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Research Note

Identification of novel donors for yield contributing traits from Chickpea Adaptive Trials (CAT) of ICARDA for base broadening of Indian chickpea (*Cicer arietinum* L.)

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Abstract
The Chickpea Adaptation Trial (CAT) of International Center for Agricultural Research in the Dry Areas (ICARDA), comprising of 36 genotypes was raised during *rabi* 2019-20 for estimation of variability, heritability and association among yield and its components characters. The experiment was carried out in a randomized complete block (RCBD) design with two replications. Analysis of variance showed significant variability among the genotypes used for the study. Days to flowering and days to maturity were observed to record high heritability, which indicated the influence of dominant and epistatic gene action for these traits. Character association study among yield and yield contributing traits revealed that seed yield exhibited significant positively correlation with test weight. All the chickpea genotypes were grouped into three discrete clusters with higher genetic diversity for different traits suggesting good amount of variability among the genotypes.

Keywords: Chickpea, Adaptation Trial, Variability, Correlation, Clustering.

Chickpea (*Cicer arietnum* L.) is a self-pollinated grain legume with diploid chromosomal number of 2n=16 and having genome size of 738 Mb containing 28,269 genes (Varshney *et al.*,2013). It is a cool season crop cultivated in over 50 countries (Upadhyaya *et al.*, 2011). With annual production of around 10.41 Mt from an area of approximately 9.54 Mha, India contributes major share of world's chickpea area (70%) and production (67%) and the average yield is approximately 912 kg/ha (FAOSTAT, 2019). Basically, there are two types of chickpea cultivated worldwide, *Kabuli* and *Desi*, introducing two diverse gene pools (Nawroz and Hero, 2011). Earlier studies have suggested that the chickpea from Indian subcontinent has a narrow genetic pool (Bharadwaj *et al.*, 2011) which is limiting the genetic improvement of chickpea through conventional breeding efforts. Variability is prerequisite for effective plant breeding program for obtaining desirable genotypes. Information on correlations among seed yield and its component traits can hasten the progress of selection. Seed traits like seed size is very important factor in improving yield and productivity of chickpea (Tapan *et al.*,2015). The present investigation tries to identify novel sources for yield improvement in chickpea from the Chickpea Adaptation Trial (CAT) of ICARDA for base broadening.

Chickpea Adaptation Trial (CAT) comprising of 36 lines obtained from ICARDA were evaluated in post rainy season during *rabi* 2019-20 under timely planting conditions with a check variety, Pusa 3022. The field

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experiment was conducted at the farm of ICAR-Indian Agricultural Research Institute, New Delhi (28.63° N, 77.17° E). The genotypes were evaluated in randomized block design with two replications. Each genotype was planted in a single row of four meters length with a spacing of 30 cm between rows and 15 cm between plants. The recommended agronomic practices were followed during the crop season for proper crop growth. Observations were recorded on six parameters *viz*., days to flowering (DTF), days to maturity (DTM), plant height, test weight (TW) and seed yield (kg/ha) (**Table 2**). The mean data were subjected to descriptive statistics like mean, maximum and minimum, SD, CV were obtained using R Software. Biometrical methods were followed to estimate genotypic and phenotypic coefficient of variation (Burton 1952), heritability in broad sense (Lush 1940), genetic advance (Johnson *et al.*,1955) and correlation (Singh and Chaudhary, 1979).

Range, mean, standard deviation, analysis of variance (ANOVA), genetic variance, heritability and correlation analysis between pairs of the characters were estimated with the help of R software. Cluster analysis was done using NTSYSPC software (version 2.1 b) for making similarity index matrix. Preliminary variability study was performed with TraitStat, R package, developed by Nitesh *et al.* (2021).

