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Genetic variability and correlation studies for yield and yield attributing traits in chickpea (*Cicer arietinum* L.)

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Abstract
This study aimed to assess 248 recombinant inbred lines of chickpea in order to examine the extent of variability, heritability, genetic advance, and the relationship between various yield components and their direct and indirect effects on chickpea yield. Present study focused on eleven agro-morphological traits, including four vegetative traits (plant height, stem growth habit, number of primary branches, and number of secondary branches), one flowering trait (days to 50% flowering), six yield-related traits (days to maturity, number of pods per plant, number of seeds per pod, harvest index, 100 seed weight, and seed yield per plant). The estimation of PCV revealed higher values compared to GCV estimates for various traits including days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100 seed weight, seed yield per plant, and harvest index at both locations. On the other hand, days to 50% flowering and plant height displayed considerable heritability and significant genetic progress, indicating that these attributes are influenced by additive gene effects and can be enhanced through direct phenotypic selection. Research findings indicated a strong and meaningful positive relationship between plant height, the number of pods per plant, the number of seeds per plant, seed yield per plant and the100 seed weight. Opting for a greater number of pods and seeds per plant proves to be advantageous in maximizing the genetic advancement for seed yield.

Keywords: Yield, yield attributing traits, chickpea (*Cicer arietinum* L.)

Introduction
Historically, pulses were one of the most integral components of Indian farming and consumption patterns (Mohanty and Satyasai, 2015) [6]. Among them, chickpea (*Cicer arietinum* L.) is preferred food legume because of its diverse uses. On a global scale, it is cultivated on 15 million ha with 15.87 million tons of production (FAOSTAT, 2021) [3].
Increase in crop yield relies on the level of genetic variability found in breeding materials and the heritability of yield-related traits across generations. Genetic variability can be considered when selecting suitable parent plants, but quantitative traits are influenced by the environment. To effectively breed crops, it is necessary to separate overall variances into heritable and non-heritable components (Hamdi, 1992) [4]. The absolute variability of different traits alone cannot determine which one shows the highest degree of variability. Therefore, assessing the relative values of phenotypic and genotypic coefficient of variation provides an understanding of the variability present in a population. Estimating these coefficients, along with heritability and expected genetic advance, is valuable for improving crop yield.
Yield is a complex trait influenced by various environmental factors, hence selecting solely based on yield may not be productive in breeding programmes. Therefore, understanding the correlation among component traits and their impact on yield is crucial. Correlation coefficient helps to identify the significant traits that influence yield, such as seed yield, and assist in establishing selection criteria for enhancing multiple traits and economic yield simultaneously. Therefore, in this study, association analysis and genetic parameters was performed to evaluate the factors influencing seed yield in chickpea.

Materials and Methods
The experimental material comprised of recombinant inbred lines of chickpea developed at ICRISAT, Patancheru, assessed over two locations *viz,* ICRISAT, Patancheru and ARS, Tandur. A total of 252 genotypes (248 $F_{7:8}$ RILs derived from the cross BGD 9971 × NBeG 47 along with 4 checks) were used as experimental material for evaluation at ICRISAT, Patancheru and Agricultural Research Station, Tandur, using alpha-lattice design.

Each genotype was sown with a spacing of 60 x 20 cm (inter and intra) in an area of 1.2 m^2 plot. At ICRISAT, Patancheru, planting was completed during the second fortnight of November 2022, while in ARS, Tandur, it was during the first fortnight of December 2022. A basal dose of fertilizer was applied at the rate of 20:40:20 NPK kg per hectare. Seeds were treated with 2 g Thiram + 1 g carbendazim kg^{-1} seed before sowing for reducing seed and fungal diseases. All the other recommended package of practices were followed during the crop growth to raise a good crop.

To evaluate and ascertain the genetic variability in the chickpea genotypes, genetic parameters such as phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), broad sense heritability (h^2_{bs}), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) is essential and estimated in this study. Correlation studies are essential in plant breeding because it enables breeders to choose the most desirable combinations of attributes and better understand the association between different characteristics.

Statistical Analysis

Genotypic and Phenotypic coefficients of variability, heritability, genetic advance, genetic advance over mean and correlation analysis was obtained using R software 4.1.3 with appropriate packages.

Results and Discussion

Estimates of genetic parameters

Genetic parameters such as phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), broad sense heritability (h^2_{bs}), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) were calculated independently for seed yield and other agronomic traits in both ICRISAT, Patancheru and ARS, Tandur, to assess the level of genetic variability present in the studied characteristics (Table 1).

