod per plant	PC6	0.845	6.499	86.780
No. of seeds per pod	PC7	0.630	4.844	91.624
No. of seeds per plant	PC8	0.538	4.142	95.766
Pod length (cm)	PC9	0.320	2.465	98.231
Biological yield per plant (g)	PC10	0.177	1.362	99.592
Seed yield per plant(g)	PC11	0.033	0.253	99.845
100 seed weight (g)	PC12	0.017	0.133	99.978
Harvest index (HI) (%)	PC13	0.003	0.022	100.000

Fig. 1 : Scree plot of principal component analysis of soybean genotype between eigen value and principal components

each principal component separately loaded with various phenological and yield attributing traits under study. The PC1 was more related to the phenological and yield attributing traits viz., number of nodes per plant, number of pod cluster per plant, number of pod per plant. PC2 exhibited positive effect for harvest index allowed for higher seed yield. The third principal component was more related to yield related traits i.e., number of seeds per pod, number of seeds per plant and biological yield per plant whereas PC4 was more loaded with phenological traits *viz.,* days to flowering initiation, days to maturity and pod length. The fifth PC was more related to number of primary branches per plant, seed yield per plant and 100 seed weight. Thus, PC5 allowed for simultaneous selection of phenological and yield related traits and it can be regarded as yield factor. (Table 2 and 3). Similar results were obtained by

Divyaramakrishnan *et al.* (2014) for seed yield, number of pods per plant and number of clusters per plant, number of branches and test weight. Perera *et al.* (2017) for plant height, seeds per pod and pod length, Thippani *et al.* (2017) for pod length, 100-seed weight and number of primary branches, Jhakar *et al.* (2018) for biological yield accounted for most variability in the mungbean genotypes. Also, Thippani *et al.* (2017) found that first five principal components accounted for 78.78% of the total variation. From this study, it was clear that PC1, PC2, PC3 and PC5 were found mostly related to yield attributing traits whereas PC4 was related to phenological traits. As PC5 was constituted by most of the yield attributing traits, an intensive selection procedure can be designed to bring about rapid improvement of dependent traits i.e., yield by selecting the lines from PC5.

PC 1 includes SML 1825 which had the highest PC score 4.357 value followed by TRCRM-147 (3.630), IPM 02-3 (3.214), Pusa BM-8 (2.163) and Virat (1.861) (Table 4). It indicated that they had high value for phenological and yield related traits such as number of nodes per plant, number of pod cluster per plant, number of pod per plant. PC 2 includes the genotypes which had high PC score for VGG 16-045 (3.193), IPM 701-4 (2.774), VGG 17-038 (2.528), Pusa Vishal (1.834) and OBGG 101 (1.796). It showed they had high value for harvest index (Table 4). PC 3 includes PDM-139 (3.520) followed by Pusa Vishal (2.060), TJM-3 (2.048), HUM-1 (1.675) and IPM 410-3 (1.524), which exhibited high value for yield related traits viz., number of seeds per pod, number of seeds per plant and biological yield per plant.

PC 4 includes Pusa 9531 which recorded the highest

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No. of seeds per pod	PC7	0.630	4.844	91.624
No. of seeds per plant	PC8	0.538	4.142	95.766
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Harvest index (HI) (%)	PC13	0.003	0.022	100.000

PC score (2.805) followed by Pusa Vishal (2.253), SML 1825 (2.086), VGG 17-040 (1.286) and TMB-136 (1.108) indicated that they had high value for days to flowering initiation, days to maturity and pod length. PC 5 includes SML 1825 (2.504) which exhibited the highest PC score followed by Pusa BM-8 (2.253), Pusa Vishal (1.564), LGG 460 (1.258) and MH 1344 (1.153) indicated that they had high value for number of primary branches per plant, seed yield per plant and 100 seed weight. SML 1825 was found in PC1, PC4 and PC5 and had maximum PC score, where as Pusa Vishal was present in PC2, PC3, PC4 and PC5 and had the highest traits for phenological and yield. On the basis of top 5 PC scores in each principal component, genotypes are selected and presented as summarized form (Table 5). PC scores were calculated for all the lines in 5 principal components and utilized in finding superior genotypes for different combination of phenotypic traits. A high value of PC score of a particular genotype in a particular PC denotes high value for those variables, in that genotype which the component is representing. Thus, these score can be utilized to propose precise selection indices, whose intensity can be decided by variability explained by each of the PC.

