

# RECKONING THE INTERRELATIONSHIP AMONG DIFFERENT YIELD CONTRIBUTING TRAITS IN CHICKPEA (*Cicer arietinum* L.) GENOTYPES

## ABSTRACT

**Aims:**The enhancement of crop yield relies on the level of genetic variability found in breeding materials. An investigation was conducted on chickpea germplasm lines to analyze the existing variability, as well as the correlation and path analysis related to yield and its contributing traits viz., days to 50 *per cent* flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, test weight, protein content and seed yield per plant.

**Study design:** The investigation was carried out in an augmented block design with 6 blocks.

**Place and Duration of Study:** Agricultural and Horticultural Research Station, Bhavikere, Chikmagalur, during Rabi 2023.

**Methodology:**96 germplasm lines collected from different sources were utilized in the study with 4 checks. Data were 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 studied traits. 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 pods per plant, test weight, protein content and seed yield per plant. Correlation studies revealed that, seed yield was in positive association with test weight, number of secondary branches per plant, number of pods per plant, number of primary branches per plant and protein content. Test weight showed the highest positive direct effect on seed yield followed by plant height, number of primary branches per plant, number of pods per plant and number of seeds per pod.

**Conclusion:** This study indicated that yield improvement initiatives should focus on traits such as the number of pods per plant, number of primary branches per plant, test weight and seed yield per plant in breeding programs.

*Keywords: Chickpea, GCV, PCV, Heritability, Genetic advance as per cent of mean*

## 1. INTRODUCTION

“Chickpea (*Cicer arietinum* L.), also known as Gram, Bengal gram, Egyptian pea, Chana, or garbanzo bean, was one of the first grain legumes to be domesticated in the ancient world by humans” [1]. “The genus *Cicer* belongs to the sub-family Papilionaceae within the family Leguminosae and has a diploid genome consisting of eight pairs of chromosomes ( $2n=2x=16$ ), with a genome size of 738 Mbp” [3,4]. Chickpea crops are broadly classified into two types: the desi type, featuring small, angular, brown seeds with high fiber content, primarily cultivated in South Asia and Africa, and the kabuli type, which has larger seeds with less fiber content and is cultivated in the Mediterranean region [4]. Chickpea seeds are recognized for their nutritional benefits, including rich fiber, unsaturated fatty acids, and  $\beta$ -carotene [5].

Chickpea is one of the richest vegetarian sources of protein. As the food security and biofortification are the global concerns, chickpea plays a vital role in addressing these issues as it

is the rich source for quality protein, which is essential in enhancing human immune system and body metabolism rate. Worldwide, chickpea cultivation spans 148.11 million hectares, yielding 180.95 million tonnes with an average productivity of 1222 kg/ha. India leads the world in chickpea production, contributing 73.46% of the global output. The country cultivates chickpea across 107.40 million hectares, producing 135.44 million tonnes at a productivity of 1261 kg/ha. In Karnataka, chickpea cultivation covers 10.56 million hectares, yielding 6.87 million tonnes at a productivity of 650 kg/ha [6]. Kalaburagi ranks first in Karnataka for area, production and productivity, followed by Bijapur, Bidar, Gadag and Dharwad districts.

“Genetic improvement of all crops mainly depends on the magnitude of genetic variability present in the plant breeding material. The estimation of PCV and GCV are required for understanding the effects of environment on various traits. Estimation of heritability and genetic advance in a population gives information about the future gain in the following generations. The partitioning of correlation into direct and indirect effects by path coefficients analysis was suggested by Wright . which gives us important information on the relative advantages of the selection criteria's traits. Path coefficient analysis is essential to determine the direct effects of traits on other traits as well as their indirect effects on other traits” [7].

## 2. MATERIALS AND METHODS

The present experiment was carried out during rabi season 2023-2024 in the PG research block of Agricultural and Horticultural Research Station, Bhavikere, Chikmagalur, Karnataka. Ninety six chickpea genotypes along with four checks obtained from Zonal Agricultural Research Station, Kalaburgi, Karnataka were used in the study. The genotypes were grown in Augmented Block Design with six blocks. Each entry was sown in three rows of one meter length having 10 plants per row. Standard package of practices were followed to raise a good crop with row to row distance of 30 cm and plant to plant distance of 10 cm.

