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

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Abstract
A field experiment was conducted to examine the genetic divergence using Mahalanobis D^2 statistics among one hundred urdbean genotypes. Significant genotypic differences were observed for twelve characters studied indicating the considerable amount of variation among the genotypes. Cluster II consisted maximum number of accessions (21) followed by cluster I and III (17) and cluster VII, X and XI consisted one accession only. The inter cluster distances were greater than intra cluster distances revealing that considerable amount if genetic diversity existed among the accessions. Higher cluster mean values for plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of days to maturity and seed yield per plant was observed in cluster VII indicating the usefulness of the genotypes present in this cluster. The genotype P 1070 may serve as potential parent for hybridization programme in the improvement of yield.

Keywords: Divergence, Mahalonobis D^2 analysis and blackgram

Introduction
Urdbean (*Vigna mungo* (L.) Hepper) belongs to the leguminacea family, is an important pulse crop in India. In India it may be cultivated throughout the year over wide range of agro climatic zones. But mainly grows in kharif and rabi seasons. Blackgram is a self-pollinated crop and is lacking variability. The choice of divergent parents for hybridization programme is one of the important considerations for creating genetic variability. Several biometrical approaches have been shown to be usefull in selecting parents for successful hybridization programme. D^2 analysis has been found to be most effective and widely used for the classification of parental lines. The importance of genetic diversity of parents in a hybridization programme has been emphasized as the crosses involving genetically diverse parents and likely to produce high heterotic effects and also desirable segregants in the later segregating generations. Several workers emphasized the need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations (Gupta *et al.* 2005, Katiyar and Dixit 2010) [4, 7]. Genetic diversity arises due to geographical separation, crossable barriers or due pattern of evaluation. The present study was conducted with an objective to select the diverse parents for further use in urdbean breeding programme.

Material and Methods
The experimental material comprised of one hundred genetically diverse genotypes along with four checks (*viz.*, Vamban 8, KU 96-8, Sekhar 3 and WBU 108) collected from different parts of the country. All the entries were evaluated at Regional Agricultural Research Station, Lam, Guntur, A.P during kharif 2015 under Augmented completely randomized design II in three blocks. Each genotype was sown in single row with spacing of 30 x10 cm. all the prophylactic measures were taken to grow a healthy crop. The observations were recorded on five randomly selected plants of each genotype at various phenophases of the crop. Observation on plot basis was recorded for days to 50% flowering and days to maturity. Average of five plants in respect of plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight leaf area, SPAD, chlorophyll content and seed yield per plant was used for mahalanobis D^2 analysis was employed to assess the genetic diversity.

Results and Discussion

The analysis of variance of thirteen yield and yield attributing characters of urdbean are summarized in table 1. A total of one hundred genotypes were grouped into eleven clusters using Tocher's method (Table 2). The distribution of one hundred genotypes into eleven clusters was at random with maximum number of genotypes in clusters II (21 genotypes) followed by clusters I and III (17 genotypes), cluster VI (16 genotypes), clusters IV and IX (8 genotypes), cluster V (7 genotypes) and cluster VIII (3 genotypes). The clusters, VII, X and XI were solitary with zero intra cluster D^2 values. The formation of distinct solitary clusters may be due to the fact that geographical barriers preventing gene flow or intense natural and human selection for diverse and adaptable gene complexes.

This pattern of grouping has indicated that the diversity need not be necessarily related to geographical diversity and it may be the outcome of several other factors like natural selection, exchange of breeding material, genetic drift and environmental variation. Similar results were obtained earlier by Sagar *et al*. (2001) [6], Chauhan *et al*. (2005) [2] and Bhattacharya and Vijayalaxmi (2005) [1].

