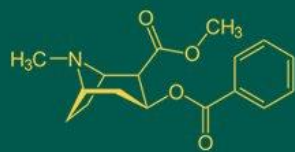


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Quantitative trait association and genetic diversity analysis in chickpea (*Cicer arietinum* L.) genotypes

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Abstract

Chickpea is grown on a large scale in India but the productivity is very low as compared to other chickpea-growing countries. Because, in India, the crop is affected by many biotic and abiotic stresses and also has a narrow genetic base in germplasm lines, which are the prerequisite of any breeding program for developing high-yield varieties. Understanding the genetic associations between yield components is crucial for developing superior chickpea cultivars. This study evaluated 53 chickpea genotypes for nine morpho-agronomic traits to identify key selection criteria through correlation and cluster analysis. Correlation analysis revealed seeds per plant as the strongest yield predictor (0.738), followed by pods per plant (0.480) and seeds per pod (0.591). Plant height showed significant positive association with productivity ($r = 0.341$ with pods per plant). Cluster analysis identified substantial genetic divergence, with clusters VI and IX exhibiting maximum inter-cluster distance (6.4736), suitable for divergent hybridization. Cluster V demonstrated superior yield performance (12.71 g/plant) alongside highest seeds per plant (74.73) and seeds per pod (1.80). These findings provide breeders with precise morphological markers and genetically diverse germplasm for efficient selection and development of high-yielding chickpea varieties.

Keywords: Chickpea (*Cicer arietinum* L.), correlation analysis, genetic diversity, yield components, cluster analysis, plant breeding

Introduction

Chickpea (*Cicer arietinum* L.) holds a prominent position in global pulse production and serves as a crucial source of protein in human nutrition, particularly in developing countries. The crop's significance extends beyond its nutritional value, encompassing its role in sustainable agriculture through biological nitrogen fixation and soil health improvement. As global demand for protein-rich foods increases and climate challenges intensify, the need for improved chickpea varieties has become increasingly urgent. Genetic improvement in chickpea relies heavily on understanding the extent of genetic variability, heritability and genetic advance of economically important traits. These parameters are fundamental to designing effective breeding strategies and achieving genetic gain through selection (Kumar *et al.*, 2021) [17]. Recent studies involving diverse chickpea germplasm have revealed substantial genetic variation for various agronomic and physiological traits, providing opportunities for crop improvement. Recent advances in genomic tools and technologies have enhanced our understanding of the genetic basis of important traits in chickpea. Assessment of genetic variability, correlation coefficient analysis among diverse genotypes has revealed promising traits such as hundred seed weight, seed per plant and pods per plant were found to be significant for yield. Kumar *et al.*, identified several genotypes with superior performance under drought conditions, exhibiting high heritability for drought tolerance-related traits. Globally, chickpea cultivation spans approximately 17.8 million hectares, producing 17.2 million metric tons annually, with India leading production at 11.4 million tons (FAOSTAT, 2023). In India, Madhya Pradesh, Maharashtra, Rajasthan, and Uttar Pradesh are the top chickpea-producing states, contributing significantly to national production (ICRISAT, 2023). The significant genetic variability observed among 53 genotypes, combined with high heritability and genetic advance for key traits, suggests good prospects for genetic improvement through selection.

Understanding the genetic control of complex traits through the study of genetic parameters has facilitated the development of improved breeding strategies. The integration of conventional breeding approaches with modern genomic tools offers promising avenues for chickpea improvement, particularly in addressing emerging challenges related to climate change and food security.

Material Methods

This research was conducted at School of Agriculture, ITM University, Gwalior during the growing season of rabi 2024-25, study was carried out on 50+3 (Checks: Samriddhi, IPC 0677 and RVS-203) genotypes of Chickpea varieties at Crop research centre-1 collected from The seeds collection via.,

MTA from IIPR (Indian Institute for Pulse Research) and different geographical location of country and collected as germplasm of the university. The experiment was laid out in a augmented block design with replicated checks. All other agronomic factors except the factor under study were kept constant. Usual cultural practices were adopted to maintain a good crop. The observations recorded includes days to 50% Flowering, days to maturity, primary branches, plant height, pods per plant, seeds per plant, seeds per pod, 100-seed weight and seed yield per plant were recorded on plot and plant basis. The data collected were subjected to statistical analysis. Phenotypic and genotypic correlation coefficients among different characters were estimated.