The observations were taken on five randomly selected plants from the middle of the plot for the collection of the data on the various quantitative traits like plant height(cm), Number of primary branches, number of secondary branches, number of pods per plants, number of seeds per pod, test weight (g), seed yield per plant (g) and protein content (%), while the data for days to 50 per cent flowering and days to maturity were taken on plot basis when 50 percent of the plants showed flowering and maturity. The analysis of variance was done using R- statistic programme. Heritability in broad sense was calculated by the formula suggested by Allard [8]. Genetic advance was studied by the formula suggest by Johnson et al. [9]. Path coefficient analysis was carried out according to Dewey and Lu [10].

## 3. RESULTS AND DISCUSSION

### 3.1 Analysis of variance

The analysis of variance revealed significant differences among the genotypes for the traits studied. The study identified substantial genetic variability within and between chickpea genotypes for several characteristics, including days to 50 per cent flowering, days to maturity, plant height, number of primary, secondary branches per plant, number of pods per plant, number of seeds per pod, test weight, protein content and seed yield per plant (Table 1). These results are consistent with those reported by Ashwini et al. [11] and Sanjay et al. [12].

### 3.2 Phenotypic and Genotypic Coefficient of Variation

According to Burton and Devane [13], they classified PCV and GCV value as high (>20%), medium (10-20%) and low (<10%). On the basis of this, the present study indicated that four characters showed high PCV and GCV values viz., test weight (23.20% and 22.31%), protein content (28.84% and 28.39%), number of pods per plant (29.51% and 28.09%) and seed yield per plant (38.23% and 30.32%). Moderate PCV and GCV were observed for days to 50 per cent

flowering, plant height, number of primary branches per plant, number of secondary branches per plant and number of seeds per pod indicating that there is variation in these traits. These results suggests that improvement can be made, as the impact of environmental factors is relatively minimal. The low values of PCV and GCV was observed for days to maturity indicated that there is less variability in this trait. Hence, this trait might not be ideal for selection in a crop improvement program (Table 2). These findings align with the results reported by Ningwalet al.[14], Vikram et al. [15] and Banik *et al.* [16].

### 3.3 Heritability ( $h^2$ )

Robinson et al.[17] classified heritability values as high (>60%), moderate (30-60%) and values less than 10% low. High heritability was observed for days to 50 per cent flowering (78.91%), days to maturity (89.98%), plant height (88.25%), number of primary branches per plant (84.49%), number of secondary branches per plant (73.71%), number of pods per plant (90.60%), number of seeds per pod (85.69%), test weight (92.44%), protein content (96.88%) and seed yield per plant (62.89%). Similar findings were delineated by Kumari et al. [18] and Srikanth et al. [19] which revealed the broad genetic base and effectiveness of selection for these traits (Figure 1).

### 3.4 Genetic advance as percent of mean (GAM)

Falconer and Mackay [20] classified genetic advance as *per cent* of mean as low (0-10%), medium (10 - 20%) and high (20% and above). The genetic advance as *per cent* of mean (GAM) was found to be high for traits such as plant height (27.94), number of primary branches per plant (31.40), number of secondary branches per plant (21.28), number of pods per plant (55.15), number of seeds per pod (25.24), test weight (44.25), protein content (57.65) and seed yield per plant (49.60), which suggests that these traits are controlled by additive gene action (Figure 1). Hence, selection for these traits can be effective. Conversely, moderate GAM values were observed for days to 50 per cent flowering and days to maturity (19.52 and 13.62 respectively). These results are in conformity with the findings of Gediyaet al.[21], Kumar et al.[22] and Karthikeyan et al.[23].

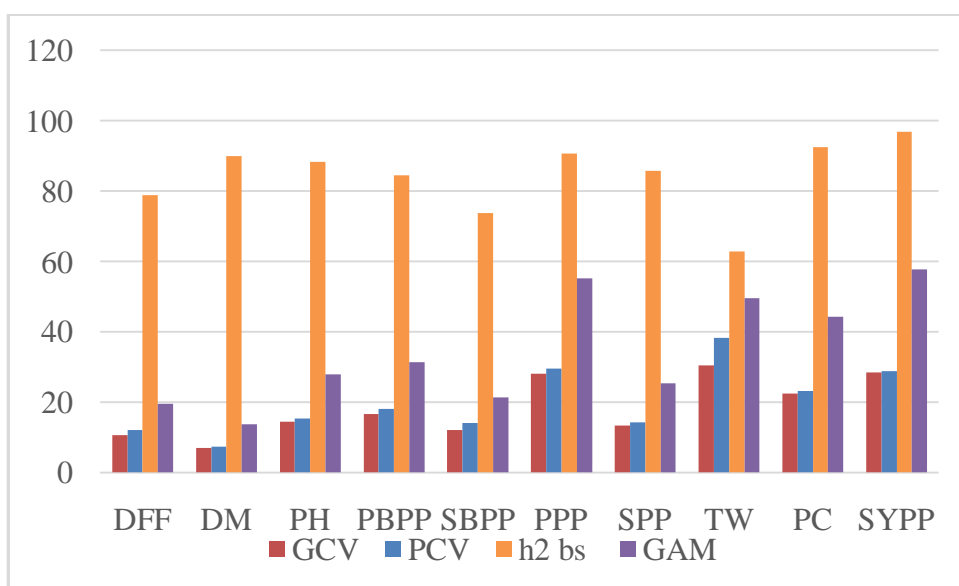
### 3.5 Phenotypic correlation coefficient

