

INVESTIGATION OF GENETIC DIVERGENCE IN CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES

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ABSTRACT

An experiment with fifty one genotypes of Chickpea carried out to study the nature and magnitude of genetic divergence using Mahalanobis's D² Statistics, in randomized block design with two replications. The data for eight important quantitative traits recorded from the genotypes raised. The fifty one Chickpea genotypes were grouped into five clusters. Cluster I was largest with forty genotypes followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster I and V, followed by cluster II and V suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters viz. 100 seed weight, No. of pods per plant and Days to 50% flowering contributed maximum in manifestation of genetic diversity. Seed yield plant⁻¹ had maximum Phenotypic and Genotypic Coefficient of Variation (PCV and GCV), followed by 100 seed weight. High magnitude of heritability (broad sense) was recorded for 100 seed weight. High heritability coupled with high genetic advance was observed for number of pod per plant, 100 seed weight, Days to 50% flowering and Plant height suggesting that, the role of additive gene effect and possibilities of achieving high genetic progress through selection. The genotypes IC-270936, IC-487323, IC-350889, Vishal, Digvijay, IC-442831, IC-268927, IC-327656, IC-299779, EC-490044 and IC-269004 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an integral part of an Indian agriculture since time immemorial, because of its intrinsic value in terms of higher protein content, carbohydrates, minerals, nitrogen fixing ability and indispensability as alternative crop for crop diversification. On the basis of cultivated area, chickpea ranks 19th among the crops, and is grown in 34 countries of the world. Area under pulses in India, Pakistan, Nepal, and Bangladesh covers about 90% of the world acreage (Saxena, 2001).

Limited or lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of grain legumes including chickpea (Ramanujam, 1975). When the parents utilized in across are genetically similar, it is quite likely that the different lines derived reveals low diversity. On the contrary, when diverse parents are used in obtaining a segregating population, the derived lines reveal greater diversity despite sharing a common percentage (Katiyar, 1978).

Yield components are the primary objectives under study for crop improvement as because Grafius (1978) suggested that there may not be genes for yield per se but rather for the various components, the multiplicative interactions of which result in the artifact of yield. In any program aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F1 hybrids and broad spectrum of variability in segregating

generations. Mahalanobis's D² statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis have greatly been emphasized (Murty and Arunachalam, 1966). Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters toward divergence and effectiveness of selection (Venkateswarlu, 2001; Manivannan et al., 2002; Patil et al., 2003; Bisht et al., 2005). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the green gram genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

For realizing genetic diversity among the parents with their direct and indirect effects of different traits on seed yield and selection of best diverse parents for Chickpea breeding programme at MPKV, Rahuri present investigation was undertaken.

MATERIALS AND METHODS

The experimental material comprising Fifty one genotypes of Chickpea was grown during Rabi- 2012 in a Randomized Block Design with two replication at Pulses Improvement Project, Mahatma Phule Agriculture University, Rahuri. Data were recorded on five randomly tagged plants for viz., days for 50 % flowering, days to maturity, plant height, 100 seed weight, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of pods plant⁻¹, protein

Table 1: Estimates of variability parameters for nine different characters of Chickpea

Sr. No.	Name of the characters	Range	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A.	G.A. as % of mean
1.	Days to 50 % flowering	42.50-72.02	46.30	48.49	2.18	12.91	13.21	95.49	17.55	33.32
2.	Days to maturity	98.00-119.00	16.01	18.13	2.11	3.72	3.96	88.33	9.931	9.245
3.	Plant height (cm)	32.80-64.70	35.79	39.05	3.25	13.72	14.33	91.68	15.12	34.70
4.	No. primary branches plant ¹	2.90-6.30	0.70	0.99	0.29	18.65	22.20	70.58	1.858	41.36
5.	No. of secondary branches plant ¹	7.20-20.10	7.58	8.61	1.03	23.52	25.08	87.95	6.816	58.23
6.	No. of pods plant ¹	30.20-104.20	276.00	293.37	17.36	27.23	28.08	94.08	42.54	69.74
7.	100 seed weight (g)	9.59-32.45	34.14	34.56	0.41	37.35	37.58	98.80	15.33	98.03
8.	Seed yield plant ¹ (g)	3.60-21.03	13.37	13.77	0.39	39.77	40.35	97.14	9.517	103.48
9.	Protein content (%)	17.38-25.12	1.687	3.095	1.40	5.882	7.966	54.50	2.532	11.466

