Evaluation of Genetic Variability, Heritability and Genetic Advance of Chickpea (*Cicer arietinum* L.) Genotypes under Organic Condition

ABSTRACT

Aims: The improvement in crop yield depends upon the magnitude of genetic variability available in breeding material and the extent to which the yield component traits are heritable from generation to generation.
Study design: Randomized Block Design.
Place and Duration of Study: Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Bundelkhand University, Jhansi (U.P.) between October 2019 and June 2020.
Methodology: A field experiment was conducted using twenty-two genotypes of chickpea in Randomized Block Design (RBD) with three replications along with plot size of 1.20 x 1 m and the plant geometry was maintained at 10cm X 30cm during Rabi 2019-20. The material was shown on 23rd October, 2019. Observations were recorded on the basis of five random competitive plants selected from each genotype separately for yield and its attributing parameters were evaluated as per standard procedure.
Results: The genotypes were highly significant for all characters expect day to 50% germination, number of primary branches per plant, root fresh weight and root dry weight. High phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were observed for number of nodules per plant, number of pods per plant and number of seeds per pod. High heritability coupled with high genetic advance as percentage of mean for number of nodules per plant, number of pods per plant, number of seeds per pod, test weight, seed yield per plant and biological yield per plant.
Conclusion: Highly significant genetic variability present in the existing material which can be used in breeding programme for crop improvement. High heritability coupled with high genetic advance for number of nodules per plant, number of pods per plant, number of seeds per pod, test weight, seed yield per plant and biological yield per plant, hence, that these traits can be improved through direct selection.

Keywords: Chickpea, genetic variability, genetic advance, heritability and seed yield.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinated Rabi legume crop which having 2n=2x=16 chromosomes with genome size of 732 Mb and an important part of Indian diet. Vavilov (1926) designated Southwest Asia and the Mediterranean as primary and Ethiopia as secondary centers of diversity. India contributes major share of world's chickpea area (70%), production (67%) and continues to be the largest chickpea producing nation. To meet domestic demand, India also imports large quantity of *Desi* chickpea, but in past decade, it has emerged as a major exporter of *Kabuli* chickpea. In India, chickpea is mostly cultivated as a rainfed crop (68% area) in all parts of the country [1].

The improvement in crop yield depends upon the magnitude of genetic variability available in breeding material and the extent to which the yield component traits are heritable from generation to generation. The genetic variability can thus be a choice for selecting suitable parents; however, the quantitative characters are prone for environmental influence that necessitates the partitioning of overall variances as heritable and non-heritable components for efficient breeding programme. Absolute variability in different characters cannot be the decisive factor for deciding as to which character is showing the highest degree of variability. The relative values of phenotypic and genotypic coefficient of variation, therefore, gives an idea about the magnitude of variability present in a population, since, the estimate of genotypic and phenotypic coefficient of variation, heritability and expected genetic advance are useful for yield improvement and the above values were estimated to know the scope of improvement in the yield of chickpea [2].

India is also greater consumer as well as importer of chickpea in the world. In India, chickpea is grown about 9.93 m ha area and producing 9.53 m tonne grain with productivity of 960 kg per ha. In Uttar Pradesh, it is cultivated on area of 577 thousand ha with grain yield production is 475 thousand tonne and productivity of chickpea crops is 824 kg per ha, respectively 2013-14. It is cultivated throughout the country excepting high altitude and costal region. However, the major chickpea producing state are Madhya Pradesh, Rajasthan, Maharashtra, Karnataka and Andhra Pradesh which contribute more than 90 per cent of the national production. Despite its great importance, chickpea cultivation is neglected as little attention is given towards its improvement. There are various reasons for the low production of crop like lack of genetic variability, absence of suitable ideotype, susceptibility to biotic and abiotic stresses and planting in marginal areas of farming. Hence, it is vital to improve the productivity of chickpea. This can be achieved by studying the genetic architecture of the crop [3].

The knowledge of the inheritance of various quantitative and qualitative traits through estimation of genetic parameters like phenotypic and genotypic coefficients of variability, heritability and genetic advance is a prerequisite in conducting an effective breeding programme. Before starting any breeding program, it is necessary to assess the nature and magnitude of genetic variability in the population to improve the yield and its component traits. Along with genetic variability, knowledge of heritability and genetic advance is essential to formulate selection criteria for improvement of seed yield. Heritability is the heritable portion of phenotypic variance which is a good index of transmission of traits from parents to their offspring. Heritability in broad sense provides an idea about the additive and non-additive gene action in the expression of traits. The estimates of heritability along with genetic advance are more important than genetic advance alone to know the resulting effect of the best individuals [4]. Keeping in view these points, the present investigation is conducted to assess the variability, heritability and genetic advance among genotypes of chickpea.

