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

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Genetic divergence as measured by D^2 technique was studied for seed yield and its components in 56 genotypes of chickpea. The genotypes were grouped into six clusters and the maximum intra-cluster distance was observed in cluster II comprising five genotypes. Clusters IV and V followed by I and IV, III and IV were identified as genetically divergent. Considering cluster mean and genetic distances hybridization involving genotypes BGD 116, BGD 115, KGDM 1181, BCP 17, BGM 524, BG 256, KGDB 1178 of cluster VI for seed yield plant^{-1}, hundred seed weight and plant height; H 95-25, H 95-37 and H95-30 of cluster IV for pods plant^{-1}; ICCV 97030, GCP 9610, ICCV 97039 of cluster II for early maturity; ICCV 97032, JSC 3 and ICCV 97034 of cluster I for primary branches plant^{-1} and early flowering; RSG 966, IPC 97-1, IPC 96-46, ICCV 97022 of cluster V for seed yield plant^{-1}, pods plant^{-1} and bold seed are expected to produce wider genetic variability and promising segregants for seed yield and other desirable traits.

Key words : Chickpea, *Cicer arietinum* L., Correlation, Genetic Divergence

Grain yield is a complex character and is attributed to several physiological and metric traits. Determination of the nature and magnitude of genetic diversity and variability for the character under improvement is a prerequisite before launching any breeding programme. The present study on 46 chickpea accessions was aimed at (i) estimating the magnitude of genetic variability among selected genotypes for seed yield, (ii) determining the grouping pattern of genotypes in different clusters, (iiii) identify genetically diverse and agronomically desirable parents to be used in breeding programme for high seed yield.

Materials and Methods

Fifty-six genotypes of diverse origin were grown in randomized complete block design with three replications at Research Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (IGAU), during *rabi* 2000-01 (Table 1). C 235 (small seeded), Vijay and JG 74 (medium seeded), BG 391 and BG 256 (bold seeded) recommended for Chhattisgarh state were included as standard varieties. Each plot consisted of 4 rows of 4 m length with 30 and 10 cm spacing between and within row, respectively. Recommended package of practices was adopted to raise a good crop. Basal dose of 20 kg N and 50 kg P_2O_5 was applied at the time of sowing. Two sprays of Monocrotophos 36 EC @ 750 ml/ha were applied to protect the crop from *Helicoverpa armigera.* Five competitive plants from each genotype were randomly selected for recording plant height (cm), primary branches/plant, pods/plant, seeds/pod, 100-seed weight (g) and seed yield/plant (g). Phenological observations were recorded on plot basis. The data were subjected to the Mahalanobis (1936) D^2 statistics to measure the genetic

Table 1. List of 56 genotypes of chickpea selected for analysis of genetic divergence of seed yield

Designation	No. of genotypes	Source
H 95-122, H 95-25, H 95-37, H 95-30	4	Haryana
PBG-78, C-235 (C), FG 559, FG 712, GL 96047, GL 96004,	6	Punjab
CSJD 901, GCP 9504, CSJD 869, RSG 964, GCP 9516,	9	Rajasthan
GNG 1275, RSG 966, GNG 469, GCP 9610		
Phule G 95007, Vijay (C), Phule G 93009, BCP 17	4	Maharashtra
ICCV 97017, ICCV 97001, ICCV 97031, ICCV 93118, ICCV 97033, ICCV 97038, ICCV 97016, ICCV 97024, ICCV 97039, ICCV 97030,	14	Andhra Pradesh
ICCV 97034, ICCV 97032, ICCV 95138, ICCV 97022	4	Madhya Pradesh
IG 338, JG 74(C), RG 938, JSC 3 (C),		
PG 97-6, IPC 96-27, IPC 97-1, I PC 96-46, KGDB 1178, KGDM 1181	6	Uttar Pradesh
BGD 112, BGD 109, BGD 72(C), BGD 115, BGD 116	5	Karnataka
BG 391(C), BGM 528, BGM 524, BG 256 (C)	4	New Delhi

