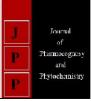


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#### **KD Bhoite**

Zonal Agriculture Research Station, Igatpuri, Dist. Nashik, Maharashtra, India

#### **GN Deore**

Zonal Agriculture Research Station, Igatpuri, Dist. Nashik, Maharashtra, India

#### DV Kusalkar

Zonal Agriculture Research Station, Igatpuri, Dist. Nashik, Maharashtra, India

# Studies on genetic variability and heritability in chickpea (*Cicer arientum* L.)

# KD Bhoite, GN Deore and DV Kusalkar

#### Abstract

The present investigation was conducted to estimate the genetic variability and character association existing among 60 chickpea genotypes including two checks which were evaluated during *Rabi* 2017-18 under randomized block design having two replications. Analysis of variance revealed significant differences among the genotypes for all the characters studied. Maximum heritability was observed for all the studied characters except plant spread. The traits *viz*; 100 seed weight, seed yield per plant, lower first pod from found level, number of pods per plant, number of primary branches per plant and number of secondary branches per plant showed high estimates of broad sense heritability accompanied by high genetic advance as per cent of mean indicating that these characters governed by additive gene action. However, the characters like a number of pods per plant, 100 seed weight, number of primary branches per plant and number of secondary branches per plant would be effective for increasing seed yield in chickpea.

Keywords: chickpea, genetic variability, heritability, genetic advance

#### 1. Introduction

Pulses are important constituents of the Indian diet and supply a major part of the protein requirement. Among the pulses, chickpea is important *rabi* crop of India. It is well adapted to grow on residual soil moisture in the post rainy season because of its deep and prolific root system. Chickpea provides high quality protein, particularly for vegetarians. It is also used as a feed for livestock and has a significant role in farming systems as a substitute for fallow in cereal rotations, where it contributes to the sustainability of production and reduces the need for nitrogen fertilization through fixing atmospheric nitrogen.

Chickpea (*Cicer arietinum* L.) is an annual, self-pollinated, diploid (2n=16) grain legume crop grown in a wide range of environments including the Mediterranean, South and West Asia, North America, and North and East Africa. India is the largest producer of chickpea in the world sharing 65.2% of area and 65.4% of production. In India the area under chickpea was 10.20 million ha, production was 9.38 million tones and productivity was 919 kg/ha during 2016-17. Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Gujarat, Andhra Pradesh and Karnataka are the major chickpea producing states sharing over 95 % area. (Anonymous, 2017)<sup>[3]</sup>. In Maharashtra, the area under chickpea was 19.29 lakh ha., production was 19.41 lakh tones and productivity was 1006 kg/ha during the year 2016-17. (Anonymous, 2017)<sup>[4]</sup>.

Plant genetic resources are the basis of global food security. They comprise a diversity of genetic material contained in traditional varieties, modern cultivars, crop wild relatives and other wild species. To meet the need for more food, it would be necessary to make better use of a broader range of the world's plant genetic diversity (Karaoz and Zencirci 2005) and Nature and magnitude of genetic variability and heritability in a population as genetic and non-genetic factors are pre-requisites in any successful hybridization programme to get desirable segregants.

Although the cultivation of chickpea is very wide in India, the productivity of legume in general and chickpea in particular have remained stagnant over the years. Therefore, there is an urgent need to enhance its production and productivity to meet protein requirement of India. Hence, the present investigation was aimed to estimate the genetic variability and heritability for different quantitative characters in 60 genotypes of chickpea.