The magnitude of estimated PCV found higher than GCV estimates for days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100 seed weight, seed yield per plant and harvest index at both the locations and for days to flowering, plant height and growth habit at Tandur. However, estimated PCV and GCV found similar magnitude for days to flowering, growth habit, plant height and primary branches at ICRISAT and for number of primary branches at Tandur. The estimated GCV was high (> 20.00%) for growth habit (34.5902) only at ICRISAT. The moderate levels of GCV (11.00 – 20.00%) was recorded for days to flowering (16.3652), days to maturity (12.17410, plant height (14.9442), number of pods per plant (10.8381) and seed yield per plant (10.8562) at ICRISAT and for number of secondary branches per plant (14.2269), number of pods per plant (19.8661), seed yield per plant (12.3067) and harvest index (12.3067) at Tandur. The magnitude of GCV recorded was low for number of primary branches per plant (2.9819), number of secondary branches per plant 97.1378), number of seeds per plant (6.2786), 100 seed weight (8.4194) and harvest index (7.61) at ICRISAT and for days to flowering (0.5072), days to maturity (0.6842), growth habit (3.1888), plant height (8.3347), number of primary branches per plant (4.6342), number of seeds per plant (4.2556) and100 seed weight (8.7843) at Tandur.

The degree of genetic variability present for these traits in the genetic material determines the usefulness of agronomic traits as selection criteria in any breeding effort. The magnitude of estimated PCV was found to be larger than GCV estimations for DM, SRBN, NPPP, NSPP, 100 SW, SYPP and HI across locations, indicating that these attributes are mostly affected by location or environments. Similarly, Parameshwarappa *et al.*, (2012) [7] also observed higher PCV estimates than GCV for primary branches per plant, secondary branches per plant, pods per plant, and seeds per plant, seed yield per plant and biomass per plant at across locations.

Days to flowering (0.8948), plant height (0.7743), and days to maturity (0.4884) exhibited high and moderate estimates of heritability at ICRISAT. Conversely, the remaining traits at ICRISAT, as well as all traits in Tandur, displayed lower heritability. Similar results of higher heritability estimates for days to flowering and days to maturity was observed by Banik *et al.*, (2018) [2] and Parameshwarappa *et al.*, (2012) [7].

The estimated genetic advance over % of the mean (GAM) was high exclusively for days to flowering (31.8905), growth habit (71.2561) and plant height (27.0888) at ICRISAT. In contrast, moderate estimates of GAM was observed for number of secondary branches per plant (18.1139), number of pods per plant (11.5178) and seed yield per plant (12.7043) only at Tandur. Low estimates were observed for days to maturity (5.1801), number of primary branches per plant (2.6837), number of secondary branches per plant (2.5639), number of pods per plant (4.1848), number of seeds per plant (1.7171), 100 seed weight (5.2477), seed yield per plant (5.2308) and harvest index (4.7267) at ICRISAT and for days to flowering (0.0326), days to maturity (0.1544), growth habit (0.6187), plant height (7.0184), number of primary branches per plant (4.8808), number of seeds per plant (2.1147), 100 seed weight (6.4957) and harvest index (9.2136) at Tandur.

The efficiency of a trait's selection in breeding can be determined by its heritability in conjunction with genetic advance over mean (Johnson *et al.*, 1955). In one or both of the experimental locations, the days to 50% flowering and plant height showed strong heritability together with significant genetic advance, indicating that these traits are controlled by additive gene action and can be enhanced through simple phenotypic selection. Similar findings have also been reported for days to 50% flowering and plant height by Banik *et al.*, (2018) [2] and Parameshwarappa *et al.*, (2012) [7].

Correlation analysis

Plant types need to be reconstructed by breeding activities that involves stem growth patterns in order to increase crop production, make it lodging-resistant, and make it responsive to better agronomy. Correlation plays a significant role in plant breeding as it helps plant breeders to understand the relationship between different traits and select the most desirable combinations, to improve plant varieties. Since, growth habit is associated with various morphological characters, phenotypic correlation coefficients thus estimated for various agronomic and economically important traits based on the evaluation data of the two locations are given in Table 2. Stem growth habit in the study showed positive and highly significant association with days to flowering (0.120), days to maturity (0.084), plant height (0.161) and secondary branches per plant (0.080) whereas negatively associated with economically important traits. In order to improve in the desired direction, it is also crucial to comprehend the strength and direction of associations among the characteristics that demonstrated a substantial correlation with seed yield. Present study showed seed yield per plant having highly significant and positive association with plant height (0.198), number of pods per plant (0.763), number of seeds per plant (0.825) and 100 seed weight (0.077). Number of pods per plant showed highly significant, positive association with plant height (0.227), 100 seed weight with secondary branches (0.110) whereas number of seeds per plant showed positive, highly significant association with both plant height (0.227) and number of pods per plant (0.831). Similarly, harvest index showed positive and highly significant association with plant height (0.140), number of pods per plant (0.107), number of seeds per plant (0.157), 100 seed weight (0.167) and seed yield per plant (0.290). However, there is no association found between growth habit and other economically important traits in the population. Seed yield per plant showed negative correlation with days to flowering (-0.131), days to maturity (-0.061) and primary branches (-0.013). Similarly, 100 seed weight showed negative and highly significant association with number of seeds per plant (-0.109).

