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Computation of Genetic Variability and Divergence Analysis in Advance Breeding Lines of Chickpea

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ABSTRACT: The information related to genetic variability and diversity is most important for breeding programme. Presence of genetic divergence amid the parents is an essential criteria to expand the probabilities of selecting better genotypes for several traits. If highly diverse parents are available, the chances of enhancing individual trait also increased. The existing research was envisioned to know the amount of genetic variability and diversity amongst genotypes of *desi* chickpea (*Cicer arietinum* L.) and to categorize highly divergent parents for various upcoming hybridization programmes. Genetic variability and diversity amongst the parentages is crucial to increase the chances of selection for superior segregates related to several yield attributing traits. The high value of GCV%, high heritability coupled with genetic advance as percentage of mean was recorded for 100 seed weight. Forty two *desi* chickpea lines were composed into 9 clusters based on divergence analysis. Cluster I was the biggest amongst all the clusters having 18 genotypes followed by cluster II contain 11 genotypes and cluster III had 7 genotypes. Cluster IV to Cluster IX, each with a single genotype. The maximum genotypes grouped into cluster I indicated unidirectional selection for individual character. On the basis of intra and inter cluster distance, the advance breeding lines namely, JG 74 × ICC 4958-2, JG 23 × ICC 251741, JG 74 × ICC 4958-1, JG 11 × JG 14, ICC 181109 and JG 24 were identified as promising lines and might be used as a parent in chickpea improvement programme.

Keywords: Genetic diversity, variability, cluster, hybridization programme and divergence analysis.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a major food legume crop mainly grown in continents of tropical and subtropical (Fikre and Bekele, 2019). It is third significant legume of South Asia in the wide-reaching just after common bean and field peas. The nutritional property of chickpea is higher as compared to pigeonpea in relative to the anti-nutritional aspects and digestibility. In chickpea protein is available in simplest form therefore it is at par to mungbean and urdbean. It is predominantly grown-up in rainfed agronomical conditions with available residual soil moisture, so the produce profoundly agonizes due to water and high temperature stress in Central and Peninsular India. In India chickpea was cultivated in an area of 9.93 mha with a production of 10.8 mt (Agricultural Statistics at a Glance, 2020).

Extent of genetic variability amongst the advance lines is the key to accomplishment of any breeding podium. The information related to genetic divergence of advance breeding lines is advantageous tool in management of several gene banks as well as breeding experimentations. Genetic diversity amongst the parentages is highly essential to increase the chances of selection for superior segregates related to several yield attributing traits. The percentage for enlightening desirable character is high when the parents are more diverse in origin. Genotypes from distinctive geographical sections are frequently included in hybridization programme.

MATERIAL AND METHOD

The experimental material for the existing study consists 42 advance breeding lines of chickpea. The investigational research was laid out in randomized block design (RCBD) with three replications during two *rabi* seasons 2020-21 and 2021-22 at Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV Jabalpur. Each research plot having of 2 rows of 4.0 m length. Inter and intra-row spacing was kept at 30.0 and 10.0 cm respectively. Prescribed agronomical practices were implemented to grow sufficient plant population. Ten modest evocative plants are carefully chosen at random from each and every plot among replication and labelled for recording the further quantitative observations on yield and its contributing traits, like, days to 50% flowering, days to maturity, plant height (cm), height of first fruiting node (cm), number of primary branches per plant, number of secondary branches per plant, 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). Pooled statistical analysis was done by using Window-Stat 9.1 software. Genetic diversity was studied using Mahalanobis's D^2 (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The statistical method which divides the total variation into various components and delivers base for the test of significance. The analysis of variance indicated that extremely significant alterations were reported among the genotypes for all the studied characters (Table 1 and Fig. 2). Among forty two genotypes, the genotype ICCV 15104 mature earliest (107 days),while ICC 191609 (120 days) taken maximum days to mature. The highest total number of pods per plant & number of effective pods per plant was recorded by JG 36 (109.4 & 103.6, respectively), while the genotype ICCV 15118 (43.6 & 38.3, respectively) having lowest total and effective pods per plant.

