GENETIC DIVERGENCE AND HYBRID PERFORMANCE IN CHICKPEA

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ABSTRACT

Multivariate analysis was done to find out genetic divergence among 28 chickpea populations comprising 7 parents and 21 hybrids from all possible crosses among the parents. The inter- and intracluster D^2 values of the parental clusters and the pattern of distribution of hybrids vis-a-vis their respective parents across the clusters suggest that there was appreciable genetic diversity among the parents as well as hybrids. Parental genotypes originating from the same geographical region also did not show any affinity among themselves in the formation of clusters, thus, showing lack of correspondence between geographical and genetic diversity. Study of relationship between divergence of the parents and heterosis in the hybrids revealed that the parents separated by D^2 values of medium magnitude generally showed higher heterosis for different characters.

Key words: *Cicer arietinum*, multivariate analysis, diversity, heterosis, chickpea.

Variability, which is the genetic base of a crop, is the basic requirement for making progress in crop breeding. Therefore, in any breeding programme inclusion of genetically diverse parents is essential in order to create new reservoirs of genetic variability which, in turn, would help in recombining genes from diverse sources. In different crosses involving diverse parents, it is important to know the relationship between parents and heterosis in their hybrids. The present investigation has assessed genetic diversity in a set of 7 chickpea genotypes and 21 hybrids between them through multivariate analysis.

MATERIALS AND METHODS

The material comprised 7 parents, 3 each from India (F 61, Pusa 209, K 4) and Iran (NEC 1196, P 4353-1, NEC 802), and 1 from USSR (P 9656). The seven parents along with all the 21 possible hybrids among them were grown in rabi 1982-1983 in randomised complete block design with three replications. Each treatment was raised in 4 m long single-row plots with 60×20 cm spacing. Five random plants

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per plot were used to record observations on 12 quantitative traits (Table 1). Analysis of variance and covariance was done with the help of plot means. The original data were transformed to standardise uncorrelated variables by the pivotal condensation method [1]. Total 378 D^2 values corresponding to all the 28 possible pairs of entries were computed. Divergence between any two populations was obtained as sum of squares of differences in the transformed values of the corresponding varieties. Based on these D^2 values, the 28 populations were grouped into clusters using the Tocher's method [1]. Heterosis was calculated as percentage increase or decrease of F_1 over the midparental (MP) value for pods and seeds/plant, seeds/pod, 100-seed wt., and seed yield/plant. Critical difference (CD) calculated from their appropriate standard error of difference was used to test the significance of F_1 mean over MP value.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) showed that differences among 28 entries (7 parents and 21 F_1) were significant with respect to all characters studied except protein and methionine content. The test of significance based on Wilk's criterion also revealed highly significant differences among the populations for the pooled effects of all the characters. The D^2 values ranged from 2.20 to 147.71, indicating sufficient divergence in the populations for different characters. The 28 chickpea populations were grouped into 13 clusters (Table 2). Seven parents from three distinct geographical regions, India, Iran and USSR, were clubbed into four clusters: I, II, V and VII. Not more than two parental genotypes were included in a single cluster, and one cluster (VII) had only one genotype. Average intra- and intercluster

Table 1. Mean squares from the ANOVA of parents and F_1 in chickpea

Character	Replications (d.f. 2)	Treatments (d.f. 27)	Error (d.f. 54)
Days to flowering	8.90	20.80**	4.35
Days to maturity	18.20	20.15**	4.50
Plant height	8.80	266.53**	38.15
Branches/plant	11.02	108.60**	17.43
Pods/plant	10767.50	64153.76**	15530.76
Seeds/plant	21112.00	102062.11**	30619.87
Seeds/pod	0.09	0.20**	0.07
100-seed wt.	0.31	52.68**	4.27
Seed yield/plant	15.08	5308.22**	668.67
Protein content in seed	5.81	4.33	6.47
Methionine content in flour	0.01	0.01	0.01
Methionine content in protein	0.11	0.04*	0.02

*, **Significant at 5% and 1% levels, respectively.

