

## Original Research Article

# **Heritability, Genetic advance and Correlation Analysis for grain yield and yield components of chickpea (*Cicer arietinum* L.)**

### **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 result showed that most traits demonstrated high heritability, except for days to maturity, which displayed moderate heritability. The traits like pods per plant, 100 seed weight, number of nodules per plant, grain yield per plant and harvest index exhibited a significant genetic advance. Grain yield exhibited positive and significant genetic correlations with pods per plant, root length, 100 seed weight, number of nodules per plant, and harvest index but negative correlations with traits like days to maturity and plant height. Correlated response analysis highlighted traits that positively influenced grain yield and suggested indirect selection or index selection for improvement. Conversely, traits showing negative correlations namely days to 50% flowering, days to maturity and plant height may benefit from recurrent selection methods.

**Keywords:** Chickpea, Genetic correlation, Grain yield, Heritability, Selection

### **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 tonnes and 999 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 were 11.95 million hectares, 11.95 million tonnes and 1000 kg/ha, respectively. 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.* (2020) 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.

## **Materials and methods**

The current investigation took place at TCA, 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. Throughout the growing season, the weather conditions were conducive to the typical growth and development of chickpea crops. The aim was to assess the heritability, genetic correlation, and genetic advance concerning grain yield per plant and its associated characteristics in chickpea. 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 in line x tester mating design in 2021-22. The 45 crossings and 18 parental lines were organized in a RBD Design with three replications during the 2022-23 period. Standard agronomic methodologies were employed to ensure optimal crop growth. The calculation of broad-sense heritability followed the formula outlined by Singh and Chaudhary (1979).

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

where  $H_b^2$  - broadsense heritability

$\sigma_G^2$  - genotypic variance

$\sigma_P^2$  - phenotypic variance

Genetic correlations ( $r_g$ ) of thirteen characters with grain yield were evaluated by the formula;

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

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) was estimated as according to Falconer, 1989;

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

Where;  $h_x$ - heritability of grain yield,

$h_y$ - heritability of other character,

$r_g$ -genotypic correlation between grain yield and other character.

Genetic advance (GA) estimation was done according to Allard's (1964), given as,

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

Where,  $i$ - selection intensity

$H^2$ - heritability

$\sigma_p^2$  is phenotypic variance

## Results and discussion

### 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 0.490. This indicates that most of the variation present in the studied characters are 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 (0.901) and the lowest by the character, days to maturity. The trait, grain yield per plant (0.760) also came within the range of 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 shown by the harvest index (3.786) and the least by nodules dry weight (0.078). Other traits showing high genetic advance includes, 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 or marker-assisted 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 increase these traits by exploiting non-additive gene effects. The outcomes of this study are in agreement with the research conducted by Kishor *et al.* in 2018, Sohail *et al.* in the same year, followed by Meena *et al.* in 2021, Balpandeet *et al.* and Upadhyay *et al.* in 2022, Chauhan *et al.* and Nunavathet *et al.* in 2023, as well as Karthikeyan *et al.*, whose work was published in 2022.

### 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 increased in one character is associated with the decreased in the other character.

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Table 1: Heritability, Genetic Correlation and Advance, Correlated Response in fourteen characters.

Characters	Mean of Squares	Heritability (h <sup>2</sup> )	Genetic Correlation with Grain Yield (r <sub>g</sub> )	Correlated Response (CR/R)	GA
1. Days to 50 % flowering	32.224**	0.622	-0.492	-0.601	1.174
2. Days to Maturity	72.858**	0.490	-0.470	-0.729	1.094
3. Plant height (cm)	75.075**	0.806	-0.266	-0.251	1.799
4. Primary branches per plant	0.413**	0.802	0.702	0.665	0.150
5. Secondary branches per plant	7.134**	0.846	0.798	0.717	0.733
6. Pods per plant	81.861**	0.799	0.878*	0.835	2.848
7. Root Length (cm)	14.951**	0.725	0.878*	0.920	1.155
8. Root Volume	0.414**	0.838	0.844	0.765	0.200
9. 100 Seed weight (g)	37.332**	0.901	0.929**	0.784	2.772
10. Number of nodules per plant	40.336**	0.812	0.913**	0.855	2.529
11. Nodule Fresh Weight (g)	0.543**	0.835	0.810	0.840	0.301
12. Nodule Dry Weight (g)	0.021**	0.892	0.805	0.893	0.078
13. Grain yield per plant (g)	54.127**	0.760	-	-	3.081
14. Harvest Index	86.491**	0.827	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

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 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 (1989). 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 generation. Overall, the traits, 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 and colleagues in 2018, followed by Anusha *et al.* in 2020, Karthikeyan *et al.* in 2022, Traore *et al.* in the same year, Ningwalet *et al.* in 2023, and Rao's work in 2023, all align with the findings discussed, highlighting the consistency and reproducibility of these observations across different research efforts.

## **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 selection via phenotypic or marker-assisted methods. 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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