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Genetic Diversity Analysis of Chickpea Genotypes (*Cicer arietinum* L.) for Seed Yield and Morpho-genetic Traits

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ABSTRACT

Background: Based on D^2 analysis 53 chickpea genotypes were grouped into seven clusters. Among the VII clusters, cluster I consists of 30 genotypes forming the largest cluster followed by cluster II with 16 genotypes, cluster VII with three genotypes and cluster III, IV, V and VI with one genotype each. Inter cluster distance were found to higher than intra cluster distance which depicted wide genetic diversity among the chickpea genotypes under study. Contribution of various characters towards expression of total genetic divergence indicated that seed yield (27.77%) contributed maximum (24.74%) followed by biological yield and number of pods per plant (20.43%). The clustering pattern of genotype demonstrated that clustering does not follow any particular cluster pattern with respect to origin. The pattern of cluster analysis of the first principal component had the largest eigenroot 4.18 per cent of total variation followed by 3.53, 2.91, 2.02, 1.45, 1.26 and 1.15 from second to seven principal components. The eigenroot of first principal component accounted for 19.91 per cent of total variation followed by second to seven principal components which accounted for 16.82, 13.84, 9.62, 6.90, 5.99 and 5.48 per cent of total variations present in the genotypes.

Method: The study was carried out at Pulses Research Sub-Station (PRSS), Samba and Advanced Center for Rain-fed Agriculture (ACRA), Rakh Dhiansar during *Rabi* seasons 2017-18 and 2018-19. The experimental material comprising of 48 chickpea (*Cicer arietinum* L.) genotypes along with 5 checks were evaluated in augmented block design.

Result: The genotypes of cluster II, V and VII had highest inter-cluster distances as well as higher cluster means for most of the yield component traits indicating that these genotypes were most diverse can be used as parents in hybridization programme of chickpea breeding. The variation present in the chickpea genotypes under study can be exploited through selection and hybridization among identified genotypes for breeding high yielding chickpea genotypes.

Key words: *Cicer arietinum* L., Cluster analysis, Genetic diversity, PCA.

INTRODUCTION

The Mahalanobis (1936) D^2 analysis is an important method for quantifying population divergence. Many research using this method have found that spatial separation isn't always linked to genetic diversity. As a result, it offers a better idea of the extent of divergence and is independent of sample size, as well as a foundation for selecting parental lines for future breeding programmes.

The aim of present experiment was to group genotypes based on their divergences. Several researchers investigated genetic variation, clustering patterns, the relative contribution of distinct characters to divergence and the efficacy of selection (Raj *et al.*, 2019). The present experiment was designed to investigate the genetic divergence and clustering pattern of chickpea genotypes in order to select appropriate parents for use in hybridization programmes and to investigate the genetic parameters that influence yield. According to Murthy and Arunachalam (1966), multivariate analysis with "Mahalanobis D^2 statistics" is a powerful method for determining the function of various quantitative characters in determining the maximum divergence and establishing the relationship between genetic and geographic divergence. Knowing the origins of genetic diversity for various characters is critical, since the primary goal of plant breeders is to increase yield and efficiency by developing superior varieties. An inquiry into the existence and degree of divergence is useful for understanding the course of evolution and classifying populations into groups based on diversity, particularly when one or two characters are overlapping.

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MATERIALS AND METHODS

The present study was carried out in augmented design at two locations, Advanced Center for Rain-fed Agriculture (ACRA), Rakh Dhiansar and Pulses Research Sub-Station (PRSS), Samba, of SKUAST-Jammu, during *Rabi* season of 2017-18 and 2018-19. The experimental materials used

for present study comprised of 48 genotypes along with 5 checks of chickpea (C*icer arietinum* L.). The genotypes were diverse with respect to morphological and important economical traits. Among 48 genotypes and HC-5, CSJ-515, RSG-888, DKG-964 and BG-372 were undertaken as standard check. The seed materials for present study were received from Pulses Research Sub-Station (PRSS), Samba, of SKUAST-Jammu, during *Rabi* season 2017- 18. The experiment was based on augmented design as suggested by Federer (1956, 1975) and Raghava Rao (1975) with the purpose of evaluating and doing statistical analysis, of a large number of new selections. The yield of new selection was adjusted for block differences, which was measured by check varieties in every block. Experimental materials were allocated in six blocks in augmented block design with 5 checks distributed randomly in each block.

