SHORT COMMUNICATION

D^2 Analysis for Physiological Traits in the Progenies of Urdbean (*Vigna mungo* (L.) Hepper)

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Keywords: D^2 statistics, Genetic divergence, *Vigna mungo*, Physiological traits

Minor genes, whose effects could be identified by plant morphology have been exploited for genetic improvement of grain legumes, but this has not led to spectacular gains in the yield potential. The analysis of constraints to increasing genetic potential of these crops reveal the existence of wide differences between the actual biological potential and the highest levels achieved through the present available base. Further, the selection of diverse parents belonging to distant groups leads to a wide spectrum of gene combinations for the quantitative inherited physiological traits. The D^2 analysis measures the amount of genetic diversity in a given population in respect of several physiological characters including seed yield considered together. In urdbean, D^2 statistics has been studied in the parents and their F_2 progenies. The intermating of unlike leads to greater opportunity for crossing over which releases latent variation by breaking up the predominantly repulsion phase linkages (Thoday, 1960).The present study aims at analyzing the genetic divergence among progenies and their parents in urdbean, using Mahalanobis, $^sD^2$ statistics by a software (SPSS programme), a powerful tool in discerning divergence among groups based upon multiple growth characters and assessing the relative contribution of different components to total divergence (Rao, 1952; Murty and Arunachalam, 1966). Such a measure will eventually help in breeding programme, aimed at evolving superior genotypes.

The materials for the present study comprised twelve genetically diverse lines of urdbean (HPU-1, VB-17, HPBU-124, HPBU-125, HPBU-126, HPBU-128, HPBU-129, HPBU-130, HPBU-131, HPBU-133, UL-338 and MX-17) which were crossed with four diverse pollen parents (T-9, PDU-1, UG-218 and Palampur-93) in a line x tester mating design (Kempthorne,1957). The resultant 48 F_2, along with 16 parents were evaluated for their performance at the Regional Research Station, Himachal Pradesh Agricultural University, Bajaura (31°48′ N 77°00′E, 1099 amsl) during *kharif* 2003. The experiment was laid out in Randomized Block Design with three replications. All the agronomic practices were followed for raising the crop.

Data for physiological traits were recorded on 20 randomly selected plants within each replication of each cross, 40 and 60 days after sowing. The following physiological traits were included in the study,

1. Leaf Area Plant^{-1} (LAP)

Leaf area plant^{-1} (cm^2) was computed by leaf area meter (Delta-T-Devices, Cambridge, England). After completing the observations on leaf area, clipped leaves and stem portions of each plant were dried in an oven for 48 hours at 65°C. The samples of dried leaves stem and branches were weighed on the Electronic Balance (ADCO Model-AD200B). The following physiological traits were computed using the formulae of Redford (1967).

2. Crop Growth Rate (CGR), (g day^{-1})

$$CGR = (W_2 - W_1)/ (t_2 - t_1)$$

where W_2 and W_1 are dry plant weights measured in two consecutive harvests over time interval $t_2 - t_1$.

3. Leaf Growth Rate (LGR), (cm^2 day^{-1})

$$LGR = (A_2 - A_1)/ (t_2 - t_1)$$

where A_1 and A_2 are the leaf areas at times t_1 and t_2, respectively.

4. Net Assimilation Rate (NAR), (mg dm^{-2})

$$NAR = (W_2 - W_1) (InA_2 - InA_1)/ (A_2 - A_1) (t_2 - t_1)$$

where, InA_2 and InA_1 are the natural log values of leaf area at times t_2 and t_1, respectively.

5. Leaf Area Ratio (LAR), (dm^2 g^{-1})

$$LAR = \frac{\text{Leaf area (A)}}{\text{Total dry plant weight (W)}}$$

6. Seed Yield Plant^{-1} (SYP), (g)

Twenty plants per replication were selected at random and seed yield plant^{-1} was recorded.

Following analysis of variance, genetic divergence was studied using Mahalanobis D^2 statistics as described by Rao (1952). D^2 values based on uncorrelated variables were used to classify the parents and crosses. The constellation of groups was formed according to Tocher, s method (Rao, ibid). The relative contribution of each trait to the total D^2 value between each pair of genotype was determined following the procedure outlined by Bhatt (1970).

