



# Heritability, Genetic Advance and Correlation Analysis for Grain Yield and Yield Components of Chickpea (*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 experiment was performed to evaluate heritability, genetic advance and genetic correlation for grain yield and its components, in F<sub>1</sub> populations by line x tester fashion. The results showed that most traits demonstrated high heritability, except for days to maturity (49%), which displayed moderate heritability. The traits like pods per plant (2.848), 100 seed weight (2.772), number of nodules per plant (2.529), grain yield per plant (3.081) and harvest index (3.786) exhibited a significant genetic advance. Grain yield exhibited positive and significant genetic correlations with pods per plant (0.878), root length (0.878), 100 seed weight (0.929), number of nodules per plant

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(0.913), and harvest index (0.964) but negative correlations with traits like days to maturity (-0.492) and plant height (-0.266). Correlated response analysis highlighted traits that positively influenced grain yield and suggested indirect selection or index selection for improvement.

**Keywords:** Chickpea; genetic correlation; grain yield; heritability; selection.

## 1. INTRODUCTION

One among the most significant legume crops in the world, particularly in the semi-arid parts of Asia and Africa, is the chickpea (*Cicer arietinum* L.). It offers an abundant supply of vitamins, minerals, dietary fiber, and protein., and has multiple benefits for human health and the environment. According to the latest data from FAOSTAT (2021), the world area, production and productivity of chickpea in 2021 were 15.97 million hectares, 15.97 million metric tons and 1000 kg/ha, respectively. India, commanding over two-thirds of the global chickpea production and covering a substantial portion of the world's agricultural land, stands as the foremost producer of this vital legume. India's area, production and productivity of chickpea in 2021-22 were 10.91 million hectares, 13.75 million tons and 1260 kg/ha, respectively [1]. These numbers demonstrate that although India has made significant strides in recent years to increase the acreage and output of chickpeas, it still lags behind numerous other nations in terms of productivity.

The chickpea production is restricted by various number of stresses, such as drought, heat, salinity, diseases, and pests. Therefore, improving the grain yield and its components traits, is a major goal of chickpea breeding programs. Heritability, genetic advance, and correlation analysis are important parameters for evaluating the genetic potential and variability of chickpea genotypes for grain yield and its components traits. The percentage of phenotypic variation attributed to genetic sources is known as heritability. It can be calculated in a various ways., such as analysis of variance, parent-offspring regression, or response to selection. Heritability can be influenced by the environment, the genetic background, and the interaction between them. Various research findings have reported different estimates of heritability for different traits in chickpea.

Genetic advance is the expected gain in the mean value of a trait after one cycle of selection. Various research findings have reported different

estimates of genetic advance for different traits in chickpea. For example, Anusha et al. [2] conducted research on 25 different chickpea genotypes within a single environment. Their findings revealed a substantial genetic advance (GA%) for key traits such as the number of pods per plant, plant height, etc.

Direct selection of grain yield trait in chickpea may not serve efficient due to its complex nature which depends on various factors such as genetic, environmental and management factors. Hence, indirect selection based on secondary traits that are highly correlated with grain yield and have high heritability and additive gene action may be more preferable for improving chickpea yield. Correlation analysis is the study of the association between two or more traits. These parameters can help breeders to identify the most suitable selection criteria and breeding methods for improving chickpea yield and quality. Considering the importance of the aforementioned information, the outcomes of the evaluation of line x tester populations were analyzed to ascertain the heritability, genetic correlation, and genetic advance for the observed characteristics in chickpea.