Abbreviations: GCV = Genotypic coefficient of variation; b.s. = Broad sense; h^2 = Heritability; PCV = Phenotypic coefficient of variation; G.A = Genetic advance; σ^2_g = Genotypic variation; σ^2_p = Phenotypic variation; σ^2_e = Environmental variation

Table 2: Distribution of 51 genotypes of Chickpea in different clusters

Cluster No.	Number of genotypes	Genotypes included
I	40	IC-327947, IC-486995, IC-269044, IC-269021, IC-269031, IC-268978, IC-268985, IC-555401, IC-299246, IC-485859, IC-327890, EC-555278, IC-269093, IC-269147, IC-269128, IC-269034, IC-506753, IC-268930, Vijay, IC-269111, IC-269056, IC-269045, IC-268992, IC-269002, IC-269009, IC-269003, IC-487344, IC-424303, IC-269015, IC-113160, IC628970, IC-269120, IC-268946, IC-269090, IC-268947, IC-269092, IC-269113, IC-299118, IC-327596, IC-486938.
II	8	IC-270936, IC-487323, IC-350889, Vishal, Digvijay, IC-442831, IC-268927, IC-327656.
III	1	IC-299779.
IV	1	EC-490044.
V	1	IC-269004.

Table 3: Cluster means for different traits in Chickpea

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant ¹	No. of secondary branches plant ¹	No. of pods plant ¹	100 seed weight (g)	Seed yield plant ¹ (g)	Protein content (%)
I	52.70	107.28	42.72	4.45	11.87	63.12	12.85	8.06	22.19
II	49.25	105.38	42.94	4.45	11.50	58.31	26.21	15.37	21.78
III	60.50	116.50	55.80	5.30	8.60	40.70	27.87	11.35	22.75
IV	71.00	119.00	64.70	4.00	9.10	30.20	23.43	7.09	17.95
V	53.50	108.50	49.70	6.30	12.60	48.80	22.81	5.15	23.66
Population mean	57.39	111.33	51.17	4.90	10.73	48.22	22.63	9.40	21.66

content and seed yield plant⁻¹. Wilks (1932) criteria were used to test the significance differences in mean values of all the eight characters. Statistical analysis: Mahalanobis (1936) defined the distance between two populations as D^2 , which was obtained by Tochers method, described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1985). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated. The experimental data was analyzed statistically by the method of analysis of variance for single factor (Gomez and Gomez, 1984) and lastly to find out the significance mean difference between varieties different genetic parameters were estimated. Analysis of variance was performed to test the significance of difference among the genotypes for the characters studied, as suggested by Panse and Sukhatme (1985). Genetic variability parameters were estimated by the method proposed by Johnson *et al.* (1955).

Fifty one genotypes of Chickpea showed significant differences among all characters under study. The relative contribution (Table 5) of different characters towards divergence showed 100 Seed weight (g) contributed maximum towards divergence followed by number of pods per plant and days to 50 per cent flowering (cm) which was also observed by Manivannan *et al.* (2002) and Raje and Rao (2000) in green gram, Gupta and Singh (1970) found that the same characters are positively associated with yield and are the main yield components.

The parameters of genetic variability revealed high PCV and GCV values for seed yield per plant followed by 100 seed weight, number of pods per plant and number of secondary branches per plant and number of primary branches per plant respectively, (Table 1) indicating that these traits could be used as selection indices for yield improvement, similar finding were reported by Sable *et al.* (2000), Gumber *et al.* (2002), Borate *et al.* (2010), Nagy *et al.* (2013) in pigeonpea and Garje *et al.* (2013) in green gram. High heritability (> 60 %) was observed in all the characters studied. The high heritability with high genetic advance was recorded for the character 100

RESULTS AND DISCUSSION

Table 4: Intra cluster and inter cluster D and D² values (in parenthesis) of 5 clusters of Chickpea

Clusters	I	II	III	IV	V
I	9.91	20.43	25.02	24.23	31.59
	-98.2	-417.38	-626	-587.09	-997.92
II		11.84	16.82	22.85	26.42
		-140.18	-282.91	-522.12	-698.01
III			0	11.92	14.82
			0	-142.08	-219.63
IV				0	18.65
				0	-347.82
V					0
					0

