RESEARCH ARTICLE

ASSESSMENT OF GENETIC DIVERSITY IN CHICKPEA (*CICER ARIETINUM* L.) GERMPLASM

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Received-03.07.2017, Revised-21.07.2017

Abstract: Genetic diversity among 100 accessions of chickpea collected from different agro-ecological zones of India was assessed for several quantitative and qualitative traits. These accessions were grown in the augmented design with 5 intermittent checks *viz*., HK 94-134, KWR 108, GCP-105, Udai and Pant G-186 after every tenth row. Wide range of variability was observed for both qualitative and quantitative traits studied. All the chickpea genotypes were grouped into 11 discrete clusters with higher genetic diversity for different traits. Maximum 12 genotypes consisted by cluster II, IV, VII followed by cluster I, III and VI were having 11 genotypes. The highest intra-cluster distance was recorded for cluster II (23.214) followed by cluster VIII (16.218). The maximum inter-cluster distance was observed between cluster IV and XI (70.776) followed by cluster III and XI (58.599). The above result indicates that these genotypes having sufficient genetic diversity to generate segregants through crossing programme.

Keywords: Chickpea, Accessions, Cluster Distance, Augmented, Genetic Diversity

INTRODUCTION

Chickpea is popularly known as King of pulses. In India, total pulses are grown on an area of 23.47 m ha with production of 18.34 m t and productivity of 751 kg/ha in 2012-13.Chickpea (*Cicer arietinum* L.) is the premier pulse crop of India covering 8.19 m ha area and production contributing 7.17 m t with the productivity of 929 kg/ha. The area, production and productivity of Uttar Pradesh has been 0.56 m ha, 0.38 m t, 683 kg/ha respectively in year 2014-15 (Anonymous 2015). Despite its nutritional value and economic importance too, chickpea production is relatively low in country; this is primarily due to poor genetic makeup of the native cultivars. The choice of potential genetically diverse parents for use in hybridization programme is based on the hypothesis that crosses involving divergent parents offer greater possibility of obtaining desirable segregants in the segregating generation which shows the need of research work.`

In chickpea, there are some reports available on the evaluation of genetic stock in agro-morphological traits (Singh et al. 1990, Farshadfar and Farshadfar 2008, Ali et al. 2010, Wadikar et al. 2010). These reports suggest that pod/plant, 100 seed weight (g), plant height and number of primary branches/plant are the major yield contributing traits (Singh et al. 1990). To strengthen ongoing breeding program, study of the available natural genetic variation is of immense importance. It is imperative to collect and evaluate germplasm precisely to draw valid conclusions. Generally, morphological variations are used to partition the available germplasm into small groups/clusters based on similarity and dissimilarity coefficients (Anderson 1984). Genetic variation present in germplasm arrays and the genetic relationships among genotypes are very useful for efficient conservation as well as utilization of genetic resources in breeding programme. Evaluation of germplasm increases the efficiency to make desirable selection whereas diversity index provides the information regarding the extent of variation present in the population. Therefore, an experiment was conducted to assess genetic diversity for different trait for yield and also their contribution towards genetic diversity.

MATERIAL AND METHOD

The experimental material comprising 100 accessions collected from agro-ecological zones of India were grown in an augmented design (Federe 1956) with five intermittent checks viz., HK 94-134, KWR 108, GCP-105, Udai and Pant G- 186 after every tenth row during rabi 2013-14 at Student's Instructional Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Faizabad (U.P.). Each line was grown in single row of 4m length representing a plot in non-replicated way, while checks were replicated ten times. Row to row and plant to plant spacing was kept 30cm and 10cm, respectively. Data were recorded on the basis of five randomly selected plant for different traits like number of primary branches/plant, number of secondary branches/plant, plant height (cm), pods/plant, seeds/ pod, biological yield/plant (g), seed yield/plant(g), harvest index (%)

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and 100-seed weight (g) whereas days to 50% flowering and days to maturity were recorded on plot basis.