## 2. MATERIALS AND METHODS

The current investigation took place at Tirhut College of Agriculture, Dholi, throughout the rabi seasons of 2021-22 and 2022-23. At an elevation of 55 meters above mean sea level, Dholi occupies a geographical position at 25.9°N latitude and 85.9°E longitude. The soil composition consists of sandy loam with a moderate organic matter content, originating from alluvial deposits. During the 2022-23 year, Dholi received an average rainfall of 1200 mm, with the majority occurring between July and September, while the crop received 0.25 mm of rainfall during the growing season. Throughout the growing season, the weather conditions were conducive for growth and development of chickpea crops. The studied materials involved 15 lines, namely, DC-17-1111, DC-17-1104, HC5, Rajendra Chana 1, DC-17-115, Vihar, ICCV-96970, JG-315, JG-62, ICCV-17-115,

KGP-59, GCP-105, PG-186, BG-372, GNG-2299 and three testers, namely GNG-2372, RSG-888, GNG-2207, crossed to produce forty-five F<sub>1</sub> hybrids following line x tester mating design in 2021-22. The 45 crosses and 18 parental lines were laid out in a Randomized block Design with three replications during Rabi- 2022-23. Standard agronomic methodologies were employed to ensure optimal crop growth. The calculation of broad-sense heritability was done following the formula outlined by Singh and Chaudhary [3].

$$H_b^2 = \sigma_G^2 / \sigma_P^2 \times 100$$

Where

$$H_b^2 - \text{broad sense heritability}$$

$$\sigma_G^2 - \text{genotypic variance}$$

$$\sigma_P^2 - \text{phenotypic variance}$$

Genetic correlations ( $r_g$ ) of thirteen characters with grain yield were evaluated by the formula, [4].

$$r_g = \frac{cov_{GCA(i,j)}}{\sqrt{[\sigma_{gca(i)}^2 \times \sigma_{gca(j)}^2]}}$$

where

$COV_{GCA(i,j)}$ , - covariance parameter of GCA between grain yield (i) and character (j), and  $\sigma_{gca(i)}^2$ ,  $\sigma_{gca(j)}^2$  - variance components of grain yield (i) and character (j), respectively.

Correlation response (CR) between grain yield and other characters was estimated as according to Falconer, [5], as follows

$$CR = (h_x / h_y) r_g$$

Where,

$h_x$  - heritability of grain yield,  
 $h_y$  - heritability of other character under consideration  
 $r_g$  - genotypic correlation between grain yield and other character.

Genetic advance (GA) estimation was done according to Allard's [6], given as,

$$GA = ih^2 \sqrt{\sigma_p^2}$$

Where,

$i$  - selection intensity  
 $H^2$  - heritability  
 $\sigma_p^2$  is phenotypic variance

### 3. RESULTS AND DISCUSSION

#### 3.1 Heritability and Genetic Advance

Heritability can be grouped as high (above 60%), moderate (between 30% to 60%) and low below 30%). The traits under investigation demonstrated considerable broad-sense heritability, with the exception of the trait 'days to maturity,' which showed a moderate heritability score of 49.02%. This indicates that most of the variation present in the studied characters was due to genetic differences among the genotypes and that the traits are less affected by environmental conditions. The highest heritability was shown by the character, 100 seed weight (90.11%) and the lowest by the character, days to maturity (49.02%). The trait, grain yield per plant (76.03%) also exhibited high heritability. Hence, all the studied characters, excluding days to maturity can be easily improved by direct selection. For genetic advance, the maximum value was showed by the harvest index (3.786) and the least by nodules dry weight (0.078). Other traits showing high genetic advance include, plant height, pods per plant, 100 seed weight, number of nodules per plant and harvest index indicating that selection would be more effective for improving these traits. Furthermore, the traits grain yield per plant, pods per plant, 100 seed weight and harvest index had high heritability and high genetic advance, hence, simple phenotypic selection can be used to improve these traits by exploiting additive gene effects. While the traits, days to 50% flowering and days to maturity exhibited less heritability and low genetic advance, hence, the breeding methods like hybridization or mutation breeding can be used to create new variability and improve these traits by exploiting non-additive gene effects. The outcomes of this study are in agreement with the research conducted by Kishor et al. [7], Sohail et al. [8], followed by Meena et al. [9], Balpande et al. [10] and Upadhyay et al. [11], Chauhan et al. [12] and Nunavath et al. [13,] as well as Karthikeyan et al., [14].

