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Assessment of Variability and Genetic Parameters in Agro-Physiological Traits of Chickpea (Cicer arietinum L.) under Rainfed Condition

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

An experiment was conducted during *rabi* season of 2017-18 to estimate the genetic parameters of variation including heritability and genetic advance for agro-physiological characters *viz.*, days to flower initiation, days to 50 *per cent* flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per plant, biological yield per plant (g), seed yield per plant (g), 100-seed weight (g), root length (cm), relative water content and harvest index (%) in 20 genotypes of chickpea. High phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were observed for characters *viz.*, number of branches per plant, seeds per plant and 100-seed weight. The magnitude of phenotypic coefficient of variance and their corresponding genotypic coefficient of variance for all the characters were observed in good agreement reflecting the narrow range of environmental influence in the manifestation of the characters. High heritability was

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recorded for number of branches per plant, 100-seed weight, seeds per plant, pods per plant and biological yield per plant. High heritability combined with high genetic advance was observed for seeds per plant, pods per plant and 100-seed weight which indicated that these traits were governed by additive gene effects and phenotypic selection would be effective in early generations for these characters.

Keywords: Agro-physiological characters; chickpea; genetic parameters; genetic variability and Seed yield.

1. INTRODUCTION

Chickpea (Cicer arietinum L.) is a self-pollinated diploid (2n = 2x = 16) food legume that belongs to family Leguminosae. It is also known as Gram, Indian pea and Bengal gram. It is most important pulse crop of India contributing about 30 per cent of total pulse acreage and about 40 per cent of total pulse production of the nation. India ranked first in area and production in the world with cultivated area of 9.55 million ha and production of 9.94 million tons with productivity of 1041 kg per ha. In Madhya Pradesh, it covers an area of 31.03 lakh ha with production of 39.97 lakh tons and productivity of 1288 kg per ha [1]. Chickpea seeds contain on an average 23 per cent protein, 64 per cent total carbohydrates (47 per cent starch, 6 per cent soluble sugar), 5 per cent fat, 6 per cent crude fiber and 2 per cent ash. It is also reported to contain high mineral content: phosphorus (340 mg/100 g), calcium (190 mg/100 g), magnesium (140 mg/100 g), iron (7 mg/100 g), zinc (3 mg/100 g) [2]. Hence, it is considered as one of the important component of the indian diet.

Its productivity in the country and state is low because chickpea is grown on low input marginal lands and mostly cultivated on residual moisture in the Indian subcontinent. Among various constraints for its low productivity, drought stress particularly at the end of the growing season is a major constraint to chickpea production and yield stability in rainfed regions. With unpredictability of the drought stress and continuous population explosion, there is a high need to develop highyielding chickpea varieties with improved drought tolerance [3]. Thus, for improving chickpea productivity under rainfed situations, it is essential to explore the knowledge on genetic variability in the experimental materials. The success of any crop improvement programme depends upon the nature and magnitude of genetic variability and heritability, which provides better opportunity in selecting desired types [4]. The high heritability combined with high genetic advance for any trait indicates effectiveness of

selection. It is essential to increase the production of chickpea to fulfill the protein requirement of increasing population. The seed vield of chickpea is a complex and multiplicative character. which is highly influenced by environmental variations. Success of crop improvement programme depends upon the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. Information on nature and magnitude of variability present due to genetic and non genetic is an important prerequisite causes for systematic breeding programme. Therefore, the present investigation aimed to estimate genetic variability, heritability and genetic advance for agro-physiological traits of in a set of genotypes of chickpea under rainfed condition of Indore, Madhya Pradesh, India.

2. MATERIALS AND METHODS

The experimental material used in the present study comprised of twenty genotypes of chickpea. The present experiment was laid down during Rabi 2017-18 in a Randomized Complete Block Design (RCBD) in three replications of 5.00 m \times 1.50 m plot size with maintaining the plant geometry at 30 cm × 10 cm. The investigation was carried out at the Research Farm, AICRP on Dryland Agriculture, College of Agriculture, Indore (M.P.), which is situated between latitude 20°43' N and longitude 76°54' E and at an altitude of 567 meters above the mean sea level in Malwa plateau of western part of Madhya Pradesh. It has sub-tropical and semiarid climate having a temperature ranged from 5.7 C to 43.5 C in winter and summer, respectively. All recommended package of practices were adopted to raise good and healthy crop. Observations were recorded on plot as well as single plant basis. Observations on plot basis were recorded for days to flower initiation, days to 50 per cent flowering, days to maturity, while observations on single plant basis were recorded from five randomly selected plants from each entry and each replication for number of branches per plant, plant height (cm), number of pods per plant, number of seeds per plant, biological yield per plant (g),100-seed weight (g), seed yield per plant (g), harvest index (%), relative water content and root length (cm) were used for statistical analysis. The genotypic and phenotypic variances were estimated according to the formula suggested by Johnson et al. [5].

Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were computed as *per cent* following the method suggested by Burton & Devane [6]. Heritability in broad sense (h^2 bs) was computed using the formula adopted by Allard [7]. The expected genetic advance (GA) for different characters under selection was estimated using the formula suggested by Johnson et al. [5]. Genetic advance over mean was estimated by using the following formula proposed by Comstock & Robinson [8].

GCV and PCV were computed as percent the method suggested by Burton & Devane [6]. Heritability in broad sense (h² bs) was computed using the formula adopted by Allard [7]. The expected genetic advance (GA) for different characters under selection was estimated using the formula suggested by Johnson et al. [55]. Genetic advance over mean was estimated by using the following formula proposed by Comstock & Robinson [8]. For recording root length, the soil from the roots is removed by rinsing the roots in running water. The total length of root is obtained by measuring the length of tap and branch roots of the chickpea root system. Relative water content (RWC) in chickpea crop upper portion node 5^{th} , 6^{th} , 7^{th} '', 7th leaves was plugged and removed leaf from leaflets for calculating the RWC [9].

3. RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among genotypes for all the characters studied (Table 2) which indicated significant differences among highly the genotypes for all the characters viz., plant height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant (g), 100-seed weight (g), days to flower initiation, days to 50 per cent flowering, days to maturity, harvest index (%), seed yield per plant (g), root length (cm) and relative water content indicating the genotypes under study were genetically diverse for all the quantitative traits. These findings were in conformity with the findings of Vaghela et al.

(2009) for seed yield per plant and number of pods per plant; Borate et al. [10] for days to first flower initiation, number of branches, plant height; Malik et al. [11], for pods per plant, branches per plant, biological yield per plant, grain yield and harvest index; Shweta et al. [12] for seed yield per plant and pods per plant; Ramanappa et al. [13] for days to 50 per cent flowering, plant height (cm), number of branches per plant, days to maturity, 100 seed weight (g), harvest index in chickpea: Kuldeep et al. [14] for seed yield per plant, 100-seed weight, harvest index, number of effective pods per plant, total number of pods per plant and number of branches; Dev et al. [15] for 100-seed weight, number of pods per plant and plant height. Hasan and Deb [16] for number of pods number of seeds per plant and per plant.

The parameters of genetic variability viz., mean, range, phenotypic coefficient of variation (PCV), coefficient of variation genotypic (GCV), heritability in broad sense (h²_{bs}) and expected genetic advance as per cent of mean were estimated for all these characters (Table 3). The plant height ranged from 32.27 (Vishal) to 42.92 (JG 322) cm, with an average of 38.16 cm. Genotypes viz., Ujjain 21, JG 14, JG 130, RVG 202, Green Gram, KAK 2, RVG 201, IG 593 and JG 322 showed more plant height (cm) than the average. The number of branches per plant ranged from 3.12 (JG 130) to 7.18 (IG 370) with an average of 4.44 branches per plant. Six genotypes viz., JG 412, JG 11, IG 593, Ujjain 21, JG 6 and IG 370 exhibited more branches per plant. The pods per plant ranged from 49.54 (IG 593) to 87.24 (JG 16) with an average of 65.22. Twelve genotypes viz., KAK 2, Ujjain 21, JG 11, IG 370, JG 322, JG 218, JG 12, JG 130, RVG 201, RVG 202, Green Gram and JG 16 exhibited higher number pods per plant. The number of seeds per plant ranged from 39.83 (JG 6) to 107.46 (JG 16) with an average of 61.61. Nine genotypes viz., JG 338, RVG 201, JG 322, JG 130, Green Gram, JG 12, Ujjain 21, Vishal and JG 16 exhibited higher seeds per plant. The biological yield per plant ranged from 18.16 g. (JAKI 9218) to 37.08 g. (JG 130). The 100-seed weight (g) ranged from 15.27 (Ujjain 21) to 35.74 (KAK 2) with an average of 23.20 g. The days to flower initiation ranged from 47.38 (RVG 203) to 53.90 (RVG 202) days, with average of 51.16 days. The days to 50 per cent flowering ranged from 51.50 (RVG 203 and KAK 2) to 60.43 (JG 6) with general mean of 56.36 days. The days to maturity ranged from 119.48 (RVG 203) to

