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## Study of variability, heritability and genetic advance for some quantitative traits in chickpea (*Cicer arietinum* L.)

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### Abstract

The present investigation is carried out with 65 treatments (50 F<sub>1</sub>s + 15 Parents) in RBD to find out genetic variability, heritability and genetic advance percent of mean. Analysis of variance for the design of experiment revealed that mean squares due to treatments were highly significant for all the eleven characters studied, while mean squares due to replications were found non-significant in both timely and late sown condition. The high estimates of PCV and GCV (>20%) were recorded for seed yield per plant, 100 seed weight, secondary branches per plant, and biological yield per plant and moderate estimates (10-20%) were recorded for pods per plant and harvest index in both environments. The high estimates of heritability in broad sense (>75%) were found for 100 seed weight, seed yield per plant, days to 50 per cent flowering, biological yield per plant, plant height, harvest index and secondary branches per plant in both the environments. High genetic advance in per cent of mean (>20%) were recorded for seed yield per plant, 100 seed weight, secondary branches per plant, biological yield per plant, pods per plant and harvest index in both the environments. High heritability coupled with high genetic advance in per cent of mean were found for 100 seed weight, biological yield per plant, seed yield per plant, harvest index, secondary branches per plant and pods per plant in E1 and E2..

**Keywords:** Variability, Heritability, Genetic Advance, Quantitative traits and Chickpea.

### Introduction

Chickpea [*Cicer arietinum* (L.) 2n=2x=16] belongs to genus *Cicer*, family Fabaceae, and sub family Papilionaceae. It is an annual, self-pollinated diploid pulse crop with a genome size of 750 Mbp (Arumuganathan and Earle 1991).<sup>[1]</sup> Chickpea is an important food legume of the semiarid tropics and is an important food legume of the semiarid tropics and the warm temperature zones and widely cultivated in Asia, Africa (East and North) and Europe. India is producing 7.06 mt of chickpea with 840 kg/ha productivity from an area of 8.39 m ha area which is one of the major chickpea producing country (Anonymous, 2016).<sup>[2]</sup> In Uttar Pradesh, chickpea production was 164.00 thousand tones with average yield of 612 kg/ha from an area of 268.00 thousand hectare in year 2015-16 (Anonymous, 2016).<sup>[2]</sup> It is desirable crop due to its good nutritional value as it contain on an average of 4.5% fat, 8% crude fiber, 22% protein, 63% carbohydrate and 2.7% ash (Wood and Grusak, 2007).<sup>[3]</sup> Besides its nutritional value, it is an important contributor to soil fertility as it provides nitrogen to soil due to nitrogen fixation ability with help of bacteria (*Rhizobium* sp.) (Gul *et al.*, 2011).<sup>[4]</sup> India due to harmful effect of terminal drought and heat stresses. There are major constraints in warmer short-season environments for chickpea production.

The variability is the character of economic importance is basic prerequisite for improvement. Lack of adequate variability has been implicated as one of the major limitation in improving the productivity of chickpea. The extent of genetic variability has been considered as an important factor, which is an essential prerequisite for a successful hybridization aimed at producing high yielding progenies. The knowledge of heritability helps the plant breeder in predicting the behaviour of the succeeding generations, making desirable selection and assessing the magnitude of genetic improvement through selection. The present study was therefore conducted to assess the extent of genetic variability, heritability and genetic advance for eleven traits in chickpea genotypes. The information obtained will be utilized in devising the breeding strategy in chickpea improvement.

### Method and materials

The experiment was conducted at Students Instructional Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) during *rabi* 2013-15 on 65 treatments (50 F<sub>1</sub>s + 15 Parents) in Randomized Block design with three replications.

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Each line was grown in one row of 4 meter length. Row to row and plant to plant spacing was kept 30 cm and 10 cm, respectively. On the basis of 15 randomly selected plants data were recorded on primary branches per plant, secondary branches per plant, plant height (cm), pods per plant, seeds per pod, biological yield per plant (g), seed yield per plant (g), harvest index (%) and 100 seed weight (g) except days to 50% flowering and days to maturity which were recorded on plot basis. Data in each experiment of all entries was subjected to analysis of variances following Panse and Sukhatme (1967), heritability in broad sense (Hbs) and genetic advance (GA) as per Johanson *et al.*, (1955).

### Result and discussion

Analysis of variance for the design of experiments has been presented in the Table 1 for all the eleven characters. The mean squares due to treatments were highly significant for all the characters studied while, mean squares due to replications were found non-significant for all the characters in both the environments. The existence of genetic variability in the population provides ample opportunities for selection being effective. The pool of genotypes was therefore assessed for the variability analysis. The existence of wide diversity among the constituent genotypes with regard to the characters under study was confirmed through various statistical parameters. The basic material therefore, offers positive opportunities for investigation furtherance of the aforesaid objectives.

