Theoretical and Applied Genetics 45, 211–214 (1974)

Genetic Divergence and Hybrid Performance in Mung Bean

S. RAMANUJAM, A. S. TIWARI and R. B. MEHRA

Division of Genetics, Indian Agricultural Research Institute, New Delhi (India)

Summary. Genetic divergence in 35 populations (10 parents and 25 F_1's) of mung bean was studied by D^2 and canonical analyses. The ten parents formed as many as eight separate clusters, suggesting that the genetic divergence between them was quite substantial. The parent BR-2 was highly divergent from all the other entries. It was found that flowering time, maturity, seed density and seed size (100-seed weight) contributed substantially to the divergence. Canonical analysis supported the divergence pattern obtained by D^2 analysis and the contribution of different characters to genetic divergence. The relationship between genetic divergence (D^2) and heterosis was evaluated. In general, there was fair agreement between the extent of heterosis and the genetic divergence between the parents.

Adequate genetic diversity is a basic requirement of breeding programmes. In pulses, where little information is available, the importance of studies on genetic divergence is obvious. The results of such an investigation in mung bean (*Phaseolus aureus* Roxb.) are presented and discussed in this paper.

Materials and Methods

Ten parental genotypes of diverse origin and 25 F_1 crosses involving them were grown in kharif 1971 in a randomized block design with three replications, at the Division of Genetics, Indian Agricultural Research Institute, New Delhi. Observations were recorded on yield/plant in gm., number of branches/plant, number of seeds/pod, 100-seed weight in gm., days to flowering, days to maturity, proportion of leaf axils which bore an inflorescence, number of pods/plant, % protein in flour, and seed density. The original measurements were transformed to standardised, uncorrelated variables by pivotal condensation (Rao, 1952). The divergence between any two populations was obtained as the sum of squares of the differences in the value of the corresponding transformed variates. Based on these D^2 values, the 35 populations were grouped into clusters using Tocher's method (Rao 1952). Canonical analysis was according to Anderson (1958).

Heterosis was measured as the percentage of the deviation of F_1 value from the mid-parent value to the mid-parent value.

Results and Discussion

ANOVA (Table 1) revealed significant differences among the populations for each of the ten characters. Simultaneous test of significance based on Wilks's criterion also revealed significant differences among the populations for the pooled effects of all the characters. The D^2 values corresponding to every possible pair (595) of the 35 centries are on record in Tiwari (1973).

The 35 mung populations studied could be grouped into 19 clusters (Fig. 1). The highest inter-cluster distance was between clusters I and XIX ($D^2 = 1231.96$) while the lowest was between I and II ($D^2 = 20.5$).

The cluster-means (Table 2) for the various characters considered together with the inter- and intra-cluster D^2 estimates provided interesting evidence on the nature of genetic divergence.

Such assessment of the contribution of different characters to genetic diversity in D^2 analysis, revealed the importance of seed density, maturity time, seed size and flowering time. Yield and its components, such as number of pods/plant and seeds/pod, had limited influence on genetic diversity. Canonical analysis (Table 3) also revealed the importance of maturity and flowering time in the first vector and seed density and seed size in the second. There was, therefore, considerable agreement between the findings of D^2 analysis and the principal component approach for the contribution of different characters to genetic divergence. Murty and Arunachalam (1966), who considered the effect of breeding systems on genetic diversity, reported the importance of the contribution of flowering time to genetic diversity in a number of crop plants, including such selfpollinators

Table 1. *ANOVA (RBD) for ten characters studied in 35 genotypes of mung bean*

Source of variation	d. f.	Yield/ plant	Branches /plant	Seeds/ pod	100-seed weight	Days to flowering	Days to maturity	Effective axils/ plant	Pods/ plant	% protein	Grain density
Replications	2	0.80	2.76	0.40	0.20	10.03**	1.22	15.87*	48.74**	23.50**	0.001
Treatments	34	12.18**	1.24**	2.86**	0.99**	197.32**	249.49**	40.40**	59.81**	4.21**	0.016**
Error	68	2.30	0.29	0.64	0.15	3.18	3.23	9.10	18.20	1.28	0.001

