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Short Communications

Genetic Variability and Association Study for Quantitative Traits in Chickpea (*Cicer arietinum* L.) Genotypes

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Chickpea (*Cicer arietinum* L.), a self-pollinated legume belonging to the Fabaceae family (2n = 16), is a vital pulse crop widely grown and consumed in India. Cross pollination by insects occurs occasionally in this crop (Ahmad *et al*., 2005). It serves as a major source of dietary protein, especially for vegetarian populations and offers a balanced nutritional profile with 25 to 29% protein, 41-50.8% carbohydrates, essential minerals and unsaturated fatty acids like oleic and linoleic acids. Its affordability and high nutrient value make it an indispensable crop in food and nutritional security. Chickpea is considered one of the oldest and most commonly cultivated legumes in the world from the Fabaceae family (Ullah *et al*., 2020). Chickpea exists in two distinct types: *desi* (Microsperma) - adapted to semi-arid tropics, and *kabuli* (Macrosperma) - suited to temperate climates. *Kabuli* type is considered to be having higher protein than *desi* types (Singh *et al*., 2009). In Rajasthan, Chickpea grown in area of 2.047 m ha producing 2.52 mt with average productivity of 1230 kg ha^{-1} (Anonymous, 2025). Despite its significance, the national average yield of chickpea remains low and unstable, which are largely attributed to a narrow genetic base among cultivated varieties and restricts their potential to respond to environmental and biological stresses. Enhancing yield and stability, therefore, depends on broadening genetic diversity and identifying traits that significantly contribute to productivity.

The efficacy of the breeding programme critically depends on the extent of variability and heritability (Pal *et al*., 2018). Genetic variability serves as a key indicator, offering essential sources of variation upon which plant breeders can effectively act (Gaur *et al*., 2020; Verma *et*. *al*., 2018). Understanding the extent of genetic variability and interrelationships among yield related traits is critical for effective selection and breeding. Yield in chickpea is a polygenic trait, influenced by several interconnected components. Hence, selection based solely on yield may not be efficient. Instead, identifying key traits with high heritability, genetic advance and understanding their direct and indirect effects on seed yield can significantly improve selection efficiency. Correlation analysis reveals the degree of association between traits while path coefficient analysis helps partition these correlations into direct and

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Table 1. Variability parameters for seed yield and its related traits in chickpea

Traits	Maximum	Minimum	Grand mean	GCV	PCV	Heritability (Broad sense)	Genetic advance as % of mean
F	80.00	50.00	62.00	12.88	13.24	94.67	25.82
PH	81.30	39.00	59.75	15.71	16.64	89.12	30.56
PP	104.70	18.70	53.67	29.39	30.10	95.30	59.10
M	141.00	111.00	124.97	6.05	6.25	93.52	12.05
TW	30.20	11.60	20.27	19.01	20.16	88.85	36.90
PSH	3.00	1.00	1.21	17.57	36.60	23.04	17.37
Yield	1600.00	360.00	956.74	20.66	22.53	84.12	39.04