Indian J. Plant Genet. Resour. 16(1): 64-67 (2003)

divergence. The varieties were grouped into clusters by Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance revealed highly significant differences among the genotypes for all the characters under study (Table 2). High genotypic coefficient of variation (GCV) was found for seed yield/plant, pods/plant and 100-seed weight (Table 3). However, moderate values of GCV were recorded for seeds/pod, primary branches/plant, plant height and days to first flower. It indicated the scope for improvement of these traits in the material under the present study. Similar findings have also been reported in chickpea by earlier workers (Singh *et al.*, 1986; Bejiga *et al.*, 1991; Tripathi and Arora, 1991; Rao *et al.,* 1994). Genotypes exhibited a wide range of variation for most of the traits except seeds/pod and primary branches/plant (Table 3).

The 56 genotypes were grouped into six clusters, suggesting adequate scope for selecting superior and diverse parents to be exploited in a breeding programme (Table 4). Maximum number of genotypes (15) were accommodated in cluster III followed by 14 in cluster VI, 13 in cluster V, 6 in cluster I, 5 in cluster II and 3 genotypes in cluster IV. The maximum intra-cluster distance (D=1.988) was observed in cluster II followed by cluster I (D=1.880) and V (D=1.865), indicating existence of considerable genetic divergence among constituent genotypes (Table 4). Hence, parents within the cluster can be chosen for hybridization programme.

The relative distance (Table 5) of each cluster from other clusters (inter-cluster distances) indicated greater divergence between cluster IV and V (D=4.635) followed by I and IV (D=4.459), III and IV (D=4.344). Selection of genetically diverged parents from above clusters would produce a broad spectrum of variability, which may enable further selection for high seed yield and other desirable traits.

The cluster means of genotypes (Table 6) revealed that the average cluster mean was higher for seed yield in cluster VI followed by cluster IV; for size in cluster VI followed by cluster II, I and V; for pods plant^{-1} in cluster IV followed by VI and II; for primary branches plant^{-1} in cluster I followed by IV and VI; for early maturity in cluster II followed by III, IV and VI.

The genotype with high mean value in any cluster can either directly be used for adoption as pure line variety or can be used in hybridization for yield improvement. The genotypes ICCV 97032, JSC 3, ICCV 97034 of cluster I for primary branches/plant and early flowering; ICCV 97030, GCP 9610, ICCV 97039 of cluster II for early maturity; H 95-25, H 95-37, H 95-30 of cluster IV for pods/plant; BGD 116, BGD 115, KGDM 1181, BCP 17, BGM 524, BG 256, KGDB 1178 of cluster VI for seed yield/plant, 100-seed weight

Table 2. Analysis of variance for different characters

		Mean Squares							
Source	d.f.	Days to first flower	Days to maturity	Plant height	Primary branches/plant	Pods/plant	Seeds/ pod	100-seed weight	Seed yield/ plant
Replication	2	6.438	6.063	0.938	0.003	0.046	0.040	0.781	0.140
Treatment	55	85.861**	51.786**	70.478**	0.257**	420.043**	0.096**	73.119**	31.906**
Error	110	0.301	0.326	0.001	0.006	0.00009	0.0002	0.596	0.001

** = Significant at $p<0.01$

Table 3. Estimates of mean, range, genotypic coefficient of variation and genetic correlation for different characters

Characters	Mean	Range		GCV	r_g with seed yield
		Min.	Max.		
Days to first flower	58.88	44.00	70.00	9.07	0.556**
Days to maturity	104.21	96.00	118.00	3.97	-0.153
Plant height (cm)	49.67	39.40	59.40	9.76	0.210
Primary branches/plant	2.70	2.00	3.53	10.72	0.418**
Pods/plant	41.64	18.00	83.67	28.41	0.750**
Seeds/pod	1.39	1.77	1.03	12.82	-0.332**
100-seed weight (g)	20.36	13.24	31.50	24.15	0.577**
Seed yield/plant (g)	9.72	4.96	18.60	33.55	–

