The Pharma Innovation Journal 2021; 10(4): 250-253

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(4): 250-253

www.thepharmajournal.com
Received: 02-01-2021
Accepted: 26-02-2021

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Principal components of genetic diversity in black gram [*Vigna mungo* (L.) Hepper]

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DOI: https://doi.org/10.22271/tpi.2021.v10.i4d.5935

Abstract
Forty black gram [*Vigna mungo* (L.) Hepper] genotypes were evaluated using principal component analysis to estimate the extent of genetic diversity for ten different yield and its component traits. The first three principal components *viz*., PC I, PC II and PC III with eigen values more than one contributed around 80% of the variability for the genotypes studied. PC I contributed 46.834% towards variability and the traits responsible for its contribution are *viz*., number of clusters per plant, grain yield per plant, number of branches per plant and number of seeds per pod. The second axis (PC II) contributed 18.951% variability and variation at this axis is due to the accumulated genetic variation of traits *viz*., days to 50% flowering, days to maturity, grain yield per plant and number of clusters per plant. While PC III and PC IV accumulated 13.807% and 5.765% respectively. Therefore on a cumulative note, first four axes contributed about 85.357% of total variance among 10 characters for all the forty genotypes under study. In the current investigation, four lines (TU 94-2, PU 31, IPU 94-1 and LBG 623) are identified from the depicted 2D & 3D figures as diverse genotypes, which may yield transgressive segregants or heterotic F_1s based on nature of gene action of the trait in question.

Keywords: Genetic diversity, Eigen value, principal components, black gram, *Vigna mungo*

Introduction
Black gram (*Vigna mungo* (L.) Hepper) is one of the important pulse crops in India. It is a short duration, self-pollinated and diploid grain legume (2n =2x=22). It is believed that black gram was domesticated from a wild progenitor of *Vigna mungo* var. *silvestris* in India (Kaewwongwal *et al*., 2015) [1]. Black gram seeds have high nutritive value with protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins (Singh and Singh, 2013) [2]. It is also one of the important kharif and spring/summer pulse crop of many South Asian countries like of India, Pakistan, Nepal, Bangladesh, Thailand and Korea (Ghafoor and Arshad, 2008) [3]. In spite of its importance, the productivity of this crop is relatively low. India is the largest producer and consumer of black gram. The annual production of black gram in India is 3060 thousand tonnes from 5602 thousand hectares with an average productivity of 546 kg/ha, while in Andhra Pradesh it is grown in an area of 318 thousand hectares with a production of 310.56 thousand tonnes and productivity of around 977 kg/ha. (Ministry of Agriculture, 2018) [4]. The major constraints in achieving higher productivity are lack of exploitable genetic variability, absence of suitable ideotype, poor harvest index, susceptibility to biotic and abiotic stresses, non-availability of quality seeds of improved varieties and narrow genetic base which occur due to repeated usage of few parents with high degree of relatedness in crossing programmes (Hadimani *et al*., 2016) [5]. In order to improve yield, new black gram varieties must be developed. An assessment of the genetic diversity of pulses is an important initial step in any research programme to improve crop yield. Multivariate analysis such as principal component analysis (PCA) and cluster analysis serve as potential tools in evaluating the phenotypic diversity, identifying genetically distant clusters of genotypes and selecting important traits contributing to the total variation in the genotypes. These analyses provide information that could help in better selection of parental genotypes with specific traits and in devising breeding strategies for trait improvement. Principal component analysis (PCA) allows natural grouping of the genotypes and is precise indicator of differences among genotypes. PCA is very helpful for identification of plant characters that categorize the distinctiveness among promising genotypes (Chakravorty *et al*., 2013) [6].

Principal component analysis (PCA) and two-way cluster analysis are two important statistical programs that aid in selecting elite genotypes for breeding programme that meet the goal of a breeder for the development of improved varieties (Mohammadi and Prasanna, 2003) [7]. To address the requirement of identifying diverse lines, forty black gram genotypes were evaluated by PCA to identify genetically diverse genotypes and to identify traits that contribute to variability in the population.

Materials and Methods

Forty genotypes of black gram obtained from various research stations *viz*., RARS Lam, ARS Gantasala and Baba Atomic Research Centre (BARC) were evaluated in Randomised Complete Block Design with three replications during *Kharif*, 2019 at Advanced PG Centre, Lam, Guntur. Each genotype was raised in two rows of three meter length with a spacing of 30 x10 cm between and within the rows, respectively. Observations on yield component traits *viz*., plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, test weight and grain yield per plant were recorded on randomly selected five plants per replication and their mean values were subjected to statistical analysis. However, observations on days to 50% flowering and days to maturity were recorded on plot basis. PCA was carried out to know the stages of divergence and the traits contributing at each stage or axis towards diversity and principal component scores were used as variables instead of attributes for clustering procedures, thereby making the results equivalent to those from initially standardized data as the correlation matrix was used for its study. In PCA on correlation matrix, the standardization of columns (here characters) created 10 new variables for 40 genotypes without changing their relative positions. All these 10 new variables are the principal components (PCI, PCII …….PC X) and each principal component is a linear combination of the 10 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one and these loadings are viewed as weights defining the contribution of characters in respective principal component. Like regression coefficients, loadings sign (+ / -) are indicative of the direction of contribution. But unlike regression, only the relative contributions are important, so all signs can be changed without affecting the analysis (Jackson, 1991) [8].