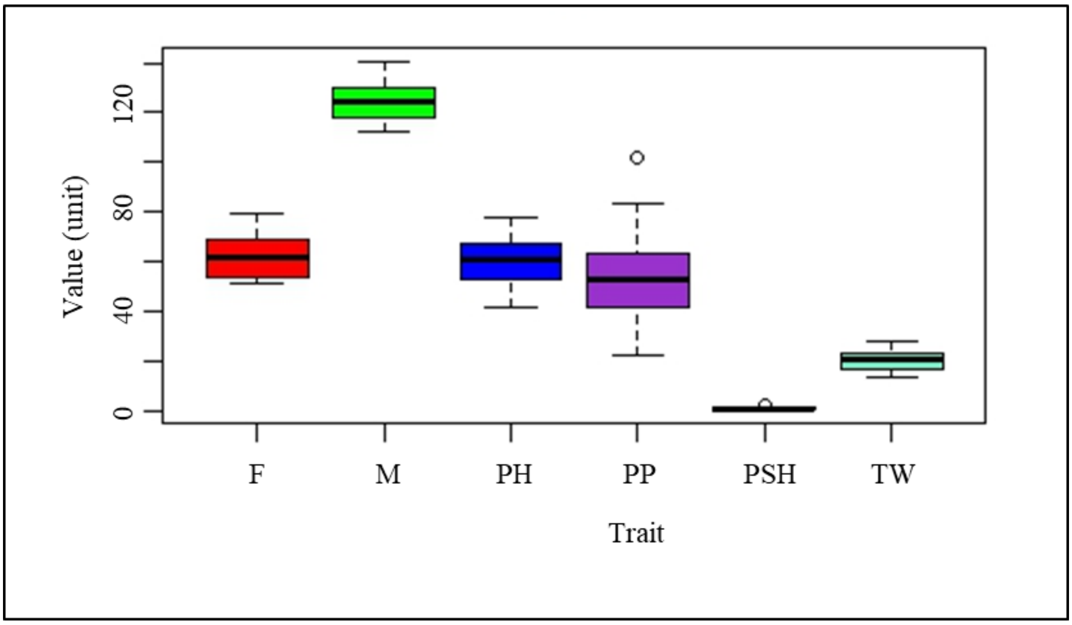
F- days to 50% Flowering; PH- Plant height; PP- Pods plant^{-1}; M- Days to Maturity; TW- Test weight; PSH- Plant stand at harvest; Yield-Grain Yield; PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation.

indirect effects offering deeper insight into trait contribution towards yield. These tools are indispensable in identifying reliable selection criteria and have been effectively employed in chickpea improvement programs by numerous researchers. In this context, the present study was undertaken to assess the genetic variability, trait correlations and path coefficients among various quantitative traits in chickpea. The objective of this study was to identify key traits contributing to seed yield and develop a robust selection strategy to aid in the breeding of high-yielding chickpea genotypes, particularly under rainfed conditions.

A total of 46 genotypes of chickpea were undertaken for present study collected from different centers of All India Coordinated Improvement Project of Chickpea. The present study was conducted in randomized block design (RBD) with three replications at Rajasthan Agricultural Research Institute (SKNAU), Durgapura, Jaipur (Rajasthan), India during *rabi* season, 2024-25. The genotypes were sown in first week of November under timely sown conditions. The experimental unit was four row plots of 4 m long and spacing between row to row was kept to 30 cm and plant to plant was 10 cm. The NPK 20:40:00 fertilizer was applied as basal dose. The data were recorded from 05 randomly selected plants for each genotype. The considered traits are days to 50% flowering (F), plant height (PH) (cm), Pods plant^{-1} (PP), days to maturity (M), test weight (TW) (g), grain yield (Yield) (kg ha^{-1}) and plant stand at harvest (PSH) (0-9 Scale). The genetic parameters *viz*., mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance as a percent of mean were estimated by applying formula followed by Burton and Devane (1953). Further, genotypic and phenotypic correlation coefficients for the undertaken traits were calculated as per the method of Al-Jibouri *et al.* (1958). Path analysis was done as per method given by Dewey and Lu (1959).

The evaluation of chickpea genotypes for genetic variability, heritability, correlation, and path coefficient analysis revealed significant genetic differences across all studied traits, indicating substantial scope for selection and genetic improvement.

