



## **Assessment of Genetic Variability, Heritability and Genetic Advance Studies for Yield Mentioning Traits in Chickpea Elite Genotypes (*Cicer arietinum* L.)**

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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**

The present investigation has been done to conduct an Assessment of Genetic Variability, Heritability, and Genetic Advance Studies for Yield and Quality Traits in Chickpea Elite Genotypes (*Cicer arietinum* L.). The experiment is laid out in Randomized Block Design (RBD) with three replications to minimize the error. The experiment was carried out during the Rabi 2020-2021. The analysis has been done with ten characters having plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length, days to 50% flowering, 100- seed weight, pod yield per plant, pod yield per plot as a dependent variable. High genotypic coefficient variation and phenotypic coefficient of variation were found in seed yield per plant (25.5 and 25.9), seed yield per plot (25.4 and 25.8) and several seeds per pod (15.7 and 28.5) displayed the negligible influence of the environment on the phenotypic expression of the character. High heritability coupled with high genetic advance was seen in seed yield per plant (90 and 51.8), seed yield per plot (97.1 and 51.6), number of secondary branches per plant (90 and 27.8), number of primary branches per plant (70 and 23.3), number of pods per plant (96 and 20.6), and pod length (95 and 38.9), indicating an additive gene effect. Therefore, these characteristics can be used in further breeding programs for crop advancement.

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## 1. INTRODUCTION

“The chickpea (*Cicer arietinum* L.) is an annual legume of the family Fabaceae, chickpea seeds are high in protein. It is one of the earliest cultivated legumes. Chickpea is a cool-season grain legume that may withstand hot temperatures during fruiting and ripening. It is thought to have originated in South-East Anatolia and neighboring Syria and Iran, where the earliest remains date back to around 7000 BC. It was introduced to the Mediterranean Basin, Africa, and the Indian subcontinent before 2000 BC. *Cicer arietinum* from sea level up to an altitude of 2500 m in areas where temperatures range from 15°C to 29°C” [1-3]. “Chickpeas are mainly cultivated in the cool, dry season of the semi-arid tropics on residual moisture. The plant will be adapted to tropical climates with moderate temperatures and is successfully cultivated under irrigation in the cool season of many tropical countries. Globally, chickpea has yield levels of about 850 kg/ha. The crop yields in the developing regions are very low. However, in the case of chickpeas, some developing regions have exceeded the developed countries in terms of yield levels. The yield level in South and South-East Asia has increased by 13% from 717 kg/ha in 1994-1996 to 812 kg/ha in 2008-2010, growing at an annual rate of 0.8%. The mean annual production share of chickpea by region from 2008 to 2017 revealed that Asia shares 83% globally. In 2019, world production of chickpea was 14 million tonnes, led by India with 70% of the global total, and Turkey as a secondary producer of chickpea [4,5].

Variability is the either presence of or the generation of genetic differences. It is defined as “the formation of individuals differing in genotype, or the presence of genotypically different individuals, in contrast to environmentally induced differences which as a rule, cause only temporary, nonheritable changes of the genotypes.” Genetic variability in a population is important for biodiversity. The genotypic and phenotypic coefficients of variation help understand the existing variability in the populations whereas, the estimates of heritability and genetic advance provide the indices of transmissibility of characters. Thus, estimates of

variability like coefficients of variation, heritability, and genetic advance are very useful for devising suitable selection strategies for developing high-yielding genotypes in chickpea crops.

## 2. MATERIALS AND METHODS

Thirty chickpea genotypes obtained from different sources were sown in a Randomized Block Design (RBD) with three replications in the Crop Research Centre (CRC), Department of Genetics and Plant Breeding, School of Agriculture, ITM University, Gwalior, during 2021-2022. Each genotype was planted in a separate plot, with a plant-to-plant and row-to-row distance of 10 and 30 cm, respectively. Recommended cultural practices were carried out to grow a successful crop. Observations are recorded on ten traits viz. Plant height, Days to 50% flowering, number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod, pod length, seed index, yield per plant, and Seed yield per plot.

The data were subjected to analysis using R Studio by Raj Popat et al. [6].

## 3. RESULTS AND DISCUSSION

The Analysis of Variance (Table 1) showed significant differences among the 30 genotypes of chickpea for all the ten characters studied, which indicate the presence of a sufficient amount of genetic variability among the genotypes and hence revealed the scope of improvement in a breeding program. Fisher, R.A. [7].

Range of variability for plant height (56.6- 83.3 cm), days to 50% flowering (62.3- 85.3), number of primary branches (11.6–19.3), number of secondary branches (53.6 -93.6), number of pods per plant (124.6– 174.6), number of seeds per pod (1.3– 2.6), pod length (1.2 - 2.5cm), seed index (15.6–21.6), yield per plant (32.6-102g) and Seed yield per plot (0.9-3) were observed Table 2. Similar findings were previously reported in the mean performance of plant height, several primary branches per plant, and several secondary branches per plant by Alwawi et al. [2], Ali et al. [1], Muhammad et al. [8], and Meena et al. [9].