The loadings for first principal component were chosen so as to make its variance as large as possible. Loadings of second principal component were chosen such that the variance of PC II is as large as possible, subject to the constraint that PC I and PC II are uncorrelated. The process was continued to create 10 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984) [9]

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating several significant principal components having Eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993) [10]. Results of PCA and cluster analysis are discussed here under.

Results and Discussion

The differentiation occurred in any population at during different evolutionary stages, is represented by different axes and these axes together represent total divergence. A certain proportion of total variability is created at each stage of differentiation or axis. To understand this differentiation, variances (Eigen values), variability in %, cumulatively accumulated variability and component loading of the 10 different traits were estimated and presented in Table 1. Nearly 80% of the variation in the genotypes studied for 10 polygenic traits was due to 1st three components (PC I, II, III) having eigen values greater than unity. And partitioning of total variance through principal component analysis showed that the first four principal components contributed 85.357 percent towards the total variability (Table 1).

Table 1: Eigen values, cumulative percent variance and component loading of first four principal components for traits in black gram

	PC I	PC II	PC III	PC IV
Eugene Value (Root)	4.683	1.895	1.381	0.576
% Var. Exp.	46.834	18.951	13.807	5.765
Cum. Var. Exp.	46.834	65.785	79.592	85.357
Days to 50% flowering	0.014	0.649	0.295	0.030
Plant height (cm)	0.191	-0.175	0.618	-0.595
Number of branches per plant	0.379	-0.208	-0.175	-0.356
Number of clusters per plant	0.397	0.104	-0.316	0.004
Number of pods per plant	0.318	-0.043	-0.441	-0.242
Pod length (cm)	0.369	-0.059	0.158	0.550
Number of seeds per pod	0.374	-0.196	0.243	0.099
Test weight (g)	0.352	0.043	0.323	0.229
Days to maturity	0.118	0.636	-0.060	-0.294
Grain yield per plant (g)	0.384	0.210	-0.119	0.098

The first principal component (PC I) contributed 46.834% towards variability. Characters *viz*., number of clusters per plant (0.397), grain yield per plant (0.384), number of branches per plant (0.379) and number of seeds per pod (0.374) explained the maximum variance in this component. The second axis (PC II) contributed 18.951 percent variability and variation at this axis is because of accumulated genetic variation of traits *viz*., days to 50% flowering (0.649), days to maturity (0.636), grain yield per plant (0.210) and number of clusters per plant (0.104). PC III contributed 13.807 percent of heritable variation and has significant positive loadings of plant height (0.618), test weight (0.323) and days to 50 percent flowering (0.295). And the fourth principal component (PC IV) was characterized by 5.765 percent contribution towards the total variability. This axis showed positive loadings for pod length (0.550), test weight (0.229) and number of seeds per pod (0.099). The cumulative variability percentage for first component is 46.834, while it

is 65.785 for PC II, 79.592 for PC III and 85.357 for PC IV. The PCA scores for 40 black gram genotypes in the first three principal components were computed and were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated (Table 2).

Table 2: PCA scores of respective vectors for 40 black gram genotypes

S. No.	Genotype	PC I X vector	PC II Y vector	PC III Z vector
1	MBG 1053	21.173	19.647	13.664
2	TBG 106	26.494	23.376	9.585
3	GKB 2	24.074	21.181	13.035
4	PU 31	21.033	19.452	10.341
5	PU 212	20.087	20.901	16.994
6	TBG 104	23.779	20.092	13.380
7	VBG 4-008	22.173	20.601	13.148
8	VBG 14-016	24.829	22.819	14.158
9	GKB 4	22.390	21.131	12.154
10	VBG 13-003	26.393	20.830	12.817
11	MBG 1046	25.908	22.019	11.250
12	VBG 4-14	24.808	19.960	13.897
13	GAVT 12	27.722	20.069	9.500
14	GKB 3	22.121	20.057	13.376
15	MBG 1050	24.940	21.211	13.628
16	GBG 12	28.278	25.173	11.168
17	LBG 20	24.179	19.961	14.889
18	LBG 787	21.642	24.677	15.933
19	GAVT 7	28.500	22.906	9.740
20	GKB 1	22.224	19.515	17.068
21	LBG 726	19.599	20.384	14.769
22	LBG 752	21.925	23.695	15.603
23	LBG 771	20.170	20.287	17.701
24	VBG 12-110	21.974	20.791	13.004
25	MBG 1069	23.594	20.226	14.091
26	GBG 1	23.911	20.990	13.041
27	LBG 623	21.926	23.308	16.264
28	MBG 207	17.438	20.960	13.235
29	VAMBAN 8	16.034	19.771	13.104
30	UAHS BG 1	19.685	25.560	13.928
31	UAHS BG 7	24.333	24.683	11.731
32	UAHS BG 8	22.204	25.677	11.543
33	UAHS BG 2	18.877	23.083	13.116
34	UAHS BG 3	25.326	24.456	14.342
35	UAHS BG 6	17.762	21.311	15.038
36	IPU 7-3	17.166	24.868	13.352
37	IPU 94-1	16.734	21.501	11.230
38	IPU 2-43	23.960	25.194	13.208
39	TU 94-2	20.017	21.950	11.140
40	KPU 26	17.097	20.459	13.786

