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Genetic variability studies in chickpea (*Cicer arietinum* L.) for yield and yield related traits

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ABSTRACT
In present investigation, 113 chickpea genotypes including Anuradha, BG 256, L 550 and DCP 92-3 as check varieties respectively were evaluated on the basis of 14 biometrical traits in a field experiment during rabi seasons of two consecutive years 2013-14 and 2014-15, District seed farm, Kalyani Simanta, Nadia, West Bengal. The experiment was laid out in augmented design with six blocks. The analysis of variance revealed significant differences for all the traits studied among the genotypes except number of secondary branches per plant. The phenotypic variance was higher than the corresponding genotypic variance against all the traits studied. High estimates of GCV and PCV observed for characters like number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 pod weight, 100 seed weight, volume expansion and seed yield per plant. Characters like days to 50% flowering and seed length showed low levels of GCV and PCV signifying lesser possibility of improvement in these characters through selection. High estimates of heritability coupled with high genetic advance as percent of mean were obtained for all the characters under study except for days to 50% flowering and seed length indicating that these traits were under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. High heritability with moderate to low genetic advance as percent of mean was observed for days to 50% flowering and seed length. This indicates the influence of non-additive gene action and considerable influence of environment on the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis.
Key words: Chickpea, Genetic variability, PCV, GCV, Heritability

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INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinated and diploid (2n=16) crop species with a genome size of 931Mb (http;//www.rbgkew.org.uk/cval/), is the most important food legume crop of South Asia and the third most important food legume crop in the world after beans (*Phaseolus vulgaris* L.) and Peas (*Pisum sativum*.L.), in terms of annual production (FAOSTAT 2013). Chickpea is the only cultivated species of the genus Cicer which has 43 species (van der Maesen, 1987). Chickpea is a valuable source of dietary protein in many parts of the world for humans and in some cases, animal feed. The crop sown after chickpea is benefited by improved soil fertility (mainly through N2 fixation by chickpea), particularly in the rainfed areas. There are mainly two kinds of chickpeas commercially grown, Desi has small, darker seeds and a rough coat and is cultivated mostly in the Indian subcontinent, Ethiopia, Mexico and Iran (Mansfeld, 2008). Kabuli has lighter coloured, larger seeds and a smoother coat and mainly grown in southern Europe, Northen Africa, Afghanistan, Chile and also was introduced during eighteen century to the Indian subcontinent (Mansfeld, 2008). Desi chickpeas have markedly higher fiber content than kabulis and hence a very low glycemic index, which may make them suitable for the people with low blood sugar problems (Mendosa, 2007). Chickpea is grown in tropical, subtropical and temperate regions. Kabuli type is grown in temperate region, while the desi type chickpea is grown in the semi-arid tropics (Muehlbauer and Singh, 1987; Malhotra et al. 1987). Chickpea is an excellent source of protein and carbohydrate and its protein is of high quality as compared to other pulse crops (Ercan et al., 1995), In general, protein

content in chick pea varies from 12.4-31.5 % (Hulse, 1975). Chickpeas are a rich source of protein, vitamin A and iron (Bender and Bender, 2005).

Chickpea is cool season legume crop, globally it is grown over an area of 13.57 million hectare with production of 13.11 million tons and productivity of 966 kg ha−1 (FAO 2013). India is the largest chickpea producing country accounting for 67% of the global chickpea production covering about 9.60 million ha. area with annual production of 8.83 million tons grain. The present yield level is 920 kg ha−1, which is far below the potential yield (5000 kg ha−1) of the crop. In India, West Bengal also a chickpea growing state, it is grown over an area of 24.9 thousand ha. with annual production of 29.3 thousand tons and productivity of 1175 kg ha-1 (Directorate of Economics and Statistics, Govt. of West Bengal; 2013). The major chickpea producing states are Madhya Pradesh, Uttar Pradesh, Rajasthan, Karnataka, and Maharashtra etc.

Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population and the germplasm serves as a valuable source of base population and provide scope for wide variability (Ramya and Senthilkumar, 2009). The importance of broad genetic base in evolving new cultivars by incorporating new genes in the existing one is well organized. Being a self-pollinated crop, chickpea exhibits a good amount of variability for various characters. Co-efficient of variation is useful in the assessment of genetic variability for the particular characters. Heritability denotes the proportion of phenotypic variation due to genotypes thus help the breeders to select the elite genotype for a character. Based on the evaluation for different morphological characters and yield attributes, the breeder can easily identify the various desirable characters present in different genotypes and quite often use them in breeding programme to improve the yield and quality. Genotypic and phenotypic variances make available the information of variability only but the heritable portion of this variation is determined by the estimates of heritability. For that reason awareness of these values of the resources in which breeders are paying attention is of enormous importance. High heritability estimates signify the effectiveness of these characters through selection for crop improvement, as less environmental influences are involved in it (Maniee et al.,2009).

