

## Short Communication

## Multi-variate analysis in blackgram (*Vigna mungo* (L). Hepper) for diverse agro morphological traits

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### ABSTRACT

**Fifty-two blackgram germplasm lines were evaluated for ten agro-morphological traits through multivariate analyses to estimate the genetic diversity, pattern of variation and relationship among tested individuals and their correlation analysis. First three principal components exhibited more than 1.0 eigen values and exhibited 65.0% total variability. Number of clusters/plant, number of pods/plant, number of seeds/pod and plant height had highest positive eigen vector value in PC<sub>1</sub> indicated the large effect in the overall variation of genotypes. From the biplot, the characters *viz.*, number of branches/plant, hundred seed weight, single plant yield, plant height, number of clusters/plant, hypocotyl colour and number of seeds/pod contributed to the maximum divergence. Five major groups were formed as clusters *viz.*, I, II, III, IV and V consisting of 19, 2, 11, 2 and 18 genotypes, respectively. The genotypes from diverse clusters can be utilized for hybridization programs in blackgram.**

**Key words:** Blackgram, Cluster analysis, Genetic diversity, PCA

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Blackgram (*Vigna mungo* (L). Hepper) originated in South Asia, where it has been in cultivation from ancient times and it is one of the most highly valued pulses of India. Black gram is highly nutritious as it contains high levels of protein (25g/100g), potassium (983mg/100g), calcium (138 mg/100g), iron (7.57mg/100g), niacin (1.447mg/100g), Thiamine (0.273mg/100g) and riboflavin (0.254 mg/100g) (<https://www.gbif.org>). India is the world's largest producer as well as consumer of blackgram and it is very extensively used in Indian cuisine. In India, blackgram is cultivated in an area of 5.03 Million ha with a production of 3.28 Million tonnes and productivity of 652 Kg/ha during 2017-18 (DES, Ministry of Agri. & FW (DAC&FW), Govt. of India, 2017-18).

The constraints in the limited productivity of blackgram are limited availability of high yielding varieties, low seed or varietal replacement, non-availability of quality seeds, susceptibility to pests and diseases, drought or moisture stress, salinity, alkalinity and lack of life saving irrigation (Vasanthakumar, 2016). Reduced genetic variability and diversity among crop plant species has raised serious concern among agricultural workers (Bhandari *et al.* 2017) and further development in crop varieties will be a laborious task. Genetic diversity becomes more important in context of climate change and related unforeseen events, and is the reservoir of many novel traits conferring tolerance to various biotic and abiotic

stresses; hence genetic diversity plays a vital role in heterosis and transgressive segregation (Bhandari *et al.* 2017).

Multivariate statistical tools include Principal Component Analysis (PCA), cluster analysis and discriminate analysis (Oyelola, 2004). PCA may be used to disclose patterns and eliminate redundancy in data sets as variations regularly occur in crop species for yield and grain quality (Maji and Shaibu, 2012). The primary benefit of PCA is to measure the significance of each dimension for relating the variability of a data set. Cluster analysis is a prominent tool for determining clustering patterns to establish relationships between genetic divergence as well as it is a measure of estimating the cophenetic correlation coefficient. Hence, the present investigation was carried out on a set of blackgram germplasm accessions with an objective of identification of genetically diverse germplasm through multivariate analysis by taking into account of agro-morphological traits. Similar works were reported by Rajasekhar *et al.* 2020; Mohanlal *et al.* 2018; Thirumalai and Murugan, 2020; Ghafoor and Arshad, 2008; Jeberson *et al.* 2019.

A total of 52 blackgram germplasm accessions collected from various sources (Table 1) were used for the study. Field experiments were carried out at 'D' block of Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam, Tamil Nadu during 2019-2020. Each

