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An insight of Genetic Diversity Analysis in Advance Breeding Lines of Chickpea (*Cicer arietinum* L.)

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ABSTRACT: Assessment of genetic divergence and characterization of breeding lines helps plant breeders to select parents in their breeding programme to generate new variability and development of superior cultivars and different populations for various genetic studies of economically important traits. Research with thirty genotypes of chickpea carried out to study the magnitude and nature of genetic divergence using the Mahalanobis's D^2 statistics, with three replication in randomized complete block design. The data for fourteen important quantitative traits were recorded from the advance breeding lines of chickpea raised. The thirty chickpea genotypes were classified into five clusters. Cluster I was largest with twenty two genotypes followed by cluster II with five genotypes and remaining clusters (III, IV, and V) were monogenotypic. Three characters viz. days to maturity, no. of pods per plant, biological yield and hundred seed weight contributed maximum in manifestation of genetic diversity. The genotypes ICCV191618, JG 63-14407, JG2016-74315, JG 2021-1424 JG18-251097 and JG2016-36 were notified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea.

Keywords: Chickpea, Genetic diversity, Cluster, Divergence analysis.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a diploid crop plant ($2n = 2x = 16$) with an approximately 740 Mb haploid genome size (Varshney *et at.,* 2013). Southeastern Turkey and adjoining area of Syria and Ethiopia are the primary Vavilovian centers of origin and secondary center of diversity respectively. India, the largest chickpea-producing country, with a 75% share of global production (Gaur *et at.,* 2019) and it produced in 50 countries, of which Australia, Myanmar, Pakistan, Turkey, Canada, Ethiopia, India, Iran, Mexico, and the USA are the major producers (Dixit *et at.,* 2019). Among crucial food legumes crops, the chickpea ranked second from beans (*Phaseolus vulgaris* L.) in the area of yield and it holds third position as an important cultivated legume crop in the world after soybean and dry bean (Srivastava *et at.,* 2017). In terms of the pulse production across the world, chickpea contributes about 12% in which more than 70% production contributed by different countries of Asia continent. However, the highest percentage is noted for yield in India is 70% of total world yield (Aswathi *et at.,* 2019). It is a cheap and major source of protein for vegans. Furthermore, it is also rich source of minerals (magnesium, phosphorus, calcium, zinc and iron) unsaturated fatty acids, β-carotene and fiber which are considered good for health and well-being.

The principle and procedure of Mahalanobis's D^2-statistics (1936) helps has made possible to point-out genetically diverged parents which computes the degree of divergence and provides the idea about the relative contribution of each and every component traits towards the total divergence. The understanding and knowledge of genetic diversity has a significant impression on the crops improvement research. Evaluation of genetic diversity in breeding lines can facilitate identification of diverse heterotic group with possible breeding values in substantiation of breeding potential of breeding lines in breeding programme. Genetic distance plays a definite role for efficient choice of parents for hybridization programme (Saha *et at.,* 2018). More diverse the parents within the rational limits, the more the probability of obtaining heterotic broader spectrum of variability in the segregating populations. Modern agriculture production and plant breeding techniques narrowed and limited the base for the genetic diversity of chickpea. Therefore, the present investigation has been outlined to evaluate the genetic diversity among the chickpea breeding lines for important traits. Therefore, it's time to explore diversity and novel sources of variation that might be used in plant breeding programmes.

MATERIAL AND METHODS

The experimental material consisted 30 advance breeding lines of chickpea. The investigational research

was laid out with three replication in randomized complete block design (RCBD) during *rabi* seasons 2020-21 at Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV Jabalpur. Research plot was divided into 2 rows of 4.0 m length for each genotype. Intra and inter-row spacing was kept at 10.0 and 30.0 cm respectively and recommended agronomical practices were put into effect to grow sufficient plant population. Five plants are selected randomly from each plot among replication and labeled for observing the further quantitative parameters on yield and its contributing traits, like, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, days to maturity, plant height (cm), height of first fruiting node (cm), stem thickness (mm), total number of effective pods per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). The data recorded were subjected to D^2 statistics to unveil the genetic diversity among the breeding lines as suggested by Mahalanobis (1936). Grouping of breeding lines into different clusters was done as per the method suggested by Rao (1952). The statistical data were analyzed using INDOSTAT version 9.1 software programme.

