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Research Article

Genetic diversity analysis in blackgram [*Vigna mungo* (L.) Hepper]

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Abstract
A study was conducted focusing on assessing the level of variability represent among the hundred and two blackgram genotypes based on Mahalanobis's D^2 statistics for nine quantitative traits. Out of eighteen clusters, the maximum inter cluster distance was observed between cluster XVI and XV. Cluster XVIII had a low mean value for days to 50% flowering, cluster XIII had a high mean value for plant height, the number of primary branches per plant and cluster XVII recorded the highest number of pods per plant. High heritability coupled with high GAM was observed for plant height, the number of primary branches per plant, the number of clusters/plants, the number of seeds per pod, hundred seed weight, protein content, and single plant yield. From the association analysis single plant yield was positively and significantly associated with the number of clusters per plant and the number of pods per plant. Hence, simultaneous selection of the above traits would be more rewarding to bring genetic improvement in black gram breeding programmes.

Key words
Blackgram, Correlation, Variability, Heritability, Genetic Diversity.

INTRODUCTION

Black gram (*Vigna mungo* L. Hepper), also called urdbean is a member of the Asian *Vigna* crop group. It is extensively used only in India and now grown in the Southern United States, West Indies, Japan and other tropics and subtropics (Delic *et al*., 2009). Seed yield of black gram is low, being about 450–800 kg/ha (Gupta *et al.,* 2013). The major constraints in achieving higher productivity are lack of exploitable genetic variability, absence of suitable ideotype for different cropping systems poor harvest index, susceptibility to biotic and abiotic stresses, non-availability of quality seeds of improved varieties and narrow genetic base occur due to repeated usage of few parents with a high degree of relatedness in crossing programmes. Limited variability has been exploited in varietal development programmes in black gram (Jayamani and Sathya, 2013).

To increase the potential of a black gram as food and feed, it is necessary to study and exploit the genetic diversity of this crop. Genetic diversity is a pre-requisite for any crop improvement program as it helps in estimating and establishing genetic relationship in germplasm collection, identifying diverse parental combinations to create segregating progenies with maximum genetic variability and superior recombinations for further selection and introgressing desirable genes from diverse germplasm. The D^2 analysis proposed by Mahalanobis (1936) is an effective tool in quantifying the degree of genetic divergence among the genotypes. Keeping the above in view, the present study was undertaken to identify the best performing germplasm of black gram based on quantitative traits using Mahalanobis D^2 statistics and Tocher's method.

MATERIALS AND METHODS

In the present study, 102 genotypes of black gram (**Table 1**) were evaluated at the Department of Plant Breeding and Genetics in Agricultural College and