The ANOVA revealed significant genetic variability among all the 36 genotypes except for days to flowering (**Table 1**). Days to flowering ranged from 52 days to 59 days with an average of 55 days while the days to maturity ranged from 135 days to 140 days with an average of 138 days. Plant height ranged from 56 cm to 92 cm with a mean value of 77 cm. Test weight ranged from 20 g to 40 g for 100 seeds. Seed yield ranged from 680 kg/ha to 2300 kg/ha with a mean of 1520 kg/ha. Coefficient of variation at phenotypic and genotypic level was relatively high for plant height and test weight and was moderate for seed yield/ha., days to flowering and days to maturity. The magnitude of PCV was higher than GCV for all traits indicating the influence of environment on expression of these traits. Heritability estimates were high for days to flowering (84.32%), days to maturity (80.21%) and test weight (99.64%). All traits showed high heritability except plant height (58.41%) and yield/ha. (42.40%), which exhibited moderate heritability (**Table 2**). High heritability of all the traits was also reflected by the minor difference in magnitudes of PCV and GCV. High estimates of heritability of the traits under study could be due to the larger genetic variability of the genotypes. Saleem *et al.* (2008), Durga *et al.* (2007), Thapa *et al.* (2022) and Arshad *et al.* (2004) observed high heritability in chickpea for days to flowering, days to maturity, test weight and plant height. High values obtained for heritability and genotypic variation indicated the presence of additive genetic effects, because of which conventional selection methods can be practiced for developing superior varieties Noor *et al.* (2003). Meanwhile, those traits are heavily controlled by the environment showed very low values for heritability and genotypic variation Arshad *et al.* (2004).

Character association among yield and yield contributing traits were studied through analysis of correlation coeffecients and the same are furnished in **table 3.** Seed yield showed positive correlation with days to flowering, days to maturity, plant height and test weight. Thus for improvement of yield in chick pea, days to flowering, days to maturity, plant height and test weight could be used as selection criteria. Days to flowering showed positive correlation with plant height and seed yield per hectare and negative correlation was observed with days to maturity and test weight. Days to maturity exhibited negatively significant correlation with days to flowering. Similar findings were reported by Sanjay *et al.* (2017), Samyuktha *et al.* (2018) and Agarwal *et al.* (2018).

Clustering of the 36 chickpea genotypes was done on the basis of Non-hierarchical Euclidean cluster distance and similarity index matrix using NTSYSPC software (version 2.1 b) . The clustering pattern reveled three prominent groups (**Fig. 1. and Table 4**). Among the clusters, cluster II was the largest with 28 genotypes, while cluster I was observed to be composed of seven genotypes, while cluster III was solitary. The cluster II was further

Table 1. ANOVA for the characters of 36 chickpea genotypes.

			ANOVA		
Traits	**DF**	**SS**	**MSS**	**F VALUE**	**Significant**
DTF	35	150.28	4.29	0.87	0.66
DTM	35	93.81	2.68	1.29	0.22*
PH	35	5067.20	144.77	61.51	0.00*
TW	35	1272.40	36.35	30.67	0.00*
SY	35	12.44	0.35	279.13	0.00*

*Significant at 5%

DTF-Days to flowering (Number of days), DTM- Days to maturity (Number of days), PH-Plant height (cm), TW-Test weight (gram), SY-Seed yield (Kg/ha).

Table 2. Character means, range, coefficient of variation, heritability and variances of 36 chickpea genotypes.