On the basis of D^2 analysis, the intra and inter cluster distances for all eleven clusters were presented in table 3 and table 4. The maximum intra cluster distance was observed in the cluster XI (16.12) followed by cluster III (15.90), cluster VII (15.73), cluster IX (15.32), cluster V (12.64), cluster VIII (11.87), cluster X (11.76), cluster VI (10.13), cluster IV (9.43), cluster I (8.66) and cluster II (3.36). Cluster I with 17 genotypes was 2nd largest and the closest to the cluster II (19.18) and farthest to cluster VI (51.44). Cluster II with 21 genotypes was the largest and was closest to cluster VIII (31.57) and farthest to cluster VI (69.99). There were seventeen genotypes in cluster III and was the second largest cluster. This cluster was the closest to cluster I (19.79) and farthest to cluster VI (47.49). Cluster IV comprise of eight genotypes was the nearest to cluster V (17.11) and farthest to cluster XI (62.64). There were seven genotypes in cluster V which was the nearest to cluster IV (17.11) and farthest cluster XI (60.91). Cluster VI had sixteen genotypes and was closer to cluster IV (19.00) and farthest to cluster XI (81.87). Cluster VII was solitary with genotype P 1070 and was the closest to cluster VIII (19.30) and farthest to cluster XI (52.13). There were three genotypes in the cluster VIII and was the nearest to cluster I (21.03) and farthest to cluster XI (52.99). Cluster IX had eight genotypes and was the nearest to cluster X (18.84) and farthest to cluster II (44.97). Cluster X had only one genotype (TU 94-2) and was closer to cluster IX (18.84) and farthest to cluster II (37.97). Cluster XI was mono genotypic (MBG 207) and was the closest to cluster IX (40.83) and farthest to cluster VI (81.87).

Inter cluster distances were worked out considering 12 characters and inter cluster distance values ranged from 81.87 (between clusters VI and XI) to 17.11 (between clusters IV and V) indicating the wide genetic diversity between the clusters and crosses can be attempted between the genotypes of these clusters to obtain desirable transgressive segregants.

Higher cluster mean values for plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of days to maturity and seed yield per plant were observed in cluster VII (Table 5) indicating the usefulness of the genotypes present in this cluster in hybridization for developing high yielding varieties.

The additional advantage of D^2 analysis is the contribution of various characters towards the expression of genetic divergence (Table 6). The trait leaf area (49.41) had a highest contribution towards genetic divergence followed by number of pods per plant (8.86), number of branches per plant (6.87), number of seeds per pod (6.72), seed yield per plant (6.17), number of clusters per plant (5.16), plant height (4.44), pod length (2.24), days to 50% flowering (2.16), chlorophyll content (2.11), days to maturity (2.10) and SPAD (2.07). These results are in agreement with those of Ghafoor *et al*. (2001) [3] and Shanti *et al*. (2006)

From the present investigation, it was concluded that the genotype P 1070 present in cluster VII can be selected as a parent for hybridization programme. The genotypes MBG 207 and TU 94-2 which are present in cluster XI showing higher mean values for most of the yield attributing traits. The parents form these clusters can be utilized in hybridization programme for evolving high yielding varieties of urdbean.

Table 1: Augmented RBD analysis of variance for seed yield and yield component characters in blackgram (*Vigna mungo* L.)

	d.f	Days to 50% flowering	Plant height (cm)	No. of branches / plant	No. of clusters / plant	No. of pods / plant	Pod length (cm)	No. of seeds / pod	100 seed weight (g)	Days to maturity	Leaf area (cm^2)	SPAD	Chlorophyll content (mg/g)	Seed yield/ plant (g)
Entries	103	2.31**	250.13**	0.25	8.24 **	82.69**	0.15*	0.44*	0.26**	35.91**	59488.71**	45.80 **	0.16**	8.43**
Varieties	99	1.08	255.60**	0.23	7.88**	59.06**	0.08	0.23	0.21**	20.67**	58804.16**	43.96 **	0.16**	6.40 **
Block	4	6.64 **	2226.25**	0.32	30.58 **	293.94**	0.24*	0.22	1.57 **	163.70 **	364207.91 **	62.90 **	0.30 **	44.42**
Checks	3	1.93	19.92*	0.29	3.18**	8.55*	0.11	1.21**	0.10	3.87	19031.27**	7.84*	0.00	1.27 **
Error	12	0.64	5.21	0.14	0.26	1.98	0.06	0.14	0.05	1.37	1637.74	1.65	0.00	0.07