Table 1. Analysis of variance (ANOVA)

Sl. no	Characters	Replication (Df = 2)	Mean sum of squares	
			Treatment (Df =29)	Error (df =58)
1.	Plant height	430.88	87.30**	1.62
2.	Number of primary branches	243.744	12.646**	1.181
3.	Number of secondary branches	771.03	291.54**	3.85
4.	Number of pods per plant	1545.28	680.52**	6.97
5.	Number of seeds per pod	11.5111	0.5169**	0.2238
6.	Pod length	1.14411	0.35833**	0.00561
7.	Days to 50% flowering	461.01	150.52**	2.61
8.	seed index	52.811	7.965**	0.639
9.	Seed yield per plant	2548.6	1017.2**	10.0
10.	Seed yield per plot	2.31053	0.91601**	0.00896

\*\* significant at a 5% level of significance

Table 2. Mean performance of 30 genotypes for 10 characters under study

Sl. no	Genotypes	Plant height	Number of primary branches per plant	Number of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length	Days to 50% flowering	100 seed weight	Seed yield per plant	Seed yield per plot
1.	Pusa 2024	61	15.3	66	124.6	2	1.8	62.3	16.3	51	1.5
2.	IPCK- 2004-29 (Shubra)	62	14.3	72.6	135	1.6	1.4	65.3	16.6	69.6	2.1
3.	IPCK- 2004-29 (Ujjwal)	64.3	12.3	71	144	2	1.7	70.3	18	59.6	1.8
4.	Pusa- 1088	72.3	17.3	82	154	2.3	1.6	66	19	99.6	3
5.	Pusa- 1103	70	14	64.6	134.6	1.6	1.6	71.6	16.6	91	2.7
6.	JG- 130	72.3	14.6	69.6	147.3	2.6	2.0	67	18.6	79.6	2.4
7.	JG- 63	72.3	13.3	73	162.3	2	2.3	71	19.3	63	1.9
8.	JGK- 2	66	11.6	68.6	125	2.3	1.8	63	16	81	2.4
9.	JGK- 3	64.6	14.3	71.3	134	1.6	1.5	69	18.6	99.6	3
10.	JG- 226	68	16	82.6	164.3	2	2.4	64.6	18.3	64	1.9
11.	JG- 6	65.6	14.6	66.3	131.6	1.6	2.3	71.6	20	49.6	1.5
12.	JGK- 14	62.3	14	66.3	131.3	1.3	1.5	65	15.6	75.3	2.2
13.	JGK- 1	64.3	18.3	85.3	147.3	2.3	1.4	67	19.3	81.6	2.4
14.	RMG-1079	66.3	15.3	65	135.6	1.6	2.1	76	20.3	62	1.8

Sl. no	Genotypes	Plant height	Number of primary branches per plant	Number of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length	Days to 50% flowering	100 seed weight	Seed yield per plant	Seed yield per plot
15.	ML-1299	74.6	18	88.3	165.3	2.3	1.4	75.3	17.6	102	3.0
16	PVSA-672	59	13	67	137	2.3	1.6	73.3	17.3	35	1
17	RMG-1041	56.6	12	58.6	133.6	1.6	2.1	81.3	20	70	2.1
18	RMG-1015	63.3	15.6	67	147.3	2.6	1.6	79.6	17	55	1.6
19	Jyoti	62	15.3	57.3	127.3	1.6	1.6	84.6	21.3	77.3	2.3
20	C-115	65	12.6	53.6	134.6	2	1.2	81	16.6	88.6	2.6
21	C-113	65.6	13.3	65	141.3	2.6	1.5	69.3	17	58.6	1.7
22	C-223	74.3	17.6	79.6	166.6	1.3	1.7	73.3	16.6	96.3	2.9
23	JG-24	64.6	14.6	66	157	2	1.2	81	19.3	68.3	2
24	C-1014	83.3	14	66.3	164	1.6	1.4	82.3	17.6	55	1.6
25	C-1023	67	15.3	66.6	145	2.3	1.4	75.3	21.6	32.6	0.9
26	C-137	67.6	19.3	93.6	174.6	1.6	1.6	69	17	83	2.5
27	C-210	65	14.6	63.6	145.3	2.6	1.9	77	19.6	68.6	2
28	C-126	71	19	86.6	166.6	1.6	2.5	84.6	15.6	94	2.8
29	C-1025	64	14	64	165	1.6	1.9	82.3	18.6	58.6	1.7
30	AVTI-G5	62.6	17.3	84.6	169	1.6	2	85.3	17.3	80.6	2.4
	Grand Mean	66.5889	15.0556	71.1	147.044	1.9889	1.7711	73.5111	18.1222	71.7	2.1606
	CD 5%	2.0834	1.7763	3.2067	4.3141	0.7731	0.1224	2.6398	1.3062	5.1687	0.1547
	CD 1%	2.772	2.3634	4.2665	5.74	1.0286	0.1628	3.5123	1.7379	6.877	0.2059

### 3.1 Coefficient of Variation

The magnitude of GCV was found highest in seed yield per plant (25.5) seed yield per plot (25.4) followed by, pod length (19.3), number of seeds per pod (15.7), number of secondary branches per plant (13.7), number of primary branches per plant (12.9), number of pods per plant (10.1), days to 50% flowering (9.5), seed index (8.6) and plant height (8).

