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Genetic divergence study of chickpea (*Cicer arietinum* L.) genotypes for some seedling growth characters

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ABSTRACT

Study on few chickpea genotypes for genetic divergence was carried out with respect traits related to seedling growth in the laboratory of the department of Genetic and Plant Breeding, BCKV, Mohanpur, Nadia, West Bengal. Out of characters under study, the highest contributor towards total divergence was shoot length (26.821%). The genotypes could be grouped into 8 clusters based on the relative magnitude of D^2 values. Cluster I had the highest number of genotypes i.e. 56. The values of intra-cluster distances varied from 12.425 (cluster I) to 99.684 (cluster VII). The highest intra-cluster distance was observed for cluster VI (99.684). Dendrogram was drawn by taking Euclidean distance as a measure of genetic distance following 'Unweight Pair Group Method using Arithmetic Averages' (UPGMA). The genotypes IPC 2010-37, AGBL 122 and 24017-1-1 hold a greater distance and are were widely apart from ICCV 13305, ICCV 13306 and AGBL 134. Therefore hybridization may yield greater heterosis.

Keywords : Chickpea, divergence, D^2 values, dendrogram and UPGMA

Pulses play a key role in crop rotation having their ability to fix nitrogen. Among pulses, chickpea is a common one which is widely cultivated for its typically yellow-brown pea-like seeds. Chickpea is considered as the third most important pulse in the world, being widely grown in many subtropical and warm temperate regions. The developing countries share more than 95 per cent of the area, production and consumption of chickpea (Ahmad *et al*., 2012). Lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of grain legumes including chickpea (Ramanujam, 1975). The knowledge of genetic diversity helps in the tagging of germplasm, identification of gene stock and the establishment of core collections. The agriculture practices and successive breeding has narrowed down the genetic base of cultivated chickpea. This has promoted the search for new sources of variation that might be useful for chickpea breeding program. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F_1 hybrids and a broad spectrum of variability in segregating generations. Quantitative traits provide an estimate of genetic diversity and numerical taxonomic techniques including principal component and cluster analysis have been successfully used to classify and measure the pattern of genetic diversity in germplasm. Mahalanobis's D^2 statistics is a powerful tool for quantifying the degree of variability at the genotype level (Johnson *et al.*, 2015). The objectives of the present studies were to assess the amount of genetic diversity in a collection of chickpea genotypes based on some seedling growth parameters and to identify the potential genotypes for future utilization in chickpea breeding programs.

MATERIALS AND METHODS

The experiment was carried out in the laboratory of the department of Genetic and Plant Breeding, BCKV, Mohanpur, Nadia, West Bengal. The seed materials used in the experiment (Table 1) were supplied by AICRP on Chickpea, Kalyani Centre, BCKV, Nadia, West Bengal. Sixty healthy, viable seeds of each Chickpea genotype were surface sterilized by immersing the seeds in 70 per cent ethanol for two minutes followed by washing thoroughly with distilled water. Ten seeds of a genotype were arranged in a row with even space over a glass plate (20 x 30 cm) wrapped with a blotting paper. To prevent the seeds from sliding down when the set was kept in a slant position in a stand, another glass strip (20 x 2 cm) was placed over the seeds with the help of a piece of thermocol at the two ends and guarder in such a way that the seeds remained in their position and the seedlings grew without any hindrance. The whole set was then placed in a transparent polythene bag.

An asymmetrical Factorial Completely Randomized Design was followed for the experiment and there were six sets for each genotype representing three replications for control and three replications for treatment were arranged. The seeds were then allowed to germinate and under indoor laboratory condition with sufficient light, 70-80 per cent relative humidity and at a temperature range of 20-25 °C. Data from six randomly selected competitive seedlings on the nine growth parameters *viz*. root length, shoot length, total seedling length, root fresh weight, shoot fresh weight, total fresh weight, root dry

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Table 1: List of the ninety-six genotypes of chickpea (*Cicer arietinum* L.) used in the experiment

