

Original Research Article

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## Assessment of Genetic Diversity in Chickpea (*Cicer arietinum* L.) Germplasm under Normal Sown Condition of Bihar

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### ABSTRACT

An experiment was conducted during Rabi 2016-17 at Pulses Research farm, Bihar Agricultural University, Sabour (Bhagalpur) to study the existing genetic diversity in thirty six Desi chickpea genotypes under normal sown condition. All the genotypes were grouped into seven clusters as per Ward minimum variance method revealed the presence of considerable amount of genetic diversity in the material with each other for different yield and yield attributing traits. The cluster II containing the maximum of 13 genotypes followed by 9 genotypes in cluster I, 5 genotypes in cluster III, 3 genotypes each in cluster IV and V, 2 genotypes in cluster in cluster VI and mono-genotypes in cluster. The intra-cluster  $D^2$  value ranged from 0.00 to 421.27 while, inter-cluster D value ranged from 402.80 to 3912.66. The highest intra-cluster distance was exhibited by cluster I (421.27) followed by cluster VI (316.27) and III (315.69). The highest inter cluster distance was observed between cluster II and VII (3912.66) followed by cluster II and VII (3831.40), cluster III and VI (2804.51) and cluster IV and VII. The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes. The genotypes of cluster VII showed the highest mean values for grain yield per plant, harvest index, biological yield per plant, primary and secondary branches per plant, plant height and days to maturity, while cluster VI showed the highest mean for grain yield per plot, total number of pods per plant, effective pods per plant and days to 50% flowering. The cluster V had highest mean value for 100 seed weight and canopy temperature at vegetative stage. The cluster IV recorded highest mean value for chlorophyll index, while cluster III exhibited highest mean value for canopy temperature at pollen formation stage. The promising genotypes for grain yield per plant, harvest index, biological yield per plant, grain yield per plot, total number of pods per plant, effective pods per plant, primary and secondary branches per plant, plant height, on the basis of mean values which could be utilized for hybridization programme for the development of high yielding genotypes. Among the fifteen traits studied, maximum contribution was made by 100-seed weight (46.83%) (Table-4) followed by total number of pods per plant (22.22%), grain yield per plant (12.54%), grain yield per plot (5.34%) and harvest index (3.49%). Therefore, these characters may be given importance during hybridization programme.

#### Keywords

Chickpea, Genetic diversity,  $D^2$  statistics and grain yield

#### Article Info

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## Introduction

Chickpea (*Cicer arietinum* L.), a cool season crop is the largest produced food legume in South Asia and the third largest globally after common bean and field pea. India is the largest chickpea producer with 65% global production and chickpea constitutes about 40% of India's total pulse production. In spite of India being the largest chickpea producing country, a deficit exists in domestic production and demand which is met through imports. In India, the total area under chickpea is 8.25 M ha with 7.33 million tonnes production with productivity 889 kg/ha and the total area in Bihar reached 60.0 thousand ha with 57.50 thousand tonnes of production with productivity of 958 kg/ha (2014-15: Agricultural Statistics Division, Directorate of Economics and Statistics, Dept. of Agriculture and Cooperation).

Limited or lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of chickpea (Johnson *et al.*, 2015). 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. 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 F<sub>1</sub> hybrids and broad spectrum of variability in segregating generations. Mahalanobis's D<sup>2</sup> statistics is a powerful tool in quantifying the degree of variability at the genotype level. Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters toward divergence and effectiveness of selection (Patil *et al.*, 2003;

Bisht *et al.*, 2005; Johnson *et al.*, 2015). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the chickpea genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

## Materials and Methods

The experimental material consisted of thirty six chickpea genotypes were sown on 10<sup>th</sup> November, 2016 at Pulses Research farm, Bhatti, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid out in a randomized complete block design with three replications during Rabi 2016-17 under All India Coordinated Research Project on Chickpea. The plot size was 4.8 m<sup>2</sup>, with 1 row of 4 m length. Inter row spacing distance was kept 30 cm and plant to plant spacing was 30 x 10 cm. The recommended packages of practices were followed to raise a healthy crop.