Data analysis was done for both qualitative and quantitative traits. Analysis of variance (ANOVA) for augmented design for all attributes (qualitative and quantitative) was done using statistical software, Windostat ver. 8.0 (Khetan 2009). Based on adjusted mean data Euclidean distance (diversity index) was calculated using Numerical Taxonomy and Multivariate Analysis System (NTSYSpc) ver. 2.1 (Rohlf 2000). Dendrogram and cluster groupings using unweighted pair group with arithmetic averaging (upGMA) clustering algorithm was done based on Euclidean distance matrix through SAHN option of NTSYS pc ver. 2.2.

RESULT

On the basis of non-hierarchical Euclidean cluster analysis all the accessions were grouped into 11 discrete clusters with higher genetic diversity for different traits (Table 2).The maximum contribution of genetic diversity was found within biological yield/plant followed by pods/plant. Based on the genetic diversity analysis, maximum numbers of genotypes were grouped in cluster II (12), IV (11) and VII (10). The enlarge intra-cluster value was observed for cluster II (23.214) followed by VIII (16.218) and IX (13.230). The maximum inter-cluster distance was recorded between cluster IV and XI (70.776) followed by cluster III and XI (58.599). Maximum Inter-cluster distances between cluster VII and XI (52.789), cluster II and IX (51.714), cluster V and XI (50.088).

Mean performance value for different traits studied revealed that the highest mean value for days to 50% flowering ($\bar{X}$ =85.88) and days to maturity ($\bar{X}$ =145.64) were observed in cluster II indicates their delayed onset of flowering and maturing nature than the remaining germplasm (Table 3). While, cluster XI for days to 50% flowering ($\bar{X}$ =66.00) and days to maturity ($\bar{X}$ =123.68) having lowest value indicating their earliness towards both characters. Genotypes of long plant stature were grouped under cluster II ($\bar{X}$ =64.24) and of short stature in cluster X ($\bar{X}$ =41.27). Genotypes having highest number of podsplant^{-1}were placed in cluster II ($\bar{X}$ =53.40) and of lowest value in cluster IX ($\bar{X}$ =24.71). Genotypes of cluster II were also having highest biological yieldplant^{-1} ($\bar{X}$ =81.46) while, its lowest value was recorded in cluster IV ($\bar{X}$ =53.71). Number of primary and secondary branches were higher in the genotypes of cluster XI ($\bar{X}$ =3.34) and ($\bar{X}$ =7.43) respectively. Whereas, lowest mean value for both characters recorded in cluster IV ($\bar{X}$ =1.97) and ($\bar{X}$ =4.14), respectively. Highest mean value for seeds pod^{-1}was exhibited in cluster XI ($\bar{X}$ =2.29) and its lowest value was found in cluster VII ($\bar{X}$ =1.59). High seed yielding genotypes were grouped in cluster XI ($\bar{X}$ =31.03) whereas, of low mean value in cluster IV ($\bar{X}$ =11.10). Cluster XI also represented high mean value for harvest index ($\bar{X}$ =39.04) and its value was lowest in cluster IV ($\bar{X}$ =20.93). 100 seed weight mean value was found highest in cluster VIII ($\bar{X}$ =40.01) while, it was lowest in cluster VI ($\bar{X}$ =21.66).

DISCUSSION AND CONCLUSION

In order to investigate specific and general adaptation of chickpea in India, wide range of germplasm accession has been collected. On the basis of non-hierarchical Euclidean cluster analysis (Mahalanobis 1936), all the genotypes were grouped into 11 discrete clusters with higher genetic diversity for different traits indicating that present study can have an important implication for future investigations to produce higher yielding variety by suitable crop improvement programme. In the present accessions, considerable variation was present for all the important quantitative characters. The maximum contribution of genetic diversity was found for biological yield per plant followed by pods per plant. The similar results were also reported by Kumar et al. (2013). Therefore, selection based on these traits would be fruitful. In the present study higher order inter-cluster distances was observed indicating ample genetic variation was present for seed yield per plant. Similar observations have also reported by Sreelakshmi et al. (2011) and Sewak et al. (2012).

