



Genetic Diversity Analysis and Identification of Promising Lines for Hybridization in Chickpea (*Cicer arietinum* L.)

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ABSTRACT

Forty genotypes of chickpea were evaluated for assessing genetic divergence for different quantitative characters for improving yield potential of chickpea by using Mahalanobis D² statistics. The genotypes were grouped into seven clusters suggesting a considerable amount of genetic diversity in the material. The intra-cluster D² value ranged from 0.00 to 9.06 while, intercluster D² value ranged from 4.07 to 55.71. The maximum intra cluster distance was exhibited by cluster V followed by cluster II and cluster I. Cluster III had mono- genotype and emerged with contained highest cluster mean value grain yield per plot. Cluster II has the highest mean value for number of pods per plant and the lowest mean value for days to 50% flowering, days to maturity and plant height. Maximum contribution toward the total divergence was exhibited by 100-seed weight followed by number of pods per plant and minimum by days to maturity. Cluster IV and VI showing maximum inter cluster distance and crossing of genotypes Sabour chana-1 (BRC-1), GCP 105, PBC 503, DC 16-2, NBeG 776, RVSSG 42, G2016-43, GL 14042, IPC 2013-21, GNG 2338, GNG 2375 and KWR 108 from cluster VI suggested for improving grain yield per plot, 100-seed weight and earliness in flowering and ultimately enhancing the yield and chances of getting better recombinants in segregating generations.

Keywords: Chickpea, genetic diversity grain yield Mahalanobis D



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INTRODUCTION

Chickpea (*Cicer arietinum* L.), a member of *Fabaceae* family, is one of the most important *rabi* pulse crop in India contributing 20% to the pulse production in the world. Chickpea (*Cicer arietinum* L.) with a genome size of 732 Mbp is a self-pollinated, diploid (2n = 2x = 16) cool season pulse crop grown in more than 44 countries representing all the continents under eight geographically diverse agro-climatic conditions (Croser *et al.*, 2003). India is the largest chickpea producer accounting a share of about 67% in global chickpea production with about 8.39 m ha area, 7.06 m t production and 840 kg/ha productivity (Singh *et al.*, 2015). The area occupied under chickpea cultivation in Bihar is 59.37 thousand hectares with productivity of 986 kg/ha. This is only 4% of pulse production of the country. Particular reference to chickpea in Bihar, the area of chickpea has declined from 2.45 lakh in 1975-76 to 0.56 lakh hectares in 2010-11 although productivity has increased from 550 kg/ha to 1000 kg/ha during the same period. Highest productivity of 1430 kg/ha was recorded in Bihar state in 2012-2013.

Genetic crop improvement depends upon exploitation of traits diversity available in the gene pool by providing useful information in parents' selection and their further utilization through plant breeding approaches. Diversified germplasm is a source that may have genes of biotic and abiotic stress

resistance for future breeding programs. Recent plant breeding practices have narrowed genetic base of cultivated chickpea. However, characterization of newly developed genotypes for economic traits will assist in the development of superior cultivars (Naveed *et al.*, 2015). D² analysis which has been given by Mahalanobis (1936) is a very potent technique of measuring genetic divergence. Now it is reliably and extensively used in plants for measuring genetic divergence (Kuldeep *et al.*, 2015). The aim of forming clusters and finding the intra and inter cluster divergence is to provide the base for selecting parents for a planned breeding programme. The knowledge of genetic diversity has a significant impact on the improvement of crop plants and this information has been successfully used for efficient germplasm management, fingerprinting and genotype selection. In views of these facts, the current research was undertaken to assess the magnitude of genetic diversity and characters contributing to genetic diversity among chickpea genotypes.