S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype
1	AGBL 110	**25**	24017-2-1	**49**	FLIP07-127C	**73**	ICCV 13306
2	AGBL 122	**26**	24018-2-1	**50**	FLIP07-3C	**74**	ICCV 13307
3	AGBL 134	**27**	24031-3-1	**51**	FLIP07-176C	**75**	ICCV 13308
4	AGBL 146	**28**	24032-2-1	**52**	ICC 7441	**76**	ICCV 13309
5	AGBL 158	**29**	24034-4-1	**53**	ICC 8621	**77**	ICCV 13311
6	AGBL 160	**30**	24042-1-1	**54**	ICC 14402	**78**	ICCV 13312
7	AGBL 172	**31**	24042-5-1	**55**	ICC 15618	**79**	ICCV 13314
8	AGBL 184	**32**	24043-4-1	**56**	ICC 16207	**80**	ICCV 13316
9	GJG 0184	**33**	IPC 2010-25	**57**	ICC 3325	**81**	ICCV 13317
10	GAG 1107	**34**	IPC 2010-37	**58**	ICC 15868	**82**	ICCV 13318
11	GAG 1111	**35**	IPC 2008-89	**59**	ICC 1098	**83**	ICCV 14103
12	GJG 1211	**36**	IPC 2010-219	**60**	ICCV 13101	**84**	ICCV 14106
13	GJG 1304	**37**	IPC 2011-69	**61**	ICCV 13102	**85**	ICCV 14107
14	24001-4-1	**38**	IPC 2011-141	**62**	ICCV 13103	**86**	ICCV 14108
15	24002-4-3	**39**	IPC 2011-70	**63**	ICCV 13104	**87**	ICCV 14112
16	24003-1-1	**40**	IPC 2011-64	**64**	ICCV 13105	**88**	ICCV 14118
17	24003-2-1	**41**	IPC 2011-123	**65**	ICCV 13106	**89**	JG 16
18	24004-3-1	**42**	IPC 2010-94	**66**	ICCV 13107	**90**	GG 1
19	24005-3-1	**43**	FLIP17-218C	**67**	ICCV 13109	**91**	GG 4
20	24006-2-1	**44**	FLIP07-40C	**68**	ICCV 13111	**92**	RSG 888
21	24007-5-1	**45**	FLIP07-266C	**69**	ICCV 13116	**93**	DCP 92-3
22	24015-2-1	**46**	FLIP01-36C	**70**	ICCV 13117	**94**	JG 11
23	24015-4-1	**47**	FLIP07-249C	**71**	ICCV 13118	**95**	ICCV 93511
24	24017-1-1	**48**	FLIP01-29C	**72**	ICCV 13305	**96**	ICC 4958

Table 2: Contribution of individual character towards total genetic divergence.

S. N.	Characters	Contribution (%)	Times 1st ranked
1.	Root length	10.314	8
2.	Shoot length	26.821	22
3.	Total length	17.150	14
4.	Root fresh weight	4.394	4
5.	Shoot fresh weight	1.227	1
6.	Total fresh weight	14.458	12
7.	Root dry weight	9.802	8
8.	Shoot dry weight	6.674	5
9.	Total dry weight	9.159	7

weight, shoot dry weight and total dry weight was recorded from 10 days old seedlings from each plate. The statistical analysis was carried out by using computer-based software *i.e.* SPSS for diversity analysis. The multivariate analysis of D^2 statistics was carried out according to Mahalanobis (1936) and Euclidean distance and UPGMA was used for diversity analysis. The cultivars were grouped in different cluster following Tocher's method. The contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1985). Grouping of variety into various clusters was done based on D^2 values and average intra and inter-cluster distance were estimated.

RESULTS AND DISCUSSION

In the present investigation, nine seedling growth parameters have been studied to evaluate the pattern and extent of genetic variability and relatedness among 96 genotypes of chickpea.

Contribution of individual characters towards divergence

Contribution of individual character to the divergence among genotype is presented in table-2. The highest

Table 3: Grouping of 96 genotypes grown under control condition into different clusters

Cluster	No. of genotypes	Genotypes
I	56	24015-2-1; 24017-2-1; FLIP07-176C; FLIP07-127C; ICCV 14118; 24004-3-1; ICC 8621; 24001-4-1; IPC 2010-25; ICCV 14103; ICC 16207; ICC 15618; FLIP01-29C; ICC 14402; ICC 3325; ICCV 13104; JG 16; FLIP07-3C; 24006-2-1; ICCV 14106; ICCV 14107; ICC 1098; GJG 0814; ICCV 13101; GJG 0919; GJG 1211; 24003-3-1; 24031-3-1; ICC 7441; AGBL 146; ICCV 13317; ICCV 13103; ICCV 13318; GG 4; FLIP06-40C; AGBL 134; IPC 2011-123; ICCV 13118; 24042-5-1; ICCV 13106; 24007-5-1; 24043-4-1; ICCV 13107; IPC 2011-69; GJG 0904; ICCV 13102; AGBL 160; ICCV 13312; 24003-1-1; ICCV 14112; ICCV 13305; ICCV 13314; FLIP07-249C; ICCV 13316; GG 1; IPC 2008-89
II	12	24031-1-1; FLIP07-36C; IPC 2010-94; IPC 2011-70; ICCV 13311; ICCV 13116; AGBL 158; 24018-2-1; ICCV 13111; GAG 1107; ICCV 13307; AGBL 110
III	8	GJG 1311; 24034-4-1; 24032-2-1; 24015-4-1; 24005-3-1; 24042-1-1; IPC 2010-219; 24002-4-3
IV	7	FLIP07-218C; FLIP07-255C; FLIP 07266C; ICCV 13309; ICCV 13306; ICC15868; ICCV13105
V	5	ICCV 13109; ICCV 13117; IPC 2011-141; AGBL 184; AGBL 172
VI	6	GAG 1111; GJG 1304; ICCV 14108; ICCV 13308; 24017-1-1; AGBL 122
VII	1	IPC 2011-64
VIII	1	IPC 2010-37

