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Genetic divergence analysis in *kabuli* chickpea (*Cicer arietinum* L.)

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Abstract
Genetic diversity using Mahalanobis D^2 statistics was studied in 22 genotypes of *kabuli* chickpea (*Cicer arietinum* L.) for seed yield, its components and seed quality traits. The 22 genotypes were grouped into three clusters based on D^2 analysis. The cluster I and III were largest which consisted of 9 genotypes each and cluster II had 4 genotypes. The maximum inter-cluster distance was observed in between cluster II and III followed by cluster I and II whereas, cluster I and III with minimum distance. The maximum intra-cluster distance was observed in cluster II followed by cluster III and cluster I with minimum intra-cluster distances. The genotypes KAK-2 and HK-06-163 of cluster I having high seed yield per plant could be included in hybridization programme. The genotypes belonging to cluster II *viz.*, RVSSG-11, RVSSG-12, Phule G-09311 and phule G-09316 could be utilized as parents in future breeding programme.

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

Introduction
Chickpea is an economically important crop in India, Middle East, North Africa and Ethiopia. It is the third most important pulse crop in the world next to *Phaseolus vulgaris* and *Pisum sativum.* In India, over 70 per cent of the world's chickpea crop is produced (Joshi *et al*. 2006) [2]. Chickpeas are classified based on seed size, shape and color such as *desi* with small, angular and coloured seeds, whereas *kabuli* with large, ram shaped and beige coloured seeds (Singh and Saxena 1999) [7]. Seed size is an important trait for trade and component of yield and adaptation in chickpea (Upadhaya *et al*. 2006) [9].
Genetic diversity is one of the criteria of parent selection in the hybridization programme. The availability of transgressive segregants in any breeding program depends upon the diversity between the parents involves. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2-statistics has made possible to choose genetically diverged parents. The D^2 statistics also measures the degree of diversification and determines the relative proportion of each component character to the total divergence. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis. Quantification of genetic diversity in existing groups of germplasm for yield and its components is very important in planning breeding programme of crop plants. It not only helps in selection of parents to get superior recombinants but also in understanding the pattern of variation for different characters and hence improving choices of selecting better segregants for various important traits. However, information available on genetic diversity in *kabuli* chickpea is limited (Prakash, 2006) [5]. Therefore, the present study was carried out to analyze the genetic diversity in *kabuli* chickpea genotypes in order to select the potential parents for hybridization programme.

Material and Methods
The experimental materials used in the present study consisted of 22 genotypes of *kabuli* chickpea (*Cicer arietinum* L.) obtained from AICRP on chickpea, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.). These were evaluated in randomized complete block design with three replications at Research cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh) during *rabi* season of 2011-12. The distance between plants within rows was 20 cm, and spacing between rows was 40 cm. The recommended package of practices was followed throughout the period of crop growth. Observations were recorded on five competitive plants in each genotype per replication and mean value per plant was obtained. Mahalanobis (1936) [4] D^2 statistic analysis was used for assessing genetic divergence among 22 *kabuli* chickpea genotypes and genotypes were grouped into different clusters according to Torcher's method as described by Rao (1952) [6].

Results and Discussion

A set of 22 genotypes of *kabuli* chickpea were subjected to D^2 analysis for seventeen characters. Based on D^2 values three clusters were formed (Table 1). This indicated that substantial diversity existed in the all the genotypes evaluated in the present study. This is in agreement with earlier reports, indicating substantial diversity in *kabuli* chickpea materials. The present study also suggests that, there is no relationship between geographic and genetic diversity as genotypes chosen from different eco-geographical regions are grouped in same cluster.

The 22 genotypes of *kabuli* chickpea were grouped into three different clusters. The cluster I and III were largest which consisted of nine genotypes each while, cluster II having four genotypes. From the clustering pattern, it was revealed that, the genotype collected from different region were independent of their genetic origin. Hence, the genotypes studied are reliable enough for hybridization and selection.

The maximum inter-cluster distance was observed in between cluster II and III (5.507) followed by cluster I and II (4.526) whereas, cluster I and III (3.576) with minimum distance. This suggested that, the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregantes or desirable combinations for development of useful genetic stocks or varieties. The maximum intra-cluster distance was observed in cluster II (3.394) followed by cluster III (3.071) and cluster I (2.989) (Table 2).The minimum intra-cluster distances indicating minimal diversity (difference) for the genes under study.