Table 1. List of blackgram germplasm accessions used in the study

Sl. No	Germplasm	Source
1	IC 436852	NBPGR, New Delhi
2	KKM1	AC & RI, Killikulam
3	ABG 11032	TRRI, Aduthurai
4	VBG 13017	NPRC, Vamban
5	RU 1515	AC & RI, Madurai
6	IC 436765	NBPGR, New Delhi
7	ABG 11028	TRRI, Aduthurai
8	IC 28198	NBPGR, New Delhi
9	KKB 14009	AC & RI, Killikulam
10	KKB 1445	AC & RI, Killikulam
11	KKB 1449	AC & RI, Killikulam
12	IC 343936	NBPGR, New Delhi
13	ABG 11015	TRRI, Aduthurai
14	KKB 14032	AC & RI, Killikulam
15	VBG 11042	NPRC, Vamban
16	RU 153	AC & RI, Madurai
17	KKB 1552	AC & RI, Killikulam
18	KKB 14038	AC & RI, Killikulam
19	RU 15009	AC & RI, Madurai
20	CO 6	Department of Pulses, Coimbatore
21	RU 159	AC & RI, Madurai
22	VBG 11018	NPRC, Vamban
23	KKB 14034	AC & RI, Killikulam
24	KKB 1443	AC & RI, Killikulam
25	VBN 6	NPRC, Vamban
26	KKB 1444	AC & RI, Killikulam
27	RU 1516	AC & RI, Madurai
28	KKB 1442	AC & RI, Killikulam
29	KKB 14040	AC & RI, Killikulam
30	IC 436621	NBPGR, New Delhi
31	KKB 14005	AC & RI, Killikulam
32	KKB 1448	AC & RI, Killikulam
33	IC 436626	NBPGR, New Delhi
34	ADT 6	TRRI, Aduthurai
35	IC 343857	NBPGR, New Delhi
36	VBN 4	NPRC, Vamban
37	VBG 10024	NPRC, Vamban
38	VBG 11040	NPRC, Vamban
39	IC 343885	NBPGR, New Delhi
40	ADT 3	TRRI, Aduthurai
41	ABG 11036	TRRI, Aduthurai
42	IC 436720	NBPGR, New Delhi
43	ADT 5	TRRI, Aduthurai
44	ABG 11037	TRRI, Aduthurai
45	IC 281999	NBPGR, New Delhi
46	ABG 11011	TRRI, Aduthurai
47	IC 436811	NBPGR, New Delhi
48	IC 436910	NBPGR, New Delhi
49	KKB 1420	AC & RI, Killikulam
50	KKB 1441	AC & RI, Killikulam
51	KKB 14001	AC & RI, Killikulam
52	RU 1513	AC & RI, Madurai

genotype was sown in 3 meter row to accommodate 20 plants per row with spacing of 30 x 10 cm. The experiment was conducted by adopting Randomized

Block Design (RBD) replicated twice. On the tenth day after sowing the crop was thinned out, leaving one healthy seedling per hill. Recommended agronomic practices were adapted and need based plant protection measures were taken. From each replication, five random plants were tagged for observing agro morphological characters. The observations on hypocotyl colour, seedling vigour, days to 50% flowering, plant height (cm), number of branches/plant, number of clusters/plant, number of pods/plant, number of seeds/pod, hundred seed weight (g) and single plant yield (g) were recorded. The data on hypocotyl colour and seedling vigour were recorded based on descriptors ([https://www.bioversityinternational.org/Descriptors\\_vigna\\_mungo.pdf](https://www.bioversityinternational.org/Descriptors_vigna_mungo.pdf)). The mean value of the five plants was computed and taken for analysis.

PCA was performed to classify the patterns of variation. The PCs (Principal Components) with eigen values greater than one were selected as proposed by Jeffers (1967). Correlations between the original traits and the respective PCs were calculated. Statistical analysis was carried out using the software STAR 2.0. The principal component analysis was computed using the following equation:  $PC_1 = \sum a_j X_j$  where,  $a_j X_j$  = Linear coefficient - Eigen vectors. Cluster analysis was performed using agglomerative clustering method adopting Euclidean distance measure (Blashfield, 1976).

PCA is a well known multivariate statistical technique and a potent tool in modern data analysis used to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1978) and also to rank genotypes on the basis of PC scores. In the present study, PCA was performed using yield and related traits in 52 blackgram germplasm accessions. The proportion of variance, cumulative proportion and eigen values are given in Table 2. Out of ten PCs, three exhibited more than 1.0 eigen values and exhibited 65.0 % total variability among the characters studied. The principal components having more than one eigen value showed more variation for the selection of the diverse parents in blackgram germplasm accessions. Among the three principal components, PC<sub>1</sub> shared high proportion of total variation 39 % followed by PC<sub>2</sub> (16.00%) and PC<sub>3</sub> (10.00%) with eigen values of 3.92, 1.63 and 1.02 respectively (Fig 1). Semi curve line was obtained after PC<sub>3</sub> followed by straight line with little variances observed in each PC. From the scree plot, it is clear that the maximum variation was observed in PC<sub>1</sub> and hence the traits present in this PC contributed more variation for diversity. Ghafoor and