Table 4. Clustering pattern based on D^2 statistics in chickpea

Cluster	Number of genotypes	Name of genotypes
I	6	Vijay, ICCV 97038, ICCV 97016, ICCV 97034, JSC 3, ICCV 97032
II	5	JG 74, ICCV 97039, ICCV 97030, RG 938, GCP 9610
III	15	H 95-122, PBG 78, CSJD 901, GCP 9504, C 235, CSJD 869, FG 559, ICCV 97017, FG 712, IG 338, ICCV 97001, ICCV 97031, PG 97-6, RSG 964, GCP 9516
IV	3	H 95-25, H 95-37, H 95-30
V	13	Phule G 95007, ICCV 93118, BGD 112, ICCV 97033, BGD 109, GL 96047, Phule G 93009, ICCV 97024, RSG 966, IPC 97-1, ICCV 95138, IPC 96-46, ICCV 97022
VI	14	GL 96004, BG 391, GNG 1275, IPC 96-27, BGM 528, BGD 72, GNG 469, BGM 524, BG 256, BGD 115, BGD 116, KGDB 1178, KGDM 1181, BCP 17

Table 5. Mean intra-cluster (diagonal and bold) and inter-cluster distances among six clusters in chickpea

Cluster	I	II	III	IV	V	VI
I	**1.880**					
II	2.638	**1.988**				
III	3.281	3.244	**1.727**			
IV	4.459	4.052	4.344	**1.448**		
V	2.583	2.911	2.389	4.635	**1.865**	
VI	3.421	2.989	3.995	2.950	3.095	**1.692**

Table 6. Cluster means for seed yield and its components in chickpea

Cluster	Days to first flower	Days to maturity	Plant height (cm)	Primary branches/plant	Pods/plant	Seeds/pod	100-seed weight (g)	Seed yield/ plant
I	55.00	108.00	45.24	3.11	35.67	1.34	21.83	8.57
II	57.00	100.40	44.17	2.68	40.53	1.15	22.82	9.21
III	55.53	102.40	48.57	2.52	38.87	1.60	14.85	7.44
IV	68.67	102.67	45.73	2.89	69.56	1.41	17.15	13.10
V	58.46	107.31	52.50	2.54	32.15	1.38	21.02	7.67
VI	63.07	103.36	52.92	2.83	50.40	1.29	24.82	14.02

and plant height are expected to produce superior segregants in segregating generations as these genotypes were found to possess higher genotypic mean values for their respective traits and occupy different clusters. Beside these, four genotypes viz., RSG 966, IPC 97-1, IPC 96-46 and ICCV 97022 from cluster V can also be utilized in breeding programme for higher seed yield, pods/plant and bold seed size. Thus, these genotypes hold great promise as parents in hybridization programme for creating valuable genetic variability and obtaining promising segregants for higher seed yield in segregating generations.

In the present study seed yield/plant had significant and positive genotypic correlation with days to first flower, primary branches/plant, pods/plant and 100-seed weight, indicating that indirect selection for these traits can bring out improvement in seed yield (Table 3). Therefore, seed size, pods/plant, primary branches/plant and days to first flower should form the basis for selection of parents for hybridization from distantly placed clusters. It is clear that selection for bold seed size will also bring improvement in seed yield of chickpea. Similar results have also been reported by Bejiga *et al.* (1991), Shinde and Saraf (1991), Rao *et al.* (1994), Gumber *et al.* (2000) and Kulkarni (2001). Besides, bold seed size undoubtedly gets premium in the market. Hence, genotypes like BGD 116, BGD 115, KGDM 1181, BCP 17, BGM 524, BG 256, KGDB 1178 from cluster VI can be exploited in breeding programme for higher seed yield and bold seed size.

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