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Research Note

Genetic variability studies in extra large and large seeded *kabuli* chickpea (*Cicer arietinum*)

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Abstract
Thirty *kabuli* chickpea genotypes were evaluated in a randomized block design with three replications. Analysis of variance revealed significant genotypic differences for all the nineteen characters with wide range of variability. Estimates of genotypic and phenotypic co-efficients of variation were high for number of pods per plant and number of seeds per plant. High heritability accompanied with high genetic advance was shown by days to 50% flowering, plant height, the number of pods per plant, the number of seeds per plant, 100 grain volume, cooking time for soaked seeds, 100 seed weight, shoot biomass per plant, harvest index and seed yield per plant which indicated that the heritability is due to additive gene effects and selection of plants can be done directly on the basis of phenotypic expression of these characters.

Keywords
Genetic variability, Chickpea, Heritability.

Chickpea [*Cicer arietinum* (L.) 2n=2x=16] belongs to genus Cicer, family Fabaceae, and sub family Papilionaceae. It is an annual, self-pollinating, diploid pulse crop with a genome size of 750 Mbp (Akanksha *et al*., 2016). Chickpea is an important food legume and on an average, chickpea seed contains 23% protein, 64% carbohydrates, 47% starch, 5% fat, 6% crude fiber, 6% soluble sugar and 3% ash. The mineral component is high, phosphorus (340 mg/100 g), calcium (190 mg/100 g), magnesium (140 mg/100g), iron (7 mg/100g) and zinc (3 mg/100 g). Chickpea protein has the highest digestibility when compared to other dry edible legumes (Ujinwal *et al*., 2019). It has the ability to fix atmospheric nitrogen and improve soil fertility with low added cost of production (Ali *et al*., 2008).

Globally chickpea is the second most important pulse crop, grown in an area of 14.60 M ha with a production of 14.8 M tons and an average productivity of 1014 kg ha^{-1}. In India, chickpea is grown annually in an area of 9.54 M ha with 9.07 M tons of production and 951.4 kg ha^{-1} productivity (FAOSTAT, 2019). Although, the major crop improvements have been made in the recent years through the evolution of high yielding and disease resistant chickpea cultivars, breeding for improved types is a continuous process and requires strenuous efforts by breeders (Ali *et al*., 2008). For any crop improvement programme, genetic variability is the first pre-requisite for development of new varieties. The choice of best yield attribute can be made on the basis of the extent of genetic variability present in the genetic materials. Heritability measures the fraction of phenotypic variability that can be attributed to genetic variation. Genetic advance provides information on possible improvement of mean genotypic value of particular character through selection. Hence, the present investigation was aimed to estimate the phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance for 19 different characters in chickpea.

The present investigation was taken up during *Rabi* 2018-19 at Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh, India. Thirty genotypes of

chickpea *viz*., NBeG 399, NBeG 440, NBeG 458, NBeG 719, NBeG 723, NBeG 724, NBeG 789, NBeG 805, NBeG 810, NBeG 829 NBeG 833, NBeG 835, NBeG 837, NBeG 844, NBeG 1010, ICCV 171301, ICCV 171302, ICCV 171303, ICCV 171305, ICCV 171306, ICCV 171313, ICCV 177314, Phule G 15307, RKGK 499 NBeG 119, MNK 1, JGK 5, Phule G0517, KAK 2, Vihar were sown in a Randomized Block Design with three replications. Each genotype was sown in a double row plot of 3m length with inter row spacing of 30 cm and intra row spacing of 10 cm. Two supplemental irrigations ere provided through sprinklers at 35 and 55 days after sowing for irrigated condition. Observations were recorded for 19 parameters *viz*., days to 50% flowering, days to physiological maturity, SCMR, plant height, the number of primary branches per plant, the number of secondary branches per plant, the number of pods per plant, the number of seeds per plant, seed diameter, protein content, 100 seed weight, 100 grain volume, water absorption after soaking, volume expansion after soaking, cooking time for raw seeds, cooking time for soaked seeds, shoot biomass per plant, harvest index and seed yield per plant. The total variability present in each character among 30 genotypes was tested for significance by using analysis of variance as described by Panse and Sukhatme (1961).

