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Cataloguing for Diverse Advance Breeding Lines of *Desi* Chickpea (*Cicer arietinum* L.) for Phenological and Yield Attributing Traits

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ABSTRACT: Generally plant breeder, select the parents on the basis of phenotypic divergence, however, for effectual breeding programme; the proficiency in genetic divergence among parents with reference to the phenological and quantitative traits which are to be improved is indispensable. The present experiment was carried out at breeding farm of JNKVV, Jabalpur, Madhya Pradesh during *Rabi* cropping seasons of timely sown during both 2019-20 and 2020-21 Genetic divergence by using Mahalanobis D^2 statistics was studied in 30 *Desi* chickpea lines including 3 checks for yield and yield contributing traits Under study, the genotypes fall into ten clusters based on D^2 analysis. The cluster I and V were largest with the large number of genotypes *i.e.* 16 and 6 respectively, whereas, rest of clusters had one genotype each. Maximum intra cluster distance was observed in cluster V (D^2 = 7.29) followed by cluster I (D^2 = 6.43). The maximum inter-cluster distance was observed in between cluster IV and IX (D^2 = 13.27) followed by cluster II and cluster IX (D^2 = 12.36), whereas, cluster V and VIII with minimum distance (D^2 = 9.00). On the basis of intra and inter cluster distance, genotypes namely; BRC 302, JG 14, Phule G 1018-9-6, JG12 × JG 16-3, DC16-116, JG63 × ICC4958 and JG74 × ICCV4958 were identified as superior genotypes and could be adopted as parents in further precise breeding programme of chickpea.

Keywords: *Desi* chickpea, Mahalanobis D^2 statistics, Genetic divergence.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a major food crop, especially in tropical and subtropical climates (Fikre and Bekele 2019) and third most important pulse crop in the world next to *Phaseolus vulgaris* and *Pisum sativum*. In India, over 67 per cent of the world's chickpea crop is produced (Joshi *et al*. 2006). Genetic variability is important indices for plant breeders because it provides a source of variation as well as raw material for yield enhancement (Gaur *et al.* 2020; Verma *et al.* 2018). The magnitude of genetic variability present in breeding material has a significant impact on the amount of progress that has been made in crop improvement as a result of selection (Gautam *et al.* 2021) Genetic divergence helps in selection of parents to develop superior recombinants and understanding the pattern of variation for different traits. For any crop improvement programme, the availability of superior segregates depends upon the divergence between the parents involves, hence, for selection of parent, it can be one of the most important criteria for in hybridization programme. The procedure of Mahalanobis's D^2-statistics helps has made possible to identify genetically diverged parents which measures the degree of divergence and provides the conclusive idea about the relative proportion of each component traits towards total divergence. Therefore, the present investigation was implemented to scrutinize the genetic diversity in *desi* chickpea genotypes in order to select the promising parents for hybridization programme.

MATERIAL AND METHODS

The experimental materials consisted of 30 genotypes of *desi* chickpea collected from AICRP on chickpea Department of Plant breeding and Genetics, JNKVV, Jabalpur, Madhya Pradesh and ICRISAT, Patancheru, Hyderabad. These were evaluated in randomized complete block design with three replications at Research cum breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Jabalpur, Madhya Pradesh during *rabi* season of timely sown during both 2019-20 and 2020-21. The rows/ plot were 2 and the row length was 4.0m with maintained spacing between rows was 30 cm. The recommended package of practices was followed throughout the period of crop growth. Five competitive plants were taken into consideration for observation for each genotype per replication and mean value per plant was obtained. Mahalanobis (1928) D^2

statistical analysis was used for Pooled data of *rabi* 2019-20 and 2020-21 for assessing genetic divergence among 30 *desi* chickpea genotypes and genotypes were grouped into different clusters according to Torcher's method as described by Rao, (1952).

RESULTS AND DISCUSSION

In the present study, 30 genotypes of *desi* chickpea lines were subjected to Mahalanobis D^2 statistical analysis for four phonological traits *viz.*, days to flower initiation, days to 50 % flowering, days to pod initiation, days to maturity and rest of ten quantitative traits (Table 1 and Fig. 1). Based on D^2 analysis, ten clusters were formed, which indicated the existence of ample genetic diversity in the present experimental material i.e. in all the genotypes. The cluster I and V were larger consisted of sixteen and six genotypes respectively, whereas, rest of clusters had one genotype each (Table 1). Hence, from this cluster analysis, it depicted that genotypes were independent of their genetic origin irrespective collection of different region. Therefore, the genotypes in the present study are worthy for adequate selection and hybridization programme.

