Comparative Manifestation of Genetic Diversity for Grain Yield and Its Component Traits in Urdbean under Two Cropping Systems

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Nature and magnitude of comparative genetic diverisity was assessed using Mahalanobis's D^2 statistics in 64 genotypes (16 parents and 48 F_2 crosses) of urdbean genotype grown in monoculture and in association with maize. All the genotypes were grouped in 9 clusters in case of monocluture, while 7 clusters were formed for intercropping. Some genotypes had consistently the similar clustering pattern in both the cropping systems while others were affected by the cropping system in expressing the genetic diversity. The performance of some genotypes varied from cropping system to another, while that of others remained unaffected. Breeding programme to develop varieties suitable for monoculture, intercrop and both the cropping systems has been suggested.

Key words: Urdbean, Cropping system, Genetic divergence, Cluster analysis

Urdbean is cultivated in India as a sole or monoculture crop. However, its intercropping with maize is a common practice in some hilly tracts of North India. This practice aims at (i) ensure against total crop failures under abnormal weather conditions, (ii) increase in total productivity per unit land area and (iii) equitable and judicious utilization of land resources and farming inputs. The Indian Urdbean Breeding Programme has concentrated mainly on the development of high yielding varieties adapted to sole cropping. The varieties developed to date are also being intercropped with maize under the assumption that correlated improvement will occur in the intercrop. However, significant genotype x cropping system interactions have been reported in climbing bean genotypes (Francis *et al.*, 1978a, 1978b) and segregating soybean populations (Gupta *et al.*, 1981). Most of the available information on genetic divergence of urdbean was only under monoculture or sole crop and we have no information as to how the genetic diversity of the urdbean genotypes is altered when intercropped with maize. The selection of genetically diverse parents belonging to distant groups lead to a wide spectrum of gene combinations for polygenically inherited traits. The present study aims at analyzing the genetic divergence of 48 F_2 crosses and their parents under both the cropping systems using Mahalanobis's D^2 statistics, a powerful tool in discerning divergence among groups based upon multiple characters and assessing the relative contribution of different components to the total divergence (Rao, 1952, Murty and Amnachalam, 1966). Such a measure will eventually help in breeding programmes by intermating of unlikes leads to greater opportunity for crossing over which releases latent variation by breaking up the predominantly repulsion phase linkages (Thoday, 1960) at evolving superior genotypes required for different cropping systems.

Materials and Methods

The material for the present study consisting 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) 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 crosses alongwith 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). The experiment was conducted in Randomized Block Design with three replications under two sets of cropping systems *viz* monoculture and intercropping with maize. Each entry in sole crop, sub-plots comprised two rows of urdbean each 2m long and 30 cm apart. Under associated cropping, sub-plot treatments were identical except that a row of a locally recommended variety of maize (Early Composite) was added between successive two rows of urdbean. The plants of urdbean and maize were spaced at 8 and 20 cm within rows, respectively. All the recommended agronomic practices were followed for raising the crop.

Observations were recorded on 5 and 20 randomly selected plants/replication for parents and F_2's, respectively on X_1 : seed yield/plant (g), X_2 : harvest index (%), X_3: 100-seed weight (g), x_4: seeds/pod, X_5: pods/plant, X_6: biological yield/plant (g), X_7 : plant height (cm), X_8: pod bearing branches/plant, X_9: days to 50% flowering, X_{10}: days to maturity. Data were analyzed based on the procedure described by Rao (1952), the values of D^2 between pairs of genotypes were computed. The composition of groups was formed according to Tocher's method.

Results and Discussion

The composition of each cluster in two cropping systems are presented in Table 1. As many as 13 genotypes were grouped in cluster I under monoculture, followed by 10 in clusters II and IX, 9 in clusters VI and VIII and 8 in cluster III, 2 each in IV and V and 1 in cluster VII. In case of intercropping, 16 genotypes were grouped in cluster I followed by 12 in clusters II and VII, 10 in cluster IV, 9 in cluster V, 4 in III and 1 in cluster VI. The clustering pattern of progenies was independent of parental cross combinations, i.e., progenies of cross and there parents were grouped in different clusters under two cropping systems. The clustering pattern of some genotypes was not consistent. This can easily be attributed to the effect of cropping system on the genotypes in expressing the genetic diversity. This also demonstrated simultaneously that the conclusions drawn on the basis of a study of genetic diversity of parents and progenies in monoculture cannot be applicable in intercropping. Grouping of populations into clusters have been reported to alter from environment to environment (Somayajulu *et al*, 1970, Upadhya and Murty 1970, Jatasra and Paroda, 1983).

