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GENETIC DIVERGENCE IN CHICKPEA[1]

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ABSTRACT

The grouping of genotypes from different ecogeographical areas in the same cluster confirmed that there is no parallelism between genetic diversity and geographical distribution. The pattern of clustering was highly influenced by environment and while making general statement on this aspect, the experimental conditions should be taken into consideration. To make worthwhile improvement in chickpea, 100-seed weight, pods per plant, flowering period and harvest index, in that order, should be taken into account. The clustering pattern of genotypes has revealed that *Desi* and *Kabuli* types are different from each other. Hence, crossing among these two types may provide more desirable segregants.

VARIETIES from geographically diverse localities are generally included in hybridization programmes presuming genetic diversity and greater likelihood of recovering promising segregants. However, this being an inferential criterion, it cannot be successfully utilized for discrimination between parents. Selection of parents based on the extent of genetic divergence has been successfully utilized in different crop species by Moll *et al.* (1962), Miller and Marani (1963), Murty and Anand (1966) and Bhatt (1970). The problem of selection may further be simplified if one could identify the characters responsible for descrimination between parents. The reports available on this aspect in chickpea are rather scanty. Therefore, the present investigation was aimed at ascertaining the nature and magnitude of genetic diversity among a set of chickpea cultivars.

MATERIALS AND METHODS

The material consisted of 32 genotypes of chickpea originating from 13 different countries of Asia, Africa, Europe and North America. This material represented wide range of variation in respect of several morphological, developmental and agronomic characters (Table 1). The material was evaluated in eight environments in a randomized complete block design (RBD) with three replications each at Pantnagar, Nagina and Bulandshahr during the 1976–77 and 1977–78 crop seasons. The details of the environments are setout in Table 2. Data were collected on ten quantitative characters, viz., days to 50% flower, days to maturity, plant height, primary branches/plant, secondary branches/plant, pod/plant, seeds/pod, yield/plant, 100-seed weight and harvest index. Mahalanobis' D^2 statistic was used to measure genetic divergence as suggested by Rao (1952). The per cent contribution of a character towards genetic divergence was calculated as the percentage of combinations in which the character has been ranked first.

RESULTS

The analysis of variance showed significant differences among the entries for all the characters. All the genotypes could be grouped into eight clusters.

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TABLE 1

Origin, morphological and agronomical characterstics of chickpea lines

Sl. No.	Line	Origin	Seed colour	Flower colour	General characteristics
1	P-3552	Iran	Yellow	Pink	*Desi*
2	K-4·68	India (U.P.)	Yellow	Pink	*Desi*
3	850-3/27	India (U.P.)	Brown	Pink	*Desi*, upright growth habit
4	Kaka	Iran	Black	Pink	*Desi*
5	G-130	India (Punjab)	Yellow	Pink	*Desi*
6	NEC-240	U.S.S.R.	YB	Pinkish white	*Desi*, erect
7	H-208	India (Haryana)	Yellow	Pink	*Desi*, drought tolerant
8	P-840	Moracco	Brown	Pink	*Desi*
9	P-896	Afghanistan	Yellow	Pink	*Desi*, 2 pods/peduncle
10	Annigeri-1	India (Karnataka)	Yellow	Pink	*Desi*, early
11	B-110	India (West Bengal)	Brown	Pink	*Desi*
12	USA-613	U.S.A.	YB	Pink	*Desi*, tall
13	P-1081-1	Nigeria	YB	White	*Desi*, fertilizer responsive
14	NEC-1639	Pakistan	YB	Pink	*Desi*, tall, erect
15	P-2974	Iran	YB	Pink	*Desi*
16	JG-62	India (M.P.)	Yellow	Pink	*Desi*, early, 2 pods/ peduncle
17	Pant G-110	India (U.P.)	YB	Pink	*Desi*
18	Hima	India (Haryana)	Green	Pink	*Desi*, vegetable type
19	V-4	Mexico	Brown	Pink	*Desi*, large seed size
20	Radhey	India (U.P.)	Brown	Pink	*Desi*
21	NEC-1604	Egypt	SW	White	*Kabuli*
22	GL-651	India (Punjab)	SW	White	*Kabuli*
23	Hyb. 16-3	India (U.P.)	SW	White	*Kabuli*, 2 pods per peduncle
24	L-532	India (Punjab)	SW	White	*Kabuli*
25	P-3896	Iran	SW	White	*Kabuli*
26	L-550	India (Punjab)	SW	White	*Kabuli*
27	K-4	India (U.P.)	SW	White	*Kabuli*, wide adaptation
28	NEC-1607	Lebanon	SW	White	*Kabuli*, large seed size
29	Jam	Iran	SW	White	*Kabuli*
30	Giza	Egypt	SW	White	*Kabuli*, small seed size
31	NEC-10	Jordan	SW	White	*Kabuli*, large seed
32	Pink-2	India (M.P.)	Pink	White	—

