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Research Note

Genetic diversity in working germplasm collection of kabuli chickpea (*Cicer arietinum* L.)

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Abstract
Genetic diversity was assessed in working germplasm collection comprising of 207 kabuli chickpea accessions for seven yield attributes. Wide genetic variation was seen in the kabuli germplasm for seven important yield and yield traits. Genetic diversity in the germplasm was evident in the form of 13 distinct clusters, out of which cluster I accommodated maximum number with 67 genotypes followed by cluster III with 62 genotypes. The diversity of the genotypes was mainly due to phenological traits days to 50 % flowering, which contributed 39.41 per cent to the total diversity followed by days to maturity (35.76 %). Variation is seed size (100- seed weight) contributed 14.29 per cent to the total diversity measured. The genotypes in cluster IX were the most divergent which was shown by their higher intra cluster distance (9.04) followed by the genotypes in cluster XII, VI and V. The diversity between cluster X and cluster VI was the highest as their inter cluster distance was the highest (27.25) followed by cluster XII and VI (26.05). Low inter cluster distance (3.86) was observed between clusters X and VII. The most promising and divergent kabuli germplasm lines LBeG 7, NBeG 855, ICCV 08313, ICCV 083308, ICC 15568 and NBeG 731 were identified for inclusion in hybridization for realizing desirable transgressive segregants.

Keywords: Chickpea, kabuli, yield traits, genetic diversity, inter and intra cluster distance.

Chickpea is the most dominant food legume crop in the world. Chickpea seed contains 17-24 % of protein, 61.2% carbohydrates, 9.8 % moisture (Smartt, 1976) and essential amino acids like isoleucine, leusine, lysine, phenylalanine and valine (Karim and Fattah, 2006). Introduction of chickpea crop in a cereal based crop rotation can break the disease and pest cycle and increase the productivity of the entire rotation (Jodha and Subbarao, 1987) and also plays an important role in sustaining soil fertility (Singh and Shiv, 2013).

India is the largest producer of chickpea in the world contributes about 70 % in area i.e. 10.56 million ha with production and productivity of 11.22 million tons and 1063 kg/ ha, respectively (FAOSTAT, 2019). In India, Madhya Pradesh is the largest producer sharing 40 % of total production followed by Maharashtra. During recent years chickpea has to spread to Southern India and being grown in larger areas in Karnataka and Andhra Pradesh. In Andhra Pradesh, the area under chickpea cultivation is 4.59 lakh ha with the production of 5.59 lakh tones and productivity of 1218 kg/ha (Directorate of Economics and Statistics, Planning Department, Andhra Pradesh, 2019-20). Farmers in Andhra Pradesh also showing interest in growing large seeded kabuli chickpea as the market prices of these kabuli types are higher compared to desi varieties. The demand for extra-large seeded kabuli types was met through import mainly from Mexico and Turkey (Yadav *et al.,* 2004). Breeding and selection for large-seeded kabuli chickpea varieties, therefore, is an imperative requisite to meet the farmer's demand and concern. Cultivation of kabuli chickpeas raises the status of chickpea from a poor farmer's subsistence crop to a cash crop (Kashiwagi *et al.,* 2007). Regional Agricultural Research Station (RARS), Nandyal of Acharya N.G. Ranga Agricultural University (ANGRAU) is responsible for location specific research in chickpea crop in Andhra Pradesh. The first step in the utilization of germplsam in crop improvement is its evaluation for genetic diversity for economically important traits. Genetic divergence among the parents to be utilised in the varietal improvement is pre-requisite and vital to generate variability for selection in segregating generations for developing new and improved varieties (Nimbalkar *et al*., 2017).

Therefore, the present study was planned with 207 kabuli chickpea genotypes during *rabi*, 2019-20 in a Randomized Block Design (RBD) with two replications at the experimental farm of Regional Agricultural Research Station (RARS), Nandyal of Andhra Pradesh. Each line was raised in two rows of 4 m length with a spacing of 30 cm between the rows and 10 cm between the plants. Data were recorded on seven characters *viz*., days to 50% flowering, days to maturity, number of primary branches,