RESULT AND DISCUSSION

Genetic diversity is the fundamental requirement of any of the breeding programme targeted at genetic amelioration of yield (Shafique *et at.*, 2016). The evaluation of genetic diversity is crucial not only for crop improvements but also structured management and conservation of germplasm resources. In present research of investigation, thirty advance breeding lines of chickpea were fall into five clusters based on divergence analysis were depicted in Table 1 and Fig1., cluster I was the largest amongst all the clusters having 22 advance breeding lines followed by cluster II contain 5 advance breeding lines, while cluster III (JG 2021-1424), cluster IV (JG18-251097) and cluster V (JG2016-36) was monogenotypic, each with a single advance breeding line. Therefore this result revealed that the advance breeding lines are independent and collected from different sections must be incorporate in the hybridization research programme. The maximum advance breeding lines grouped into cluster I pointed unidirectional selection for individual character or lines from almost similar geographical point of origin.

The genetic divergence percentage contributions through all the 14 quantifiable traits under research are described in Table 2 & Fig. 2. The percent involvement of individual traits in the direction of the total divergence was observed highest for total no of pods per plant (57.38%). However, traits like, days to maturity (17.70%), plant height (9.20%), hundred seed weight (14.02%), biological yield (14.02%), also contributed high percentage toward divergence after total no of pods per plant. Trait, total no of effective pods per plant contributed a 6.44 % in total divergence, these findings of divergence contribution with similar variation was also reported by Biswal and Babbar (2022); Tiwari and Babbar (2017); Gediya *et al.* (2018). For magnification of genetic gains, the diverse parents should be used in the crossing programme with different allele combination to get the transgressive segregants. Furthermore, for crop improvement programme, the availability of superior segregates rely on the divergence between the parents involves, as a consequences, for the selection of parent; it can be one of the key criteria in hybridization programme.

Cluster mean for various traits presented in the table3. Cluster V gives maximum value 66 days and cluster III revealed lowest value (58days) for days to 50 % flowering. A maximum day taken to maturity was found in cluster V (108 days), whereas minimum was found in cluster III (98.3days), similarly for pant height cluster I (60.9cm) showed highest and cluster IV (53.3cm) lowest values respectively. Highest and lowest height of first fruiting node was falling in cluster I (26.3cm) and cluster IV (18.9cm) respectively. Highest stem thickness value was observed in cluster V (3.2 mm) and lowest was found in both cluster II (2.9mm) and cluster III (2.9mm). For no of primary branches per plant highest value fall under cluster IV and lowest in cluster II, similarly highest and lowest value of no of secondary branches per plant was observed in cluster IV and III respectively. Maximum total no of pods per plant were observed under cluster II and minimum in cluster IV, similarly for no of effective pods per plant highest value were observed in cluster V and lowest were observed in cluster IV (59.9). While considering the no of seed per pod maximum value found in cluster III and lowest found in cluster V (1.2). Hundred seed weight were highest and lowest in cluster IV (43.2g) and cluster II (20.5g) respectively, similarly biological yield showed maximum value in cluster V (62.2g) and lowest in cluster I (40.02g) respectively. Harvest index revealed highest value in cluster III and lowest in cluster I (52.2%). Considering seed yield per plant highest value were observed in cluster V (36.8g) and lowest were observed in cluster I (20.6g). In the plant breeding basic requirement for any breeding objective is selection of suitable parents and off spring for further improvement program. So in the study the genotype (JG2016-36) of cluster V may be used for further crop improvement studies by more focusing on the traits *viz*, days to maturity, total no of pod per plant, 100seed weight and biological yield per plant. These similar results were in closed harmony with Vijaya Kumar *et al.* (2017); Aswathi *et al.* (2019); Biswal and Babbar (2022); Katkani *et al.* (2022). Therefore, this present research exemplify that there is an adequate possibility for obtaining genetic diversity which helps in the improvement of chickpea breeding plan.

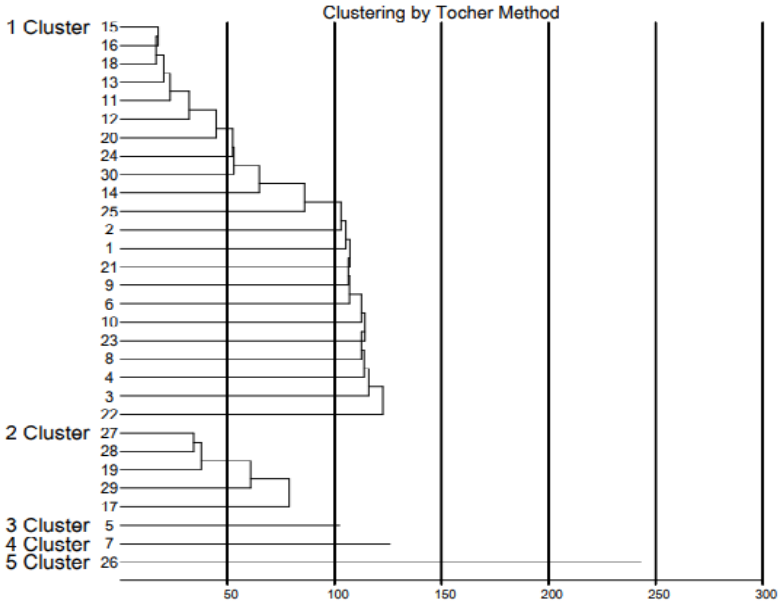

Fig. 1. Grouping of advance breeding lines into different clusters.