Table 1. Pedigree details of blackgram genotypes

S. No.	Germplasm accessions	Pedigree	S. No.	Germplasm accessions	Pedigree
1	KU-12-668	Selection from TU 94-2	26	VBG-11-037	ADT 5 x *Vigna mungo* var. *silvestris*
2	ABG-11-004	VBN 1 x VBN 3-3	27	IC281999	Kolhar, Adilabad, A P
3	IC436720	Landrace-Bhimpur, Adilabad, AP	28	IC 413304	Landrace- Gangwar, Medak,
4	VBG-12-042	VBN 5 x COBG 757	29	IC343939	Land race
5	VBG-11-018	VBG 73 x *Vigna mungo* var. *silvestris*	30	IC343885	Land race
6	IC-436784	Land race	31	VBG-11-050	ADT 5 x *Vigna mungo* var. *silvestris*
7	VBG-12-005	VBN 3 x *Vigna mungo* var. *silvestris*	32	IC 281994	Singango, Adilabad, AP
8	ABG-11-011	RBU 38 x TMV 1/4/1	33	IC 436758	Land race
9	VBG-11-020	VBN 5 x VBG 04-001	34	KKB-14-011	IPU 2006-01 x TNY local
10	IC-398989	Landrace- Vinjamur, Nellore, AP	35	VBG 13-023	VBN 5 x VBN 4
11	VBG.12.034	VBN 1 x KU 238	36	VBG 10053	VBN 2 x VBN 04003
12	IPU.0233	-	37	IC 281989	Pochara, Adilabad, A P
13	VBG10.010	AD 75 x *Vigna mungo* var. *silvestris*	38	IC 282002	Machkal, Adilabad, A P
14	KU.12.39	Selection from COBG 10-05	39	ABG 11-030	CO 5 x AC 196/3/3
15	ABG.11.013	VBN 4 x Co(Bg) 629/8/3	40	IC 282007	Narsapur, Madak, AP
16	IC281986	Lakkanpur, Adilabad, AP	41	IC 281993	Singango, Adilabad, AP
17	VBG-11-043	AD 75 x *Vigna mungo* var. *silvestris*	42	VBG-14-003	KU 216 x VBN 3
18	KU-11-680	Selection from IPU 99-33	43	IC 282008	Land race
19	ABG-11-028	Co(Bg) 671 X ADT 5	44	IC 281792	Land race
20	ABG-11-032	Co 5 x VBN 4/6/1	45	VBG 11-028	ADT 5 x *Vigna mungo* var. *silvestris*
21	ABG-11-011	RBU 38 x TMV 1/4/1	46	VBG-12-121	VBN 3 x AM 6
22	IC343967	Rampachodavaram East Godavari, A P	47	IC 281980	Thumikipad, Khammam, AP
23	VBG-11-044	VBG 73 x *Vignamungo* var. *silvestris*	48	IC 281982	Pashathand, Adilabad, AP
24	ADT-5	Pure line selection from kanpur	49	KKB-14-001	IPU 2006-01 x ADT 3
25	VBG-11-046	ADT 5 x *Vignamungo var. silvestris*	50	IC 281977	Penpahad, Nalgonda, AP
51	VBG 14-015	VBN 5 x PU 31	77	VBG-12-122	VBN 3 x AM 6
52	VBG 11045	VBG 73x Vignamungo var. silvestris	78	VBG 11024	ADT 5x*Vigna mungo* var. silvestris
53	VBG-11-041	ADT5 x *Vigna mungo* var. silvestris	79	IC 436736	Landrace-Lokari, Adilabad, A P
54	IC398970	Kammapalli, Prakasam, A P	80	VBG-14-013	Selection from ACM 05 007
55	IC281987	Chinchalli, Adilabad, AP	81	IC282004	Improved cultivar- Mudhol, Adilabad, A P
56	KKB 14-003	IPU 2006-01 x TNY local	82	VBG 10-024	VBG 73 x *Vigna mungo* var. silvestris
57	VBG-12-122	VBN 3 x AM 6	83	VBG-11-027	ADT 5 x *Vigna mungo* var. silvestris
58	VBG-12-039	VBN 1 x PU 31	84	VBG-11-042	ADT 5 x *Vigna mungo* var. silvestris
59	IC281978	Aathukur,Khammam,AP	85	VBG 12-093	VBG 73 x *Vigna mungo* var. silvestris
60	IC436724	Lokari, Adilabad, A P	86	IC343962	Others- Sunnampadu, East Godavari, A P
61	ABG-11-035	Co(Bg) 671 X Co(Bg) 647/3/3	87	IC281982	Improved cultivar- Pashathand, Adilabad, A P
62	ABG-11-037	Co(Bg) 671 x ADT 5	88	IC335331	Others- Mimillapally, Ponnur, Guntur, A P
63	VBG-11-033	VBG 73 x *Vigna mungo* var. *silvestris*	89	VBG-11-029	VBG 73 x *Vigna mungo* var. *silvestris*
64	ABG-11-015	RBU 38 x TMV 1/1/1	90	IC281991	Kolhar, Adilabad, A P
65	IC343943	Others- Chandhurthi, East Godavari, A P	91	ABG-11-036	Co(Bg) 671 X Co(Bg) 647/1/4
66	VBG-12-034	VBN 1 x KU 238	92	VBG-11-040	VBN 1 x *Vigna mungo* var. silvestris
67	KKB 06-012	VBN3 x COBG 643	93	VBG-13-019	VBN 3 x *Vigna mungo* var. silvestris
68	IC436765	Liguguda, Adilabad, A P	94	IC281990	Daltabad, Adilabad, A P
69	VBG 12062	PU 31 x CO 6	95	IC436536	Siripuram, RangaReddy, A P
70	IC 281992	Singango, Adilabad, A P	96	IC343947	Others- Seethapally, East Godavari,AP
71	IC281984	Improved cultivar- Rolemanda, Adilabad,A P	97	KU-11-667	Selection from UH 07-06
72	VBG 13-017	VBN 3 x *Vigna mungo* var. *silvestris*	98	IC281995	Singango, Adilabad, A P
73	IC436727	Landrace- Lokari, Adilabad, AP	99	KKB-05-011	CoBg 643 x VBN 3
74	IC282001	Improved cultivar- Machkal, Adilabad, A P	100	APK-1	ADT 2 x RU 1
75	IC436811	Landrace- Gottipattar, Adilabad, A P	101	VBN 4	CO 4 x PDU 102
76	VBG-12-056	PU 31 x CO 6	102	ADT 3	Pureline selection from Tirunelveli local

Research Institute, Killikulam, Tamil Nadu, during 2016-17. The collected germplasm lines were sown in a randomized block design (RBD) with two replications. Each genotype was planted in 3 meter row to accommodate 20 plants per row with a spacing of 30 x 10 cm. Observations were recorded on five randomly selected plants from each genotype for each replication for various yield attributes *viz*., days to 50% flowering, plant height (cm), the number of primary branches per plant, the number of clusters per plant, the number of pods per plant, the number of seeds per pod, hundred seed weight (g), protein content (g) and single plant yield (g). The data were subjected to statistical analysis using (Mahalanobis, 1936) D^2 statistics and the Tochers method as described by Rao (1952) for determining group constellation. Average inter and intra cluster distances were estimated as per the procedure outlined by Singh and Choudhary (1977). The various genetic parameters *viz.,* Genotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV), heritability (h^2) and Genetic Advance as a percentage of Mean (GAM) were calculated by adopting the formulae given by Johnson *et al.* (1955). The genotypic correlation coefficient was calculated based on the formulae given by Snedecor (1961).

