Genetic Divergence in Chickpea (*Cicer arietinum* L.)

OP Kashyap and NK Rastogi

Department of Plant Breeding and Genetics, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492 006, Chhattisgarh

Genetic divergence as measured by D^2 technique was studied for seed yield and its components in 60 chickpea germplasm accessions. The analysis of variance revealed significant differences among the genotypes for each character under study. The genotypes were grouped into 6 clusters and the maximum intra-cluster distance was observed in cluster I comprising 14 genotypes. Cluster III and VI were identified as genetically divergent. Considering the cluster means and cluster distances, IG 327, IG 326, IG 323, IG 311, IG 314 of cluster V; ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007, IG 313 of cluster VI; ICCV 91004, ICCV 91003, ICCV 89228 of cluster III; ICCV 91008, ICCV 91012, ICCV 89224 of cluster I were the most promising genotypes. They may be utilized in future breeding programme to obtain high heterotic effect or to develop desirable recombinants.

Key Words: Chickpea, *Cicer arietinum* L., Genetic divergence

Chickpea being the most important among pulse crops can change the scenario of pulse production in the country if improved cultivars of high and stable seed yield along with disease and pest resistance to biotic and abiotic stresses are developed. Determination of the nature and magnitude of genetic diversity and variability for the character under improvement is a prerequisite for any breeding programme. The present study was aimed at determining the grouping pattern of genotypes and identifying genetically diverse and agronomically desirable parents to be used in breeding programme for high seed yield.

Materials and Methods

The material for the study consisted of 60 chickpea germplasm accessions. Forty were received from International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh (ICRISAT) and 20 accessions were locally collected from Chhattisgarh. The material was grown in a Randomized Complete Block Design with two replications at Research Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur. Each accession was grown in plots of 3 rows of 2 m length at spacing of 30 cm between rows and 10 cm between plants in a row. The nutrients (N:P:K) were applied @ 20 : 50 : 20 kg/ha as DAP and muriate of potash. Two sprays of monocrotophos 40 EC @ 750 ml/ha were applied to protect the crop from *Heliothis armigera*. Observations were recorded on five randomly selected plants per replication for seed yield (g) and its components *viz.*, days to 50% flowering, plant height (cm), number of secondary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant and 100-seed weight (g). The data were subjected to the Mahalanobis (1936) D^2 statistics to measure the genetic divergence. The varieties were grouped into a number of clusters by Tocher's method as described by Rao (1952). The criterion was that any two varieties on an average showing lower D^2 values were grouped into the same cluster while those showing high D^2 values were grouped into different clusters.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for each character, indicating the existence of variability among the genotypes for the characters studied. Based on the relative magnitude of D^2 values 60 genotypes were grouped into 6 clusters (Table 1). Maximum number of 14 genotypes were accommodated in cluster I followed by 12 in cluster II, 11 each in clusters IV and VI, 7 in cluster V and 5 genotypes in cluster III (Table 2). The maximum intra-cluster distance (D = 2.242) was observed in cluster I followed by cluster III (D = 2.009) and cluster VI (D = 1.789). The minimum intra-cluster value (D = 1.553) exhibited by cluster II indicated limited genetic divergence among the 12 genotypes.

The relative divergence of each cluster from other clusters (inter-cluster distances) indicated greater divergence between clusters III and VI (D = 4.116) followed by clusters II and III (D = 3.942) and clusters III and IV (D = 3.865). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield components studied, which may enable further selection and improvement in seed yield. The hybrids developed from the selected genotypes within limits of compatibility of these clusters may produce high magnitude of heterosis or desirable

Table 1. Clustering of 60 genotypes based on D² statistic

Cluster	No. of genotypes	Genotypes
I	14	ICCV 89224, ICCV 89238, ICCV 91001, ICCV 91006, ICCV 91008, ICCV 91012, ICCV 91013, ICCV 91014, ICCV 91016, ICCV 91017, ICCV 91018, ICCV 91130, ICCV 89205, ICCV 89220
II	12	IG 316, IG 322, IG 324, ICCV 91129, ICCV 89214, ICCV 89302, ICCV 89303, ICCV 89304, ICCV 89308, ICCV 89311, JG 74(C), ICCV 89325
III	5	ICCV 89215, ICCV 89216, ICCV 89228, ICCV 91003, ICCV 91004,
IV	11	IG 315, IG 317, IG 318, IG 319,s IG 321, IG 325, IG 328, IG 329, ICCV 89213, ICCV 89305, ICCV 89310
V	7	ICC 4918, IG 311, IG 314, IG 320, IG 323, IG 326, IG 327
VI	11	ICCV 89222, ICCV 91007, ICCV 91020, ICCV 91024, IG 312, IG 313, ICCV 91128, ICCV 89204S, ICCV 89209, ICCV 89240, ICCV 89243

Table 2. Mean intra-cluster (diagonal and bold) and inter-cluster distances among six clusters