Mean performance value for different traits studied revealed that the highest mean value for days to 50% flowering and days to maturity were observed in cluster II whereas lowest values for cluster XI indicates their delayed onset of flowering and maturing and earliness towards both characters, respectively. Such higher order differences in mean performance were also observed for other important quantitative traits in different clusters. This result was supported by Kumar et al. (2013) Singh and Shiva Nath (2012). These results indicated that genotypes within above clusters showed more valuable heterotic pool for different character and therefore can be used to augment the yield and related attributes by using genotypes from cluster having maximum inter-cluster and intra-cluster distance to develop the transgressive segregants.

Table 1. Clustering pattern of 105 chickpea genotypes on the basis of Non-hierarchical Euclidean cluster analysis of eleven characters

Cluster number	**Number of genotypes**	**Genotypes**
I	11	NDGK 98-8,IPCK 2009-164, GNG-2196,HK-2, Phule G 0517, BG-3026, BDNGK 798, BG 3040. GSJK-27, KAK-2, HK94-134 (ch).
II	12	NDGK99-9, HK-4, GNG 2182 ,BG 1003, BG-3039,SKUA-C-23311,NDGK-11-32, BGD-1076,BDNGK-931, IPCK 2009-47, BDNG 801,BG-1003
III	11	NDGK 11-31, IPCK 2006-56, GLK-27242, HK 06-171, BG 3014, IPC 0811, GNG 1969, AKG-1001, L 550, Udai (ch).
IV	12	ICCV 95334,BBG-2, RSG-811, BGD-1072,CSJ-515, GL-26083, IPC 2003-27, BG-256, CSJ-8962, ICC-14872,HK 06-163, KWR-108(Ch)
V	7	IPCK 06-143, BG 3033, H 0449, BGM 569, JG-22, PD G 84-16, BG-3031
VI	11	BG 267, CSJK-72, CSJK 66, BPNGK 798, PG 0120, BGD 1071, C-235, BGD-1068, ICCV-08108, GCP-105 (ch), Pant G-186(Ch)
VII	12	JGK-16, GNG-2047, GJG 1001, CSJ-697,CSJ-724, BGD 1057, RVSSG-1, BAUG-13, BGD-1059, SBD-377, BG 3032, GNG-1999
VIII	10	CSJK-70, GNG-2112, DC 2012-1, GBM-2, BGD 1024, K 850, GL 1362, DKG-986, GNG-1969, Phule G-07112
IX	6	IPCK 2005-46, Phule G 09305, ICCV 05107, BG 3003, ICC-15929, ICCV 92944
X	6	IPCK 08-120, Phule G 9316, JG-19, Phule G 8202-16, HK 08-206, BGM 570
XI	7	HK 06-171, GNG 2104, HK-09-219, JGK-1, HK 08-212, BG-3027, GNG-2171

Table 2. Estimates of average intra and inter cluster distance for 11 clusters in chickpea accessions

Cluster number	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**
I	**9.405**	24.429	21.06	30.032	22.301	26.433	31.450	24.900	34.728	21.514	36.743
II		**23.214**	27.857	43.246	29.833	34.354	47.451	49.743	51.714	35.259	56.912
III			**6.687**	13.05	13.273	12.057	19.649	26.346	25.956	27.322	58.599
IV				**8.022**	14.549	14.857	17.242	32.217	27.232	25.956	70.776
V					**9.198**	11.320	17.230	29.139	19.189	16.968	50.088
VI						**6.520**	15.015	31.982	16.980	20.518	44.428
VII							**10.098**	28.824	22.108	19.633	52.789
VIII								**16.218**	27.332	26.755	41.199
IX									**13.230**	21.687	35.572
X										**8.659**	28.173
XI											**0.000**

Note: Bold figures indicate intra cluster distance.

