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Short Communication

Divergence analysis in *kabuli* chickpea (*Cicer arietinum* L.)

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The role of genetic diversity and its significance has been recognized for the selection of desirable parents in breeding programme to obtain high heterotic response and transgressive segregents. The genetic diversity in *desi* chickpea (*Cicer arietinum* L.) genotypes has been studied by many workers [1-2]. However, information available on genetic diversity in *kabuli* chickpea is limited. Therefore, this study was carried out to analyze the genetic diversity in *kabuli* chickpea genotypes in order to select the potential parents for breeding programme. Eighty one genotypes of *kabuli* chickpea representing diverse collection of local selections, breeding lines, cultivars and commercial varieties were grown in randomized block design in three replications during *rabi* 2003-04. Each genotype was sown in single row plot of 3.5 meter length. Observations were recorded for eight morphological characters namely days to 50% flowering, days to maturity, plant height (cm), pods per plant, 100-seed weight (g), seeds per pod, secondary branches per plant and grain yield per plant (g). The genetic divergence among genotypes was computed by means of Mahalanobis' D^2 technique [3]. The difference between the genotypes for the set of characters was tested and the genotypes were grouped into clusters following Tocher's method [4]. The relative contribution of characters towards divergence was estimated using canonical analysis.

Genetic divergence: The analysis of variance showed a wide range of variation and significant difference for all the characters. Using "V" statistics, the analysis of dispersion for the test of significance of difference in the mean values based on Wilks' criterion revealed significant differences among the genotypes for aggregate eight characters. On the basis of relative magnitude of D^2 values, the 81 genotypes were grouped into 10 clusters each having 10, 26, 11, 01, 14, 09, 03, 05, 01 and 01 genotypes, respectively (Table 1). The composition of clusters were revealed that genotypes of a cluster developed at a wide range of eco-geographical areas, thereby suggested that genetic differences and similarities among the genotypes were irrespective of the areas. This allows us to select parents for hybridization on the basis of genetic diversity and not merely on the basis of eco-geographical variation.

Table 1. Grouping of genotypes into different clusters, number and names of genotypes and source

Clusters	No. of genotypes	Genotypes	Source
I	10	BG 267, L 550, GNG 1340, ICCV 96309, ICCV 96301, GNG 912, GNG 149, GNG 1289, GNG 966, GNG 1166	Delhi, Punjab, Rajasthan, Andhra Pradesh
II	26	ICCV 96307, ICCV 96314, BG 1107, RSG 585, ICCV 96313, GNG 1386, BG 1105, ICCV 92337, PG 93303, BG 1083, GNG 1390, BG 1088, GNG 1388, ICCV 95311, PFGK 1170, HK 98-155, ICCV 96009, GNG 971, GNG 1392, BG 1091, GNG 1382, HK-00-297, GNG 1280, ICCV 2, ICCV 96315, ICCV 96311	Andhra Pradesh, Delhi, Rajasthan, Maharastra, Punjab, Haryana
III	11	BG 1053, GNG 1499, BG 1003, ICCV 93306, ICCV 32, GNG 1292, HK-00-329, GNG 1389, BG 1106, SCS-1, PB 95311	Delhi, Rajasthan, Andhra Pradesh, Haryana, Jammu & Kashmir, Punjab
IV	01	GNG 1285	Rajasthan
V	14	ICCV 96010, ICCV 97306, ICCV 96306, H-98-158, ICCV 95317, BG 1090, IPCK 992, IPCK 9778, ICCV 97314, HK 89-112, BG 1059, GNG 1284, ICCV 92321, ICCV 92317	Andhra Pradesh, Haryana, Delhi, Uttar Pradesh, Rajasthan
VI	09	GNG 1350, ICCV 96308, ICCV 92325, GNG 1107, GNG 1345, ICCV 96312, JKG 92337, PG 93308, GNG 1286	Rajasthan, Andhra Pradesh, Madhya Pradesh, Maharastra
VII	03	GNG 1103, GNG 1287, GCP 107	Rajasthan
VIII	05	MPJGK 3, PG 3332, ICCV 96319, LbeG 7, MPJGK 2	Madhya Pradesh, Maharastra, Andhra Pradesh, Uttar Pradesh
IX	01	ICCV 96316	Andhra Pradesh
X	01	ICCV 96304	Andhra Pradesh