RESULTS AND DISCUSSION

The mean performance showed a wide range of variation for most of the characters under study. The mean performance of genotypes for days to 50 per cent flowering ranged from 30.00 (VBG 12034, VBG 10010) and to 44.50 (KKB 14011) days. The plant height recorded the mean value of 43.02 cm with a range of 22.40 cm (KU 1239) to 59.90 cm (ABG 11036). The mean performance of the trait number of primary branches per plant was 5.84 and the range varied from 3.20 (IC281978) to 11.60 (ABG 11030). The number of clusters per plant recorded the mean of 7.88 with the range of 3.20 (IC 282002) to 18.40 (IC 281982). The mean obtained for the trait number of pods per plant was 28.97 with the range varied between 15.20 (VBG 11024) and 49.60 (KU 11667). The mean obtained for the trait was 6.51 which revealed significant in 14 genotypes. The trait number of seeds per pod exhibited the minimum of 5.00 (VBG 12122, IC 281980) and the maximum 8.00 (VBG 13023) based on the mean value. The range recorded for single plant yield varied from 3.17 g (ABG 11011) to 6.60 g (IC 335331) with an average of 4.67 g and seventeen genotypes had shown significantly higher values for this trait based on the mean value. The range recorded for single plant yield varied from 4.02 g (IC 343947) to 29.10 g (IC 343962) with an average of 11.13 g and thirty-three genotypes had shown significantly higher value for this trait based on the mean value. The range recorded for protein content varied from 17.20 g (VBG 11044) to 28.44 g (ABG 11015) with an average of 23.07 g and 28 genotypes had shown significantly higher value for this trait based on the mean value. Based on overall mean performance, the genotypes IC 343885 and IC 335331 are suitable to improve the yield, and also other characters *viz*., the number of clusters per plant and the number of pods per plant. The genotypes KKB 14001 AND KKB 14003, IC 343885 are suitable to improve the number of pods and clusters per plant. Therefore, these genotypes can be used in the future breeding programme for improving the seed yield and other characters (**Table 2**).

Table 2. Mean performance of 9 characters in blackgram genotypes

S. No.	Name of genotypes	Days to 50 % flowering	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Single plant yield (g)	Protein content (g)
1	KU 12668	37.50*	33.50	5.60	8.30	33.20 *	7.16	4.36	7.09	23.51
2	ABG 11004	40.00	42.30	6.60 *	10.70 *	42.80 *	6.50	3.54	10.80	26.91*
3	IC 436720	39.50	48.10 *	5.40	9.50 *	28.50	6.60	6.56 *	16.40 *	27.71*
4	VBG 12042	31.50*	44.20	5.80	9.90 *	29.70	6.33	4.80	16.70 *	22.00
5	VBG 11018	34.00*	46.80 *	5.80	9.60 *	19.20	6.50	4.84	22.70 *	22.27
6	IC 436784	40.50	51.70 *	6.80 *	6.10	30.50	6.60	3.63	8.15	25.78*
7	VBG 12005	32.50*	45.80 *	7.00 *	10.80 *	43.20 *	6.00	4.32	9.80	20.83
8	ABG 11011	34.50*	49.30 *	7.00 *	6.40	25.60	7.25	3.17	11.30	27.27*
9	VBG 11020	34.00*	36.00	5.80	7.80	31.20 *	6.25	4.86	17.87 *	18.99
10	IC 398989	31.50*	57.50 *	5.80	11.00 *	33.00 *	6.70	4.42	7.00	24.51
11	VBG 12034	30.00*	43.00	5.60	7.80	31.20 *	6.25	4.54	11.54	23.48
12	IPU 0233	31.50*	34.00	5.60	8.40	25.20	7.20	4.60	11.00	24.18
13	VBG 10010	30.00*	29.75	6.20	7.20	36.00 *	7.20	4.77	11.34	20.93
14	KU 1239	33.00*	22.40	4.80	6.60	26.40	7.00	4.95	9.06	17.80
15	ABG 11013	40.00	44.90 *	5.20	5.70	28.50	6.40	4.25	8.20	23.93
16	IC 281986	36.00*	46.30 *	5.40	5.70	28.50	7.70 *	5.44 *	9.82	21.53
17	VBG 11043	38.50	43.60	4.50	7.90	23.70	6.40	4.07	5.94	22.65
18	KU-11-680	37.50*	25.75	4.80	8.10	40.50 *	6.00	4.33	12.98 *	19.58
19	ABG 11028	36.00*	36.70	4.60	6.20	31.00 *	6.00	4.60	10.36	25.80*
20	ABG 11032	40.50	53.30 *	4.80	6.10	30.50	7.00	5.54 *	13.05 *	26.79*
21	ABG 11011	32.00*	48.90 *	3.80	11.00 *	44.00 *	6.33	3.17	7.97	27.27*