Through the results obtained from the ANOVA the genetic parameters were estimated as follows

Variance
The genotypic and phenotypic variances were calculated according to the formulae proposed by Burton and Devane (1953).

$$\text{Genotypic variance}(\sigma_g^2) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{\text{Number of replications}}$$

Phenotypic variance ($\sigma_p^2\sigma_p^2$) = Genotypic variance

$(\sigma_g^2) + \text{Error variance } (\sigma_e^2)$

Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed by the formulae given by Burton (1952).

$$\text{GCV}(\%) = \frac{\text{Genotypic standard deviation}}{\text{General Mean}} \text{x } 100$$

$$\text{PCV}(\%) = \frac{\text{Phenotypic standard deviation}}{\text{General Mean}} \text{x } 100$$

Broad sense Heritability

Heritability in broad sense was estimated by using formula given by Lush (1940).

$$\text{Broad sence Heritability}(h_b^2) = \frac{\text{Genotypic variance}(\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \text{x } 100$$

Phenotypic variance ($\sigma_p^2\sigma_p^2$) = Genotypic variance

$(\sigma_g^2) + \text{Error variance } (\sigma_e^2)$ $(\sigma_g^2) + \text{Error variance } (\sigma_e^2)$

Genetic advance

The genetic advance was estimated by the formula given by Johnson *et al.* (1955a).

$$GA = K.\sigma_p.h_b^2$$

where,

GA = Genetic advance

$\sigma_p\sigma_p$ = Phenotypic standard deviation

$h_b^2h_b^2$ = Broad sense Heritability

k = Selection differential at 5% selection intensity (2.06)

Genetic advance as per cent of mean (GAM)
Genetic advance as per cent of mean was calculated as per the formula.

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance (GA)}}{\text{Grand Mean}(\bar{X})} \text{x } 100$$

The results of ANOVA for 19 characters in 30 genotypes of *kabuli* chickpea were presented in Table 1. Analysis of variance revealed highly significant differences among the thirty genotypes for all the traits.

From the table 2 depicted, a close correspondence between genotypic and phenotypic coefficient of variation can be seen for all the recorded traits and accordingly less influenced by the environment. Number of pods per plant (21.60%, 24.94%) and the number of seeds per plant (28.09%, 30.23%) showed high estimates of GCV and PCV which indicates that the environmental influence on the expression of these traits were minor. Thus selection can be applied on the traits to isolate more promising line. Similar results were reported by Vaghela *et al*. (2009), Saki *et al*. (2009), Pandey *et al*. (2013), Hagos *et al*. (2018).

Table 1. Analysis of variance for 19 characters in *kabuli* chickpea

S.No	Character	Mean sum of squares		
		Replications	Treatments	Error
		(df : 2)	(df: 29)	(df: 58)
1	Days to 50% flowering	1.91	121.57**	2.20
2	Days to Physiological maturity	2.63	93.14**	1.71
3	SCMR	17.01	41.74**	12.77
4	Plant height (cm)	7.91	106.55**	4.00
5	Number of primary branches per plant	0.06	0.15**	0.06
6	Number of secondary branches per plant	2.40	7.86**	2.02
7	Number of pods per plant	8.61	48.19**	4.82
8	Number of seeds per plant	18.61	131.24**	6.60
9	Seed diameter (mm)	0.13	0.45**	0.06
10	Protein content (%)	5.54	15.87**	2.50
11	100 grain volume (ml)	1.64	105.42**	2.23
12	Water absorption after soaking (%)	7.19	27.92**	6.12
13	Volume expansion after soaking (%)	4.86	50.18**	3.80
14	Cooking time for raw seeds (min)	10.54	160.68**	3.95
15	Cooking time for soaked seeds (min)	31.11	136.59**	11.23
16	100 seed weight (g)	0.04	115.25**	2.66
17	Shoot biomass per plant (g)	2.73	16.41**	2.38
18	Harvest index (%)	2.30	124.79**	6.14
19	Seed yield (g/plant)	1.45	5.19**	0.61

* Significant at P ≤ 0.05; ** Significant at P ≤ 0.01

The estimates of genetic variability parameters for 19 characters in 30 genotypes were presented in Table 2

Table 2. Estimates of genetic parameters for 19 characters in 30 chickpea genotypes

