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MULTIVARIATE ANALYSIS ON GENETIC DIVERGENCE IN DIFFERENT ENVIRONMENTS IN BLACK GRAM GENOTYPES

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ABSTRACT
Twenty two blackgram genotypes collected from all over the country were grown at two locations during *Zaid* and *Kharif* seasons in 2013 to evaluate the genetic variability and to determine the genetically diverse genotypes that could be used in hybridization programme for yield enchancement of black gram. Ten morphological characters were studied. Mahalanobis D^2 statistics was used to group the 22 genotypes into five clusters. In E1, cluster I was found to be largest that contained 7 genotypes. Intra-cluster distances between the genotypes were maximum for cluster I (27) while inter-cluster distance ranged from 5.78-12.04. In E2, cluster III was found to be largest that contained 9 genotypes. Intra-cluster distances between the genotypes were maximum for cluster III (48.6) while inter-cluster distance ranged from 6.56-18.70. The per cent contribution towards total genetic divergence was maximum for the number of branches per plant, followed by pod length in both the environments. Ward's cluster analysis divided the 22 genotypes into 2 clusters *viz*., Cluster I and II with 11 genotypes in each cluster in E1 and with 13 and 9 genotypes in E2. IPU2K-21, UH-86-5, SHEKHAR-2 and U-17 can be used as parents in hybridization programme for development of superior blackgram cultivars.

INTRODUCTION

India is the largest producer and consumer of pulses in the world contributing around 25-28% of the total global production. The country grows a variety of pulse crops, such as chickpea, pigeonpea, greengram, blackgram, peas and lentils under a wide range of agro-climate conditions (Patel *et al*., 2014). Majority of Indian population is vegetarian; pulses are the excellent source of protein, carbohydrate, dietary fibre, vitamins and minerals (Deepshikha, 2014). Black gram {*Vigna mungo* (L.) Hepper} (2n = 2x = 22) which belongs to family *Leguminosase*, is an important food legume of *Vigna* group. The seeds of black gram contain a moderately high amount of calories (calorific value of 350 cal/100g), carbohydrates (56.6%), proteins (26.2%) and fat (1.2%). It is also rich in essential mineral and vitamins essential for human body (Shafique *et al.,* 2011). The present productivity of these pulse crops is not only low also static for past several years. There is widening gap between demand and supply with about 20% of the total demand met by import. The major constraints for achieving higher yield in this crop are inherently low yielding potential of the varieties due to lack of genetic variability, absence of suitable ideotypes for different cropping systems, a poor harvest index and susceptibility to abiotic stresses or biotic stresses (Sarobol 1997; Souframanien and Gopalakrishna 2004; Srinives 2006). The entire success of plant breeding programme of any crop largely depends on the wide range of variability present in that crop. It is the range of genetic variability in respect of important economic characters present in the population upon which is based on the effectiveness of selection. Genetic variability is a prerequisite for response to selection in respect of any biological population (Neema and Palanisamy, 2004). Genetic diversity is an essential requirement for increasing crop productivity through breeding. Selection of diverse parents in breeding programme helps in isolation of superior recombinants. The D^2 analysis is one of the very important multivariate analysis developed by Mahalanobis (1936) to study the genetic divergence amongst a set of genotypes. Mahalanobis D^2 statistics based on morphological data thus provides a quantitative method to determine the divergence among biological populations. Because of the greater influence of environments, the morphological characters often do not reliably portray the genetic divergence. However, the evaluation of genotypes over different environments can reduce the influence of environment and genotype x environment interaction (Gumber *et al.,* 2006). In the present study, 22 genotypes of blackgram in two different environments were evaluated for estimating genetic divergence based on ten morphological characters. The objective of this study was to assess the genetic divergence available in 22 genotypes of blackgram under two different environment based on Euclidean distances for the identification of genetically diverse and agronomically superior accessions.

MATERIALS AND METHODS

Seeds of 22 genotypes of black gram were procured from ARS, Durgapura, Jobner Agriculture University, Jaipur. Source details of the genotypes used are given in Table 1. The experiment was conducted in Randomised Block Design with three replication at ARS, Durgapura, Jobner Agriculture

University, Jaipur, designated as environment E1 and at Plant Breeding Research Farm, RCA, MPUAT, Udaipur, designated environment E2. Plant to plant and row to row distance of 30 cm and 10 cm were maintained at each location for maintaining crop geometry. Recommended package of practices were adopted for raising good and healthy crop. The five competitive plants from each of the replication were tagged and observations were taken from these tagged plants at various stages of the plant growth. Data were recorded for ten morphological character namely; plant height (cm), days to 50% flowering, number of branches per plant, days to maturity, number of pods per plant, pod length (cm), 1000 seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%). Mean values were computed and data were analyzed for analysis of variance as suggested by Panse and Sukhatme (1985) and analysed by Mahalonobis D^2 statistics. The genotypes were grouped by Tochers method as suggested by Rao (1952). In this study, the morphological data based grouping of 22 genotypes of black gram was done using Ward's minimum variance method (Ward, 1963) using the IBM SPSS statistics software.