MATERIALS AND METHODS

The experimental material consisted of forty chickpea genotypes were sown on 15th November 2017 at Pulses Research farm, Bhatti, Bihar Agricultural University, Sabour (Bhagalpur). Atmospheric temperature varied from 3.8 0°C minimum in January to 44.5 0°C maximum in May. The experiment was laid out in a randomized complete block design with three replications during Rabi 2017-18 under All India Coordinated Research Project on Chickpea. The plot size was 4.8 m², with 1 row of 4.0 m length. Inter-row spacing distance was kept 30 cm and plant to plant spacing was 30 x 10

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cm. The recommended packages of practices were followed to raise a healthy crop. Data were recorded on six quantitative traits viz. days to 50% flowering, days to maturity, plant height (cm), the total number of pods per plant, 100 seed weight (g), grain yield per plant (g) 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^2 statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method. 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 eight clusters as per

Table1: Distribution of forty chickpea genotypes in various clusters

| Cluster | No. of Genotypes | Name of Genotypes |
|---------|------------------|---|
| I | 10 | CSJ 907, BG 3075, RKG 13 -75, NBeG 738, KGD 99 -4, BDNG 2015 -16, DBGV 206, BGD 138, RVSSG 41, NBeG 776 |
| II | 16 | GJG 1403, GNG 2338, BG 3706, BRC -1, GCP 105, Phule G 0818, GL 13001, RKG 13 -380, AKG 1303, BAUG 108, GJG 1416, H 13 -36, RVSSG 42, H12 -63, PG177, PG 214 J |
| III | 1 | DC 16-2 |
| IV | 5 | GL 14042, GNG 2325, IPC 2013 -21, JG 2016 -44, CSJ 866 |
| V | 6 | PBC 503, G 2016 -43, RG 2011 -02, Phule G 0810, PBC 514, NDG 15 -6 |
| VI | 1 | IPC 2012-108 |
| VII | 1 | KWR 108 |

Tocher's method, with cluster II containing the maximum of 16 genotypes followed by 10 genotypes in cluster I, 6 genotypes in cluster V, 5 genotypes in cluster IV and mono-genotypes in cluster III, VI and VII. (Table 1 and Fig. 1). It means the overall genetic similarity was found in the germplasm 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 Lal *et al.* (2001), Raval and Dobariya (2004), Paramesharappa *et al.* (2011) and Parashi *et al.* (2013). The possible reason for grouping of genotypes of different places into one cluster could be a free exchange of germplasm among the breeder of a different region or unidirectional selection practiced by a breeder in tailoring the promising cultivar for selection of the different region.