YB – Yellow brown; SW – Salmon white.

The grouping based on Mahalanobis D^2 statistic does not conform to the geographical origin of the genotypes (Table 2).

The number of genotypes included in a cluster varied from one environment to another (Table 2). It is highly desirable that the extent of genetic divergence between populations reflected through any analysis should be comparatively stable over environments to be of utility to the plant breeders. However, the grouping pattern of genotypes in the present study was not consistant across environments.

Similar results have also been reported by Katiyar (1978) in this crop. Various genotypes had shifted their positions from one cluster to other across environments. The genotypes from different geographical regions were found to cluster together. Only P-3552 (Iran) occupied the same cluster across eight environments. Genotype 850-3/27 was included in cluster II in E4, E5 and E6 while it occupied cluster III in E1, E3, E7, and E8. In a few cases genotypes from a particular state occupied the same cluster. Similarly, the genotypes belonging to different geographical regions have also been observed to cluster together. For example, cluster I in E1 was represented by genotypes originated from Iran, India, Morocco, Nigeria and Pakistan. While in E2 cluster I had genotypes from Iran, India, USA and Egypt.

Inter and intra-cluster distance was calculated in all the environments. In E1, the maximum and minimum inter-cluster D^2 values were observed between the clusters III and IX ($D^2=985\cdot75$) and, II and V ($D^2=140\cdot66$). In E2, maximum and minimum inter-cluster D^2 values were found between clusters III and VII ($D^2=2364\cdot61$) and, I and V ($D^2=351\cdot95$) in that order. In E3, maximum and minimum inter-cluster D^2 values were observed between clusters VI and VIII ($D^2=419\cdot66$) and, V and VIII ($D^2=71\cdot38$), respectively. Maximum and minimum inter cluster D^2 values were found between clusters IV and IX ($D^2=469\cdot00$) and, I and V ($D^2=42\cdot88$), respectively in E4. In E5, maximum and minimum inter-cluster D^2 values were observed between clusters V and VIII ($D^2=1423\cdot00$) and, III and VIII ($D^2=64\cdot85$), respectively. Maximum and minimum D^2 values were observed between clusters IV and IX ($D^2=893\cdot50$) and, I and III ($D^2=106\cdot00$) in E6. In E7, maximum and minimum D^2 values were found in between clusters and I and VI ($D^2=14249\cdot00$) and, IV and VIII ($D^2=290\cdot87$), respectively. Maximum and minimum D^2 values were observed between clusters IV and VIII ($D^2=489\cdot70$) and, III and VII ($D^2=92\cdot33$) in E8.

Intra-cluster D^2 values ranged from $0\cdot00$ to $154\cdot35$ in E1, from $0\cdot00$ to $1548\cdot00$ in E2, from $0\cdot00$ to $58\cdot06$ in E3, from $0\cdot00$ to $37\cdot66$ in E4, from $0\cdot00$ to $91\cdot33$ in E5, from $0\cdot00$ to $100\cdot00$ in E6, from $0\cdot00$ to $684\cdot33$ in E7 and from $0\cdot00$ to $72\cdot33$ in E8, respectively.