Table 1: Grouping of *Desi* Chickpea Genotypes in Different Clusters using D^2 Statistics in Pooled Analysis.

Clusters	Number of genotypes included	Genotypes
I	16	ICCV 15118, GJG 1503, BG 3091, RKG17-04, NOG 15-5, BG 3092,RVSSG-60, RKG 13-205, BRC 305, JSC 55, JG2017-49, JG12 JG 16-1, ICC 96029 × JG315, IPC 2010-14, PG 187, JG24
II	1	BRC 302
III	1	JG 14
IV	1	Phule G 1018-9-6
V	6	GNG 2367, RG 2011-04, GL 14015, PG 205, JG 11 × JG 14, JG 36
VI	1	JG12 × JG 16-3
VII	1	DC16-116
VIII	1	JG63 × ICC4958
IX	1	JG74 × ICCV4958
X	1	JG 2016-1614

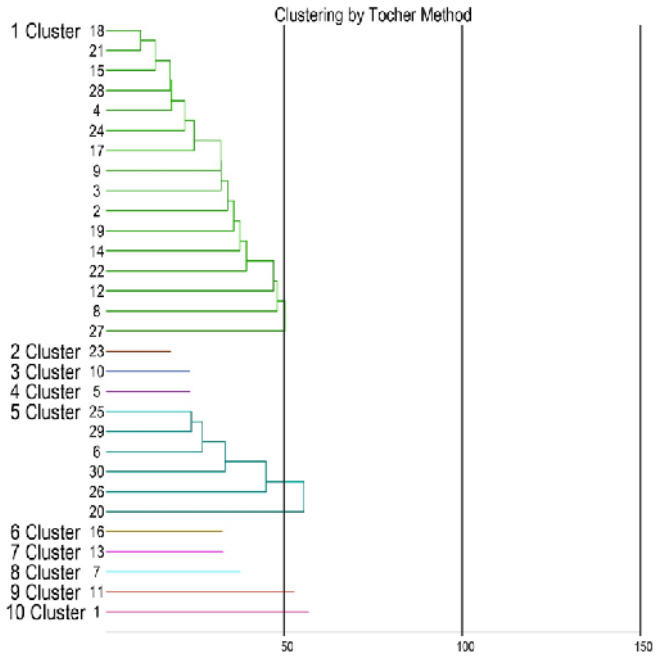

Fig. 1. Distribution of Chickpea Genotypes in Different Clusters in Pooled Analysis.

The maximum inter-cluster distance was observed in between cluster IV and IX (13.27) followed by cluster II and cluster IX (12.36), cluster IV and cluster VI (12.34), cluster VIII and cluster IX (12.12), cluster II and cluster VI (11.68), cluster VI and cluster IX (11.93), cluster VI and cluster X (11.44), cluster VIII and cluster X (11.43), cluster III and cluster X (11.26), cluster V and cluster IX (11.24), cluster VII and cluster X (11.05), cluster IV and cluster VII (10.96), cluster II and cluster X (10.61), cluster VII and cluster IX

(10.60), cluster III and cluster IV (10.34), cluster III and cluster V (10.22), cluster IX and cluster X (9.95), cluster II and cluster III (9.83), cluster V and cluster X (9.71), cluster I and cluster X (9.57), cluster IV and cluster X (9.50), cluster III and cluster VIII (9.47), cluster VI and cluster VII (9.42), cluster IV and cluster V (9.11), whereas, cluster V and cluster VIII (9.00) with minimum distance. This suggested that, getting higher frequency of desirable segregates or better combination from parents included from these clusters for development of promising varieties in hybridization programme. The maximum intra-cluster distance was observed in cluster V (7.29) followed by cluster I (6.43), whereas, the remaining clusters revealed zero value for Intra cluster distance (Table 2). This suggested that, cluster V and I were polygenotypic with higher diversity and rest 8 clusters with zero intra cluster distance were monogenotypic indicating minimal diversity in the present study.

Table 2: Inter and Intra Cluster distances in Pooled Analysis.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**6.43**	8.29	8.13	8.98	8.02	8.34	8.23	8.36	8.82	9.57
II		**0.00**	9.83	4.86	8.65	11.68	8.81	8.76	12.36	10.61
III			**0.00**	10.34	10.22	5.72	11.05	9.47	12.08	11.26
IV				**0.00**	9.11	12.34	10.96	7.95	13.27	9.50
V					**7.29**	9.66	8.52	9.00	11.24	9.71
VI						**0.00**	9.42	10.01	11.93	11.44
VII							**0.00**	11.34	10.60	11.05
VIII								**0.00**	12.12	11.43
IX									**0.00**	9.95
X										**0.00**