Observations were recorded for 09 morphological traits *viz*., plant height (cm), number of pods per plant, number of seeds per pod, pod length (cm), number of days to maturity, seed yield (g/plant), 100 seed weight (g), biological yield (g/plant) and harvest index (%) as per standard procedures.

RESULTS AND DISCUSSION

The variation among the chickpea genotypes in this study would provide ample opportunities for the genetic improvement of the crop through direct selection of genotypes or through hybridization using as parents possessing the desirable traits. Analysis of variance was carried out among 48 chickpea genotypes along with 5 checks using Augmented Block Design (Federer, 1956). Significant differences were found among all the genotypes for all the traits.

Genetic divergence, which is due to genetic factors, is the basis for heritable improvement. The plant breeders have always therefore, been fascinated by great amount of diversity in crop plants as could serve as raw material for crop improvement program. The precise information about the genetic divergence is therefore, crucial for effective breeding programme. The genetically diverse parents are known to produce higher heterotic effects and consequently give desirable recombinants in the breeding material. Multivariate analysis as shown by Mahalanobis (1936) D^2 statistics, is a measure that appraises the genetic variability quantitatively among a set of genotypes.

The estimate of D^2 values (Tocher's mthod) ranged from 300.47 to 1242.4. Clearly indicating the presence of adequate diversity among genotypes under study. The aim of measuring inter and intra cluster divergence is to provide the basis for hybridization programme. The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to the different clusters and will not give expected desired heterotic response and segregants in further generations. Consequently, breeding programme should be designed that, the parents are selected from different clusters with wider genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.,* 1965). Therefore, while selecting the parents by considering the genetic diversity, their performance and cluster mean for the characters also need due consideration in the crop improvement progrmme. In the present study (Fig 1), maximum genotypes (30) were included in cluster I followed by cluster II (16), cluster VII (3), cluster III, IV, V and VI had single genotype in each (Table 1). The maximum (Fig 2) intra (diagonal value) cluster distance (1242.4) was observed between cluster VII and cluster VI, followed by cluster II and I (746.75), cluster V and cluster IV (721.69), cluster IV and cluster III (709.66). Table 2 indicating wide divergence among the cluster. This

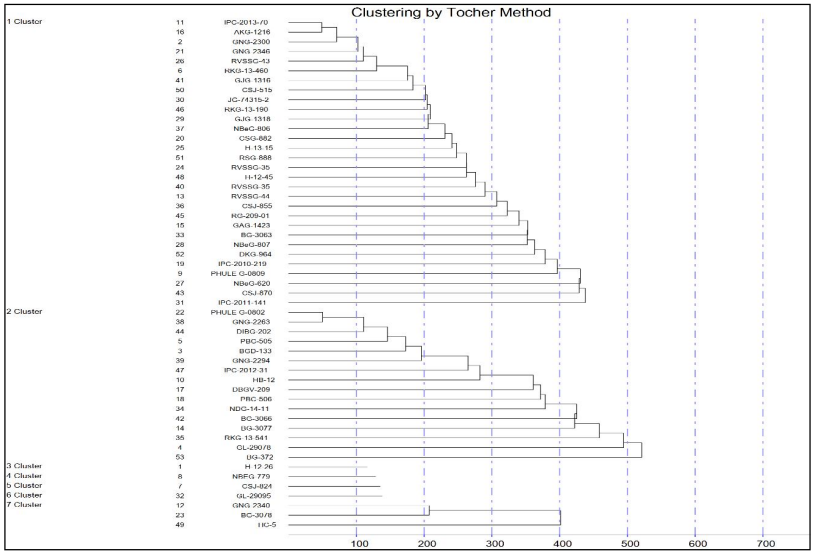

Fig 1: Clustering pattern of fifty three chickpea genotypes by Tocher's method.

