Indian J. Genet., 57 (1): 87–90 (1997)

GENETIC DIVERSITY AMONG CHICKPEA ACCESSIONS

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(Received: February 15, 1993; accepted: June 19, 1996)

ABSTRACT

Multivariate analysis of divergence among 60 entries of chickpea for seven developmental characters led to their grouping into five clusters. Grouping of entries in different clusters was not related to their geographic origin. The intercluster D^2 values ranged from 8.0 to 38.2. Based on mean performance, genetic distance and clustering pattern, hybridization involving parents from clusters II and V may give higher yielding varieties.

Key words: Genetic diversity, *Cicer arietinum* L., chickpea.

Multivariate analysis by Mahalanobis' D^2 statistic is a powerful tool in quantifying the degree of divergence among all possible pairs of population at genotypic level before effecting actual crosses in modelling the varieties in a desired genetic architecture. Thus, a study was conducted to determine the extent of genetic divergence, so that more or less homogenous groups can be made for making appropriate choice of the parents for hybridization and developing the varieties.

MATERIALS AND METHODS

The material for the present investigation consisted of sixty entries collected from various places. They were grown at Defence Agricultural Research Laboratory Field Station Hawalbagh. The experiment was laid out in randomized block design with three replications during 1990–91. Each genotype was grown in 4-row plot of 3 m long with 30 cm row-to-row and 10 cm plant-to-plant distance. The data recorded on 10 plants from each entry on seven quantitative traits were subjected to multivariate analysis using Mahalanobis' D^2 statistics [1]. The genotypes were grouped into clusters by the Tocher's method as described by Rao [2].

RESULTS AND DISCUSSION

Analysis of variance of means revealed significant differences amongst the genotypes for all the characters. The coefficient of variation was maximum for number of pods per plant followed by seed yield per plant. Khan et al. [3] also reported the coefficient of genotypic variation were maximum for pods per plant (32.8%) followed by grain yield (25.9%). The coefficient of variation at environmental level also showed similar pattern but magnitude of the values were less than corresponding genotypic value.

The 60 genotypes were grouped into 5 clusters (Table 1). Cluster I contained maximum number of genotypes (36). These genotype were of late flowering duration, medium pod number and medium grain yield per plant. Cluster II comprised 15 genotypes of similar number of primary and secondary branches to that of cluster I but comparatively less number of pods and lower grain yield. Five genotypes fell in cluster III were earlier than the genotype in other cluster but having similar seed yield per plant. Clusters IV and V had two genotypes each of late duration and higher grain yield. The cluster pattern of the genotypes