The advance breeding line namely JG 2016- 9651 recorded smallest seed (14.7 g) and lowest harvest index (38.6%), whereas the genotype ICCV 15118 had largest seed size (35.2 g).Maximum harvest index was noted by JG 63 × ICC 1205 (60.0 %). The uppermost seed yield per plant was gained by, ICC 191606 (26.5 g) and lowermost yield per plant was observed in JG 63 × ICC 4958 (14.0 g) under timely planting condition. The execution of any of breeding strategy significantly depends on the range of genetic variation existing in the population and the assortment to which the suitable traits are heritable. The genetic variability is the percentage for deviation covered in a population and an outcome of different additive and non-additive gene effects.

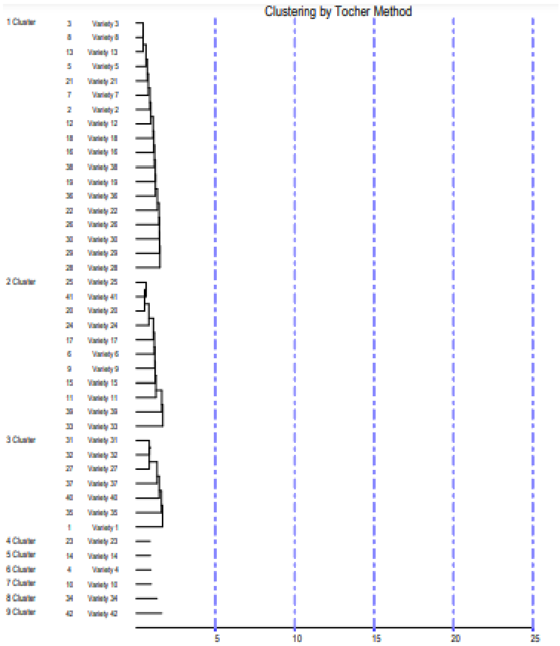

Fig. 1. Distribution of chickpea genotypes in various clusters in pooled analysis.

Table 1: Genetic parameters of variability for yield and its attributing traits.

Character	Range			GCV (%)	PCV (%)	h^2 (bs) %	GA as % of mean
	Min.	Max.	Av.				
DTF	59.67	72.16	66.09	4.9	6.4	40.1	7.9
DM	107.33	120.0	113.69	2.5	3.2	61.8	3.9
PH	49.90	73.48	58.99	8.4	11.8	50.3	12.2
NPBPP	2.42	3.78	2.90	9.6	18.1	65.2	18.3
NSBPP	12.62	19.16	15.84	8.41	17.4	47.3	16.4
TNPPP	43.68	109.46	69.34	23.80	32.4	53.8	35.9
HFFN	16.54	27.52	22.21	12.70	18.6	46.4	17.8
ST	2.40	3.77	3.07	6.46	12.0	39.4	12.6
NEPPP	38.83	103.64	64.23	25.59	34.6	78.8	38.9
NSPP	1.94	3.44	2.39	10.81	15.3	49.9	21.4
100 SW	14.74	35.24	23.83	21.71	22.6	91.7	42.8
BY	29.05	56.58	39.40	13.53	24.2	71.3	24.9
HI	38.59	60.04	49.04	6.84	16.8	78.6	30.9
SYPP	14.07	26.57	19.01	14.10	22.7	82.4	22.8