According to the first PC score, SML 1825 had highest score followed by TRCRM-147, IPM 02-3 and Pusa BM-8 etc., indicating that they were more related to number of nodes per plant, number of pod cluster per plant, number of pod per plant. The highest PC scores in PC2 were recorded by VGG 16-045, IPM 701-4, and VGG17-038 were closely related to harvest index. In PC3, highest PC score was exhibited by PDM-139 followed by Pusa Vishal and TJM-3 for number of seeds per pod, number of seeds per plant and biological yield per plant. At the same time, PC scores of genotypes Pusa 9531 followed by Pusa Vishal and SML 1825, etc. in PC 4 related to days to flowering initiation, days to maturity and pod length. PC scores for PC 5 exhibited yield characteristics viz. number of primary branches per plant, seed yield per plant and 100 seed weight in genotypes SML 1825, Pusa BM-8 and Pusa Vishal (Table 5). Thus, breeder can select lines having the highest score with desirable combination of quantitative and qualitative traits for further breeding programme.

Conclusion:
It can be concluded that PC analysis highlights the

Table 2 : Five PC values of rotation component matrix for thirteen variables of thirty six genotypes of mungbean

Traits	Principal components				
	PC1	PC2	PC3	PC4	PC5
Days to flowering initiation	0.066	-0.375	0.125	0.319	-0.047
Days to maturity	-0.020	-0.476	0.133	0.232	0.103
No. of primary branches per plant	0.269	-0.178	-0.227	0.106	0.526
No. of nodes per plant	0.325	-0.162	-0.327	-0.034	0.290
No. of pod cluster per plant	0.383	-0.116	-0.183	-0.286	0.165
No. of pod per plant	0.418	0.014	0.237	-0.288	-0.020
No. of seeds per pod	0.131	0.257	0.446	0.300	0.066
No. of seeds per plant	0.403	0.156	0.431	-0.055	0.021
Pod length (cm)	-0.051	-0.255	0.249	0.458	0.207
Biological yield per plant (g)	-0.140	-0.378	0.354	-0.413	0.071
Seed yield per plant(g)	-0.247	0.083	0.365	-0.332	0.504
100 seed weight (g)	-0.482	-0.064	-0.106	-0.147	0.293
Harvest index (HI) (%)	-0.036	0.502	-0.058	0.248	0.454

Extraction method: Principal component analysis; * represents more related traits in each principal component

Table 3 : Interpretation of rotated component matrix for the traits having values >0.5 in each PCs

Traits	PC1	PC2	PC3	PC4	PC5
	No. of nodes per plant	Harvest index (HI) (%)	No. of seeds per pod	Days to flowering initiation	No. of primary branches per plant
	No. of pod cluster per plant	-	No. of seeds per plant	Days to maturity	Seed yield per plant(g)
	No. of pod per plant	-	Biological yield per plant (g)	Pod length(cm)	100 seed weight (g)

