

## Assessment of genetic diversity of cultivated chickpea (*Cicer arietinum* L.)

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**Abstract:** An investigation was carried out among the twenty five genotypes of chickpea to study the nature and magnitude of genetic divergence using Mahalanobis's  $D^2$  Statistics. The data were recorded on ten important quantitative traits from the genotypes raised in Randomized Block Design having three replication. The twenty five chick pea genotypes were grouped into six clusters. The cluster I shows largest cluster with eight genotypes. Highest inter cluster distance was observed between cluster III and cluster VI, followed by cluster I and VI. Three characters viz. harvest Index, 100 seed weight and number of pods per plant contributed maximum in manifestation of genetic diversity. Number of pods per plant had maximum Phenotypic and Genotypic Coefficient of Variation (PCV and GCV), followed by Biological yield per plant and 100 Seed weight. A moderate to high degree of Heritability and Genetic Advance was observed for number of Pods per pant, Harvest index and Biological yield. The genotypes KPJ 59, PBJ 1 and Pusa 329 were identified as genetically diverse parents, which can be utilized for future crop improvement programme

**Key words:** Chickpea,  $D^2$  statistics, genetic variability, inter cluster distance and intra cluster distance

### INTRODUCTION

The knowledge of genetic diversity is a useful tool in gene-bank management and breeding experiments like tagging of germplasm, identification and/or elimination of duplicates in the gene stock and establishment of core collections Genetic diversity among the parents is a prerequisite to improve the chances of selecting better segregants for various characters. The more diverse the parents within reasonable limits, the more are the chances of improving the characters under consideration. Varieties from distinct geographic regions are usually selected for hybridization programme presuming the presence of considerable genetic diversity among them. The present study was envisaged to measure the genetic diversity among the genotypes of *Cicer arietinum* L. and to identify divergent parents for future hybridization programmes for yield improvement.

### MATERIALS AND METHODS

The experimental material comprising 25 genotypes of chickpea was grown during rabi (winter) 2007-2008 in a Randomized Block Design with three replication at Central Research Farm of Allahabad Agricultural Institute-Deemed University, Allahabad. Data were recorded on five randomly tagged plants for plant height (cm), Number of branches per plant, Days to 50% flowering, Number of pods per plant, 100 seed weight (g), Days to maturity, Biological yield per plant (g), Harvest index (%), yield per plant (g) and yield per hectare (q). Pooled data were subjected to statistical analysis. Wilks criteria was used to test the significance of pooled differences in mean values of all the 10 characters.

Table 1: Distribution of 25 genotypes of chick pea into different clusters

Cluster number	Number of genotypes	Genotypes
I	8	PG 12, Pusa 261, GL 769, GPF 2, RSG 931, JG 74, Radhey, Pant G 114,
II	5	Pusa 312, Pusa 209, B 108, PG 5, JG 130
III	3	RAU 52, Pusa372, DCP 92-3
IV	6	Pusa 244, Pusa 240, Pusa 256, Saki 9516, Pusa 329, Avrodhi
V	2	Pusa 212, PBG 1
VI	1	KPJ 59

Genetic diversity was studied using Mahalanobis's  $D^2$  and clustering of genotypes was done according to Toucher's method

The pooled analysis of variance for the experimental design showed highly significant differences among genotypes for all the characters studied. Multivariate analysis based on Mahalanobis's  $D^2$  statistic grouped the genotypes into 6 clusters, (table 1). Similar findings have been reported by Kumar (1997). This suggested the presence of high degree of divergence in the material studied.

### RESULTS AND DISCUSSION

Significant differences were observed among 25 genotypes of chickpea for all characters under study. Among the 10 character studies harvest index, 100 seed weight, pods per plant and biological yield per plant contributed maximum in the manifestation of genetic divergence. Higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for Number of pods per plant & Harvest index respectively, indicating that these traits could be used as selection indices for yield improvement. Number of pods per plant and 100 seed weight exhibited high values of

Table 2: Cluster mean values of 6 clusters for 10 characters in 25 genotypes of chickpea