124.97 (JG 12) with an average of 122.69 days. Out of 20 genotypes, seven genotypes viz., RVG 203, Vishal, JG 412, JG 338, JG 130, Ujjain 21 and JG 14 exhibited earliness for maturity. The harvest index (%) ranged from 44.63 (JG 130) to 61.04 % (RVG 201) with an average of 54.63. The seed yield per plant (g) ranged from 10.12 g (JAKI 9218) to 18.61 g (IG 593), with an average of 13.54 g. Eight genotypes viz., JG 12, RVG 201, Vishal, JG 130, JG 322, KAK 2, JG 16 and IG 593 showed higher seed yield per plant (g). The root length (cm) ranged from 12.64 (JG 14) to 18.62 (JG 130) cm, with an average of 15.06 cm. Out of 20 genotypes, nine genotypes viz., Green Gram, IG 370, JAKI 9218, JG 338, JG 11, JG 218, Vishal, IG 593 and JG 130 identified as deep rooting genotypes which may have the advantage of accessing subsoil reserves of water when the top soil dried out later in the season. Chen et al. (2017) reported the role of root system as the capacity of roots to grow into the subsoil is significant for avoiding terminal drought stress in water-limited soils. The range for RWC was 56.93 (RVG 201) to 76.78 % (JG 322) with general mean of 66.01 per cent. Eight genotypes viz., JG 6, KAK 2, Green Gram, IG 593, IG 370, JG 412, JG 130 and JG 322 showed higher relative water content. Sachdeva et al. [17] concluded that maintaining higher RWC (%) enabling genotypes to perform better in terms of physiological processes under stress and decreasing in RWC signifying their vulnerability to drought stress. The values of mean and range revealed that there were wide ranges of genetic variability among genotypes for various agrophysiological traits.

The phenotypic coefficient of variation was marginally higher than the corresponding genotypic coefficient of variation for all the characters (Table 3). The genotypic coefficient of variation and phenotypic coefficient of variation were categorized as low (<10 %), moderate (10-20 %) and high (>20 %) as suggested by Sivasubramanian and Madhavamenon [18]. The phenotypic coefficient of variation (PCV) was recorded high for number of branches per plant (25.71 %), followed by number of seeds per plant (25.47 %), 100-seed weight (22.42 %), seed yield per plant (20.68 %) and biological yield per plant (20.33 %). While, number of pods per plant (15.44 %), harvest index (13.79 %), root length (13.90 %) and relative water content (12.43 %) recorded moderate PCV. The genotypic coefficient of variation (GCV) was recorded the highest for number of branches per plant (25.31 %) followed by number of seeds per plant (24.50 %) and 100-seed weight (21.75 %). While, the moderate GCV was recorded for biological yield per plant (18.47 %), seed yield per plant (16.80 %), number of pods per plant (14.35 %) and root length (10.41 %). The estimated GCV and PCV helped in getting a clear understanding of the variability present among various genotypes.

S. No.	Name of Genotypes	Pedigree
1	Ujjain 21	Selection from local material
2	JG 14	(GW 5/7 × P 327) × ICCL 83149
3	JG 218	ICCV 4 × P 1353
4	Vishal	K 850 × ICCL 80074
5	IG 593	-
6	RVG 203	(ICCV 37 × GW 5/7) × ICCV 107
7	JG 322	CHAFFA × BG 1
8	JG 6	(ICCV 10 × K 850) × (H 208 × RS 11)
9	RVG 201	PG 5 × BHEEMA
10	JG 16	ICCC $4 \times ICCV 10$
11	JG 130	(Phule G 5 × Narsinghpur Bold) × JG 74
12	Green Gram	BGD 112 × JSC 37
13	IG 370	-
14	JG 338	-
15	JAK 19218	(ICCV 37 × GW 5/7) × ICCV 107
16	KAK 2	(ICCC 2 × Surutato 77) × ICC 7344-ICCX 870026 PB-PB-14P-BP-62 AK- 7AK-BAK
17	JG 412	(Phule G 5 × Narsinghpur Bold) × ICCV 37
18	JG 12	(N. Bold \times PG 5) \times PG 5
19	RVG 202	(JAKI-9226 × DCP 20) × JG 412
20	JG 11	[(Phule G 5 × Narsinghpur Bold) × ICCC 37] ICCX-860263-BF-BP-91BP

