Original Research Article

Principle component analysis for yield and quality traits of blackgram [*Vigna mungo* (L.) Hepper]

Abstract

The study consists of fifty nine blackgram [*Vigna mungo* (L.) Hepper] genotypes which were evaluated for fourteen traits of both quantitative and qualitative. In order to determine the relationship and genetic diversity among 59 blackgram genotypes a field experiment was conducted at Regional Agricultural Research station, Lam, Guntur district , Andhra Pradesh state during *Kharif*, 2019. Principal component analysis for various yield contributing traits was done to evaluate diversity and some quantitative and qualitative traits which had more effects on diversity. Results of PCA revealed out of five principle components ,four principle components with eigen value >1. The first five components obtained from Principal component analysis (PC 1 to PC 5) accounted for about 76.73% of the total variation for fourteen quantitative and qualitative traits. Out of total principal components retained PC 1, PC 2, PC 3, PC 4 and PC 5 with values of 35.42%, 14.85%, 11.14%, 8.75% and 6.56% respectively. The results of 2D and 3D scatter diagram revealed LBG 904 , LBG 752 and TBG 129 genotypes to be most diverse. By utilizing these diverse genotypes as parents in hybridization suggested for obtaining desirable transgressive segregants towards development of high yield with nutritional quality. The clustering of blackgram genotypes based on the yield and quality attributing traits would be helpful to identifying the appropriate genotypes for effective utilization in upcoming breeding programmes. The outcomes of principal component analysis revealed that wide genetic variability occurs between these blackgram genotypes and proposed their potential value in blackgram yield and quality improvement.

Key words : Principle component analysis, genetic divergence, yield, blackgram, PCA

1.INTRODUCTION :

Black gram [*Vigna mungo* (L.) Hepper] with chromosome number of 2n = 22 belonging to the family Leguminosae and subfamily Papilionaceous is a self-pollinating, short duration and widely cultivated grain legume (Naga *et al*., 2006). *Vigna mungo* var. *silvestris* is progenitor of black gram (Kaewwongwal *et al*., 2015) India is primary centre of origin (Vavilov, 1926). black gram grain is a rich source of protein, fibre, several vitamins and essential minerals such as calcium and iron (Reddy *et al*., 1982). Black gram is the best source of protein for vegetarian persons (Pandey *et al.*, 2016). India is the largest producer and consumer of blackgram/urd and also the world’s major contributor in blackgram production. India produces about 3060 thousand tonnes of blackgram annually from about 5602 thousand hectares of area, with an average productivity of 546 Kg per hectare, while in Adhra Pradesh about 310.56 thousand tonnes of blackgram annually from about 318 thousand hectares of area, with an average productivity of around 977 Kg per hectare.(Ministry of Agriculture, 2018)

In any hybridization programme Genetic diversity is prerequisite . Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable recombination (Jayamani and Sathya, 2013). Assessment of the nature and extent of genetic variability for qualitative, quantitative traits and genetic diversity within the black gram genotype is necessary for crop improvement interms of crop yield and quality. Principal component analysis (PCA) allows not only the natural grouping of the genotypes and is also precise indicator among genotypes differences. The main advantage of using Principal component analysis is that each genotype can be assigned to one group only. PCA has been used to identify redundancy of the genotypes with similar traits and their elimination (Adams, 1995). The present investigation was undertaken in this context to study the nature and magnitude of genetic diversity among 59 blackgram genotypes for yield, yield component and quality traits using Principal component analysis (PCA).

2. MATERIALS AND METHODS

The experimental material consisted of 59 blackgram genotypes obtained from IIPR, Kanpur and from MULLaRP scheme of Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh state. Details of the genotypes studied in the present investigation are presented in Table 1. All the 59 genotypes were sown during *Kharif* 2019-20 Regional Agricultural Research Station, Lam, Guntur of the university ANGRAU, AP. Experiment was laid in an augmented design without replication with five blocks and four check varieties. Four check varieties randomized in each block. The plot size was 2 rows of 3 meter length and spacing maintained was 30 x 10 cm. The observations were recorded on traits viz., days to flowering, plant height (cm), branches per plant, cluster per plant, pods per plant, pod length (cm), seeds per pod, days to maturity, 100 seed weight (gm), grain yield per plant (gm), Harvest index (%), protein content (%), Iron content (mg/100g) and Zinc content (mg/100g).The observations recorded on ten randomly selected plants from the middle of the row avoiding the plants from the border and are tagged. observations on test weight, days to 50% flowering and days to maturity and all the quality parameters *viz.,* Protein, Iron, and Zinc were recorded on plot basis. Total variance among the 55 genotypes and 4 check entries were separated into different sources (‘genotypes + check entries’, ‘ genotypes’, ’check entries’ and ‘genotypes *vs* check entries’) using Augmented design (Federer, 1956). Principal component analysis was carried out using the software Window Stat Version 8.5.