Table 1: List of chickpea genotypes

S.No.	Genotype	S.No.	Genotype	S.No.	Genotype
1	BG 3043	19	ICC 4918	37	IPC 15132
2	BG 3062	20	ICC 4958	38	IPC 17351
3	CSI 515	21	ICC 5168	39	IPC 1840
4	Digvijay	22	ICC 5320	40	IPC 1859
5	GCI 3001	23	ICC 5434	41	IPC 20156
6	GL 88341	24	ICC 5783	42	IPC 20198
7	GNG 2299	25	ICC 8400	43	IPC 2064
8	GOK CC	26	ICC 9001	44	IPCK 02
9	HC 5	27	ICC 92944	45	IPCK 18185
10	ICC 10301	28	IG 14	46	IPCK 1923
11	ICC 10685	29	ILWC 105	47	IPCK1920
12	ICC 12031	30	IPC 0562	48	JG 11
13	ICC 12118	31	IPC 0611	49	KWR 108
14	ICC 12237	32	IPC 0756	50	MNK 1
15	ICC 14871	33	IPC 0883	51	C1: Samriddhi,
16	ICC 237	34	IPC 10121	52	C2: IPC 0677
17	ICC 3935	35	IPC 10134	53	C3: RVS-203
18	ICC 42439	36	IPC 1062		

Results

Correlation coefficient analysis

Days to 50% flowering (DFF) exhibited a significant positive correlation with days to maturity (0.412). The positive association with days to maturity confirms that later-flowering genotypes tend to have a longer crop duration, a trend consistent with reports by Bakhsh *et al.* (1998) [18] and Wahid and Ahmed (1998). The largely non-significant relationships with yield components suggest that flowering time alone may not directly govern productivity under the conditions studied. Days to maturity (DM) exhibited a significant negative correlation with pods per plant (-0.332). Non-significant positive associations were recorded with seed yield per plant (0.242), seeds per plant (0.028), seeds per pod (0.130), and 100-seed weight (0.008) consistent with findings of Arora and Kumar and Bakhsh *et al.* (1998) [18]. Primary branches per plant (PB) showed non-significant negative correlations with seed yield per plant (-0.083), plant height (-0.078), and 100-seed weight (-0.204) table 2 fig. 1. Non-significant positive correlations were observed with pods per plant (0.043), seeds per plant (0.041), and seeds per pod (0.159). The compensatory role of other yield components may explain this pattern, as noted by Sarvaliya (1993). Plant height (PH) showed significant positive associations with pods per plant (0.341) and 100-seed weight (0.313). Taller plants appear to provide a larger framework for pod-bearing nodes, consistent with Tripathi (1995) and Yousefi. Pods per plant (PPP) displayed a highly

significant positive correlation with seed yield per plant (0.480) and seeds per plant (0.385). A significant positive association was noted with plant height (0.341) and a significant negative correlation with days to maturity (-0.332). The strong link between pod number and yield underscores its importance as a selection criterion, as documented by Yadav (1990), Jethwa (1994), and Singh. Seeds per plant (SPP) demonstrated highly significant positive correlations with seed yield per plant (0.738) and seeds per pod (0.770). A significant positive association was found with pods per plant (0.385). The highest correlation with seed yield (0.738) confirms seeds per plant as the most reliable yield predictor, consistent with Singh, Bakhsh *et al.* (1998) [18]. Seeds per pod (SPPD) exhibited highly significant positive correlations with seed yield per plant (0.591) and seeds per plant (0.770).

The strong interrelationship between seeds per pod and seeds per plant (0.770) indicates that selection for higher seeds per pod simultaneously increases total seed count, as reported by Ozdemir (1996) and Jethwa (1994). 100-seed weight (SW) showed a significant positive correlation with seed yield per plant (0.420) and plant height (0.313). The significant link between seed weight and yield confirms seed size as a reliable selection criterion, consistent with Yadav (1990) and Singh (1997). The negative associations with pod and seed number reflect the classical size number trade-off noted by Mani and Bahl (1990). Seed yield per plant (YPP) is the primary trait of interest and recorded

highly significant positive correlations with seeds per plant (0.738) and seeds per pod (0.591). A highly significant positive association was also found with pods per plant (0.480). Significant positive correlations were observed with 100-seed weight (0.420). The results confirm that seeds per plant, seeds per pod, and pods per plant are the most influential contributors to yield, and should be prioritized in selection programmes, in agreement with Singh *et al.* (1997), Bakhsh *et al.* (1998)^[18], and Kumar.