The estimates of mean, range, variability, heritability (broad Sense) and genetic advance per cent of mean of both E<sub>1</sub> and E<sub>2</sub> have been presented in Table 2. The seed yield per plant among parents ranged from 10.91g (ICCV 10) to 41.92g (ICCV 05107) in E<sub>1</sub> and from 9.62g (ICCV 10) to 18.76g (HK 94-134) in E<sub>2</sub>. While among crosses, the lowest seed yield per plant 16.33g was produced by the cross combination (KWR 108 X BG 5058) and highest yield 40.89g was exhibited by the cross combination (ICCV 05107 X Subhra) in E<sub>1</sub>, whereas in E<sub>2</sub> the lowest seed yield per plant 9.45g produced by the cross combination (KAK 2 X BG 372) and its highest value 23.14g was found for the cross combination (ICCV 05107 X Subhra). Pods per plant among parents ranged from 51.20 (BG 5058) to 84.03 (ICCV 05107) in E<sub>1</sub> and from 32.37 (BG 5058) to 57.13 (KWR 108) in E<sub>2</sub>. Among the crosses, it ranged from 51.30 (ICCV 05107 X ICCV 10) to 101.50 (IPC 2004-52 X Phule G 5) in E<sub>1</sub> and from 36.93 (KAK 2 X Phule G 5) to 62.70 (IPC 2004-52 X Phule G 5) in E<sub>2</sub>.

In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits in both the environments. The high estimates of phenotypic and genotypic coefficient of variation (>20%) were recorded for seed yield per plant, 100 seed weight, secondary branches per plant, and biological yield per plant in both the environments. The characters which exhibited moderate estimates (10-20%) of PCV and GCV were pods per plant and harvest index in both environments, whereas primary branches per plant and seeds per pod exhibited moderate estimate of PCV and low GCV in both E<sub>1</sub> and E<sub>2</sub> environments except aforesaid characters and remaining traits viz., days to 50 per cent flowering, days to maturity and plant height in both environments showed low estimates (<10%) of PCV and GCV in E<sub>1</sub> and E<sub>2</sub>. These findings were in conformity with finding of Ali *et al.* (2008),<sup>[7]</sup> Chaurasia *et al.* (2009), Dwevedi and Lal (2009), Vaghela *et al.* (2009),

Borate *et al.* (2010),<sup>[11]</sup> Sreelakshmi *et al.* (2010)<sup>[12]</sup> and Johnson *et al.* (2015).<sup>[17]</sup>

The high estimates of heritability in broad sense (>75%) were found for 100 seed weight, seed yield per plant, days to 50 per cent flowering, biological yield per plant, plant height, harvest index and secondary branches per plant in both the environments; while, days to maturity and pods per plant in E<sub>2</sub> only. The moderate estimates of heritability (50-75%) were found for pods per plant and days to maturity in E<sub>2</sub>. Whereas, the low estimate of broad sense heritability was found for primary branches per plant in E<sub>2</sub> and seeds per pod in both the environments.

High genetic advance in per cent of mean (>20%) were recorded for seed yield per plant, 100 seed weight, secondary branches per plant, biological yield per plant, pods per plant and harvest index in both the environments. Whereas, moderate estimates (10-20%) of genetic advance in per cent of mean were estimated for plant height and primary branches per plant in both the environments; while for seeds per pod, only in E<sub>2</sub>. Low genetic advance in per cent of mean (<10%) were estimated for days to 50% flowering and days to maturity in both environments and for seeds per pod only in E<sub>2</sub>.

High heritability coupled with high genetic advance in per cent of mean were found for 100 seed weight, biological yield per plant, seed yield per plant, harvest index, secondary branches per plant and pods per plant in both environments. It indicates that most likely the heritability is due to additive gene effects and selection may be effective. Whereas, high heritability coupled with moderate genetic advance in per cent of mean was recorded for plant height in both the environments. High heritability coupled with low genetic advance in per cent of mean was found for days to 50 % flowering and days to maturity in both the environments, indicates presence of non-additive gene action, thus selection for such trait may not be rewarding. Similar findings were reported by Chauhan and Singh (2000),<sup>[13]</sup> Arshad *et al.* (2003),<sup>[14]</sup> Chaurasia *et al.* (2009),<sup>[8]</sup> Borate *et al.* (2010),<sup>[11]</sup> Sreelakshmi *et al.* (2010),<sup>[12]</sup> Kumar *et al.* (2016)<sup>[15]</sup> Jivani *et al.* (2013)<sup>[16]</sup> and Johnson *et al.* (2015).<sup>[17]</sup>

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**Table 1:** Analysis of variance for randomized block design for 11 characters in chickpea under timely sown (E<sub>1</sub>) and late sown (E<sub>2</sub>) environments