Table 1. Grouping of 207 genotypes of kabuli chickpea into different clusters

Cluster Number	Number of genotypes	Genotype(s)
I	67	NBeG 48, NBeG 458, NBeG 706, NBeG 716, NBeG 717, NBeG 718, NBeG 720, NBeG 793, NBeG 831, NBeG 835, NBeG 836, NBeG 837, NBeG 839, NBeG 845, ICC 030147, ICC 3645, ICC 8261, ICC 14194, ICC 15568, ICCV 04305, ICCV 05306,ICCV 06304, ICCV 06306, ICCV 06307, ICCV 07301, ICCV 07310, ICCV 08302, ICCV 08303, ICCV 08305, ICCV 08306, ICCV 08311, ICCV 08313, ICCV 10303, ICCV 10306, ICCV 11301, ICCV 11303,ICCV 11312, ICCV 11314, ICCV 11317, ICCV 14507, ICCV 89224, ICCV 95333, ICCV 96322, IPCK-12-313, B-12, BG-1053CSJK-74, GJG-0724, GNG-1581, HK-06-163, HK-08-206, JGK-18, K 005, K 009, PG-05107, PG-12407, RVSSG-56, Virat, NBeG 471, ICCV 15308, NBeG 790, NBeG 841, B-218, ICEL-5, JGK-13, JGK-16, K 002.
II	21	NBeG 419, NBeG 456, NBeG 457, NBeG 842, NBeG 844, NBeG 846, ICC 12487, ICCV 08301 , ICCV 10301, ICCV 10305, ICCV 10307, ICCV 10308, ICCV 10314, ICCV 10315, ICCV 10401, ICCV 10410, ICCV 89314, ICCV 97105, ICCV 97306, IPCK-08-130 ,NBeG 444.
III	62	NBeG 42, NBeG 119, NBeG 124, NBeG 241, NBeG 324, NBeG 367, NBeG 399, NBeG 403, NBeG 415, NBeG 459, NBeG 510, NBeG 529, NBeG 705, NBeG 779, NBeG 721, NBeG 802, ICC 030144, ICCV 03402, ICCV 04301, ICCV 05303, ICCV 06301, ICCV 06305, ICCV 07302, ICCV 09310, ICCV 09312, ICCV 09313, ICCV 09315, ICCV 09317, ICCV 11318, ICCV 12301, ICCV 12302, ICCV 12304, ICCV 12305, ICCV 12306, ICCV 12307, ICCV 12310, ICCV 12311, ICCV 12312, ICCV 12314, ICCV 12316, ICCV 12318, AKG-2002-1,BG-3025,CSJK-42, GNG-1958, JGK-03-304, JGK-17, KAK-2, L-551,PG-0215-2, RVSSG-62, Vihar,NBeG 177,NBeG374,ICCV 15304,ICCV 09303,ICCV 09306 ,ICCV 10310,ICCV 10404, NBeG 466, BG-2094, BG-3012.
IV	17	NBeG 840, NBeG855, ICCV 01301, ICCV 11302, ICCV 11305, ICCV 11307, ICCV 11309, IPCK-06-143, IPCK-0762, HK-06-173, HK-08-163, HK-08-231, NBeG 464, GNG-1886, ICCV 11304, BG-5023, HK-08-212.
V	16	NBeG 122, NBeG 732, ICCV 07312, ICCV 08308, ICCV 08312, ICCV 10409, ICCV 11313, CSJK-25, CSJK-68, Doller-3, K 001, K 003, K 850, Kripa, MNK-1, CSJK-24.
VI	3	IPCK-11-129, GNG-1499, GNG-1969.
VII	1	NBeG 810
VIII	1	L-550
IX	11	NBeG 104, NBeG 440, NBeG 460, NBeG 528, NBeG 722, NBeG 799, NBeG 800, ICC 16216, ICCV 08304, ICCV 08310, ICCV-2.
X	1	NBeG 163
XI	1	NBeG 178
XII	5	NBeG 723, NBeG 731, NBeG 832, NBeG 833, K 007.
XIII	1	LBeG 7

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plant height (cm), number of pods, 100- seed weight (g) and seed yield per plant (g). Genetic diversity analyses were done as per Mahalanobis (1936), Rao (1952) and Singh and Chaudhari (1979).

The analysis of variance revealed significant mean sum of squares for all the traits which is an indication of noteworthy variability among the genotypes. The genetic diversity among 207 kabuli chickpea accessions was arrived by employing D^2 statistics which grouped them into dissimilar clusters (**Table 1**). The diversity of the germplasm is amply evident in the form of 13 clusters, separated by inter cluster distances as small as 3.86 (X and VII) to as high as 227.25 (X and VI). Cluster I was the largest which consisted of 67 genotypes, followed by cluster III with 62 genotypes. Cluster II, IV, V, IX, XII and VI had 21, 17, 16, 11, 5 and 3 genotypes respectively, while remaining clusters VII, VIII, X, XI and XIII had only one genotype each. Devi *et al*. (2004) reported that the pattern of clustering had no general association between ecological distributions of genotypes. This is evident in case of cluster I, as it had more number of genotypes and most of them originated from different places. Diversity among these genotypes might be due to selection criteria employed for one particular trait, selection pressure exercised and the differential adoption in environments (Murthy and Arunachalam, 1996). Study of relative importance of the characters makes it possible to discard characteristics that contribute less to the discrimination of the evaluated materials, reducing costs and labour in the next experiments. Phenological traits *viz.*, days to 50 % flowering (39.41 %) and days to maturity (35.76 %) contributed maximum to the total diversity. These traits were followed by 100-seed weight (14.29 %), plant height (5.06 %), seed yield per plant (3.38 %) and number of pods per plant (1.60 %) (**Table 2**). The similar results were reported by Kuldeep *et al*. (2015).

