Indian J. Genet., 58(3): 337-342 (1998)

GENETIC DIVERGENCE IN CHICKPEA (*CICER ARIETINUM* L.)

ARUN KUMAR, RAM KRISHNA[1] AND S. K. CHATURVEDI[2]

Indian Agricultural Research Institute, New Delhi 110 012

(Received: December 12, 1997; accepted: October 20, 1998)

ABSTRACT

In order to assess the divergence among the 17 genotypes, 5 each developed through mutation breeding and intra- and interspecific hybridization and two standard checks in chickpea, Mahalanobis' D^2 statistics was applied. These genotypes were grouped into five clusters. Clusters II, I and III had 6, 5 and 4 genotypes, respectively. On the other hand, the clusters IV and V had only one genotype each. The genotypes falling in cluster III had the maximum divergence which were closely followed by those of clusters II and I. The maximum and minimum divergence was revealed between clusters II and V and between III and V, respectively. In general, the clusters II and V exhibited high and low mean values, respectively for most of the characters. It has been suggested that for varietal improvement the hybridization among the genotypes of divergent clusters should be done rather than depending on those genotypes of the cluster having minimum divergence.

Key words: Chickpea, *Cicer arietinum, Cicer reticulatum,* genetic divergence.

Chickpea is most important grain legume, occupying first position both in area and production among the pulses grown in India. Recently, it has got setback in area on account of competition with high yielding and input responsive crops like wheat in irrigated and mustard in rainfed areas. It failed in competition on account of its low yield potential. In order to make this crop competitive with those grown during winter season breeding of high yielding and input responsive varieties is only solution. For achieving this goal, suitable base material on which further improvement could be effected is most important pre-requisite. Chickpea being an autogamous crop, the generation of variability through natural means is limited. Hence, the chances of selection of desirable parents for breeding improved varieties are also limited. It is therefore, essential to generate variability by artificial means for making breeding programmes effective. In the present investigation, genetic divergence among the genotypes developed through three methods viz., intraspecific

---

[1] Professor and Head, Department of Genetics and Plant Breeding, C. S. Azad University of Agriculture and Technology, Kanpur 208002

[2] Senior Scientist (Breeding), Indian Institute of Pulses Research, Kanpur 208024.

and inter specific hybridization and mutation breeding has been worked out by using Mahalanobis D^2 statistics in order to assess the potentiality of breeding method in terms of generating variability.

MATERIALS AND METHODS

The investigation was conducted on 17 genotypes of chickpea, 5 each developed through mutation breeding (IPC 92-33, IPC 92-34, IPC92-35, IPC92-36 and IPC92-39), interspecific hybridization between *Cicer arietinum* × *C. reticulatum* (IPC41, IPC 42, IPC 43, IPC 45 and IPC 71) and intra-specific hybridization (IPC 92-4, IPC 92-5, IPC 92-6, IPC 92-7 and IPC 92-8) and two standard checks (BG 256 and KPG 59). These genotypes were raised in completely randomised block design with three replications. The observations on five randomly selected plants in each population were recorded on 13 quantitative traits viz., days to 50% flowering and maturity; plant height; number of branches; first podding node; internode length; number of branches and pods per plant; number of seeds per pod; biological and grain yield plant; 100 seed weight; and protein content.

The genetic divergence and related statistics were estimated by using D^2 statistics as suggested by Rao [1]

RESULTS AND DISCUSSION

The analysis of variance showed existence of significant differences among the genotypes in respect of all characters, excepting number of branches per plant. The differences among the genotypes were also found when aggregate effect of all characters was tested by Wilk's criterion. The D^2 values for all 136 comparisons between pairs of genotypes are given in Table 1. On the basis of divergence, 17 genotypes under investigation have been grouped into five clusters (Table 2). Having six genotypes the cluster II has been found the largest. The clusters I and III had 5 and 4 genotypes, respectively. The clusters IV and V had only one genotype each. The divergence within the cluster indicates the divergence among the genotypes falling in the same cluster. On the other hand, intercluster divergence suggest the distance (divergence) between the genotypes of different clusters. The data (Table 3) suggested minimum distance between the genotypes falling in cluster III which was closely followed between those falling in clusters II and I. When the clusters were compared for divergence, the maximum distance was observed between clusters II and V and minimum between III and V. From cluster mean values (Table 4) it is clear that among clusters showing maximum divergence, the differences in cluster means were substantially high for all characters, excepting days to maturity, number

---

Table 1. The values of D^2 for cominations of 17 genotypes in chickpea

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1.	84.75	75.64	36.60	63.41	297.82	271.94	345.88	884.34	309.01	749.24	648.00	704.37	719.46	832.02	268.57	273.48
2.		130.16	149.50	100.21	474.16	467.79	553.02	1159.49	483.58	969.15	1113.12	885.82	947.17	1048.48	431.84	428.67
3.			64.47	32.01	305.04	268.01	317.08	796.64	288.15	229.71	805.28	669.48	704.44	775.95	257.65	335.65
4.				85.58	311.17	289.05	336.90	815.96	297.25	704.93	824.73	670.82	666.38	779.90	279.50	278.96
5.					265.33	274.53	310.55	772.31	267.87	703.01	776.18	656.88	679.37	755.68	235.29	287.30
6.						144.50	30.59	217.63	31.96	173.83	221.08	150.22	153.20	226.93	34.57	37.88
7.							82.06	346.77	104.19	275.49	288.25	238.48	281.72	252.79	87.24	184.05
8.								198.06	13.75	152.07	190.31	26.17	135.06	162.62	18.15	76.39
9.									241.23	72.91	23.67	76.23	83.90	100.08	307.01	291.40
10.										169.08	128.48	130.15	146.28	174.05	15.37	55.36
11.											45.21	13.81	40.45	20.71	224.10	175.24
12.												38.10	73.33	57.07	226.37	281.31
13.													32.47	29.06	189.41	162.93
14.														79.09	206.61	144.41
15.															235.79	266.26
16.																72.59

