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DIVERGENCE ANALYSIS IN CHICKPEA

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ABSTRACT

The observations on 80 chickpea genotypes collected from different geographical areas were recorded for eighteen characters. The data were subjected to divergence analysis. Based on D^2 values 80 genotypes were grouped into eleven clusters. The highest numbers of genotypes were included in cluster I (60) followed by cluster II (7). No definite relationship was observed between genetic diversity and geographical distribution. Based on inter-cluster distances, crossing between BGM-419 and KPG33 are expected to produce a broad spectrum of variability in segregating generations to isolate transgressive segregants for yield and its components.

In the crop improvement programme, the importance of existing genetic variability/ diversity in the available material has been emphasized by several workers (Joshi and Dhawan, 1966; Murty and Arunachalam, 1966). The more diverse the parents more are the chances of increased spectrum of genetic variability. Divergence analysis by means of Mahalanobis's (1928) D^2 statistics is a powerful tool in quantifying the degree of divergence at genotypic level. The present study aims at analyzing the genetic divergence in 80 chickpea genotypes.

Eighty chickpea genotypes, collected from different areas of the country, were planted in R.B.D. with three replications during *rabi* 1998 at Crop Research Station, G.B. Pant University of Agriculture and Technology, Pantnagar. Each genotype comprised of a single row of 4 meters length. The row-to-row and plant-to-plant distances were maintained at 30 and 10 cm. respectively. The observations were recorded on a sample of ten random plants from each plot for days to initial flowering, days to 50 per cent flowering, days of 100 per cent flowering days to maturity, reproductive period (days), plant length (cm), canopy spread (cm), length of pod bearing branch (cm), primary branches per plant, secondary branches per plant, first pod forming node, pods per plant, seeds per pod, seeds per plant, 100-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). The data were subjected to divergence analysis of Mahalanobis (1928) following Rao (1952). The clustering was done following Tocher's method as described by Rao (1952). Intra- and inter-cluster distances and clusters mean for the characters were also computed.

The analysis of variance showed significant difference among the genotypes of all the characters. Based on D^2 values all the genotypes could be grouped into eleven clusters (Table 1) and the genotypes within each cluster were closer to each other than the genotypes pooling up in different clusters.

The maximum number of genotypes (60) was included in cluster I followed by 7 genotypes in cluster II, 3 genotypes in cluster V, 2 genotypes each in cluster III and cluster IV. Six clusters *viz*., VI, VII, VIII, IX, X and XI included one genotype each. Apart from cluster III and single genotype clusters, all the clusters were observed to be heterogeneous which included genotypes from different geographic areas. This situation indicated no parallelism between genetic diversity and geographical distribution. Similar trend was also reported by earlier worked in chickpea (Arora, 1990;

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Table 1. Grouping of eighty chickpea genotypes in different clusters

Cluster	Genotypes	Origin
I	BG267, BG298, BG 303, BG 312, BG 314, BG 316, BG 318, BG 319, BG 327, BG 328, BG 329, BG 331, BG 332, BG 333, BG 424, BG 431, BG 447, BG 448, BGM450, BGM 452, BGM 453, BGM 454, BGM 455, BGM 457	Delhi
	K850, K959, K999, KPG59, KPG102, KSB203, KSB209, KSB210, KSB213, Pant G114, PDG43-37, PDG83-34, PDG84-14, PDG85-5, PDG85-17, Radhey	Uttar Pradesh
	L345, L550, L59, GF16, GL769, GL1002, GL83-35, GL83-119	Punjab
	ICCV13, ICCV14, ICCV15, ICCC14, ICCC32, ICCC42, ICCC49	Andhra Pradesh
	GNG149, GNG257, GNG309, GNG398	Rajasthan
	H82-2	Haryana
II	BG272, BG315	Delhi
	KSB220, PDG85-6	Uttar Pradesh
	GNG421, GNG422	Rajasthan
	HK85-103	Haryana
III	PDG34-16, PDG85-3	Uttar Pradesh
IV	BGM449	Delhi
	H85-65	Haryana
V	BG256, K989	Uttar Pradesh
	RSG143-1	Rajasthan
VI	K1032	Uttar Pradesh
VII	PDG85-4	Uttar Pradesh
VIII	PDG83-13	Uttar Pradesh
IX	BGM456	Delhi
X	BGM419	Delhi
XI	KPG33	Uttar Pradesh

Table 2. Intra- and Inter- cluster distances in chickpea

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	19.87	28.64	32.49	27.50	31.90	41.63	35.94	31.11	32.48	45.46	63.95
II		23.59	41.08	36.47	40.07	47.00	45.56	38.67	41.59	49.86	68.34
III			25.17	48.08	40.43	62.31	48.06	47.93	59.34	64.93	72.34
IV				28.70	41.71	45.42	42.54	54.01	33.96	59.27	68.29
V					29.94	50.77	48.28	44.16	40.42	53.79	73.56
VI						0	54.10	50.25	48.21	67.90	83.75
VII							0	37.10	56.84	63.86	82.46
VIII								0	38.90	52.16	64.33
IX									0	66.29	65.28
X										0	105.06
XI											0

Kumar and Arora, 1992). These results emphasize the necessity of quantitative assessment of genetic diversity to identify suitable parents in chickpea.

Maximum diversity was associated with genotypes from Uttar Pradesh, followed by those from Delhi as evident from their distribution in most of the clusters. The diversity observed among the genotypes of the same geographical area might probably be due to eco-geographical distribution, which together with human selection for seed yield characteristics has resulted in differentiation. Earlier reports (Murty and Arunachalam, 1966) have ascribed such diversity to genetic drift and selection in different environments.

The frequent movement of seed material and subsequently adaptation of agro-climatic conditions may also be responsible for such variations.

The intra-and-inter-cluster distances have been presented in Table 2. The maximum intra-cluster distance was observed for cluster V, where as the minimum intra-cluster distance was recorded in case of cluster I (excluding single genotype clusters). The inter-cluster distances, revealed the presence of considerable amount of genetic diversity among the genotypes pooled up in different clusters. This diversity was also supported by the appreciable amount of variation among the cluster means for different characters. The cluster X ranked first for harvest index, pods per plant, primary branches per plant and secondary branches per plant. Simultaneously cluster IV ranked first for first pod forming node, length of pod bearing branch and plant height.

It is obvious that varieties with narrow genetic base are affected more by seasonal variation than those with broad genetic base, particularly under rainfed conditions. Under such circumstances, availability of genetically diverse genotypes for hybridization programme becomes more important. In the present study the maximum inter-cluster distance (105.06) was observed between clusters X and XI followed by clusters VI and XI, VII and XI, and III and XI. It is apparent that cluster XI with only one genotype (KPG-33) is far from other clusters *viz.*, III, VI, VII and X indicating wide divergence between clusters.

Consequently, it is suggested that the parents BGM-419 and KPG-33 belonging to Delhi and Uttar Pradesh, respectively, falling under maximum distant groups may be crossed to get maximum heterotic effects in F1 and a broad spectrum of variability in segregating generations to isolate transgressive segregants for yield and its components.

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