



# Studies on Genetic Variability and Character Association in Chickpea Germplasm for Growth and Yield Attributes

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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**

**Aims:** The improvement in crop yield depends upon the magnitude of genetic variability available in breeding material. An investigation was carried out in chickpea germplasm lines to study variability present and correlation for growth and yield attributes viz, days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, hundred seed weight and seed yield.

**Study Design:** The investigation was carried out in an augmented design with 5 blocks.

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**Place and Duration of Study:** Zonal agricultural and horticultural research station, Babbur farm, Hiriyyur, Chitradurga during Rabi 2023.

**Methodology:** 100 germplasm lines collected from different sources were utilized in the study with 4 checks. Data was recorded and statistical analysis was carried out using R software

**Results:** The analysis of variance revealed the presence of significant differences among germplasm for all traits studied. High genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability coupled with high genetic advance as per cent of mean were recorded for traits, number of primary branches, number of pods per plant, hundred seed weight and seed yield. Correlation studies revealed that, seed yield was in positive association with number of pods per plant, plant height and hundred seed weight.

**Conclusion:** Through this study, it is clear that yield improvement programs could prioritize traits like the number of pods per plant, plant height, hundred seed weight and seed yield in breeding programmes.

**Keywords:** Chickpea; GCV; PCV; heritability; genetic advance as per cent of mean.

## 1. INTRODUCTION

Chickpea (*Cicer arietinum* L.), the most widely cultivated pulse crop globally, belongs to the family Leguminosae and has a chromosome count of  $2n=16$  with a genome size of approximately 738 Mbp [1]. Of the 43 species in the *Cicer* genus, only one is cultivated, while the rest are wild species. In India, chickpea is grown on 9.99 million hectares, including 0.713 million hectares in Karnataka [2]. Chickpea is a vital alternative protein source in densely populated countries like India, providing 18-21% protein, 50-60% carbohydrates, 10-20% fibre, essential minerals, vitamins and unsaturated fatty acids like linoleic and oleic acids. Its nutritional benefits support human health by aiding in the prevention of cardiovascular diseases, type-2 diabetes, digestive disorders and certain cancers [3].

Chickpea has played a major role in the realization of the pulse revolution in India making the country self-sufficient in pulses. There has been a remarkable increase in chickpea production from a level of 7.33 million tonnes in 2014-15, to an all-time high of 13.98 million tonnes during 2021-22 with an increase of more than 34% chickpea productivity and during 2022-23, production was 13.54 million tonnes [4]. Despite recent growth in chickpea production, challenges like climate change, emerging diseases and market issues remain significant. To overcome these issues through crop improvement, genetic variability and diversity studies are the fundamental requirement.

The phenotypic expression of any plant characteristic is primarily determined by the plant's genetic makeup, along with environmental influences that affect variability, though the focus

is on inherent genetic variation. The success of genetic improvement in any trait depends on the level of variability present within the gene pool for that trait and the selection applied to the germplasm resources. The correlation analysis provides a way to identify the key traits that have an impact on a dependent trait and helps in simultaneous improvement of various characters along with economic yield. Therefore, present study was conducted to evaluate genetic variability and correlation among germplasm lines.

## 2. MATERIALS AND METHODS

The experimental material comprised of 100 germplasm lines with 4 checks. A field experiment was conducted during rabi 2023 at the Zonal Agricultural and Horticultural Research Station, Hiriyyur to evaluate genetic variability and correlation. The experiment was laid out in an augmented design with five blocks as outlined by Federer [5]. Each block contained 20 germplasm lines and 4 checks. Row spacing of 30 cm and plant to plant spacing of 10 cm was maintained. Each line was sown in a single row of 3 m wherein each row consists of 30 plants.

Five randomly selected plants in all the germplasm lines were used for taking the observations on eight yield and yield attributing traits viz, days to fifty per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, hundred seed weight and seed yield (kg/ha). The average of observations recorded on the five plants was considered for statistical analysis. Variability and correlation analysis were performed using R package *augmented RCBD* [6].