also suggests that genetic architecture of the genotypes in one cluster differs entirely from those included in the other cluster giving scope for hybridization programme for improvement of chickpea genotypes. The inter cluster distance (640.04) was minimum between VI and V indicating close relationship between those clusters suggesting that the genotypes in this cluster may be used as parents in hybridization programme to obtain desirable recombination's. At intra cluster level, cluster VII had the highest value (470.46) which indicating that this cluster is more heterogeneous. However, the lowest intra-cluster distance was observed in cluster III, IV, V and VI indicating that the strains of these

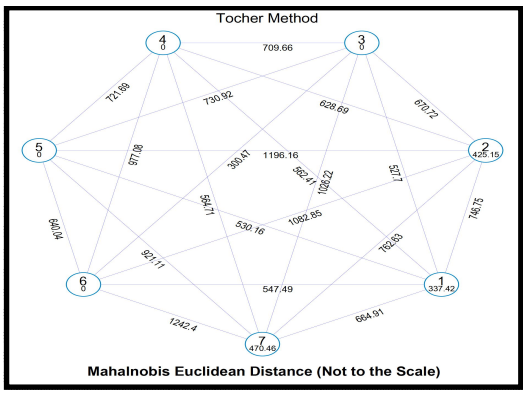

Fig 2: Divergence average intra and inter cluster distance among grouped fifty-three chickpea genotypes.

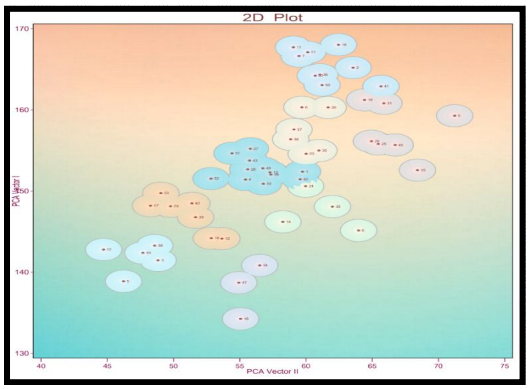

Fig 3: 2D Plot for different characters on the basis of PCA.

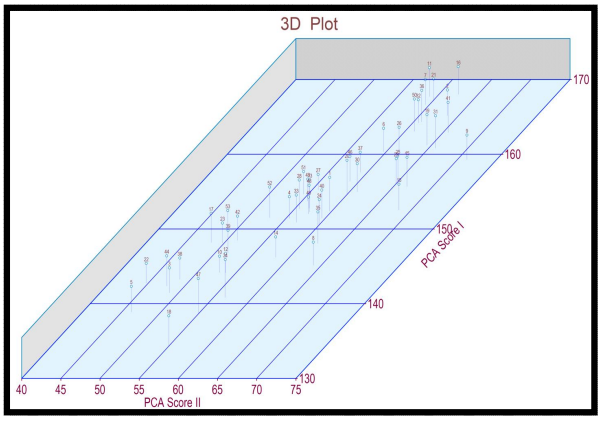

Fig 4: 3D Plot for different characters on the basis of PCA.

clusters resemble on another genetically and appeared to have evolved from common the genepool. The cluster mean for all 09 morphological traits are presented in (Table 3) from the data it can be seen that considerable difference exists for all the studied. It showed that cluster mean for plant height in cluster VII (67.54) and the lowest in cluster VI (44.78). Pods per plant highest in cluster VII (65.17) and lowest in cluster V (50.25), number of seeds per pod highest in cluster V (1.78) and lowest in cluster VI (1.48), pod length (cm) highest in cluster VII (2.10) and lowest in cluster III (1.63), days to maturity highest in cluster VI (149.25) and lowest in cluster II (127.64), seed yield highest in cluster V (14.92) and lowest in cluster IV (8.74), 100 seed weight highest in cluster VI (17.75) and lowest in cluster III (12.71), biological yield highest in cluster V (28.27) and lowest in cluster IV (18.97), harvest index highest in cluster VII (52.97) and lowest in cluster III (44.52). These results are in agreement with the finding by Singh *et al.* (2016), Gediya *et al.,* (2018), Raj *et al.,* (2019), Manasa *et al.,* (2020).

