Exploring Genetic Diversity in Chickpea (*Cicer arietinum* L.) Under Normal Sown Condition of Bihar

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Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: The present investigation was undertaken to study the nature and magnitude of genetic diversity among chickpea genotypes.
Study Design: The experimental material comprised of forty genotypes of chickpea in Rabi 2016-17 at Pulse Research Farm, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid in a randomised complete block design with three replications during Rabi with the inclusion of the recommended packages and practices needed for a healthy crop
Results and Discussion: Analysis of variance revealed highly significant differences among the forty genotypes for all the characters studied indicating that significant amount of genetic variability present in the material. The cluster I had maximum elven genotypes followed by cluster VI, 08 genotypes, cluster III, 07 genotypes and IV having five genotypes, while cluster II and V had four genotypes, respectively. The cluster VII was mono-genotypic having one genotype. The intra-cluster D^2 value ranged from 0.00 to 25.16 while, inter-cluster D^2 value ranged from 30.73 to 204.05. The maximum intra cluster distance was exhibited by cluster V followed by cluster I and cluster IV. The maximum inter-cluster distance was observed between cluster II and VII (204.05), followed by cluster II and V (170.79) and cluster III and V (157.56) suggesting that the genetic

architecture of the genotypes in one cluster differ entirely from those included in other clusters. The genotypes BAUG 108, H12-63, RKG13-380, AKG1303 and KWR108 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea.

Conclusion: 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.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is one of the most important legumes for consumption in India as well as worldwide. In grain legumes, it ranks second in acreage and third in production with productivity of 913 kg/ha [1]. India is the largest producer of chickpea in the world sharing 65.2% of area and 65.4% of production. Chickpea was grown in 9.93 million ha area, with the production of 9.53 million tons and productivity of 960 kg/ha. Chickpea seeds contain 17.7 per cent protein, 0.49 per cent lysine, 0.11 per cent methionine, 56.6 per cent carbohydrates, a considerable amount of calcium, phosphorus, iron and vitamin B. India is the largest producer of chickpea sharing 67% of the total chickpea production in the world but still remains as its importer. The growing population demands the development of high yielding varieties to meet their consumption needs. Genetic improvement of the crop can be brought by utilizing the diversity in gene pool. The germplasm with high diversity acts as a source of biotic and abiotic stress resistance which could be employed to reduce the losses in production of chickpea by using promising lines for hybridisation programmes. Plant breeding practices have to lead to narrowing of the genetic base of cultivated chickpea. However, newly developed genotypes characterisation for economic traits will help in superior cultivar development (Naveed et al., 2015).The determination of genetic variability, heritability and genetic advance is necessary in selection of superior genotypes.D^2 statistical analysis is a tool which measures the degree of divergence among the population. Murthy and Arunachalam [2] viewed multivariate analysis with "Mahalanobis D^2 statistics" a strong tool to know the pattern of clustering to verify the relationship between genetic and geographic divergence and to discover the importance of different quantitative traits towards the maximum divergence. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic diversity among chickpea genotypes.

2. MATERIALS AND METHODS

The experimental material comprised of forty genotypes of chickpea in Rabi 2016-17 at Pulse Research Farm, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid in a randomised complete block design with three replications during Rabi 2016-17 with the inclusion of the recommended packages and practices needed for a healthy crop. Data for six quantitative traits were recorded viz. days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, 100 seed weight (g) and grain yield per plot. The days to 50% flowering, days to maturity, and seed yield per plot were accounted on a plot basis and plant height, number of pods per plant and 100 seed weight (g) were documented from a random sample of five plants in each plot. Genetic divergence was determined by using D^2 statistics of Mahalanobis [3] and clustering of genotypes was done according to Ward's Minimum Variance method. The percentage contribution of studied characters towards genetic divergence was computed according to Singh and Chaudhary [4].

3. RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for all the six characters studied indicating a significant amount of genetic variability present in the material. All the genotypes were grouped into seven clusters as per Ward's minimum variance method (Table 1, and Fig. 1), the cluster I had maximum elven genotypes followed by cluster VI, 08 genotypes, cluster III, 07 genotypes and IV having five genotypes, while cluster II and V had four genotypes, respectively. The cluster VII was mono-genotypic having one genotype. The intra-cluster D^2 value ranged from 0.00 to 25.16 while, inter-cluster D^2 value ranged from 30.73 to 204.05 (Table 2). The maximum intra cluster distance was exhibited by cluster V followed by cluster I and cluster IV. The

maximum inter-cluster distance was observed between cluster II and VII (204.05), followed by cluster II and V (170.79) and cluster III and V (157.56) suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Cluster III had exhibited highest cluster mean value for grain yield per plot, while cluster V had high mean for 100-seed weight (Table 3). Cluster II has the highest mean value for a number of pods per plant and earliness in flowering and maturity. Maximum contribution toward the total

divergence was exhibited by 100-seed weight followed by seed yield per plant, biological yield, number of pods per plant and harvest index. The genotypes BAUG 108, H12-63, RKG13-380, AKG1303 and KWR108 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea. 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.

