Indian Journal of Agricultural Sciences **84** (10): 1278–9, October 2014/Short Communication

Diversity studies in chickpea (*Cicer arietinum*)

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Received: 18 December 2012; Revised accepted: 15 July 2014

Key words: Chickpea, D^2statistics, Genetic variability, Inter cluster distance and Intra cluster distance

The knowledge of genetic diversity is a useful tool in gene-bank management and breeding experiments like tagging of germplasm, identification and/or elimination of duplicates in the gene stock and establishment of core collections. Genetic diversity among the parents is a prerequisite to improve the chances of selecting better segregates for various characters. The more diverse the parents within reasonable limits, the more are the chances of improving the characters under consideration. Varieties from distinct geographic regions are usually selected for hybridization programme presuming the presence of considerable genetic diversity among them. The present study was envisaged to measure the genetic diversity among the genotypes of chickpea (*Cicer arietinum* L.) and to identify divergent parents for future hybridization programmes for yield improvement.

The experimental material for the present study comprised of 70 genotypes of chickpea. Out of seventy accessions, 50 were received from ICARDA and 20 genotypes were from ICRISAT. The experimental trail was laid out in randomised block design with three replications during *rabi* 2010-11 at Pulses Research Station, Habak, Shalimar ($34^{o}15^{\times}$ N latitude and $74^{o}84^{\times}$ E longitude) at 1524 m above mean sea level. Each experimental plot consisted of 4 rows of 3 m length. The inter and intra-row spacing was maintained at 30 and 10 cm respectively. Uniform standard plant population was maintained. Recommended package of practices were adopted to raise a good crop. Ten competitive representative plants were selected at random from each experimental plot in each replication and tagged for recording the biometrical observations on eleven morphological, maturity, quality, yield and yield component traits, viz. days to 50% flowering and maturity, plant height, number of primary branches, number of pods/plant, number of seeds/pod, seed yield/plant, 100-seed weight, biological yield/plant, harvest index and protein content. Genetic diversity was studied using Mahalanobis's D^2 (1936) and clustering of genotypes was done according to Toucher's method.

Seventy genotypes got grouped into five clusters (Table 1). Cluster pattern revealed that, cluster I was largest consisting of 52 genotypes followed by cluster II with 9 genotypes, cluster IV with 7 genotypes. The remaining clusters III, V were both solitary, each with a single genotype. The maximum genotypes grouped in cluster I depict either the same geographical origin or unidirectional selection practiced for a particular trait at several places producing similar phenotypes and aggregated in one cluster. The formation of solitary clusters may be due to intensive natural or human selection for diverse adaptive gene complex. The average D^2 values of intra and inter cluster distances (Table 2) revealed that maximum intra-cluster distance was shown

Table 1 Distribution of different chickpea genotypes into clusters based on D^2statistics

Cluster	Number of genotypes in cluster	Name of the genotypes
I	52	SKC-163, SKC-10315, SKC-93, SKC-4, SKC-107, SKC-74, SKC-3279, SKC-11, SKC-10305, SKC-10310, SKC-39, SKC-10301, SKC-80, SKC-3, SKC-10302, SKC-10304, SKC-115, SKC-90, SKC-108, SKC-70, SKC-112, SKC-1929, SKC-37, SKC-10314, SKC-120, SKC-62, SKC-12, SKC-22, SKC-11, SKC-68, SKC-10, SKC-68, SKC-63, SKC-10313, SKC-10312, SKC-8, SKC-10319, SKC-10311, SKC-9, SKC-104, SKC-10308, SKC-10306, SKC-10303, SKC-68, SKC-116, SKC-263, SKC-113, SKC-10307, SKC-7, SKC-12004, SKC-121, SKC-16.
II	09	SKC-10317, SKC-6, SKC-10317, SKC-5, SKC-9, SKC-10309, SKC-10318, SKC-17, SKC-65.
III	01	SKC-1.
IV	07	SKC-23, SKC-33, SKC-117, SKC-40, SKC-482, SKC-67, SKC-97.
V	01	SKC-95.