TABLE 2

Grouping of 32 chickpea genotypes into various clusters over eight environments utilizing Mahalanobis D^2 statistic

Cluster	ENVIRONMENTS*							
	E1	E2	E3	E4	E5	E6	E7	E8
I	1,7,8,13,** 14,16	1,2,3,4,7, 10,12,13, 25,26,30	1,4,5,7,14, 18,19	1,2,4,5,7, 17,18,19	1,2,5,7,13, 14,18,32	1,2,4,5,6,7, 9,18,25,30		1,8,13,4
II	2,4,5,6,9, 17	5,11,14,20, 23	2,8,11,12, 13,17	3,12,15,20, 22,23,24, 26,27	3,20	3	2,4,7,8,9, 10,13,15, 19,20	2,5,6,76,15, 17,19,25,30
III	3,15	6,9,24	3,24,28	6,11,30	4,6,11,15, 16,17,22,23, 27	8,11,14,16, 17	3,11,12,14, 21	3,10,24
IV	10,12,24	8,15,18,19	6,30	8,13	8	10	5,24,25,28	4,11,16,18, 32
V	11	16,17	9,15,20,22, 25,26,27	10,25,32	9	12,15,20 24,27	6,16,32	12,20,26
VI	18,19,20,22	21,29	10	14,31	10,25,26	13,19	17,23	21,23,27,29
VII	21,23,25,26, 27	22	16,32	16	12,19,29	21,23,26	18,26,30	22
VIII	28,29,31	27,28	21,23,29	21,29	21,24,29,31	22,29,32	27,29	28,31
IX	30,32	31,32	31	28	30	28,31	22,31	—

*E1=Pantnagar, normal planting; E2=Bulandshahr, normal planting; E3=Pantnagar, normal planting; E4=Pantnagar, late planting; E5=Bulandshahr, normal planting; E6=Bulandshahr, late planting; E7=Nagina, normal planting; and E8=Nagina, late planting.

In E1 and E2 planting was done in Rabi 1976–77, and for rest of the environments, planting was done in rabi, 1977–78.

**These numbers refer to genotypes as per Table 1.

Discussion

The genetic architecture of a population is controlled by the breeding behaviour of the individuals. Changes in breeding systems have accelerated the genetic divergence in natural populations. Chickpea is a predominantly autogamous crop and no information is available suggesting a change in its breeding behaviour under varied environmental conditions. Discrimination of desirable parents for a successful hybridization programme is a difficult task for a plant breeder. Generally, geographic diversity has been considered as a measure of genetic diversity. However, this is an inferential criterion and it may not be so effective in quantifying or differentiating between populations.

The pattern of distribution of 32 genotypes in various clusters showed that there was considerable genetic diversity in the material. Most of the *Kabuli* types were included in clusters IV to VII. However, *Kabuli* types from different countries were randomly distributed. In general, the major clusters in all the eight environments had genotypes from varying sources. Therefore, it can be concluded that there is no parallelism between genetic and geographical diversity in the material under investigation. The selection of parental material for hybridization, merely based on geographic diversity, may be an arbitrary and futile exercise. In D^2 statistic analysis, the grouping of genotypes from heterogeneous geographic regions into one cluster is expected because of the free exchange of breeding material from one country to another. It is highly desirable that the extent of genetic divergence between populations reflected through any analysis should be comparatively stable over environments to be of utility to plant breeders. However, the grouping pattern of genotypes in the present study was not consistent across the environments. The random distribution of genotypes is expected because these estimates have been obtained on the quantitative characters which themselves are liable to be highly influenced by genotype environment interactions. Therefore, when these estimates are obtained over a number of environments it is likely that grouping may not be exactly identical.

One line from Iran (P-3552) always occupied cluster I in all the environments. This genotype expressed the maximum divergence from other genotypes. Genotype, 850–3/27 shuttled from cluster II to III in varying environments. USA-613 (U.S.A.) was included in a cluster along with Asian group. It may, therefore, be tentatively said that USA-613 is a recent introduction to U.S.A. from Asia. Similarly, V4 from Mexico was also included in a cluster along with Asian group. Chickpea is not native to Mexico. Its introduction to Mexico by Spaniards dates back to the early Post-Columbian era. Random distribution of African material into different clusters suggests that chickpea has been introduced to Africa from Asia, possible with the mass immigration of Asian workers to African continent during British colonial rule.

Statistical distances (D^2 values) represent the index of genetic diversity among the clusters. It would, therefore, be logical to effect crosses between

genotypes belonging to the clusters separated by high estimated statistical distances. The maximum inter-cluster distance of cluster VIII from the rest over eight environments cannot be explained on the basis of geographical distance alone. Geographic barriers preventing gene flow or intense natural or human selection for diverse adaptive gene complexes must be responsible for this genetic divergence.

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