Characters df.	Sources of variation					
	Replications		Treatments		Error	
	2		64		128	
	E <sub>1</sub>	E <sub>2</sub>	E <sub>1</sub>	E <sub>2</sub>	E <sub>1</sub>	E <sub>2</sub>
Days to 50% flowering	0.68	0.94	46.97**	34.38**	1.06	0.98
Days to maturity	0.77	0.01	31.97**	7.25**	1.07	0.89
Plant height (cm)	1.89	8.46	64.02**	47.41**	2.41	2.94
Primary branches per plant	0.10	0.00	0.65**	0.25**	0.18	0.07
Secondary branches per plant	1.46	1.05	17.87**	20.58**	1.61	2.02
Pods per plant	21.64	1.07	453.40**	157.31**	23.86	17.73
Seeds per pod	0.01	0.00	0.03**	0.04**	0.01	0.01
100 seed weight (g)	0.78	0.45	171.15**	97.04**	0.57	0.59
Biological yield per plant (g)	9.23	8.93	656.88**	208.20**	23.21	9.00
Seed yield per plant (g)	0.89	1.97	130.58**	29.02**	2.82	0.89
Harvest index (%)	0.64	1.57	48.30**	50.87**	3.65	2.53

\*\*\* Significant at 5% and 1% probability levels, respectively.

Where, E<sub>1</sub> (Timely Sown) and E<sub>2</sub> (Late sown)

**Table 2:** General Mean, range, coefficient of variation, heritability and genetic advance for 11 characters in chickpea, in timely and late sown environments.

Characters		General mean $\pm$ SE	Range		Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
			Parents	Crosses	Phenotypic	Genotypic		
Days to 50% flowering	E <sub>1</sub>	97 $\pm$ 0.59	91-105	92-107	4.18	4.04	93.54	8.06
	E <sub>2</sub>	74 $\pm$ 0.57	68-80	67-81	4.69	4.49	91.87	8.87
Days to maturity	E <sub>1</sub>	143 $\pm$ 0.60	139-151	138-153	2.36	2.24	90.62	4.40
	E <sub>2</sub>	128 $\pm$ 0.54	125-130	125-131	1.35	1.14	70.44	1.97
Plant height	E <sub>1</sub>	49.65 $\pm$ 0.90	40.27-55.40	39.97-59.57	9.65	9.13	89.48	17.78
	E <sub>2</sub>	45.64 $\pm$ 0.99	38.23-49.53	38.23-60.63	9.24	8.44	83.43	15.87
Primary Branches plant <sup>-1</sup>	E <sub>1</sub>	4.35 $\pm$ 0.24	2.97-4.90	3.50-5.53	13.31	9.10	46.74	12.81
	E <sub>2</sub>	3.31 $\pm$ 0.15	2.63-3.67	2.77-4.30	11.00	7.44	45.69	10.36
Secondary branches plant <sup>-1</sup>	E <sub>1</sub>	10.03 $\pm$ 0.73	5.87-14.00	6.13-19.90	26.44	23.22	77.12	42.00
	E <sub>2</sub>	9.55 $\pm$ 0.82	5.60-14.00	5.90-19.60	30.00	26.05	75.39	46.59
Pods per plant	E <sub>1</sub>	74.72 $\pm$ 2.82	51.20-84.03	51.30-101.50	17.30	16.01	85.72	30.54
	E <sub>2</sub>	49.46 $\pm$ 2.43	32.37-57.13	36.93-62.70	16.21	13.79	72.41	24.17
Seeds per pod	E <sub>1</sub>	1.21 $\pm$ 0.07	1.07-1.50	1.00-1.47	11.80	6.40	29.36	7.14
	E <sub>2</sub>	1.23 $\pm$ 0.07	1.07-1.60	1.07-1.60	13.33	8.08	36.77	10.09
100 seed weight (g)	E <sub>1</sub>	28.84 $\pm$ 0.44	14.97-45.05	21.02-47.90	26.28	26.15	98.99	53.59
	E <sub>2</sub>	25.03 $\pm$ 0.44	13.50-36.19	15.77-38.33	22.86	22.66	98.20	46.25
Biological yield plant <sup>-1</sup> (g)	E <sub>1</sub>	66.52 $\pm$ 2.78	32.47-105.00	47.83-115.00	23.02	21.85	90.09	42.72
	E <sub>2</sub>	42.96 $\pm$ 1.73	30.67-58.10	25.17-64.17	20.21	18.97	88.05	36.66
Seed yield plant <sup>-1</sup> (g)	E <sub>1</sub>	23.56 $\pm$ 0.97	10.91-41.92	16.33-40.89	28.60	27.69	93.78	55.25
	E <sub>2</sub>	13.72 $\pm$ 0.54	9.62-18.76	9.45-23.14	23.35	22.31	91.31	43.92
Harvest index (%)	E <sub>1</sub>	35.24 $\pm$ 1.10	24.98-40.79	26.38-41.52	12.22	10.95	80.28	20.20
	E <sub>2</sub>	32.07 $\pm$ 0.92	24.51-36.69	21.43-38.53	13.47	12.52	86.42	23.97

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