The coefficient of variability both at phenotypic and genotypic levels was computed by applying the formula, as suggested by Burton and De Vane [7].

$$\text{PCV per cent} = \frac{\text{Phenotypic variance}}{\text{Grand mean}} \times 100$$

$$\text{GCV per cent} = \frac{\text{Genotypic variance}}{\text{Grand mean}} \times 100$$

GCV and PCV values were categorized as low, moderate and high values as suggested by Sivasubramanian and Menon [8], which is as follows. Low (0-10%); Moderate (10-20%); High (>20%)

Heritability (broad sense) was estimated as the ratio of genotypic variance to the total variance as suggested by Lush [9].

$$\text{Heritability (H}^2\text{)} = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

Heritability was classified as low (0 – 30%), moderate (30.1 – 60 %) and high (> 60%), as given by Robinson and Comstock [10].

The genetic advance as per cent mean was calculated using the formula given below.

Genetic advance as per cent of mean =

$$\frac{\text{GA}}{\text{Grand mean}} \times 100$$

Where, GA is predicted genetic advance calculated using the formula given by Johnson et al. [11].

$$\text{GA} = h^2 \times K \times \sigma_p$$

Where,

$h^2$  = Heritability in broad sense

$K$  = Selection differential, which is equal to 2.06 at 5 per cent intensity of selection

$\sigma_p$  = Phenotypic standard deviation

The genetic advance as per cent of mean was classified as suggested by Johnson et al. [11] as low (0 – 10%), moderate (10.1 – 20%), and high (>20%).

### 3. RESULTS AND DISCUSSION

#### 3.1 Analysis of Variance

Analysis of variance revealed significant variations for days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant,

number of seeds per pod, hundred seed weight and seed yield indicating the presence of sufficient genetic variability in evaluated germplasm lines (Table 1). These results are in accordance with the results of Janghel et al. [12] and Ram et al. [13] and signifies the potential for incorporating promising genotypes in future breeding programs for enhancing yield and its contributing traits.

#### 3.2 Variability Studies

Selection of any breeding method in crop improvement mainly relies on the genetic characteristics of the population. This can be known by variability studies including genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability and genetic advance as per cent of mean. High GCV and PCV were observed for traits primary branches (37.49% and 39.09%), number of pods per plant (47.88% and 49.2%), hundred seed weight (30.37% and 31.23%) and seed yield (35.67% and 36.84%). PCV is slightly higher than GCV for all these traits indicating the influence of environment. The presence of ample amount of variation reveals the effectiveness of selection (Table 2) and the results are in line with findings of Karthikeyan et al. [14], Mihoariya et al. [15] and Sanjay et al. [16].

The characters primary branches (91.99% and 74.18%), number of pods per plant (94.69% and 96.13%), hundred seed weight (94.59% and 60.94%) and seed yield (93.77% and 71.26%) showed high heritability coupled with high genetic advance as percent of mean (Fig. 1) denoting, these traits were under additive gene action and selection for these traits are rewarding. The results are in conformity with the findings of Singh et al. [17], Prasanthi et al. [18], Ram et al. [19] and Tamatam et al. [20].

#### 3.3 Correlation Studies

Correlation studies give a clear view of character association which is generally due to linkage, pleiotropy, physiological association in development and biochemical pathways. Correlation analysis is very essential to know the mutual relationship between two variables as it measures the degree of closeness and the linear relationship between two variables. The phenotypic correlation for eight characters of chickpea germplasm lines were recorded to elucidate the association present among them.

