Indian J. Pl. Genet. Resources 12(1): 46-49, 1999

GENETIC DIVERGENCE IN CHICKPEA

A. SIROHI, A. SINGH, K. S. PANWAR AND K. C. CHAUHAN[1], Himachal Pradesh Krishi Vishvavidyalaya, Research Sub Station, Berthin 174 029 (Himachal Pradesh)

A wide range of genetic divergence was noted in 25 genotypes of Chickpea for six yield related traits. These strains were grouped into 7 clusters. The cultivars within a cluster showed smaller D^2 values than those belonging to two different clusters. 100-seed weight and seed yield per plant were chiefly responsible for genetic divergence. Based on inter-cluster distances, crossing of cluster IV genotypes with V, VI and VII was suggested to get maximum heterotic effect in F_1 and a broad spectrum of variability in the segregating generations to isolate superior individuals for yield and its components.

Key words : Chickpea, genetic divergence, phenotypic diversity.

Chickpea (*Cicer arietinum* L.) is one of the important pulse crop under cultivation in India since ancient times. It is one of the main source of protein and certain essential amino acids to largely vegetarian diet. Much of the area under Chickpea crop is concentrated in states of Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, Rajasthan, Bihar, West Bengal and Maharashtra.

These regions have wide agro-climatic variations/agricultural situations. Information on the nature and degree of genetic variability present in chickpea lines would help in the understanding of evolutionary mechanism involved in intra-specific divergence and choice of desirable parents for evolving superior varieties. The present investigation was, therefore, aimed at assessing the genetic divergence among 25 strains of Chickpea using Mahalanobis D^2 for future breeding programme that could lead to the isolation of desired segregants in the succeeding generations.

MATERIALS AND METHODS

Twenty five chickpea lines of which C-235 (small seeded) and HPG-17 (bold seeded) formed recommended varieties, were evaluated in four rabi seasons w.e.f. 1991 to 1994. The experiment was laid out in RBD with two replications in the last week of October every year at the Experimental Farm of Himachal Pradesh Krishi Vishvavidyalaya, Research Sub Station, Berthin (600 m amsl). Each plot consisted of 4 rows of 4 m length with 30 cm and 10 cm spacings between and within row, respectively. Observations were recorded on ten randomly selected plants from each entry excluding the border rows in each replication for six quantitative traits viz; days to 50 per cent flowering, days to maturity, plant height (cm), pods per plant, 100-seed weight (g) and seed yield per plant (g). Mahalanobis's (1936) D^2 statistic was used to assess genetic divergence on four season's pooled data. Genotypes were

[1]Deptt. of Tree Improvement & Genetic Resources, College of Forestry, Dr YS Parmar University of Horticulture & Forestry, Solan 173 230 (HP)

Table 1. Pedegree, disease reaction, agronomic score and source of the lines

Sr. No.	Lines/cultivars	Disease reactions		Agronomic score	Source
		Ascochyta blight	Root rot		
1.	ICCX 810800	R	T	Very good	Received from ICRISAT as developed lines for future breeding programme and evaluation as such
2.	ICCX 810737	T	T	Good	
3.	ICCX 90201	T	T	-do-	
4.	HPG-8	S	S	-do-	Developed from breeding material received from ICRISAT in F_2 generation through selection in advanced generations
5.	HPG-14	S	MS	-do-	
6.	HPG-25	T	MS	-do-	
7.	HPG-34	S	T	-do-	
8.	HPG-35	S	MS	-do-	
9.	HPG-41	T	MS	-do-	
10.	HPG-72	S	MS	-do-	
11.	H75-35	S	T	-do-	
12.	H76-102	T	MS	-do-	
13.	H86-100	T	T	-do-	
14.	H86-21	T	T	-do-	
15.	HPG-5	S	T	-do-	Developed through pure line selection from HAUC-1
16.	HPG-17	T	T	-do-	Developed through pure line selection from H84-72.
17.	HPG-4	S	S	Very good	Developed through hybridization programme o the station (Research Sub-Station, Berthin) through material received from International Chickpea Coordinated tri (Desi, long duration, 1987) on the basis of specific taits (i.e. *Ascochyta* blight resistance)
18.	HPG-27	S	T	Good	
19.	HPG-28	S	S	-do-	
20.	HPG-33	S	T	-do-	
21.	HPG-36	S	MS	-do-	
22.	HPG-39	T	T	-do-	
23.	HPG-40	T	T	-do-	
24.	HPG-81	S	T	-do-	
25.	C-235	S	S	Good	Old released, widely adapted/cultivated variety of chickpea

R = Resistant, T = Tolerant, S = Susceptible, MS = Mildely susceptible

grouped into different clusters according to Tocher's method (Rao, 1952). Pedigree, disease reaction, agronomic score and source of the lines are appended in Table 1.