Table 1: Distribution of advance breeding lines of chickpea in different clusters.

Cluster	No. of genotypes	Name of Advance breeding lines
I	22	JG74315-14, JG 63-14407, JG 2022-23, JG 2022-26, JG14, JG 2021-1617, JG2022-75, JG16-4958, ICCV181109, ICCV181108, ICCV181603, ICCV191616,ICCV191604, ICCV181106, ICCV191618, ICCV191609, ICCCV191608, ICCCV191606, ICCV15104, JG2016-14-16-11, ICCV191608, NBeG-47
II	5	ICCV191618, JG 63-14407, JG2016-74315, JG36, JG24
III	1	JG 2021-1424
IV	1	JG18-251097
V	1	JG2016-36

Table 2: Contribution of quantitative traits towards clustering.

Source	Times Ranked 1st	Contribution (%)
Days to 50% flowering	10	2.3
Days to maturity	77	17.7
Plant height (cm)	40	9.2
Height of first fruiting node (cm)	14	3.2
Stem thickness (mm)	2	0.46
Number of primary branches per plant	10	2.3
Number of secondary branches per plant	8	1.8
Total number of pods per plant	97	22.3
Number of effective pods per plant	28	6.4
Number of seeds per pod	1	0.23
100 seed weight (g)	61	14
Biological yield (g)	61	14
Harvest index (%)	10	2.3
Seed yield per plant (g)	16	3.6

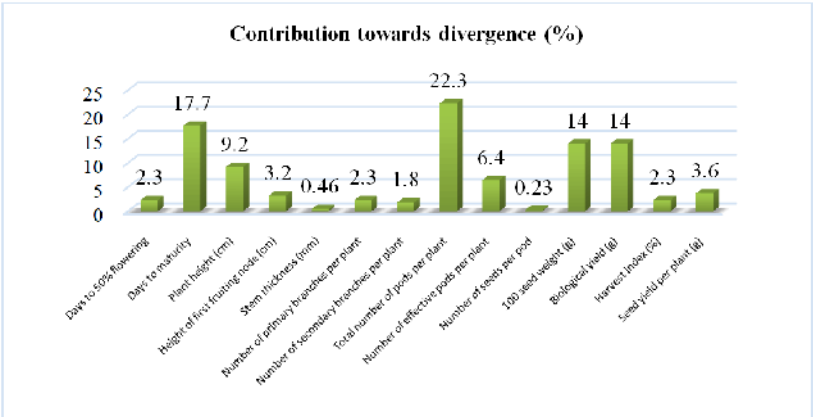

Fig. 2. Contribution of fourteen quantitative traits towards clustering.

Table 3: Cluster mean for seed yield and its attributing traits: - Torchers method.

Cluster	DTF	DM	PH	HFFN	ST	NPBPP	NSBPP	TNPP	NEPPP	NSPP	HSW	BY	HI	SYPP
I	61	107	60.9	26.3	3.1	3.1	19.66	74.2	63.5	1.2	25.2	40.0	52.2	20.6
II	58	102	53.4	20.2	2.9	2.86	21.46	104.7	96.2	1.3	20.5	45.0	53.4	23.9
III	56	98	56.1	21.9	2.9	3.13	19.05	82.3	66.8	1.5	33.8	56.7	63.2	35.8
IV	59	106	53.3	18.9	3.1	3.38	26.05	64.1	59.9	1.3	43.2	50.5	53.6	26.8
V	66	108	59.2	25.0	3.2	2.79	19.07	145.4	130.8	1.2	34.8	62.2	59.0	36.8

Where, DTF: days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number of primary branches per plant, NSBPP: Number of secondary branches per plant, TNPPP: Total number of pods per plant, HFFN (cm): Height of first fruiting node, ST (mm): Stem thickness, NEPPP: Number of effective pods per plant, NSPP: Number of seeds per pod, HSW (g): 100 Seed weight, BY (g): Biological yield per plant, HI (%): Harvest index, SYPP (g): Seed yield per plant.

Table 4: Intra and Inter cluster distance.

Cluster	I	II	III	IV	V
I	**10.23**	13.60	14.38	15.02	22.08
II		**8.86**	14.92	18.47	17.25
III			**0.00**	11.22	18.51
IV				**0.00**	20.59
V					**0.00**

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Conflict of interest. None.

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