Present study revealed high significant positive correlation among plant height, number of pods per plant, number of seeds per plant, seed yield per plant and 100 seed weight. Selection for higher number of pods and seeds per plant is useful in maximizing genetic gain for seed yield. Toker and Cagirgan in 2004 [8] grain yield showed significant positive association with plant height and number of pods per plant. Similarly, Yucel *et al.*, 2006 [10] observed significant positive correlation of seed yield with plant height and number of seeds per pod. Vaghela *et al.*, (2009) [9] reported positive and significant association between seed yield and number of pods per plant, number of seeds per pod, 100 seed weight. However, present study revealed negative correlation for seed yield with days to flowering, days to maturity and number of primary ranches per plant. Ali *et al.*, in 2010 showed negative correlation of days to flowering with seed yield.

Table 1: Genetic variability, heritability (h^2_{bs}), genetic advance (GA) and genetic advance over % of the mean (GAM) for agronomic traits and other economically important traits at ICRISAT, Patancheru and ARS, Tandur

Character	ICRISAT					Tandur				
	GCV	PCV	(h^2_{bs})	GA	GAM	GCV	PCV	(h^2_{bs})	GA	GAM
DF	16.3652	17.3001	0.8948	13.3548	31.8905	0.5072	16.2712	0.001	0.0147	0.0326
DM	12.1741	23.9681	0.4984	4.9229	5.1801	0.6842	6.249	0.012	0.1481	0.1544
GH	34.5902	34.5902	0.0075	1.0236	71.2561	3.1888	33.9452	0.0088	0.0091	0.6187
PH	14.9442	16.9834	0.7743	13.7009	27.0888	8.3347	20.3895	0.1671	3.1496	7.0184
PRBN	2.9819	6.8143	0.1915	0.027	2.6837	4.6342	9.0554	0.2619	0.0494	4.8808
SRBN	7.1378	40.9149	0.0304	0.0903	2.5639	14.2269	23.0181	0.382	0.9882	18.1139
NPPP	10.8381	57.8235	0.0351	20.5162	4.1848	19.8661	70.5866	0.0792	24.8803	11.5178
NSPP	6.2786	47.2941	0.0176	12.9421	1.7171	4.2556	17.6421	0.0582	2.0361	2.1147
100 SW	8.4194	27.8263	0.0915	1.1074	5.2477	8.7843	24.4705	0.1289	1.5499	6.4957
SYPP	10.8562	46.4149	0.0547	1.6583	5.2308	12.3067	24.5587	0.2511	2.4559	12.7043
HI	7.61	25.2394	0.0909	0.0206	4.7267	12.823	36.7382	0.1218	0.0352	9.2136

Table 2: Correlation analysis for agronomic and other economically important traits for the RIL population

Characters	DF	DM	GH	PH	PRBN	SRBN	NPPP	NSPP	100 SW	SYPP	HI
DF	1.000	0.471**	0.120**	0.064*	0.032	0.149**	-0.114**	-0.166**	0.000	-0.131**	-0.064*
DM		1.000	0.084**	0.073**	0.029	0.119**	-0.065*	-0.105**	-0.006	-0.061*	-0.029
GH			1.000	0.161**	0.007	0.080**	0.001	-0.022	-0.029	-0.030	-0.034
PH				1.000	0.031	-0.121**	0.227**	0.251**	-0.002	0.198**	0.140**
PRBN					1.000	0.050*	-0.058*	-0.077**	0.021	-0.013	0.030
SRBN						1.000	-0.275**	-0.452**	0.110**	-0.302**	-0.200**
NPPP							1.000	0.831**	-0.028	0.763**	0.107**
NSPP								1.000	-0.109**	0.825**	0.157**
100 SW									1.000	0.077**	0.167**
SYPP										1.000	0.290**
HI											1.000

**- Significant at 1% level of significance
*- Significant at 5% level of significance

Conclusion

Present study showed higher magnitude of estimated PCV than GCV for days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100 seed weight, seed yield per plant and harvest index at both the locations. Days to 50% flowering and plant height exhibit notable heritability and significant genetic advancement, suggesting that these characteristics are influenced by additive gene effects and can be improved through straightforward phenotypic selection. This study demonstrated a strong and meaningful positive association between various factors, including plant height, the number of pods per plant, the number of seeds per plant, seed yield per plant and 100 seed weight. By focusing on increasing the number of pods and seeds per plant, one can effectively enhance the genetic gain for seed yield, thereby maximizing overall productivity.

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