S.No.	Characters	GCV (%)	PCV (%)	Heritability (%)	GA	GA as % of mean
1	Days to 50% flowering	12.82	13.17	94.80	12.65	25.71
2	Days to Physiological maturity	6.52	6.70	94.70	11.07	13.06
3	SCMR	6.03	8.18	43.10	4.20	8.15
4	Plant height (cm)	14.52	15.35	89.50	11.40	28.30
5	Number of primary branches per plant	4.84	8.56	32.00	0.20	5.64
6	Number of secondary branches per plant	13.60	19.40	49.10	2.02	19.64
7	Number of pods per plant	21.60	24.94	75.00	6.78	38.53
8	Number of seeds per plant	28.09	30.23	86.30	12.34	53.74
9	Seed diameter (mm)	4.61	5.56	68.80	0.62	7.89
10	Protein content (%)	11.25	14.05	64.10	3.48	18.55
11	100 grain volume (ml)	16.28	16.80	93.90	11.71	32.50
12	Water absorption after soaking (%)	4.84	6.57	54.30	4.09	7.35
13	Volume expansion after soaking (%)	7.02	7.84	80.30	7.26	12.96
14	Cooking time for raw seeds (min)	8.11	8.41	93.00	14.36	16.11
15	Cooking time for soaked seeds (min)	15.57	17.54	78.80	11.82	28.47
16	100 seed weight (g)	14.43	14.94	93.40	12.20	28.73
17	Shoot biomass per plant (g)	12.14	14.92	66.20	3.63	20.36
18	Harvest index (%)	14.17	15.23	86.60	12.05	27.16
19	Seed yield (g/plant)	15.40	18.20	71.60	2.16	26.85

The characters like days to 50% flowering (12.82%, 13.17%), plant height (14.52%, 15.35%), the number of secondary branches per plant (13.60%, 19.40%), protein content (11.25%, 14.05%), 100 grain volume (16.28%, 16.80%), cooking time for soaked seeds (15.57%, 17.54%), 100 seed weight (14.43%, 14.94%), shoot biomass per plant (12.14%, 14.92%), harvest index (14.17%, 15.23%) and seed yield (15.40%, 18.20%) showed moderate estimates of GCV and PCV that suggested vigorous selection to improve these traits.

Similar results were reported for days to 50% flowering by Vaghela *et al.* (2009), Padmavathi *et al*. (2013), Pandey *et al.* (2013), Barad *et al*. (2018) and for plant height by Jeena *et al*. (2005), Vaghela *et al.* (2009), Arora *et al*. (2018), Barad *et al*. (2018) and for the number of secondary branches per plant by Padmavathi *et al*. (2013), Barad *et al*. (2018) and for 100 seed weight by Saleem *et al.* (2002), Akhtar *et al*. (2011) and for harvest index by Padmavathi *et al*. (2013), Akanksha *et al.* (2016), Kumar *et al.* (2016) and for shoot biomass by Jeena *et al*. (2005), Ali *et al*. (2010), Kumar *et al.* (2016) and for seed yield Ali *et al*. (2008), Hagos *et al.* (2018).

However, the low magnitude of GCV and PCV was observed for days to physiological maturity (6.52%, 6.70%), SCMR (6.03%, 8.18%), the number of primary branches per plant (4.84%, 8.56%), seed diameter (4.61%, 5.56%), Water absorption after soaking (4.84%, 6.57%), volume expansion after soaking (7.02%, 7.84%) and cooking time for raw seeds (8.11%, 8.41%) which indicated that the breeders should go for source of high variability for these traits to make improvement. Low GCV and PCV for days to physiological maturity was supported by Jeena *et al*. (2005), Saki *et al.* (2009), Akhtar *et al*. (2011) and for number of primary branches per plant was repoted by Ali *et al*. (2010), Hagos *et al.* (2018).

Days to 50% flowering (94.80%), days to physiological maturity (94.70%), 100 grain volume (93.90%), 100 seed weight (93.40%), cooking time for raw seeds (93.00%), plant height (89.50%), harvest index (86.60%), the number of seeds per plant (86.30%), volume expansion after soaking (80.30%), cooking time for soaked seeds (78.80%), the number of pods per plant (75.00%), seed yield (71.6%), seed diameter (68.80%), shoot biomass per plant (66.20%) and protein content (64.10%) showed high estimates of heritability.