#### 2. Material and methods

The experiment was conducted during *Rabi*, 2017-18 at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra. The experimental material comprised of 60 chickpea genotypes including two checks *viz*; Phule Vikram and JAKI-9218 depicted in (Table 1) was obtained from Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri,

Corresponding Author: KD Bhoite Zonal Agriculture Research Station, Igatpuri, Dist. Nashik, Maharashtra, India Dr. PDKV, Akola, Maharashtra, IIPR, Kanpur, JNKVV, Jabalpur, ICRISAT, Hyderabad, ARS, Nandyal, and ARS, Sabour. These genotypes of chickpea were evaluated in a Randomized Block Design (RBD) with two replications. Each genotype was sown in single row of 3 m length with spacing 45 cm between row and 10 cm within rows. The land selected for the experiment was medium black which was brought to fine tilth. The fertilizer dose is 25: 50: 30 NPK kg/ha and applied at the time of sowing in order to facilitate easy and better germination. The operations like thinning, weeding, hoeing and plant protection measures were carried out regularly to ensure satisfactory crop growth. Observations were recorded on 11 randomly selected plants in each entry and replication for ten characters viz., days to 50% flowering, days to maturity, plant height, plant spread, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, lower first pod from ground level, 100-seed weight, protein content and seed yield per plant. The mean data of each character was subjected to analysis of variance to test the level of significance among the genotypes for different characters according to the method suggested by Panse and Sukhatme, (1967)<sup>[12]</sup>. The genotypic coefficient (GCV) and phenotypic coefficient of variations (PCV) were estimated as per the formulae suggested by Burton (1952)<sup>[6]</sup> while, heritability in a broad sense was calculated by using the formulae suggested by Allard (1960) [2]

## 3. Results and discussion

The seed yield is a highly variable and complex character and is a result of cumulative effects of its component characters. The analysis of variance revealed that the mean sum of square due to treatments (genotypes) for all the characters studied is found to be significant (Table 2). This suggested that the genotypes selected for research were quite variable and considerable amount of variability existed among them. Hence, it provides ample scope for selection of different quantitative and qualitative characters for yield improvement in chickpea (Table 1). Similar results were reported by Banik *et al.* (2018)<sup>[10]</sup> and Srivastava *et al.* (2017)<sup>[14]</sup>.

# 3.1 Estimates of Components of Variation

The estimates of GCV, PCV, heritability (b.s.) and genetic advance as per cent of mean for different characters studied are presented in Table 3. An estimate of GCV and PCV for all characters studied revealed that the phenotypic coefficient of variation (PCV) was higher than their corresponding genotypic coefficient of variation (GCV), indicating the influence of environment on the expression of these characters and suggesting sufficient amount of variability and thus offer better scope for genetic improvement through selection of these traits. The magnitude of genotypic coefficient of variation (GCV) was highest for seed yield per plant (36.52 %) followed by number of pods per plant (32.64 %), number of secondary branches per plant (23.13%). The medium variation exhibited for number of primary branches per plant (19.92%), 100 seed weight (19.19 %), lower first pod from found level (17.08 %) and plant spread (12.12 %). Low variation were observed for days to 50% flowering (9.23 %), plant height (8.65 %), protein content (6.86 %) and days to maturity (4.62%).

The high estimates of PCV were observed for seed yield per plant (37.44 %) followed by number of pods per plant (34.52 %) and number of secondary branches per plant (25.57 %). The medium PCV recorded in number of primary branches per plant (22.35 %), 100 seed weight (19.26 %), lower first pod from found level (17.86 %) and plant spread (16.21 %). However, the low PCV were observed for days to 50% flowering (9.42 %), plant height (10.21 %), protein content (7.00 %) and days to maturity (5.11 %). Similar results were reported by Thakur *et al.* (2008) <sup>[15]</sup> and Kumar *et al.* (2012) <sup>[8]</sup>.