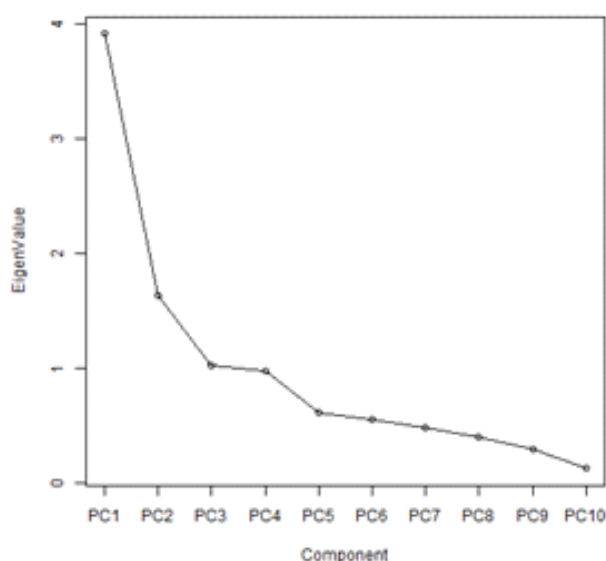


Fig. 1. Scree plot for different PCs in blackgram germplasm

Arshad (2008) studied the multivariate analyses for quantitative traits in blackgram and according to them, first two PCs contributing more than half of the variance were plotted to observe the relationships between genotypes. Singh *et al.* (2010) studied principal component and cluster analysis in blackgram advanced genotypes and the first eight PCA together explained 98.79% of variance present in the material and the genotypes were grouped into five clusters. Jeberson *et al.* (2019) studied the principal component and cluster analyses in black gram under Foot-hills conditions of Manipur. According to them, the first three principal components, having the eigen values more than 1, contributed 84.52% towards variability among the 25 genotypes screened for quantitative

traits. Mohanlal *et al.* (2018) reported that first component had contribution from the traits *viz.*, number of pods per plant, pod length, number of seeds per pod, seed yield per plant which accounted 35.44% to the total variability in blackgram. They confirmed that the remaining variability of 20.06%, 12.39% and 11.23% was accounted by second, third and fourth principal components by various traits *viz.*, number of branches, pod weight and 100 seed weight and the cumulative variance of 79.12% of total variation among eleven characters was explained by the first four axes.

To conclude the critical limit for the coefficients of the proper vectors, coefficients with greater than 0.3 possess large effect to be considered in the overall variation present in the genotypes (Raji, 2002). Eigen vectors of the PCs for different traits are presented in Table 3. The results showed that number of clusters/plant and number of pods/plant had highest positive value (0.41) followed by number of seeds/pod (0.39) and plant height (0.36) in PC<sub>1</sub>. Days to fifty per cent flowering (0.65) and number of branches/plant (0.45) recorded highest positive values in PC<sub>2</sub>. Katiyar *et al.* (2016) studied the biplot analysis for genetic diversity in thirty diverse blackgram genotypes and from their studies, PCA transformed all the metric traits into single index of similarity, yielded 20 eigen vectors and eigen roots and the maximum eigen root value 7.01 was obtained by eigen vector 1 followed by 4.18, 1.75, 1.52 and 1.17 respectively for rest of the vectors.

In the present investigation, the first two PCs (PC<sub>1</sub> and PC<sub>2</sub>) were plotted against each other in biplot to observe the relation among the blackgram germplasm lines based on the observed yield and related characters (Fig.2). Genotypes *viz.*, VBG 13017, ABG 11037, ABG 11015, VBG 10024, KKB 1448, IC 436626,

Table 2. Proportion of variance, cumulative proportion and eigen values of blackgram germplasm accessions

Statistics	PC <sub>1</sub>	PC <sub>2</sub>	PC <sub>3</sub>	PC <sub>4</sub>	PC <sub>5</sub>	PC <sub>6</sub>	PC <sub>7</sub>	PC <sub>8</sub>	PC <sub>9</sub>	PC <sub>10</sub>
Proportion of Variance	39.0	16.0	10.0	10.0	6.0	5.0	5.0	4.0	3.0	2.0
Cumulative Proportion	39.0	55.0	65.0	75.0	81.0	86.0	91.0	95.0	98.0	1.00
Eigen Values	3.92	1.63	1.02	0.98	0.61	0.55	0.47	0.40	0.29	0.12

