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Research Note

Genetic divergence studies in blackgram (*Vigna mungo* L. Hepper)

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Abstract

Divergence among 112 genotypes for yield and yield contributing traits was carried out by using mahalanobisD^2 statistics. The maximum inter cluster distance was observed between cluster XII and IV (18.80) followed by cluster VI and IV (18.79). The maximum intra cluster distance was reported in cluster XII (14.74).The crosses which involve parents from these more divergent clusters will yield relatively good amount of heterosis in F_1 and high frequency of transgressive segregants and genetic variability in subsequent generationsBased on the mean performance and diversity studies the genotypes KU 11-667, ABG 11-036, IC 436729 and IC 335331 were found to be the best for further yield improvement.

Key words
Blackgram, D^2 analysis.

Blackgram is one of the important pulse crops, occupying unique position in Indian Agriculture. Among pulses, it stands fourth in production and acreage. It is cultivated almost in all parts of India and adopts well to wide range of soil types. It covers an area of about 5.03 million hectares with production of3.28 million tonnes. Its productivity is only 650 kg/ha. In Tamil Nadu, blackgram covers an area of about 4.06 lakh hectare with production of 3.01 lakh tonnes and productivity of741 kg/ha during 2017-18. Many breeding efforts have been carried out to improve the yield level of this crop and to break the yield plateau, but it could not be done because of narrow genetic base of parents used in hybridization.

Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of producing desirable recombinants. Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at genotypic level. Therefore, an attempt has been made in the present investigation with a view to estimate genetic divergence among a set of 112 genotypes.

The present investigation was carried out with 112 blackgram genotypes from National Pulses Research Centre, Vamban, Agriculture Regional Station, Aruppukottaiand National Bureau of Plant Genetic Resources, Hyderabad. The genotypeswere evaluatedatDepartment of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam in a randomized block design (RBD) with two replications. Each genotype was sown in 3 meter row to accommodate 20 plants per row with a spacing of 30x15 cm. Recommended agronomic practices and need based plant protection measures were taken. Five randomly taken plants were considered to record data for days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and yield per plant (g). The mean values of five plants were taken for the analysis of genetic divergence following Mahalanobis (1936). The genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

The analysis of variance for randomized block design revealed highly significant differences among accessions for all the characters under investigation indicating the presence of a considerable magnitude of genetic variability among 112 accessions of black gram(Table-1). The multivariate analysis giving the D^2values between 112 accessions, all these entries were grouped into thirteen clusters (Table 2).

Averageintra and inter cluster D^2 values were worked out from divergence analysis (Table 3). The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Similar findings were also reported by Panigrahi *et al*. (2014). He studied with 44 genotypes (17 land races genotypes from diverse origin and 27 mutants) with a view to identify the best genetic diversity using Mahalanobis‟s D^2 technique. These genotypes were grouped into twelve clusters. Clusters II and cluster V had maximum of nine genotypes each followed by cluster IV having eight genotypes. The inter cluster distance were greater than the intra cluster distance revealing the considerable amount of genetic diversity existed among the accession.

In the present investigation, among the thirteen clusters, the cluster V had highest33genotypes followed by cluster I twenty eight genotypes, cluster XII thirteen genotypes , cluster IV ten genotypes, cluster II eight genotypes, cluster XIII six genotypes and cluster III three genotypes. The cluster VI, VII, VIII, IX, X and XI had two genotypes each. Cluster XII had the maximum intra-cluster distance indicating presence of substantial divergence between genotypes followed by cluster XIII whereas minimum intra-cluster distance was observed in the cluster VI and cluster VII.

The maximum inter cluster distance was observed between cluster XII and II followed by cluster XIII and VI, while minimum inter-cluster distance was recorded between cluster XI and IX. The crosses between parents from these more divergent clusters may yield relatively good heterosis in F_1, high frequency of transgressive segregants and useful recombinants in subsequent generations.

Minimum inter-cluster distance was observed between clusters IX and XI followed by the clusters IX and VI and IX and VII suggesting lack of diversity amongthe genotypes of these clusters.Kumar *et al.* (2002) studied 19 genotypes of urdbean using Mahalanobis‟s D2 statistics. The results revealed significant genotypic differences and the genotypes were classified into five clusters. Cluster I was the largest with 10 genotypes and cluster V having only one genotype which was highly divergent. The inter-cluster distance was minimum (27.14) between cluster I and II and maximum (77.30) between cluster II and III.