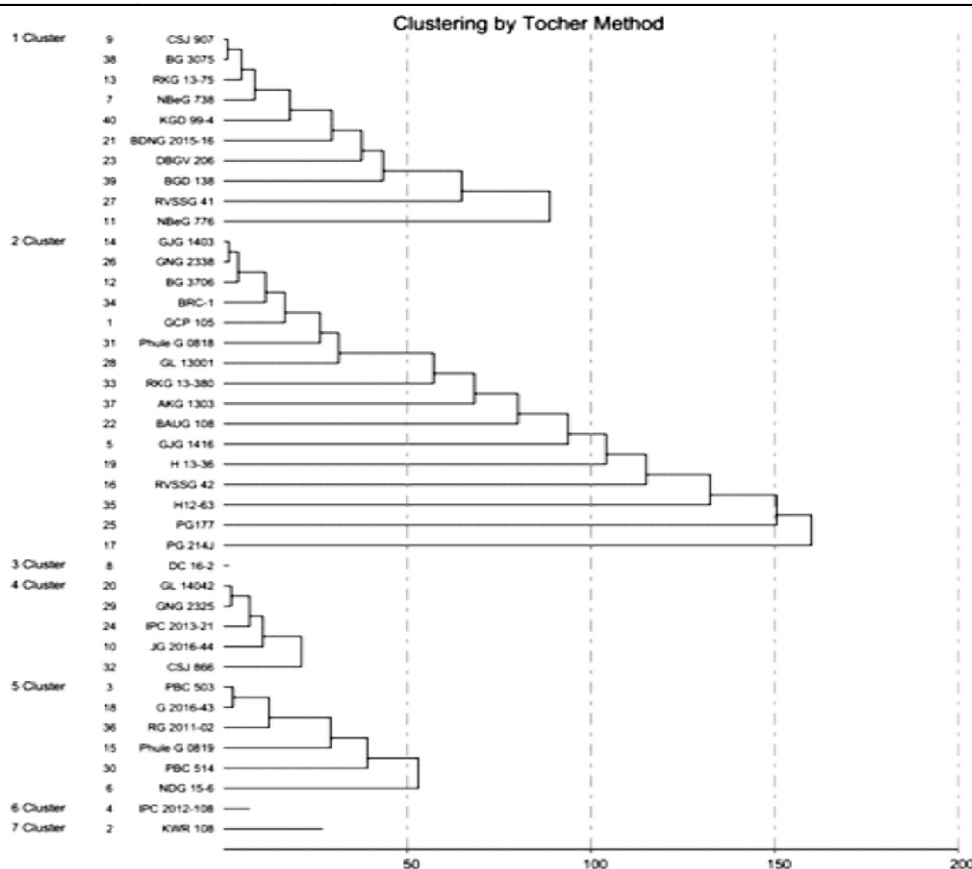


Fig.1: Cluster analysis dendrogram of forty chickpea genotypes

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

| Clusters | I | II | III | IV | V | VI | VII |
|----------|------|-------|-------|-------|-------|-------|-------|
| I | 6.58 | 24.52 | 10.02 | 17.01 | 21.72 | 18.11 | 38.71 |
| II | | 8.77 | 15.70 | 19.78 | 29.82 | 53.51 | 49.82 |
| III | | | 0.00 | 5.88 | 33.31 | 36.97 | 31.23 |
| IV | | | | 4.07 | 49.53 | 55.71 | 49.04 |
| V | | | | | 9.06 | 14.99 | 49.78 |
| VI | | | | | | 0.00 | 49.86 |
| VII | | | | | | | 0.00 |

The highest intra-cluster distance was exhibited by cluster V (9.08) followed by cluster II (8.77) and cluster I (Table 2) (6.58). The intra cluster distance was maximum in cluster V followed by cluster II which indicated that hybridization involving genotypes within the same clusters may result in cross combination. The highest inter-cluster distance was observed between cluster IV and VI (55.71), followed by cluster II and VI (55.51), cluster VI and VII (49.86) and cluster II and VII (49.82). 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. 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.

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 per plant | 100- seed weight (g) | Grain yield per plot (g) |
|---------|-----------------------|------------------|-------------------|-----------------------|----------------------|--------------------------|
| I | 74.13 | 134.90 | 64.06 | 73.23 | 27.91 | 862.97 |
| II | 73.04 | 134.15 | 66.48 | 137.62 | 23.00 | 989.15 |
| II | 76.33 | 135.33 | 77.26 | 84.33 | 22.57 | 1069.33 |
| IV | 73.67 | 134.40 | 64.09 | 81.00 | 18.02 | 1050.07 |
| V | 73.50 | 135.00 | 64.59 | 119.22 | 35.92 | 868.78 |
| VI | 75.80 | 135.33 | 66.22 | 65.67 | 38.94 | 876.67 |
| VII | 94.00 | 139.67 | 80.27 | 102.40 | 25.91 | 911.00 |

The genotypes of cluster III revealed highest mean values (Table 3) for grain yield per plot while cluster VI showed the highest mean value for 100 seed weight. Cluster II recorded highest mean value for number of pods per plant and the minimum mean value for days to 50% flowering and days to maturity and on the basis of mean values which could be utilized for hybridization programme for the development of high yielding genotypes. The highest mean value for plant height was exhibited by cluster VII and minimum by cluster I.

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

| Source | Times ranked | Contribution % |
|----------------------------|--------------|----------------|
| Days to 50% Flowering | 51 | 6.54 |
| Days to maturity | 4 | 0.51 |
| Plant height (cm) | 36 | 4.62 |
| Total number of pods/plant | 312 | 40.00 |
| 100 -seed weight (g) | 359 | 46.03 |
| Grain yield/ plant (g) | 18 | 2.31 |

Among the six traits studied, maximum contribution was made by 100 seed weight (46.03%) (Table 4 and Fig. 2), 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 Agrawal *et al.* (2018). Therefore, these characters may be given importance during hybridization programme.