S. No.	Genotype Name	DTF	DTM	PH	TW	SY
1	FLIP88-85C	54.00	139.00	82.00	32.50	680.00
2	FLIP12-202C	53.00	138.00	73.00	29.00	870.00
3	FLIP12-131C	55.00	138.00	71.00	39.00	1000.00
4	FLIP12-261C	55.00	140.00	84.00	31.50	1010.00
5	FLIP12-138C	55.00	138.00	78.00	29.00	1020.00
6	FLIP12-55C	57.00	138.00	66.00	28.50	1120.00
7	FLIP12-145C	54.00	138.00	61.00	23.00	1130.00
8	FLIP12-161C	54.00	137.00	68.00	32.50	1160.00
9	ILC482	54.00	139.00	70.00	27.00	1170.00
10	FLIP12-176C	58.00	137.00	57.00	28.50	1200.00
11	FLIP12-19C	54.00	136.00	81.00	31.00	1230.00
12	FLIP12-281C	55.00	136.00	76.00	25.00	1230.00
13	FLIP12-333C	58.00	138.00	81.00	31.00	1290.00
14	FLIP12-09C	56.00	139.00	75.00	31.00	1320.00
15	FLIP12-342C	55.00	137.00	71.00	32.50	1360.00
16	FLIP12-334C	54.00	139.00	77.00	28.50	1410.00
17	FLIP12-53C	57.00	136.00	89.00	31.00	1530.00
18	FLIP12-278C	56.00	140.00	77.00	32.50	1550.00
19	FLIP12-196C	55.00	138.00	86.00	28.50	1600.00
20	FLIP12-192C	53.00	137.00	91.00	25.00	1600.00
21	FLIP12-263C	57.00	136.00	71.00	30.00	1620.00
22	FLIP12-107C	56.00	137.00	73.00	32.50	1630.00
23	FLIP12-146C	55.00	137.00	89.00	25.00	1630.00
24	FLIP12-276C	54.00	139.00	78.00	34.00	1650.00
25	FLIP 82-150C	58.00	137.00	79.00	23.00	1670.00
26	FLIP12-330C	54.00	137.00	77.00	28.50	1680.00
27	FLIP12-85C	55.00	139.00	81.00	23.00	1720.00
28	FLIP93-93C	53.00	137.00	63.00	23.00	1740.00
29	FLIP12-86C	54.00	139.00	86.00	21.00	1840.00
30	FLIP12-195C	53.00	139.00	84.00	22.50	1990.00
31	FLIP12-319C	56.00	137.00	89.00	32.50	2000.00
32	FLIP12-139C	53.00	140.00	77.00	21.00	2100.00
33	FLIP12-128C	55.00	137.00	71.00	33.00	2170.00
34	FLIP12-169C	56.00	139.00	89.00	34.50	2290.00
35	FLIP12-193C	54.00	139.00	74.00	27.50	2310.00
36	Pusa 3022	57.00	137.00	66.00	29.00	2310.00
	Mean	54.81	137.65	76.57	28.79	1520.00
	Minimum	52.00	135.00	56.00	20.00	680.00
	Maximum	59.00	140.00	92.00	40.00	2300.00
	SE	2.22	1.44	1.53	1.09	0.04
	Std. Deviation	1.47	1.16	8.51	4.26	4.21
	CV	4.06	1.05	2.00	3.78	2.34
	GCV %	18.22	4.66	96.40	78.10	34.02
	PCV %	27.92	9.87	97.23	79.44	34.09
	Heritability (bs)	84.32	80.21	58.41	99.64	42.40

GCV: Genotypic Coefficient of variation, PCV: Phenotypic Coefficient of variation Genotypic, SE: Standard error, CV: Coefficient of variation. DTF-Days to flowering (Number of days), DTM- Days to maturity (Number of days), PH-Plant height (cm), TW-Test weight (gram), SY-Seed yield (Kg/ha).