2. MATERIAL AND METHODS

2.1 Experimental site

The field experiment was conducted at Agriculture Research Farm, Karguaji, Institute of Agricultural Sciences, Bundelkhand University, Jhansi, Uttar Pradesh during Rabi-2019. Geographically, it is located at 25^0.45” N latitude and 78^0.61 E longitudes at an altitude of 271 m above the mean sea level in semi-arid tract of central India.

2.2 Experimental material

The experimental material consisting of twenty-two genotypes was procured from Indian Institute of Pulse Research, Kanpur is given in Table-1.

Table-1: List of chickpea genotypes used in present investigation

S. No.	Name of genotype	S. No.	Name of genotype
1.	T39.1	12.	KWR108
2.	PDF- 02.E	13.	GNG469
3.	BG3043	14.	JG14
4.	IPC.71	15.	NBCG47
5.	RVGK101	16.	JG130
6.	IPC08-11	17.	JAKI9218
7.	JG24	18.	GG2
8.	IPC06.77	19.	ICC92030
9.	ILWC21	20.	ICC4958
10.	IPC05.64	21.	ICC5434
11.	CSG8962	22.	T.39A

2.3 Experimental design

The experimental material consisting of 22 genotypes of chickpea was evaluated in Randomized Block Design with three replications with the plot size of 1.20m x 1m and the plant geometry was maintained at 10cm X 30cm. The material was shown on 23rd October, 2019. All recommended package of practices was followed to raise good chickpea crop during the conduct of experiment.

2.4 Recording of data

Observations were recorded on plot basis as well as single plant basis. Plot basis data were recorded for days to 50 per cent germination, days to 50 per cent flowering and days to maturity; while single plant basis data recording was done for plant height, number of nodules per plant, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight, number of primary branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, test weight and seed yield per plant. Five randomly competitive plants were taken for single plant recording of data.

2.5 Statistical analysis

The data on various characters were subjected to statistical analysis by using appropriate method of analysis of variance as described by Panse and Sukhatme,1985 [5]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton, 1952 [6]. Heritability in broad sense was estimated according to Burton and De Vane, 1953 [7]. The estimates of genetic advance were obtained by the formula given by Johnson et al., 1955 [4].

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

Genetic variability in any crop improvement program is a basic requirement for deciding the efficiency of selection. Its existence is essential for resistance to biotic and abiotic factors as well as for wide adaptability. The assessment of genetic variability was main objective of present investigation. The analysis of variance presented in Table 2, indicated that mean sum of squares due to genotypes were significantly different at 1% and 5% level of significant expect day to 50% germination, number of primary branches per plant, root fresh weight and root dry weight suggesting that the genotypes were genetically divergent and presence of sufficient genetic variability in the existing material. Similar findings were earlier reported [8].

. Table: 2. Analysis of variance for various characters of chickpea genotypes

S. No.	Characters	Replication [2]	Genotype [22]	Error [44]
1	Day to 50% germination	0.14	0.67	0.74
2	Days to 50% flowering	1.27	69.29**	1.69
3	Days to maturity	0.06	17.86**	1.25

4	Plant height (cm)	44.27*	37.04**	11.81
5	No. of nodules per plant	2.42	85.68**	7.43
6	No of primary branches per plant	0.34	0.45	0.32
7	Shoot fresh weight (g)	29.02	230.31**	65.61
8	Root fresh weight (g)	0.27	0.67	0.46
9	Shoot dry Weight (g)	46.81	100.26*	45.75
10	Root dry weight (g)	0.16	0.42	0.36
11	Number of pod per plant	1155.57*	4449.82**	270.27
12	No of seed per pod	0.02	0.90**	0.03
13	Test weight (g)	2.82	100.20**	3.64
14	Biological yield per plant (g)	7.43	752.56**	33.04
15	Harvest Index	0.51	3.53**	0.58
16	Seed yield per plant (g)	1.72	191.07**	7.29

*, ** Significant at 5% and 1% respectively.