Intra-cluster average D^2 values for monoculture ranged from 10.10 to 16.47 while 9.78 to 12.84 under intercropping system (Table 2). Relatively low values of intra-cluster average D^2 suggested the presence of narrow genetic variation within a cluster. Inter-cluster D^2 is a measure of genetic distance between two clusters and was observed to be the highest (58.09) between clusters IV and V and the lowest (17.05) between clusters II and III in monoculture, while it was the highest (98.33) between cluster I and VI and the lowest (14.27) between cluster I and IV in the intercropping. Intra- and inter-cluster average D^2 values were higher in magnitude under monocropping than intercropping except cluster VI of intercropping. The cluster means for all the characters were higher in magnitude under monoculture than the intercrop (Table 3). It was due to the effect of intercropping on urdbean genotypes.

The urdbean breeding for higher seed yield is of great significance for both cropping systems. Direct relationship between progeny mean and number of superior genotypes to the best check has been reported by Bakshi Ram *et al.* (1996). Therefore, the mean performance of progenies is very important in deciding which of the crosses should be repeated or not in order to get better segregants. The mean performance of seed yield of diverse cluster combinations in two cropping systems indicated that means of cluster combination I (6.48) and III (6.58) were lower in magnitude under monoculture, while cluster combination V (4.34) in intercropping system. Hence, the hybridization among genotypes from these cluster combination might result in enhancement in genetic variability towards negative direction. Hybridization among genotypes from these cluster combinations may not improve the population mean performance but the variance and the range of frequency distribution are expected to increase (Allicchio and Palenzona, 1974) due to crossing over which releases latent variation by breaking up the predominantly repulsion phase linkage (Thoday, 1960).

Further, mean of cluster combination IV (HPBU-131 x PDU-1 and HPBU-133 x UG-218), followed by cluster VII (HPBU-130 x PDU-1) was the maximum in monoculture, whereas, similar clusters also consisting various genotypes under intercropping system. Therefore, subsequent cross-breeding programme among genotypes of these cluster combinations for important seed yield and component traits is expected to increase variability in the further mapping population with desirable mean performance suitable for both the cropping systems could be undertaken.

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Table 1. Distribution of parents and their progenies in different clusters under two cropping systems

		Monoculture				Intercropping	
Cluster	Number of genotypes	Parents	Progenies	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-126 x T-9, HPBU-128 x UG-218, HPBU-128 x Palampur-93, HPBU-130 x UG-218, HPBU-133 x PDU-1, UL-338 xUG-218, MX-17 x Palampur-93	I	16	MX-17, T-9, PDU-1, UG-218	HPU-1 x T-9, HPU-1 x Palampur-93, VB-17 x PDU-1, VB-17 x UG-218, VB-17x Palampur-93, HPBU-124 x T-9, HPBU-124 x PDU-1, HPBU-125 x T-9, HPBU-126 x UG-218, HPBU-128 x T-9, HPBU- 129 x T-9, HPBU- 1 3 1 x Palampur-93
II	10	HPU-1, HPBU-130, HPBU-131, MX- 17, UL.1-338	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	II	12	VB-17, HPBU-124, HPBU-125, HPBU-126, Palampur-93	HPBU-125 x UG-218, HPBU-125 x Palampur-93, HPBU-129 x Palampur-93, HPBU-130 x T-9, HPBU-130 x UG-218, MX-17 x T-9, MX-17 x PDU-1
III	08	–	HPU-1 xUG-218, HPBU-124 xUG-218, HPBU- 126 x UG-2 1 8, VB- 17 x UG-218, HPBU-128 x T-9, HPBU-129 x UG-218, HPBU-129 x Palampur-93, UL-338 x T-9	III	04	–	HPBU-125 x PDU-1, HPBU-128 x Palampur-93, UL-338 x T-9, UL-338 x Palampur-93
IV 1,	02	–	HPBU-131 x PDU-1, HPBU-133 x UG-218	IV	10	UL-338	VB-17 x T-9, HPBU-126 x PDU- HPBU-126 x Palampur-93, HPBU-128 x PDU-1, HPBU-129 x PDU-1, HPBU-130 x PDU-1, HPBU-130 x Palampur-93, HPBU-131 x T-9, MX-17 x UG-218
V	02	_	VB-17 x Palampur-93, HPBU-125 x Palampur-93	V	09	–	HPU-1 x UG-218, HPBU-129 x UG-218, HPBU-131 x PDU-1, HPBU -131 x UG- 218, HPBU-133 x T-9, HPBU-133 x PDU-1, HPBU-133 x UG-218, HPBU- 133 x Palampur-93
VI	09	HPBU-128, HPBU-129, VB-17	HPBU-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	VI	01	HPU-1	–
VII	01	–	HPBU-130X PDU-1	VII	12	HPU-1, HPBU-128, HPBU-129, HPBU-1 30, HPBU-131, HPBU-133	HPU-1 x PDU-1, HPBU-124 x UG-218, HPBU-126 x T-9, HPBU-128 x UG-218, UL-338 x PDU-1, MX- 17 x Palampur-93
VIII	09	HPBU-126	HPBU-125 x PDU-1, HPBU -125 x UG- 218, HPBU-126 x PDU-1, HPBU-129 x T-9, HPBU-124 x Palampur-93, HPBU- 130 x Palampur-93, MX- 17 x T-9, MX- 17x 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-338x Palampur-93				