## 3.1.1 Range of variability

The general mean for seed yield per plant was (8.97 g). Genotype NO.37/55 produced highest seed yield per plant (18.25 g) and the genotype IPC 2010-14 produced lowest seed yield per plant (4.28 g). The highest and lowest number of pods per plant exhibited in genotype JG 2016-1206301 (49) and NO.44/20011(13.33) respectively. The mean performance for number of pods per plant was 27.40. The variation for 100 seed weight ranged between 15.75 (SAGL-152402) to 36.90 g (NO.37/55) with average mean 24.03 g. The maximum plant spread recorded in genotype NO.44/20037 (19.99 cm), whereas minimum plant spread showed by genotype IPC 2010-14 (10.66 cm). The mean performance for plant spread was 14.42 cm. The variation in days to 50% flowering was ranged between 47 (SAGL 152401) and 65 (IPC 2008-83) days with general mean 53.88 days. While, for days to maturity it was between 84 (SAGL 152401) and 101 (IPC 2008-83) days. The mean performance for this trait was 93.22 days. The general mean for plant height was 42.94 cm. The genotype NO.44/20084 was tall (56.33 cm) and NBeG 873 was dwarf (34.99) among the all the tested genotypes for plant height. Number of primary branches per plant ranged from 1.66 (No. 44/20012) to 4.83 (Phule G-0914-6-17) and Number of secondary branches per plant ranged from 4.83 (Phule G-0914-6-17) to 14.66 (SAGL 152199) with mean performance (7.99). Mushtaq et al. (2013)<sup>[11]</sup> reported genetic variability for seed yield, flowering date, days to maturity. Akhtar et al. (2011)<sup>[1]</sup> reported highest range of variability for pods per plant. Borate et al. (2010)<sup>[5]</sup> reported a considerable range of variability for secondary branches and plant height.

# 3.1.2 Heritability and genetic advance

Maximum heritability was observed for 100 seed weight (99.4%) followed by days to 50 per cent flowering (96.00%), Protein content (96.00), seed yield per plant (95.1%), lower first pod from found level (91.4%), number of pods/plant (89.4%), number of secondary branches per plant (81.8%), days to maturity (81.5%), Number of primary branches/plant (79.4%) and Plant height (71.8%). High heritability (>60%) was observed for all the studied characters except plant spread.

Ĝenetic advance is a measure of genetic gain under selection which depends upon main factors viz., genetic variability, heritability, selection index. The range of genetic advance observed from 1.08 to 17.42. Low estimate of GA were observed for all the characters under study except for number of pods per plant (17.42) and days to 50% flowering (10.03). Saleem *et al.* (2002)<sup>[13]</sup> assessed that 100 seed weight, days to 50% flowering were characterised by high (b.s.) heritability estimates, which indicated the presence of a considerable proportion of total variability due to genetic causes. Farshadfar *et al.* (2013)<sup>[7]</sup> reported that heritability estimates were high for hundred seed weight and seed yield.

In the present investigation, 100 seed weight, seed yield per plant, lower first pod from found level, number of pods per plant, number of primary branches per plant and number of secondary branches per plant showed high estimates of broad

these traits could be more effective for desired genetic improvement. It is supported by similar findings of Kumari *et al.* (2013)<sup>[9]</sup>.

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S.N.	Source/Genotype	S.N.	Source/Genotype M.P.K.V Rahuri			
5.N.	ICRISAT, Hyderabad	5.N.				
1	NO.44/20001	31	Phule G-0805-17-5			
2	NO.44/20037	32	Phule G-0913-2-11			
3	NO.44/20084	33	Phule G-0914-6-17			
4	NO.44/20012	34	Phule G-0808-30-9			
5	NO.44/20095	35	Phule G-0914-6-6			
6	NO.44/20076	36	Phule G-0914-8-14			
7	NO.44/20068	37	Phule G-0914-8-20			
8	NO.37/55	38	Phule G-14101			
9	NO.44/20046	39	Phule G-0919-4-8			
10	NO.44/20096	40	Phule Vikram-Check			
11	NO.44/20081		ARS, Sabour			
12	NO.44/20011	41	SAGL 152199			
13	NO.44/20090	42	SAGL 152216			
14	NO.44/20060	43	SAGL 152317			
15	NO.44/20063	44	SAGL 152402			
	Dr. PDKV, Akola	45	SAGL 152404			
16	JAKI -9218-Check	46	SAGL 152210			
	ARS, Nandyal	47	SAGL 152278			
17	NBeG-776	48	SAGL 152401			
18	NBeG-873	49	SAGL 152403			
	I.I.P.R Kanpur	50	SAGL 152405			
19	IPC 2014-48		JNKVV, Jabalpur			
20	IPC 2014-120	51	JG 2016-11			
21	IPC 2015-120	52	JG 2016-141611			
22	IPC 2015-85	53	JG 2016-638474			
23	IPC 2012-49	54	JG 2016-1206301			
24	IPC 2012-30	55	JG 2016-96054958			
25	IPC 2010-14	56	JG 2016-1614			
26	IPC 2007-13	57	JG 2016-634958			
27	IPC 2008-11	58	JG 2016-921814			
28	IPC 2008-83	59	JG 2016-5522411			
29	IPC 2006-127	60	JG 2016-960506301			
30	IPC 2010-216					

