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Genetic Divergence for Nodulation and Yield contributing traits In Chickpea (*Cicer arietinum* L.)

PREETI VERMA[1] AND R.S. WALDIA
Department of Plant Breeding, College of Agriculture, CCSHAU, Hisar (HR)- 125004

Abstract

*Genetic divergence was estimated among a set of twenty one genotypes comprising of six diverse parents (*desi / kabuli *and nodulating / non nodulating) and their fifteen F_1 crosses using D^2 statistic for thirteen yield contributing and nodulating traits. Significant differences were observed for all the characters among the genotypes which were grouped into eight clusters. Maximum intra cluster distance was observed in cluster II while maximum inter cluster distance was observed between cluster VI and VIII followed by cluster VII and VIII. Based on inter- cluster distances, crossing of genotypes of cluster VI with that of VIII, III and V, and between VII and VIII was suggested to get maximum heterotic effect and a broad spectrum of variability in the segregating generations to isolate superior individuals for yield and its components.*

Key words: *chickpea, cluster, D2 analysis, desi, kabuli, nodulation*

Introduction

Chickpea is the third most important food legume worldwide with major production areas in the Indian sub continent, West Asia and North Africa (WANA). Despite considerable efforts, productivity of the crop has not yet been significantly improved. Therefore, the major concern of breeders is to increase the genetic potential for yield. Variability for nodulation in the host cultivars remains to be exploited although indications of its existence have long been found. Exploiting genotypic variability in nodulation through breeding has been a recent effort and the studies report the identification of progenies with increased yield along with nitrogen fixation and stress the need for appropriate selection pressure in favour of nitrogen fixation.

The more diverse the parents within reasonable limits, the more are the chances of obtaining heterotic F_1s, broader spectrum of variability in the segregating populations and also improving the characters under consideration. Meager attempts have been done to study genetic diversity for nodulation characters *viz*., nodule number, nodule weight, nitrogen content, leghaemoglobin content and root weight etc. The present study was, therefore, conducted with a view to identify divergent parents or complex crosses for future hybridization programmes for yield improvement of chickpea.

Materials and Methods

The experimental material comprising of twenty one genotypes of chickpea including six parents (table 1) and their fifteen crosses was raised during *rabi* 2004 – 05 in randomized block design with three replications at Pulses Research Farm, CCSHAU, Hisar (HR). Three major phenotypic groups of parents were formulated on the basis of nodulation *viz*. Group I: Non nodulating parents (ICC 4918 & ICC 4993); Group II: Medium nodulating parents (H 96 – 99 & HC – 1); Group III: High nodulating parents (HC – 2 & HC – 3). The row and plant spacing was maintained at 30 and 15 cm, respectively. Five plants were randomly selected from each genotype in each replication and observations were recorded for 13 characters *viz*. plant height(cm), number of secondary branches, number of pods per plant,100-seed weight(g), biological yield(g), seed yield(g), number of nodules, nodule weight(g), nitrogen content(%), leghaemoglobin content(mg/g), harvest index(%), root weight(g) and plant weight(g). Genetic diversity was studied using Mahalanobis's D^2 statistics (1936).

Results and Discussion

The results revealed that the genotypes varied significantly for all the 13 characters studied. On the basis of D^2 values, 21 genotypes were grouped into eight clusters (Table 2). In a similar study, Dwevedi & Gaibriyal (2009) grouped 25 genotypes in six clusters while Tomar *et al*. (2011) grouped 45 genotypes in eight clusters. In the present study, cluster I had the maximum number of 5 genotypes. Three genotypes each in clusters II to V, two in cluster VI and only one genotype fell in each of the clusters VII and VIII suggesting that these two genotypes (HC 2 and ICC – 4993 X HC 3) were the most diverse as compared to the others. Clusters II, III, IV, V and VII included F_1 crosses only, which showed that the genetic architecture of the crosses were altogether different from the parental lines. The placement of non

Present address
[1] Agricultural Research Station, Kota (MPUAT, Udaipur)

Table 1: Pedigree and origin of chickpea parents used in the study

S.No.	Genotype	Pedigree	Year of release	Origin
1	ICC 4918(desi)	Pureline selection from Annigeri	1992	ICRISAT
2	ICC 4993(kabuli)	Pureline selection from Rabat	1992	ICRISAT
3	H 96 – 99(desi)	H89-78 x H86-84	2005	CCS HAU, Hisar
4	HC 1(desi)	F61 x L550	1989	CCS HAU, Hisar
5	HC 2(desi)	S208 x E100 Ym	-	CCS HAU, Hisar
6	HC 3(desi)	L550 x E100 Ym	1999	CCS HAU, Hisar

nodulating and nodulating genotypes into separate clusters indicated that a group of genotypes which are having more or less similar nature constituted same clusters on the basis of their performance and *vice versa*.

Intra cluster and inter cluster D^2 values were computed for the eight clusters (table 3). The intra-cluster D^2 value was maximum in cluster II (4.260) while it was least being zero in clusters VII and VIII as they both had only one genotype. Similar results were earlier reported by Dwevedi & Gaibriyal (2009). The maximum inter-cluster distance of 9.677 was found between clusters VI and VIII followed by clusters VII and VIII (7.908) indicating that the genotypes falling in these clusters were highly divergent from each other implying large amount of diversity within and between groups, which could be exploited in breeding programmes. The minimum distance between cluster I & III (3.697), I & IV (3.747) and I & V (3.846) indicate them to be genetically closure clusters as all these clusters included mostly the crosses. Selection of parents (for hybridization) or crosses (for attempting further crossing for developing double cross or three way cross) from such clusters may be avoided as it may result in narrow genetic base.