Table 1. Details of the blackgram genotypes studied and their sources

Sl. N	Genotype	Source	Sl. N	Genotype	Source

1	KU 96-7	CSA,Kanpur	31	PU 1501	GBPU A&T, Pantnagar
2	MBG 1070	ARS,Madhira	32	OBG 102	OUAT, Bhubaneswar
3	LBG 918	RARS,Lam	33	TBG 129	RARS,Tirupati
4	IPU 17-1	IIPR, Kanpur	34	LBG 776	RARS,Lam
5	DBGV 16	UAS, Dharwad	35	WBU 108	PORS,Berhampore
6	OBG 103	OUAT, Bhubaneswar	36	KPU1720-140	ARS, Kota
7	DKU 90	CSK HPKV, Palampur	37	LBG 709	RARS,Lam
8	Uttara	IIPR, Kanpur	38	TU 50	BARC,Mumbai
9	VBG 09-005	NPRC, Pudukkottai	39	LBG 868	RARS,Lam
10	KPU 52-87	ARS,Kota	40	TU 40	BARC,Mumbai
11	PU 31	GBPUAT, Pantnagar	41	MU 52	MSSC Ltd, Akola
12	KU 17-04	CSAU,Kanpur	42	RU 03-22-4	IGKVV, Raipur
13	DKU 116	Dhaulakuan	43	KUG 818	PAU, Ludhiana
14	CO 5	NPRC,Vamban	44	VBG 12-110	NPRC, Vamban
15	GJU 1509	SDAU,S.K nagar	45	NUL 242	Nirmal seed
16	LBG 854	RARS,Lam	46	ADT 5	TNAU,Aduthurai
17	VBG 17-026	NPRC, Vamban	47	ADT6	TNAU,Aduthurai
18	VBN -5	NPRC,Vamban	48	VBG 17-029	NPRC, Vamban
19	OBG 41	OUAT, Bhubaneswar	49	OBG 101	OUAT, Bhubaneswar
20	VBG 12-062	NPRC,Vamban	50	IPU 11-6	IIPR, Kanpur
21	LBG -623	RARS,Lam	51	IPU 1702	IIPR, Kanpur
22	TU 44	BARC, Mumbai	52	LBG 972	RARS,Lam
23	ADBG 13023	TNAU,Aduthurai	53	LBG 885	RARS,Lam
24	AKU 1608	PDKV, Akola	54	LBG 883	RARS,Lam
25	IPU 12-5	IIPR, Kanpur	55	LBG 880	RARS,Lam
26	VBG 13-003	NPRC, Vamban	56	LBG 787	RARS,Lam
27	LBG 904	RARS,Lam	57	IPU 2-43	IIPR, Kanpur
28	SBC 50	RARS, Shillongani	58	LBG 752	RARS,Lam
29	TJU 134	BARC, Mumbai	59	TU 94-2	BARC, Mumbai
30	PU 1541	GBPU A&T, Pantnagar			

3.RESULTS AND DISCUSSION :

In the present study, PCA was estimated for fourteen traits of fifty nine genotypes of blackgram. The first principle component (PC1) contributed 35.423% towards variability. Characters *viz.*, grain yield per plant (0.414), number of pods per plant (0.373) and harvest index (0.379) explained the maximum variance in first principle component(PC1). The second axis (PC 2) contributed 14.853% variability and variation at this axis is because of the following traits *viz.*, days to maturity (0.433), plant height (0.354) and iron content. PC 3 contributed 11.146 % of variation with loading of days to 50% flowering(0.291) , days to maturity (0.209) and number of branches per plant (0.167) . The fourth principle component (PC 4) was characterized by 8.750 percent contributed towards the total variability. This axis showed positive loadings for Zinc content (0.316) , number of branches per plant (0.297) and days to 50% flowering(0.148) and the fifth principle component (PC 5) was characterized by 6.563 percent contributed towards the total variability. This axis showed positive loadings for number of seeds per pod (0.338), pod length (0.301) and days to maturity (0.205).