** Significant at 1% level

* Significant at 5% level

d.f : degrees of freedom

Table 2: Clustering pattern of blackgram (V*igna mungo* L.) genotypes by Tocher's method

Cluster number	No. of genotypes	Name of genotype (s)
I	17	VBG 10-014, UH07-06, RU-44, KU 1006, PU 30, P 205, LBG 766, CPS 35, VBG04-005, KPU 26, CN 8072, LBG 797, ACM 05-007, AKU10-4, LBG 758, NUL 388, LBG 726
II	21	LBG 765, OBG 35, PGRU3-38, P 1032, UH 2289, Uttara, LBG 788, UG 708, LBG 746, PU 31, P 112, LBG 710, PLU 2146, TU 136, UPU 88-86, LBG 780, P 710, IPU 10-4, LBG 794, UH 07-13, IPU 2-43
III	17	PLU 710, LBG 823, LBG 812, NDU12-300, WBG 26, LBG 791, LBG 818, LBG 799, LBG 815, NDUK 20, LBG 801, P 705, LBG 805, LBG 798, LBG 806, LBG 782, SMS 131
IV	8	LBG 767, LBG 808,LBG 784, LBG 822, LBG 726, LBG 770, LBG 777, LBG 795

V	7	LBG 747, LBG 623, KKBU-5011, KPU 67-08, SPS 26, COBG 1045, P 1053
VI	16	TBG 104, LBG 20, LBG 785, KU 323, TU10-3, P 726, T9, LBG 783, LBG 787, RVSU11-8, U 150, LBG 786, PU 212, PBG 32, PGRU 99058, LBG 752
VII	1	P-1070
VIII	3	LBG 772, LBG 802, LBG 753
IX	8	GKU 02-1, P 1060, P 728, LBG 798, UH 85-5, KU 708, LBG 771, TU 68
X	1	TU 94-2
XI	1	MBG 207

Table 3: Average Intra and inter cluster D ^{2} values among thirteen characters in blackgram genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX`	X	XI
I	8.66	19.18	19.79	26.25	31.70	51.44	22.18	21.03	30.15	26.94	48.63
II		3.36	32.45	39.12	41.79	69.99	33.98	31.57	44.97	37.97	56.98
III			15.90	31.92	30.01	47.49	24.48	24.00	33.88	26.34	45.51
IV				9.43	17.11	19.00	24.38	20.97	22.23	23.11	62.64
V					12.64	19.39	23.32	21.66	28.30	25.33	60.92
VI						10.13	30.42	31.68	28.79	34.38	81.87
VII							15.73	19.31	20.78	22.95	52.14
VIII								11.87	24.75	21.77	52.99
IX									15.32	18.84	40.83
X										11.76	32.57
XI											16.12

Note: Diagonal values are intra-cluster distances, off-diagonal values are inter cluster Distances

Table 4: The nearest and farthest clusters from each cluster based on D^2 value using Tocher's method

Cluster Number	Nearest cluster with D^2 value	Farthest cluster with D^2 value
I	II (19.18)	VI (51.44)
II	VIII (31.57)	VI (69.99)
III	I (19.79)	VI (47.49)
IV	V (17.11)	XI (62.64)
V	IV (17.11)	XI (60.91)
VI	IV (19.00)	XI (81.87)
VII	VIII (19.30)	XI (52.13)
VIII	I (21.03)	XI (52.99)
IX	X (18.84)	II (44.97)
X	IX (18.84)	II (37.97)
XI	IX(40.83)	VI (81.87)

Table 5: Mean values of 11 clusters estimated by Tocher's method from 100 blackgram (*Vigna mungo* L.) genotypes