RESULTS AND DISCUSSION

Analysis of variance revealed the presence of genetic variability for all the six traits studied. Significant values of X^2 in pooled analysis (X^2 144 = 1682.36, Wilk's criterion) showed that the lines differed among themselves. Based on D^2 values of pooled data, 25 genotypes were grouped into seven clusters (Table 2) Among these, cluster-II consisted of nine followed by cluster-IV (five), cluster III and V with three each and cluster I and VI with two genotypes. The cluster VII represented only one genotype. The inter and intra cluster distances is presented in Table 3.

Table 2. Clustering pattern based on D^2-statistic in chickpea

Cluster	No. of genotypes	Genotypes
I	2	ICC × 810800, ICC × 810737
II	9	HPG4, HPG14, HPG25, HPG33, GPG34, HPG39, HPG4, HPG72, H76-102
III	3	HPG8, HPG27, ICCV 90201
IV	5	HPG17, HPG28, H75-35, H86-21, H86-100
V	3	C-235, HPG38, HPG41
VI	2	HPG35, HPG81
VII	1	HPG5

A persual of Table 3 indicates that maximum inter cluster distance was observed between cluster IV and V followed by IV and VI, IV and VII, II and V and I and V, suggesting wide diversity between these groups. Contrary to it, least inter cluster distance between VI and VII clusters indicated the close relationship. Maximum intracluster distance was observed for cluster II, followed by cluster IV depicting diversity among the lines. Cluster VII gave zero intracluster distance, since it was represented by a single genotype.

Further, it appeared that the D^2 values for 248 pairs of genotypes were appreciably higher for 100-seed weight than for any other character. This fact was further substantiated by actual contribution of each character based on 300 pairs of 25 genotypes exist. 100-seed weight alone contributed 82.6 per cent and was followed by seed yield per plant by 8.3 per cent. The cluster means of genotypes for seven clusters as presented in Table 4 reveal that only 100-seed weight and seed yield per plant contributed maximum to divergence. The mean values of these characters

Table 3. Intra and inter-cluster distance (D) values in chickpea

Character	I	II	III	IV	V	VI	VII
I	3.42	206.14	150.98	558.73	683.19	322.06	193.55
II		61.11	121.08	293.33	958.99	426.98	452.15
III			8.42	659.43	454.06	136.81	168.45
IV				60.28	2099.53	1256.87	1196.77
V					41.156	155.25	203.87
VI						55.50	115.19
VII							0.00

varied widely in different clusters. Cluster IV was distinguished by genotypes having maximum mean values for 100 seed weight, plant height and seed yield per plant whereas, cluster V showed minimum values for 100-seed weight and plant height. The cultivars of cluster VII and II for number of pods per plant and those of clusters V and VII for days to 50 per cent flowering registered the maximum and minimum values.

Table 4. Cluster means for different characters in chickpea

Character	No. of genotypes	Days to 50% flower	Days to maturity	Plant height	Pods/ plant	100-seed weight (g)	Seed yield/ plant
I	2	135.8	190.5	55.7	60.4	20.10	9.03
II	9	139.7	191.5	65.6	55.4	21.47	11.54
III	3	138.1	190.9	58.02	56.7	21.09	9.44
IV	5	137.0	194.3	66.3	58.3	25.74	12.73
V	3	139.9	191.6	53.7	60.1	13.65	8.83
VI	2	138.0	195.8	57.87	55.8	18.45	10.92
VII	1	122.6	191.2	56.7	62.5	15.98	8.05

The importance of genotypic diversity for selection of parents for successful hybridization programme is quite obvious. Therefore, it was observed from the present study that traits viz; seed weight and seed yield per plant, which contributed maximum to the total divergence, should form the basis for selection of parents for hybridization among distantly placed clusters, keeping in view their yield potential to obtain a good amount of heterosis. These results are corroborative with the findings of Asawa *et al.* (1981), Singh *et al.* (1982), Jain *et al.* (1981) and Adhikari *et al.* (1983). From the above study, it is suggested that for creating maximum genetic variability, crossing among the genotypes of clusters IV and V, VI and IV, II and V; I and V would be useful. Crosses in the above combinations are expected to provide enough variability to select for high yielding segregants in the segregating generations.

REFERENCES

Adhikari, G. and M.P. Pandey. 1983. Genetic divergence in Chickpea. *Indian J. Genet.* **43**(2): 188-192.

Asawa, B.M., R.K. Chandra and V.K. Mathoo. 1981. Genetic divergence in Chickpea (*Cicer arietinum*). *Indian J. Agri. Sci.* **51**(II): 762-767.

Jain, K.C. B.P. Pandya and K. Pande. 1981. Genetic divergence in chickpea. *Indian J. Genet.* **41**(2): 220-225.

Mahalanobis, P.C. 1936. On the generalized distance in statistic. *Proc. Nat. Inst. Sci. India.* **2**: 49-55.

Rao, C.R. 1952. Advanced statistical methods in Biometrical Research, John Wiley and Sons, Inc, New York.

Singh, K.P., S.N. Kakkar, V.P. Singh and B.D. Chaudhary. 1982. Genetic divergence in chickpea (*Cicer arietinum*). *Indian J. Agri. Sci.* **52**(8): 492-496.