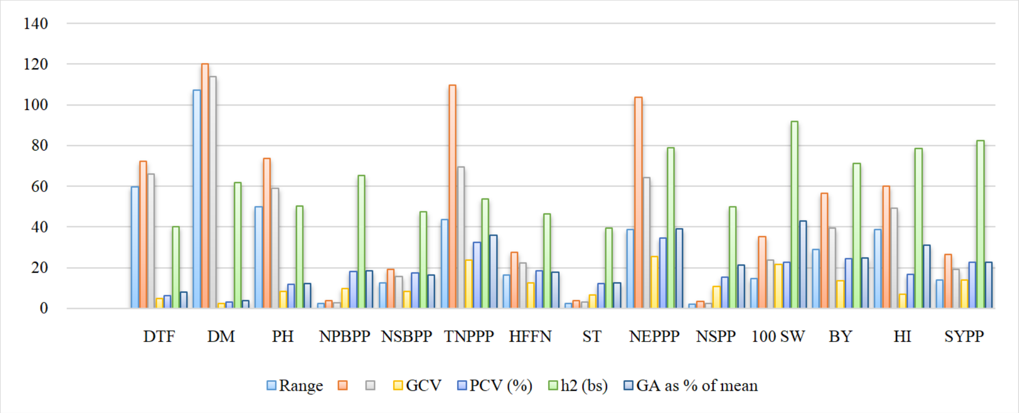

Fig. 2. Genetic parameters of variability for yield and its attributing traits.

The values of phenotypic coefficient was observed higher as compared to genotypic coefficient under timely planting condition. The maximum amount of genotypic coefficient of variation was observed for the trait number of effective pods per plant (25.5%) followed by total number of pods per plant (23.8%) and 100 seed weight (21.7%). Similar results are accordance with the findings of Kumar *et al.* (2018) for 100 seed weight, Jida*et al.* (2019) for total number of pods per plant, Kumar *et al.* (2020) for number of effective pods per plant and total number of pods perplant, Ram *et al.* (2021) for100 seed weight and Xalxo *et al.* (2021) for number of effective pods per plant &100 seed weight.

The high extent of heritability was detected in 100 seed weight (91.7%) followed by seed yield per plant (82.4%), number of effective pods per plant (78.8%), harvest index (78.6%) and biological yield per plant (71.3%). High genetic advance as percentage of mean was recorded for 100 seed weight (42.8%) followed by number of effective pods per plant (38.9%), total number of pods per plant (35.9%), harvest index (30.9%), biological yield per plant (24.9%), seed yield per plant (22.8%) and number of seeds per pod (21.4%) on the basis of pooled analysis. High heritability along-with high genetic advance as percentage of mean was presented by100 seed weight, seed yield per plant, number of effective pods per plant, harvest index and biological yield per plant. The outcomes in line with the earlier results of Hussain *et al.* (2017) for harvest index, biological yield per plant, number of effective pods per plant, 100 seed weight and total number of pods per plant, Honappa *et al.* (2018) for biological yield per plant, number of seeds per pod, seed yield per plant and 100 seed weight, Tsehaye *et al.* (2020) for seed yield per plant and number of pods per plant, Gautam *et al.* (2021) for100 seed weight, seed yield per plant, and biological yield per plant, Ram *et al.* (2021) for 100 seed weight, number of effective pods per plant and biological yield per plant and Xalxo *et al.* (2021) for 100 seed weight.

The high value of GCV% and high heritability coupled with genetic advance as percentage of mean was documented for 100 seed weight, whereas high GCV% and genetic advance as percentage of mean was noted for effective pods per plant, total number of pods per plant and 100 seed weight. These outcomes displayed that sufficient variations are obtainable for these traits in the material under study which conceals massive opportunity of chickpea improvement for these traits. These above revealed traits can be incorporated in selection criteria for concurrently improving the seed yield per plant in advance breeding lines of chickpea.

Forty two *desi* chickpea advance breeding lines were composed into 9 Clusters based on pooled divergence analysis. Disseminations of genotypes into dissimilar clusters were depicted in Table 2 and Fig 1. Cluster I was the biggest amongst all the clusters having 18 genotypes followed by Cluster II contain 11 genotypes and Cluster III had 7 genotypes. Cluster IV to Cluster IX, each with a single genotype. Therefore this investigation gives information that the genotypes are independent and collected from different sections must be incorporate in hybridization programme. The maximum genotypes grouped into Cluster I indicated unidirectional selection for individual character or them from similar geographical origin accumulated in one cluster.