Table 1: List of 60 genotypes of chickpea

Table 2: Analysis of variance for eleven different characters in chickpea

S.N.	Characters	Mean sum of squares				
		Replication (d.f. 1)	Genotype (d.f. 59)	Error (d.f. 59)		
1	Days to 50% flowering	0.533	50.480**	1.042		
2	Days to maturity	4.033	41.227**	4.203		
3	Plant height (cm)	8.018	33.026**	5.424		
4	Number of primary branches per plant	1.476	0.780**	0.089		
5	Number of secondary branches per plant	10.800	7.593**	0.759		
6	Number of pods per plant	131.712	169.450**	9.471		
7	Lower first pod from ground level	0.732	39.759**	1.779		
8	100 seed weight (g)	2.703	42.676**	0.136		
9	Plant spread (cm)	47.276	8.524**	2.408		
10	Protein content (%)	0.353	5.009**	0.100		
11	Seed yield per plant (g)	5.980	22.010**	0.549		

\*, \*\* indicate significant at 5 and 1 per cent level, respectively

Note: Figures in the parenthesis indicates the degrees of freedom

S. N.	Characters	Moon	Range Min. Max.		GCV %	PCV %	b.s. %	G.A.	Genetic advance as % mean
	Characters		Min.	Max.					
1	Days to 50% flowering	53.88	47	65	9.23	9.42	96.0	10.03	18.62
2	Days to maturity	93.22	84	101	4.62	5.11	81.5	8.00	8.58
3	Plant height (cm)	42.94	34.99	56.33	8.65	10.21	71.8	6.48	15.10
4	Number of primary branches per plant	2.95	1.66	4.83	19.92	22.35	79.4	1.07	36.57
5	Number of secondary branches per plant	7.99	4.83	14.66	23.13	25.57	81.8	3.44	43.10
6	Number of pods per plant	27.40	13.13	49.0	32.64	34.52	89.4	17.42	63.59
7	Lower first pod from ground level	25.52	15.16	38.33	17.08	17.86	91.4	8.58	33.64
8	100 seed weight (g)	24.03	15.75	36.90	19.19	19.26	99.4	9.47	39.42
9	Plant spread (cm)	14.42	10.66	19.99	12.12	16.21	55.9	2.60	18.68
10	Protein content (%)	22.83	18.74	25.78	6.86	7.00	96.0	3.16	13.85
11	Seed yield per plant (g)	8.97	4.28	18.25	36.52	37.44	95.1	6.58	73.38

Table 3: Estimates of variability parameters for eleven characters in chickpea

## 4. Conclusion

The assessments of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as per cent of mean indicated that selection must be done in the characters like number of pods per plant, 100 seed weight, seed yield per plant and number of secondary branches per plant for improving the yield in chickpea. High heritability associated with high genetic advance as per cent of the mean was observed for 100 seed weight, seed yield per plant, lower first pod from found level, number of pods per plant, number of primary branches per plant and number of secondary branches per plant indicating that these characters governed by additive gene action. Hence, selection for genetic improvement characters like a number of pods per plant, 100 seed weight, number of primary branches per plant and number of secondary branches per plant would be effective for increasing seed yield in chickpea.

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