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22	IC 343967	33.00*	48.10 *	5.60	9.20 *	36.80 *	6.25	4.59	9.32	21.17
23	VBG 11044	39.00	48.55 *	5.80	8.25	24.75	6.00	4.42	10.48	17.20
24	ADT 5	33.50*	42.25	5.80	8.70	26.10	7.00	4.86	16.60 *	24.36
25	VBG 11046	34.00*	29.20	5.40	4.40	22.00	5.80	4.31	10.13	21.50
26	VBG 14015	42.50	36.80	4.40	5.10	20.40	7.60 *	3.80	8.00	25.77*
27	VBG 11045	37.50*	43.60	3.80	4.20	16.80	6.33	3.82	9.82	21.45
28	VBG 11041	40.00	39.45	3.40	4.50	18.00	6.28	5.31	15.48 *	20.24
29	IC 398970	38.00*	51.80 *	3.60	9.00 *	27.00	6.37	6.41 *	11.38	22.42
30	IC 281987	35.00*	40.20	3.60	3.85	19.25	6.80	4.56	29.00*	25.23*
31	KKB 14003	34.50 *	31.24	4.60	15.80 *	48.40 *	5.62	4.20	4.38	21.30
32	VBG 12122	40.00	37.10	3.80	6.90	27.60	5.00	5.16	6.81	22.33
33	VBG 12039	40.00	45.10 *	3.80	9.10 *	27.30	6.80	4.87	9.47	17.50
34	IC 281978	30.50*	35.90	3.20	8.00	24.00	6.00	4.56	8.77	23.64
35	IC 436724	37.50*	52.10 *	4.20	7.10	28.40	6.27	4.62	11.63	23.24
36	ABG 11035	43.00	54.20 *	5.80	7.40	37.00 *	6.37	6.02 *	7.70	22.88
37	ABG 11037	43.00	54.00 *	6.00	5.60	28.00	6.75	4.65	14.61 *	25.66*
38	VBG 11033	32.00*	45.00 *	5.60	6.30	25.20	6.00	4.36	8.17	18.99
39	ABG 11015	41.50	49.70 *	5.40	4.80	24.00	7.00	4.86	7.54	28.44*
40	IC 343943	33.50*	47.10 *	3.40	8.80 *	26.40	7.50 *	5.41 *	8.45	23.43
41	VBG 12034	42.50	43.00	4.40	4.60	23.00	6.20	4.54	13.20 *	23.48
42	KKB 06012	43.00	41.00	4.30	13.60 *	24.00	7.30 *	4.30	8.20	20.10
43	IC 436765	39.00	45.80 *	4.80	7.00	35.00 *	5.20	5.34 *	8.07	24.94*
44	VBG 12062	43.50	39.80	5.60	7.40	29.60	6.65	4.14	16.58 *	23.17
45	IC 281992	32.50*	51.35 *	5.40	4.90	24.50	6.25	5.62 *	9.32	22.16
46	IC 281984	36.50*	45.00 *	4.40	7.20	36.00 *	6.30	6.30 *	9.30	23.35
47	VBG 13017	37.00*	25.00	4.20	4.60	23.00	5.50	5.20	6.47	25.03*
48	IC 436727	36.00*	48.10 *	5.40	8.40	25.20	7.00	5.57 *	7.30	26.95*
49	IC 282001	35.00*	48.55 *	5.00	10.80 *	32.40 *	7.30 *	5.29	14.74 *	20.88
50	IC 436811	32.00*	36.45	4.80	10.80 *	32.40 *	7.50 *	6.44 *	5.15	27.13*
51	VBG 12056	31.50*	32.70	6.80 *	7.60	30.40	6.10	4.37	8.09	23.78
52	VBG 11037	36.50*	49.10 *	5.60	4.00	16.00	7.10	5.15	7.16	22.18
53	IC 281999	37.00*	54.70 *	5.80	10.40 *	41.60 *	5.40	4.54	10.09	25.91*
54	IC 413304	41.00	44.95 *	5.20	5.80	17.40	6.00	5.44 *	7.34	26.78*
55	IC 343939	36.50*	47.00 *	5.20	7.20	21.60	7.00	5.18	14.28 *	22.37
56	IC 343885	35.00*	46.10 *	5.80	10.20 *	40.80 *	6.70	5.50 *	17.40 *	26.21*
57	VBG 11050	33.00*	37.90	4.80	9.00*	24.00	6.25	5.52 *	13.80 *	18.26
58	IC 281994	36.50*	44.80 *	4.40	4.20	21.00	6.75	4.51	17.80 *	24.19
59	IC 436758	35.00*	46.10 *	6.00	4.90	24.50	7.00	4.49	8.53	19.11
60	KKB 14011	44.50	41.80	5.40	14.80 *	37.80 *	6.50	3.60	8.30	21.30
61	VBG 13023	37.50*	43.70	5.20	5.00	25.00	8.00*	4.63	5.30	22.16
62	VBG 10053	33.00 *	25.10	8.80 *	3.80	19.00	7.00	4.34	6.38	22.88
63	IC 281989	37.00*	46.60 *	5.80	5.20	26.00	7.50 *	5.27	8.12	20.94
64	IC 282002	38.50	52.30 *	7.80 *	3.20	16.00	7.80 *	6.20 *	15.90 *	19.58
65	ABG 11030	39.00	53.20 *	11.60 *	7.60	38.00 *	6.25	3.60	6.51	27.97*
66	IC 282007	37.00*	38.90	7.50 *	5.20	26.00	7.90 *	4.62	19.60 *	24.36
67	IC 281993	38.00*	54.70 *	8.60 *	4.60	23.00	7.10	4.61	9.70	26.39*
68	VBG 14003	37.50*	45.00 *	10.00 *	8.00	32.00 *	5.66	3.55	12.95 *	19.81
69	IC 282008	35.00*	41.00 *	9.20 *	8.40	25.20	7.50 *	3.97	6.07	21.86
70	IC 281792	43.50	58.80 *	10.65 *	5.20	26.00	7.40 *	4.30	14.30 *	22.14
71	VBG 11028	35.00*	44.80 *	6.80 *	9.80 *	29.40	5.83	4.61	13.09 *	22.90
72	VBG 12121	31.00*	30.70	7.20 *	7.20	21.60	5.25	4.41	15.18 *	25.02
73	IC 281980	35.50*	43.70	5.60	5.60	28.00	5.00	4.28	14.37 *	24.65
74	IC 281982	34.00 *	44.70 *	8.45 *	18.40 *	28.00	6.25	4.00	7.98	23.37
75	KKB 14001	37.50*	29.46	7.80 *	5.60	48.80 *	6.80	4.20	9.30	21.24
76	IC 281977	38.50	46.90 *	8.40 *	5.60	28.00	7.00	4.59	14.30 *	23.22
77	VBG 12122	37.50*	37.10	6.00	5.80	29.00	7.00	5.16	6.14	24.06
78	VBG 11024	38.00*	48.50 *	6.40 *	7.60	15.20	7.00	5.18	9.84	19.66
79	IC 436736	36.00*	52.00 *	9.40 *	6.80	27.20	5.75	4.66	8.90	23.73
80	VBG 14013	33.50*	38.50	6.80 *	7.40	29.60	6.66	4.62	5.00	21.36
81	IC282004	34.50*	44.00	7.00 *	8.80 *	26.40	6.20	4.74	19.80 *	22.33
82	VBG 10024	31.00*	29.60	7.40 *	7.20	36.00 *	6.30	3.43	11.70	20.17
83	VBG 11027	38.00*	41.90	6.80 *	10.00 *	20.00	5.80	4.34	11.70	22.52
84	VBG 11042	38.00*	43.00	5.40	10.00 *	22.00	6.60	4.13	18.80 *	25.41*
85	VBG 12093	33.50 *	44.10	8.00 *	7.80	23.40	6.80	4.88	5.06	21.56