RESULTS AND DISCUSSION

The mean sum of squares due to genotypes varied significantly for all the quantitative characters except for days to maturity under two environments, indicating existence of wide range of variability among the genotypes (Table 2). The findings were in accordance with Reddy *et al*. (2011), Reni *et al*. (2013), Singh et al. (2014) in blackgram and Katiyar and Kant in lentil (2015). Based on D^2 value the 22 genotypes could be grouped into five clusters in both the locations. But there was difference in the constitution of clusters between locations indicating genotype x location interaction (Tables 3 and 4). These results are in accordance with the finding of Neema and Palanisamy, (2004). They studied the genetic divergence in a Diallel mating

Table 1: Details of the genotypes used for present studied

S. No.	Genotype Code	Genotype	Source Centre
1.	G1	U-9	IIPR, Kanpur
2.	G2	UTTARA	IIPR, Kanpur
3.	G3	IPU2K-21	IIPR, Kanpur
4.	G4	UH-86-5	HAU, Hisar
5.	G5	PLU-144	IARI, Delhi
6.	G6	RUG-8	RAU, Durgapura
7.	G7	SPS-29	IIPR, Kanpur
8.	G8	UL-23	Uttar Pradesh
9.	G9	NHKD-31	IIPR, Breeding line
10.	G10	PANT-U30	GBPAU&T, Pant nagar
11.	G11	IC-16511	NBPGR, New Delhi
12.	G12	UH-177	HAU, Hisar
13.	G13	PLU-1	IARI, Delhi
14.	G14	IPU99-233	IIPR, Kanpur
15.	G15	SHEKHAR-2	CSAUAT, Kanpur
16.	G16	PLU-446	IIPR, Kanpur
17.	G17	BG-369	Andhra Pradesh
18.	G18	U-17	IIPR, Kanpur
19.	G19	HPU-180	Himachal Pradesh
20.	G20	STY-2289	IIPR, Breeding line
21.	G21	IPU99-176	IIPR, Kanpur
22.	G22	STY-2834	IIPR, Breeding line

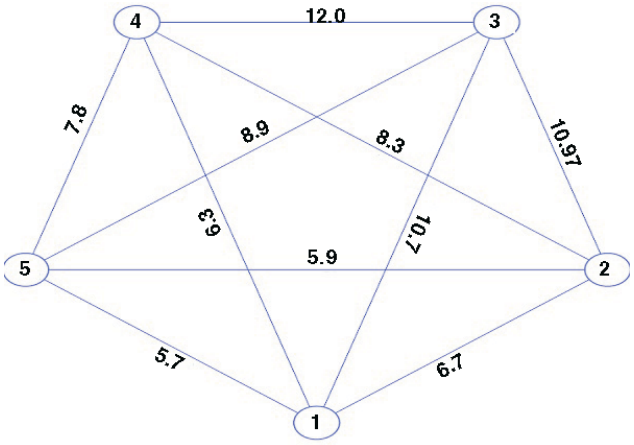

Figure 1: Intra- and inter-cluster distances for 5 groups of 22 genotypes of *V. mungo* L. in E1

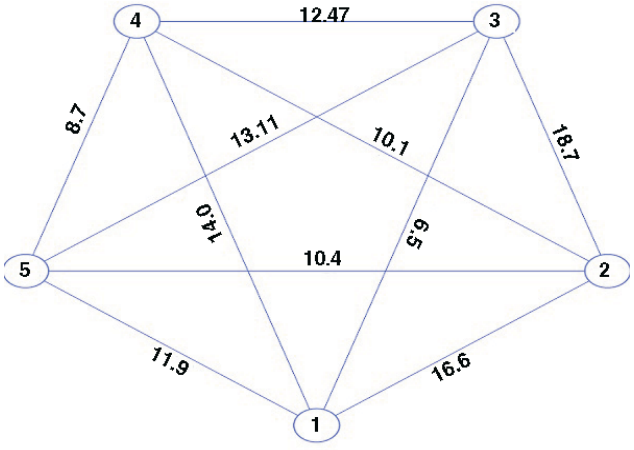

Figure 2: Intra- and inter-cluster distances for 5 groups of 22 genotypes of *V. mungo* L. in E2

system of cowpea. The clustering was conducted for two different locations and at both locations, six clusters were constituted by them. However, the constitution differed between the locations.

