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

A key Rabi legume crop in India, the chickpea (Cicer arietinum L.) has 2n=2x=16 chromosomes and a 732 Mb genome. Southwest Asia, the Mediterranean, and Ethiopia were identified by Vavilov (1926) as the key diversification hubs. With a 70% global area and 67% global output contribution, India dominates the chickpea industry. To meet demand, the country imports Desi chickpeas, but in the past ten years it has started to export Kabuli chickpeas. Rainfed farming accounts for 68% of all agricultural land in India [1].

The level of genetic variability in breeding material and the inheritability of yield-related traits across generations are key factors in agricultural yield enhancement. Parent selection is made easier by genetic variation, but because quantitative features are more sensitive to environmental influence, it is necessary to divide variations into heritable and non-heritable components for successful breeding. The relative values of phenotypic and genotypic coefficients of variation give insight into population variability because the absolute variability in many traits by itself is insufficient to identify the most variable trait. Yield improvement is aided by assessing heritability, genetic advance estimates, and the genotypic and phenotypic coefficient of variation [2].

India is a large importer and consumer of chickpeas on a global scale. In India, chickpea farming is practiced over a huge area of over 9.93 million hectares, producing roughly 9.53 million tonnes of grain at a production rate of 960 kilos per hectare. In Uttar Pradesh specifically, the crop is grown over 577 thousand hectares, producing 475 thousand tonnes of grain output and 824 kg of chickpea crop productivity in the 2013–14 season. Except for high altitude and coastal regions, this crop is planted everywhere across the nation. Despite the fact that it is extremely important, little effort is put into improving chickpea farming. Crop output is low for a number of reasons, including genetic instability, a lack of acceptable ideotypes, vulnerability to biotic and abiotic stressors, and planting in unproductive regions of the farm. Therefore, increasing chickpea yield is essential. Studying the crop's genetic structure can help with this [3].

Estimating genetic parameters including phenotypic and genotypic coefficients of variability, heritability, and genetic progress is necessary to comprehend the inheritance patterns of both quantitative and qualitative features. These conditions must be met in order to successfully run breeding operations. It is crucial to assess the kind and degree of genetic variability within the population before beginning any breeding endeavor, especially with regard to yield and its component qualities. For developing selection criteria targeted at improving seed production, understanding heritability and genetic advancement are equally as important as understanding genetic variability. The heritable component of phenotypic variance is represented by heritability, which serves as a marker for the inheritance of traits from one generation to the next. Insights into the additive and non-additive gene actions impacting trait expression are provided through broad-sense heritability. In this perspective, the evaluation of heritability in conjunction with genetic progress is more important than genetic progress alone since it offers a thorough knowledge of the effects of better individuals [4]. Given these factors, the current investigation's goal is to evaluate the genetic advance, heritability, and variability of different chickpea genotypes

2. MATERIAL AND METHODS

2.1 Experimental site

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

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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

In order to determine the effectiveness of selection, genetic diversity is a fundamental necessity for any crop development effort. Its existence is necessary for both broad adaptation and resistance to biotic and abiotic influences. The major goal of the current work was to evaluate genetic variability. 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 gives evidence that these attributes are sufficiently variable in populations where genetic variables are more important, and it also lays the groundwork for choosing desirable genotypes of chickpea. Low estimates of variability were observed for days to 50% flowering, days to maturity, plant height and harvest index. This implied that selection will not be successful for these traits due to the minimal genetic variability that these traits exhibit in the population. Similar outcomes have already been reported. [12, 13].

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

S. No.	Character	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	Genetic 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 allows for the evaluation of attributes that are passed down from one generation to the next. Breeders place a great deal of importance on heritability in general because it shows how reliably a genotype can be verified 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. For plant height and shoot fresh weight, moderate heritability was found, showing environmental effect and necessitating high intensity selection for development of these variables. Similar outcomes were previously reported [15].

3.3 Genetic advance

Genetic advance contributes to enhancing the average genetic value of chosen plants above parental populations, quantifying the genetic progress achieved through selection. It's crucial to consider alongside genetic advance for effective genotype selection. 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. Because of the masking influence of the environment on the traits in question, genetic advance values fluctuated greatly. As a result, genetic advance as a percentage of mean was estimated to anticipate genetic gain in order to achieve a relative comparison of attributes in connection to the environment. (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, coupled with moderate genetic advances as a percentage of the mean, was observed in days to 50% flowering. This outcome could be attributed to the influence of additive gene action on their expression and phenotypic selection for favourable traits. Conversely, high heritability accompanied by low genetic advances was evident in the harvest index. This finding indicated the prevalence of non-additive gene action in the manifestation of this trait. These results align with prior research findings [17, 18].

4. CONCLUSION

Based on the findings of the current investigation, substantial genetic variability exists in the current material, offering potential for crop improvement through breeding programs. Traits such as 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 exhibit high heritability coupled with genetic advance, indicating their suitability for direct selection to enhance overall yield

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