Cluster grouping: The cluster distance was ranging from 0.00 to 7.02 within clusters and from 5.98 to 13.44 between clusters (Table 2). This indicated that the clusters were homogeneous within themselves and heterogeneous between themselves. The highest inter-cluster genetic distance was found between cluster VII and VIII (13.44) followed by III and VIII (12.96) I and VIII (12.94) VIII and X (12.76) and I and IX (11.02). The distance was lowest between clusters II and IV (6.24) followed by IV and VI (6.53), II and III (6.72), II and V (6.73) and II and X (6.73). Cluster VIII showed maximum genetic distance and cluster II showed maximum closeness to all other clusters. The genotypes were also grouped (arbitrary) on the basis of seed weight. It was observed that out of 81 genotypes, 24 had 100-seed weight less than 25g, 33 genotypes between 25-30g and 24 genotypes above 30g. This grouping was done just to find out whether arbitrary classification has any correlation with cluster grouping done on the basis of genetic distance. But no relationship was found in both the classifications. Even, only four lines having 100-seed weight less than 20g were classified in two different clusters. Same was the case with five genotypes having 100-seed weight of more than 35g. They were classified in three different clusters. It also supports the significance of genetic diversity analysis for better breeding improvement.

Table 2. Intra (diagonal) and inter-cluster divergence for ten clusters in *kabuli* chickpea

Cluster no.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**4.13**	7.09	6.27	7.22	10.27	7.40	7.98	12.94	11.02	8.43
II		**4.85**	6.72	6.24	6.73	7.41	8.54	9.55	7.64	6.73
III			**5.50**	8.87	9.43	8.51	7.74	12.96	10.64	7.94
IV				**0.00**	8.24	6.53	8.10	8.79	6.95	8.46
V					**5.91**	8.40	10.94	7.68	8.25	9.67
VI						**6.51**	9.36	10.29	9.37	8.47
VII							**7.02**	13.44	10.87	9.81
VIII								**6.56**	10.05	12.76
IX									**0.00**	7.71
X										**0.00**

Cluster means: The diversity in the present material was also supported by the appreciable amount of variation among cluster means for different characters (Table 3). Cluster X showed highest mean for plant height (94cm), number of pods per plant (55.2), secondary branches per plant (12.67) and grain yield per plant (15.64 g), cluster IX for days to maturity (150 days) and 100-seed weight (39.57g), cluster VII for seeds per pod and cluster III for days to 50% flowering (106.79 days). The characters grain yield per plant (32.35%), 100-seed weight (22.87) and seeds per pod (17.65%) were the major contributors towards genetic divergence.

A perusal of the above results suggest that genotypes from the cluster I, III, VIII, IX and X may yield better recombinants. Besides grain yield, pods per plant, seeds per pod and secondary branches per plant were found important traits for selecting better yielding genotypes. Looking towards the importance of bold seeded *kabuli* chickpea the genotypes ICCV 96316, PG 3332, MPJGK-2 and ICCV 96319 belonging to cluster VIII and IX can be included in the breeding programme to improve the seed size.

Table 3. Mean performance of different clusters for yield and yield attributing traits in *kabuli* chickpea

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Secondary branches/ plant	Pods per plant	Seeds per pod	100-seed weight (g)	Grain yield per plant (g)
I	105.20	148.13	71.53	9.57	40.96	1.61	22.11	13.37
II	105.38	148.78	80.50	9.58	35.89	1.27	28.06	11.49
III	106.79	149.70	87.70	8.79	34.94	1.59	24.39	12.25
IV	101.33	148.00	63.00	8.00	32.40	1.27	29.53	13.08
V	105.43	148.79	78.74	9.33	32.41	1.27	32.19	8.16
VI	104.78	148.41	69.33	10.22	39.29	1.16	24.47	11.79
VII	105.44	148.56	64.44	9.11	42.13	1.80	27.11	13.23
VIII	101.00	147.47	71.47	8.80	30.40	1.19	34.26	6.78
IX	105.67	150.00	67.00	9.33	36.40	1.00	39.57	13.61
X	106.67	147.33	94.00	12.67	55.20	1.10	30.47	15.64
Percent contribution to genetic divergence	8.89	2.96	12.81	0.43	2.04	17.65	22.87	32.35

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