S. No	Cluster No. Character	I	II	III	IV	V	VI
1	Plant height	54.64	54.53	48.23	58.36	57.33	63.53
2	Branches/plant	3.10	3.24	3.20	3.16	3.47	3.66
3	Days to 50% flowering	84.92	88.20	89.89	90.28	84.33	88.67
4	No. of pods per plant	56.83	70.90	72.45	55.36	105.22	125.69
5	100 Seed weight	16.40	16.92	18.27	27.94	17.18	17.29
6	Days to maturity	146.20	146.33	148.67	148.56	150.33	147.67
7	Biological yield per plant	44.58	55.91	58.72	53.31	55.05	91.33
8	Harvest index	27.11	28.02	29.42	31.50	33.03	24.60
9	Seed yield per plant	13.94	15.16	17.18	16.73	18.13	22.30
10	Seed yield per ha	23.01	25.26	28.60	28.73	30.21	34.00

Table 3: Intra (diagonal) and inter-cluster average distances ( $D^2$ ) for 10 characters in 25 genotypes of chickpea.

Cluster number	I	II	III	IV	V	VI
I	107.53 (10.36)	150.96 (12.28)	270.68 (16.45)	331.84 (18.2)	468.65 (21.64)	109.95 (33.31)
II		67.17 (8.19)	358.96 (18.94)	271.34 (16.47)	266.05 (16.31)	611.19 (11.71)
III			74.20 (8.61)	487.06 (22.06)	379.57 (19.48)	1233.94 (11.63)
IV				139.18 (11.79)	562.87 (23.72)	964.12 (31.05)
V					119.47 (10.93)	367.50 (19.70)
VI						0.00

heritability (in broad sense) Similar findings have been reported by Burli *et al.* (2004). Number of pods per plant and biological yield per plant exhibited high value of genetic advance as percent of mean. 25 genotypes were grouped into VI clusters using Mahalanobis  $D^2$  statistics and Tocher's method. The cluster I was the largest and consisted of 8 genotypes followed by clusters IV which had 6 genotypes. The cluster II had 5 genotypes, cluster III had 3 genotypes and cluster V had 2 genotypes. Cluster VI was unique in having only one genotype. Highest inter cluster distance is observed between cluster III & cluster VI followed by I & VI and IV and VI, respectively The grouping pattern did not show any relationship between genetic divergence and geographic diversity which has been the point of debate in the past. Murthy and Arunachalam (1996) reported that genetic drift and selection in different environments could cause greater diversity than the geographic distance. Cluster means were found highest for different characters. Cluster VI showed highest mean performance for plant height, Branches per plant, Number of pods per plant, Biological yield per plant, and Seed yield per plant and Seed yield per hectare. Cluster V recorded maximum performance for days to maturity and Harvest index. Cluster IV showed higher mean performance for days to 50% flowering and 100 seed weight. Average intra and inter-cluster  $D^2$  values among 25 genotypes revealed that cluster VI showed no intra-cluster  $D^2$  value as it had only one genotypes. The cluster IV showed maximum intra-cluster  $D^2$  value (139.18) followed by cluster V (119.47) and cluster I (107.53) revealing the inclusion of diversion of diverse genotypes in these clusters. The inter cluster  $D^2$  values ranged from 150.96 to 1233.94. Maximum inter cluster  $D^2$  value was observed between cluster III and IV (1233.94) which indicated that the genotypes included in these different clusters may give high heterotic response and thereby better segregants Similar findings have been

reported by Lal *et al.*, 2001. Minimum inter cluster  $D^2$  value was observed between cluster II and VI (150.96) indicating the close relationship among the genotypes included in these two clusters. The average cluster means for 10 characters (Table 3) indicated that genotypes indicated cluster I were of early maturity days and averaged plant height. Cluster III showed early flowering habit with shortest plant height. Cluster IV showed higher mean performance for days to 50% flowering and 100 seed weight, where as cluster V showed maximum performance for days to maturity and harvest index. Similar findings have been reported by Sable *et al.* (2000). The cluster VI showed maximum number of primary branches, maximum number or pods per plant, Biological yield per plant, seed yield per plant and seed yield per hectare. The genotypes included in the diverse clusters namely, VI and V hold good promise as parents for obtaining potential hybrids and thereby crating greater variability of these characters to improve the yield. Concomitant result has been reported by Kumar *et al.* (1997)

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