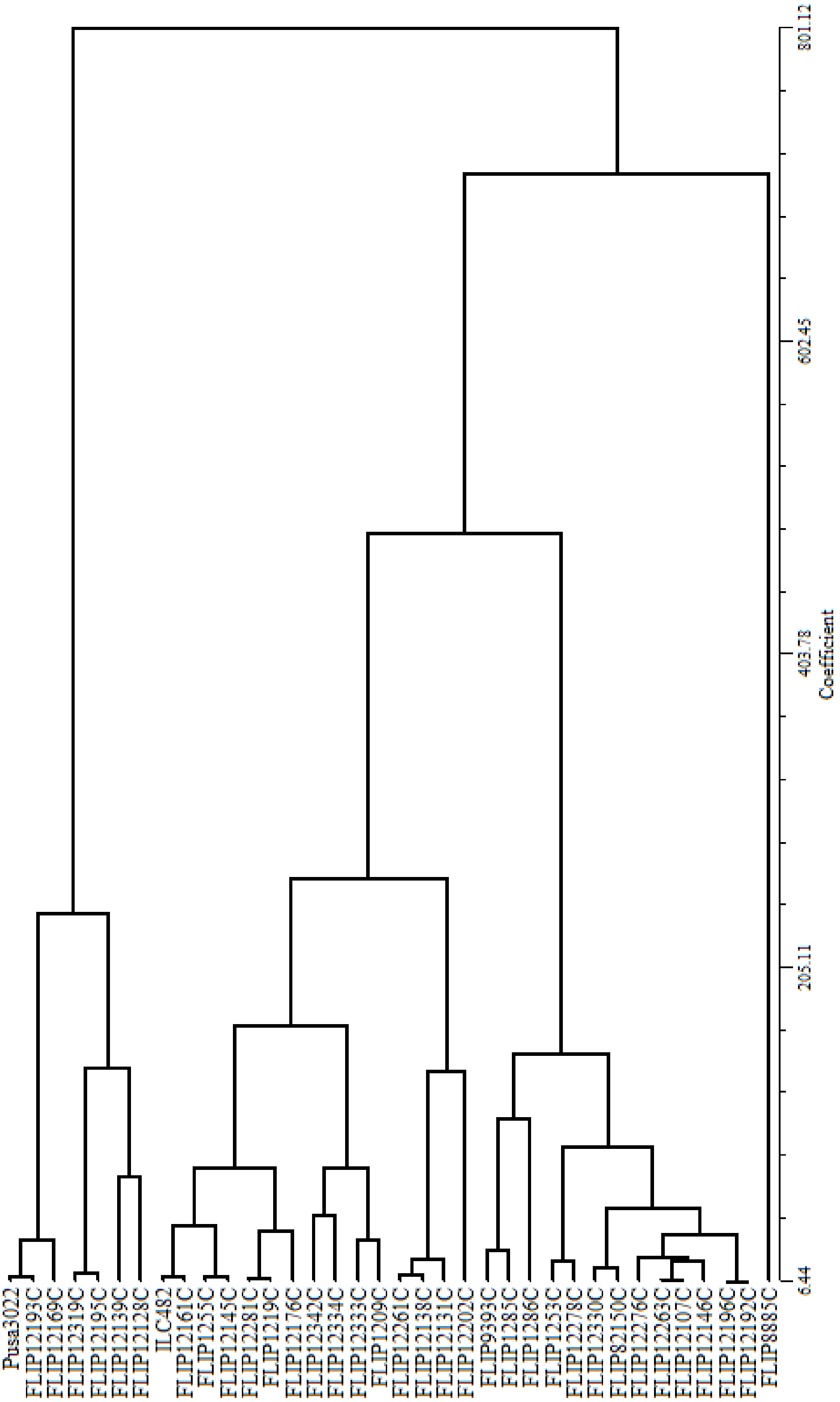

Fig. 1. Sequential agglomerative hierarchical non-overlapping (SAHN) clustering of the 36 chickpea genotypes

Table 3. Estimates of phenotypic correlation coefficient among chickpea lines.

Traits	DTF	DTM	PH	TW	SY
DTF	1				
DTM	-0.285*	1			
PH	0.07	0.070	1		
TW	-0.093*	0.069	-0.01	1	
SY	0.017	0.051	0.199	0.221*	1

DTF-Days to flowering (Number of days), DTM- Days to maturity (Number of days), PH-Plant height (cm), TW-Test weight (gram), SY-Seed yield (Kg/ha).