Table 4: Intra (diagonal) and inter cluster distance (D) in 96 genotypes.

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	12.425	80.322	89.927	97.155	179.714	99.239	118.647	200.561
Cluster 2		14.326	46.324	92.632	143.624	92.687	104.826	116.685
Cluster 3			15.327	79.321	119.47	96.909	122.414	113.117
Cluster 4				20.424	77.832	118.536	174.292	172.805
Cluster 5					45.326	151.804	123.327	115.743
Cluster 6						69.801	137.832	120.488
Cluster 7							99.684	151.801
Cluster 8								74.485

contributor towards total divergence was shoot length (26.821%) followed by total length (17.150%). Similar kinds of observations were made by earlier workers (Sen *et al.,* 2016 and Patil *et al.,* 2005). Remaining traits had low contribution towards genetic divergence and hence, they were of less importance. Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important. Since shoot length contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

Grouping of genotypes into different clusters

Clusters were formed based on the relative magnitude of D^2 values, following Tocher's method described by Rao (1952) with the criterion that the intra-cluster values should be less than that of inter-cluster values. Following the principle, the genotypes could be grouped into 8 clusters. The cluster members were presented in table 3. Cluster I had the highest number of genotypes *i.e.* 56 followed by clusters II with 12 genotypes. Genotypes within the same cluster were considered to be closely related as compared to genotypes in other clusters. Monogenotypic clusters (Cluster VII and VIII) indicate that such genotypes might have completely different genetic makeup from the remaining genotypes and from each other, thus leading to the formation of separate cluster (Sen *et al.,* 2016).

Average Intra and inter-cluster distances

Average intra and inter-cluster distances of 96 genotypes were presented in table 4**.** The values of intra-cluster distances varied from 12.425 (cluster I) to 99.684

