

Original Research Article

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

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

Place and Duration of Study: Zonal agricultural and horticultural research station, Babbur farm, Hiriyur, 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. MATERIAL 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 (1961). 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, number of 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 RCB*. [Give the scale for gcvpcv heritability and GAM for classifying into high medium and low. Also give the formulas of gcv, pcv, heritability and GAM along with the references.](#)

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3. RESULTS AND DISCUSSION [\(references should be numbered consecutively throughout the article, beginning with \[1\] for the first-cited reference, and should be cited in the text by numerals in a square bracket. For example; cell cycle arrest and apoptosis induction are targeted in the strategy of cancer therapy \[1\]\).](#)

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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. [5].

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). The results are in line with findings of Karthikeyan et al. [6], Mihoariya et al. [7] and Sanjay et al. [8].

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 (Figure 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. [9], Prasanthi et al. [10], Ram et al. [11] and Tamatam et al. [12].

3.1 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.

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 (0.3448) and plant height (0.2639) suggesting these are major yield contributing traits and traits like hundred seed weight (0.1448) and days to fifty per cent flowering (0.01195) expressed non-significant positive association which were in accordance with the findings of Kaur et al. [13], Dawane et al. [14] and Jain et al. [15]. Selection for these traits helps in indirect selection of yield (Figure 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. [14] and Pattanayak et al. [16].

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

Source of variation	DF	DF	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 variation (%)		of h ² 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

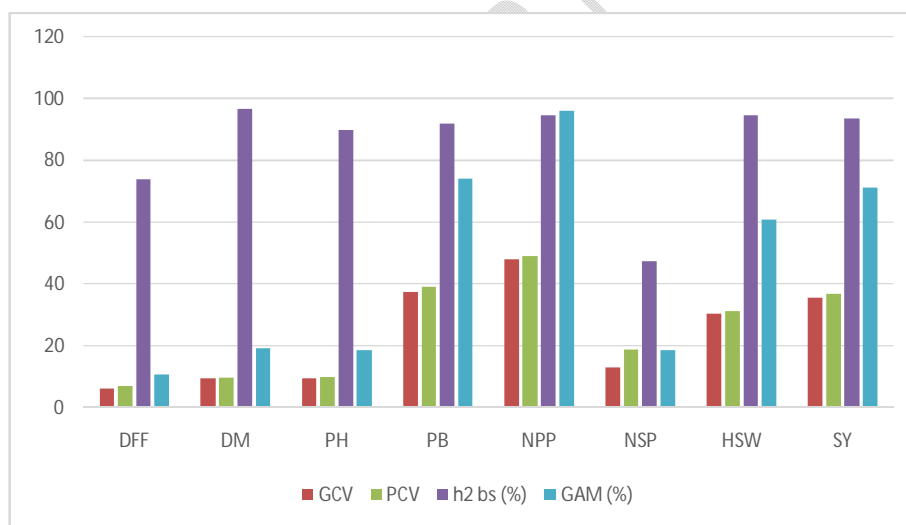


Figure 1: pattern of GCV, PCV, heritability and genetic advance as percent of mean (GAM) for various traits in chickpea germplasm lines

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

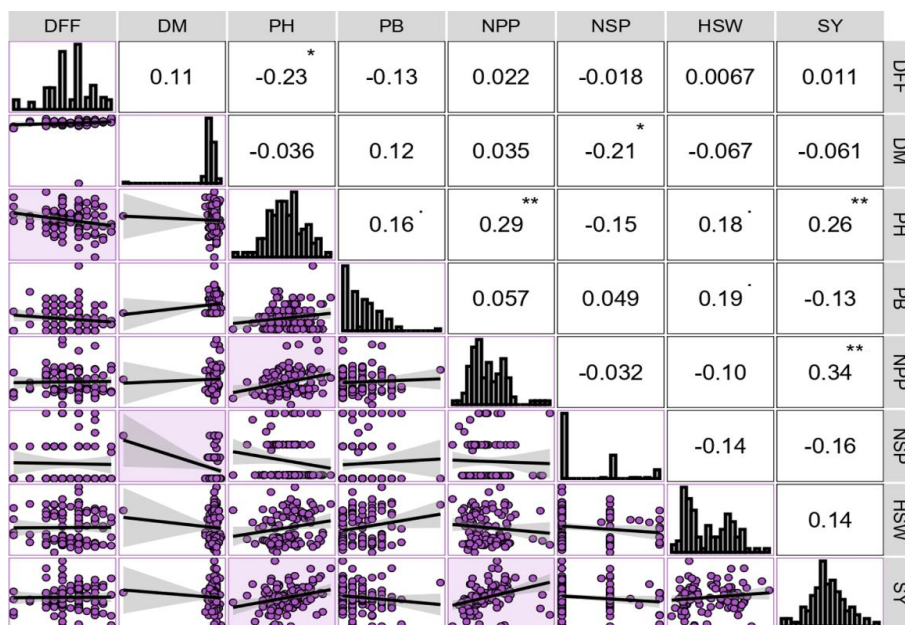


Figure 2: Correlation coefficients for yield and yield attributing traits

*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

4. CONCLUSION

The chickpea germplasm evaluated in the present investigation demonstrated considerable variation for growth and yield attributing traits. Traits like number of pods per plant, plant height and hundred seed weight have high GCV, PCV, heritability and genetic advance as percent of mean indicating ample amount of variation and effectiveness of selection. Traits like number of pods per plant, number of primary branches and hundred seed weight are in positive association with seed yield and can be considered as an essential criterion for selecting higher yields. Therefore, characters like plant height, number of primary branches, number of pods per plant, hundred seed weight and seed yield can be prioritised for further chickpea improvement.

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