The wide genetic diversity that exists in the available genotypes provides ample scope for further improvement. Importance of genetic diversity for selecting parents in combination-breeding programme of different crops to recover transgressive segregates has been emphasized (Singh and Ramanujam, 1981; Cox and Murphy, 1990). Even though a lot of research work has been conducted on variability and divergence in chickpea but the variation is a continuous process. Therefore there is a lot of scope for finding new variations among different genotypes. Keeping this in view, the investigations was carried with the following objective to estimate the extent of genetic variability present among the released cultivers in India and their utilization in breeding chickpea for the Gangetic plains of West Bengal.

MATERIAL AND METHODS

The experiments were carried out during rabi (November-March) seasons of 2013-14 and 2014-15 at the District Seed Farm, AB block, Kalyani Simanta, BCKV, (Latitude 22o58′ N and Longitude 88o32′ E), West Bengal, India. After harvesting seeds from each genotype were taken for analysis. The laboratory works were carried out in Laboratories of Department of Genetics and Plant Breeding and Department of Agronomy, Faculty of Agriculture, BCKV, Mohanpur. The experimental materials consisted of 113 varieties of chick pea including four checks namely L 550, BG 256 and Anuradha and DCP 92-3 (table.1). The standard crop management practice was fallowed. The different yield related traits recorded were presented in table.2. The biochemical analysis of protein content of seeds was analyzed through by Micro-Kjeldahl method. The analysis of variance for different characters was carried out season wise as well as for pooled data in IASRI (online software) in order to assess the genetic variability among genotypes as given by Sahu and Das (2009). The level of significance was tested at 5% using F test.

Table. 1: list chickpea varieties for variability estimates

Sl. No.	Variety	type									
1	Anuradha (ch)	Desi	33	GNG 146	Desi	65	RSG 807	Desi	97	PKV Kabuli 4	Kabuli
2	DCP 92-3 (ch)	Desi	34	RSG 2	Desi	66	PBG 1	Desi	98	BG 1053	Kabuli
3	L 550 (ch)	Kabuli	35	Pusa 209	Desi	67	Vaibhav	Desi	99	HK 1	kabuli
4	BG 256 (ch)	Desi	36	Pusa 329	Desi	68	Pusa 547	Desi	100	L 551	Kabuli
5	RSG 888	Desi	37	GG 2	Desi	69	Pusa 261	Desi	101	Pusa 1088	Kabuli
6	Pusa 212	Desi	38	RSG 896	Desi	70	PDG 4	Desi	102	Virat	Kabuli
7	CSJD 884	Desi	39	HC 3	Desi	71	RSG 973	Desi	103	Bahar	Kabuli
8	Pusa 244	Desi	40	Digvijay	Desi	72	RSG 931	Desi	104	L 552	Kabuli

9	SJK 6	Kabuli	41	GG 3	Desi	73	Pusa 362	Desi	105	BG 1003	Kabuli
10	RAU 52	Desi	42	AKG 30312	Desi	74	Pusa 372	Desi	106	GNG 1292	Kabuli
11	RSG 902	Desi	43	BGM 408	Desi	75	KWR 108	Desi	107	Pusa 1150	Kabuli
12	GNG 663	Desi	44	PKV Haritha	Desi	76	GNG 1488	Desi	108	Pusa 118	Kabuli
13	Pusa 72	Desi	45	ICCV 37	Desi	77	GNG 469	Desi	109	HK 4	Kabuli
14	CSG 140	Desi	46	RSG 11	Desi	78	ICCV 10	Desi	110	HK 98 155	Kabuli
15	PDG 3	Desi	47	GCP 105	Desi	79	AKGS 1	Desi	111	ICPK 02	Kabuli
16	Pusa 240	Desi	48	Chaffa	Desi	80	RSG 945	Desi	112	Gulak 1	Desi
17	RSG 963	Desi	49	Pusa 391	Desi	81	Vijay	Desi	113	RSGK 21	Kabuli
18	RSG 895	Desi	50	JG 218	Desi	82	KPG 59	Desi			
19	AVRODHI	Desi	51	JG 315	Desi	83	Dahod Yellow	Desi			
20	JG 14	Desi	52	Annigeri	Desi	84	HG 1	Desi			
21	JG 16(9576)	Desi	53	RSG 959	Desi	85	PDG 5	Desi			
22	JG 11	Desi	54	GL 769	Desi	86	GNG 1958	Desi			
23	JG 6	Desi	55	Sadhabahar	Desi	87	Pusa 267	Kabuli			
24	GCP 101	Desi	56	Pule G 12	Desi	88	PKV Kabuli 2	Kabuli			
25	JG 130	Desi	57	RSG 991	Desi	89	IPCK 200	Kabuli			
26	HC 5	Desi	58	Rajas	Desi	90	HK 2	Kabuli			
27	RSG 974	Desi	59	GNG 1581	Desi	91	GNG 1969	Kabuli			
28	C 235	Desi	60	Radhey	Desi	92	RSGK 6	Kabuli			
29	PBG 5	Desi	61	Panth G 114	Desi	93	JGK 1	Kabuli			
30	V P G 5	Desi	62	RSG 10	Desi	94	GNG 1499	Kabuli			
31	GPF 2	Desi	63	JAKI 9218	Desi	95	ICPK 2004-29	Kabuli			
32	JGG 1	Desi	64	Pusa 1130	Desi	96	Pusa 128	Kabuli			