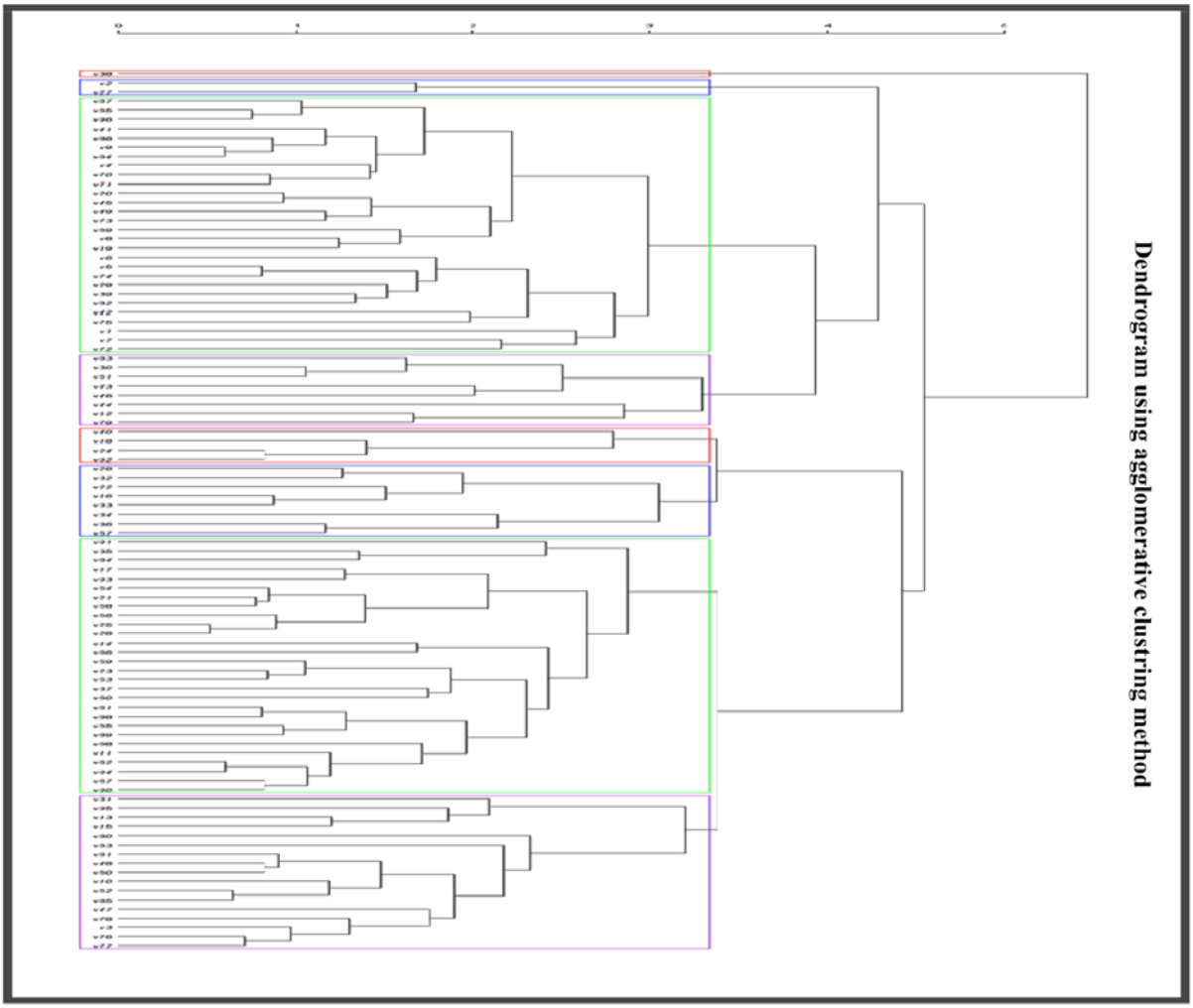

Fig. 1: Dendrogram based on Euclidean distance using the method of average linkage (UPGMA) of 96 genotypes of chickpea.

(cluster VII). Intra and inter cluster distances might arise due to differential genetic makeup of the genotypes (Win *et al.*, 2011). The intra-cluster values indicated the distance of genotype falling in the same cluster. High intra-cluster values indicated heterogeneity of genotypes in spite of belonging to the same cluster. The above result indicated the presence of a very high degree of heterogeneity in cluster VII. This intra-cluster heterogeneity might serve as a guideline to select desirable parents for recombination breeding programme even from the same cluster.

Average inter-cluster distances ranged from 46.324 (between cluster II and III) to 200.561 (between cluster I and VIII). Minimum inter-cluster distance indicated that the genotypes between these clusters maintained less divergence. From the divergence analysis it may be concluded that genotypes belonging to different clusters separated by high estimated Mahalanobis distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. Thus, the genotypes of cluster I and cluster VIII may be selected for hybridization program.

Dendrogram

A graphical tree diagram **(**Fig.1**)** was drawn by taking Euclidean distance as a measure following method of the unweight Pair Group Method using Arithmetic Averages (UPGMA). Dendrogram of 96 genotypes**.** Based on the 9 variables, the 96 genotypes were divided into 8 clusters. The interpretation was done based upon dissimilarity scale among the different clusters. The genotypes IPC 2010-37, AGBL 122 and 24017-1-1 hold a greater distance from ICCV 13305, ICCV 13306 and AGBL 134. These genotypes were widely apart from the formers and therefore hybridization may yield greater heterosis. Fikru *et al*. (2014) studied eleven

morphological variables of 228 lentil genotypes and analyzed genetic diversity by applying the method of Mahalanobis's generalized distances (D^2) and a cluster analysis following the method of the Unweight Pair Group Method using Arithmetic Averages (UPGMA).

It was concluded from the present study that the highest contributor towards total divergence was shoot length followed by total length and total fresh weight. The pattern of distribution of 96 genotypes in various clusters revealed the existence of considerable genetic diversity in the material. The genotypes were grouped into 8 clusters. The highest intra-cluster distance was observed for cluster VI (99.684). Hence, genotypes belonging to this cluster can be utilized as parents in future breeding programmes with the desirable genotypes belonging to clusters VII. Dendrogram study revealed that the genotypes *viz*. IPC 2010-37, AGBL 122 and 24017-1-1 hold a greater distance from ICCV 13305, ICCV 13306 and AGBL 134. These genotypes were widely apart from the formers and therefore hybridization may yield greater heterosis.

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