Inter-cluster divergence

The analysis of inter-cluster average K values (Table 3 & 4) revealed that Clusters VI and IX showed the highest inter-cluster distance at (6.4736), indicating significant genetic diversity between the genotypes in these clusters. Conversely, Clusters II and IV exhibited the lowest inter-cluster distance at (2.1269). According to the K-means cluster diversity analysis, the most genetically divergent pairs of clusters were. VI-IX (6.47), V-IX (5.75), V-VII (5.30), III-VI (5.16), I-IX (5.08). The clusters with the lowest inter-cluster average K values were II-IV (2.126), I-V (2.53), IV-VIII (2.547), III-VII (3.00). The pairwise distance matrix revealed substantial genetic divergence among nine chickpea clusters, with inter-cluster distances ranging from 2.1269 (Clusters 2–4) to 6.4736 (Clusters 6–9). The close affinity between Clusters 2 and 4 suggests shared pedigree, whereas Cluster 9 exhibited marked distinctiveness from all other groups, indicating a unique gene pool. Intra-cluster distances varied from 2.109 (Cluster 8) to 3.692 (Cluster 7), reflecting differential within-group homogeneity. Such patterns reflect the complex genetic architecture of chickpea germplasm, where crosses between highly divergent clusters maximise heterotic potential and trait recombination (Farahani *et al.*, 2019; Janghel *et al.*, 2021; Bhor *et al.*, 2025)^[16, 15, 17].

Cluster mean performance

Days to 50% flowering had shown the highest cluster mean value in cluster VII (71.63) and the lowest cluster mean value for cluster IX (50.47). Days to maturity had shown the highest cluster mean value in cluster II (126.19) and the lowest cluster mean value for cluster VII (112.14). Primary branches per plant shows highest cluster mean value in cluster VII (4.48) and the lowest cluster mean value for cluster IV (2.76) Table 5. Plant Height had shown highest cluster mean value in cluster III (41.36) and lowest cluster mean value for cluster VII (19.36). Pods per plant had shown highest cluster mean value in cluster III (43.85) and lowest cluster mean value for cluster VI (25.93). Seeds per plant had shown highest cluster mean value in cluster V (74.73) and lowest cluster mean value for cluster VI (25.93). Seeds per pod had shown highest cluster mean value in cluster V (1.80) and lowest cluster mean value for cluster VII and IX (1.11). Seeds weight had shown highest cluster mean value in cluster VI (34.98) and lowest cluster mean value for cluster II (14.78). Yield per Plant had shown highest cluster mean value in cluster V (12.71) and lowest cluster mean value for cluster II (4.11).

Discussion

The correlation analysis of 53 chickpea genotypes for nine morpho-agronomic traits revealed significant associations governing yield determination. Days to flowering demonstrated a positive correlation with days to maturity (0.412), confirming that late-flowering genotypes possess prolonged crop durations, consistent with contemporary findings by Mohan and Thiyagarajan (2019)^[6], Rahangdale *et al.*, (2023)^[10] and Rajput *et al.*, (2023)^[9]. However, days to maturity exhibited a weak negative correlation with pods per plant (-0.332), suggesting that extended growing periods alone do not guarantee superior pod production. This contrasts with some breeding programs where selection for late-maturing types resulted in enhanced productivity (Nagar and Karnawat, 2023)^[7]. The observed variation in these relationships underscores the genotype-specific nature of phenological trait interactions.

Yield component analysis identified seeds per plant as the most reliable yield predictor (0.738), substantiating recent multivariate analyses by Kumar *et al.* (2025)^[4] and Pal (2024)^[12]. Seeds per pod demonstrated highly significant interdependence with seeds per plant (0.770) and both traits displayed strong positive association with seed yield (0.591 and 0.738, respectively). Pods per plant showed robust positive correlation with yield ($r = 0.480$), reinforcing its value as a selection criterion (Lambe *et al.*, 2024). Notably, 100-seed weight maintained significant positive correlation with yield (0.420) despite negative associations with pod and seed numbers, exemplifying the classical size-number trade-off (Akbar *et al.*, 2025)^[1]. This trade-off offers strategic flexibility; breeders can simultaneously pursue either seed quality or quantity depending on market preferences and environmental adaptation requirements.