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86	IC 343962	37.00*	46.40 *	5.60	8.40	25.20	6.00	4.53	29.10 *	23.33
87	IC 281982	34.00 *	44.70 *	5.40	8.60	25.80	6.70	4.00	12.34 *	26.45*
88	IC 335331	35.00*	53.20 *	5.80	8.60	43.00 *	6.00	6.60 *	15.40 *	24.33
89	VBG 11029	34.50 *	47.80 *	5.60	16.20 *	32.40 *	6.00	4.69	15.40 *	17.29
90	IC281991	35.50*	39.80	6.00	8.20	24.60	5.87	4.53	18.45 *	25.79*
91	ABG 11036	37.50*	59.90 *	6.60 *	9.80 *	49.00 *	6.20	4.72	17.70 *	27.77*
92	VBG 11040	33.00 *	29.20	6.00	7.20	21.60	6.06	4.68	15.73 *	28.21*
93	VBG 13019	39.00	35.10	7.40 *	10.80 *	32.40 *	6.65	4.43	8.00	17.80
94	IC 281990	36.00*	36.50	4.60	7.20	36.00 *	5.97	3.88	8.41	21.06
95	IC 436536	35.50*	45.50 *	4.20	10.00 *	30.00	7.30 *	4.63	4.30	26.22*
96	IC 343947	36.00*	43.60	4.60	4.60	23.00	6.85	4.61	4.02	22.31
97	KU 11667	38.50	46.40 *	5.20	12.40 *	49.60 *	6.87	4.40	9.74	21.41
98	IC 281995	35.00	49.10 *	4.30	8.00	24.00	6.00	5.37 *	7.17	18.99
99	KKB 05011	41.50	40.60	6.00	14.20 *	48.60 *	5.37	4.40	9.01	26.52*
100	APK 1	33.00 *	36.00	5.80	7.00	35.00 *	6.13	4.06	9.62	22.00
101	VBN 4	36.50	37.10	7.00 *	10.80 *	32.40 *	5.33	3.96	9.25	24.31
102	ADT 3	36.00	44.80 *	5.80	7.00	24.00	7.70 *	3.81	8.18	22.45
	Mean	36.40	43.02	5.84	7.88	28.97	6.51	4.67	11.13	23.07
	Range	30.00-44.50	22.40-59.90	3.20-11.60	3.20-18.40	15.20-49.60	5.00-8.00	3.17-6.60	4.02-29.10	17.20-28.44
	SED	0.71	0.68	0.26	0.31	0.62	0.28	0.23	0.35	0.58
	CD (0.05)	2.00	1.90	0.74	0.87	1.75	0.78	0.65	0.99	1.62
	CD (0.01)	2.65	2.52	0.98	1.16	2.31	1.04	0.86	1.31	2.14