Table 2. Intra- and inter- cluster VD^2 values under two urdbean cropping systems

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
Monoculture									
I	**10.10**	24.96	24.28	40.23	39.51	18.68	39.25	20.27	17.73
II		**15.64**	17.05	43.35	21.80	25.05	38.76	19.46	21.17
III			**16.47**	47.31	30.16	30.02	46.61	30.81	17.22
IV				**12.53**	58.09	25.62	47.09	43.15	37.57
V					**13.02**	38.89	48.56	28.55	40.99
VI						**11.22**	35.54	21.20	22.74
VII							–	34.45	41.38
VIII								**13.90**	29.15
IX									**13.71**
Intercropping									
I	**9.78**	19.36	31.29	14.27	16.23	98.33	15.11		
II		**9.88**	18.71	15.87	17.22	95.64	15.67		
III			**11.89**	23.94	21.94	97.23	24.89		
IV				**11.79**	18.64	97.17	17.86		
V					**12.84**	97.29	20.29		
VI						–	96.10		
VII							**12.43**		

Table 3. Cluster means of characters under two urdbean cropping systems

Character	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
Monoculture									
X_1	6.48	9.04	6.58	11.34	7.15	8.63	9.97	8.61	8.01
X_2	38.83	41.90	37.15	24.00	41.39	32.64	40.86	42.36	38.58
X_3	5.04	4.96	4.87	5.20	4.88	5.11	4.92	4.82	4.88
X_4	5.21	5.24	5.33	5.79	5.44	5.25	4.68	5.14	5.18
X_5	26.40	35.53	25.21	37.35	28.44	31.06	44.71	35.90	31.95
X_6	18.34	23.86	18.37	50.62	21.29	30.35	24.65	22.05	21.78
X_7	45.44	48.26	44.80	57.26	50.25	56.60	56.28	47.83	47.55
X_8	8.02	9.21	8.25	8.79	8.43	9.31	10.44	9.55	9.15
X_9	41.84	40.90	41.06	42.70	41.15	41.71	42.00	41.46	40.86
X_{10}	89.13	89.40	91.78	93.35	91.00	90.69	92.50	88.13	89.60
Intercropping									
X_1	5.68	5.96	5.74	6.37	4.34	5.55	5.49		
X_2	36.64	38.18	36.27	39.86	33.07	4.29	38.13		
X_3	4.74	4.27	4.93	4.42	4.55	4.23	4.39		
X_4	4.99	4.70	4.56	4.83	4.99	4.99	4.75		
X_5	26.50	28.26	27.20	36.05	29.83	37.40	24.45		
X_6	14.66	15.00	14.23	16.55	12.12	12.27	13.69		
X_7	40.85	45.41	32.98	36.72	33.46	46.44	46.25		
X_8	7.20	7.75	7.75	7.52	6.57	6.69	7.59		
X_9	44.47	45.26	44.15	43.02	42.26	45.20	44.63		
X_{10}	96.50	94.54	94.13	95.38	95.89	96.00	94.65		

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