Table 2. Distribution of 17 genotypes of chickpea among five clusters

Cluster	No. of genotypes	Names of genotypes
I	5	IPC 92-4, IPC 92-6, IPC 92-8, BG 256, KPG 59
II	6	IPC 92-33, IPC 92-34, IPC 92-35, IPC 92-36, IPC 92-39, IPC 92-7
III	4	IPC 41, IPC 43, IPC 45, IPC 71
IV	1	IPC 92-5
V	1	IPC 42

Table 3. Inter- and intracluster (diagonal) distances involving 17 genotypes of chickpea

Cluster	I	II	III	IV	V
I	6.218	14.097	17.149	10.980	21.780
II		7.215	27.415	16.752	31.950
III			7.722	16.612	10.751
IV				0.000	21.638
V					0.000

Table 4. Clusterwise mean values of 13 characters in chickpea

Character	Cluster				
	I	II	III	IV	V
1. Days to 50% flowering	76.67	70.79	89.00	80.33	89.67
2. Days to maturity	120.55	120.85	128.50	124.00	120.67
3. Plant height (cm)	55.85	62.93	54.73	73.53	55.60
4. No. of branches/plant	6.88	6.47	7.30	6.47	6.87
5. First podding node	14.40	12.26	17.63	17.73	17.53
6. Internode length (cm)	2.09	3.11	1.62	2.31	1.59
7. No. of pods/plant	28.60	25.58	27.83	23.73	22.87
8. No. of seeds/pod	1.13	1.09	1.09	1.07	1.06
9. Biological yield/plant (g)	17.00	19.24	12.47	15.33	12.93
10. Grain yield/plant (g)	6.80	7.64	4.07	5.40	2.90
11. Harvest Index (%)	39.93	37.66	29.22	39.01	22.43
12. 100 seed weight (g)	23.63	27.88	13.72	26.80	13.50
13. Protein content (%)	22.81	23.35	22.23	22.43	17.21

of branches per plant, first podding node and number of seeds per pod. In general, the cluster II had high mean values for a large number of characters, whereas cluster V showed lower magnitude of mean values.

Contribution of characters to divergence : The contribution of individual characters to the divergence has been worked out in terms of number of times it appeared first (Table 5). Days to 50% flowering and maturity; biological yield per plant; and harvest index contributed nothing towards the genetic divergence. On the other hand, the character internode length (31.62%), followed by 100 seed weight (26.47%) and protein content (25.00%) contributed maximum towards genetic divergence. The remaining 5 characters contributed very low to this parameter.

Table 5. Contribution of individual trial in the divergence among 17 genotypes of chickpea.

	Trait	No. of times ranked	Contibution (%)
1.	Days to 50% flowering	0	0.00
2.	Days to maturity	0	0.00
3.	Plant height	4	2.94
4.	No. of branches/plant	6	4.41
5.	First podding node	1	0.74
6.	Internode length	43	31.62
7.	No. of pods/plant	4	2.94
8.	No. of seeds/pod	1	0.74
9.	Biological yield/plant	0	0.00
10.	Grain yield/plant	2	1.47
11.	Harvest Index	0	0.00
12.	100 seed weight	36	26.47
13.	Protein content	34	25.00

The genetic diversity is directly related to the success of hybridization for developing new varieties/ releasing variability. Mahalanobis D^2 statistics was applied for grouping 17 genotypes of chickpea derived through three breeding methods. In all, five clusters/ groups were formed. The cluster I had five genotypes, three of them were derived from intervarietal crossing and two were the standard checks, which are also the result of intervarietal crossing. Since, the varieties involved in the initial crosses for developing the three genotypes and two standard checks were not much divergent this resulted in their placement in one cluster. Similarly, in cluster II, out of six genotypes, five were derived from mutation breeding using single parental variety. Since, mutations are mostly at micro levels they may not have created divergence to the extent that they could fall in different clusters. In cluster III also, all the four genotypes have been developed from interspecific cross involving cultivated species, *Cicer arietinum* and wild species, *Cicer reticulatum* in which only one alien source is involved. Therefore, these four genotypes fell only in one cluster. Sandhu and Gumber [2] and Kumar *et al.* [3] also drew similar conclusions, while studying genetic divergence in chickpea.

The distance among the genotypes of the same cluster and of different clusters has also been worked out. The variation in the intracluster distance could not be observed in clusters I, II and III. On the other hand, maximum divergence among the characters of cluster III was noticed. The clusters II and V were found showing maximum divergence. This can be explained on the basis of the fact that the genotypes of the cluster II were developed through mutation breeding using a single genotype as parent and the genotype failing in cluster V has been developed through interspecific hybridization between two lines having divergent genes. Therefore, hybridization between the genotypes of these two clusters, will lead to accumulation of favourable genes in a single variety. In view of this, it is suggested that for varietal development, the crosses between the genotypes of divergent clusters should be made rather than between the genotypes of those clusters which have the minimum divergence. It is also suggested that for creating variability and developing the varieties a large number of divergent lines, instead of few wild species, should be used in the interspecific hybridization.

REFERENCES

1. C. R. Rao, 1952. Advanced Statistical Methods in Biometric Research. John Wiley and Sons, Inc., New York.
2. T. S. Sandhu and R. K. Gumber. 1991. Genetic divergence in chickpea. International Chickpea Newsletter., **21**: 18-19.
3. J. Kumar, P. N. Bahl and D. B. Raju. 1984. Variability in relation to geographical ditribution in chickpea. Indian J. Genet., **44**(1): 164-172.