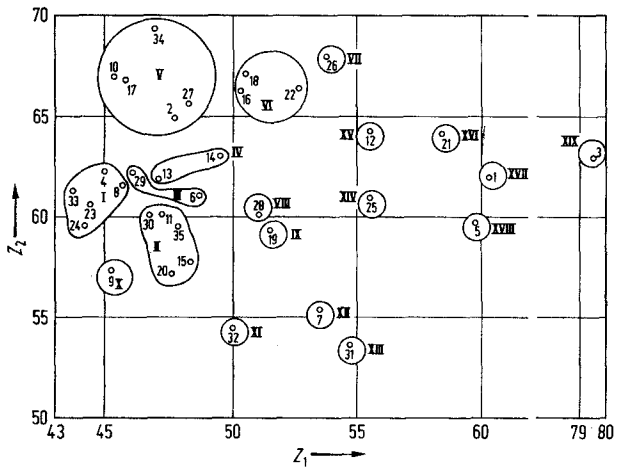

Fig. 1. Two dimensional representation of divergence of 35 genotypes of mung bean (10 parents and 25 hybrids) using the first two canonical vectors (Z_1, Z_2) as coordinates. The groupings obtained from D^2 analysis are superimposed. The genotypes included in the different clusters are: I. T. 44, 'Pusa Baisakhi', T. 44 × Hyb. 45, T. 44 × R. 1, 'Pusa Baisakhi' × R. 1; II. K. 11 × B. 1, K. 11 × Khar. 1, BR. 2 × T. 44, J. 781 × 'Pusa Baisakhi', R. 1 × 'Madira',; III. Khar. 1, Khar. 1 × 'Madira'; IV. K. 11 × T. 44, K. 11 × Hyb. 45; V. B. 1, 'Madira', B. 1 × T. 44, Khar. 1 × 'Pusa Baisakhi', 'Pusa Baisakhi' × 'Madira'; VI. B. 1 × BR. 2, B. 1 × Hyb. 45, B.R. 2 × 'Pusa Baisakhi'; VII. Khar. 1 × J. 781; VIII. Khar. 1 × R. 1; IX. B. 1 × J. 781; X. R. 1; XI. J781 × 'Madira'; XII. J. 781; XIII. J. 781 × R. 1; XIV. Hyb. 45 × 'Madira'; XV. K. 11 × BR. 2; XVI. BR. 2 × Hyb. 45; XVII. K. 11; XVIII. Hyb. 45; XIX. BR. 2.

as wheat and linseed. Seed density has been less studied. Murty and Arunachalam (1966) reported an important role for seed density, but found seed size to have limited influence on genetic diversity in these crops. In the present study, seed size also made a fair contribution to genetic diversity, as has also been reported in a number of crops including mung bean (Gupta and Singh, 1970) by earlier workers. Perhaps the considerable human selection exerted for seed size in pulse crops is responsible for this.

It is interesting to note that the ten parents showed considerable diversity among themselves and formed as many as eight well-separated clusters (Fig. 1). The parents T.44 and 'Pusa Baisakhi' in cluster I, and B-1 and 'Madira' in cluster V, are the only parents placed together. The parent BR-2 was highly divergent from all the other entries. The 25 hybrids fell into as many as 14 different clusters in the D^2 analysis, many of the clusters consisting of one or two hybrids and often considerably separated from the clusters containing the parents (e. g. crosses of parent K-11). In some instances the hybrids occupied the same cluster as one of their parents, while in others hybrids having one parent in common occupied the same cluster. It was also noted that hybrids involving one common parent may be widely dispersed (e. g., five hybrids of BR-2 occupied four distantly situated clusters, II, VI, XV and XVI). All these results suggest that substantial diversity exists among the parental genotypes and that considerable variation has been generated from these crosses though only a limited number of parents were involved. The alleged lack of genetic variability in mung bean, and presumably other pulses, therefore needs to be re-examined.

