

Divergence Studies in Blackgram [*Vigna mungo* (L.) Hepper] Genotypes under Rice Fallow Situation

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ABSTRACT

Forty five genotypes of blackgram were studied for genetic divergence employing Mahalanobis' D^2 statistics for yield and yield contributing characters. These genotypes were grouped into seven clusters. Out of seven clusters, cluster III was largest comprising of seventeen genotypes followed by cluster II with sixteen genotypes, cluster I with eight and cluster IV, V, VI, VII with one genotype. Maximum intra cluster distance was observed in cluster III (28.69) followed by cluster II (15.81) and cluster I (10.15), indicating that divergence existed among genotypes of the above clusters. The maximum inter cluster distance (210.34) was observed between cluster IV and VII followed by cluster VI and VII (140.66), cluster III and VI (110.51), cluster II and VII (107.97), cluster IV and V (104.4) and cluster I and VII (93.53). The genotypes of these clusters may therefore be used as parents in the crossing programme to generate the breeding material with high diversity. The maximum contribution towards genetic divergence was by 100 seed weight (33.74%) followed by days to 50% flowering (18.59), days to maturity (16.46) and number of branches per plant (7.37).

Key words: *Black gram, yield and yield component characters, Divergence, Mahalanobis D^2 analysis and Tocher's method*

Blackgram (*Vigna mungo* (L.) Hepper) is the third important pulse crop of India and is also known as urdbean/mash. It is a tropical, self-pollinated and diploid ($2n=22$) legume grown for its dry seeds. In India, it occupies in an area of 31 lakh ha producing 14 lakh tons with a productivity of 451.61 kg/ha (www.Indiastat.com, 2016-17). In Andhra Pradesh, it is mainly cultivated under rice fallows in coastal A.P. in an area of 5.03 lakh ha with a production and productivity of 3.29 lakh tons and 659 kg/ha, respectively. (www.Indiastat.com, 2016-17).

Urdbean cultivation has been very popular in rice fallows particularly in coastal Andhra Pradesh and certain areas of Tamilnadu and Odisha. In recent years, there has been a significant increase in area under rice fallow blackgram but production and productivity of this crop is very low due to the paucity of suitable varieties with adaptation to local conditions. The major constraints in achieving higher yield of this crop are lack of genetic variability, absence of suitable ideotypes for different cropping systems and poor harvest index.

Genetic diversity has been considered as an important factor which is also an essential pre-requisite for hybridization programme to obtain high yielding genotypes. D^2 analysis is widely followed to measure the genetic distance among the lines and also to identify characters contributing for genetic divergence. The present investigation was taken up to measure the genetic divergence among the genotypes, so as to

identify genetically diverse parents for further use in crop improvement programme.

MATERIAL AND METHODS

The field experiment was conducted during rabi, 2017-18 at Agricultural Research Station, Ghantasala, Krishna District, Andhra Pradesh. The material for the present study comprised of 45 genotypes of blackgram obtained from ARS, Madhira (4), National Pulse Research Centre, Vamban, (2) and ARS, Ghantasala (39). The genotypes were sown on 15.12.2017 in plot No.22 of block II in a randomized complete block design with three replications. Each genotype was sown in six rows of 4m length in each replication with a spacing of 30 cm between rows and 10 cm between plants. The crop was provided with normal cultural operations namely, thinning, pathways cutting and weeding and need based plant protection measures.

Five plants per genotype were randomly selected from two central rows for recording data on 12 characters namely, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%). Standard statistical procedures were used for multivariate analysis given by Mahalanobis (1936) and grouping of the biodiversified genotypes into different clusters was done using Tocher's technique (Rao, 1952).

Table 1. Clustering pattern of 45 genotypes of Blackgram by Tocher's method under rice fallow situation

Cluster number	No. of genotypes	Name of genotype (s)
I	8	LBG-685, LBG-752, MBG-1053, LBG-787, GBG-12, MASH-114, LBG-788, KKB05011
II	16	PU-31, GBG-1, TBG-104, T9, LBG-709, WBG-108, TU-94-2, DPU 88 31 x VBG 4-008, VBG4-008, LBG-20, GP-6, Uttara, GP-31, KUG 216 x BG 018-2, TU-18, GP-27
III	17	LBG-645, GP-13, MBG-1069, MBG-1050, Buttaminumu, LBG-402, IPU 2-43, MBG-1046, LBG-17, PU-40, LBG-648, LBG-623, VBG 4-14, GP-12, GP-15, GP-14, KUG 216×SPS 5
IV	1	GP-11
V	1	GP-33
VI	1	KUG 216×PU 40
VII	1	Thootiminumu