Data were recorded on fifteen quantitative traits viz. days to 50% flowering, days to maturity, chlorophyll index, canopy temperature at vegetative stage, canopy temperature at pollen formation stage, primary branches per plant, secondary branches per plant, plant height (cm), total number of pods per plant, effective pods per plant, 100 seed weight (g), grain yield per plant (g), biological yield per plant, harvest index and grain yield per plot (g). The days to 50% flowering, days to maturity, and grain yield per plot were recorded on a plot basis and plant height and number of pods per plant and 100-seed weight were recorded from a random sample of five plants in each plot. Genetic divergence was estimated by using D<sup>2</sup> statistics of Mahalanobis (1936) and clustering of genotypes was done according Ward minimum variance method as suggested by Ward (1963). The per cent contribution of

characters towards genetic divergence was calculated according to Singh and Chaudhary (1985).

## Results and Discussion

All the genotypes were grouped into seven clusters as per Ward minimum variance method, with cluster II containing the maximum of 13 genotypes followed by 9 genotypes in cluster I, 5 genotypes in cluster III, 3 genotypes each in cluster IV and V, 2 genotypes in cluster in cluster VI and mono-genotypes in cluster VII (Table 1 and Fig. 1). The pattern of distribution of 36 genotypes in various clusters revealed existence of considerable genetic diversity in the material. It means the overall genetic similarity was found in the germplasms were presented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of Raval and Dobariya (2004), Parameshwarappa *et al.*, 2011, Parashi *et al.*, 2013, Kuldeep *et al.*, 2015 and Kuldeep *et al.*, 2015. The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region. The intra-cluster  $D^2$  value ranged from 0.00 to 421.27 while, inter-cluster D value ranged from 402.80 to 3912.66 (Table 2 and Fig. 2) in Ward minimum variance method. The highest intra-cluster distance was exhibited by cluster I (421.27) followed by cluster VI (316.27) and III (315.69). The intra cluster distance was maximum in cluster I followed by cluster VI which indicated that hybridization involving genotypes within the same clusters may result in cross combination. The highest inter cluster distance was

observed between cluster II and VII (3912.66) followed by cluster II and VII (3831.40), cluster III and VI (2804.51) and cluster IV and VII. These lines may be utilized in further breeding programme for the exploitation of hybrid vigour and suggesting wide diversity between them and genotypes in these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Lal *et al.*, 2011). Therefore, crosses between the members of clusters separated by inter-cluster distances are likely seemed to be beneficial for further improvement. Significant differences among the genotypes for different characters indicated variations among the genotypes favorable for their use in the breeding programs. Crosses between parents with maximum divergence would be more responsive to improvement since they are likely to produce higher heterosis and desirable genetic recombination (Kuldeep *et al.*, 2015). The genotypes of cluster VII showed the highest mean values (Table 3) for grain yield per plant, harvest index, biological yield per plant, primary and secondary branches per plant, plant height and days to maturity, while cluster VI showed the highest mean for grain yield per plot, total number of pods per plant, effective pods per plant and days to 50% flowering. The cluster V had highest mean value for 100 seed weight and canopy temperature at vegetative stage. The cluster IV recorded highest mean value for chlorophyll index, while cluster III exhibited highest mean value for canopy temperature at pollen formation stage. The promising genotypes for grain yield per plant, harvest index, biological yield per plant, grain yield per plot, total number of pods per plant, effective pods per plant, primary and secondary branches per plant, plant height, on

the basis of mean values which could be utilized for hybridization programme for the development of high yielding genotypes. Similar results were reported by Garje *et al.*, (2013), Meshram *et al.*, (2013), Nagy *et al.*, (2013) and Singh *et al.*, (2014). Among the fifteen traits studied, maximum contribution was made by 100-seed weight (46.83%) (Table 4) followed by total number of pods per plant (22.22%), grain yield per plant (12.54%), grain yield per plot (5.34%) and harvest index (3.49%). Therefore, these characters may be given importance during hybridization programme. On the basis of divergence classes the potential parent's viz. PhuleG1310, BRC-4, JG16, KPG 59, KWR 108, PG170, GNG2304, GNG2299, PG186, GNG 2264, GL29098, BG372, CSJ887, GCP105 can be used in the hybridization

programme for chickpea improvement to obtain better transgressive segregants. This finding are in accordance with that of Wadikar *et al.*, (2010), Akthar *et al.*, (2011), Parameshwarappa *et al.*, (2011), Jayalakshmi *et al.*, (2012), Puri *et al.*, (2013), Gaikwad *et al.*, (2014) and Johnson *et al.*, (2015). The high inter cluster distance was observed between clusters, suggesting wide diversity between them and genotypes in these clusters could be used as parents in hybridization programme to develop high yielding chickpea genotypes under normal sown condition because crosses between genetically divergent lines will generate heterotic sergeants. Among the fifteen traits studied, maximum contribution was made by plot yield followed by plant stand at harvest and number of pods per plant.