Table 3. Contribution of different traits towards total variance in blackgram germplasm accessions

Traits	PC <sub>1</sub>	PC <sub>2</sub>	PC <sub>3</sub>	PC <sub>4</sub>	PC <sub>5</sub>	PC <sub>6</sub>	PC <sub>7</sub>	PC <sub>8</sub>	PC <sub>9</sub>	PC <sub>10</sub>
Hypocotyl colour	0.12	-0.48	<b>0.61</b>	-0.16	0.25	0.18	-0.37	0.33	-0.06	0.14
Seedling vigour	0.20	-0.27	-0.24	0.71	-0.03	0.51	0.12	0.19	0.00	0.06
Days to 50% flowering	-0.09	<b>0.65</b>	0.19	0.00	-0.39	0.32	-0.21	0.39	-0.04	0.29
Plant height	<b>0.36</b>	0.06	-0.10	0.36	-0.16	-0.47	-0.67	-0.06	-0.18	-0.10
No.of.branches/plant	0.24	<b>0.45</b>	-0.07	0.10	0.82	-0.02	-0.02	0.11	0.20	0.09
No.of.pods/plant	<b>0.41</b>	0.01	-0.12	-0.31	-0.19	0.33	-0.20	-0.03	0.57	-0.46
No of pods/pod	<b>0.41</b>	-0.15	-0.33	-0.31	-0.10	0.00	0.01	-0.14	0.03	0.75
No. of seeds/pod	<b>0.39</b>	-0.02	0.11	0.00	-0.18	-0.45	0.49	0.59	0.07	-0.09
100 seed weight	0.29	0.15	<b>0.62</b>	0.28	-0.12	-0.01	0.24	-0.55	0.20	0.13
Single plant yield	<b>0.42</b>	0.15	0.01	-0.22	0.06	0.28	0.16	-0.12	-0.75	-0.28

IC 343885, IC 436910, KKB 1441, KKB 1552, KKM 1, RU 1515, ABG 11011, IC 436811 and ABG 11032 formed a group in right top corner of the biplot showed positive values of both the PCs and the traits *viz.*, number of branches/plant, hundred seed weight,

single plant yield, plant height and number of clusters/plant placed in the same quadrant contributed the maximum divergence. PC<sub>1</sub> and PC<sub>3</sub> were plotted against each other in another biplot and genotypes *viz.*, ABG 11015, IC 343857, KKB 1445, KKB

Table 4. Hierarchical clustering in blackgram germplasm

Cluster	Frequency	Cluster Membership
I	19	IC 436852, VBG 13017, RU 1515, IC 436765, IC 28198, RU 15009, RU 159, KKB 1443, VBN 6, RU 1516, KKB 1448, IC 436626, VBN 4, VBG 10024, VBG 11040, IC 343885, ABG 11037, ABG 11011 and IC 436811
II	2	KKM1 and ABG 11032
III	11	ABG 11028, KKB 14009, KKB 1445, KKB 1449, RU 153, KKB 14038, VBG 11018, KKB 1444, ADT 3, ABG 11036 and IC 436720
IV	2	IC 343936 and IC 281999
V	18	ABG 11015, KKB 14032, VBG 11042, KKB 1553, CO 6, KKB 14034, KKB 1442, KKB 14040, IC 436621, KKB 14005, ADT 6, IC 343857, ADT 5, IC 436910, KKB 1420, KKB 1441, KKB 14001 and RU 1513