Clusters	1	2	3	4	5	6
1	**5.027**	13.757	10.208	11.290	14.669	7.231
	(2.242)	(3.709)	(3.195)	(3.360)	(3.830)	(2.689)
2		**2.412**	15.539	2.849	13.513	5.527
		(1.553)	(3.942)	(1.688)	(3.676)	(2.351)
3			**4.036**	14.938	12.076	16.941
			(2.009)	(3.865)	(3.475)	(4.116)
4				**2.856**	8.387	5.396
				(1.690)	(2.896)	(2.323)
5					**2.921**	9.474
					(1.709)	(3.078)
6						**3.201**
						(1.789)

Note : D values given in parenthesis and D² values above in the diagonal and non-diagonal

transgressive segregants, which would be rewarding in chickpea improvement programme. Arora and Tripathi (1991), Kumar *et al.* (1998), Sirohi *et al.* (1999) and Yadav *et al.* (2000) also found similar degree of diversity in chickpea.

The cluster mean value for seed yield and its components are furnished in Table 3. There was a wide range of variation in cluster mean values for most of the traits except days to 50% flowering and secondary branches per plant. The average cluster-wise mean for different characters showed that the genotypes included

in cluster V, such as IG 327, IG 326, IG 323 and IG 311 had maximum seed yield per plant. Genotypes IG 327, IG 314 and IG 326 of cluster V exhibited maximum number of pods per plant. The genotypes ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007 and IG 313 forming separate cluster (VI) had maximum 100-seed weight. ICCV 91004, ICCV 91003 and ICCV 89228 in cluster III had maximum number of seeds per plant. Genotypes ICCV 91016, ICCV 91008 and ICCV 91018 of cluster I flowered earlier while ICCV 91012, ICCV 89224, ICCV 91008 possessed maximum plant height. Of the cluster I genotypes ICCV 91008, ICCV 91012 and ICCV 89224 had maximum number of secondary branches per plant.

Crosses among the parents having genetic divergence are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. In the present investigation hybridization among the genotypes IC 327, IG 326, IG 323, IG 311, IG 314 of cluster V (for seed yield per plant and pods per plant), ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007, IG 313 of cluster VI (for 100-seed weight), ICCV 91004, ICCV 91003, ICCV 89228 of cluster III (for seeds per plant), ICCV 91008, ICCV 91012 and ICCV 89224 of cluster I (for earliness, plant height, secondary branches)

Table 3. Cluster means for different characters

Cluster	No. of genotypes	D/F 50%	Plant height (cm)	Branches/ plant	Pods/ plant	Seeds/ plant	Seeds/ pod	100-seed wt(g)	Seed yield/ plant
I	14	55.35	54.29	3.27	59.35	1.42	74.09	21.93	5.60
II	12	60.75	45.29	2.43	46.25	1.19	50.44	17.41	6.22
III	5	56.84	44.20	2.68	70.40	1.64	101.58	19.79	5.40
IV	11	62.39	47.15	2.95	48.39	1.28	58.54	14.22	7.96
V	7	60.94	45.41	3.04	73.21	1.21	84.06	17.13	12.73
VI	11	60.60	50.63	2.91	51.08	1.15	56.85	24.00	9.14
MEAN		59.46	48.64	2.90	55.74	1.29	66.80	19.25	7.62
RANGE	MIN.	51.95	39.15	2.13	31.60	1.09	36.05	11.93	2.75
	MAX.	67.05	59.75	4.34	85.20	1.04	113.90	31.91	17.89
CV(%)		2.19	2.84	4.96	2.51	11.51	2.15	3.98	5.97

(Table 4) are expected to give promising and desirable recombinants in segregating generations because they possess desirable features as seen from their cluster means.

Table 4. Promising genotypes for different characters

S.No.	Characters	Genotypes
1	Seed yield	IG 327, IG 326, IG 323, IG 311
2	100-seed weight	ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007, IG 313
3	Pods per plant	IG 327, IG 314, IG 326
4	Seeds per plant	ICCV 91004, ICCV 91003, ICCV 89228
5	Days to 50 % flowering	ICCV 91016, ICCV 91008, ICCV 91018
6	No. of branches	ICCV 91008, ICCV 91012, ICCV 89224
7	Plant height	ICCV 91012, ICCV 89224, ICCV 91008

References

Arora PP and KN Tripathi (1991) Evaluation of chickpea germplasm for yield and its components. *Indian J. Pulses Res.* **4**: 89-90.

Kumar A, R Krishna and SK Chaturvedi (1998) Genetic divergence in chickpea (*Cicer arietinum* L.). *Indian J. Genet.* **58**: 337-342.

Mahalanobis PC (1936) On the generalized distance in statistic. *Proc. Natl. Acad. Sci. India.* **2**: 49-55.

Rao CR (1952) *Advanced Statistical Methods in Biometrical Research*, John Wiley and Sons, Inc. New York.

Sirohi A, A Singh, KS Panwar and KC Chauhan (1999) Genetic divergence in chickpea. *Indian J. Pl. Genet. Resour.* **12**: 46-49.

Yadav VS, SS Yadav, J Kumar and D Singh (2000) Phenotypic diversity in chickpea under different environments. *Ann. Agric. Res.* **21**: 48-50.