According to D^2 values genotypes HC-5, BG-3078 and GNG-2340 were found to be most diverse genotype followed by BGD-133, PBC-505, PHULE G-0802, GNG-2263, DIBG-202, GNG-2294, IPC-2012-31, HB-12, DBGV-209, PBC-506, NDG-14-11, BG-3066, BG-3077, RKG-13-541, GL-29078 and BG-372.

Seed yield (27.77%) contributed highest for divergence followed by biological yield (24.73%) and number of pod per plant (20.43%) indicating that these characters were considerably responsible for total divergence in the material under study (Table 4). Similar results were obtained by Jivani *et al.,* (2013), Jaya laksmi *et al.,* (2014), Parhe *et al.,* (2015) and Jakhar *et al*., (2016).

A large number of variables are often measured by plant breeders, some of which may not be sufficient discriminatory power for germplasm evaluation, characterization and management. Principal component analysis (PCA) involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The principal component analysis is a multivariate analysis used to study kind of variation present in the selected population. Owing to lack of knowledge regarding relative importance and usefulness of variables, the investigator tries to include all the possible variables and makes the data matrix perceivably large, complicated and beyond comprehension. Therefore, the investigator requires a technique for systematic reduction and summarization of data sets. Basically a well-known data reduction technique *i.e*. principal component analysis initiated by Pearson (1901), offers solution to this complex problem by transforming the original set of variables into smaller set of linear combinations that account for most of the variability of the original data set. The adjective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out if the total variability and also to rank germplasms on the basis of PC scores.

Table 1: Distribution of fifty-three chickpea genotypes in various clusters based on D^2 statistics (Tocher's Method).

Cluster no.	Number of genotypes	Name of genotypes
I	30	RKG-13-460, IPC-2013-70, AKG-1216, GNG-2346, RVSSG-43, GNG-2300, GJG-1316, CSJ-515, JG-74315-2, RKG-13-190, GJG-1316, NBeG-806, CSG-882, H-13-15, RSG-888, RVSSG-35, H-12-45, RVSSG-35, RVSSG-44, CSJ-855, RG-209-01, GAG-1423, BG-3063, NBEG-807, DKG-964, IPC-2010-219, PHULE-G-0809, NBEG-620, CSJ-870, IPC-2010-141
II	16	BGD-133, PBC-505, PHULE G-0802, GNG-2263, DIBG-202, GNG-2294, IPC-2012-31, HB-12, DBGV-209, PBC-506, NDG-14-11, BG-3066, BG-3077, RKG-13-541, GL-29078, BG-372
III	1	H-12-26
IV	1	NBEG-779
V	1	CSJ-824
VI	1	GL-29078
VII	3	HC-5, BG-3078, GNG-2340

Table 2: Mean Inter and Intra (diagonal) cluster distance among seven cluster in chickpea genotypes by Tocher's method.

Clusters	I	II	III	IV	V	VI	VII
I	337.42	746.75	527.7	562.41	530.16	547.49	664.91
II		425.15	670.72	628.69	1196.16	1082.85	762.63
III			0	709.66	730.92	300.47	1026.22
IV				0	721.69	977.08	564.71
V					0	640.04	921.11
VI						0	1242.40
VII							470.46

Table 3: Cluster means for nine morphological traits in chickpea genotypes by Tocher's methods.

Characters	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII
Plant height (cm)	60.87	54.18	45.85	63.08	65.75	44.78	67.54
Number of pods per plant	64.34	64.80	61.75	52.75	50.25	59.75	65.17
Number of seeds per pod	1.59	1.62	1.53	1.68	1.78	1.48	1.56
Pod length (cm)	1.88	2.07	1.63	1.78	1.75	1.98	2.10
Number of days to Maturity	141.52	127.64	142.25	136.00	145.00	149.25	140.67
Seed yield (g/plant)	12.13	11.61	9.97	8.74	14.92	14.34	13.14
100 seed weight (g)	16.92	16.91	12.71	17.44	13.86	17.75	14.46
Biological yield (g/plant)	23.49	22.92	21.63	18.97	28.27	27.51	24.74
Harvest index (%)	51.32	50.00	44.52	45.78	52.56	52.01	52.97

Table 4: Percentage contribution of nine morphological and yield attributing traits towards Divergence.

