



Studies of Genetic Variability, Heritability and Genetic Advance in Yield Component Traits in Chickpea (*Cicer arietinum* L.)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Twenty diverse genotypes of chickpea including three checks viz., GNG 158, GNG 1488, PNG 469- checks, were carried out under Agriculture Research farm, Department of Genetics of Plant Breeding, Lovely Professional University, Phagwara (Punjab). This experiment was conducted in Randomized Block Design (RBD) with three replications, during rabi 2021-2022. To estimate genetic variability, heritability and genetic advance percent of the mean. analysis of variance for the design of experiments has been present for all the twelve traits The analysis of variance estimation demonstrated that the mean sum of squares attributed to genotypes were significant for all of the characters, suggesting that there was enough genetic diversity among the genotypes. The current study found that the Phenotypic Coefficient of Variation (PCV) was greater than the corresponding Genotypic Coefficient of Variation (GCV) for all traits, which could be attributed to genotype-environment interaction to some degree or another, explaining environmental factors influencing the expression of these characters. In the present study, moderate PCV, GCV were observed in No. of secondary branches per plant, 100 seed weight, No. of primary branches per plant, Harvest index, biological yield per plant, No. of pods per plant, Plant height and Seed yield per plant. Low value of PCV and GCV were recorded in No. of seeds per pod, protein content, Days to maturity and Days to 50% flowering, shows the magnitude of PCV and GCV were low and indicating limited

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scope for improvement. The genotypic correlation coefficient was higher in magnitude than their corresponding phenotypic one, indicating there by strong inherent association between different traits studied. The phenotypic expression of correlation was less due to multiple influences of environmental components in the view of correspondence selection on phenotypic basis would be effective.

Keywords: Genetic variability; PCV; GCV; chickpea; heritability; genetic advance.

1. INTRODUCTION

Food and Nutrition Security remain far from being reached, and in many parts of the world, the biggest problem is still hidden hunger [1]. Pulses, which are high in protein, are an essential part of the Indian diet. Pulses are generated with the least number of resources; hence they are less expensive than animal protein. In compared to other vegetables, pulses are high in protein, less costly, and may be utilized in a variety of cropping systems without interfering with the primary cereal crops. Aside from being a good source of protein, they are also beneficial to agriculture since they improve soil health and fertility by fixing nitrogen organically. Chickpea (*Cicer arietinum* L.), also referred as gram, Bengal gramme, chhola, and garbanzo bean, was one of the first grain legumes produced by humans [2]. The third-largest pulse crop in the world, chickpeas have a worldwide yield of 14.25 million tonnes [1]. It is an essential part of the major farming production systems, particularly in South Asia and Africa. Chickpeas (23–24%) are a highly affordable, nutrient-dense source of protein that are also said to have a well-balanced amino acid profile [3]. It is a self-pollinated crop from of the Papilionaceae subfamily of the Family Fabaceae [4]. Chickpeas are diploid with $2n=16$ chromosomes. Chickpeas is the most important pulse crop, with extensive acceptance and use. During the rabi, chickpea is typically farmed in marginal rainfed regions. It is a temperate and subtropical bean plant that flourishes in both tropical and temperate regions. Chickpea is classified into two market types: desi and Kabuli [5]. In addition to proteins, chickpeas are a major source of more over 15 minerals, including zinc and iron (Fe) (Zn) [6]. The desi types, which account for around 85 percent of chickpea area, are distinguished by small, angular-shaped, dark-colored seeds with a rough surface, pink flowers, anthocyanin pigment on the stem, and either a semi-spreading or semi erect growth habit. India is the world's leading producer of chickpeas, both in terms of land and output. It might be attributed to a variety of causes, including a favorable

environment, high-yielding seeds, increased farmer acceptance, and a wide market. More than half of India's chickpea output is produced in states such as Madhya Pradesh, Maharashtra, and Rajasthan. Chickpeas account for over 70 percent of total of India's pulse exporting [7]. Chickpeas are split and eaten as dal, as well as whole fried or boiled seeds. As a source of nourishment, animals eat husk and dal bits. Green, immature chickpeas are eaten as a vegetable in India and Pakistan, while chickpea flour is frequently used in snacks and sweets. Animals love the nourishment that straw provides. The lack of genetic variety for the majority of agronomic attributes is a major barrier to the development of pulse crops. Currently, it is simple to transfer genes from (*C. reticulatum*) chickpea to (*C. arietinum* L) chickpea. However, important genes from other species of the genus *Cicer* cannot be utilized because of incompatibility issues. Using novel techniques like embryo rescue and somatic hybridization, beneficial genes from other cicer species may be introduced into the domesticated chickpea, *Cicer arietinum* [8].