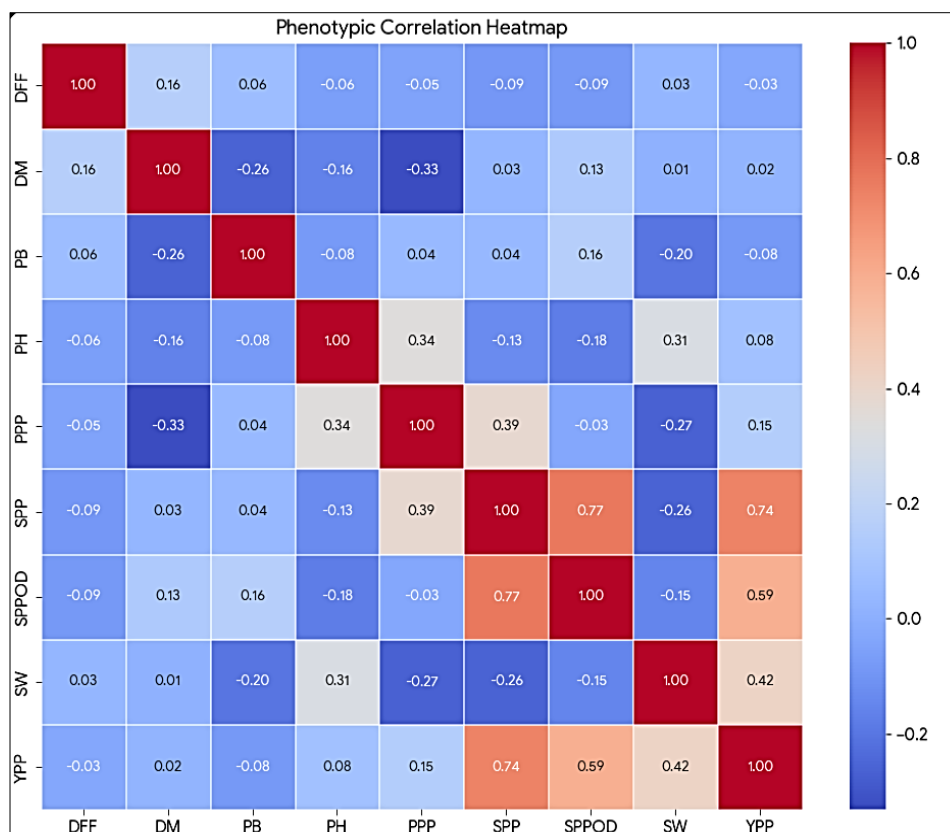
Plant height showed significant positive associations with both pods per plant (0.341) and 100-seed weight (0.313), supporting the hypothesis that taller genotypes provide superior pod-bearing framework (Deepa *et al.*, 2023)^[2]. Primary branches per plant exhibited negligible correlations with yield components, suggesting compensatory mechanisms operate in yield determination. The cluster analysis identified substantial genetic divergence among the 53 genotypes, with clusters VI and IX showing the maximum inter-cluster distance (6.4736), similar to findings by Shivwanshi and Babbar (2019)^[13], Barela *et al.*, (2022)^[8] and Jain *et al.*, (2024)^[11] who reported inter-cluster distances of 6.7 in chickpea germplasm. This genetic divergence provides excellent parental combinations for hybridization programmes. Cluster V demonstrated superior mean performance for yield per plant (12.71 g) alongside highest seeds per plant (74.73) and seeds per pod (1.80), identifying this cluster as a valuable source for direct selection or elite parent material, consistent with Singh *et al.* (2022)^[14].

Integrated selection prioritizing seeds per plant, pods per plant, and plant height would efficiently combine high-yielding potential with agronomic suitability for varied environments. The identified genotypic variation and clustering patterns provide breeders with substantial genetic resources for developing superior chickpea cultivars through both direct selection and divergent crossing strategies, potentially improving chickpea productivity in diverse growing regions globally (Dawane *et al.*, 2020)^[3].

Table 2: Correlation coefficient heat map for nine traits of chickpea

	DFD	DM	PB	PH	PPP	SPP	SPPD	SW	YPP
DFD	1	0.158	0.062	-0.063	-0.049	-0.092	-0.087	0.027	-0.032
DM		1	-0.261	-0.161	-0.332*	0.028	0.13	0.008	0.242
PB			1	-0.078	0.043	0.041	0.159	-0.204	-0.083
PH				1	0.341*	-0.132	-0.179	0.313*	0.079
PPP					1	0.385*	-0.035	-0.265	0.48*
SPP						1	0.77*	-0.261	0.738*
SPPD							1	-0.151	0.591*
SW								1	0.42*
YPP									1

Note: Bold r-values with star indicate significance at $p \leq 0.05$ (*) or $p \leq 0.01$ (**). r-values without star denote non-significant correlations. DFD = Days to 50% Flowering; DM = Days to Maturity; PB = Primary Branches; PH = Plant Height; PPP = Pods per Plant; SPP = Seeds per Plant; SPPD = Seeds per Pod; SW = 100-Seed Weight; YPP = Seed Yield per Plant.