Seed yield per plant exhibited significant positive association with test weight (0.64\*\*), number of secondary branches per plant (0.34\*\*), number of pods per plant (0.24\*), number of primary branches per plant (0.22\*) and protein content (0.21\*). Consequently, yield can be improved by utilizing these yield-attributing traits for direct selection. Non-significant positive association was noted with plant height and number of seeds per pod. In contrast, seed yield per plant exhibited non-significant negative correlation with days to maturity (-0.19) and days to 50 per cent flowering (-0.09), which will be helpful in the development of early maturing varieties (Table 3 and Figure 2). The above results were well supported by the similar findings of Gediyaet al. [21] and Karthikeyan et al. [23].

### 3.6 Path coefficient analysis

To know the direct and indirect effects of these traits on seed yield correlations were further partitioned into direct and indirect genotypic and phenotypic effects through path coefficient analysis (Table 4). Path coefficient analysis was carried out by taking grain yield per plant as dependent variables and rest of the traits as independent variables. Test weight (0.7058), plant height (0.0466), number of primary branches per plant (0.1107), number of pods per plant (0.0934)

and number of seeds per pod (0.0658) also exhibited a positive direct effect on seed yield. The significant positive direct effects of these traits underscore their strong association with seed yield per plant. These results are in confirmation with the reports of Karthikeyan et al. [23], Kaur and Bharadwaj[24], Yadav et al. [25]. In the current study, the residual effect is 0.3938, indicating that 60.62 per cent of the variability in seed yield is explained by the yield-contributing traits analyzed. This suggests that there are other factors beyond the traits examined that also influence the seed yield.



**Figure 1: pattern of gcv, pcv, heritability and genetic advance as percent of mean for various traits in chickpea germplasm lines**

*DFF- Days to 50 percent flowering, DM- Days to maturity, PH- Plant height, PBPP- Number of primary branches per plant, SBPP- Number of secondary branches per plant, PPP- Number of pods per plant, SPP- Number of seeds per pod, TW- Test weight, PC- Protein content, SYPP- Seed yield per plant*

**Table 1: Analysis of variance for yield and its attributing characters of chickpea genotypes**

<b>SOURCE OF VARIATION</b>	<b>df</b>	<b>DFF</b>	<b>DM</b>	<b>PH</b>	<b>PBPP</b>	<b>SBPP</b>	<b>PPP</b>	<b>SPP</b>	<b>TW</b>	<b>PC</b>	<b>SYPP</b>
Block (eliminating treatment)	5	3.87	2.77	5	0.01	0.2	8.2	0	4.98	0.43	1.91
Genotypes+ Checks (eliminating block)	99	39.5**	40.5**	48.86**	0.31**	4.8**	79.41**	0.04**	63.65**	28.97**	14.14**
Genotypes	95	40.56**	53.98**	42.61**	0.19**	1.42**	51.11**	0.03**	32.89**	27.67**	4.24*
Checks	3	115.89**	31.44**	215.45**	2.05**	23.01**	119.92**	0.06**	838.05**	59.99**	92.82**
Checks vs Genotypes	1	180.07**	45.63*	570.11**	6.71**	281.54**	3185.64**	1.47**	1434.24**	275.59**	760.86**
<b>Error</b>	15	8.56	5.41	5.01	0.03	0.37	4.8	0	2.49	0.86	1.57

\*\* Significant at 1% \* significant at 5% DFF- Days to 50 percent flowering, DM- Days to maturity, PH- Plant height, PBPP- Number of primary branches per plant, SBPP- Number of secondary branches per plant, PPP- Number of pods per plant, SPP- Number of seeds per pod, TW- Test weight, PC- Protein content, SYPP- Seed yield per plant