The magnitude of PCV was found highest in the number of seeds per pod (28.5), seed yield per plant (25.9), seed yield per plot (25.8), followed by pod length (19.8), number of primary branches per plant (14.8), number of secondary branches per plant (14), number of pods per plant (10.3), days to 50% flowering (9.8), seed index (9.6) and plant height (8.2).

The Estimates of Phenotypic Coefficient of Variation (PCV) for all the 10 characters under study were found to be higher than the Genotypic Coefficient of Variation (GCV) indicating the

influence of the environment on the phenotypic expression of these characters.

These results are by results reported the values of the phenotypic coefficient of variations were higher than the genotypic coefficient of variations showing the influence of the environment on the recorded characters by Arshad et al. [3] and Khan et al. [10] suggested that the seeds per pod had maximum PCV and GCV followed by test weight.

### 3.2 Heritability and Genetic Advance

The magnitude of heritability ranged from 97.1 to 30 in seed yield per plot and the number of seeds per pod respectively. The highest heritability was seen in seed yield per plot (97.1) followed by the number of pods per plant (96), and pod length (95). Days to 50% flowering (94), seed yield per plant (90), number of secondary branches per plant (90), plant height (90), seed index (79), number of primary branches per plant (70), and number of seeds per pod (30) (Table 4).

**Table 3. Coefficient of variation (GCV, PCV) for all the characters under study**

Sl. no	Characters	Genotypic coefficient of variation	Phenotypic coefficient of variation
1	Plant height	8	8.2
2	Days to 50% flowering	9.5	9.8
3	Number of primary branches per plant	12.9	14.8
4	Number of secondary branches per plant	13.7	14
5	Number of pods per plant	10.1	10.3
6	Number of seeds per pod	15.7	28.5
7	Pod length	19.3	19.8
8	seed index	8.6	9.6
9	Seed yield per plant	25.5	25.9
10	Seed yield per plot	25.4	25.8

**Table 4. Heritability, genetic advance, and genetic advance as percent mean for all the characters under study**

sl. no	Characters	Heritability h <sup>2</sup> (bs) (%)	Genetic advance (%)	GA as a percent of the mean (%)
1	Plant height	90	10.7	16
2	Days to 50% flowering	94	14	19.1
3	Number of primary branches per plant	70	3.51	23.3
4	Number of secondary branches per plant	90	19.7	27.8
5	Number of pods per plant	96	30.3	20.6
6	Number of seeds per pod	30	0.3	17.8
7	Pod length	95	0.6	38.9
8	100 seed weight	79	2.8	15.8
9	Seed yield per plant	90	37.19	51.8
10	Seed yield per plot	97.1	1.1	51.6

Genetic advances ranged from 0.3 to 37.19 in the number of seeds per pod and seed yield per plant respectively.

High heritability coupled with high genetic advance is seen in seed yield per plant, High heritability coupled with high genetic advance indicates additive gene action which is beneficial for crop improvement.

These results were to the findings of Babbar et al. [4], Qurban Ali et al. [11], Gul, R, et al. [5], and Kadiri Kusuma et al. [12] who observed high heritability for the number of seeds per pod and high genetic advance as percent of the mean for the number of primary branches per plant.

#### 4. CONCLUSION

This paper discusses genetic variation, heritability, and genetic variability in 30 chickpea genotypes. The study has employed entirely routine and standard methods. The results have shown that some genotypes have a significant yield and heritability, which can be used in subsequent seed breeding research. It appears that the identified genotypes are good breeding. In this study, it is concluded that among the 30 genotypes of chickpea, the two genotypes C-136, C-1014, GNG-1958, C-223, C-126, C-128, C-115, and C-137 were found to be superior in terms of yield. Seed yield per plant, number of seeds per pod, seed yield per plot, and pod length exhibited high GCV, PCV, and other genetical parameters revealed that the higher heritability and genetic advance as percent of mean were for several pods per plant, days to 50% flowering, seed yield per plant, number of secondary branches per plant, plant height. The above-mentioned characters will prove helpful for a selection of the desirable yield-related traits as they possess additive gene action which is completely transferable.

#### 5. FUTURE SCOPE

Chickpea has low digestible carbohydrates with a good amount of protein, important fats, and a variety of minerals and vitamins. It is a very nutrient-dense pulse crop that has health value for pregnant women and young children. Its growth depends on zinc, a mineral that is abundant in chickpeas. The current high rates of population increase would exacerbate the discrepancy between the country's demand and its output for chickpeas. This circumstance highlights the necessity of breeding Chickpea

crops to increase the yield. For increasing the yield, the need for a variable population of chickpeas concerning desirable traits is required to evaluate. Hence, the genetic variability, heritability, and genetic advance were evaluated in chickpea genotypes. The identified genotypes having valuable traits would be utilized further in the breeding programs.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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