The cumulative variability percentage for first component is 35.423, while it is 50.276 for PC 2, 61.422 for PC 3, 70.173 for PC 4 and 76.736 for PC 5 (Table 1). The PCA scores for 59 blackgram genotypes in the first three principle components were computed and were considered as three axes as X,Y and Z and squared genotype from these three axes were calculated (Table 2). The pattern of spreading of the genotypes in these clusters was detected to be at random with no reference to geographical diversity as genotypes from different geographical regions were clustered in the same as well as different clusters.The PCA scores for 59 genotypes plotted in graph to get the 2D (PCA I as X axis and PCA II as Y axis) and 3D (PCA I as X axis, PCA II as Y axis and PCA III as Z axis) scatter diagram (Fig. 1 and Fig. 2).

The diverse genotypes numbered 27 (LBG 904),58 (LBG 752), and 33(TBG 129) which are far away from other genotypes in the 2 dimention and 3 dimention diagram (Fig 1 & 2) may used as parents in hybridization to exploit the transgressive segregants.

Usage of PCA for getting 2D & 3D digrams and to understand the genetic diversity was earlier used in various crops Jadhav *et al.,(*2014) in finger millet, Naik *et al.,* (2016) in cotton and Nainu *et al.,* (2020) in mungbean for identifying promising parents and to produce superior segregants in subsequent generations.

Table 2. Eigen value, per cent variance and percent cumulative variance for five principal components (PCs) and factor loading between PCs and traits studied in blackgram (*Vigna mungo*(L.) Hepper)

Canonical Roots Analysis (P. C. A.)						
	Components	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
	Eigene Value (Root)	4.95926	2.07946	1.56049	1.22509	0.91885
	% Var. Exp.	35.42328	14.8533	11.14639	8.75061	6.56322

	Cum. Var. Exp.	35.42328	50.27658	61.42296	70.17357	76.73679
	Characters	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
1	Days to 50% Flowering	0.27311	0.27958	0.29113	0.14814	0.09769
2	Days to maturity	0.2272	0.43322	0.20978	0.00721	0.20514
3	Plsnt height (cm)	0.22832	0.35434	0.15533	-0.03623	0.05019
4	Number of branches per plant	0.26926	0.27798	0.16774	0.29795	0.09285
5	Number of clusters per plant	0.32718	-0.39255	0.03246	0.12817	0.02131
6	Number of pods per plant	0.37304	-0.32604	0.07726	0.09448	-0.02828
7	Pod length (cm)	0.19888	-0.03188	-0.52202	-0.01192	0.30183
8	Number of seeds per pod	0.29012	0.02819	-0.36248	-0.17266	0.3382
9	100-Seed weight (g)	0.17746	0.15724	0.07679	-0.42969	-0.66854
10	Harvest Index (%)	0.37911	-0.23543	0.0894	-0.04726	-0.13137
11	Protein content (%)	0.09716	0.12295	-0.10932	-0.71973	0.15591
12	Iron content (mg/100g)	0.10224	0.32065	-0.41532	0.15348	-0.15554
13	Zinc content (mg/100g)	0.11112	0.17104	-0.4559	0.3168	-0.45407
14	Grain Yield Per plant (g)	0.41446	-0.20438	0.04332	-0.06169	-0.10775

Table 3. The PCA scores of genotypes of 59 genotypes of blackgram (*Vigna mungo* (L.) Hepper)

		PCA I	**PCA II**	**PCA III**			**PCA I**	**PCA II**	**PCA III**
Sl. N	**Genotype**	**X Vector**	**Y Vector**	**Z Vector**	**SL N**	**Genotype**	**X Vector**	**Y Vector**	**Z Vector**