The mean values for seed yield and yield attributing traits were compared across the clusters and are depicted in Table 3 and 4. Cluster mean for days to flower initiation was found high in cluster VII (55 days), while, it was lowest for cluster X (47 days). Cluster mean for days to 50% flowering was maximum in cluster VII (62 days), while, it was the lowest in cluster IV (53.33 days). Cluster VII had highest mean value (75 days) of days to pod initiation, whereas, it was showed lowest in cluster III, r IV and VIII (67 days). Cluster II had highest mean value (117 days) of days to maturity, while it revealed minimum for cluster VI (105 days). Cluster mean for Plant height was high in cluster IX (64.53 cm), whereas, it was lowest in cluster IV (38.6 cm). Cluster II, III, VI, VIII and IX had maximum mean value (4.0) for number of primary branches per plant, whereas, it was noted low in cluster IV, VII and X (3.33). Cluster mean for number of secondary branches per plant was found highest in cluster VIII (8.67), while, noted lowest for cluster X (6.67). Cluster mean for total number of pods per plant revealed maximum in cluster X (114), whereas, it was found lowest for cluster III (51). Cluster X (77) had highest mean value for number of effective pods per plant and observed lowest for cluster VI (37). Cluster X had maximum mean value (1.78) for number of seeds per pod, whereas, it was found lowest for cluster VIII (1.4). For 100 seed weight, highest cluster mean was found in cluster vii (27.63g), while, it was noted low in cluster X (18.63g). Cluster VII had high cluster mean value (71.37 g) for biological yield per plant, while it was found lowest for cluster X (17.4 g). Cluster VIII had highest seed yield per plant (30.47 g), whereas, it was lowest for cluster X (14.33 g).

Table 3: Maximum and Minimum Cluster Mean Values for Yield and its Attributing Traits in Pooled analysis.

Traits	Cluster Mean Values (10 clusters)	
	Min	**Max**
DTFI	VIII, X	VII
DT50%F	IV	VII
DTPI	III, IV,VII	VII
DTM	VI	II
PH	IV	IX
PB	IV, VII, X	II, III, VI, VIII, IX
SB	X	VIII
TNPPP	III	X
NEPP	VI	X
NSPP	VIII	X
100 SW	X	VII
BY	X	VII
HI (%)	VI	X
SYPP	X	VIII

Table 4: Cluster Mean for Seed Yield and its Attributing Traits in *Desi* Chickpea Genotypes in Pooled Analysis.

Characters		DTFI	DT50%F	DTPI	DTM	PH	PB	SB	TNPPP	NEPPP	NSPP	100 SW	BY	HI	SYPP
Clusters	I	49.69	56.02	66.56	108.06	50.69	3.73	7.85	63.21	43.65	1.45	24.84	43.56	48.53	23.86
	II	51.00	56.00	68.00	117.00	41.53	4.00	8.00	59.00	47.00	1.66	23.43	55.43	45.30	21.20
	III	48.00	54.00	67.00	114.00	47.57	4.00	7.67	51.00	39.00	1.67	24.20	35.57	57.30	23.23
	IV	48.00	53.33	67.00	115.00	38.60	3.33	7.00	77.00	52.00	1.73	20.43	63.37	49.57	24.20
	V	54.72	60.28	71.50	111.17	52.62	3.94	8.33	74.17	47.17	1.52	23.18	53.46	52.09	24.41
	VI	51.00	59.00	69.33	105.00	48.57	4.00	7.33	57.00	37.00	1.44	27.53	33.33	57.30	24.37
	VII	55.00	62.00	75.00	116.00	43.77	3.33	7.67	56.00	39.00	1.55	27.63	35.50	40.43	20.27
	VIII	47.00	56.00	67.00	107.00	58.50	4.00	8.67	57.00	38.00	1.40	27.53	71.37	52.43	30.47
	IX	50.00	56.00	68.33	106.00	64.53	4.00	8.00	87.00	68.00	1.44	26.57	27.53	46.30	24.50
	X	47.00	54.00	69.00	110.00	47.40	3.33	6.67	114.00	77.00	1.78	18.63	17.40	59.43	14.33

Where,
DTF: Days to flower initiation, DT50%F: Days to 50% flowering, DTPI : Days to pod initiation, DTM : Days to maturity, PH : Plant high, PB : Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total Number of pods per plant, 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 plant.

In the present study, percentage contributions of yield and yield contributing traits towards total genetic divergence were presented in Table 5. Highest contribution toward the total divergence was revealed for seed yield per plant (22.99 %) followed by biological yield per plant (16.55 %), harvest index (15.86 %), days to flower initiation (11.26 %) and number of effective pods per plant (10.11 %). Negligence contribution towards divergence was found for remaining traits under study.