The intra and inter cluster D^2 average values are depicted in Table 3. On the basis of D^2 values, 42 genotypes of chickpea were classified into nine Clusters. Intra cluster distance wide ranging from 0.00 to 4.77. Cluster III displayed highest intra Cluster D^2 value (D^2 = 4.77) followed by Cluster II (D^2 = 4.01) and Cluster I (D^2 = 3.64) ,whereas six clusters like, Cluster IV, V, VI,VII,VIII and IX had one genotype in each cluster, these revealed zero value for Intra cluster distance. These monogenotypic masses representing minimum diversity in the present study. The uppermost inter cluster divergence distance was detected between genotypes of Cluster II and Cluster IX (31.76) followed by Cluster IV & IX (25.72) , Cluster V and Cluster IX

(21.73), Cluster II & III (21.49), Cluster VI and Cluster IX (15.87), Cluster I and Cluster IX (15.35), Cluster VII and Cluster IX (14.43), Cluster III & V (14.34), Cluster II and Cluster VII (13.68), Cluster II and Custer VIII (12.70), Cluster III and Cluster IV (12.30), Custer VII and Cluster IX (12.07), Cluster III and Cluster VI (11.27), Cluster V and Cluster VIII (10.56) and Cluster VII and Cluster VIII (10.40),while the lowest distance was recorded between Cluster V and Cluster VI (3.89) followed by Cluster I & Cluster VI (4.54) and Cluster VI and Cluster VII (4.64). The cluster IX revealed the highest inter cluster distance with further clusters and therefore should be utilized in crossing programme. The outcomes specify that remarkable possibilities were available for incorporation of allelic resources existing in these accessions by using a sound & systematic breeding methodology to improve high yielding quality recombination's.

The cluster mean for various studied traits in pooled analysis are existing in (Table 3). Cluster VIII (69. days) revealed highest mean and Cluster VII was found earliest with cluster mean of 59. days for days to 50% flowering. Days to maturity, Cluster IX taken maximum days with mean of 118 days and Cluster IV mature earliest in 109 days. For plant height the tallest and shortest cluster is Cluster IX (68.7 cm) and Cluster VII (51.2 cm). Maximum number of primary branches per plant were recorded in Cluster VI (3.78) and highest secondary branches per plant was documented in Cluster IX (17.29), whereas lowest number of primary &secondary branches per plant were noted in Cluster IV (2.47, 13.41 respectively). The maximum total number of pods and effective pods per plant were found in Cluster IX with mean value of 98.92 and 95.72 respectively, whereas lowest was documented in Cluster IV with average of 51.24, 40.84respectively. Height of first fruiting node (26.84 cm) was found uppermost in Cluster VI and lowermost in Cluster VII (18.22 cm). Utmost stem thickness (3.31 mm) and lowest biological yield per plant (35.79 g) were noted in Cluster VI, minimum stem thickness (2.92 mm) is found in Cluster II while highest biological yield per plant (50.14 g) were noted in Cluster VII. Uppermost number of seeds per pod was counted in Cluster V having mean value of 3.45 and lowermost was found in Cluster III with 2.20mean. Cluster IX had maximum 100 seed weight (34.07 g), whereas minimum was documented in Cluster II (17.21 g). Harvest index was highest in cluster IX with mean value of 55.44% and minimum in cluster VII (46.20%). Maximum seed yield per plant was present in Cluster VII (23.18 g), while minimum was recorded in Cluster VI with 16.59 g mean value. These findings approved in earlier research of Dhuria and Babbar (2016); Tiwari and Babbar (2017); Thakur *et al.* (2018); Gediya *et al.* (2018); Johnson *et al.* (2019); Ponnuru *et al.* (2019); Janghel (2020); Dar *et al.* (2020); Boparai *et al.* (2021); Biswal *et al.* (2022).