The mean values for different characters were compared across the clusters and are presented in (Table 3). Cluster I had highest seed yield per plant (15.33 g) followed by cluster II (13.53 g) whereas, it was lowest for cluster III (11.58 g). Comparison of cluster mean for different important characters showed that cluster mean for days to 50% flowering was high in cluster III (70.52 days) followed by cluster I (68.96 days) while, it was lowest for cluster II (67.50 days). Clusters mean for days to maturity was found high in cluster III (115.52 days) followed by cluster II (109.08 days) while, it was noted low for cluster I (108.59 days). Cluster mean for plant height was high in cluster II (53.49 cm) followed by cluster I (52.42 cm) while, it was low for cluster III (50.53 cm). Cluster mean for primary branches per plant was maximum in cluster I (3.76) followed by cluster II (3.60) while, it was the lowest in cluster III (3.29). Cluster mean for secondary branches per plant was high in cluster I (9.27) followed by cluster III (8.49) while, it was low for cluster II (6.83). Cluster mean for pods per plant was maximum for cluster I (58.94) followed by cluster III (50.38) while, it was minimum in cluster II (42.83). Cluster I had highest mean value (40.08 g) of biological yield per plant followed by cluster II (35.14 g) whereas, it was lowest in cluster III (30.96 g). Cluster II had maximum 100-seed weight (38.36 g) followed by cluster I (28.27 g) while, it was lowest in cluster III (23.61 g). Cluster mean for harvest index was found high in cluster I (38.40%) followed by cluster II (38.39%) whereas, it was noted low in cluster III (38.30%). Cluster II (0.41 g/seed) had highest mean value of hydration capacity followed by cluster I (0.30 g/seed) while, it was lowest in cluster III (0.25 g/seed). Cluster mean for hydration index was high in cluster III (1.02) whereas, it was lowest in cluster I and II (1.00) each. Swelling capacity was found highest in cluster II (0.47 ml/seed) followed by cluster I (0.33 ml/seed) while, it lowest for cluster III (0.29 ml/ seed). Cluster mean for swelling index was highest in cluster III (1.20) followed by cluster II (1.17) whereas, it was noted low in cluster I (1.08). Seed volume was found maximum in cluster II (0.40 ml/seed) followed by cluster I (0.31 ml/seed) while, it was minimum for cluster III (0.25 ml/seed). Cluster mean for protein content was highest in cluster III (20.51%) followed by cluster II (20.49%) and lowest for cluster I (20.19%). Cooking time was found high in cluster III (79.00 min) followed by cluster I (74.44 min) while, it was noted least in cluster II (61.17 min).

The cluster mean for various traits showed that different cluster respond differentially for various traits. The cluster I showed best performance for early maturity, high mean values for primary branches per plant, secondary branches per plant, pods per plant, seed yield per plant and biological yield per plant. The cluster II showed best performance for early flowering, high mean values for test weight, hydration capacity, swelling capacity, seed volume while, it had least mean value for cooking time. The cluster I, II and III were found to exhibit nearly equal cluster mean values for harvest index, hydration index and protein content.

The above findings clearly showing the wide variation from one cluster to another in respect of cluster means, which indicated that genotypes performance for various characters, were separated into different clusters. The three clusters in the aforesaid genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although, genotypes originated in same place or geographic region were also found to be grouped together in same cluster, the instances of grouping of genotypes of different origin or geographic region in same cluster were observed in case of all the three clusters. This suggests lacks of parallelism between genetic and geographic diversity. Darshanlal *et al.* (2001) [1], Katiyar *et al.* (2004) [3] and Joshi *et al*. (2006) [2] reported no relationship between geographic distribution and genetic divergence. Therefore, the selection of parental material for hybridization programme, simply based on geographic diversity may not be a successful exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more rewarding than the choice on the basis of geographic diversity advocating lack of definite relationship between genetic and geographic diversity in *kabuli* chickpea. Hence, this study suggests that there is a lot of scope for harnessing genetic diversity existing in the improvement of *kabuli* chickpea crop in future.

The clustering of genotypes from different ecogeographical locations into one cluster could be attributed to possible free exchange of breeding material or even varieties from one place to another (Verma and Mehta, 1976) [10].

Results indicated that, the genotypes from the clusters having maximum distance between them may be utilized as parents in crossing programme to isolate desirable segregates for seed yield and quality components. In present study the cluster II and III were found to exhibit maximum inter-cluster distance whereas, cluster II with maximum intra-cluster distance. The twenty two genotypes of *kabuli* chickpea had shown considerable divergences for different characters.

Based on the results obtained from present study, it is concluded that, the mean values of clusters for different characters and *per se* performance of the genotypes grouped in the respective clusters could be selected for a viable hybridization programme for improving a particular traits. The present finding clearly indicates that, for different desirable traits, parents can easily be chosen out from any cluster depending upon its merit (Table 4). RVSSG-12 and RVSSG-11 of cluster II for early flowering; for high test weight (42.29 g) and swelling capacity (0.51 ml/seed) Phule

G-09311 of cluster II; for maximum hydration capacity (0.50 g/seed) and seed volume (0.44 ml/seed) RVSSG -12 of cluster II; for least cooking time (50 min) Phule G-09316 of cluster II; for harvest index HK-08-231(44.33%), BGD-128 (43.89%) and JGK-1(43.82%) of cluster III; for hydration index BDNGK-798 (1.17) of cluster III; for high protein content CSJK-1 (22.75%), HK-06-152 (22.08%) of cluster III could be utilized in hybridization programme to give desirable transgressive segregants in F_2 or onward generations. Beside this, genotypes KAK-2 and HK-06-163 of cluster I having high seed yield per plant could also be included in hybridization programme.