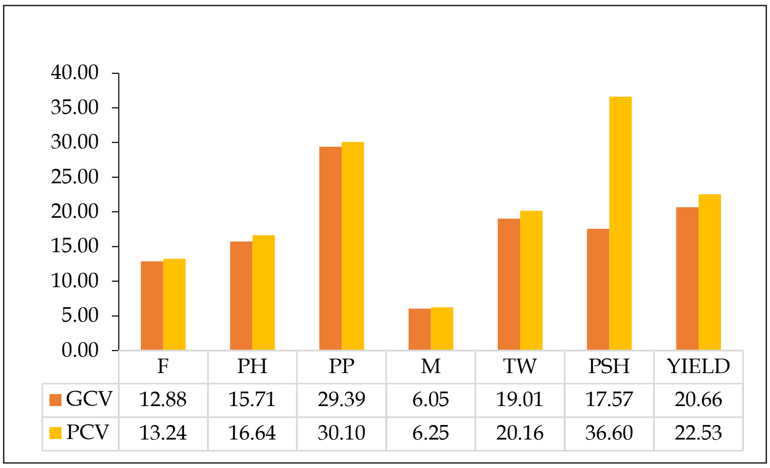
Highly significant differences among genotypes for all traits revealed the presence of sufficient genetic variability, which is a prerequisite for any crop improvement program. The genotypic coefficient of variation (GCV) ranged from 6.05% for Maturity to 29.38% for pods per Plant, while grain yield also exhibited a high GCV (Table 1, Fig. 1). These findings are in agreement with those reported by Bhanu *et al.* (2017) and Tharu *et al.* (2021), who also observed high GCV for reproductive and yield traits in chickpea genotypes indicating a strong genetic influence on these traits. The phenotypic coefficient of variation (PCV) exceeded the GCV for all traits, ranging from 6.25% to 36.60%, implying the involvement of environmental factors in trait expression (Fig. 2). However, the small difference between PCV and GCV in traits such as flowering, maturity, plant height and test weight suggested minimal environmental influence, which supports previous findings by Saroj *et al.* (2023) and Kumar *et al.* (2023), where similar closeness in GCV and PCV was observed. Broad-sense heritability (h^2BS) estimates were high for all traits except plant stand at harvest, which recorded a low value of 23.04%. Heritability



F- days to 50% Flowering; M- Days to Maturity; PH- Plant height; PP- Pods plant^{-1}; PSH- Plant stand at harvest; TW- Test weight.
Fig 1. Box plot analysis of variability in chickpea.

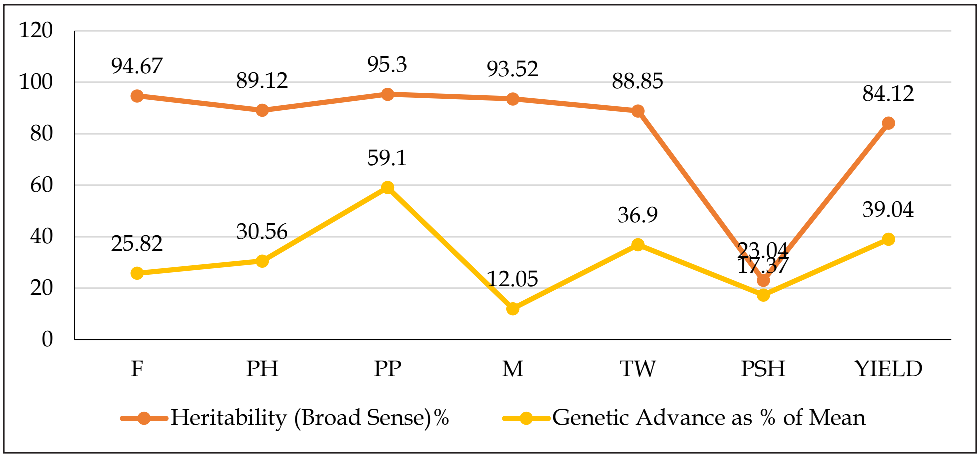
was particularly high for pods per plant (95.30%), flowering (94.67%), maturity (93.52%), plant height (89.12%), test weight (88.85%), and grain yield (84.12%) (Table 1, Fig. 3). These findings are in line with the results of Bhanu *et al*. (2017), Gautam *et al*. (2021) and Kumar *et al*. (2023), who suggested that high heritability indicates the predominance of additive genetic effects and the effectiveness of direct selection. Genetic advance as a percentage of mean was highest for pods per plant (59.10%), followed by grain yield (39.03%) and test weight (36.89%), indicating a high potential for genetic gain through selection. High heritability accompanied by high genetic advance in these traits suggests the presence of additive gene action, which has been reported by Tharu *et al*. (2021) and Sharma *et al*. (2022) in earlier studies on chickpea. Conversely, low heritability and genetic advance as a percentage of mean for plant stand at harvest suggest the need for more stable environmental conditions or improved management for effective phenotypic selection.