Genetic divergence analysis was carried out by calculating D^2 values from the means of 102 genotypes of black gram for nine characters. The genotypes were grouped into 18 clusters (**Table 3**). Among the 18 clusters, cluster 1 contains the maximum number of 50 genotypes followed by cluster II (16 No.), cluster IX (14 No.) and cluster III (8 No.). Clusters *viz.*, IV, V, VI, VII, VIII, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII had one genotype each. The intra and inter cluster D^2 values are presented in **Table 4**. The intra-cluster distance values ranged from

Table 3. Clustering pattern of studied genotypes in blackgram

Cluster number	Number of genotypes	Genotypes
I	50	IC 281986, IC 281989, IC 436758, VBG 11033, IC 281992, ABG 11013, VBG 13023, IC 281995, VBG 11043, IC 343947, ABG 11028, IC 281978, VBG 11046, VBG 11024, IC 436727, IC 343943, VBG 12039, VBG 11044, IC 436724, ABG 11015, VBG 12093, IC 436784, IC 281982, VBG 12034, IC 398970, IC 436765, VBG 12122, VBG 14013, IC 281984, VBG 11028, IC 281990, ADT 3, APK 1, IC 343967, VBG 12122 , IPU 0233, KU 12668, VBG 12056, VBN 4, IC 282008, IC 436536, IC 281980, VBG 11027, IC 436736, ABG 11011, IC 343939, IC 413304, VBG 11050, IC 281977, VBG 12034
II	16	IC 281792, VBG 11040, IC 281991, ADT 5, VBG 11042, VBG 10024, IC 282002, VBG 12062, VBG 11020, VBG 12042, IC 281994, IC 436720, VBG 11018, IC 282001, VBG 11041, ABG 11037
III	8	VBG 10010, VBG 10024, KU 11680, VBG 13019, KU 1239, VBG 11 046, VBG 13017, VBG 10053
IV	1	ABG 11032
V	1	VBG 11037
VI	1	VBG 11045
VII	1	IC 281993
VIII	1	VBG 12005
IX	14	IC 343885, IC 335331, IC 281999, ABG 11004, KU 11667, ABG 11011, KKB 05011, KKB 14011, ABG 11035, IC 398989, ABG 11030, VBG 14003, VBG 11029, ABG 11036
X	1	IC 436811
XI	1	KKB 06012
XII	1	IC 282002
XIII	1	IC 281792
XIV	1	IC 343962
XV	1	IC 281987
XVI	1	KKB 14003
XVII	1	KKB 14001
XVIII	1	IC 281982

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0.00 to 23.08. The maximum intra cluster D^2 value was observed in cluster IX (23.08) followed by cluster III (19.98) and cluster II (17.95). The inter cluster distance values ranged from 15.20 to 72.84. The maximum inter cluster distance was observed between cluster XVI and XV (72.84) followed by XIV and XVI (66.07) that indicated wide divergence existed among the genotypes of these clusters. From the studies, inter cluster distance was more than the intra cluster distances. Similar results were reported by Kavani *et al*. (2007). The least value of inter-cluster D^2 value was observed in between cluster VII and XIII (15.20) suggested that the genotype in one cluster is in close proximity with the genotype in the other cluster of pair. Hence, genotypes from both clusters may not be useful in breeding programmes. This is in agreement with Kumar *et al*. (2015).