Cluster No.	Days to 50% flowering	Plant height (cm)	No. of branches / plant	No. of clusters / plant	No. of pods / plant	Pod length (cm)	No. of seeds / pod	100 seed weight (g)	Days to maturity	Leaf area (cm²)	SPAD	Chlorophyll content (mg/g)	Seed yield/ plant (g)
I	40.13	36.29	2.34	4.86	21.66	4.52	6.27	4.31	79.04	464.48	37.76	1.06	5.80
II	40.02	49.48	2.48	6.46	24.97	4.70	6.29	4.56	79.59	369.09	38.03	0.97	8.26
III	41.05	42.43	1.20	7.60	28.84	4.64	6.28	4.75	79.26	1797.35	37.04	0.91	8.38
IV	41.68	38.09	1.42	6.41	26.67	4.52	6.06	4.92	80.45	822.19	35.93	1.04	7.58
V	40.36	51.71	2.76	7.18	30.73	4.69	6.56	4.66	82.06	702.39	34.55	0.75	8.90
VI	40.09	47.02	2.45	6.70	26.86	4.69	6.50	4.60	79.26	249.33	38.97	0.99	7.94
VII	40.90	66.70	3.90	11.66	39.46	4.52	6.34	4.74	86.20	421.60	37.83	1.36	15.03
VIII	42.07	40.15	1.41	7.36	26.41	4.72	6.50	4.89	77.87	1065.10	37.00	1.44	7.70
IX	40.59	47.56	2.65	5.44	25.55	4.73	6.13	4.70	81.33	534.19	37.62	0.92	6.88
X	44.40	43.15	0.82	3.16	13.51	4.44	5.96	5.14	79.20	1329.85	37.18	0.94	4.11
XI	41.40	44.45	0.82	4.16	14.51	4.44	5.06	5.04	77.20	619.35	35.28	0.27	4.01

Note: Bold figures indicate minimum and maximum values in each character

Table 6: Contribution of different characters towards genetic divergence in blackgram (*Vigna mungo* L.) genotypes

S. No.	Source	No. of times ranked Ist	Contribution (%)
1	Days to 50% flowering	100	2.16 (%)
2	Plant height (cm)	238	4.44 (%)
3	No. of branches / plant	350	6.87 (%)
4	No. of clusters / plant	256	5.16 (%)
5	No. of pods / plant	450	8.86 (%)
6	Pod length(cm)	140	2.24 (%)
7	No. of seeds/ pod	360	6.72 (%)
8	100 Seed weight (g)	80	1.69 (%)
9	Days to maturity	120	2.10 (%)
10	Leaf area (cm²)	3698	49.41 (%)