The intra-cluster D^2 values ranged from 0.00 to 27 in E1 and from 7.20 to 48.6 in E2; the average intra-cluster distance between the genotypes was maximum (27) for the cluster I followed in descending order by cluster IV (25.6), II (15.7) and V (11.6) in E1 while the average intra-cluster distance between the genotypes was maximum (48.6) for cluster III followed in descending order by cluster V (27.5), III (19.10), II (8.2) and IV (7.2), respectively in E2 (Fig. 1 and 2).

Further, the inter-cluster distance was noted maximum between cluster III and IV (12.04) and minimum (5.78) between cluster I and V in E1 whereas maximum inter-cluster distance was noted between cluster II and III (18.70) and minimum (6.56) between cluster I and III in E2, respectively. Similar findings has been reported by Kumar *et al*. (2006).

Ushakumari *et al*. 2000 grouped 50 genotypes of cowpea

Table 2: ANOVA for the 10 chosen characters in 22 genotypes of *V. mungo* L. (E1 and E2)

S. No.	Characters	Env.	Mean Squares		
		df	Replication(2)	Genotypes(21)	Error(42)
1.	Days to 50% flowering	E1	2.94	17.6*	7.87
		E2	2.17	8.86*	4.66
2.	Days to maturity	E1	10.78	17.40	17.64
		E2	2.33	9.5	17.76
3.	Plant height (cm)	E1	0.36	25.05**	2.01
		E2	10.36	111.64**	6.87
4.	Number of branches per plant	E1	.002	0.39**	0.015
		E2	0.015	0.18**	.008
5.	Number of pods per plant	E1	1.5	13.7**	1.65
		E2	3.72	60.15**	2.65
6.	Pod length (cm)	E1	0.20	0.97**	0.11
		E2	0.08	0.47**	0.16
7.	1000 seed weight (g)	E1	10.42	23.89**	7.17
		E2	4.22	36.23**	6.46
8.	Seed yield per plant (g)	E1	0.03	0.39**	0.10
		E2	0.10	2.7**	0.18
9.	Biological yield per plant (g)	E1	0.65	5.1**	1.05
		E2	3.2	13.87**	2.33
10.	Harvest index (%)	E1	7.52	15.7*	6.90
		E2	13.62	20.97**	7.38

* , ** Significant at 5% and 1% probability level, respectively

Table 3: Cluster profile of 22 genotypes of *V. mungo* L. in E1 location:

Cluster	No. of genotypes	Genotypes
I	7	U-9, UTTARA, PLU-144, SHEKHAR-2, PLU-446, IPU99-176 and STY-2834
II	5	IPU2K-21, UH-86-5, IC-16511, PLU-1 and BG-369
III	1	UH-177
IV	6	RUG-8, SPS-29, UL-23, NHKD-31, IPU99-233 and U-17
V	3	PANT-U30, HPU-180 and STY-2289

Table 4: Cluster profile of 22 genotypes of *V. mungo* L. in E2 location:

Cluster	No. of genotypes	Genotypes
I	4	U-9, PLU-1, IPU99-176 and STY-2834
II	2	UTTARA and UH-177
III	9	IPU2K-21, UL-23, NHKD-31, PANT-U30, IC-16511, IPU99-233, PLU-446, BG-369 and STY-2289
IV	2	UH-86-5 and HPU-180
V	5	PLU-144, RUG-8, SPS-29, SHEKHAR-2 and U-17

Table 5: Cluster means and overall average values for various characters in 22 genotypes of *V. mungo* L. (E1)

Cluster	No. of Genotype	Days to 50% maturity (days)	Days to maturity (days)	Plant height (cm)	Number of branches / plant	Number of pods / plant	Pod length (cm)	1000 seed weight (g)	Seed yield /plant (g)	Biological yield/ plant (g)	Harvest Index (%):
I	7	39	79	18.19	1.52	16.56	4.04	41.5	4.17	13.82	30.27
II	5	36	78	17.86	1.26	17.69	3.66	35.7	3.75	12.27	30.66
III	1	38	79	26.33	2	19.2	5.66	37.4	4.02	15.6	25.81
IV	6	42	83	17.16	1.28	15.93	3.89	38	3.7	12.94	28.72
V	3	37	78	18.67	1.66	15.84	4	38.5	3.6	13.87	26.09
Mean	4.4	38.4	79.4	19.64	1.54	17.04	4.25	38.22	3.84	13.7	28.31
Treat MSS		24.2	23.81	18.41	0.206	4.26	0.85	26.1	0.28	3.54	15.1
Err MSS		1.56	1.56	5.98	0.113	4.64	0.2	3.69	0.098	1.27	2.92
F Ratio		15.52	15.25	3.07	1.81	0.917	4.23	7.05	2.85	2.77	5.16
Percent con tribution towards variability		0	0	0.045	0.172	0.477	0.015	0.002	0.056	0.061	0.007