2. MATERIALS AND METHODS

The present investigation entitled “Study of Genetic Variability, heritability and genetic Advance in Chickpea (*Cicer arietinum* L.)” was conducted during Rabi, 2021-2022. In the experiment twenty 20 diverse genotypes including three checks viz., GNG 158, GNG 1488, PNG 469- checks of chickpea, were carried out under Agriculture Research farm, Dept of Genetics of Plant Breeding, Lovely Professional University, Phagwara (Punjab). This experiment was conducted in RBD with three replications. All Observations recorded for twelve characters. The details of the genotypes used in this study are presented in (Table 1). The experimental materials consisting of twenty diverse genotypes of chickpea were sown in randomized block design in three replications. Each entry was planted in a plot size of 50 x 6 m accommodating 4 rows of 2m length, keeping row to row and plant to plant distance of 45 x 30,

respectively. All the recommended package of practices was followed to raise a good and healthy crop. In each plot, five randomly selected competitive plants were tagged to record observations except for days to 50% heading and days to maturity which were recorded on plot basis. By taking the average, the mean value for the treatment was computed. Observations recorded for twelve characters viz., Days to 50 per cent flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Number of pods per plant, Number of seeds per pod, 100-seed weight (g), Biological yield per plant (g), Harvest index (%), Protein content (%) and Seed yield per plant (g). The data acquired was subject to genetic variability, Heritability and Genetic Advance. The Analysis of variance [9],

Heritability [10], Genetic advance [11] were estimated.

3. RESULTS AND DISCUSSION

The estimates of Genetic variability, Broad sense heritability and genetic advance per cent of mean is given in Table 3.

Analysis of variance of experiment has been present in Table 2 for all the twelve characters. Analysis of variance indicated that the mean sum of square (MSS) due to genotypes were highly significant for all the characters at 1% and 5% level of significance and it indicated the presence of consisted amount of genetic variability for all the traits. Similar kind of results were also found by Meena et al. [12], Gautam et al. [13].

Table 1. List of genotypes used in the study

S. No	Name of genotype	S. No	Name of genotype
1.	GL25016	11.	CSG 515
2.	ICCL 86111	12.	ICC 3020
3.	GNG 1581	13.	JAKI 9218
4.	GNG 1488	14.	C 18443
5.	PNG 469-	15.	GNG 1958
6.	GNG 2171	16.	ICC- 5434
7.	PBG- 5	17.	PDG- 4
8.	ICC 5335	18.	Vijay
9.	SADABAHAR	19.	MDG 15-1
10.	RSG 945	20.	PBG- 7

Table 2(a-b). Mean sum of squares

Table 2(a).

Source of Variation	d.f	Days to 50% Flowering	Days to Maturity	Plant Height	No. of Primary Branches Plant-1	No. of Secondary Branches Plant-1	Number of Pods Plant-1
Replication	2	6.82**	2.87**	0.31	0.12	0.22	6.35**
Genotypes	19	13.27**	23.78**	31.99**	2.27**	4.67**	82.44**
Error	38	0.71	0.38	0.21	0.17	0.29	0.72
CV		0.78	0.44	1.43	7.81	8.41	1.75

Table 2(b).

Source of Variation	d.f	Number of Seeds Plant-1	100-grain weight	Biological yield per plant	Seed yield per plant	Protein Content	Harvest index
Replication	2	0.07*	0.09	1.67	0.87**	0.01	4.74*
Genotypes	19	0.07**	9.04**	25.84**	3.12**	3.90**	48.68**
Error	38	0.02	0.06	0.67	0.09	0.01	1.08
CV		8.21	2.35	2.83	0.43	3.42	3.38

**=significant at 5% and 1% level of probability, NS = non-significant

Table 3. Genetic parameters of variation for seed yield and its components in Chickpea