Sr. No.	Genotypes	PC1	PC2	PC3	PC4	PC5
1.	Pusa M 19-42	0.950	0.805	1.189	-3.641	-0.493
2.	MH 1344	-1.405	0.595	-0.367	-2.016	1.143
3.	OBGG 102	-0.013	1.687	-1.644	-0.411	-1.507
4.	IPM 02-3	3.214	1.241	-0.002	0.176	-2.516
5.	SKNM-1608	-0.073	-0.619	-1.699	-0.358	-0.510
6.	VGG 17-038	-0.205	2.528	1.315	-1.511	-0.398
7.	Pusa BM-8	2.163	1.000	-1.318	0.171	2.253
8.	IPM 701-4	-0.159	2.774	-1.402	0.711	0.702
9.	VGG 16-045	0.133	3.193	-0.109	0.506	0.809
10.	Pusa 9531	0.036	0.187	0.607	2.805	-1.738
11.	WBSM 48-5	-1.782	0.717	-0.202	0.933	0.493
12.	SML 1825	4.357	-1.366	-1.151	2.086	2.504
13.	IPM 604-1	0.328	0.350	-2.718	-0.345	-0.520
14.	SML 1831	-0.756	-2.597	-1.518	-1.713	0.385
15.	IPM 410-3	-0.207	-0.644	1.524	0.339	-0.882
16.	IPM 610-2	-2.470	-0.180	-0.620	0.244	0.070
17.	OBGG 101	-0.158	1.796	-0.133	-0.311	0.503
18.	IPM 205-7	-3.975	0.654	-1.738	0.367	-0.286
19.	TRCRM-147	3.630	-1.300	-2.618	-1.960	0.352
20.	VGG 17-015	0.081	-2.485	-0.539	0.646	0.300
21.	VGG 17-040	-2.807	-0.311	-0.694	1.286	-0.337
22.	MH 1451	-1.593	-0.982	-1.734	-0.011	-0.251
23.	Pusa M 19-41	1.449	-0.729	-0.581	0.026	-1.482
24.	JBM 136	-0.697	-0.599	-0.119	0.517	-0.263
25.	TJM-3	-1.982	-2.755	2.048	0.358	0.011
26.	PDM-139	0.530	-0.013	3.520	-2.123	0.743
27.	PDM-11	1.444	-1.797	1.147	0.153	-0.833
28.	LGG 460	0.568	-1.816	1.212	0.317	1.258
29.	TM-37	-2.902	0.485	1.063	-0.298	0.966
30.	Ganga-8	-2.199	-1.208	0.374	-1.179	1.031
31.	HUM-1	1.062	-0.901	1.675	0.769	-0.399
32.	SL-668	-0.243	0.997	1.292	0.221	0.268
33.	Pusa Vishal	1.020	1.834	2.060	2.253	1.564
34.	TMB-136	-1.016	-0.791	0.110	1.108	-1.172
35.	Shikha	1.813	0.402	0.825	-0.263	-1.594
36.	Virat	1.861	-0.150	0.945	0.145	-0.172

Table 4 : PCA scores of mungbean genotypes

Table 5 : Selected genotypes on the basis of PC score in decreasing order in each component

PC1	PC2	PC3	PC4	PC5
SML 1825	VGG 16-045	PDM-139	Pusa 9531	SML 1825
TRCRM-147	IPM 701-4	Pusa Vishal	Pusa Vishal	Pusa BM-8
IPM 02-3	VGG 17-038	TJM-3	SML 1825	Pusa Vishal
Pusa BM-8	Pusa Vishal	HUM-1	VGG 17-040	LGG 460
Virat	OBGG 101	IPM 410-3	TMB-136	MH 1344

characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of yield attributing traits. PCA also help in ranking of genotypes on the basis of PC scores in corresponding component. When we considered the entire PC with PC scores and character basis then Pusa Vishal ranked first because it is present in PC 2, PC3, PC4 as well as in PC 5. Pusa Vishal contributes maximum character because most of the yield related traits are present in PC 3 and PC 5. In PC 2, harvest index also

contributing towards yield attributing traits, so Pusa Vishal performs best in comparison to other genotypes and can be utilized for precise selection to the development of suitable genotypes and also used in best breeding material for the transfer of suitable traits in recipient genotypes. SML 1825 also found in PC 1 (component having maximum characters), PC 4 and PC 5 also contributes maximum characters in comparison to Pusa Vishal. On that basis, Pusa Vishal is an ideotype breeding material for selection and for further exploitation in defined breeding programme.

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