The analysis of variance revealed significant differences among genotypes for all characters studied indicating the potentiality of population to isolate parents that may produce heterotic progenies. On the basis of physiological parameters 64 genotypes (16 parents and 48 F_2 crosses) were classified into 9 clusters (Table 1). The maximum number of genotypes (13) was accommodated in cluster 1, followed by 10 genotypes each in cluster II and IX, and 9 genotypes each in cluster VI and VIII. The clustering pattern of progenies was independent of parental cross-combinations, i.e. progenies of a cross and their parents were grouped in different clusters. The estimates of inter-cluster distance between two clusters comprising progenies may be greater than those between clusters comprising progenies derived from two distinct parentages. This suggests that forces other than the divergence of the parents have operated in the differentiation of these progenies (Table 2). Intra-cluster

Table 1. Distribution of parents and their progenies in different clusters

Cluster	Number of genotypes	Parents	Progenies
I	13	T-9, PDU-1	HPU-1 x Palampur-93, HPBU-124 x T-9, HPBU-125 x T-9, HPBU-128 x UG-218, HPBU-126 x T-9, HPBU-128 x Palmpur-93, HPBU-130 x UG-218, HPBU-133 x Palampur-93, UL-338 x PDU-1, UL-338 x UG-218, MX-17 x Palampur-93
II	10	HPU-1, HPBU-130, HPBU-131, UL-338, MX-17	VB-17 x T-9, VB-17 x PDU-1, HPBU-126 x Palampur-93, HPBU-128 x PDU-1, HPBU-130 x T-9
III	08	–	HPU-1 x UG-218, HPBU-124 x UG-218, HPBU-125 x UG-218, VB-17 x UG-218, HPBU-128 x T-9, HPBU-128 x UG-218, HPBU-128 x Palampur-93, UL-338 x T-9
IV	02	–	HPBU-131 x PDU-1, HPBU-133 x UG-218
V	02	–	VB-17 x Palampur-93, HPBU-125 x Palampur-93
VI	09	HPBU-128, HPBU-129, VB-17	HPU-1 x PDU-1, HPBU-131 x T-9, HPBU-131 x UG-218, HPBU-131 x Palampur-93, HPBU-133 x PDU-1, MX-17 x PDU-1
VII	01	–	HPBU-130 x PDU-i
VIII	09	HPBU-126	HPBU-125 x PDU-1, HPBU-125 x UG-218, HPBU-125 x PDU-1, HPBU-128 x T-9, HPBU-124, Palampur-93, HPBU-130 x Palampur-93, MX-17 x T-9, MX-17 x UG-218
IX	10	HPBU-124, HPBU-125, HPBU-133, UG-218, Palampur-93	HPU-1 x T-9, HPBU-124 x PDU-1, HPBU-129 x PDU-1, HPBU-133 x T-9, UL-338 x Palampur-93

Table 2. Inter and intra cluster D^2 values in urd bean progenies

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**13.13**	20.89	44.16	13.46	53.50	44.54	18.34	23.80	34.33
II		**6.89**	34.51	31.68	48.61	39.93	20.63	32.93	32.37
III			**8.98**	49.38	24.00	11.30	38.28	42.35	19.88
IV				**9.48**	56.60	48.11	18.90	22.70	39.86
V					**5.41**	19.62	48.65	56.62	23.67
VI						**10.12**	40.68	41.84	15.20
VII							**5.45**	25.33	35.60
VIII								**12.32**	38.39
IX									**7.65**

Table 3. Cluster means of physiological characters in urd bean progenies.

Cluster	Character					
	LAP	CGR	LGR	NAR	LAR	SYP
I	12.14	0.31	46.62	75.41	15.85	6.48
II	10.46	0.23	38.91	54.77	17.16	9.04
III	8.11	0.18	29.72	58.92	19.11	6.58
IV	11.00	0.25	42.62	81.59	16.78	11.34
V	12.53	0.30	47.21	36.52	15.23	7.15
VI	12.62	0.30	48.23	72.59	16.39	8.63
VII	13.41	0.31	52.04	69.12	16.03	9.97
VIII	14.73	0.37	56.23	62.07	16.13	8.61
IX	8.24	0.19	30.18	73.42	15.82	8.01

average D^2 values varied from 5.41 to 13.13. However, the low values of intra-cluster average D^2 suggested the presence of narrow genetic variation within a cluster. Further, inter-cluster D^2 is a measure of genetic divergence between the two clusters and was observed to be the highest (56.60) between cluster IV and V and the lowest (11.30) between cluster III and VI (Table 2). Cluster means (Table 3) indicated that cluster IV, V and VII revealed highest values for almost all the characters including seed yield. Direct relationships between progeny mean and number of superior genotypes to best check has been reported by Bakshi *et al.* (1996). Therefore, the mean of progenies is very important in deciding which of the crosses should be repeated in order to get better segregants. This will provide opportunity to select better recombinants for various physiological characters and in breeding for obtaining better genetic gains.

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