Srimathy *et al.* (2012) grouped 46 blackgram genotypes into 12 clusters using Mahalanobis D^2 model. Among the characters, contribution of seed yield per plant was maximum followed by number of pods per cluster and hundred seed weight. Number of branches per plant contributed minimum to the genetic divergence leading to the inference that in general, the variability for these characters are low in blackgram genotypes used in this study. In the present investigation, the percentage contribution of different quantitative traits towards the genetic divergence was calculated (Table 4). The results indicated that the seed yield per plant contributed maximum to the total divergence followed by hundred seed weight and protein content. Days to fifty per cent flowering had least contribution to the total divergence.

The mean values of 11 characters for twelve clusters are presented in the Table 5. Cluster VIII showed the highest mean value for days to fifty percent flowering (37.25) and protein content (26.87). Cluster X recorded highest mean value (6.15) for number of primary branches per plant and pod length (4.87). Cluster III recorded highest mean value (7.37) for number of clusters per plant. Cluster II showed the highest mean value (7.84) for number of seed per pod. Cluster VI recorded the highest mean value (54.29) for plant height. Cluster III recorded highest mean value (9.30) for seed yield per plant. Cluster XI showed the highest mean value (4.87) for pod length. Cluster XII recorded the highest mean value (5.38) for hundred seed weight. Cluster XIII recorded the highest mean value (36.87) for number of pods per plant. Cluster IV showed lowest mean value for days to fifty percent flowering (33.20) and plant height (31.38).

The analysis of variance showed significant differences among the accessions for all the characters studied. The pooled divergence for all the characters within the accessions was significant. One hundred and twelve genotypes were grouped into thirteen clusters by D^2 analysis. The accessions KU 11-667 and IC 436729 may serve as potential parents for hybridization programme in the improvement of yield. VBG 12-121, VBN 7, VBG 10-024 were considered as a early flowering; KU 12-39, VBG 13-017; for dwarf; IC 343967, IC 343939 for number of primary branches per plant; KU 11-667, KU 11-680 for number of clusters per plant; IC 436729, IC 281996, KU 11-667 for number of pods per plant; IC 335331, IC 436720, IC 398998 for hundred seed weight; ABG 11-036, ABG 11-030 for protein content; KU 11-667, IC 436729, VBG 12-034 for seed yield per plant may be used as suitable parents.

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Table 1. Analysis of variance for different characters in blackgram

S. No	Characters	Grand mean	Genotype MSS	Error MSS	SD	CV%
1	**Days to 50 % flowering**	34.97	6.99**	1.66	1.87	3.69
2	**Plant height (cm)**	43.75	125.78**	2.56	7.90	3.66
3	**No. of primary branches per plant**	4.18	2.08**	0.22	1.00	11.31
4	**No. of clusters per plant**	5.32	4.86**	0.35	1.56	11.19
5	**No. of pods per plant**	27.26	109.24**	3.22	7.40	6.59
6	**Pod length (cm)**	4.70	0.21**	0.021	0.32	3.11
7	**No. of seeds per pod**	7.24	0.78**	0.14	0.60	5.34
8	**100 seed weight (g)**	4.69	0.99**	0.03	0.70	3.98
9	**Protein content (g)**	23.08	15.34**	1.00	2.76	4.34
10	**Seed yield per plant (g)**	7.81	4.76**	0.29	1.543	6.96

* - Significant at $p = 0.05$ ** - Significant at $p = 0.01$

Table 2. D^2 clusters for ten quantitative trait of blackgram

Cluster number	No. of genotypes	Genotypes
I	28	VBG 11-018 ,VBG 11-042,VBG 11-045,VBG 11-024,VBG 11-020, VBG11-027, VBG11-043, VBG11-037, VBG11-053,VBG 11-044,VBG 11-067, VBG 10-010, VBG 11-029,VBG 11-050, VBG11-041, VBG11-033,VBG 11-046, VBG11-040, VBG12-093,VBG 12-039,VBG 12-122,VBG 12-053, VBG12-034,VBG 12-005, VBG12-042,VBG 13-023, KU 12-668, VBG 12-056
II	8	VBG 13-017, VBG 13-027, VBG 13-019, VBG 14-011, VBG 14-003, VBG 14-013, VBG 14-015, ADT 3
III	3	KU 11-667, VBG 11-028, ADT 5
IV	10	KU 12-39, KU 11-680, VBG 10-024, VBG 10-053, VBN 7, VBG 12-062, VBG 12-121, VBN 4, ABG 11-028, IC282007
V	33	ABG 11-003, ABG 11-004, ABG 11-011, ABG 11-013, ABG 11-014, ABG 11-015, ABG 11-030, ABG 11-032, ABG 11-035, ABG 11-036, ABG 11-037, APK 1, IC261182, IC282001, IC282002, IC282004, IC282008, IC281977, IC281978, IC281980, IC281982, IC281984, IC281986, IC281987, IC281989, IC281990, IC281991, IC281992, IC281993, IC281994, IC281995, IC436724, IC436736
VI	2	IC398973, IC413307
VII	2	IC398956 , IC413309
VIII	2	IC398991, IC413304
IX	2	IC436536, IC436704
X	2	IC343939, IC343943
XI	2	IC343947, IC343962
XII	13	IC281996, IC281999, IC335331, IC343885, IC343967, IC398970, IC398989, IC398998, IC413306, IC436784, IC436720, IC436727, IC436747
XIII	6	VBG 11-029, IC436729, IC436758, IC436765, IC436792, IC436811

