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Research Note

Genetic divergence in mutants and land races of blackgram *(Vigna mungo [L.] Hepper)* from odisha

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Abstract
A line x tester crossing programme was taken up with ten lines and five testers with a view to identify the best Genetic diversity using Mahalanobis D-square (D^2) techniques was studied for yield and yield contributing traits of 44 (17 Land races genotypes from diverse origin and 27 mutants) blackgram genotypes of Odisha. These genotypes were grouped into twelve clusters. Cluster 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 that considerable amount of genetic diversity existed among the accession. The maximum and minimum divergence was revealed between cluster IV with XI and cluster I with X respectively. Cluster VI exhibited high mean values for number of clusters/plant, pods/plant and seeds/pod. Cluster V recorded high mean values for pod length and 100 seed weight. The characters contributing maximum towards diversity among the accessions are days to maturity (27.16 %), yield/plant (22.19 %), 100 seed weight (18.07 %) and plant height (15.85%) .These characters combining with early maturity are the major traits causing genetic divergence among the accessions. The genotypes in cluster XI with VI, XII with V and V with VI are having moderate divergence with high mean for many characters including yield and can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters

Keywords:
Black gram, divergence, yield attributes, mutants and land races

The narrow genetic base of pulse crop can be widening by use of several breeding approaches including mutation which helps in creating new base sequences. An assessment of the genetic diversity of pulses is an important first step in a program to improve crop yield. The proper estimate of nature and magnitude of diversity in a crop is essential to infer about extent of variation available for yield and its component traits. The selection of genetically divergent parents is expected to produce superior and desirable segregants following crossing (Bhatt, 1973). It is also known that germplasm collections have some valuable genes which provide tolerance to various diseases, hence characterization and evaluation of such local germplasm provides useful material for breeding good varieties. The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programmes. D^2 analysis has been found most effective and, therefore, widely used for the classification of parental lines for developing high yielding genotypes in blackgram.

Among the pulse crop, Blackgram ranks second being next to greengram in area (6.0 lakh ha.) production (2.41 lakh metric tonne) but with low productivity (6.18 q/ha) in Odisha. The limitations with the currently used blackgram germplasm in Odisha is the lack of knowledge on genetic base, low genetic diversity, poor yield and vulnerability to a wide array of insect pest and diseases under monoculture. Assessment of divergence or similarity among the genotypes would help in identification of genotypes that could be used in cross breeding programme for producing transgressive segregants. Limited systematic breeding programme for breeding superior high yielding genotypes in blackgram have been initiated. Vast scope lies for genetic improvement of blackgram through genetic diversity study done to understand the diversity in different landraces and mutants for assessment and creation of diverse line for further breeding. Hence a study on genetic divergence in mutant and local lines of Blackgram from Odisha was taken up with the view of selecting parents for hybridization programme.

The experimental materials for the present investigation comprised of 44 blackgram genotypes which included 17 Local genotypes from diverse origin of Odisha and 27 mutants. They were evaluated in randomized block design (R.B.D) with

three replications. Each entry was represented by 5 rows of 2.8 meter length with a spacing of 30 cm x l0 cm. A fertilizer dose of 20:40:20 kg NPK/ha was applied and need based plant protection measures were followed at EB-II of Plant Breeding & Genetics Department, OUAT during *Rabi*, 2011-12. The mean values of three replications were used for statistical analysis. The observations were recorded on ten quantitative traits *viz* days to 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of clusters/plant, number of pods/plant, number of seeds/plant, pod length(cm), 100 seed weight (g) and yield/plant(g). Assessment of genetic divergence was done using Mahalanobis D^2 statistic (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software as suggested by Singh and Chaudhary (1977).

The analysis of variance showed significant differences among the genotypes in respect to all the characters and indicated high genetic variability. The D^2 values for all comparisons between pairs of genotypes are calculated. On the basis of divergence 44 genotypes under investigation have been grouped into twelve distinct clusters (Table 1), indicating wide diversity in the experimental materials for majority of the characters. Distance between all pairs of genotypes was calculated using squared Euclidean distance method and the genotypes were clustered based on Tocher's method.