An interesting aspect of the analysis is the relationship between parents which fall in the same cluster. One such pair was in cluster I and involved T.44 and 'Pusa Baisakhi'. The distance between these genotypes ($D^2 = 2.5$) was very small and there

Table 2. *Cluster means for ten characters in mung bean*

Cluster No.	Population in cluster	Yield/ plant (gm)	Branches /plant	Seed/ pod	100-seed weight (gm)	Days to flowering	Days to maturity	Eff. leaf axils	Pods/ plant	% protein	Seed density (gm./cc)
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
I	5	5.21	0.77	11.49	3.15	39.46	64.13	29.08	16.37	26.65	1.32
II	5	3.54	0.84	10.32	2.72	42.67	69.07	24.00	14.35	26.09	1.26
III	2	5.93	1.23	10.51	3.90	42.17	67.83	29.08	16.90	26.73	1.41
IV	2	8.88	1.80	11.36	4.03	41.00	67.50	25.26	23.37	26.34	1.33
V	5	5.07	0.92	11.48	2.79	42.00	66.33	28.93	17.71	25.61	1.40
VI	3	8.31	1.40	12.01	2.44	44.22	71.67	26.50	25.42	25.88	1.35
VII	1	6.30	2.13	11.27	4.12	47.33	75.33	19.11	14.27	28.70	1.55
VIII	1	5.15	2.07	10.62	3.29	43.00	75.67	25.27	17.07	26.93	1.34
IX	1	4.51	1.53	9.82	2.07	44.00	75.33	21.82	16.03	27.48	1.22
X	1	5.07	1.33	10.30	3.79	42.33	65.00	33.06	14.73	26.69	1.33
XI	1	2.03	0.33	8.30	3.11	48.33	71.33	22.43	8.30	25.57	1.23
XII	1	5.67	1.97	9.89	4.66	46.67	79.00	26.25	13.48	26.65	1.37
XIII	1	4.61	1.53	9.26	3.19	45.33	83.00	26.10	13.33	28.27	1.22
XIV	1	6.99	1.53	11.80	2.55	45.33	81.33	22.15	20.40	25.45	1.26
XV	1	10.30	1.87	12.41	3.01	43.00	81.33	27.39	27.10	26.73	1.35
XVI	1	9.42	2.47	11.83	3.21	51.33	81.00	23.14	18.99	26.26	1.36
XVII	1	4.52	2.55	11.49	2.88	59.00	83.67	22.38	14.60	25.12	1.30
XVIII	1	5.36	1.67	11.12	3.13	56.67	85.67	31.79	18.31	25.03	1.38
XIX	1	3.82	3.12	9.82	2.38	84.00	108.67	25.35	17.95	29.14	1.27

Table 3. *Canonical analysis of 35 mung bean genotypes*

Canonical vectors	Yield per plant (gm.)	Branches/ plant	Seeds/pod	100 seed weight (gm.)	Days to flowering	Days to maturity	Eff. leaf axils	Pods/ plant	% protein	Seed density
Z_1	0.0154	0.1393	−0.0340	0.0125	0.6614	0.6966	−0.1766	−0.1474	0.0267	0.0509
Z_2	0.1601	0.0246	0.1597	−0.3110	0.0711	−0.1487	−0.0447	−0.0310	0.0492	0.9049
Z_3	−0.1949	0.0454	−0.0834	0.7878	0.2354	−0.1357	0.2928	0.2847	0.0414	0.2998

Variation accounted for by $\lambda 1 = 60.1\%$; $\lambda 2 = 19.9\%$; $\lambda 3 = 8.5\%$.

Table 4. *Relationship between genetic diversity and heterosis in respect of three important characters in 25 kharif-grown mung bean hybrids*