Water absorption after soaking (54.30%), the number of secondary branches per plant (49.10%), SCMR (43.10%) and the number of primary branches per plant (32.00%) recorded moderate estimates of heritability. For efficient selection, sole dependence on heritability is not sufficient. The combination of high heritability with high genetic advance will provide a clear base on the reliability of that particular trait in the selection of variable entries. High estimates of genetic advance as per cent of mean were exhibited by the number of seeds per plant (53.74%), the number of pods per plant (38.53%), 100 grain volume (32.50%), 100 seed weight (28.73%), cooking time for soaked seeds (28.47%), plant height (28.30%), harvest index (27.16%), seed yield (26.85%), days to 50% flowering (25.71%) and shoot biomass per plant (20.36%). The genetic advance as per cent of mean was moderate for the number of secondary branches per plant (19.64%), protein content (18.55%), cooking time for raw seeds (16.11%), days to physiological maturity (13.06%) and volume expansion after soaking (12.96%). While, the number of primary branches per plant (5.64%), water absorption after soaking (7.35%), seed diameter (7.89%) and SCMR (8.15%) showed low genetic advance as per cent of mean.

Estimates of heritability and genetic advance were interpreted together in order to predict the genetic gain under selection. High heritability accompanied with high genetic advance was shown by days to 50% flowering (94.80%, 25.71%), plant height (89.50%, 28.30%), the number of pods per plant (75.00%, 38.53%), the number of seeds per plant (86.30%, 53.74%), 100 grain volume (93.90%, 32.50%), cooking time for soaked seeds (78.80%, 28.47%), 100 seed weight (93.40%, 28.73%), shoot biomass per plant (66.20%, 20.36%), harvest index (86.60%, 27.16%), seed yield (71.60%, 26.85%) which indicated that heritability is due to additive gene effects and selection of plants can be done directly on the basis of phenotypic expression of these characters.

Pandey *et al.* (2013) reported high heritability coupled with high genetic advance for days to 50% flowering, plant height, the number of seeds per plant, the number of pods per plant. Vaghela *et al.* (2009) and Padmavathi *et al*. (2013) obtained similar results for harvest index. Jeena *et al*. (2005), Saki *et al.* (2009) and Padmavathi *et al*. (2013) reported similar findings for 100 seed weight, shoot biomass and seed yield.

The high heritability coupled with moderate genetic advance was observed for days to physiological maturity (94.70%, 13.06%), protein content (64.10%, 18.55%), volume expansion after soaking (80.30%, 12.96%), cooking time for raw seeds (93.00%, 16.11%). The results indicate the predominance of additive gene action in the inheritance of these characters and the desired results may be obtained by simple selection. High heritability coupled with moderate genetic advance for days to physiological maturity was in accordance with the results obtained by Jeena *et al*. (2005), Saki *et al.* (2009) and Barad *et al*. (2018), for protein content by Padmavathi *et al*. (2013).

Moderate heritability coupled with moderate genetic advance was shown by the number of secondary branches per plant (49.10%, 19.64%). Similar result of moderate heritability coupled with moderate genetic advance for the number of primary branches per plant was reported by Naveed *et al.* (2012), Hasan and Deb (2017). The

moderate heritability coupled with low genetic advance was recorded by SCMR (43.10%, 8.15%), the number of primary branches per plant (32.00%, 5.64%) and water absorption after soaking (54.30%, 7.35%).

Seed diameter (68.80%, 7.89%) recorded high heritability accompanied with low genetic advance. This, indicated that the heritability is due to non-additive gene action. Hybridization technique should be followed for further improvement of this character.

Majority of traits revealed high heritability and low level of differences among PCV and GCV which indicate less environmental influence on these traits and showed that genotypes had more influential role in the expression of these traits. Particularly, the high PCV, GCV, heritability in the broad sense and genetic advance as per cent of mean was exhibited by the number of pods per plant and the number of seeds per plant indicating that these characters are being governed by additive gene action and therefore, for further improvement, simple selection could be effective for these characters under targeted situations. The variability found in the germplasm was significant that it can be utilized successfully in different breeding programs for the betterment of existing genotypes and for the development of desirable genotypes through hybridization.

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