1	KU 96-7	67.258	45.608	24.878	31	PU 1501	72.475	32.769	25.393
2	MBG 1070	68.084	43.533	25.197	32	OBG 102	66.615	37.847	24.953
3	LBG 918	82.908	42.048	30.78	33	TBG 129	84.233	36.546	31.122
4	IPU 17-1	67.656	43.68	25.455	34	LBG 776	77.575	39.937	29.713
5	DBGV 16	72.344	38.51	26.59	35	WBU 108	62.646	33.58	23.636
6	OBG 103	66.993	44.303	26.466	36	KPU1720-140	68.284	32.614	24.874
7	DKU 90	63.891	43.296	24.968	37	LBG 709	76.493	43.074	29.774
8	Uttara	75.447	46.506	30.513	38	TU 50	70.712	40.198	26.063
9	VBG 09-005	60.486	44.99	23.94	39	LBG 868	77.049	42.532	27.985
10	KPU 52-87	63.263	44.855	24.741	40	TU 40	71.005	34.483	26.012
11	PU 31	79.856	32.953	28.255	41	MU 52	64.572	36.519	23.778
12	KU 17-04	68.064	42.215	25.552	42	RU 03-22-4	68.937	28.775	23.605
13	DKU 116	65.492	45.125	23.768	43	KUG 818	75.232	29.423	26.446
14	CO 5	64.494	46.066	25.711	44	VBG 12-110	61.227	41.14	23.534
15	GJU 1509	72.076	40.088	27.142	45	NUL 242	60.002	40.53	24.539
16	LBG 854	82.122	42.82	31.723	46	ADT 5	62.375	31.32	22.704
17	VBG 17-026	63.743	47.94	25.517	47	ADT6	69.341	42.203	25.988
18	VBN -5	73.474	37.719	26.144	48	VBG 17-029	75.618	41.1	29.654
19	OBG 41	70.214	39.44	27.367	49	OBG 101	66.132	49.011	28.065
20	VBG 12-062	60.845	47.651	26.278	50	IPU 11-6	60.098	47.568	22.765
21	LBG -623	67.281	49.084	28.553	51	IPU 1702	61.443	45.792	22.879
22	TU 44	74.522	34.986	26.853	52	LBG 972	74.255	45.487	28.396
23	ADBG 13023	76.824	35.02	25.773	53	LBG 885	81.405	40.568	30.618
24	AKU 1608	78.55	32.9	26.408	54	LBG 883	76.652	44.589	30.278
25	IPU 12-5	71.231	42.078	28.246	55	LBG 880	80.132	40.321	30.641
26	VBG 13-003	62.177	47.635	27.096	56	LBG 787A©	79.229	44.254	32.258
27	LBG 904	91.561	34.303	32.467	57	IPU 2-43A©	77.506	43.449	30.243
28	SBC 50	67.415	43.141	27.107	58	LBG 752A©	88.647	35.114	32.227
29	TJU 134	60.994	42.774	25.62	59	TU 94-2A©	65.014	50.973	28.735
30	PU 1541	70.858	36.728	27.314					

4.Conclusion: This result proposes that genotypes in clusters which are separated by high statistical distance should be utilized in potential hybridization programmes. The diverse genotypes numbered 27 (LBG 904),58 (LBG 752), and 33(TBG 129) which are far away from other genotypes in the 2 dimention and 3 dimention diagram (Fig 1 & 2) may used as parents in hybridization to exploit the transgressive segregants.