Table 2. Distribution of 28 populations (7 parents + 21 F_1) of chickpea in different clusters obtained by multivariate analysis

Cluster	No. of populatioans	Populations included
I	9	F 61 × K 4, F 61 × P 9656, F 61 × NEC 802, Pusa 209 × K 4, Pusa 209 × NEC 802, K 4 × P 4353-1, NEC 1196 × P 4353-1, Pusa 209, K 4
II	4	F 61 × P 4353-1, Pusa 209 × P 4353-1, F 61, P 4353-1
III	3	Pusa 209 × NEC 1196, Pusa 209 × P 9656, P 4353-1 × P 9656
IV	2	P 4353-1 × NEC 802, K 4 × NEC 1196
V	2	NEC 1196, P 9656
VI	1	F 61 × NEC 1196
VII	1	NEC 802
VIII	1	F 61 × Pusa 209
IX	1	NEC 1196 × P 9656
X	1	NEC 1196 × NEC 802
XI	1	K 4 × P 9656
XII	1	K 4 × NEC 802
XIII	1	P 9656 × NEC 802

D^2 values of the 13 clusters (Table 3) showed that the highest value of intracluster distance (18.1) was in cluster V which included NEC. 1196 from Iran and P 9656 from USSR, indicating diversity between the genotypes within the cluster. The next lower intracluster D^2 value was observed in cluster I, which also included two diverse types, one *desi* (Pusa 209) and one *kabuli* (K 4). Out of the three Iranian varieties, P 4353-1 was included in cluster II and NEC 802 in the distant cluster VII. The third variety (NEC 1196) formed cluster V along with variety P 9656 from the USSR. Incidentally, cluster II was also distantly placed from cluster V and these two clusters had varieties from Iran and USSR. The magnitudes of inter- and intracluster D^2 values suggest that there is considerable diversity in the parental genotypes selected for this study. Appreciable genetic diversity in chickpea has been earlier reported [2–7].

In self-pollinated crops, ecotype differentiation may be the cause of genetic diversity [8]. Another possible cause of diversity could be intense natural and human selection for diverse adaptive gene complexes. Though some of these causes might account for genetic diversity, however, this does not indicate any specific relationship between genetic and geographic diversity. In the present study three genotypes originating from the same geographical region (Iran) have shown considerable genetic diversity among themselves by occupying three different clusters. Also, genotypes from Iran got clubbed in the same clusters with those from India and USSR. This clearly shows that geographic isolation may not be the only factor responsible for genetic diversity. Lack of correspondence between geographical and genetic divergence in chickpea is known [2, 7, 9–11].

Table 3. Average intra- and intercluster D^2 values of 13 clusters of 28 populations (7 parents + 21 F_1) of chickpea

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	14.0	23.5	19.0	20.6	26.6	20.5	26.6	29.5	21.4	49.3	94.4	80.8	47.4
II		10.3	30.0	44.1	47.7	28.3	50.5	19.6	28.7	83.0	127.6	127.7	60.2
III			5.6	25.8	29.9	37.8	41.8	38.4	18.5	34.0	139.9	111.5	59.8
IV				13.6	27.1	25.1	22.5	40.3	28.3	39.0	95.8	64.2	52.6
V					18.1	36.0	35.0	62.5	29.7	65.7	120.6	102.1	87.2
VI						0.0	20.5	34.7	31.7	70.8	89.6	94.3	54.5
VII							0.0	47.3	61.0	46.6	93.7	69.2	59.9
VIII								0.0	34.0	55.7	115.4	94.5	31.4
IX									0.0	57.5	113.4	105.8	56.0
X										0.0	160.3	90.1	64.4
XI											0.0	40.1	59.6
XII												0.0	43.6
XIII													0.0

The 21 hybrids were distributed into 11 different clusters with majority of clusters having one or two hybrids. Interestingly, clusters containing hybrids were often placed away from the parental clusters. For instance, NEC 802 occupied the unipopulation cluster VII, while two of its hybrids with F 61 and Pusa 209 were included in cluster I. The other four hybrids of NEC 802 with P 4353-1, NEC 1196, K 4 and P 9656 occupied clusters IV, X, XII and XIII, respectively. Similarly, the six hybrids involving NEC 1196 as one of the parents occupied six different clusters: I, III, IV, VI, IX and X. In other cases, the hybrids occupied the same cluster in which at least one of their parents was included. The hybrids F 61 × K 4, Pusa 209 × K 4, Pusa 209 × NEC 802, and K 4 × P 4353-1 along with two of the parents, K 4 and Pusa 209, were included in cluster I. Two hybrids of F 61 and P 4353-1 were placed in cluster II. These results suggest that considerable diversity exists among the parents and substantial variation has been generated among the crosses involving these parents. Similar results were reported in chickpea [5] and in green gram [12]. The present study shows that diverse parents and hybrids can be selected on the basis of multivariate analysis and used for hybridization so that wider genetic variability becomes available for fruitful exploitation in chickpea breeding.