**Table.1** Distribution of 36 chickpea genotypes in various clusters

Cluster	No. of Genotypes	Name of Genotypes
I	09	JG 74315-14, BRC-3, IPC 2012-49, BG 3067, IPC 2012-49, GL12003, GNG 2207, H12-62, H12-55
II	13	BRC-4, JG16, KPG 59, KWR 108, PG170, GNG2304, GNG2299, PG186, GNG 2264, GL29098, BG372, CSJ887, GCP105
III	05	IPC2012-98, PBC501, DCP92-3, NDG14-24, BG3068
IV	03	GNG469, BG3043, GNG2215
V	03	NBeG507, ICCV15112, JG24
VI	02	BRC-2, BRC-1
VII	01	PhuleG1310

**Table.2** Average intra and inter cluster distance values among eight clusters for thirty six genotypes of chickpea under normal condition

Cluster	I	II	III	IV	V	VI	VII
I	421.723	509.565	827.818	1186.26	815.841	1221.331	2571.000
II		175.988	402.805	1254.806	1533.432	2123.469	3912.661
III			315.619	768.203	1698.819	2804.511	3831.403
IV				223.515	1102.483	2517.610	2486.896
V					147.343	902.239	1387.935
VI						316.279	1873.666
VII							0.000

**Table.3** Mean values of clusters of different characters towards genetic divergence in thirty six chickpea genotypes under normal sown condition

Clusters	Days to 50%	Days to Maturity	Chlorophyll Index	Canopy Temperat	Canopy Temperat	Plant Height cm	Primary Branches/	Secondary Branches/	Total Pods/Plant	Effective Pods/Plant	Biological Yield	harvest Index	100 Seed Weight	Grain yield/plant	Grain Yield/Plot
<b>I</b>	79.500	133.889	63.259	22.219	33.767	64.667	1.756	4.644	78.521	71.216	83.987	24.615	21.972	20.747	2157.511
<b>II</b>	79.231	133.538	61.013	22.060	34.490	56.135	1.538	4.054	61.654	54.058	48.531	23.374	16.750	11.096	2164.889
<b>III</b>	76.500	133.200	61.030	20.790	35.040	56.590	1.600	4.500	43.084	33.128	78.606	20.346	18.150	15.246	2030.404
<b>IV</b>	78.500	132.833	65.053	21.708	34.358	63.367	1.933	4.400	79.793	63.495	134.573	19.010	28.000	24.947	2357.502
<b>V</b>	77.167	135.333	64.787	22.342	34.233	70.733	1.600	4.133	57.552	51.981	84.217	18.317	37.750	17.063	1764.302
<b>VI</b>	80.750	135.500	63.865	21.913	34.225	65.250	1.900	4.300	163.747	158.570	109.540	19.847	26.250	21.385	2449.597
<b>VII</b>	76.000	138.000	62.770	22.175	34.475	67.000	2.600	5.600	77.220	72.518	316.800	24.780	31.750	77.220	1808.045
<b>Mean</b>	78.681	133.903	62.435	21.912	34.338	60.958	1.689	4.356	70.565	62.373	82.558	22.322	21.882	18.145	2132.939
<b>TreatMSS</b>	11.295	7.131	16.727	1.635	1.157	179.810	0.299	0.750	4710.343	4963.462	15919.722	36.111	283.061	880.402	187269.525
<b>ErrMSS</b>	11.737	10.092	8.536	1.607	3.786	93.452	0.110	0.786	388.452	348.652	559.886	20.036	17.209	52.889	208367.304
<b>F Ratio</b>	0.962	0.707	1.960	1.017	0.306	1.924	2.720	0.954	12.126	14.236	28.434	1.802	16.449	16.646	0.899
<b>Probability</b>	0.456	0.623	0.114	0.425	0.906	0.120	0.038	0.461	0.000	0.000	0.000	0.143	0.000	0.000	0.495