Table 3. Cluster means for 11 clusters in chickpea accessions

Number of cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds Per pod	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	100-seed weight (g)
I	76.889	136.331	62.862	2.444	4.944	50.340	1.874	64.419	24.824	38.510	28.144
II	85.880**	145.640**	64.236**	2.588	5.640	53.402**	1.660	81.456**	20.859	25.746	25.982
III	80.486	140.451	58.439	2.367	4.886	29.316*	1.754	54.858	11.895	22.711	26.223
IV	76.600	135.545	43.750	1.976*	4.138*	30.604	1.937	53.711*	11.101	20.927*	21.786
V	77.800	137.804	44.136	2.703	4.332	37.433	1.872	65.137	14.303	23.775	22.194
VI	76.522	135.676	43.261	2.694	5.621	32.297	1.876	54.317	12.074	21.492	21.660*
VII	67.190	125.740	44.865	2.508	4.653	33.481	1.592*	56.704	11.641	21.035	22.738
VIII	69.900	130.030	52.308	2.536	4.162	28.563	1.838	58.259	19.966	34.892	40.015**
IX	70.400	129.713	42.328	3.149	4.829	24.707	2.248	58.364	14.238	23.379	27.674
X	69.150	127.205	41.275*	2.624	4.907	44.691	1.971	80.459	21.054	27.095	25.789
XI	66.000*	123.680*	46.168	3.336**	7.432**	42.153	2.288**	75.844	31.033	39.046**	34.717

Note- * indicate lower and ** indicate higher value

ACKNOWLEDGEMENT

We thank to Dr. R.K. Mahawar for reviewing a previous version of this manuscript. Thanks to all the field assistants and technical staff of the university. I also thanks to head of Department, Genetics and Plant Breeding, N.D. Uni. of Agri. and Technology, Kumarganj, Faizabad to successfully conduct the experiment.

REFERENCES

Anonymous (2013). Agriculture Statistic Division, Directorate of Economics and Statistics, Department of Agriculture and Cooperation, U.P.

Kumar, A., Nath, S., Yadav, A.K. and Kumar, J. (2013). Study of genetic diversity among genotypes for selection of desirable parameters act on high yield in chickpea (*Cicer arietinum* L.) Progressive Research 8 (3): 614-616.

Sreelakshmi, C., Shivani, D. and Kumar, C. V. S. (2010). Genetic divergence, variability and character association studies in Bengal gram (*Cicer arietinum* L.). Electronic Journal of Plant Breeding (5): 1339-1343.

Singh, A. P. and Nath, S. (2012). Genetic diversity among the germplasm for selection of parents for hybridization programme in chickpea. Progressive Research 7 (2): 256-258.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. Proceedings of National Institute of Sciences (India) 2(1): 49-55.

Sewak, S., Iqueabal, M.A., Singh, N.P., Solanki, R.K. and Sarika (2012). Genetic diversity studies in chickpea (*Cicer arietinum*) germplasm. Journal of Food Legumes 25(1): 31-36.

Federer, W.T. (1956). Augmented (or Hoonuiaku) designs. Hawaiian Planter's Records 40: 191-207.

Khetan, M.M. (2009). Windostat version 8.0 (www.windostat.org).

Rohlf, F.J. (2000). NTSYS-pc Numerical Taxonomy and Multivariate Analysis System version 2.1. Applied Biostatistics, New York.

Ali, Q., Ahsan, M. and Farooq, J. (2010). Genetic variability and trait association in chickpea (*Cicer arietinum* L.) genotypes at seedling stage. Electronic Journal of Plant Breeding 1: 334-341.

Anderson, T.W. (1984). An Introduction to Multivari,!te Statistical Analysis (2nd ed). Wiley, New York.

Singh, K.B., Bejiga, G. and Malhotra, R.S. (1990). Association of some characters with seed yield in chickpea collections. Euphytica 9: 83- 88

Farshadfar, M. and Farshadfar, E. (2008). Genetic variability and path analysis of chickpea (Cicer arietinum) landraces and lines. Journal of Applied Sciences 8: 3951-3956.

Wadikar, P.B., Ghodke and Pole, S.P. (2010). Genetic divergence for productivity traits in chickpea. Journal of Food legumes 23: 245- 246.