The percentage assistances to genetic divergence through all the 14 quantifiable traits on pooled analysis under investigation are described in Table 5 & Fig. 3. The percent involvement of individual traits in the direction of the total divergence was documented highest for 100 seed weight (57.38%). The traits like, days to 50% flowering (9.87%), days to maturity (6.16%), total number of pods per plant (5.11%), number of seeds per pod (4.88%), number of primary branches per plant (3.14%), plant height (2.79%), number of effective pods per plant (2.67%), harvest index (2.21%), height of first fruiting node (1.74%), Seed yield per plant (1.63%) and biological yield (1.16%) have low percent of contribution These conclusions were comparable with the findings of Jayalakshmi *et al.* (2014); Tiwari and Babbar (2017); Gediya *et al.* (2018).

The fallouts evidently informed that cluster means of diverse clusters recognize the traits to be preferred for crossing on pooled analysis. The yield attributing traits werefluctuatewith respect of their involvement in the genetic divergence. Generally appearance of these traits varies due to environmental effect on the genotypes considered, besides the nature of material taken under examination (Rssool and Dar, 2014). Selection which is based on amount of genetic diversity has been effectively implemented in pulses and highly utilized in scheduling various hybridization programme. Crossing amongst genotypes having divers in origin assistances in conveying new gene pool in the population and getting higher the range of adaptation (Sandhu *et al.,* 2006). In case cluster IX might be useful as a positive donor parent for improving yield and may be stable by continual selection to obtain transgressive segregants in advance generations. On the basis of pooled analysis, It is determined that viz,100 seed weight, days to maturity, total number of pods per plant, number of seeds per pod, number of effective pods per plant and harvest index were taken in formulating selection criteria.

Table 2: Distribution of chickpea genotypes in various clusters.

Cluster No.	No. of genotypes	Name of genotypes
I	18	JG 12 × JG 16-1, PG 205, JG 26 × ICC 251741, JG 63 × ICC 4958, JG 2016- 74315, JG 12 × JG 16-3, ICC 96029 × JG 315, JG 12 × ICC 4958, JG 16 × JG 17, JG 2018- 53,JG 16 × ICC 4958, ICCV 15115, ICC 181612,ICC 15104, ICC 191604, ICC 191618, ICC 191609, ICC 191608
II	11	JG 12 × ICC 06301, JG 36, JG 12 × JG 14, JG 63 × ICC 1205, JG 74 × JG 11551, JG 2016 × 614, JG 2018-51, JG 2016- 9651, JG 2016-14-16-11, JG 2019-12-14, ICC 181667
III	7	ICC 191618, ICC 181108-1, ICC 191606, ICC 181106, ICCV 181108-2, ICC 181603, ICCV 15118
IV	1	JG 74 × ICC 4958-2
V	1	JG 23 × ICC 251741
VI	1	JG 74 × ICC 4958-1
VII	1	JG 11 X JG 14
VIII	1	ICC 181109
IX	1	JG 24

Table 3: Inter and intra cluster divergence values for different clusters.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**3.64**	8.59	8.38	4.99	6.18	4.54	5.39	5.28	15.35
II		**4.01**	21.49	8.83	8.98	7.77	13.68	12.70	31.76
III			**4.77**	12.30	14.34	11.27	7.18	7.59	7.23
IV				**0.00**	6.79	7.13	6.42	6.74	25.42
V					**0.00**	3.89	6.48	10.56	21.73
VI						**0.00**	4.64	9.36	15.87
VII							**0.00**	10.40	12.07
VIII								**0.00**	14.43
IX									**0.00**

Table 4: Cluster mean for seed yield and its attributing traits: Torcher method.