**Table 1. Heritability, genetic correlation, correlated response and genetic advance, in chickpea**

Characters	Mean of Squares	Heritability (h <sup>2</sup> ) express on % basis	Genetic correlation with grain yield (r <sub>g</sub> )	Correlated response (CR/R)	GA
1. Days to 50 % flowering	32.224**	62.20	-0.492	-0.601	1.174
2. Days to Maturity	72.858**	49.02	-0.470	-0.729	1.094
3. Plant height (cm)	75.075**	80.57	-0.266	-0.251	1.799
4. Primary branches per plant	0.413**	80.20	0.702	0.665	0.150
5. Secondary branches per plant	7.134**	84.63	0.798	0.717	0.733
6. Pods per plant	81.861**	79.90	0.878*	0.835	2.848
7. Root Length (cm)	14.951**	72.50	0.878*	0.920	1.155
8. Root Volume	0.414**	83.79	0.844	0.765	0.200
9. 100 Seed weight (g)	37.332**	90.11	0.929**	0.784	2.772
10. Number of nodules per plant	40.336**	81.20	0.913**	0.855	2.529
11. Nodule Fresh Weight (g)	0.543**	83.50	0.810	0.840	0.301
12. Nodule Dry Weight (g)	0.021**	89.21	0.805	0.893	0.078
13. Grain yield per plant (g)	54.127**	76.03	-	-	3.081
14. Harvest Index	86.491**	82.70	0.964**	0.886	3.786

\*, \*\*: level of significance at 0.05 and 0.01, respectively. h<sup>2</sup> : Broad-sense heritability (%), GA : Genetic Advance

### 3.2 Genetic Correlation and Correlated Response

The genetic correlation can be positive or negative values, spanning the range from -1 to 1. A positive genetic correlation means that the increase in one trait is also associated with the increase in the other traits as well. While in the negative correlation, the increase in one character is associated with the decrease in the other character. The study's findings revealed strong positive genotypic correlations of grain yield with ten component characters out of which five are significant, namely pods per plant, root length, 100 seed weight, number of nodules per plant, and harvest index. However the traits, days to 50% flowering, days to maturity, and plant height displayed a non-significant negative correlation with the grain output. The correlated response (CR) refers to the change in grain yield resulting from the selection of yield components through indirect selection, as described by Falconer [5]. When the value of the correlated response surpasses the threshold of one, it implies that the efficacy of indirect selection methods in enhancing grain yield is greater than

that of direct selection approaches. This indicates a more substantial genetic gain from indirect selection strategies, which could be due to the influence of multiple traits that are more effectively captured through these methods as compared to selecting solely based on grain yield. The present findings reinforce this idea, revealing a high correlated response for traits such as pods per plant, root length, root volume, 100 seed weight, number of nodules per plant, nodule fresh weight, nodule dry weight, and harvest index indicating that greater response in the grain yield can be achieved through the indirect selection of these characters in early segregating generations. Overall, the traits viz., pods per plant, root length, root volume, 100 seed weight, number of nodules per plant, nodule fresh weight, nodule dry weight, and harvest index had high genetic correlation as well as high correlated response. Hence, indirect selection or index selection can be used to improve these traits by selecting for one trait that affects another trait positively. And, days to 50% flowering, days to maturity and plant height had negative genetic correlation and negative correlated response, hence, recurrent selection

can be used to improve these traits. Concurring results have been documented by several researchers over the years. Studies conducted by Thakur [15], followed by Anusha et al. [2], Karthikeyan et al. [14], Traore et al. [16], Ningwal et al. [17], and Rekha et al., [18], all align with the findings discussed, highlighting the consistency and reproducibility of these observations across different research efforts [19].

#### 4. CONCLUSION

The study emphasizes high heritability in most traits, indicating the feasibility of direct selection for their enhancement. Traits having both high heritability and genetic advance, like grain yield per plant, 100 seed weight, and harvest index, are suitable for phenotypic selection. Traits having positive genetic correlations with grain yield suggest the effectiveness of indirect selection. Traits with negative correlations may benefit from alternative breeding approaches like recurrent selection, hybridization, or mutation breeding. The findings offer insights for breeders, providing tailored selection strategies for improving specific traits in the studied genotypes. This research aligns with prior studies, confirming consistency in observed patterns and guiding future breeding programs.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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