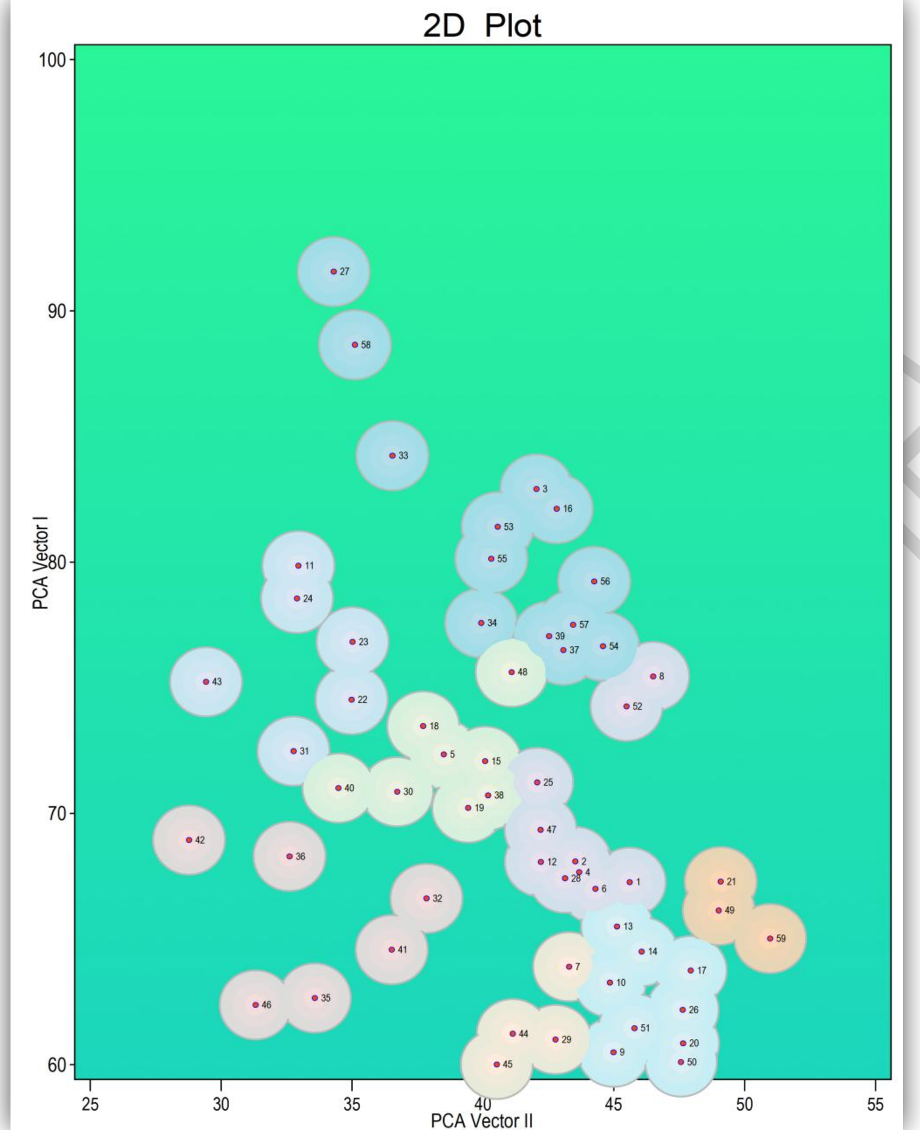

Fig 1 Two dimentional graph showing relative positions of 59 blackgram genotypes based on PCA score

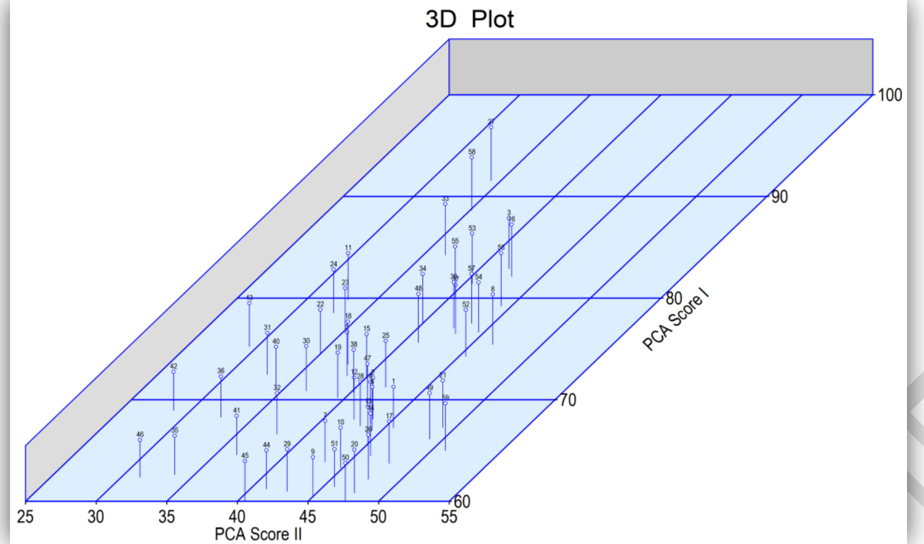

Fig 2: Three dimensional graph showing relative positions of 59 blackgram genotypes based on PCA scores

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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