Genetic variability has to be confirmed by the magnitude of variance also because range can provide only a preliminary idea about the variability. Furthermore, for comparing the variation of one character with another, the coefficient of variation which was independent of unit of measurement is preferred. The presence of narrow difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the studv characters under suggested that expression of these characters were not much influenced by environmental factor. High PCV was recorded for number of branches per plant followed by number of seeds per plant, 100-seed weight, seed yield per plant and biological yield per plant and high GCV was recorded for number of branches per plant followed by number of seeds per plant and 100-seed weight indicating that there is considerable scope for selection to improve these characters. Results were in accordance with the findings of Vaghela et al. (2009), Borate et al. [10], Sreelakshmi et al. [19], Babbar et al. [20], Dar et al. [21], Shweta et al. [12], Jain et al. [22], Kuldeep et al. [14], Dev et al. [15] and Hasan and Deb [16]. The characters showing less difference between the GCV and PCV are more governed by genetic factors for the expression of them. Thus. desired improvement of these traits may be achieved by simple selection procedure. The results were in agreement with the findings of Mohamed et al. [23].

Heritability measures the contribution of genetic variability to phenotypic variability observed for quantitative characters. The classification for estimate of h²_(BS) was made as suggested by Robinson et al. [24] as low (<50 %), moderate (50-70 %) and high (>70 %). A illustrious heritability was observed for the characters viz. number of branches per plant (93.93 %), followed by, 100-seed weight (91.33 %), number of seeds per plant (89.73 %), number of pods per plant (83.72 %) and biological yield per plant (79.81 %). While the moderate heritability was observed for characters viz., plant height (66.56 %), followed by seed yield per plant (63.99 %), days to 50 % flowering (60.96 %), days to flower initiation (58.37 %) and root length (54.45 %) (Table3).

Genetic advance as *per cent* of mean was recorded for yield and its contributing characters (Table 3). It was categorized as suggested by Johanson et al. [5] *i.e.*, High (>20%), Medium (10-20%), Low (<10%). Genetic advance as

percent of mean was high for number of branches per plant (51.29 %) followed by number of seeds per plant (48.55 %), 100-seed weight (43.47 %), biological yield per plant (34.51 %), seed yield per plant (28.10 %) and number of pods per plant (27.46 %). Genetic advance as *per cent* of mean was moderate for root length (16.06 %) followed by plant height (11.35 %). While, low genetic advance as percentage of mean were recorded for days to 50 *per cent* flowering (7.92 %), relative water content (7.88 %), days to flower initiation (6.46 %), harvest index (5.24 %) and days to maturity (1.30 %).

In present investigation higher PCV, GCV, heritability and genetic advance as per cent of mean were observed for number of branches per plant (25.71 %, 25.31 %, 93.93 % and 51.29 %), number of seeds per plant (25.47 %, 24.50 %, 89.73 % and 48.55 %) and 100-seed weight (22.42 %, 21.75 %, 91.33 % and 43.47 %). In any crop improvement programme, the most basic information required was the extent of the inheritance potential of the genotypes for the traits under consideration. various Thus. heritability estimates help in the selection of elite genotypes from genetically diverse populations. A higher magnitude of the broad sense heritability (h_{BS}^{2}) estimate for quantitative characters indicates effectiveness of selection on the basis of phenotypic performance. However, it does not show any indication of the amount of genetic progress for selecting the best individuals which is possible only by using the estimates of genetic advance.