Table 1: Grouping of *kabuli* chickpea genotypes in different clusters

Cluster	Genotypes	Number of genotypes included
I	GNG-2112, GNG-2104, BG-3025, IPCK-07-62, HK-06-163, IPCK-06-143, HK-06-171, KAK-2, BG-3026	9
II	RVSSG-12, Phule G-09311, RVSSG-11, Phule G-09316	4
III	HK-08-212, HK-08-231, JGK-1, BGD-128, BDNGK-798, BGM-571, HK-06-152, CSJK-1, GNG-1969	9
Total		22

Table 2: Estimation of average intra- and inter-cluster distances for three clusters in *kabuli* chickpea genotypes

Clusters	I	II	III
I	2.989		
II	4.526	3.394	
III	3.576	5.507	3.071

Diagonal and bold values indicates the intra-cluster distances

Table 3: Cluster mean for different traits in *kabuli* chickpea genotypes

S.N.	Characters	Clusters		
		I	II	III
1.	Days to 50% flowering	68.96	67.50	70.52
2.	Days to maturity	108.59	109.08	115.52
3.	Plant height (cm)	52.42	53.49	50.53
4.	Primary branches per plant	3.76	3.60	3.29
5.	Secondary branches per plant	9.27	6.83	8.49
6.	Pods per plant	58.94	42.83	50.38
7.	Seed yield per plant (g)	15.33	13.53	11.58
8.	Biological yield per plant (g)	40.08	35.14	30.96
9.	100-seed weight (g)	28.27	38.36	23.61
10.	Harvest index (%)	38.40	38.39	38.30
11.	Hydration capacity (g/seed)	0.30	0.41	0.25
12.	Hydration index	1.00	1.00	1.02
13.	Swelling capacity (ml/seed)	0.33	0.47	0.29
14.	Swelling index	1.08	1.17	1.20
15.	Seed volume (ml/seed)	0.31	0.40	0.25
16.	Protein content (%)	20.19	20.49	20.51
17.	Cooking time (min)	74.44	61.17	79.00

Table 4: Desirable genotypes based on cluster mean for different traits

S. No	Characters	Clusters		
		I	II	III
1.	Days to 50% flowering	KAK-2, IPCK-07-62	RVSSG-12, RVSSG-11	BGM-571
2.	Days to maturity	HK-06-163	RVSSG-11	JGK-1, HK-08-212
3.	Plant height (cm)	BG-3025, IPCK-06-143	Phule G-09311	CSJK-1, HK-08-212, HK-06-152, BGM-571
4.	Primary branches per plant	HK-06-163, IPCK-07-62, GNG-2104	Phule G-09311	BDNGK-798, CSJK-1
5.	Secondary branches per plant	HK-06-163	Phule G-09311	BDNGK-798, BGD-128, HK-06-52
6.	Pods per plant	HK-06-163, IPCK-07-62, BG-3025	Phule G-09316, Phule G-09311	GNG-1969, BGD-128, CSJK-1
7.	Seed yield per plant (g)	KAK-2, HK-06-163	Phule G-09316, Phule G-09311	BGD-128, HK-08-231
8.	Biological yield per plant (g)	HK-06-163	Phule G-09316	HK-06-152, BDNGK-798
9.	100-seed weight (g)	KAK-2	Phule G-09311	BGD-128
10.	Harvest index (%)	KAK-2	Phule G-09311, Phule G-09316	HK-08-231, BGD-128, JGK-1
11.	Hydration capacity (g/seed)	HK-06-171, KAK-2	RVSSG-12	BDNGK-798, BGM-571, CSJK-1
12.	Hydration index	HK-06-171	RVSSG-12	BDNGK-798
13..	Swelling capacity (ml/seed)	KAK-2	Phule G-09311	BDNGK-798, BGD-128
14.	Swelling index	HK-06-163	Phule G-09316	HK-08-231
15.	Seed volume (ml/seed)	KAK-2	RVSSG-12, Phule G-09311	CSJK-1, JGK-1
16.	Protein content (%)	GNG-2104	Phule G-09316	CSJK-1, HK-06-152
17.	Cooking time (min)	IPCK-07-62, BG-3026	Phule G-09316	BGM-571

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