Table 4. Clustering pattern of 36 chickpea genotypes on the basis of Non-hierarchical Euclidean cluster analysis of five characters.

Cluster number	Number of genotypes	Genotypes
I	7	Pusa3022, FLIP12193C, FLIP12169C, FLIP12319C, FLIP12195C, FLIP12139C, FLIP12128C
II A	15	ILC-482, FLIP12161C, FLIP1255C, FLIP12145C, FLIP12281C, FLIP1219C, FLIP12176C, FLIP12342C, FLIP12334C, FLIP12333C, FLIP1209C, FLIP12261C, FLIP12138C, FLIP12131C, FLIP12202C
II B	13	FLIP9393C, FLIP1285C, FLIP1286C, FLIP1253C, FLIP12278C, FLIP12330C, FLIP82150C, FLIP12276C, FLIP12263C, FLIP12107C, FLIP12146C, FLIP12196C, FLIP12192C
III	1	FLIP8885C

subdivided into two major group among which major group IIA was observed to be composed of 15 genotypes and IIB was composed of 13 genotypes.. Mean performance value for different traits studied revealed that the highest mean value for days to 50% flowering (54.90) and days to maturity (139.00) were recorded in cluster IIA and cluster III respectively indicating that the genotypes of these clusters were delayed in flowering and maturity than the remaining genotypes (**Table 5**). Clusters III and cluster IIB recorded lowest value for days to 50% flowering (54.00) and days to maturity (137.38) indicating their earliness towards both traits respectively. Genotypes of cluster III were also having highest plant height (82.00) while, its lowest value was recorded in cluster IIA (72.53). High seed yielding genotypes were grouped in cluster I (2168.00 kg/ha) whereas, the ones with low mean yield were grouped in cluster III (682.00 kg/ha). Test weight mean value was found highest in cluster III (32.50), while it was lowest in cluster IIB (27.46). The genotypes FLIP12193C and FLIP12169C were found to be having maximum similarity with Pusa 3022 (Check) as they fall on a single branch. The genotype FLIP8885C was observed to be lowest yielder and hence could have been clustered separately from others. The above result indicates that sufficient genetic diversity existed among these genotypes and hence crossing among the diverse genotypes could result in generation of superior segregants. Similar finding was reported by Naveed *et al.* (2015). Raman and Singh (1987) and Vijayakumar *et al.* (2017) suggested that genotypes coming under those clusters which have high inter cluster distances between them could be used in plant breeding programmes for achieving more variation, which complements the present study.

Table 5. Cluster means for three clusters in chickpea genotypes.

Cluster number	Number of genotypes	DTF	DTM	PH	TW	SY
I	7	54.71	138.07	78.29	28.57	2168.26**
II A	15	54.90**	137.60	72.53*	29.80	1168.44
II B	13	54.81	137.38*	79.88	27.46*	1649.38
III	1	54.00*	139.00**	82.00**	32.50**	682.46*

Note- * indicate lower and ** indicate higher value. DTF-Days to flowering (No. of days), DTM- Days to maturity (No. of days), PH-Plant height (cm), TW-Test weight (gram), SY-Seed yield (Kg/ha.).

Plant yield values of some genotypes were comparable to the standard check Pusa-3022. FLIP12-193C, FLIP12-169C, FLIP12-128C and FLIP12-1139C were higher yielding and thus are promising indicating their suitability to be used as donors.

Based on the study it was observed that the genotypes FLIP12-193C, FLIP12-169C, FLIP12-128C and FLIP12-1139C were comparable to the standard check Pusa-3022, for seed yield and could be used as donors for yield improvement. Good amount of variability among the genotypes was noticed for all the traits presenting scope for selection. The high values of heritability and strong correlation coefficients indicated that Test weight, plant height, days to maturity and seed yield (kg/ha.) could be reliably used to improve chickpea yield through indirect selection.

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