The clustering pattern of genotypes confirmed the presence of wide diversity. Among the twelve clusters, clusters II and V had maximum number of genotypes of nine each, cluster IV had eight genotypes followed by cluster VII with three genotypes. Cluster I, III, VI, VIII, IX, X and XI were digenotypic clusters. Cluster XII had solitary genotype. It is obvious that the genotypes have grouped into different cluster irrespective of their geographical origins and parental sources as local land races of odisha have grouped them into two distinct groups (cluster II and cluster IV). Mutant of same parents also grouped into different clusters and of different parents grouped in one cluster. The mutant and land races were in separate cluster proving their genetic closeness and widerness. As the land races are being cultivated since long time and they have adopted to a specific climate and geographical regions, they might have grouped them among themselves. On the other hand the mutants are derivatives of high yielding parents which have arisen due to different mutagenic treatments, hence almost making clusters among themselves only but of different clusters also. This indicated the importance of mutagens in creating variability which can be exploited by recombination breeding. It means that the genetic constitution of the varieties was more important than their origin and distribution (Rai *et al*., 2009). The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand inter cluster divergence suggests the distance (divergence) between the genotypes of different clusters. Inter and intra cluster D^2 values were worked out from divergence analysis. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation.

The composition of cluster and values of inter and intra cluster distances are given in Table 2. The inter cluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accession. The intra cluster distance ranged from 0.00 to 7.65 and the inter cluster distance ranged from 3.10 to 15.07, indicating that the selected genotypes were highly divergent. Minimum intra cluster distance had been recorded with cluster XII (0.00) due to the presence of solitary accession followed by cluster I (2.32) and cluster III (2.74). It indicated that these accessions were closely related in their evolutionary process and passed through similar evolutionary factor. These genotypes within the cluster were less divergent. This might be due to the unidirectional selection practised in past and that has resulted in uniformity and less divergent between these genotypes. Cluster V had highest intra cluster distance (7.65) followed by cluster IV (6.63), cluster XI (6.32) and cluster VII (6.32). The maximum inter cluster distance was observed between cluster IV and XI (15.07) followed by cluster II and XI (14.27) and cluster IV and V (14.14), suggesting that the genotypes belonging to these cluster may further be used as parents for hybridization programme to develop desirable hybrids because crosses between genetically divergent parents will generate transgressive segregants (Shafique *et al*., 2011 and Chauhan *et al.* 2008).

The cluster mean values were estimated over genotypes for ten yield attributing characters in blackgram related to yield, which revealed that a wide range of variation (Table 3). Minimum days to 50% flowering was observed in genotype of cluster XII followed by cluster III. A maximum day to 50% flowering was recorded in cluster VIII. Earliest maturing entries were belonged to cluster XII followed by cluster I. Genotypes requiring longest period to mature belonged to cluster II. Highest mean value for plant height was recorded with cluster XI. Cluster XII had lowest mean value for plant height. Number of primary branches/plant was more with the genotypes of cluster V. The maximum number of cluster/plant was observed in

cluster VI. Similarly genotypes belonged to cluster VI had maximum pod/plant and seed/pod. Highest mean values for pod length and 100 seed weight were more in genotypes of cluster V. Cluster XI registered with highest yield/plant followed by cluster XII and cluster V.

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component characters appeared first in rank and its respective percent contribution towards genetic divergence was presented in Table 4. Among the yield attributing traits the maximum contribution towards divergence was made by days to maturity (27.16%) followed by yield/plant (22.19%), 100 seed weight (18.07%) and plant height (15.85%). On the basis of yield performance and some specialized characters genotypes of cluster V with VI, V with XII and VI with XI are more diverse. Promising genotypes from each cluster for specific traits which can be further utilized in breeding programme are presented in Table 5. From the above study it can be concluded the diversity in blackgram genotypes for yield and yield attributing characters may be due to early maturity, number of cluster/plant, pod/plant, seed/pod, pod length and 100 seed weight results are similar with the reports of Pariya *et al.*, 1997, Singh *et al.* 2012 and Ali *et al*. 2008.

The pattern of distribution of genotypes into various clusters indicates that geographical diversity having no parallelism with clustering pattern which was in agreement with earlier reports in black gram (Ganesh Ram *et al.* 1997; Sagar. *et al.* 2001). The genotypes belonging to different clusters having maximum divergence can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters (Panigrahi *et al*. 2014). However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster and that should be utilized in breeding Programme.