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Table 2 Average inter cluster (Above diagonal) and intra cluster (Diagonal) D^2values

Cluster	I	II	III	IV	V
I	98.87	267.59	259.94	358.28	1522.93
II		97.13	556.91	758.63	2233.05
III			0.00	145.52	757.74
IV				154.56	596.96
V					

Table 3 Cluster means for yield, yield component traits and quality of chickpea accessions (*Cicer arietinum*)

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant	Number of pods/ plant	Number of seeds/ pod	100-seed weight (g)	Seed yield/ plant (g)	Biological yield (g)	Harvest index	Protein content (%)
I	143.99	174.31	46.32	3.24	36.14	1.10	35.32	6.21	15.98	0.27	21.70
II	142.15	172.33	45.08	2.53	26.81	1.08	27.93	4.72	13.99	0.26	23.41
III	144.33	174.00	49.60	4.27	40.67	1.10	35.73	7.17	14.20	0.33	22.42
IV	143.14	173.43	45.24	3.93	46.69	1.24	37.54	7.36	16.20	0.31	20.73
V	144.67	173.67	47.87	4.67	60.92	1.20	39.59	8.33	15.53	0.34	18.64

by cluster IV (154.56) followed by cluster I (98.87) and cluster II (97.13).

When diversity among the clusters was studied, it showed a range of 145.52 to 2233.05. Clusters II and V showed maximum inter cluster distances of 2233.05 followed by that between clusters I and V (1522.93), clusters II and IV (758.63) and between clusters III and V (757.74). The lowest inter cluster distance was noticed between clusters III and IV (145.52), followed by that between cluster I and III (259.94).

Cluster V expressed maximum inter-cluster distance with most other clusters and hence can be used in the hybridization programme. The results clearly indicate that tremendous potential exists for introgressing the allelic resources present in these genotypes through a systematic breeding and selection approach so as to recover high yielding quality recombinants.

Number of pods per plant contributed maximum towards divergence. Cluster V being monogenotypic had maximum number of primary branches per plant, more number of pods per plant, maximum 100-seed weight, maximum seed yield per plant and high harvest index (Table 3). Cluster IV consisting of seven genotypes had maximum number of seeds per pod and high biomass. Cluster III consisting of single genotype had maximum plant height. Cluster II consisting of nine genotypes had high protein content. The above results suggest that cluster V consisting of single genotype can be used as one of the parents in breeding programme for enhancing yield.

The results clearly indicate that cluster means of different clusters identify the characters to be chosen for hybridization. Munshi *et al*. (2000) observed that cluster means and coefficient of variations are an interacting picture of diversity. The contributing characters differ in respect of their contributions to the genetic diversity. Mostly expression of these characters differs due to environmental influence on the genotypes studied, besides the nature of genetic material under investigation. The choice of parents is of paramount importance in any breeding programme. Selection based on extent of genetic divergence has been successfully adopted in pulses and has been used in planning hybridization programme. Hybridization among diverse genotypes helps in bringing new gene pool in population and expanding the range of adaptation (Sandhu *et al*. 2006). For instance cluster V can be used as a successful donor parent for enhancing yield and can be fixed by continued selection of transgressive segregants in advance generations. It is concluded that characters like days to maturity, total pods per plant, 100-seed weight, seed yield per plant were considered as selection criteria.

SUMMARY

Genetic diversity is a useful tool in gene bank management and breeding experiments like tagging of germless, identification and/or elimination of duplication in the gene stock and establishment of core collections. The present study was envisaged to measure the genetic diversity among the genotypes of chickpea (*Cicer arietinum* L.) and to identify divergent parents for future hybridization programmes of yield improvement. Characters like days to maturity, total pods/plant, 100-seed weight, seed yield/plant can be considered as selection criteria.

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