Cluster	DTF	DM	PH	NPBPP	NSBPP	TNPPP	HFFN	ST	NEPPP	NSPP	100SW	BY	HI	SYPP
I	65	113	58.8	2.82	15.66	59.	21.6	3.06	55.3	2.39	24.49	36.43	48.37	17.39
II	66	113.	55.5	2.84	16.94	84.	21.2	2.92	78.9	2.43	17.21	39.26	48.23	18.80
III	69.00	115.60	63.08	3.02	14.95	69.	25.1	3.25	64.4	2.20	30.91	46.88	51.09	23.01
IV	62.17	109.00	55.93	2.47	13.41	51.24	18.44	3.17	40.8	2.28	23.10	38.93	50.31	18.59
V	60.17	111.67	57.71	2.99	14.17	56.50	19.79	3.19	53.8	3.45	21.59	38.13	54.44	19.87
VI	62.50	113.33	58.22	3.78	16.56	63.19	26.84	3.31	56.85	2.56	22.55	35.79	46.23	16.59
VII	59.67	110.33	51.28	3.29	17.56	70.64	18.22	3.26	62.24	2.53	28.59	50.14	46.20	23.18
VIII	69.83	111.50	73.49	2.73	13.77	73.86	23.74	3.23	72.86	2.25	24.93	36.59	48.41	17.70
IX	66.17	118.33	68.72	3.37	17.29	98.92	26.26	3.11	95.72	2.31	34.07	39.53	55.44	21.87

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

Table 5: Contribution of different traits towards clustering.

Sr.No.	Traits	Times ranked Ist	Contribution towards divergence (%)
1.	Days to 50% flowering	85	9.87
2.	Days to maturity	53	6.16
3.	Plant height cm	24	2.79
4.	Number of primary branches per plant	27	3.14
5.	Number of secondary branches per plant	3	0.35
6.	Total number of pods per plant	44	5.11
7.	Height of first fruiting node cm	15	1.74
8.	Stem thickness cm	8	0.93
9.	Number of effective pods per plant	23	2.67
10.	Number of seeds per pod	42	4.88
11.	100 seed weight g	494	57.38
12.	Biological yield g	10	1.16
13.	Harvest index%	19	2.21
14.	Seed yield per plant	14	1.63

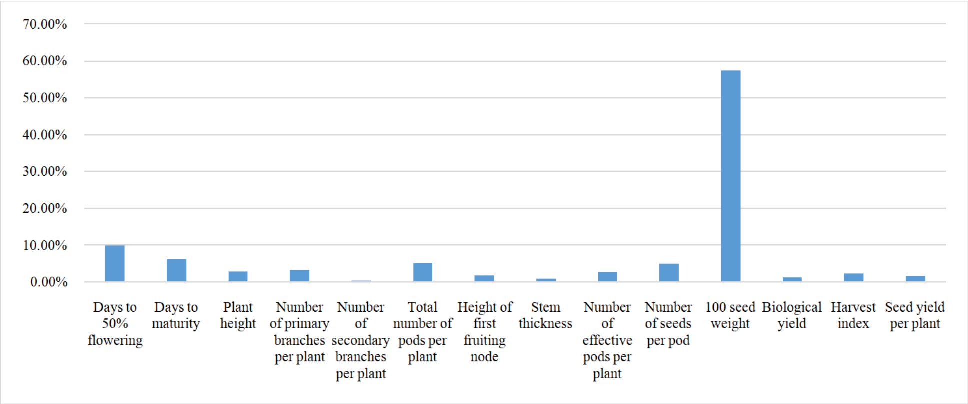

Fig. 3. Contribution of different traits towards clustering.

CONCLUSION

The high value of GCV%, high heritability coupled with genetic advance as percentage of mean was recorded for 100 seed weight. These above revealed traits can be incorporated in selection criteria for concurrently improving the seed yield per plant in advance breeding lines of chickpea. The information related to genetic divergence of advance breeding lines is advantageous tool in management of several gene banks, germplasm tagging, elimination or/and documentation of adulteration in the genetic stock and establishing of core collections. Genetic diversity amongst the parentages is highly essential to increase the chances of selection for superior segregates related to several yield attributing traits. The current research work was conducted to estimate the availability of genetic diversity amongst advance breeding lines of chickpea and to categorize distinct divergent parents aimed at future crossing/hybridization programmes for seed yield enhancement.

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Conflict of Interest. None.

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