The genotypes of clusters with high inter cluster distance are diverse and may give high heterotic response if utilized in the hybridization programme and may release hidden variability in early generations itself by breaking tight linkages (Sreelakshmi *et al.,* 2010). In present study, inter and intra cluster distances are presented in **Table 3**. The inter cluster distances were as small as 3.86 (X and VII) to as high as 27.25 (X and VI). The diversity between the genotypes of cluster X and VI was the highest followed by that between clusters XII and VI (26.05) and between clusters VII and VI (25.67). The diversity between the genotypes of clusters X and VII was

Table 2. Relative contribution of yield and yield attributes towards total genetic diversity in chickpea

Character	Contribution (%)	
Days to 50% flowering	8402	39.41
Days to maturity	7625	35.76
Number of primary branches	107	0.50
Plant height	1079	5.06
Number of pods per plant	342	1.60
Seed yield/ plant	720	3.38
100-seed weight	3046	14.29

Table 3. Average inter and intra cluster distances of 13 clusters generated among 207 chickpea genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**5.15**	8.2	9.83	8.12	8.17	13	15.26	9.44	8.66	16.83	13.75	15.64	9.48
II		**5.75**	14.85	8.8	11.98	10.25	20.93	14.48	10.62	22.6	19.28	21.11	13.46
III			**6.28**	14.01	10.58	19.93	8.27	7.89	10.47	10.01	8.06	9.84	11.91
IV				6.98	11.49	9.58	19.29	11.88	11.32	20.84	16.76	19.75	9.65
V					8	16.66	14.76	11.43	11.9	15.98	14.41	14.49	11.02
VI						8.4	25.67	17.63	15.43	27.25	22.84	26.05	14.65
VII							0	10.4	15.07	3.86	5.15	6.29	15.3
VIII								0	10.98	11.79	7.4	12.34	10.27
IX									9.04	17.05	13.7	16.01	12.25
X										0	6.11	7.56	16.44
XI											0	9.12	12.67
XII												8.66	15.74
XIII													0

Table 4. Cluster mean values for different traits in chickpea

Clusters	Days to 50% flowering	Days to maturity	Numberof primary branches	Plant height (cm)	Number of pods/ plant	Seed yield/ plant (g)	100-seed weight (g)
I	50.03	89.54	3.84	40.89	15.26	5.65	37.59
II	52.98	96.69	3.12	38.05	12.33	4.24	35.33
III	42.54	83.05	4.19	40.35	14.63	4.8	34.44
IV	56.21	90.56	3.76	43.36	21.84	5.86	31.53
V	48.28	86.66	3.81	42.98	11.34	5.43	50.02
VI	62.17	96.5	3.83	42.3	22.43	4.78	26.25
VII	37.5	76	4	42.2	18.15	5	33.1
VIII	48.5	80.5	2.5	45.65	3.8	1.9	26.5
IX	46.41	91.05	3	38.91	22.75	5.94	26.85
X	38	73	5	33.5	17.7	6.35	36.65
XI	43	76	4.5	37.95	22.85	5.55	24.45
XII	37.3	77	3.3	44.88	21.64	7.52	40.89
XIII	53.5	84	4.5	43.5	66.35	21.5	32.45

Table 5. *Per se* performance of promising genotypes

S.No.	Genotype	Cluster Number	Days to 50% flowering	Days to maturity	Number of primary branches	Plant height (cm)	Number of pods/ plant	100-seed weight (g)	Seed yield/ plant (g)
1	LBeG 7	XIII	54	84	4.5	43.5	**66.4**	32.5	**21.5**
2	NBeG 833	VII	37	75	3.5	49.5	17.5	**55.9**	5.8
3	NBeG 163	X	38	**73**	5.0	33.5	17.7	36.7	6.4
4	NBeG 855	IV	55	91	3.5	43.5	48.0	32.0	15.3
5	ICCV 08313	I	48	89	2.5	39.7	29.0	40.8	14.8
6	ICCV 08308	V	45	92	4.5	37.2	29.9	42.7	12.7
7	ICC 15568	I	50	88	4.0	41.5	33.9	33.8	11.5
8	NBeG 731	XII	38	78	4.0	49.7	24.9	44.0	10.3

the lowest due to their low inter cluster distance (3.86). Cluster VI expressed maximum inter cluster distance with most other clusters. The maximum intra cluster distance was observed in cluster IX (9.04) followed by cluster XII (8.66), VI (8.40) and V (8.00) indicating the existence of within cluster variation and diverse genotypes that fell in these clusters.

Mean values of clusters with respect to traits are useful for choosing potential genotypes for hybridization programme. Cluster mean values of 207 genotypes for seven characters are presented in **Table 4**. Promising clusters for various traits were, cluster XIII for number of pods per plant (66.35) and seed yield per plant (21.50), cluster V for 100-seed weight (50.20), cluster X for number of primary branches (5.00) and days to maturity (73). Based on *Per se* performance of genotypes (**Table 5**.) NBeG 833 (cluster VII) for 100-seed weight (55.9g), LBeG 7 (cluster XIII) for pods per plant (66.4) and seed yield per plant (21.5) and NBeG 163 (cluster X) for days to maturity (73) were identified as promising for yield attributes. Other promising genotypes for seed yield are LBeG 7, NBeG 855, ICCV 08313, ICCV 083308, ICC 15568 and NBeG 731. These genotypes identified could be included in hybridization programme for realizing desirable transgressive segregants for possible genetic improvement of kabuli chickpea.

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