Table 2. Average intra and inter-cluster D² values among seven clusters with 45 genotypes of Blackgram under rice fallow situation

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	10.15	25.85	29.26	43.64	62.63	80.83	93.53
Cluster II		15.81	49.84	35.92	37.89	39.58	107.97
Cluster III			28.69	72.29	76.22	110.51	87.35
Cluster IV				0.00	104.40	81.74	210.34
Cluster V					0.00	44.08	60.33
Cluster VI						0.00	140.66
Cluster VII							0.00

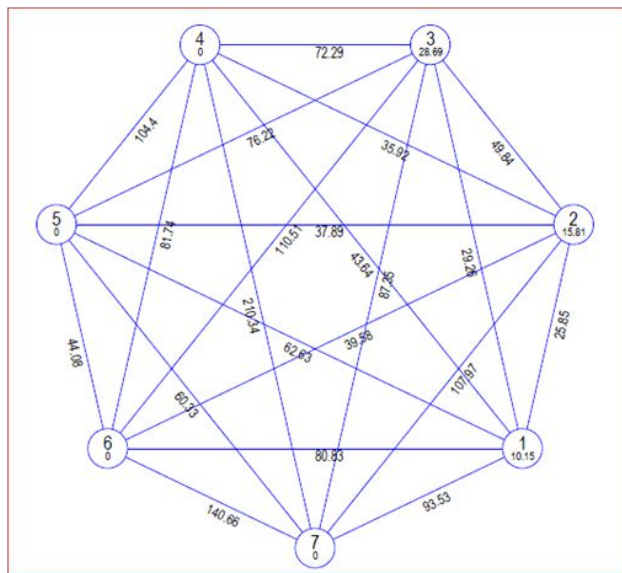
Note: Diagonal values are intra-cluster distances. Off diagonal values are inter-cluster distances.

Table 3. Mean values of seven clusters estimated by Tocher's method from 45 genotypes Blackgram under rice fallow situation

	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Branches Per Plant	Clusters Per Plant	Pods Per Plant	Pod Length (cm)	Seeds Per Pod	100 Seed Weight (g)	Biological Yield Per Plant(g)	Harvest Index (g)	Seed Yield Per Plant (g)
Cluster I	46.21	78.54	22.10	1.70	9.33	33.68	5.20	7.43	4.71	18.22	49.75	9.05
Cluster II	44.40	75.21	20.74	1.82	7.96	26.96	4.84	7.00	4.38	12.82	48.43	6.20
Cluster III	49.57	79.29	23.32	2.16	9.45	32.59	5.17	7.31	4.74	18.51	46.55	8.50
Cluster IV	43.33	71.00	21.50	2.30	8.03	25.60	4.83	6.87	5.17	13.08	44.86	5.87
Cluster V	45.00	76.00	22.53	2.80	10.60	31.73	4.63	7.00	3.58	13.98	42.35	5.95
Cluster VI	43.33	69.67	15.50	1.13	7.33	17.07	4.87	7.27	3.73	7.95	53.82	4.26
Cluster VII	53.00	83.33	29.17	2.27	8.30	29.13	5.33	8.00	3.58	21.94	40.41	8.87

Table 4. Contribution of different characters towards genetic divergence in 45 Genotypes of Blackgram under rice fallow situation

Character	Contribution (%)	Number of times ranked first
1 Days to 50% Flowering	18.59	184.00
2 Days to Maturity	16.46	163.00
3 Plant height(cm)	4.34	43.00
4 Number of Branches per Plant	7.37	73.00
5 Number of Clusters per Plant	5.05	50.00
6 Number of Pods per Plant	2.63	26.00
7 Pod Length(cm)	0.91	9.00
8 Number of Seeds per Pod	2.02	20.00
9 100 Seed Weight(g)	33.74	334.00
10 Biological Yield Per Plant (g)	3.54	35.00
11 Harvest Index(%)	0.71	7.00
12 Seed Yield Per Plant(g)	4.65	46.00

**Fig 1. Intra-cluster (D^2) and inter-cluster distance (D^2) among seven clusters of blackgram**

RESULTS AND DISCUSSION

Forty five genotypes were grouped into seven clusters based on D^2 values using the Tocher's method (Rao 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes grouped into seven clusters is shown in Table 1. Out of seven clusters, cluster III was largest comprising of 17 genotypes followed by cluster II with 16 genotypes, cluster I with eight and cluster IV, V, VI, VII by one genotype each. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at

random indicating that there is no parallelism between geographical diversity and genetic diversity.