Table 5: Contribution (%) of seed yield and yield attributing traits towards total genetic divergence in Pooled Analysis.

Source	Times Ranked 1st	Contribution %
DTFI	49	11.26
DT50%F	7	1.61
DTPI	8	1.84
DTM	0	0.00
PH	23	5.29
PB	0	0.00
SB	3	0.69
TNPPP	24	5.52
NEPPP	44	10.11
NSPP	0	0.00
100 SW	36	8.28
BY	72	16.55
HI	69	15.86
SYPP	100	22.99

Where,
DTF: Days to flower initiation, DT50% F: Days to 50% flowering, DTPI : Days to pod initiation, DTM : Days to maturity, PH : Plant high, PB : Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total Number of pods per plant, 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 plant.

Considering the, intra and inter cluster distance and cluster mean value the genotypes namely*;* BRC 302, JG 14, Phule G 1018-9-6, JG12 × JG 16-3, DC16-116, JG63 × ICC4958 and JG74 × ICCV4958 were found promising which can be used in further precise breeding programme of chickpea for achieving maximum variability for seed yield and its contributing traits that assist to evolve promising genotypes with respect to more than one trait (Table 6).

The cluster mean for seed yield and its attributing traits revealed that different cluster respond differentially for various traits under study. Hence wide variation in cluster mean with respect to different clusters suggested that genotypes performances for various traits were separated into different clusters. This denotes lacks of parallelism between genetic and geographic diversity. Lal *et al.* (2001); Katiyar *et al.* (2004); Joshi *et al.* (2006) reported no relationship between geographic distribution and genetic divergence. Therefore, for hybridization programme, selection of parental material based on geographic diversity may not be a successful exercise. The selection of suitable diverse parents would be more rewarding regarding genetic divergence analysis. Hence, this study suggested that these clusters could be used as parents in hybridization programme as hybridization between diverse parents is likely to produced superior segregates and desired wide variation. These similar results were in closed harmony with Jeena *et al.,* (2005); Dwevedi and Lal (2009); Hahid *et al.* (2010); Sreelakshmi *et al.* (2010); Prakash and Shekhawat (2012); Gaikwad *et al.* (2014); Dhuria and Babbar (2016); Aarif *et al.* (2017); Vijayakumar *et al.* (2017); Geethanjali *et al.* (2018); Thakur *et al.* (2018); Ponnuru *et al.* (2019); Dar *et al.* (2020); Boparai *et al.* (2021). Therefore, this current research illustrates that there is an enough scope for obtaining genetic diversity which helps in the advancement of chickpea breeding programme.

Table 6: List of Promising Genotypes on the basis of Cluster Means, Intra and Inter Cluster Distance in Pooled Analysis.

Promising genotypes
BRC 302, JG 14, Phule G 1018-9-6, JG12 × JG 16-3, DC16-116, JG63 × ICC4958, JG74 × ICCV4958

CONCLUSIONS

Mahalanobis (1928) D^2 statistical analysis were used for obtaining genetic divergence in the present experiment among 30 *desi* chickpea genotypes and genotypes were grouped into different clusters according to Torcher's method as described by Rao (1952). In the present study, the genotypes fall into ten clusters based on D^2 analysis. The cluster I and V were largest with the highest number of genotypes i.e. 16 and 6 respectively, whereas, rest of clusters had one genotype each. Maximum intra cluster distance was observed in cluster V (D^2 = 7.29) followed by cluster I (D^2 = 6.43). The maximum inter-cluster distance was observed in between cluster IV and IX (D^2 = 13.27) followed by cluster II and cluster IX (D^2 = 12.36),

whereas, cluster V and VIII with minimum distance (D^2 = 9.00). Genotypes having maximum inter-cluster distance should be given priorities for crossing programme for achieving desirable transgressive segregates. Hence, genetic distance had a key role for selection of diverse parents for hybridization programme. On the basis of cluster mean, intra and inter cluster distance, genotypes namely; BRC 302, JG 14, Phule G 1018-9-6, JG12 × JG 16-3, DC16-116, JG63 × ICC4958 and JG74 × ICCV4958 were identified as promising genotypes which can be used as parents in further chickpea breeding programme.

FUTURE SCOPE

This present study suggested that the promising genotypes found in respective clusters with respect to more than two traits obtained in current experiment could be used as parents in hybridization programme as hybridization between diverse parents is likely to produced superior segregates and desired wide variation which may be utilized in further breeding programme of chickpea.

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