Table. 2: list of observation recorded

Sl.No	**Characters**
1	Plant height (cm)
2	Days to 50% flowering
3	Number of primary branches per plant
4	Number of secondary branches per plant
5	Number of pods per plant
6	Number of seeds per pod
7	100 pod weight(g)
8	100 seed weight(g)
9	Harvest index (%)
10	Seed length (mm)
11	Seed breadth(mm)
12	Volume expansion (%)
13	Protein content (%)
14	Seed yield per plant(g)

Coefficient of Variation (CV):

The coefficient of variation (CV) being a unit less measurement, is a good basis for comparing the extent of variation between different characters with different scales.

$$CV = \frac{SD}{\overline{X}} \times 100$$

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957). Genotypic co-efficient of variability for all characters were estimated using the formula of Burton (1952).

$$GCV = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100 = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$$

Phenotypic co-efficient of variability for all characters were estimated using the formula of Burton (1952).

Sivasubramanian and Menon (1973) classified the PCV and GCV estimates as follows:

Low, <10%

Moderate, 10-20%

High, >20%

The broad sense heritability (h^2_{bs}) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Hanson *et al.* (1956). It is denoted by h^2

Therefore,

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} = \frac{Genotypic\ variance}{Phenotypic\ variance}$$

According to Robinson (1966) heritability estimates in cultivated plants can be placed in following categorizes.

Low, <30%

Moderate, 30-60%

High, >60%

The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson *et al.* (1955).

Genetic advance **(GA)** = $K \times h^2 \times \sigma_p$

Where,

K = A constant, the value equal to 2.06 at 5 % selection intensity

h^2 = heritability in broad sense

σ_p = phenotypic standard deviation

RESULTS AND DISCUSSION:

The results of analysis of variance for 113 genotypes of chickpea are furnished in table.3. Highly significant differences among the genotypes were observed for all the characters except number of secondary branches per plant indicating the presence of considerable amount of variability in all the characters studied. Highest magnitude of variability was recorded in number of secondary branches per plant followed by number of pods per plant and 100 seed weight.

Table.3: Analysis of variance of yield and yield related traits.

S.No.	Plant character	Source of variation with degrees of freedom (d.f.)		
		Block(5)	Genotypes (112)	Error (15)
1	Plant height at maturity(cm)	38.82029	37.96851*	12.03991
2	Days to 50 % flowering	35.76667	26.52403*	11.74444
3	No. of primary branches / plant	0.083667	0.185325*	0.051667
4	No. of secondary branches/ plant	21.74242	25.2229	16.23308
5	No of pods per plant	700.6688	553.0909*	254.0021
6	No of seeds per pod	0.054417	0.10763*	0.027583
7	100 pod weight(g)	15.15809	62.89523*	12.77345
8	100 seed weight(g)	12.81629	54.73184*	4.536898
9	Harvest index	1.264064	31.71216**	0.928704
10	Seed length(mm)	0.044514	0.669191*	0.016394
11	Seed breadth(mm)	0.03739	0.540282*	0.015539
12	Volume expansion	280.0875	1081.468*	450.565
13	Protein content (%)	0.540437	6.619896*	0.216914
14	Seed yield per plant(g)	0.768624	21.4684*	0.46522

The range, mean, genotypic, phenotypic and environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (in broad sense), genetic advance (GA) and genetic advance as percent of mean of 113 chickpea genotypes are presented in table 4. A wide range of variability was observed among the genotypes against all the characters studied. This would offer a good scope of selection for evolving promising desirable types. In general phenotypic variance was higher than the corresponding genotypic variance against all the characters. High estimates of GCV and PCV observed for characters like number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 pod weight, 100 seed weight, volume expansion and seed yield per plant, while characters like plant height, number of primary branches per plant, seed breadth, protein content and harvest index expressed moderate levels of GCV as well as PCV. Characters like days to 50% flowering and seed length showed low levels of GCV and PCV. It was also observed that are having less environmental effects.