Table 4. Average intra (diagonal) and inter cluster (between) distance of blackgram genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	17.34	24.32	25.11	19.97	20.02	20.68	20.66	26.05	28.55	22.89	20.98	27.88	28.80	43.23	46.13	39.11	33.87	30.85
II		17.95	29.38	22.21	27.46	24.05	25.75	32.70	33.24	34.07	27.93	23.10	27.71	27.79	31.34	48.07	39.43	36.60
III			19.98	33.18	31.15	28.62	33.93	31.16	36.12	25.68	27.89	37.03	40.19	47.67	48.62	37.14	28.24	37.02
IV				0.00	22.16	23.61	15.63	26.36	25.22	29.35	26.62	22.99	20.45	36.24	40.91	44.91	37.11	35.90
V					0.00	9.89	16.22	37.39	37.71	31.07	25.49	20.36	27.98	45.62	45.20	51.44	45.10	38.57
VI						0.00	21.43	39.12	39.28	32.87	24.88	20.26	30.81	40.91	38.92	51.97	44.87	40.40
VII							0.00	30.58	30.42	32.20	28.85	20.09	15.20	41.51	45.03	49.61	40.73	34.95
VIII								0.00	18.11	22.77	28.57	41.43	33.06	48.66	56.86	24.32	22.97	25.59
IX									23.08	28.37	30.27	40.60	32.23	47.09	55.21	33.15	31.51	29.78
X										0.00	21.72	42.95	42.07	55.20	58.68	24.36	29.94	25.99
XI											0.00	34.57	35.25	46.45	51.10	34.57	39.24	21.69
XII												0.00	19.98	30.78	31.51	60.27	48.51	45.39
XIII													0.00	36.04	43.06	54.71	43.01	39.45
XIV														0.00	16.28	66.07	55.55	52.55
XV															0.00	72.84	60.23	60.94
XVI																0.00	28.34	31.10
XVII																	0.00	42.11
XVIII																		0.00

The relative contribution of characters for genetic divergence in black gram is represented in **Table 5**. The maximum percentage of genetic divergence was contributed by single plant yield (30.30%) followed by the number of pods per plant (27.80 %), plant height (23.14 %) and the number of clusters per plant (10.02%).

The cluster mean for the nine characters studied in black gram is given in **Table 6**. It revealed that cluster X with one genotype (IC 436811) had the lowest mean value for days to 50 % flowering and hence this genotype could be used as a source for earliness. The highest mean value for plant height (58.80 cm) was recorded in cluster XIII. The highest mean values were recorded by cluster XVIII for the number of clusters per plant (18.40); cluster XVII for the number of pods per plant (48.80); cluster XII for the number of seeds per pod (7.80); cluster X for 100 seed weight (6.44 g) and protein content (27.13); cluster XIV

Table 5. Contribution of different traits for genetic divergence in blackgram.

Traits	Number of times ranked First	Contribution Percentage
Days to 50% flowering	79	1.53
Plant height	1192	23.14
Number of primary branches/plant	212	4.12
Number of clusters/plant	516	10.02
Number of pods/plant	1432	27.80
Number of seeds/ pod	4	0.08
100 seed weight	44	0.85
Single plant yield	1561	30.30
Protein content	111	2.15
Total	**5151**	**100.00**

for the trait single plant yield (29.10 g), hence crossing these genotypes would result in getting transgressive segregants.

The success of any breeding programme depends largely on the extent of genetic variability present in the base population. The variability parameters *viz.,* GCV, PCV heritability (h^2) and GAM for different characters are presented in **Table 7**. The highest genetic variation was observed in single plant yield (GCV 42.72 % and PCV 42.96); the number of clusters per plant (GCV 35.45 % and PCV 35.89 %); the number of pods per plant (GCV 26.99 % and PCV 27.16 %) and the number of primary branches per plant (GCV 26.39 % and PCV 27.15 %). Similar findings had been reported by Ramya *et al.* (2014). Moderate PCV and GCV were observed for the traits plant height (GCV 18.09% and PCV 18.23 %); hundred seed weight (GCV 14.29% and PCV 15.91 %) and protein content (GCV 11.52% and PCV 12.05). Similar findings had been reported for the traits of plant height and hundred seed weight by Panigrahi *et al.* (2014). Sowmini and Jayamani (2013) reported high PCV and GCV values for the number of clusters per plant and the number of pods per plant. In the present study, high heritability estimates were observed for all the characters. High heritability was recorded for single plant yield (98.9 %), the number of pods per plant (98.7 %), plant height (98.5 %), the number of clusters per plant (97.6%), the number of primary branches per plant (94.5 %), days to fifty per cent flowering (91.4 %), protein content (91.4 %), hundred seed weight (80.7 %) and the number of seeds per pod (69.8 %). High GAM was recorded for hundred seed weight (87.53 %) followed by the number of primary branches per plant (72.14%), the number of clusters/

Table 6. Cluster wise mean performance for different quantitative traits in blackgram.