into 13 clusters and reported that among the yield contributing characters, seeds/pod, branches, pods/cluster and pod length were the important traits responsible for the divergence recorded. In their study, Mahalanobis distances had ranged from 2.06 to 4.23 and maximum distance was found in the genotype PLU-446 in their E1 location. It ranged from 2.31 to 3.72 and maximum distance could be found in genotype IPU99-179 in E2 location.

Cluster mean and general mean values for 10 characters for 22 *V. mungo* L. genotypes are presented in Table 5. The

Table 6: Cluster means and overall average values for various characters in 22 genotypes of *V. mungo* L. (E2)

Cluster	No. of Genotype	Days to 50%maturity (days)	Days to maturity (days)	Plant height (cm)	Number of branches /plant	Number of pods /plant	Pod length (cm)	1000 seed weight (g)	Seed yield /plant (g)	Biological yield /plant (g)	Harvest Index (%):
I	4	36	80	33.83	1	19	4.5	38.8	5.56	18.72	29.76
II	2	38	81	47	1	26	4.6	36.2	7.66	23.6	32.57
III	9	36	80	30.11	1	22	4,4	34.5	5.53	18.59	29.82
IV	2	36	80	39.5	1	29	4.5	31.9	6.39	21.59	29.67
V	5	34	78	39.27	1	28	4.8	39.7	6.83	21.25	32.29
Mean	4.4	36	79.8	37.94	1	24.8	4.5	36.22	6.39	20.75	30.82
Treat MSS		7.02	4.28	159.6	0.039	74.41	0.15	37.68	2.94	15.77	8.01
Err MSS		1.99	2.91	8.4	0.067	7.26	0.16	6.05	0.42	1.99	6.74
F Ratio		3.5	1.47	18.99	0.577	10.24	0.93	6.2	6.9	7.8	1.18
Percent contri bution towards variability		0.029	0.255	0	0.68	0	0.46	0.003	0.002	0.001	0.35

perusal of mean data revealed that differences in the cluster means existed for all the characters studied. Results indicated that genotypes belonging to cluster II *viz.,* IPU2K-21, UH-86-5, IC-16511, PLU-1 and BG-369 showed early flowering, early maturity as well as harvest index indicating their good potential for crop productivity in Jaipur. The per cent contribution towards total genetic divergence was maximum for the characters, number of pods per plant followed by number of branches per plant and seed yield per plant. Similar results were obtained by Ghafoor *et al.* (2001). The cluster mean data revealed that differences existed for all the characters studied (Table 6), indicating that genotypes belonging to cluster V, *viz.,* PLU-144, RUG-8, SPS-29, SHEKHAR-2 and U-17 showed early flowering and early maturity with above average value for plant height, number of pods per plant, pod length, 1000 seed weight, seed yield per plant, biological yield per plant and harvest index revealing their good potential for crop productivity in Udaipur region. Their per cent contribution towards total genetic divergence was maximum for the characters number of branches per plant followed by pod length and harvest index, respectively.

Classifying Genotypes using Ward's Cluster Analysis (E1 and E2):

Ward's hierarchical cluster analyses were carried out on the basis of 10 morphological characters. It was used to measure genetic distance between the 22 *V. mungo* L. genotypes. Cluster analysis grouped the genotypes into two clusters, cluster I and II that were apart at 25 rescaled values in both the locations. In location E1, cluster I included 11 genotypes *viz.,* RUG-8, U-17, SPS-29, NHKD-31, IPU99-233, UL-23, U-9, STY-2834, PLU-144, UTTARA and SHEKHAR-2. Cluster II also included 11 genotypes *viz.,* STY-2289, IPU99-176, PLU-446, BG-369, UH-177, PLU-1, HPU-180, PANT-U30, IPU2K-21, UH-86-5 and IC-16511. In location E2, cluster I included 13 genotypes *viz.,* U-9, BG-369, IPU99-233, U-17, IPU99-176, PLU-1, STY-2834, IPU2K-21, UL-23, STY-2289, PANT-U30, IC-16511 and NHKD-31. Cluster II included 9 genotypes *viz.,* SPS-29, SHEKHAR-2, PLU-446, RUG-8, HPU-180, UH-177, PLU-144, UTTARA and UH-86-5.

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