**Table 2: Mean, range and genetic variability parameter for yield and yield related characters in chickpea genotypes**

Sl. No.	Characters	Range		Mean	Co-efficient of variation (%)		h <sup>2</sup> bs (%)	GAM (%)
		Min	Max		GCV	PCV		
1	Days to 50 <i>per cent</i> flowering	38	76	53	10.65	11.99	78.91	19.52
2	Days to maturity	89	120	100	6.96	7.34	89.98	13.62
3	Plant height (cm)	25.20	62.96	42.54	14.42	15.35	88.25	27.94
4	Number of primary branches per plant	1.66	3.55	2.40	16.56	18.01	84.49	31.40
5	Number of secondary branches per plant	5.33	14.44	8.51	12.01	13.99	73.71	21.28
6	Number of pods per plant	12.50	47.33	24.23	28.09	29.51	90.60	55.15
7	Number of seeds per pod	1.00	1.60	1.23	13.22	14.28	85.69	25.24
8	Test weight (g)	17.18	46.16	24.71	22.31	23.20	92.44	44.25
9	Protein content (%)	9.12	28.82	18.24	28.39	28.84	96.88	57.65
10	Seed yield per plant(g)	2.70	17.30	5.38	30.32	38.23	62.89	49.60

**Table 3: Phenotypic correlation coefficient for seed yield and yield attributing traits in chickpea genotypes**

\*\* Significant at 1% \* significant at 5% DFF- Days to 50 percent flowering, DM- Days to maturity, PH- Plant height, PBPP- Number of primary branches per plant, SBPP- Number of secondary branches per plant, PPP- Number of pods per plant, SPP- Number of seeds per pod, TW- Test weight, PC- Protein

Effect of traits	DFF	DM	PH	PBPP	SBPP	PPP	SPP	TW	PC	SYPP			
<b>DFF</b>	1.00	-0.1261**	-0.0705	0.0030	-0.0257	-0.0184	0.260011	0.1600354	-0.12	-0.0201	0.09	0.0153	
<b>DM</b>		1.00	-0.0739	0.0032*	0.0219	0.0155	0.210004	0.020153	-0.13	-0.0018	0.19	0.0097	
<b>PH</b>			1.00	0.0468	0.0020	0.0042	-0.16011	0.0600076	0.05	0.0028	0.13	0.0025	
<b>PBPP</b>				1.00	0.1707	0.00774	-0.14009	-0.100162	0.23*	-0.0116	0.22*	0.0260	
<b>SBPP</b>					1.00	0.02437	0.050626	-0.050122	0.10	-0.0120	0.34**	0.0232	
<b>PPP</b>						1.00	0.400934	0.050462	-0.12	0.0047	0.24*	-0.0116	
<b>SPP</b>							1.00	0.090658	-0.02	0.0057	0.11	-0.0011	
<b>TW</b>								1.00	0.0605	0.33**	0.7058	0.64**	0.2359
<b>PC</b>									1.00		0.21*		
<b>SYPP</b>										1.00			