The average intra- and inter-cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977) and are presented in Table 2. Intra cluster D^2 values ranged from zero (cluster IV, V, VI and VII) to 28.69 (cluster III). Maximum intra cluster distance was observed in cluster III (28.69) followed by cluster II (15.81) and cluster I (10.15), indicating the existence of genetic divergence among the genotypes within the above clusters. Promising genotypes included in cluster III that had the maximum intra cluster distance and comprising of LBG-645, GP-13, MBG-1069, MBG-1050, Buttaminumu, LBG-402, IPU 2-43, MBG-1046, LBG-17, PU-40, LBG-648, LBG-623, VBG 4-14, GP-12, GP-15, GP-14 and KUG 216×SPS 5.

The maximum inter cluster distance (210.34) was observed between cluster IV and VII followed by cluster VI and VII (140.66), cluster III and VI (110.51), cluster II and VII (107.97), cluster IV and V (104.4) and cluster I and VII (93.53) suggesting that the crosses between the genotypes from these clusters would give desirable recombination. This suggested that there is wide genetic diversity between these clusters. While the minimum inter cluster distance of 25.85 was recorded between cluster I and II followed by cluster I and III (29.26), cluster II and IV (35.92), and cluster II and V (37.89) indicating that genotypes of these clusters had maximum number of gene complexes.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent cluster. The greater the distance between two clusters,

the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that wider the genetic diversity between (GP-11) cluster IV and cluster VII (Thootiminumu), cluster VI (KUG 216×PU-40) and cluster VII (Thootiminumu) and cluster I (LBG-685, LBG-752, MBG-1053, LBG-787, GBG-12, MASH-114, LBG-788 and KKB05011) and cluster VII (Thootiminumu) would produce encouraging results. The genotypes of these clusters may be used as parents in the crossing programme to generate the breeding material with high diversity.

The per cent contribution (Fig.3) towards genetic divergence by all the 12 contributing characters is presented in table.4. The maximum contribution towards genetic divergence was by 100 seed weight (g) (33.74%) followed by days to 50% flowering (18.59), days to maturity (16.46), number of branches per plant (7.37), number of clusters per plant (5.05), seed yield per plant (4.65), plant height (cm) (4.34), biological yield per plant (3.54), number of pods per plant (2.63), number of seeds per pod (2.02), pod length (0.91) and harvest index (0.71). Hence parent chosen on basis of yield in association with relatively simply inherited characters like 100 seed weight, days to 50% flowering, days to maturity and number of branches per plant throw transgressive segregates for higher yield potential. These results are agreement with Niranjana and Rama Chandra (2009), Veni *et al.* (2016) and Mahesha and Gabriel (2017).

The cluster means for each of twelve characters are presented in Table 3. The data indicated that the cluster mean for days to 50% flowering (53.00), days to maturity (83.33), plant height (29.17) and number of branches per plant (2.27), pod length (5.33), number of seed per pod (8.00) and biological yield per plant (g) (21.94) was highest in cluster VII. Cluster V had high mean value for number of cluster per plant (10.60), cluster I had high mean value for number of pods per plant (33.68) and seed yield per plant (9.05), cluster IV had high mean value of 100 seed weight (5.17) and cluster VI had high mean value of harvest index (53.82). And also cluster VI (KUG 216 × PU-40) had lowest mean value for days to 50 % flowering (43.33) and days to maturity (69.67) so the genotypes of this cluster may serve as suitable for source of earliness.

A perusal of these results revealed that there was no cluster with at least one genotype with all desirable traits, which ruled out the possibility of selecting directly one genotype for immediate release. Therefore, judicious combinations of all the targeted traits require hybridization between the selected genotypes from divergent clusters.

CONCLUSION

From the above study the divergent genotypes viz., GP-11, Thootiminumu, KUG 216×PU-40, LBG-685, LBG-752, MBG-1053, LBG-787, GBG-12, MASH-114, LBG-788 and KKB05011 were found promising and may serve as potential parental genotypes for use in hybridization programmes.

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