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Table 1. Clustering of blackgram genotypes using Tocher's method

Cluster	Genotypes	Number of genotypes
I	2	PU 30-12, SARALA-5
II	9	BADAMBA LOCAL, BILIPARA LOCAL, SHERAGARH LOCAL, CHERIPALI LOCAL, KHEDAPADA LOCAL, MAHIMUNDA LOCAL, NAYAGARH LOCAL- B, DAYAPALI LOCAL, KENDRAPARA LOCAL
III	2	SARALA-8, SARALA-11
IV	8	SUDHASARANGI LOCAL, DEOGAON LOCAL, BANAPUR LOCAL, KANTAPADA LOCAL, PENDIBADI LOCAL, KALAHANDI LOCAL, BHAWANIPATNA LOCAL, BOLANGIR LOCAL,
V	9	PDU 1-3, PDU 1-7, PDU 1-9, PDU 1-10, PDU 1-11, PDU 1-12, PDU 1-15, PDU 30-8, SARALA-3
VI	2	PU 30-13, SARALA-10
VII	3	PDU 30-14, PU 30-2, PU 30-3,
VIII	2	PU 30-14, SARALA-7
IX	2	PU 30-10, PU 30-11,
X	2	SARALA-2, SARALA-4
XI	2	PU 30-9, SARALA-13
XII	1	SARALA-9

Table 2. Average intra (diagonal) and inter-cluster distance

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	2.32	10.18	4.13	10.78	10.86	4.46	6.47	4.30	5.41	3.10	10.51	5.88
II		5.72	8.17	6.31	13.60	8.92	10.01	9.38	7.38	10.12	14.27	9.31
III			2.74	8.99	11.31	3.57	7.22	5.03	4.65	4.65	11.35	3.96
IV				6.63	14.14	10.11	10.47	10.42	8.26	10.64	15.07	10.14
V					7.65	11.38	9.52	11.72	10.29	11.78	7.48	11.86
VI						3.38	7.08	4.55	5.50	5.22	10.47	5.37
VII							6.32	6.55	6.99	7.06	8.67	9.17
VIII								3.97	6.23	4.70	10.89	7.60
IX									4.11	5.89	11.05	5.07
X										5.11	11.60	6.57
XI											6.32	12.50
XII												0.000

figures given the diagonal are intra cluster distance

Table 3. Cluster wise mean values of ten characters in blackgram

Names Of Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
Days to 50% Flowering	40.85	38.11	36.90	38.37	38.45	37.49	41.19	**42.37**	38.70	41.54	38.56	*33.47*
Days to Maturity	73.13	**88.24**	75.52	87.97	74.92	76.05	79.97	79.28	77.90	74.79	75.13	*70.42*
Plant height (cm)	22.76	20.86	21.20	20.86	32.18	22.62	28.06	23.75	21.57	21.77	**35.01**	*19.01*
Primary branches/plant	1.17	1.27	1.40	*1.00*	**2.06**	1.16	1.27	1.55	1.44	1.12	1.66	1.59
No. of clusters/plant	5.07	4.66	5.25	*3.67*	4.39	**5.61**	3.89	5.53	4.52	4.93	5.03	5.18
Pods/ plant	18.49	12.21	18.39	*9.83*	15.42	**20.76**	18.55	19.61	17.75	18.84	18.11	19.69
Seeds/pod	5.09	5.46	5.45	5.42	5.19	**5.65**	*4.61*	5.38	4.83	4.94	5.40	5.27
Pod length (cm.)	4.66	*4.07*	4.89	4.14	**4.94**	4.46	4.15	4.25	4.38	4.75	4.42	4.80
100 seed weight (gm)	3.32	3.72	*3.17*	3.60	**4.41**	3.23	3.45	3.21	3.92	3.27	4.00	3.39
Yield/plant (gm)	2.98	2.91	3.05	*2.54*	3.48	3.30	3.01	3.03	3.10	2.79	**3.61**	3.49

Maximum and minimum values of each character are printed in bold and italics, respectively

Table 4. Percent contribution of different characters towards diversity in blackgram genotype

Names Of Characters	No. of times ranked 1st	Percent contribution
Days to 50% Flowering	49	5.17
Days to Maturity	257	27.16
Plant height (in cm.)	150	15.85
Primary branches/plant	26	2.74
No. of cluster/plant	28	2.95
Pod/ plant	9	0.95
Seed/pod	26	2.74
Pod length (in cm.)	20	2.11
100 seed weight (in gm.)	171	18.07
Yield/plant (in gm.)	210	22.19
Total	**946**	**100**

Table 5. Promising genotype in each cluster for specific traits

Genotype	Cluster No.	Traits for which it may be used
SARALA-9	XII	Earliness (Days to 50% Flowering)
SARALA-9	XII	Early Maturing (Days to Maturity)
SARALA-13	XI	Long stature [Plant height (in cm.)]
PDU 30-8	V	More No. Primary branches
SARALA-10	VI	More No. of cluster/plant
PU 30-13	VI	More No. of Pod/ plant
SARALA-10	VI	More No. of Seed/pod
PDU 1-10	V	Long Pod/ More Pod length (in cm.)
PDU 1-9	V	100 seed weight (in g.)
SARALA-13	XI	Maximum yield/plant (in g.)