High heritability along with high genetic advance indicates the additive gene action and the selection of such characters may be fruitful. High heritability coupled with low genetic advance is indicative of non-additive gene action. High additive gene action enables the breeder to have maximum selection response for a trait. Greater heritability estimate was observed for the characters viz., number of branches per plant, followed by, 100-seed weight, number of seeds per plant, number of pods per plant and biological yield per plant. These results were in accordance with the finding of Vaghela et al. (2009), Khan et al. [25], Babbar et al. [20], Sewak et al. [26], Parhe et al. [27] and Mallu et al. [28].

High genetic advance as *per cent* of mean was recorded for number of branches per plant, followed by number of seeds per plant, 100-seed weight, biological yield per plant, seed yield per

S. No.	Characters	Mean Sum of squares					
		Replication (2 df)	Treatment (19 df)	Error (38df)			
1	Plant height (cm)	0.64	21.65**	2.95			
2	No. of branches per plant	0.01	4.33**	0.04			
3	No. of pods per plant	3.68	276.09**	13.91			
4	No. of seeds per plant	1.27	703.81**	18.80			
5	Biological yield per plant (g)	9.35	70.89**	4.89			
6	100-seed weight (g)	0.29	77.06**	1.59			
7	Days to flower Initiation	2.80	14.56**	2.83			
8	Days to 50 % flowering	6.47	25.92**	4.41			
9	Days to maturity	2.55	7.03**	2.41			
10	Harvest Index (%)	1.57	76.55**	45.40			
11	Seed yield per plant (g)	1.82	18.22**	2.77			
12	Root length (cm)	6.97	9.31**	1.89			
13	Relative water content	219.91	108.90**	45.77			

Table 2. Analysis of variance for thirteen agro-physiological traits in chickpea

Table 3. Estimate of various parameters of genetic variability for agro-physiological traits in chickpea

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability	Genetic	Genetic advance
			Mini.	Max.	,		(Broad sense %)	advance (%)	as % of mean
1	Plant height (cm)	38.16	32.27	42.92	8.02	6.64	66.56	4.20	11.35
2	No. of branches per plant	4.44	3.12	7.18	25.71	25.31	93.93	2.21	51.29
3	No. of pods per plant	65.22	49.54	87.24	15.44	14.35	83.72	17.38	27.46
4	No. of seeds per plant	61.61	39.83	107.46	25.47	24.50	89.73	29.04	48.55
5	Biological yield per plant (g)	25.77	18.16	37.08	20.36	18.47	79.81	8.63	34.51
6	100-seed weight (g)	23.20	15.27	35.74	22.42	21.75	91.33	9.79	43.47
7	Days to flower Initiation	51.16	47.38	53.90	5.21	4.04	58.37	3.21	6.46
8	Days to 50 % flowering	56.36	51.50	60.43	6.11	4.84	60.96	4.33	7.92
9	Days to maturity	122.69	119.48	124.97	1.62	1.01	37.74	1.54	1.30
10	Harvest Index (%)	54.63	44.63	61.04	13.79	5.93	17.87	2.77	5.24
11	Seed yield per plant (g)	13.54	10.12	18.61	20.68	16.80	63.99	3.70	28.10
12	Root length (cm)	15.06	12.64	18.82	13.90	10.41	54.45	2.35	16.06
13	Relative water content	66.01	56.93	76.78	12.43	6.90	29.85	5.04	7.88

plant and number of pods per plant. The above results were in agreement with the findings of Vaghela et al. (2009), Babbar et al. [20], Shweta et al. [12], Arif et al. [29] and Bharadwaj et al. [30]. High heritability coupled with high genetic advance as per cent of mean were recorded for number of branches per plant, number of seeds per plant and 100-seed weight. Such results indicated, predominantly the presence of additive gene action in the expression of these characters and consequently chance of improving these characters through simple selection procedures appears to be more. These findings were in agreement with Vaghela et al. (2009), Borate et al. [10], Jadhav et al. [31], Arif et al. [29], Parhe et al. [32], Yadav et al. [33], Roy et al. [34] and Bharadwai et al. [30].

4. CONCLUSIONS

From the preceding discussion, it can be culminated that the analysis of variance revealed highly significant differences among genotypes for all the characters studied indicating the existence of sufficient genetic variability in the experimental material. Higher PCV, GCV, heritability and genetic advance as *per cent* of mean were observed for number of branches per plant, number of seeds per plant and 100-seed weight indicating the prevalence of additive gene action was playing major role for expression of these characters and simple selection methods may be effective for improvement of these traits.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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