S. No	Characters	Range		Mean	Co-Variance		Heritability Broad Sense (%)	Genetic Advance	GA% Mean
		Min.	Max.		GCV	PCV			
1.	Days to 50% flowering	103.67	112	108.57	1.88	1.94	94.6	4.1	3.78
2.	Days to maturity	134.67	142.33	138.07	2.02	2.04	98.4	5.71	4.13
3.	Plant height (cm)	26.43	39.27	32.19	10.11	10.14	99.3	6.68	20.76
4.	No. of primary branches per plant	4	6.67	5.27	15.88	16.5	92.5	1.66	31.46
5.	No. of secondary branches per plant	4.33	8.67	6.37	18.97	19.58	93.8	2.41	37.86
6.	Number of pods per plant	40.3	58.73	48.7	10.72	10.76	99.1	10.7	21.98
7.	Number of seeds per pod	1.47	2.07	1.76	7.16	8.59	69.5	0.22	12.3
8.	100 seed weight (g)	8	14.2	10.8	16.02	16.07	99.3	3.55	32.87
9.	Biological yield per plant (g)	23.03	36.39	28.96	11.51	11.68	97.2	5.89	20.33
10.	Seed yield per plant (g)	6.84	11.2	8.73	10	10.13	97.4	2.04	23.38
11.	Protein content (%)	20.15	24.37	22.51	5.06	5.07	99.8	2.34	10.41
12.	Harvest Index (%)	23.89	37.4	30.37	13.12	13.26	97.8	8.11	26.72

The highest estimates of PCV and GCV show that these traits have quantitative inheritance and are significantly impacted by environmental influences. While low PCV and GCV estimations imply that they are less impacted by environmental influences. In order to make inferences concerning these parameters, PCV and GCV estimations were classed as low (less than 10%), medium (10-20%), and high (more than 20%).

In the present study, moderate PCV, GCV were observed in No. of secondary branches per plant (19.58, 18.97), 100 seed weight (16.07, 16.02), No. of primary branches per plant (16.5, 15.88), Harvest index (13.26, 13.12), biological yield per plant (11.68, 11.51), No. of pods per plant (10.76, 10.72), Plant height (10.14, 10.11) and Seed yield per plant (10.13, 10). Low value of PCV and GCV were recorded in No. of seeds per pod (8.59, 7.16), protein content (5.07, 5.06), Days to maturity (2.04, 2.02) and Days to 50% flowering (1.94, 1.88), shows the magnitude of PCV and GCV were low and indicating limited scope for improvement. For all characteristics in each analysis, the phenotypic coefficient of variation was greater in magnitude than the genotypic coefficient of variation. The presence of greater magnitude of diversity in genotypes allows for crop improvement. Similar kind of results were also found by Singh et al. [14], Kumar et al. [15], Meena et al. [12].

In order to derive inferences regarding these characteristics, heritability estimates have been widely defined as low (below 30%), medium (30% and 60%), high (60% and 80%), and very high (above 80%). While genetic advance estimates have been broadly characterized as low (below 10%), medium (10-20%), and high (above 20%).

High heritability coupled with high genetic advance as percentage of mean observed in traits viz., for No. of secondary branches per plant (93.8%, 37.86) 100 seed weight (99.3%, 32.87), No. of primary branches per plant (92.5%, 31.46), Harvest Index (97.8%, 26.2), Seed yield per plant (97.4%, 23.38), Number of pods per plant (99.1%, 21.98), Plant height (99.3%, 20.76), and biological yield per plant (97.2%, 20.33) thus these characters show additive gene action in their expression. High heritability with moderate genetic advance as percentage of mean was recorded for Number of seeds per pod (69.5%, 12.3) and Protein content (99.8%, 10.41). High heritability with Low genetic

advance as percentage of mean was recorded for days to maturity (98.4%, 4.13), and days to 50% flowering (94.6%, 3.78) indicates presence of non-additive gene effects and selection may be ineffective. Similar kind of results were also found by Singh et al. [14], Kumar et al. [15], Meena et al. [12], Gautam et al. [13].

4. CONCLUSION

The finding will help to a great extent in maintenance breeding, quality seeds production, seed certification and seed testing program. It also used for screening of genotypes for quality and high yield. The PCV was higher than the GCV for all the characters. PCV, GCV is moderate were observed in No. of secondary branches per plant, 100 seed weight, No. of primary branches per plant, Harvest index, biological yield per plant, No. of pods per plant, Plant height and Seed yield per plant which suggests greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. The PCV was higher than the GCV for all the characters. PCV, GCV is moderate were observed in No. of secondary branches per plant, 100 seed weight, No. of primary branches per plant, Harvest index, biological yield per plant, No. of pods per plant, Plant height and Seed yield per plant which suggests greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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