Traits Cluster	Days to 50 % flowering	Plant height (cm)	Number of primary branches/ plant	Number of clusters/ plant	Number of pods/plant	Number of seeds/ pod	100 seed weight (g)	Single plant yield (g)	Protein content (g)
I	36.25	43.55	5.55	7.20	26.94	6.54	4.69	9.08	22.92
II	36.22	41.85	5.76	7.79	25.37	6.52	4.81	17.32	23.79
III	34.31	27.74	6.13	6.59	29.41	6.43	4.47	9.51	20.71
IV	40.50	53.30	4.80	6.10	30.50	7.00	5.54	13.05	26.79
V	36.50	49.10	5.60	4.00	16.00	7.10	5.15	7.16	22.18
VI	37.50	43.60	3.80	4.20	16.80	6.33	3.82	9.82	21.45
VII	38.00	54.70	8.60	4.60	23.00	7.10	4.61	9.70	26.39
VIII	32.50	45.80	7.00	10.80	43.20	6.00	4.32	9.80	20.83
IX	37.61	49.40	6.41	10.88	40.69	6.20	4.48	11.14	24.29
X	32.00	36.45	4.80	10.80	32.40	7.50	6.44	5.15	27.13
XI	43.00	41.00	4.30	13.60	24.00	7.30	4.30	8.20	20.10
XII	38.50	52.30	7.80	3.20	16.00	7.80	6.20	15.90	19.58
XIII	43.50	58.80	10.65	5.20	26.00	7.40	4.30	14.30	22.14
XIV	37.00	46.40	5.60	8.40	25.20	6.00	4.53	29.10	23.33
XV	35.00	40.20	3.60	3.85	19.25	6.80	4.56	29.00	25.23
XVI	34.50	31.24	4.60	15.80	48.40	5.62	4.20	4.38	21.30
XVII	37.50	29.46	7.80	5.60	48.80	6.80	4.20	9.30	21.24
XVIII	34.00	44.70	8.45	18.40	28.00	6.25	4.00	7.98	23.37
MEAN	36.91	43.86	6.18	8.16	28.8	6.70	4.70	12.21	22.93

Table 7. Variability parameters in blackgram.

Character	PCV (%)	GCV (%)	Heritability (%)	GAM
Days to 50% flowering	9.47	9.05	91.40	17.83
Plant height	18.23	18.09	98.50	36.99
Number of primary branches per plant	27.15	26.39	94.50	52.85
Number of clusters/plant	35.89	35.45	97.60	72.14
Number of pods/plant	27.16	26.99	98.70	55.24
Number of seeds/ pod	11.02	9.20	69.80	15.83
100 seed weight	15.91	14.29	80.70	26.46
Protein content	42.96	42.72	98.90	87.53
Single plant yield	12.05	11.52	91.40	22.69

plant (55.24 %), plant height (52.85%), protein content (22.69%), the number of seeds per pod (26.46%) and single plant yield (22.69%). In the present investigation, high heritability coupled with high GAM was recorded for hundred seed weight, the number of primary branches per plant, the number of clusters/plants, plant height, protein content, the number of seeds per pod and single plant yield indicating that additive gene action is involved in the genetic control of these traits. Selection can be recorded for the improvement of these characters in the future crop improvement programme. It is in agreement with the findings of Baisakh *et al.* (2014) and Reddy *et al.* (2011) in black gram.

The genotypic correlation coefficient between different characters studied is presented in **Table 8**. From the intra correlation studies, seed yield per plant had a significant and positive association of the studied genotypes in black gram with trait *viz*., the number of clusters per plant (0.348) and the number of pods per plant (0.429). A similar result was obtained by Kumar *et al.* (2014) and Kanimozhi *et al*. (2009). Days to 50% flowering had a positive and significant association with plant height (0.307); plant height had a positive and significant association with hundred seed weight (0.225) and protein content (0.210) and the number of clusters per plant had a positive and significant association with the number of pods per plant (0.514). Similar findings of association were reported by Konda *et al.* (2008).

Table 8. Genotypic correlation coefficient in blackgram.

Character	Days to 50% flowering	Plant height	Number of primary branches per plant	Number of clusters/plant	Number of pods/plant	Number of seeds/ pod	100 seed weight	Protein content	Single plant yield
Days to 50% flowering	**1.000**	0.307*	-0.004	-0.087	-0.012	0.073	0.007	0.110	-0.020
Plant height		**1.000**	0.131	0.048	0.031	0.119	0.225 *	0.210 *	0.107
Number of primary branches per plant			**1.000**	-0.007	0.089	0.070	-0.323 *	0.032	0.003
Number of clusters/plant				**1.000**	0.514 *	-0.245 *	-0.135	-0.059	0.348 *
Number of pods/plant					**1.000**	-0.270 *	-0.136	0.100	0.429 *
Number of seeds/ pod						**1.000**	0.100	-0.022	-0.086
100 seed weight							**1.000**	-0.030	0.390
Protein content								**1.000**	0.068
Single plant yield									**1.000**

It is, therefore, concluded that the genotypes belonging to different clusters having high means for desired characters and with maximum inter cluster distances (clusters *viz.,* XVI & XV and XIV & XVI respectively) could be successfully utilized in hybridization programmes. The traits *viz.,* for hundred seed weight, the number of primary branches per plant, the number of clusters/plants, plant height, protein content, the number of seeds per pod and single plant yield registered high heritability coupled with high GAM showed that the selection efficiency is high and it is due to the presence of additive gene action. Since the trait single plant yield had a positive and significant association with the number of clusters per plant and the number of pods per plant, selection of these traits would be more valuable to bring the desired improvement in black gram breeding program.

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