**Table.4** Contribution of different characters towards genetic divergence of 36 chickpea genotypes

SI. No.	Source	Contribution %	Contribution %
1.	Days to 50% Flowering	0.16	1.000
2.	Days to Maturity	0.16	1.000
3.	Chlorophyll Index	0.01	0.000
4.	Canopy Temperature @vs	0.32	2.000
5.	Canopy Temperature @pfs	0.01	0.000
6.	Plant Height (cm)	3.02	19.000
7.	Primary Branches/ Plant	1.59	10.000
8.	Secondary Branches/ Plant	0.16	1.000
9.	Total number of Pods/ Plant	22.22	140.000
10.	Effective Pods/ Plant	2.22	14.000
11.	Biological Yield per plant (g)	1.90	12.000
12.	Harvest Index (%)	3.49	22.000
13.	100 Seed Weight (g)	46.83	295.000
14.	Grain Yield/ Plant (g)	12.54	79.000
15.	Grain Yield/ plot (kg/ha)	5.34	34.000

**Fig.1** Ward minimum variance dendrogram

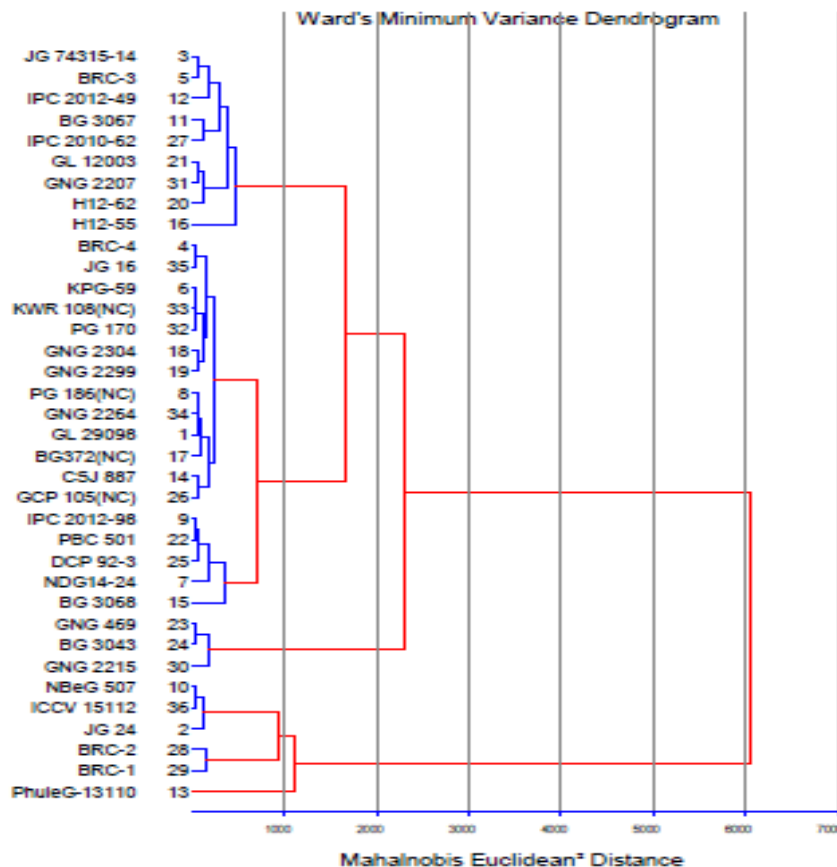
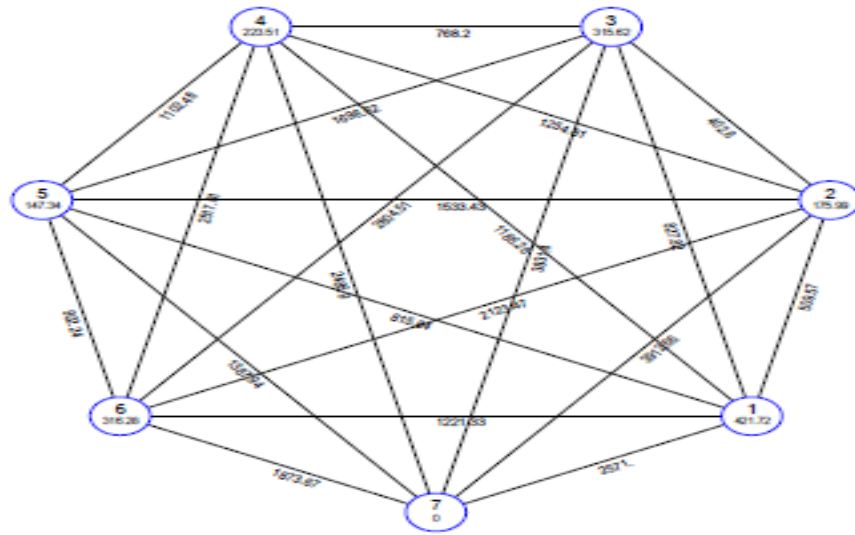
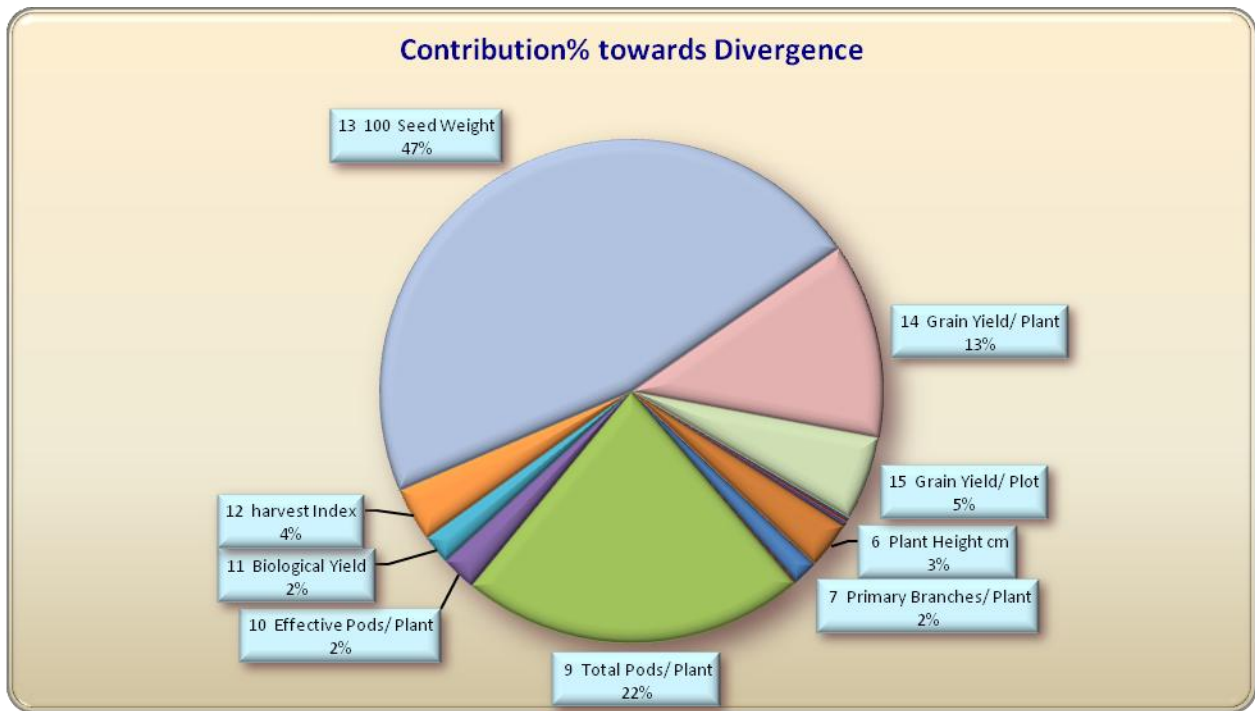




Fig.2 Euclidean<sup>2</sup> distance



Euclidean<sup>2</sup> Distance (Not to the Scale)



Therefore, these characters may be given importance during hybridization programme and offers provides the opportunity for breeding programs to improve the chickpea leading to better yield stability and profitability for growers. The above findings,

thus, would be useful for planning a comprehensive hybridization programme for obtaining desirable segregants for selection of high yielding chickpea genotypes under normal sown condition.

In the present investigation, high inter cluster distance was observed between clusters, suggesting that there are a wide diversity between them and genotypes in these clusters could be used as parents in hybridization programme to develop high yielding chickpea genotypes under normal sown condition. The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes. Considering the mean performance of genotypes, diversity of clusters they belonged and cluster means for different characters, hybridization of BRC-4, JG16, KPG 59, KWR 108, PG170, GNG2304, GNG2299, PG186, GNG 2264, GL29098, BG372, CSJ887, GCP105 of cluster II with promising genotype PhuleG1310 of cluster VII may be recommended for isolating transgressive segregants for developing high yielding rice varieties. Intercrossing of divergent genotypes with desirable traits would lead to greater opportunity for exploitation of maximum amount of heterosis and utilize them for multiple crossing programmes.

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