Table 5: Per cent contribution of different characters to genetic diversity

Sr.	Characters	Per cent contribution
1.	Days to 50 % flowering	12.47
2.	Days to maturity	8.16
3.	Plant height (cm)	7.37
4.	Number of primary branches per plant	0.94
5.	Number of secondary branches per plant	7.76
6.	Number of pods per plant	16.71
7.	100 seed weight (g)	35.69
8.	Seed yield per plant (g)	9.88
9.	Protein content (%)	1.02
	Total	100

seed weight (98.80 %) followed by seed yield per plant (97.14 %), days to 50 per cent flowering (95.49 %), number of pods per plant (94.08) and plant height (91.68 %). The estimates of GA ranged from 1.85 to 42.54 with the highest estimate in case of number of pods per plant. The highest genetic advance as per cent of mean was observed for seed yield per plant (103.48) followed by 100 seed weight (98.03), number of pods per plant (69.74) and number of secondary branches (58.23). It indicates that most likely the heritability is due to additive gene effects and selection for these traits may be rewarding. Similar findings have been reported by Samal and Jagdev (1989), Jahangirdar *et al.* (1994), Deshmukh and Patil (1995) and Meshram *et al.* (2014) in blackgram.

The Fifty one genotypes studied were grouped into five clusters (Table 2) by using Tocher's methods described by Rao (1952), cluster I with 40 genotypes, cluster II with 8 genotypes and cluster III, IV and V were mono genotypic. The inter cluster D² values varied from 11.92 to 31.59. Highest inter cluster distance is observed between the clusters I and V (D=31.59) followed by clusters-II and V (26.42), indicating wide divergence among the clusters. This also suggests that genetic architecture of the lines in one cluster differs entirely from those included in the other cluster. Minimum cluster distance was observed between cluster-III and IV, suggesting that the genotypes in this cluster may be used as parents in hybridization programme to obtain desirable recombinants. The inter cluster distance criteria is used for selection of varieties as parents for hybridization using D² analysis.

Cluster means were found highest for different characters (Table 3) viz., Cluster II showed highest mean performance for days to 50% flowering, days to maturity and seed yield per plant.

Cluster V showed higher mean performance for No. of primary branches per plant, No. of secondary branches per plant and protein content. Cluster I recorded maximum performance for number of pod per plant, Cluster III for 100 Seed weight (g) and cluster IV for plant height.

Average intra and inter cluster D² values among fifty one genotypes revealed that cluster III, IV, and V showed no intra-cluster D² value as it had only one genotypes each (Table 4). The cluster II showed maximum intra cluster D²value (11.84) followed by cluster I (9.91) revealing the inclusion of diversion of diverse genotypes in these clusters.

In the present investigation, D²values between all possible selections of fifty one genotypes ranged between 98.20 to 997.92. This high range of D² values showed the presence of good amount of diversity in the material used for the present study. Minimum inter cluster D² value was observed between cluster III and IV (142.08) indicating the close relationship among the genotypes included in these two clusters. As the D² values represent the index of genetic diversity among the cluster, it would be more appropriate to make cross between genotypes separated by high estimates of statistical distance.

Raman and Singh (1987) suggested that genotypes belonging to clusters separated by high genetic distance maybe used in hybridization program to obtain a wide spectrum of variation among the segregates and in the present study similar suggestion had been made. The genotypes included in the diverse clusters namely, II, III, IV and V hold good promise as parents for obtaining potential hybrids and thereby creating greater variability of these characters to improve the yield.

So from the above result it can be concluded that the genetic diversity was not related to geographic diversity. The cluster combinations were classified into four divergence classes, following the method suggested by Arunachalam and Bandopadhyay (1984). Crosses were suggested between clusters in a pair from inter cluster D values, which fall in divergence classes DC₁ (11), DC₂ (29), DC₃ (14) and DC₄ (only 1). Arunachalam and Bandopadhyay (1984) reported that crosses between divergent classes DC₂ and DC₃ will be more heterotic and promising than other combination of crosses. On the basis of divergence classes the potential parent's viz. IC-270931, IC-487323, IC-442831, Digvijay, IC-350889, IC-327656, Vishal, IC-327596, IC-299779, IC-269015 and IC-268947 can be used in the hybridization programme for chickpea improvement to obtain better transgressive segregants. Two characters viz. 100 seed weight (g) and Seed yield per plant (g) exhibited high heritability estimates (in broad sense). These characters should be given importance for further improvement of yield and yield components.

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