**Fig 1:** Correlation coefficient heat map for nine traits of chickpea**Table 3:** Genotypes categorized under different clusters

Cluster	Number of genotypes	Genotypes
I	8	BG 3062, HC 5, ICC 10685, ICC5168, ICC8400, IPC10121, IPC17351, JG11
II	9	GOKCC, ICC10301, ICC4918, IPC0883, IPC20156, C1, C2, C3
III	6	BG3043, ICC12118, ICC3935, ICC5320, ILWC105, IPC0611, IPC15132
IV	6	GCI3001, GL88341, ICC8400, ILWC105, IPC10134, IPC1859
V	5	DIGVIJAY, ICC14871, ICC42439, IPC1840, IPC20198,
VI	6	GL88341, ICC5783, IG14, IPC0756, IPC2064, KWR108
VII	7	ICC92944, IPC10134, IPCK02, IPCK18185, IPCK1923, IPCK1920, MNK1
VIII	1	ICC12031
IX	5	CSI515, ICC12237, ICC237, ICC4958, ICC5434

**Fig 2:** Evolved genotypic effect among 53 genotypes for yield per plant

Table 4: Inter-Intra cluster distance between various clusters among 53 chickpea genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Intra-dist (avg)
Cluster 1	2.5428	3.2617	4.1213	3.3700	2.5370	4.0825	4.0548	3.5872	5.0858	2.542
Cluster 2	3.2617	2.4589	4.1956	2.1269	4.8314	3.8615	3.0063	3.6807	5.0716	2.458
Cluster 3	4.1213	4.1956	2.4130	3.8476	4.6904	5.1640	3.7961	3.1134	4.8722	2.413
Cluster 4	3.3700	2.1269	3.8476	2.4375	4.3649	3.0781	3.8226	2.5479	4.4947	2.437
Cluster 5	2.5370	4.8314	4.6904	4.3649	3.0490	5.1260	5.3077	4.7278	5.7533	3.049
Cluster 6	4.0825	3.8615	5.1640	3.0781	5.1260	2.9279	4.7660	2.6240	6.4736	2.927
Cluster 7	4.0548	3.0063	3.7961	3.8226	5.3077	4.7660	3.6924	4.1281	5.2965	3.692
Cluster 8	3.5872	3.6807	3.1134	2.5479	4.7278	2.6240	4.1281	2.1091	4.7100	2.109
Cluster 9	5.0858	5.0716	4.8722	4.4947	5.7533	6.4736	5.2965	4.7100	0.0000	0.000

Table 5: Cluster mean for various yield and attributing traits

Cluster	n	DFE	DM	PB	PH	PPP	SPP	SPPOD	SW	YPP
Cluster 1	11	65.01	121.86	3.83	24.90	28.45	58.09	1.73	17.50	10.05
Cluster 2	11	67.20	126.19	3.73	23.87	28.30	28.30	1.27	14.78	4.11
Cluster 3	4	67.13	115.38	3.99	41.36	43.85	43.85	1.26	17.20	7.53
Cluster 4	10	65.97	124.13	2.76	27.95	30.33	33.03	1.13	19.93	6.60
Cluster 5	5	68.13	124.87	3.09	21.98	37.73	74.73	1.80	17.07	12.71
Cluster 6	3	70.47	124.69	3.29	26.37	25.93	25.93	1.30	34.98	9.39
Cluster 7	4	71.63	112.14	4.48	19.36	33.85	33.85	1.11	15.20	5.22
Cluster 8	4	64.47	118.05	3.48	35.20	33.10	33.10	1.19	29.37	9.20
Cluster 9	1	50.47	112.80	3.07	20.11	41.60	41.60	1.11	15.87	6.58

Conclusion

Study evaluated 53 chickpea genotypes across nine morpho-agronomic traits, revealing that seeds per plant (0.738), pods per plant (0.480), and seeds per pod (0.591) are the most influential yield determinants. Plant height positively associates with productivity, while the classical size-number trade-off offers breeding flexibility. Cluster analysis identified substantial genetic divergence, with clusters VI and IX showing maximum separation (6.4736), providing excellent parental combinations. Cluster V demonstrated superior yield performance (12.71 g/plant), representing an ideal source for direct selection. These findings provide breeders with precise selection criteria and genetically divergent germplasm for developing superior chickpea cultivars adapted to diverse agro-climatic regions.

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