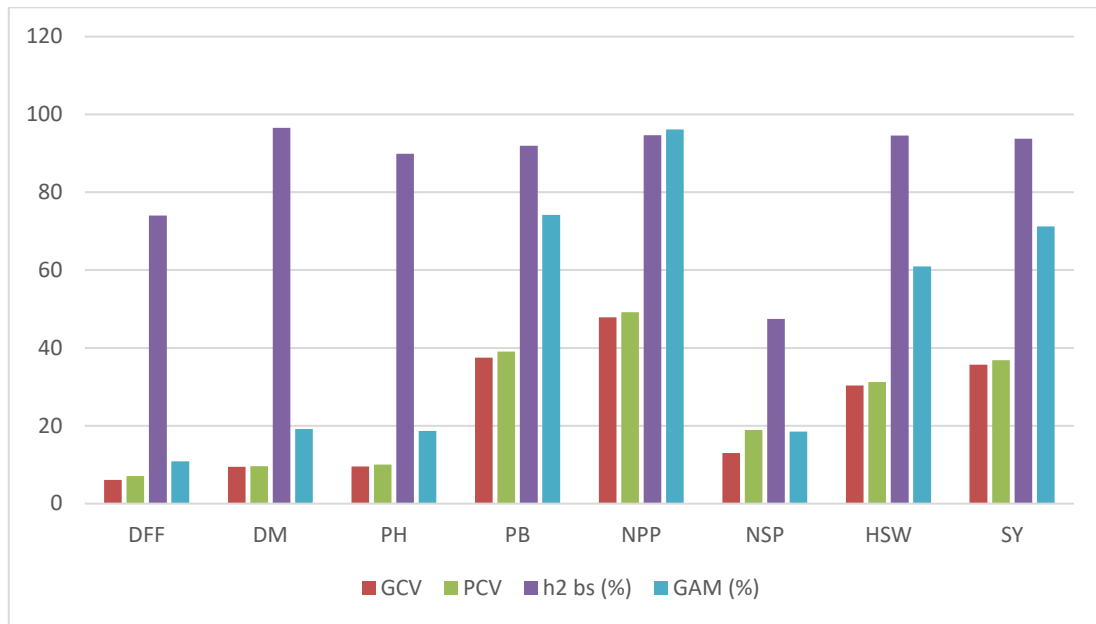
**Table 1. Analysis of variance for yield and yield attributing traits in chickpea germplasm lines**

Source of variation	DF	DFF	DM	PH	PB	NPP	NSP	HSW	SY
Block (eliminating treatment)	4	0.63	5.38	0.74	0.06	0.59	0.04	6.03	22155.42
Genotypes+ Checks (eliminating block)	103	8.17**	68.93**	10.42**	0.33**	71.12**	0.07**	28.62**	804691.03**
Genotypes	99	6.89**	73.93**	8.83**	0.39**	76.13**	0.05	44.72**	837980.33**
Checks	3	13.33**	7.92	10.73**	0.24**	28.41**	0.10*	2.56	4160565.93**
Checks vs Genotypes	1	167.48**	111.80**	268**	0.03	1019.25**	1.78	134.87	3205191.41
Error	12	1.79	2.54	0.89	0.03	1.47	0.03	2.42	52212.47

\*\* Significant at 1% \* significant at 5% DFF- Days to fifty percent flowering, DM- Days to maturity, PH- Plant height, PB- Number of primary branches, NPP- Number of pods per plant, NSP- Number of seeds per pod, HSW- Hundred seed weight, SY- Seed yield

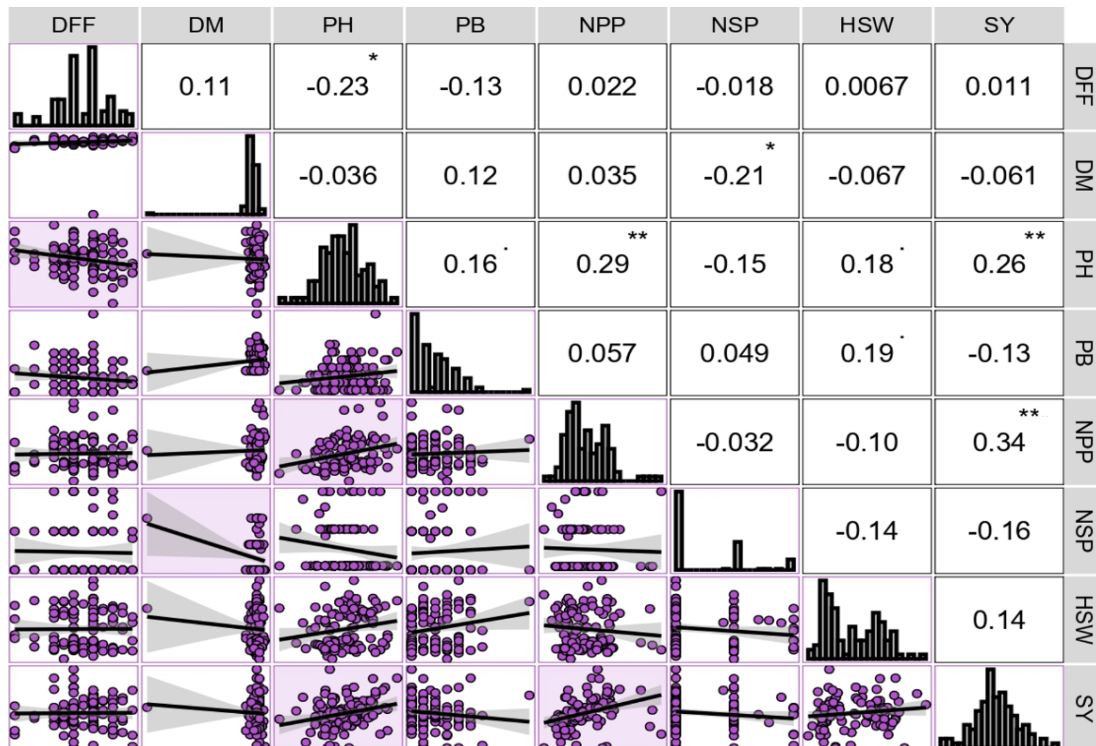
**Table 2. Mean, range and genetic variability parameters for yield and yield attributing traits in chickpea germplasm lines**