The correlation matrix revealed the nature and magnitude of interrelationships among traits. A positive correlation was found between



	F	PH	PP	M	TW	PSH	YIELD
🟧 GCV	12.88	15.71	29.39	6.05	19.01	17.57	20.66
🟨 PCV	13.24	16.64	30.10	6.25	20.16	36.60	22.53

F- days to 50% Flowering; PH- Plant height; PP- Pods plant^{-1}; M- Days to Maturity; TW- Test weight; PSH- Plant stand at harvest; Yield-Grain Yield; PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation
Fig. 2. GCV and PCV for different traits in chickpea.



F- days to 50% Flowering; PH- Plant height; PP- Pods plant^{-1}; M- Days to Maturity; TW- Test weight; PSH- Plant stand at harvest; Yield-Grain Yield

Fig. 3. Heritability for different traits in chickpea.

grain yield and pods per plant, confirming the contributory role of pods per plant in yield enhancement and same findings were also reported by Saroj *et al*. (2023) and Singh *et al*. (2023). Weak positive correlations were also recorded between yield and plant height, maturity and flowering, suggesting minimal impact of these traits on yield in this particular environment and genetic background (Table 2, Fig. 4). A strong negative correlation between yield per plot and plant stand at harvest indicated that dense plant populations or poor plant health at maturity might adversely affect productivity. Test weight also showed a moderate negative correlation with grain yield, possibly due to a resource allocation trade-off, as reported by Kumar *et al*. (2023). These negative associations are crucial in selection strategy to avoid undesirable trait combinations. A very strong positive correlation (0.96) between flowering and maturity implied a close phenological relationship, indicating that genotypes which are flowering later also matured later, which corroborates the results of Tharu *et al*. (2021) and Bhanu *et al*. (2017). A moderate positive correlation (0.27) between plant height and test weight suggested that increased plant stature might support better grain development, as reported earlier by Sharma *et al*. (2022).

Path coefficient analysis was conducted to partition the correlation into direct and indirect effects. The results revealed that flowering days had a strong positive direct effect on yield, indicating that genotypes with extended vegetative phases contributes to higher yield through increased biomass accumulation (Table: 3). This supports the findings of Kumar *et al*. (2023) and Tharu *et al*. (2021). Pods per plant and test weight also exhibited positive direct effects on yield highlighting their essential role as yield components. Direct selection for these traits could effectively enhance yield, as also suggested by Saroj *et al*. (2023). On the contrary, maturity and plant stand at harvest exerted

Table 2. Correlation coefficients for seed yield and its related traits in chickpea

Variables	Yield	F	PH	PP	M	TW	PSH
Yield	1.00	0.03	0.05	0.17*	0.06	-0.29**	-0.54**
F		1.00	0.13*	-0.08	0.96**	-0.26	-0.03
PH			1.00	0.13*	0.02	0.27**	-0.07
PP				1.00	-0.08	0.10	-0.08
M					1.00	-0.25**	-0.10
TW						1.00	0.20*
PSH							1.00

*Significant at 5% level of significance; **Significant at 1% level of significance.
Yield- Grain Yield; F- days to 50% Flowering; PH- Plant height; PP- Pods plant^{-1}; M- Days to Maturity; TW- Test weight; PSH- Plant stand at harvest.