Table 5. Cluster means of different traits in blackgram germplasm

Traits	Cluster	Minimum	Maximum	Mean	Std. Dev.
Days to 50% flowering	1	34	40	37	1.60
	2	38	38	38	0.00
	3	34	37	35	1.12
	4	40	40	40	0.00
	5	34	38	36	0.98
Plant height (cm)	1	17.40	38.60	27.57	4.70
	2	26.60	34.90	30.75	5.87
	3	22.20	36.30	29.93	3.60
	4	12.10	17.40	14.75	3.75
	5	16.13	31.95	24.51	4.10
No. of branches/plant	1	4.0	8.0	5.6	0.96
	2	5.0	6.0	5.5	0.71
	3	4.0	8.0	5.3	1.10
	4	4.0	4.0	4.0	0.00
	5	3.0	8.0	4.9	1.16
No. of clusters/plant	1	4.00	13.00	8.63	2.24
	2	17.00	24.00	20.50	4.95
	3	6.00	15.00	9.55	3.08
	4	3.00	4.00	3.50	0.71
	5	5.00	13.00	8.11	2.17
No. of pods/plant	1	7	30	18	5.72
	2	31	38	35	4.95
	3	15	28	21	4.20
	4	3	6	5	2.12
	5	5	25	15	5.30
No. of seeds/pod	1	5	6	6	0.51
	2	7	7	7	0.00
	3	6	7	6	0.30
	4	4	5	5	0.71
	5	5	6	5	0.46
100 seed weight (g)	1	3.38	5.71	4.48	0.57
	2	5.29	5.37	5.33	0.06
	3	4.18	5.99	4.99	0.57
	4	3.31	4.5	3.91	0.84
	5	3.52	5.6	4.48	0.63
Single plant yield (g)	1	2.50	10.39	5.30	1.94
	2	11.33	11.80	11.57	0.33
	3	3.65	10.48	6.18	1.97
	4	1.11	3.52	2.31	1.70
	5	2.34	8.90	4.60	1.80

1444, KKB 1448, KKB 14038, ABG 11037, IC 436910, IC 436720, ADT 6, KKB 1441, KKB 1449, ADT 3, RU 153, KKM 1 and ABG 11036 showed positive values of both the PCs and the characters *viz.*, hypocotyls colour, hundred seed weight, number of seeds/pod and single plant yield positioned in the same quadrant influencing on divergence. Ghafoor and Arshad (2008) reported that, five yield contributing traits (branches per plant, pods per plant, biomass per plant, grain yield per plant, harvest index) were important for first three PCs, hence populations in this component were categorized as high yielding with maximum number of reproductive organs.

In the present study, 52 blackgram germplasms were grouped into five clusters based on average linkage distance method of hierarchical clustering as shown in the diagram (Table 4). Five major groups were formed as clusters *viz.*, I, II, III, IV and V consisting of 19, 2, 11, 2 and 18 genotypes respectively. Cluster means of different traits of blackgram germplasm accessions are given in Table 5. Cluster I had desirable mean value for the traits *viz.*, days to 50% flowering (34 days), plant height (38.60 cm), number of branches/plant (8). Cluster II had highest mean values for the traits *viz.*, number of clusters/plant (24), number of pods/plant (38), number of seeds/pod (7) and single plant yield (11.80) whereas Cluster III had highest mean values for the traits *viz.*, days to 50% flowering (34 days), number of branches/plant (8), number of seeds/pod (7) and hundred seed weight (5.99g). Cluster V had desirable mean values for the traits *viz.*, days to 50% flowering (34 days) and number

of branches/plant (8). Hence, the genotypes belongs to these clusters can be utilized for yield improvement in blackgram breeding programs. These results are in agreement with Jeberson *et al.* (2019), Katiyar *et al.* (2016) and Kumar *et al.* (2014). Ghafoor and Arshad (2008) grouped high yielding blackgram genotypes which indicated the importance of selection in a large set of germplasm and the breeding program was suggested involving diverse parents from various clusters. In the present study, cophenetic correlation coefficient was 0.51 which indicated the more efficiency of the clustering pattern.

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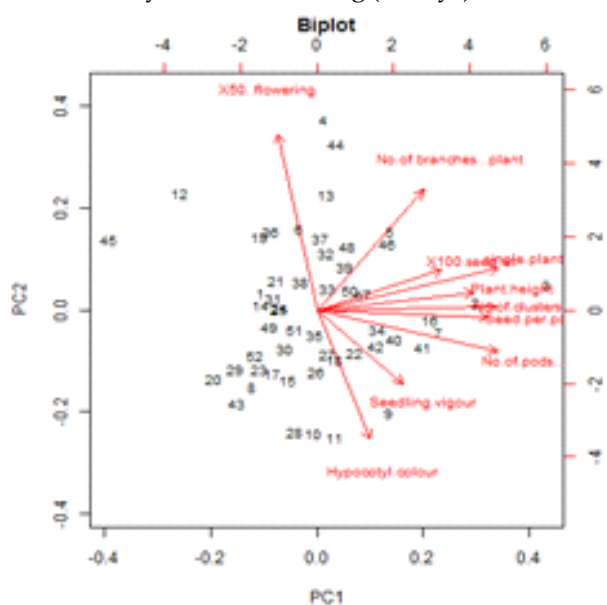


Fig. 2. The biplot of blackgram germplasm for PC<sub>1</sub> and PC<sub>2</sub>

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