Characters	Range		Mean	Co-efficient of variation (%)		h <sup>2</sup> bs (%)	GAM (%)
	Min	Max		GCV	PCV		
Days to fifty percent flowering	30.00	42.00	36.95	6.11	7.10	74.00	10.84
Days to maturity	80.00	96.00	89.26	9.47	9.63	96.56	19.19
Plant height (cm)	20.80	36.80	29.57	9.53	10.05	89.93	18.64
Number of primary branches	1.00	3.00	1.61	37.49	39.09	91.99	74.18
Number of pods per plant	3.00	51.00	17.73	47.88	49.21	94.69	96.13
Number of seeds per pod	1.00	2.00	1.15	13.03	18.92	47.42	18.51
100 seed weight (g)	11.03	38.44	21.41	30.37	31.23	94.59	60.94
Seed yield (kg/ha)	335.87	4050.00	2485.03	35.67	36.84	93.77	71.26



**Fig. 1. Pattern of GCV, PCV, Heritability and Genetic advance as percent of mean (GAM) for various traits in chickpea germplasm lines**

DFF- Days to fifty percent flowering, DM- Days to maturity, PH- Plant height, PB- Number of primary branches, NPP- Number of pods per plant, NSP- Number of seeds per pod, HSW- Hundred seed weight, SY- Seed yield



**Fig. 2. Correlation coefficients for yield and yield attributing traits**

\*Significant at  $P = 0.05$ , \*\* Significant at  $P = 0.01$  probability level

DFF- Days to fifty percent flowering, DM- Days to maturity, PH- Plant height, PB- Number of primary branches, NPP- Number of pods per plant, NSP- Number of seeds per pod, HSW- Hundred seed weight, SY- Seed yield

Yield is a complex quantitative trait influenced by environmental factors and various yield components, making genotype selection based solely on yield, less effective. Positive significant association of yield was observed with traits number of pods per plant (0.34) and plant height (0.26) suggesting these are major yield contributing traits and traits like hundred seed weight (0.14) and days to fifty per cent flowering (0.01) expressed non-significant positive association which were in accordance with the findings of Kaur et al. [21], Dawane et al. [22] and Jain et al. [23]. Selection for these traits helps in indirect selection of yield (Fig. 2). In contrast, traits like primary branches, seeds per pod and days to maturity disclosed negative relation with seed yield. Similar findings were observed from the studies of Dawane et al. [22] and Pattanayak et al. [24].

#### 4. CONCLUSION

The chickpea germplasm in this study exhibited significant variation in growth and yield traits. Traits such as number of pods per plant, plant height, and hundred seed weight showed high GCV, PCV, heritability, and genetic advance, indicating strong variation and selection potential. Additionally, traits like number of pods per plant, primary branches, and hundred seed weight were positively correlated with seed yield, making them key criteria for improving yield. Therefore, traits like plant height, primary branches, pods per plant, hundred seed weight, and seed yield should be prioritized for chickpea crop improvement.

#### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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