branch number, seed number, 1000 seed weight and oil content, in cross 2 for capsule number and in crosses 2, 3 and 4 for secondary branch number. These results indicated that selection would be more effective, when exercised at these levels for the respective traits.

However, the observed inter-generation correlation adn regression were negative in cross 4 for secondary branches at $\bar{x}$ + SD level, in cross 1 at $\bar{x}$ - SD level for capsule number and in crosses 1 and 3 for single plant yield at level. This indicated that F_2 performance was not an indicator of better F_3 performance possibly due to non-additive gene action or environmental influence (Meredith and Bridge, 1973).

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GENETIC DIVERGENCE IN CHICKPEA

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ABSTRACT

Fifty genotypes of chickpea (*Cicer arietinum* L.) were grouped into 11 clusters using Mahalanobis's D^2 statistic. Maximum distance was observed between the cluster VIII and XI. Plant height, number of secondary branches/plant, seeds/plant, 100 seed weight and seed yield/plant had shown more divergence among the clusters.

KEY WORDS : Chickpea, genetic divergence

Study of genetic diversity helps in selection of diverse parents for their use in hybridisation, as heterosis is known to depend on the extent of genetic diversity between parents. Mahalanobis's generalized distance (D^2) is used in the present investigation to ascertain the magnitude of genetic divergence and group the 50 varieties of chickpea.

MATERIALS AND METHODS

Fifty genotypes of chickpea (*Cicer arietinum* L.) were grown in randomised block design with three replications, during *rabi*, 1993-94. Each genotype was grown in two rows of 3 m length with inter and intra row spacings of 30 and 10 cm, respectively. Observations were recorded on five random competitive plants for the characters : plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of seeds per pod, number of seeds per plant, 100 seed weight (g) and seed yield per plant (g). Genetic divergence was studied using Mahalanobis's D^2 statistics as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance indicated highly significant differences among the genotypes for all the characters under study indicating the existence of a considerable variability among the genotypes.

The D^2 values between pairs of genotypes ranged from 10.7 (intracluster D^2 of IV) to 250.86 (pair VIII & XI). The group constellations were obtained on the basis of D^2 values using the method suggested by Rao (1952). Fifty genotypes were grouped into 11 clusters of which cluster I is the largest having 28 genotypes followed by 4 each in the clusters II, III, IV and V and remaining 6 clusters had only one genotype each (Table 1).

Table 1. Grouping of the 50 varieties into various clusters

Cluster	No.of strains	Name and origin of strains included		
I	28	Alternifolia (India),	Bipinnate (India),	Bronzeleaf (India).
		Ceylon-2 (India),	Cuttack gram (India),	Chara (India),
		F-61 (India),	F-370 (India),	F-187 (India),
		G-130 (India),	H-355 (India),	Horizontalis (India),
		G-130 (India),	H-355 (India),	Horizontalis (India),
		Himayatsagar Mutant (India),	J.G.39 (India),	Kaka (Iran),
		NEC-240 (USSR),	NEC-721 (Iran),	P-372-2 (India)
		P-840 Moracco,	P-1613 (India),	P-3111 (Iran),
		Pant-110 (India),	Selection-436 (India),	V-4 (Mexico),
		C.P.E.B.-28 (India),	2-52-2 (India),	3-701-13 (India)
		10-2-3-(India).		
II	4	N-31 (India),	N-59 (India),	3-1-A-3 (India).
		6-701-13 (India).		
III	4	NEC-1607 (Lebanon),	N-501 (India),	OFRA (Israel).
		T-25-1 (India).		
IV	4	P-2614 (India),	P-3090 (Iran),	P 3284 (Iran),
		Pyrouz (Iran),		
V	4	*Cicr vermajab.*(-)	P-436 (India),	Shambo (Ethiopia.
		1-9-1 (India)		
VI	1	Annegin (India)		
VII	1	*Crysanthifolia Yellow* (India)		
VIII	1	B-110 (India)		
IX	1	NEC-249 (India)		
X	1	NEC-1572 (Egypt)		
XI	1	I-13 (Iran.)		

Maximum genetic divergence was observed between clusters VIII and XI (D^2 = 250.86) followed by that between VIII and IX (D^2 = 205.47), it was least between clusters I and IX (Table 2). The intra cluster distance ranged from 3.28 to 3.91. Cluster VIII has high mean values for seeds/plant, 100 seed weight and seed yield/plant.