These three PCA scores for 40 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig 1&2) for the studied genotypes. The diverse genotypes numbered 4 (PU 31), 27 (LBG 623), 37 (IPU 94-1) and 39 (TU 94-2), which are far apart from each other in the 2 dimension & 3 dimension diagram (Fig 1&2) may result in hybrid combinations to exploit the heterosis or to produce transgressive segregants in their respective F_2 and subsequent segregation generation. Similar usage of PCA for obtaining 2D & 3D diagrams and inturn to understand the genetic diversity was earlier employed in various crops Jadhav *et al*., 2014 [11] in finger millet; Naik *et al*., 2016 [12] in cotton; Priya *et al*., 2017 [13] in rice; Ayesha and Babu., 2018 [14] in foxtail millet and Priya *et al*., 2019 [15] in mung bean to indicate the successful hybrid combination to obtain superior hybrids or transgressive segregants depending on the gene action guiding different traits.

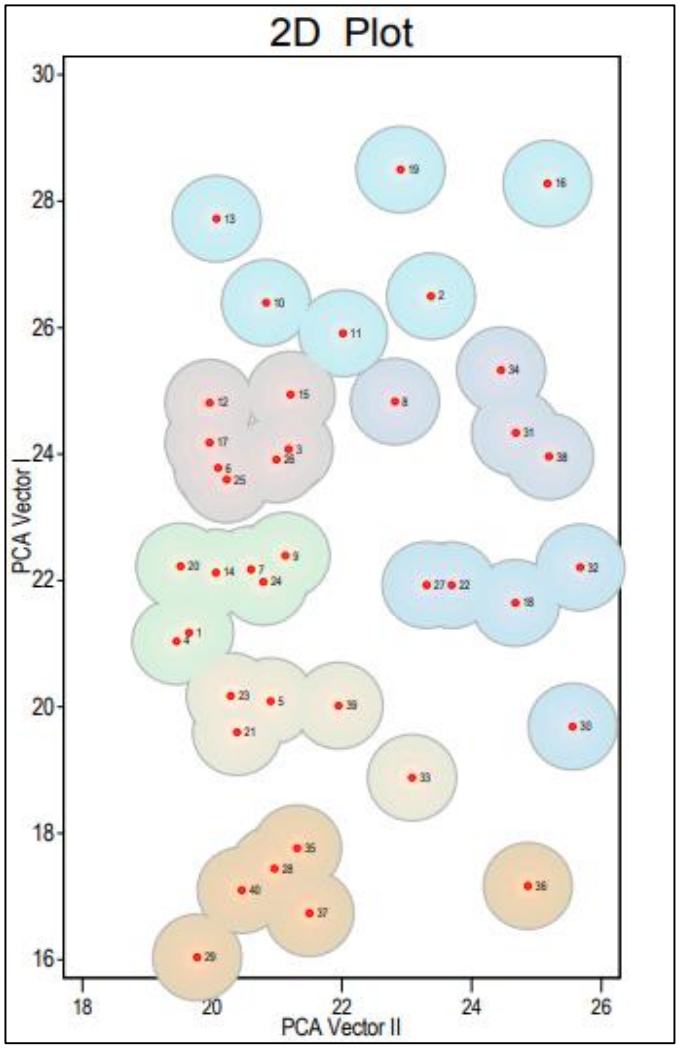

Fig 1: Two dimensional graph showing relative positions of 40 black gram genotypes based on PCA scores

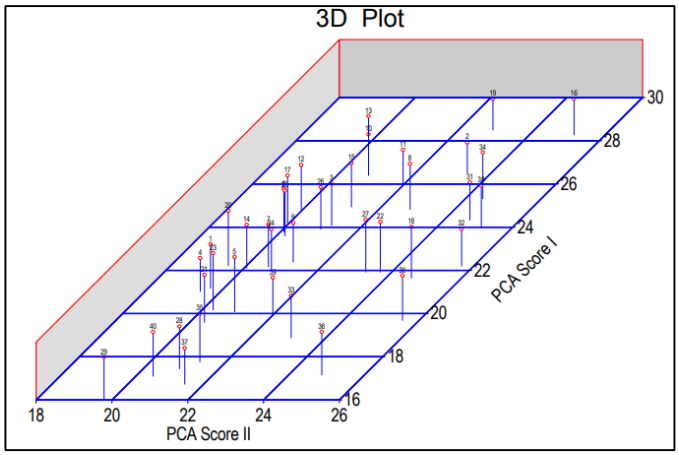

Fig 2: Three dimensional graph showing relative positions of 40 black gram genotypes based on PCA scores

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