content, SYPP- Seed yield per plant

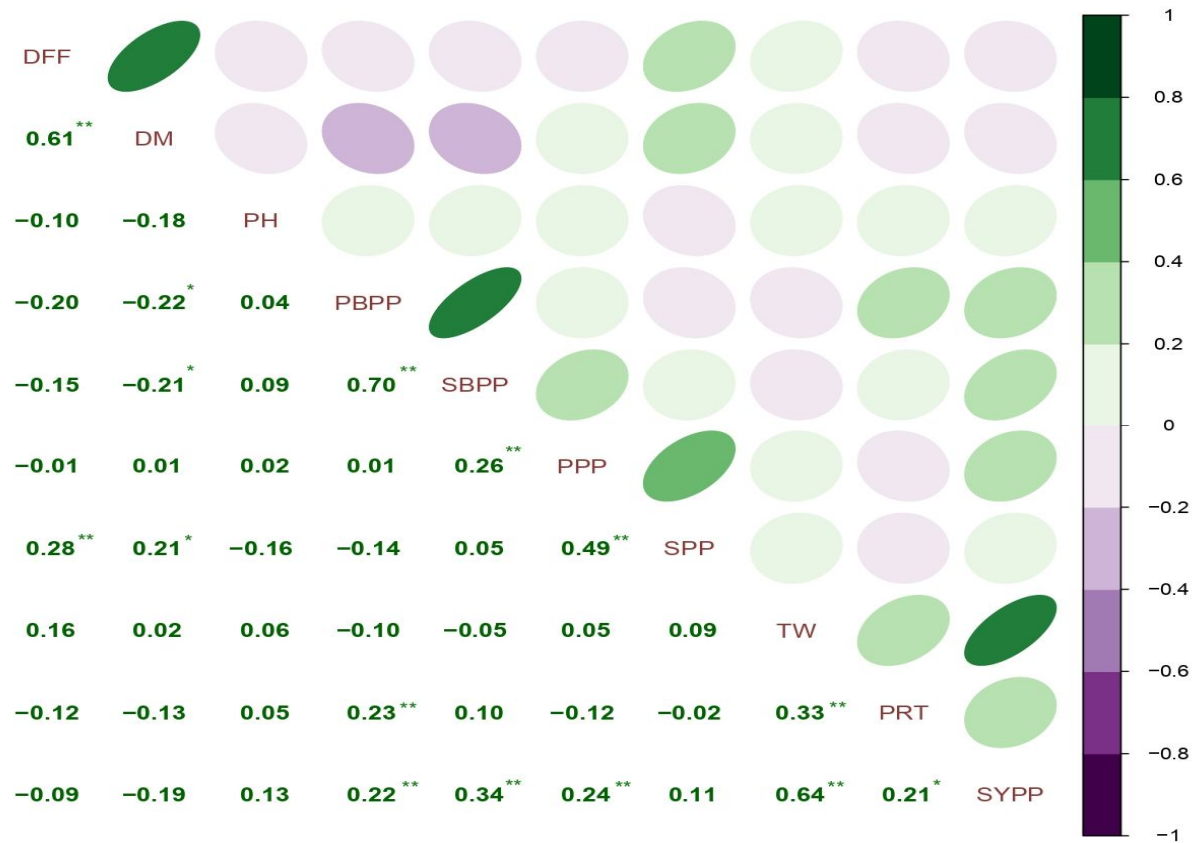
<b>PC</b>	0.0104	0.0113	-0.0046	-0.0202	-0.0082	0.0107	0.0014	-0.0287	<b>-0.0860</b>
<b>r values</b>	<b>-0.09</b>	<b>-0.19</b>	<b>0.13</b>	<b>0.22*</b>	<b>0.34**</b>	<b>0.24*</b>	<b>0.11</b>	<b>0.64**</b>	<b>0.21*</b>

**Table 4: Direct (diagonal) and indirect effect of different traits on seed yield per plant in chickpea genotypes at phenotypic level**

*Residual effect: 0.3938*

*r= correlation coefficient of component trait with seed yield*

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**Figure 2: correlation coefficients for yield and yield attributing traits**

\*\* Significant at 1% \* significant at 5%  
 DFF- Days to 50 percent flowering, DM- Days to maturity, PH- Plant height, PBPP- Number of primary branches per plant, SBPP- Number of secondary branches per plant, PPP- Number of pods per plant, SPP- Number of seeds per pod, TW- Test weight, PC- Protein content, SYPP- Seed yield per plant

#### 4. CONCLUSION

In this study, the traits such as number of pods per plant, test weight, protein content, and seed yield per plant exhibited high genotypic and phenotypic coefficient of variation (GCV and PCV), as well as high heritability and genetic advance. Focusing on these traits could lead to increased yield. The correlation coefficient analysis revealed a highly significant positive relationship between seed yield per plant and factors such as test weight, number of secondary branches per plant, number of pods per plant, number of primary branches per plant, and protein content. This suggests that these traits are key determinants of yield in chickpea. Improving seed yield per plant could be achieved by selecting for any of these traits. Path coefficient analysis showed that test weight had the strongest positive direct effect on seed yield per plant. This was followed by plant height, number of primary branches per plant, number of pods per plant, and number of seeds per pod. Therefore, focusing on these traits in the selection process would be beneficial for enhancing seed yield per plant in chickpea. The mean performance of the genotypes expressed a wide range of variability for all characters. The genotypes of desi types viz., NBeG-47, ICCX-100105-23, KCD-2304, ICCX-130116 and kabuli types viz., NBeG-440, ICCX-130124-B-B-B-B-B-8-B-B, BGM-21-10, NBeG-810 performed best for seed yield per plant.

Disclaimer (Artificial intelligence)

Option 1:

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.

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