A comparison of the mean values of the different characters in the most diverse clusters showed marked variation with respect to number of secondary branches, number of pods per plant, biological yield, seed yield, number of nodules and harvest index (table 4). Therefore, these characters might be responsible for creating divergence and differentiation among genotypes in chickpea. These findings are in agreement with that of Sirohi *et al*. (1999). The minimum plant height (52.66 cm) was recorded in cluster VII and maximum (72.33 cm) in cluster I whereas plant height in genotypes of cluster II, III, IV, V, VI and VIII showed no significant difference. In case of number of secondary branches per plant, minimum branches (15.29) were observed in cluster VI and VII (15.30) and maximum (43.88) in cluster VIII followed by cluster II (41.90). Significant differences were observed between the clusters however; clusters VI and VII were significantly inferior in producing number of branches.

In case of number of pods per plant, the minimum pods (44.12) per plant were observed in cluster VI followed by cluster VII (74.72) and maximum (199.82) in cluster V. Significant differences were observed for this trait among the clusters implying that high variations existed for number of pods per plant among various clusters.

Significant differences existed for 100 – seed weight among various clusters. Maximum weight was observed in cluster VII (28.04g) and VIII (28.00g) and minimum (15.83g) in cluster V while the other clusters were almost at par with each other.

The minimum (0) number of nodules per plant was observed in cluster VI of non – nodulating types and maximum (33.24) in cluster III. Interestingly, the same pattern like number of nodules was observed for nodule weight also; minimum (0) nodule weight in cluster VI and maximum (1.04g) in cluster III. Cluster III and cluster VIII also had the maximum values for nitrogen content, root weight and plant weight while the minimum values for these traits were observed in cluster VI and II, respectively. Thus, cluster III comprising of crosses between medium and high

Table 2: Clustering pattern of Parents and their F_1s in Chickpea

Cluster No.	Number of Entries	Genotype
1.	5	H96-99; HC1; HC3; H96-99 x HC2; H96-99 x HC 3
2.	3	ICC4918 x ICC4993; ICC4918 x HC3; ICC4993 x H96-99
3.	3	HC1 x HC2; HC1 x HC3; HC2 x HC3
4.	3	ICC 4918 x HC2; ICC4993 x HC1; ICC4993 x HC2
5.	3	ICC4918 x H96-99; ICC4918 x HC1; H96-99 x HC1
6.	2	ICC4918 ; ICC4993
7.	1	HC2
8.	1	ICC4993 x HC3

Table 3: Intra (diagonal) and inter cluster distance of Parents and their F_1s in Chickpea

Cluster	1	2	3	4	5	6	7	8
1	**2.478**	4.812	3.697	3.747	3.846	6.298	4.991	6.017
2		**4.260**	5.872	4.729	4.719	6.730	6.384	6.485
3			**3.204**	4.269	4.347	**7.588**	5.878	5.343
4				**3.205**	4.491	5.351	5.305	6.725
5					**2.894**	**7.539**	6.123	5.814
6						**1.174**	6.707	**9.677**
7							**0.000**	**7.908**
8								**0.000**

nodulating parents can be regarded as good source of Nif genes. Cluster VI showed lowest mean performance for biological yield, harvest index and seed yield while cluster VIII was characterized by highest values for these traits.

Cluster VI comprising of both non nodulating genotypes had minimum mean values for most of the important yield contributing characters studied (like number of secondary branches, number of pods, number of nodules, nodule weight, root weight, biological yield, harvest index and seed yield). On the contrary, cluster VIII had high values for the characters number of secondary branches per plant, biological yield, seed yield, harvest index, root weight and plant weight, number of pods per plant, 100- seed weight, nodule weight, nitrogen content. Inter cluster mean revealed the difference in the value for particular character between the groups indicating importance of particular cluster for choosing desirable parents for hybridization programme. On the basis of this criteria, ICC 4993 X HC -3 (cluster VIII) was identified as high yielding, genetically diverse genotype. Clusters II, III, V and VII were the next best clusters as far as other yield contributing traits are concerned. As mentioned earlier that the maximum inter cluster D2 value was observed between cluster VI and VIII; VII and VIII; VI and V and VI and III, therefore, intercrossing of these divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage. Progeny derived from such diverse crosses are expected to show wide spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in the subsequent advance generations. Hence, these genotypes might be used in multiple crossing programme to recover transgressive segregants. Our results are in conformity with the findings of Auckland and Singh (1977) who also reported that transgressive segregation with respect to growth habit, seed size, pod number and yield was greater in populations involving both *kabuli* and *desi* parentage than in populations involving only *desis*.

In a complex cross, more than two parents are crossed to produce the hybrid, which is then used to produce F_2 or is used in a backcross. Such a cross is also known as convergent cross because this crossing programme aims at converging, i.e., bringing together, genes from several parents into a single hybrid. As crop improvement progresses, the crop varieties would accumulate more and more favourable genes. In view of this, complex crosses may be expected to become routine in near future in the improvement of self pollinated crops as their improvement progresses beyond a certain level.

Besides conventional techniques, bold approaches must also be taken towards the breeding of a crop for achieving significant yield advances. The importance of crossing between the two major subgroups (*desi* and *kabuli*) of chickpea has been well established since long. With more time and study, *kabuli* x *desi* and nodulating x non nodulating introgression in the future might provide an important contribution toward achieving such advances. In view of this, the existing genetic divergence in the present experimental material can be a useful source for genetic improvement of chickpea.

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