Traits	Contribution %
Plant height (cm)	5.06
Number of pods per plant	20.43
Number of seeds per pod	9.32
Pod length (cm)	1.51
Number of days to Maturity	1.63
Seed yield (g/plant)	27.77
100 seeds Weight (g)	3.02
Biological yield (g/plant)	24.73
Harvest index (%)	6.53
Total	100

The pattern of cluster analysis of the first principal component (Table 5) had the largest eigenroot 4.181 per cent of total variation followed by 3.53, 2.91, 2.02, 1.45, 1.26 and 1.15 from second to seven principal components. The eigenroot of first principal component accounted for 19.91 per cent of total variation followed by second to seven principal components which accounted for 16.82, 13.84, 9.62, 6.90, 5.99 and 5.48 per cent of total variations present in the genotypes. The per cent of variation explained by 5^{th}, 6^{th} and 7^{th} components were small (Fig 3 and 4). These studies confirm by the earlier study of Admas and Abeje *et al.,* (2017); Temesgen *et al.,* (2015); Tesfamichael *et al.*, (2015) and Malik *et al.,* (2014).

Table 5: Eigenvector, eigenroot and associated variation for principal components analysis.

Characters	Canonical Roots Analysis (P. C. A.)						
	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector	7 Vector
Plant height (cm)	0.09	0.12	0.03	-0.33	0.04	0.22	-0.28
No. of pods per plant	-0.09	-0.11	0.09	-0.20	0.18	0.49	0.44
No. of seeds per pod	-0.07	0.07	0.15	0.09	-0.30	-0.24	-0.35
Pod length (cm)	-0.14	0.02	0.15	0.02	0.34	0.28	-0.55
Dsays to Maturity	0.32	0.24	-0.01	0.15	0.02	-0.10	0.08
Seed yield (g/plant)	0.31	-0.31	-0.26	-0.11	-0.03	0.04	-0.10
100 seed weight (g)	-0.01	0.02	0.06	0.33	-0.14	0.40	-0.42
Biological yield (g)	0.29	-0.27	-0.24	-0.16	0.10	0.02	-0.10
Harvest index	0.23	-0.24	-0.21	0.09	-0.30	0.07	-0.07
Eigene Value (Root)	4.18	3.53	2.91	2.02	1.45	1.26	1.15
% Var. Exp.	19.91	16.82	13.84	9.62	6.90	5.99	5.48
Cum. Var. Exp.	19.91	36.74	50.58	60.19	67.10	73.09	78.58

CONCLUSION

The genotypes of cluster VII, II and V (CSJ-824, HC-5, BG-3078, BGD-133, PBC-505, PHULEE G-0802, GNG-2263, DIBG-202, GNG-2294, IPC-2012-31, HB-12, DBGV-209, PBC-506, NDG-14-11, BG-3066, BG-3077, RKG-13-541, GL-29078, BG-372, GNG-2340) had highest inter-cluster distances as well as higher cluster means for most of the yield component traits indicated that these genotypes were most diverse among 53 chickpea genotypes which could be used as parents in hybridization programme of chickpea breeding. Inter cluster distances were reported to be higher than intra cluster distances, suggesting that chickpea genotypes have a high level of genetic diversity.

The variation present in the chickpea genotypes under study can be exploited for breeding high yielding chickpea cultivars through selection and hybridization among identified genotypes. For further use in breeding programmes, the promising diverse genotypes can be tested for combining ability and inheritance of yield and its contributing traits. These genotypes should be studied for genetic diversity research for another year or two in order to bring any clear conclusions about the diversity process. Genotypes from various clusters which have been described for a specific trait can be used as parents in a breeding programme to improve specific character.

Conflict of interest: None.

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