Table 1. Grouping of 60 entries of chickpea in different clusters

Cluster No.	No. of entries	Entry number with place of origin in parentheses
I	36	Pant 114 (Pantnagar), Pant 115 (Pantnagar), PR- 4423 (Kunua Hamirpur), PR-4425 (Punpal Hamirpur), PR-4426 (Rangasi Hamirpur), PR-4427 (Chineri Hamirpur), PR-4463 (Dasaram Solan), PR-4464 (Kunihar Solan), PR-4466 (Bedlak solan), PR-4468 (Panoli Solan), PR-4469 (Ramsehar Solan), PR-4470 (Ramsehar Solan), PR-4471 (Nalagarh Solan), PR-4472 (Nalagarh Solan), PR- 4473 (Nana Solan), PR-4474 (Nana Solan), PR-4475 (Raipur Solan), RFA-92 (Aleyo Essaro Ethiopia), RFA-93 (Wolte Deneba Ethiopia), RFA-93-1 (Wolte Denebra Ethiopia), RFA-94 (Denebra Ethiopia), RFA-95 (Bartilik Enuwari Ethiopia), RFA-96 (Kiro Enuwari Ethiopia), RFA-97 (Zerbelte Enuwari Ethiopia), RFA-99 (Woiramba, Enuwari Ethiopia), RFA-127 (Derort Yeduha Ethiopia), RFA-128 (Geda Eyasa Yeduha Ethiopia) RA-129 (Tiftif Yeduha Ethiopia), RFA-131 (Mankorkoya Enenaye Ethiopia), RFA-133 (Mazen Kiroj Berenta, Ethiopia), RFA-154 (Rejim Girar Barenta, Ethiopia), RFA- 186 (Workedemo ambagiorgis Ethiopia, RFA-186-2 (Workedemo ambagiorgis, Ethiopia), RFA-187 (Guntir Abo ambagiorgis Ethiopia), RFA-187-1 (Guntir Abo ambagiorgis Ethiopia), Anupam (Kanpur).
II	15	Pant 116 (Pantnagar), PR-4465 (Koti Solan), RFA- 91 (Mitre Essaro Ethiopia), RFA-92-1 (Aleyo Essaro Ethiopia), RFA-94-1 (Wolie Deneba Ethiopia), RFA-95-1 (Burtilik Enuwari Ethiopia), RFA-96-1 (Kiro Enuwari Ethiopia), RFA-97-1 (Zerbelic Enuwari Ethiopia), RFA-97-2 (Zerbelic Enuwari Ethiopia), RFA-98 (Bolo Enuwari Ethiopia), RFA-99-1 (Woiramba Enuwari Ethiopia), RFA-126 (Yegoy Yeduha Ethiopia), RFA-130 (Mankorkeya Enemeya Ethiopia), RFA-132 (Meyo Encheros Enemaye Ethiopia), RFA-132-1 (Meyo Encheros Enemaye Ethiopia)
III	5	G-130 (PAU Punjab), L-550 (PAU Punjab), PR-4467 (Panoli Solan), RFA-98-1 (Bolo Enuwari, Ethiopia), RFA-186-1 (Workedemo Ambagiorgis Ethiopia)
IV	2	PR-4422 (Amb Una), PR-4424 (Dodun Hamirpur)
V	2	PR-4471-1 (Nalagarh Solan), 850-3/27 (Pantnagar)

shows that geographic diversity is not related with genetic diversity. Therefore, the selection of entries for hybridization should be based on genetic diversity rather than geographic diversity. These results are in agreement with the earlier findings of [4–6].

The average intercluster values of ranged from 8.0 to 32.4 while intracluster distance varied from 1 to 20 (Table 2). The average D^2 value within and between cluster revealed that intracluster divergence was maximum in cluster III (D^2 20.0) which include five genotypes. Clusters IV and V with its minimum intracluster D^2 values were most compact, one followed by cluster I. The intercluster distance was maximum between clusters III and V, indicating greater genetic divergence between the genotypes belonging to these categories. The minimum intercluster differences was observed between cluster II and IV which indicates that genotypes of these clusters had maximum number of common gene complexes.

Table 2. Intercluster and intracluster (in bold) values of D in chickpea accessions

Clusters	I	II	III	IV	V
I	**8.1**	8.0	15.9	11.1	29.4
II		**10.1**	18.6	14.4	26.3
III			**20.0**	22.0	32.4
IV				**1.0**	38.2
V					**1.0**

Character means indicated substantial variation among the five cluster grouped according to D^2 analysis (Table 3). The differences among cluster means though observed for all characters but were more pronounced for number of pods per plant, 1000-seed weight and seed yield per plant. Lowest value for days to flowering were recorded in cluster III whereas late maturing genotypes were grouped in cluster I. The 1000-seed weight and seed yield per plant predominantly yield contributing character were highest in cluster V. The genotype belonging to cluster IV were having maximum number of pods per plant but were

Table 3. Character means for different clusters in chickpea

Character	Character means in different clusters				
	I	II	III	IV	V
Days to 50% flowering	116.3	112.8	110.2	115.5	115.9
Plant height (cm)	50.8	57.2	52.4	49.5	49.1
No. of primary branches	2.4	2.4	3.1	3.2	3.4
No. of secondary branches	21.4	22.4	25.4	27.5	30.4
No. of pods/plant	122.2	97.9	121.0	154.1	123.1
1000-seed weight	128.5	132.6	155.7	118.5	249.1
Seed yield/plant	19.9	18.9	21.4	22.3	22.9

late in maturity. Sixty genotypes included in this experiment exhibited wide genetic variation for all the seven characters.

The utility of multivariate analysis in selecting genetically diverse parent for successful hybridization programme have been discussed by several workers [7]. In the present study, the maximum distance (D=21.4) existed between clusters II and V. The second largest distance (D=21.2) was between clusters I and V. The crosses between genotypes in these cluster may be useful for fixing transgressive segregants [8].

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