Table .4: Variability and genetic parameters of different characters:

Plant characters	Range	Mean	GCV	PCV	H %	GA	GAM %
Plant height (cm)	51.05-84.35	64.141	10.66	10.69	99.4	14.1	21.9
Days to 50 % flowering	65.00-97.00	72.909	7.41	7.59	95.3	10.8	14.9
No of Primary branches per plant	1.80-5.00	2.503	17.12	17.91	91.4	0.85	33.7
No of secondary branches per plant	4.00-34.20	12.679	46.84	46.96	99.4	12.4	96.2
No of pods per plant	15.60-179.00	59.922	37.49	37.99	97.3	45.9	76.2
No of seeds per pod	1.00-2.45	1.603	20.78	21.55	92.9	0.66	41.2
100 pod weight (g)	19.88-71.45	33.422	24.83	25.02	98.4	17.3	50.7
100 seed weight (g)	9.23-45.35	19.816	34.13	39.30	75.4	12.4	61.0
Harvest index (%)	25.02-51.02	37.377	14.94	15.93	88.0	10.8	28.8
seed length (mm)	6.57-10.58	8.272	8.96	9.24	94.1	1.4	17.1
seed breadth (mm)	4.69-8.56	6.14	12.28	12.73	93.0	1.52	24.4
volume expansion (%)	61.42-284.84	128.58	25.65	25.75	99.2	66.2	52.6
Protein content (%)	13.80-23.56	17.365	13.31	13.98	90.6	4.5	26.1
Seed yield per plant (g)	8.80-35.90	15.229	29.38	30.56	92.4	9.0	58.1

PCV: phenotypic coefficient of variance, GCV: genotypic coefficient of variance, H %: heritability %, GA: genetic advance, GAM: genetic advance per mean

The magnitude of PCV was higher than GCV for all the traits studied, indicated environmental influences on the expression of these traits, but the influence was less as the differences between GCV and PCV were less for all the characters under study indicating that these characters were less influenced by the environment. This observation was similar with earlier findings of Borate et al (2010) and Jaydev et al (2013). High estimates of PCV and GCV was obtained for number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 pod weight, 100 seed weight, volume expansion and seed yield per plant. Therefore, there was a large scope for improvement of these traits through precise selection and hybridization. These findings were corroborated earlier by Aarif *et al.* (2014) for 100 seed weight and number of secondary branches per plant, by Shweta *et al*. (2013) for number of pods per plant, by Pramila *et al*. (2012) for number of secondary branches per plant and by Gohil and Patel (2011) for 100 seed weight and seed yield per plant.

High heritability was recorded for all the traits under study plant height, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, number of pods per plant, number of seeds per pod, 100 pod weight, 100 seed weight, seed length, seed breadth, seed yield per plant, harvest index, volume expansion and protein content. Similar observations were reported by Neelu *et al.* (2013) for seed yield per plant, by Rozina *et al.* (2011) for seed yield per plant and 100 seed weight and by Qurban *et al*. (2012) for 100 seed weight, number of pods per plant, seed yield per plant and protein content.

High estimate of genetic advance was obtained for number of pods per plant, volume expansion. Lowest genetic advance was obtained against number of primary branches per plant, number of seeds per pod, seed length, seed breadth, protein content and seed yield per plant. Number of secondary branches per plant, days to 50% flowering, plant height, 100 pod weight, 100 seed weight, harvest index had moderate levels of genetic advance. Similar results were obtained by Thakur *et al*. (2008) for number of pods per plant, by Abhishek *et al.* (2012) for number of pods per plant.

Genetic advance as percent of mean was highest for all the characters except for days to 50% flowering and seed length which had moderate level of genetic advance as per cent of mean. Similar finding was

reported earlier by Johnson *et al*. (2009) for seed yield per plant and 100 seed weight and by Vaghela *et al*. (2009) for number of pods per plant and seed yield per plant. High estimates of heritability coupled with high genetic advance as percent of mean were obtained for all the characters under study except for days to 50% flowering and seed length. These findings were similar with that of Qurban *et al.* (2012) for seed yield per plant, protein content and 100 seed weight, by Sudhanshu *et al*. (2013) , by Jivani *et al*. (2013) for seed yield per plant, harvest index and 100 seed weight, by Shweta *et al.* (2013) for secondary branches per plant, seed yield per plant, 100-seed weight, pods per plant and plant height and by Aarif *et al*. (2014) for 100 seed weight. It indicated the predominance of additive gene action for controlling these traits. Therefore, selection based on phenotypic performance would be effective for the improvement of these traits. High heritability with moderate to low genetic advance as percent of mean was observed for days to 50% flowering and seed length which suggested additive and non-additive gene action for controlling these traits.

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