It is generally believed that genetically divergent parents tend to give rise to heterotic hybrids on crossing. In the present study, relationship between genetic distance of the parents, as assessed by D^2 analysis and MP heterosis for grain yield and its components, number of pods and seeds/plant, seeds/pod and 100-seed wt. was investigated (Table 4). The distance between the parental clusters ranged from 0 to 50.5 units. The parents from clusters separated by high D^2 values (47.7 units

Table 4. Relationship between genetic diversity and MP heterosis in respect of seed yield and some of its components in chickpea

Cluster	Parent 1	Cluster	Parent 2	Inter-cluster D^2 value	MP heterosis, %				
					pods/ plant	seeds per plant	seeds/ pod	100-seed wt.	seed yield per plant
II	F 61	VII	NEC 802	50.6	−8.2	−25.8	−5.6.	−20.1	0.8
II	P 4353-1	VII	NEC 802	50.6	−7.5	−37.6	−33.9*	−7.3	−34.0
II	F 61	V	NEC 1196	47.7	−88.6*	−90.3*	−4.8	−23.1**	−91.3**
II	F 61	V	P 9656	47.7	−11.5	44.4	4.6	−5.5	−40.6
V	NEC 1196	II	P 4353-1	47.7	34.7	27.6	3.9	7.7	6.8
II	P 4353-1	V	P 9656	47.7	51.5	12.6	6.9	3.1	19.5
V	NEC 1196	VII	NEC 802	35.0	148.6**	170.5*	18.9	−20.8*	35.6
V	P 9656	VII	NEC 802	35.0	401.4**	274.4**	36.6	30.9**	410.4**
I	Pusa 209	VII	NEC 802	26.6	67.3	62.6	8.7	−0.8	74.1
I	K 4	VII	NEC 802	26.6	134.2**	124.7**	5.8	52.2**	233.3**
I	Pusa 209	V	NEC 1196	26.6	107.1**	107.3**	7.1	−13.3	32.4
I	Pusa 209	V	P 9656	26.6	87.7*	31.3	7.3	−14.1	24.4
I	K 4	V	NEC 1196	26.6	6.6	2.3	2.5	9.9	−19.6
I	K 4	V	P 9656	26.6	155.6**	78.1*	0.6	97.6**	240.3**
II	F 61	I	Pusa 209	23.5	29.4	34.6	0.7	−9.1	25.4
II	F 61	I	K 4	23.5	15.7	22.2	15.2	1.7	23.5
I	Pusa 209	II	P 4353-1	23.5	−30.8	−32.7	−2.8	−9.2	−35.5
I	K 4	II	P 4353-1	23.5	22.9	15.3	−8.2	5.7	28.2
II	F 61	II	P 4353-1	0.0	−12.9	−12.7	11.6	−18.2	−22.7
I	Pusa 209	I	K 4	0.0	4.3	9.5	12.3	−11.1	2.8
V	NEC 1196	V	P 9656	0.0	121.2*	101.1*	48.7*	−7.6	54.9

* **Significant at 5% and 1% levels, respectively.

and above) did not reveal significant heterotic response in their hybrids for different characters, except in one case for 100-seed wt. At the other extreme were the parents from clusters having low degree of divergence (less than 23.4 units) without any heterosis except in one hybrid, NEC 1196 × P 9656. In general, parental clusters separated by medium D^2 values, ranging from 26.6 to 35.0 units, exhibited significant and positive MP heterosis for seed yield and some of its components. Interestingly, three promising crosses, P 9656 × NEC 802, K 4 × P 9656 and K 4 × NEC 802, showing high heterosis for seed yield belong to this category. Though heterosis is considered to be the function of diversity but positive relationship between heterosis

and parental distance would depend on several factors including availability of optimum environment for the expression of heterosis and the extent of internal cancellation or balancing of the various components of heterosis [13]. Therefore, genetic diversity is not always directly associated with the heterosis realised. Noncorrespondence between parental distance and hybrid performance in chickpea was reported earlier [5], although some studies [12] suggested a fair degree of agreement between the extent of heterosis and parental distance in mungbean.

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