3.2 Parameters of variability

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 2.02-37.92% and 1.82- 34.71%, respectively. The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all traits studied indicating the influence of environment on the expression of these traits (Table 3). Similar results were previously reported [9, 10]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorized as low (<10%), moderate (10-20%) and high (>20%) as suggested [11]. High phenotypic coefficient of variation and genotypic coefficient of variation were found for number of nodules per plant, number of pods per plant and number of seeds per pod. This provides an evidence for the existence of sufficient variability for these traits in the population with more contribution of genetic factors and also provides the basis for selection of desirable genotypes of chickpea. Low estimates of variability were observed for days to 50% flowering, days to maturity, plant height and harvest index. This suggested the prevalence of low genetic variability for these traits in the population and selection will not be effective for these traits. Similar results were previously reported [12, 13].

Table-3: Genetic variability parameters of different traits of chickpea genotypes

S. No.	Character	GCV (%)	PCV (%)	Heritability	Genetic	Genetic

				(%)	advance	gain
1.	Days to 50% flowering	7.85	8.13	93.04	9.43	15.59
2.	Days to maturity	1.82	2.02	81.57	4.38	3.39
3.	Plant height	7.16	11.10	41.60	3.85	9.51
4.	No. of nodules per plant	21.56	24.44	77.84	9.28	39.19
5.	Shoot fresh weight	10.54	15.61	45.56	10.30	14.65
6.	Shoot dry Weight	10.44	19.58	28.42	4.68	11.47
7.	Number of pod per plant	34.71	37.92	83.75	70.37	65.43
8.	No. of seed per pod	27.50	28.84	90.97	1.06	54.04
9.	Test weight	14.07	14.84	89.84	11.08	27.46
10.	Biological yield per plant	16.10	17.18	87.89	29.91	31.10
11.	Harvest Index	1.77	2.22	62.98	1.62	2.89
12.	Seed yield per plant	14.56	15.40	89.36	15.24	28.35

3.2 Heritability

Heritability provides the assessment of transmissible traits from one generation to other. Heritability in broad sense is of remarkable significance to the breeders as its extent indicates the reliability with which a genotype can be documented by its phenotypic expression. It was recorded from 28.42% to 93.04%. According to Robinson, 1966 [14]; heritability was partitioned as high (>60%), moderate (60-30%) and low (<30%). Highest heritability was found for number of days to 50% flowering (93.04%) followed by number of seeds per pod (90.97%), test weight (89.84%), seed yield per plant (89.36), biological yield per plant (87.89%), number of pods per plant (83.75%), days to maturity (81.57%), number of nodules per plant (77.84%) and harvest index (62.98%) presented in Table 3. This revealed that the lesser influence of environment and selection for improvement of these traits may be useful due to the involvement of additive variances. Moderate heritability was observed for plant height and shoot fresh weight indicating influence of environment and requires high intensity of selection for improvement of these traits. Similar results were earlier reported by [15].

3.3 Genetic advance

Genetic advance is helpful in the improvement of mean genotypic value of selected plants over the parental populations. It measures the genetic gain under selection. It should be considered in conjugation with genetic advance for effective selection of genotypes. The estimated values of genetic advance were classified as high (>30%), moderate (20-30%) and low (<20%). Estimation of Genetic advance ranged from 1.06% to 70.37% (Table 3). The high estimate of genetic advance was recorded for number of pods per plant and moderate for biological yield per plant. Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment genetic advance as percentage of mean was calculated to predict the genetic gain (Table 3). According to Johnson et al., 1955 [4], genetic advance as percentage of mean was partitioned as high (>20%), moderate (20-10%) and low (<10%). Estimation of genetic advance as percentage of mean ranged from 2.89% to 65.43%. The high estimate of genetic advance of percentage of mean was recorded for number of pods per plant followed by number of seeds per pod, number of nodules per plant, test weight, seed yield per plant and biological yield per plant. Similar findings were earlier reported [1].

High heritability with high genetic advance as percentage of mean was recorded for number of nodules per plant, number of pods per plant, number of seeds per pod, test weight, seed yield per plant and biological yield per plant. This suggesting that these traits were under the control of additive gene action and selection will be more useful for yield improvement. The findings were in agreement to the findings of [16].

High heritability supplemented with moderate genetic advances as percentage of mean were exhibited by days to 50% flowering which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about. High heritability supplemented with low genetic advances as percentage of mean was exhibited by harvest index. This revealed the predominance of non-additive gene action in the expression of these characters. These findings collaborated the earlier findings of [17, 18].

4. CONCLUSION

On the basis of the results emanated from present investigation that highly significant genetic variability present in the existing material which can be used in breeding programme for crop improvement. High heritability coupled with high genetic advance for number of nodules per plant, number of pods per plant, number of seeds per pod, test weight, seed yield per plant and biological yield per plant, hence, that these traits can be improved through direct selection for yield improvement.

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