Cross	Divergence (D^2) between parental clusters	Per cent heterosis over mid-parent		
		Days to 50% flowering	No. of seeds pod	Grain yield/ plant (gm.)
BR-2 × Pusa Baisakhi	35.10	−29.07**	16.02**	107.59**
BR-2 × T-44	35.10	−34.95**	11.12*	6.09
B-1 × BR-2	33.21	−32.11**	19.85**	61.99**
BR-2 × Hyb. 45	20.70	−27.02**	13.09*	105.45**
K-11 × T-44	15.93	−21.21**	5.68	115.34**
T-44 × Hyb. 45	15.52	−22.08**	3.25	22.67
B-1 × Hyb. 45	14.99	−10.28**	− 0.81	71.81**
Hyb. 45 × Madira	14.99	− 7.79**	6.02	41.78
K-11 × B-1	14.67	−15.58**	− 8.88	−11.36
J-781 × Madira	14.31	9.44**	−21.12**	−60.04**
B-1 × J-781	14.31	− 2.57	− 7.19	− 2.38
K-11 × Khargone-1	13.87	−14.28**	−14.52**	50.40*
J-781 × R-1	9.81	1.87	8.23	13.99
J-781 × Pusa Baisakhi	12.36	− 2.67	− 4.04	−27.43
R-1 × Madira	9.73	2.40	− 7.56	−25.47
Khargone-1 × J-781	9.32	4.80	9.52	14.75
B-1 × T-44	6.36	− 1.98	2.42	42.97
Pusa Baisakhi × Madira	6.36	0.00	3.19	9.39
Khargone-1 × Madira	6.09	− 4.69	− 5.32	32.52
Khargone-1 × R-1	5.11	0.02	1.24	− 0.28
Pusa Baisakhi × *R*-1	4.98	4.80	10.50*	− 1.38
T-44 × R-1	4.98	− 5.25	0.87	33.48
Khargone-1 × Pusa Baisakhi	4.97	0.00	7.87	25.19
K-11 × Hyb. 45	4.80	−25.64**	− 4.42	71.86**
K-11 × BR-2	19.85	−39.84**	15.53**	147.59**

was close correspondence of the values of the three largest canonical vectors (45.09, 62.40 and 27.50 for T-44 and 45.75, 61.671 and 27.44 for 'Pusa Baisakhi'). A comparison of the performance of these two genotypes for several developmental characters, yield components and protein (25.62 and 25.32%) and methionine content (2.43 and 2.90), showed very close correspondence. This is perhaps to be expected since 'Pusa Baisakhi' is reported to be a selection from T. 44, apparently for synchronous maturity.

The concordance between the other pair of parents falling in the same cluster (B-1 and 'Madira') was not so marked. The distance ($D^2 = 24.8$) between these genotypes was greater. The values for the three largest canonical vectors for B-1 were 47.65, 64.98 and 27.64, while those for 'Madira' were 45.34, 66.90 and 31.02. It would appear that these genotypes are not as close genetically as are T. 44 and 'Pusa Baisakhi'. The resemblance between B. 1 and 'Madira' may be the result of selection for similar ecological conditions.

The relationship between genetic distance as assessed by D^2 analysis and heterosis over mid-parent has been studied for an important developmental character, an important component of yield and grain yield/ plant (Table 4). In general, there was fair agreement between the extent of heterosis and the distance between clusters in which the two parents fall. In the case of flowering time, all except one of the crosses from clusters separated by more than 10 units showed highly significant heterosis for flowering. Similarly, for number of seeds/pod, all the crosses from clusters separated by more than 20 units showed significant heterosis. For grain yield also it was generally established that to obtain heterosis, usually in a desirable direction, the crosses would need to be made between highly divergent varieties. Of course, it should be realised that genetic diversity need not

necessarily be correlated with heterosis, because of internal balancing or even cancellation of the various components of heterosis; such cancellation appears to have operated for seed yield in several hybrids.

Acknowledgements

The data on which this paper is based formed a part of the thesis submitted by A. S. Tiwari for the Ph. D. degree of the Indian Agricultural Research Institute, New Delhi. One of the authors (A. S. Tiwari) is thankful to I. C. A. R. for providing a Senior Research fellowship during the course of this study.

Literature

Anderson, T. W.: Introduction to Multivariate Statistical Analysis. New York: John Wiley and Sons 1959.

Gupta, M. P., Singh, R. B.: Genetic divergence for yield and its components in green gram. Indian J. Genet. **30**, 212–221 (1970).

Murty, B. R., Arunachalam, V.: The nature of divergence in relation to breeding system in some crop plants. Indian J. Genet. **26A**, 188–198 (1966).

Rao, C. R.: Advanced Statistical Methods in Biometric Research. New York: John Wiley and Sons 1952.

Tiwari, A. S.: Genetic analysis of yield in green gram. Unpublished Ph. D. thesis, IARI, New Delhi (1973).

Received February 19, 1974

Communicated by B. R. Murty

Professor S. Ramanujam
Dr. A. S. Tiwari
R. B. Mehra
Division of Genetics
Indian Agricultural Research Institute
New Delhi – 110012 (India)