CONCLUSION

Diverse germplasm lines possessing desirable characters which may be used in future breeding programme to get a maximum spectrum of variability for wide range of characters and for broadening the genetic base of cultivars and in order to go for programme of improving more than one economic characters. The criteria used for selection of genotype as parents for crop improvement program using D^2 analysis in the inter-cluster distance. Those genotypes with the maximum cluster distance are genetically more divergent. The hybridization programme involving genotypes IPC 2012-108, GL 14042, GNG 2325, IPC 2013-21, JG 2016-44 and CSJ 866 could be under-taken to isolate high yielding segregants since

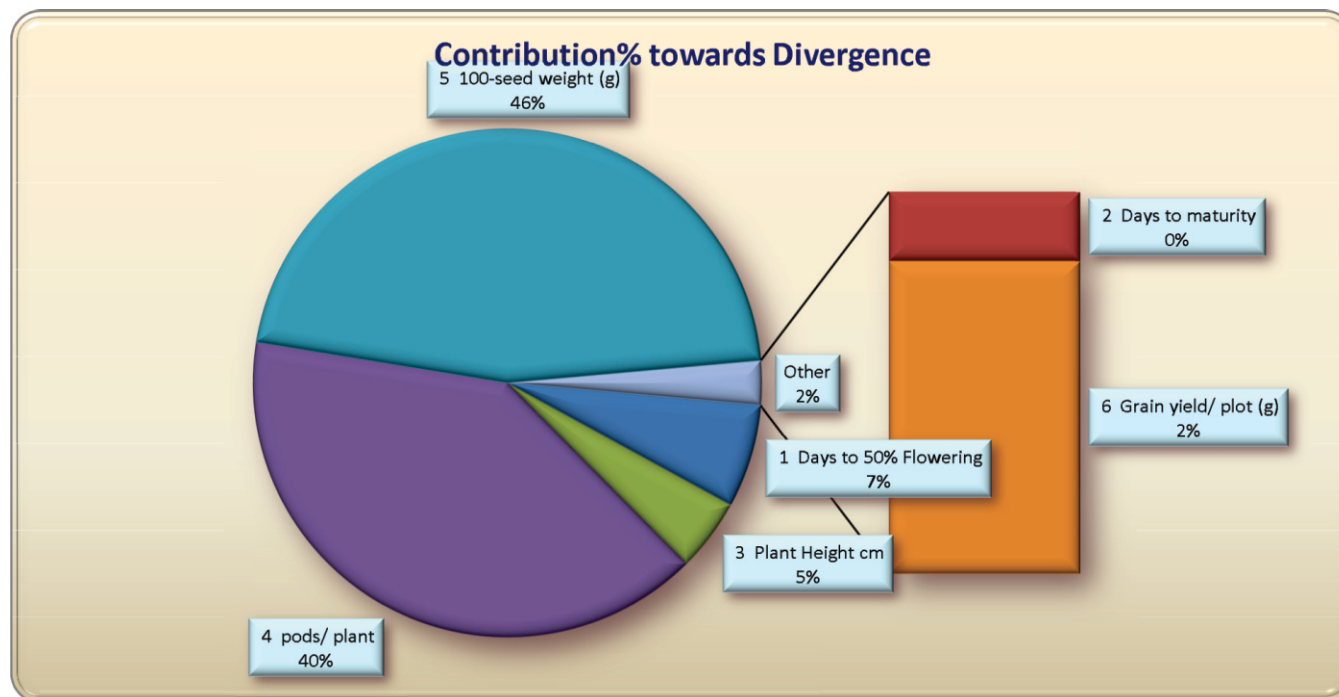


Fig. 2: Contribution of different characters towards genetic divergence of forty chickpea genotypes

these genotypes have high yielding potential, the more total number of pods per plant, high 100-seed weight and early maturity with more genetic distances. These parents could be selected for hybridization on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Therefore, progenies derived from

such diverse crosses are expected to show a wide spectrum of genetic variability and a greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants.

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