Table 3. Average of intra and inter cluster D^2 distance for ten quantitative traits of blackgram

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**12.29**	12.93	14.06	14.47	13.52	13.76	12.33	11.80	11.33	12.77	10.11	16.42	15.94
II		**12.03**	13.57	12.13	13.88	15.81	12.64	13.25	12.35	14.18	11.29	17.14	15.54
III			**12.98**	14.60	12.29	14.73	12.20	13.17	11.35	12.89	10.38	14.16	13.67
IV				**11.53**	15.56	18.79	13.90	15.43	14.39	15.82	13.25	18.80	16.36
V					**12.00**	12.12	11.05	11.26	9.70	11.99	9.57	14.06	14.11
VI						**4.82**	10.55	8.86	7.38	12.16	10.34	13.97	16.72
VII							**5.10**	11.49	7.68	12.98	8.21	15.41	15.01
VIII								**5.31**	7.75	8.02	8.30	12.96	14.33
IX									**5.49**	11.06	7.32	12.46	12.80
X										**5.79**	7.95	13.31	15.20
XI											**5.90**	12.81	12.78
XII												**14.74**	15.38
XIII													**14.60**

Table 4. Relative contribution of various characters to genetic divergence in blackgram

Characters	Number of times Ranked First	Contribution Percentage
Days to 50 % flowering	5	0.08
Plant height (cm)	531	8.54
No. of primary branches per plant	48	0.77
No. of clusters per plant	253	4.07
No. of pods per plant	515	8.28
Pod length (cm)	540	8.68
No. of seeds per pod	334	5.37
100 seed weight (g)	629	10.11
Protein content (g)	595	9.57
Seed yield per plant (g)	2766	44.49
Total	**6216**	**100.00**

Table 5. Cluster means of ten quantitative traits of blackgram

Characters **Cluster**	**Days to 50 % flowering**	**Plant height (cm)**	**No. of primary branches per plant**	**No. of clusters per plant**	**No. of pods per plant**	**Pod length (cm)**	**No. of seeds per pod**	**100 seed weight (g)**	**Protein content (g)**	**Seed yield per plant (g)**
I	34.01	41.52	**3.23**	4.93	22.04	4.86	7.00	4.56	**21.55**	7.67
II	35.00	37.47	4.46	6.35	27.49	4.77	**7.84**	4.32	21.76	6.77
III	34.67	45.18	4.50	**7.37**	33.73	4.77	7.53	4.62	22.89	**9.30**
IV	**33.20**	**31.38**	4.80	6.38	28.86	4.46	7.64	4.31	22.27	7.62
V	35.56	46.83	4.54	5.14	29.26	4.68	7.36	4.66	23.76	8.01
VI	36.75	**54.29**	3.40	4.10	19.95	4.57	6.95	4.56	26.56	**6.15**
VII	35.25	43.39	4.35	4.45	26.65	4.55	7.15	**3.64**	25.29	8.48
VIII	**37.25**	46.21	4.30	**3.95**	**19.90**	4.75	7.40	5.37	**26.87**	6.90
IX	36.75	46.98	3.40	4.15	25.75	**4.37**	6.90	4.68	25.43	7.45
X	33.75	47.08	**6.15**	4.65	21.85	**4.87**	7.80	5.29	22.90	8.13
XI	35.00	44.99	4.55	4.70	25.90	**4.87**	7.15	4.57	21.87	8.45
XII	35.96	50.79	4.48	5.81	30.51	4.61	6.91	**5.38**	24.55	8.10
XIII	35.60	43.42	4.16	4.96	**36.87**	4.65	**6.86**	5.33	22.99	8.31
MEAN	35.30	44.58	4.33	5.15	26.83	4.68	7.27	4.72	23.75	7.80