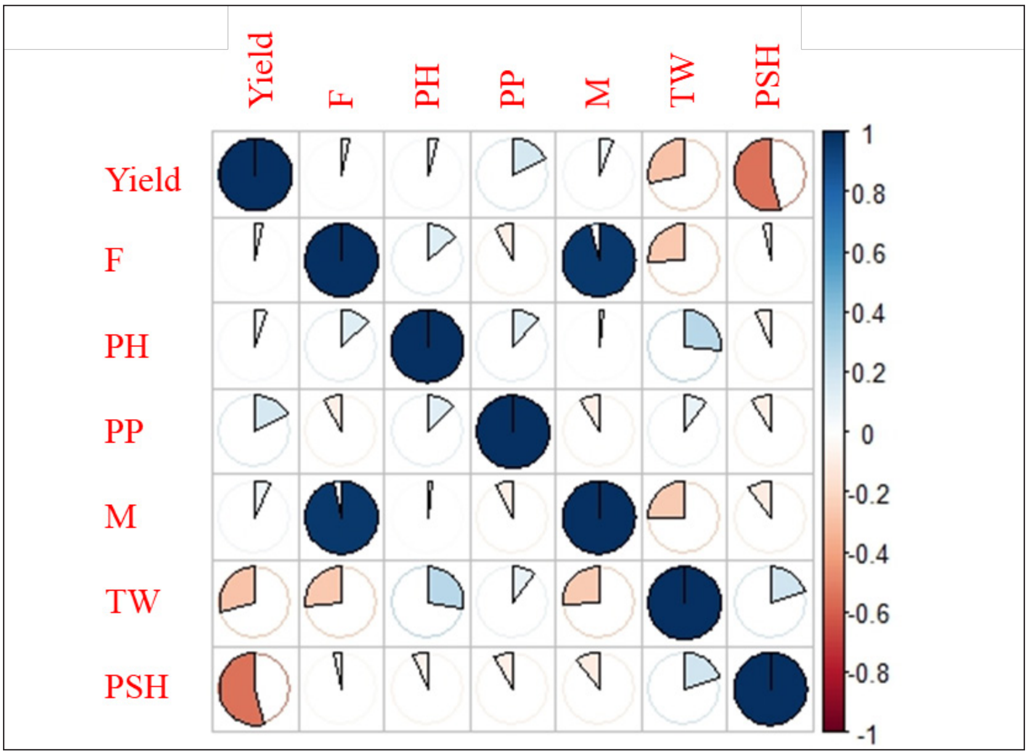
Table 3. Path Coefficient analysis showing direct and indirect effects of studied traits on seed yield in chickpea

Traits	F	PH	PP	M	TW	PSH
F	**0.94969**	-0.02197	-0.00575	-0.89921	-0.01099	0.02131
PH	0.13476	**-0.15485**	0.00915	-0.01906	0.01135	0.07305
PP	-0.07602	-0.0197	**0.07189**	0.07814	0.00412	0.11921
M	0.9164	-0.00317	-0.00603	**-0.93187**	-0.01067	0.10425
TW	-0.25961	-0.04372	0.00736	0.24748	**0.04019**	-0.29586
PSH	-0.0225	0.01258	-0.00953	0.10801	0.01322	**-0.8994**

F- days to 50% Flowering; PH- Plant height; PP- Pods plant^{-1}; M- Days to Maturity; TW- Test weight; PSH- Plant stand at harvest. (Residue effect: 0.3233)

a strong negative direct effect on yield. Early maturing genotypes might escape terminal stresses and result in higher productivity. A similar negative effect of plant stand at harvest suggests that higher plant population could lead to intra-plant competition or disease spread adversely affecting yield. These findings are consistent with those reported by Bhanu *et al*. (2017) and Sharma *et al*. (2022). Plant height showed a negative direct effect on yield, possibly due to increased lodging and resource partitioning inefficiencies in taller genotypes. This outcome is in line with observations by Tharu *et al*. (2021). The residual effect of 0.3233 indicated 67.67% of the variation in yield, while the remaining variation could be attributed to other unmeasured physiological, biochemical or environmental variables. Despite this, the traits studied provide a strong basis for effective selection in chickpea breeding programs.

The study highlights significant genetic variability and strong heritability for key agronomic traits such as pods per plant, flowering time and test weight, supporting their use in direct selection. Path analysis further validated the direct positive effects of these traits on yield, while flagging traits like maturity, plant stand at harvest and plant height as potential yield detractors under specific



Yield-Grain Yield; F- days to 50% Flowering; PH- Plant height; PP- Pods plant^{-1}; M- Days to Maturity; TW- Test weight; PSH- Plant stand at harvest
Fig. 4. Associations in different traits in chickpea.

conditions. These findings, corroborated by earlier studies, reinforce the relevance of multi-trait selection in chickpea breeding programs and provide valuable guidance for enhancing yield through genetic improvement.

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