11	SPAD	110	2.07 (%)
12	Chlorophyl1 content (mg/g)	180	2.11 (%)
13	Seed yield /plant (g)	370	6.17 (%)

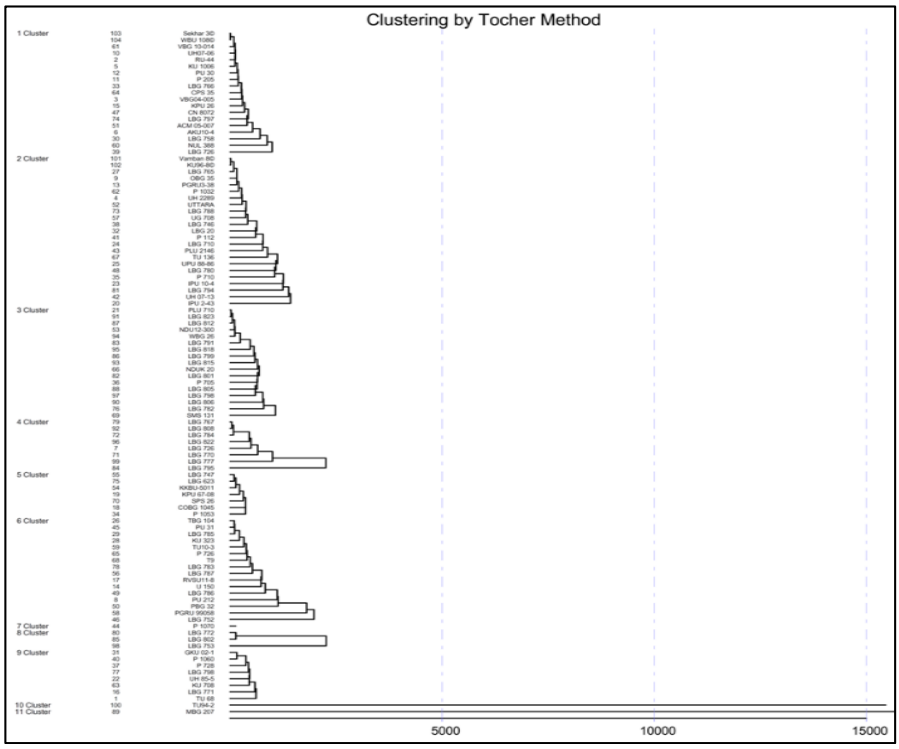

Fig 1: Dendo diagram showing relationship of 100 blackgram genotypes in eleven clusters using Tocher's Method of classification

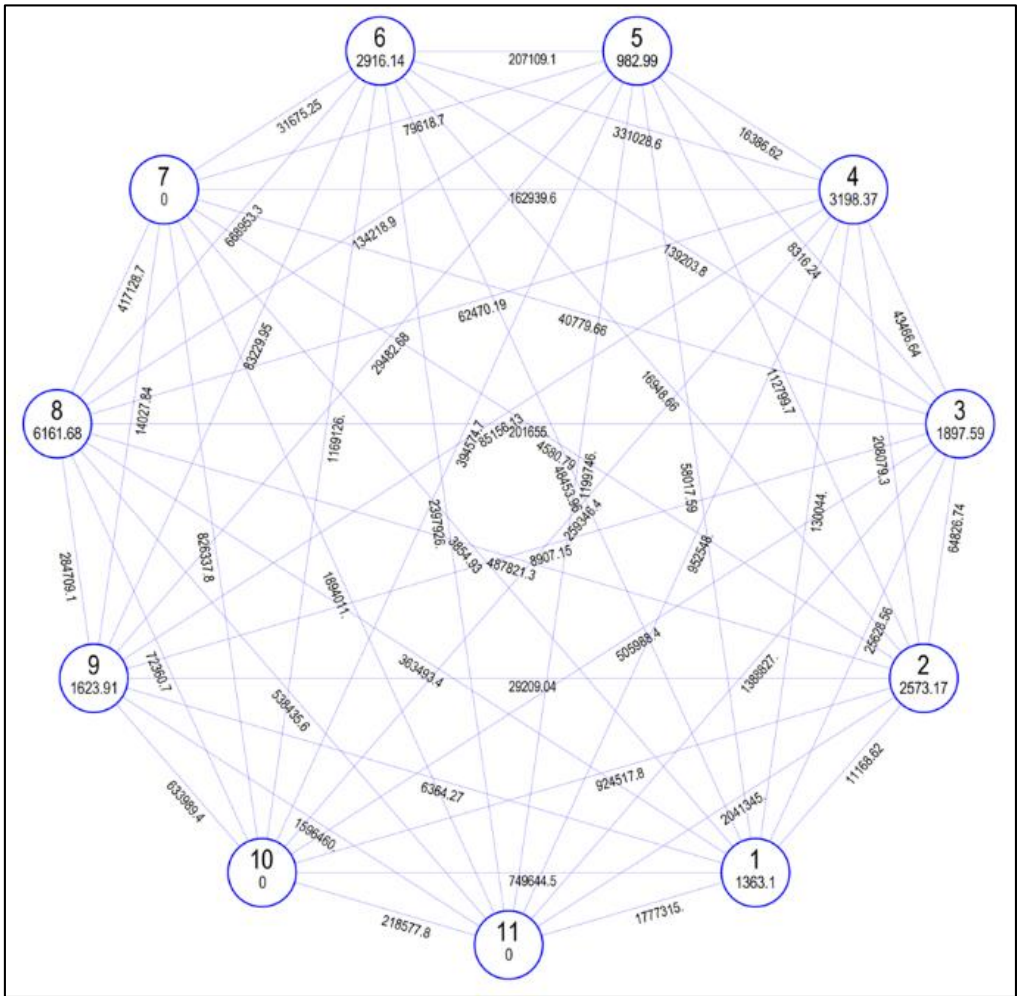

Fig 2: Intra-cluster and inter cluster distances among eleven clusters of blackgram (Tochers's Method)

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