Table 1. Distribution of forty chickpea genotypes in various clusters

Cluster	No. of genotypes	Name of genotypes
Cluster I	11	PBC 503, G2016-43, RG 2011-02, GJG 1403, GNG2338, BG 3706, GL 13001, Phule G 0818, BRC-1, KGD 99-4, GCP 105
ClusterII	04	BAUG 108, H12-63, RKG 13-80, AKG 1303
Cluster III	07	DC 16-2, NBeG 776, JG 2016-44, IPC 2013-21, GL 14042, GNG 2325, CSJ 866
Cluster IV	05	RVSSG 42, PG 214J, GJG 1416, H 13-36, PG177
Cluster V	04	IPC 2012-108, Phule G 0819, ndg 15-6, PBC 514
Cluster VI	08	NBeG 738, RKG 13-75, CSJ 907, BG 3075, BDNG 2015-16, DBGV 206, BGD 138, RVSSG41
Cluster VII	01	KWR 108

Table 2. Average intra and inter cluster distance values among seven clusters for forty genotypes of chickpea

Cluster	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster
1 Cluster	22.235	45.55	70.143	43.667	74.592	57.488	130.780
2 Cluster		9.729	88.2	40.226	170.79	126.500	204.059
3 Cluster			12.748	30.733	157.56	49.689	134.941
4 Cluster				15.834	155.07	72.355	131.486
5 Cluster					25.165	59.862	151.327
6 Cluster						15.232	120.661
7 Cluster							0.000

Table 3. Mean values of clusters of different characters towards genetic divergence in forty chickpea genotypes

| Cluster	Days to 50% flowering	Days to maturity	Plant Height cm	No. of pods/ plant	100-seed weight (g)	Grain yield/ plot (g)
1 Cluster	73.424	134.394	64.456	131.452	27.947	1004.091
2 Cluster	70.333	133.833	74.625	160.500	22.767	958.083
3 Cluster	74.190	134.333	66.674	81.143	19.188	1043.714
4 Cluster	74.733	135.000	62.733	122.733	19.375	960.867
5 Cluster	74.583	134.833	65.878	96.167	38.683	832.750
6 Cluster	73.792	134.958	63.048	68.792	28.745	818.292
7 Cluster	94.000	139.667	80.267	102.400	25.913	911.000
Mean	74.117	134.692	65.901	107.676	26.007	944.400
TreatMSS	92.307	6.133	130.652	7218.961	266.317	57708.591
ErrMSS	3.867	2.983	42.838	223.295	7.042	17994.956
F Ratio	23.870	2.056	3.050	32.329	37.817	3.207
Probability	0.000	0.095	0.022	0.000	0.000	0.018
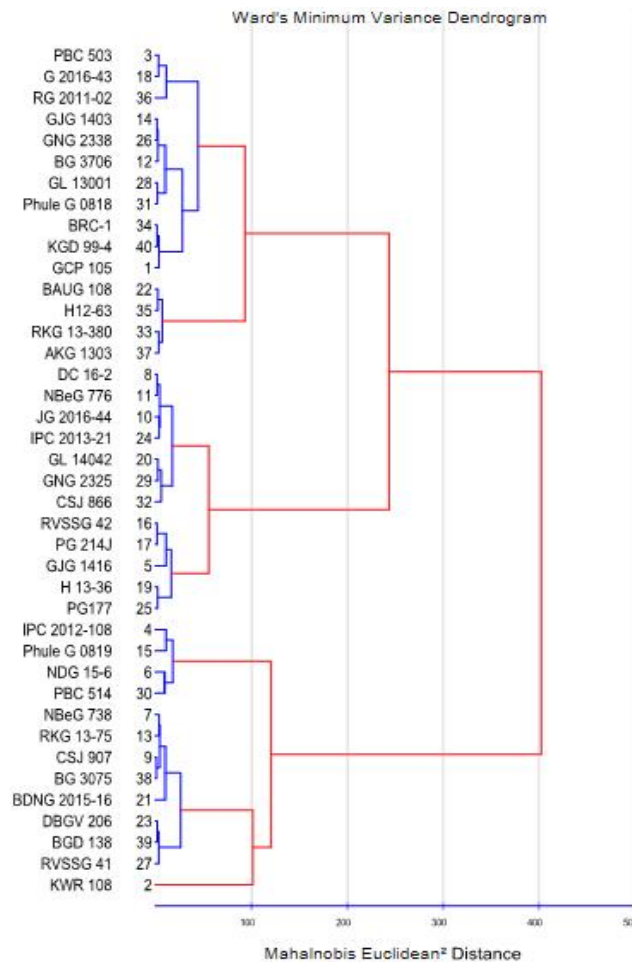
Fig. 1. Ward minimum variance dendogram

It confirmed that the overall genetic similarity found in the germplasms were present 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, also supported by previous findings of Lal et al. [5], Raval et al. [6], Paramesharappa et al. [7], Parashi et al. [8] and Agrawal et al. [9]. Free exchange of germplasm among the breeders of a different region or unidirectional selection practised by breeder in tailoringthe promising cultivar for selection of different region canbe the possible reason for grouping of genotypes of different places into one cluster.

The genotypes present in different and widely distant clusters may be utilized in a further breeding programme to exploit hybrid vigour and could be used as parents in hybridisation programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. Significant differences among the genotypes for different characters indicated variations among the genotypes acceptable 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.

Among the six traits studied, maximum contribution was made by 100 seed weight (46.03%) (Table 4), followed by number of pods per plant (40.00%), days to 50% flowering (6.54%), plant height (4.62%), grain yield per plot (2.31%). These findings are in accordance with the results of Kumar et al. [10] and Agrawal et al. [11]. Therefore, these characters may be given

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

Sl. No.	Source	Times ranked	Contribution %
1.	Days to 50% Flowering	51	6.54
2.	Days to Maturity	4	0.51
3.	Plant Height (cm)	36	4.62
4.	Total number of Pods/ Plant	312	40.00
5.	100 Seed Weight (g)	359	46.03
6.	Grain Yield/ Plant (g)	18	2.31

importance during hybridization programme. The genotypes BAUG 108, H12-63, RKG13-380, AKG1303 and KWR108 were identified as genetically diverse parents 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.

4. CONCLUSION

The genotypes BAUG 108, H12-63, RKG13-380, AKG1303 and KWR108 were identified as genetically diverse parents, which can be utilised for future crop improvement programme in Chickpea. 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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