Table 2. Inter and Intra-cluster values of D^2 and $\sqrt{D^2}$

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	15.132	73.78	106.24	35.84	33.41	37.76	44.87	157.43	23.11	28.11	138.85
	(3.89)	(8.59)	(10.31)	(5.99)	(5.78)	(6.14)	(6.69)	(12.55)	(4.81)	(5.30)	(11.78)
II		12.90	41.03	83.57	28.27	53.59	74.75	129.69	197.88	112.11	111.762
		(3.59)	(6.405)	(9.14)	(5.32)	(7.32)	(8.65)	(11.38)	(9.89)	(10.59)	(10.57)
III			15.30	60.57	64.01	108.24	133.31	184.91	112.57	115.33	37.25
			(3.91)	(7.78)	(8.00)	(10.40)	(11.55)	(13.59)	(10.61)	(10.74)	(6.10)
IV				10.73	46.09	58.92	79.71	161.19	34.73	34.55	58.94
				(3.28)	(6.79)	(7.68)	(8.93)	(12.69)	(5.89)	(5.88)	(9.68)
V					11.79	26.17	38.60	88.08	55.98	58.92	119.46
					(3.43)	(5.11)	(6.21)	(9.42)	(7.48)	(7.68)	(10.93)
VI						0.00	40.47	67.48	67.50	82 87	165.40
							(6.36)	(8.21)	(8.21)	(9.10)	(12.86)
VII							0.00	(196.03	73.35	94.97	198.00
								(14.00)	(8.56)	(9.74)	(14.07)
VIII								0.00	205.47	187.92	250.86
									(14.33)	(13 71)	(15.84)
IX									0.00	28.83	108.68
										(5.37)	(10.42)
X										0.00	122.89
											(11.08)
XI											0.00

Figures in Parantheses are the values of $\sqrt{D^2}$

Table 3. Cluster means for different charactes

Cluster	Plant height (cm)	Primary branches/	Secondary branches/	Seeds/pods	Seeds/plant	100 seed weight (g)	Seed yield/plant (g)
I	43.80	4.15	7.45	1.13	64.21	13.74	8.31
II	39.44	5.80	8.01	1.06	38.01	29.60	11.28
III	61.30	4.55	8.32	0.97	37.30	31.49	11.54
IV	62.80	3.75	9.23	1.05	67.06	18.59	12.16
V	41.01	6.00	8.40	0.96	49.20	21.92	11.04
VI	40.47	5.40	12.40	1.12	86.27	21.98	19.00
VII	34.87	7.50	12.90	1.04	58.90	15.22	9.00
VIII	43.36	5.24	10.96	0.76	92.20	32.20	29.83
IX	52.20	4.13	4.73	1.52	58.60	11.91	7.00
X	52.27	4.00	3.67	0.86	57.20	10.45	6.00
XI	82.47	3.80	7.40	1.21	44.07	28.54	12.67
Mean	50.36	4.94	9.50	1.06	59.53	21.42	12.53
Range	34.87-82.47	3.75-7.50	3.67-12.90	0.76-1.52	37.30-86.27	10.45-32.20	6.00-29.83

The pattern of distribution of genotypes from different geographical regions into different clusters was at random. This tendency of genotypes occuring in clusters across geographical boundries reveals that geographical isolation is not the only factor causing genetic diversity. As there is no parallelism between geographic distribution and genetic diversity, selection of parents for hybridisation should be based on genetic diversity rather than geographic one. The inter cluster distance also did not bear any definite relationship with regards to the geographic origin of the genotypes as the clusters involving varieties from distantly situated geographic regions and from the same region (cluster II) did not necesserily have high or low intercluster distance. Katiyar and Singh (1979) reported similar findings.

Though the cluster means (Table 3) indicated appreciable variation for most of the traits, the maximum difference between clusters was mainly due to the variation in 100 seed weight, seeds/plant, plant height, seed yield/plant and secondary branches/plant. The cluster IV, VI, VIII and XI had genotypes that would prove useful in obtaining desirable recombinants for improving yield. Selection of genotypes from divergent clusters might prove useful if they are selected with due consideration of *per se* performance. However, depending on breeder's interest and looking at subjectivity with approximate grouping by D^2 more than one genotype from a cluster could be selected for hybridisation programme, as suggested by Singh and Ramanujam (1981).

A genotype B 110, the solitary member of a quite diverse cluster VIII could be included as a potential parent in breeding programme due to its superiority in respect of the characters number of seeds/plant, high 100 seed weight and seed yield/plant.

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