

Research Paper

Multivariate analysis in chickpea (*Cicer arietinum* L.) genotypesBukke Naveen Kumar Naik¹, Suhel Mehandi^{1*}, Harikesh², Santosh Kumar Gupta³ and Sudhakar Prasad Mishra⁴

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ABSTRACT

The present study evaluated 30 chickpea (*Cicer arietinum* L.) genotypes for assessing genetic variability, trait associations and diversity analysis. The significant genotypic differences were observed for most traits, indicating substantial genetic variability, except for primary branches per plant. Days to 50% flowering showed a significant positive correlation with days to maturity and a negative correlation with hundred seed weight and biological yield per plant. Path coefficient analysis identified harvest index as having the most substantial positive direct effect on seed yield per plant, followed by biological yield per plant. Genetic diversity assessment grouped the genotypes into five clusters, indicating considerable genetic divergence. Cluster V, the largest, contained 16 genotypes and exhibited superior mean values for plant height, number of pods per plant, hundred seed weight, harvest index and seed yield per plant. The maximum inter-cluster distance was observed between Clusters IV and V, suggesting use of genotypes from these diverse clusters in crossing for obtaining transgressive segregants.

Key words: Chickpea, Correlation, Multivariate analysis, Variability

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinated crop belonging to the family Leguminosae. Chickpea is commonly known as gram, chana and Bengal gram. The chickpea plant is a diploid species with $2n = 2x = 16$ chromosomes. It is considered one of the first grain legumes domesticated by humans in the Old World (Singh *et al.* 2022, Varshney *et al.* 2013, Zohary *et al.* 2012). Pulses are nutritionally rich foods that enhance the overall value of cereal-based diets, especially for low- and middle-income populations. They are an ideal protein source for poorer communities with limited access to animal proteins. When combined with cereals, pulses provide a more balanced amino acid profile, approaching the optimal ratio for human nutrition. This makes them a key component in meeting dietary needs, particularly for those who rely on plant-based diets (FAO 2016, Mudryj *et al.* 2014).

The protein content in chickpea genotypes ranges from 12.6 to 30.5%, and both Kabuli and desi cultivars have marginal differences in protein content (Singh 1985). The average crude protein content in desi, Kabuli, and wild species was found to be 25.31%, 24.67% and 24.30%, respectively. In India, chickpea is cultivated on about 11.25 million hectares with a production of 13.52 million tonnes

and an average productivity of 1,201 kg/ha during 2022-23 (Directorate of Pulses Development, Ministry of Agriculture & Farmers Welfare 2024).

The correlation analysis revealed significant associations between seed yield and several agronomic traits at both the genotypic and phenotypic levels. In general, the genotypic correlation coefficients were higher than their phenotypic counterparts for the same trait pairs, indicating that underlying genetic relationships are strong but partially masked by environmental variation (Tiwari *et al.* 2021, Kumar *et al.* 2023). Path coefficient analysis approach helps identify which traits exert a true causal influence on yield versus those that influence yield mostly through other traits (Wright 1921, Dewey and Lu 1959). In general, genotypic path coefficients were higher than phenotypic ones, indicating that the underlying genetic relationships are stronger when environmental noise is removed (Tiwari *et al.* 2021, Kumar *et al.* 2023). Genetic diversity among parent plants can be of immense help to plant breeders in choosing desirable genotypes for a breeding programme to provide valuable information regarding cross combinations to be exploited commercially (Kumar *et al.* 2021, Singh and Narayan 2020, Toker *et al.* 2007).

MATERIALS AND METHODS

The present study used thirty chickpea genotypes (Table 1). The experiment was conducted during the 2023 and 2024 *Rabi* season at the School of Agriculture, Lovely Professional University, Punjab. The seeds were planted by dibbling, with each genotype sown in 3 replicates using a Randomized Complete Block Design (RCBD) with spacing of 45 x 10 cm

Data recording

The traits were recorded from five randomly selected competitive plants per genotype per replication following standard chickpea protocols. Primary (PB) and secondary branches (SB) were counted from ground level to main stem top and from each primary branch at maturity, respectively; number of pods per plant (NPP) comprised healthy pods bearing ≥ 3 seeds at harvest; days to 50% flowering (DFF) and maturity (DM) were noted from sowing until 50% plants flowered and 95% pods turned yellow-brown (<15% seed moisture), respectively; plant height (PH) measured distance from ground to stem/raceme top (cm); hundred seed weight (HSW) determined weight (g) of 100 air-dried seeds adjusted to 12% moisture; seed yield per plant (SYP) and biological yield per plant (BYP) recorded weights (g) of clean sun-dried seeds and total above-ground oven-dried biomass (70°C, 72 h), respectively; harvest index (HI) calculated as $(SYP/BYP) \times 100$ (%).

Statistical analysis

The analysis of variance (ANOVA) for various quantitative traits was conducted following the standard methodology proposed by Panse and Sukhatme (1985) to determine the presence of significant differences among genotypes. Correlation coefficient analysis, both genotypic and phenotypic, was carried out using the method described by Al-Jibouri *et al.* (1958) to estimate the nature and degree of association among traits.

Path coefficient analysis, aimed at partitioning the correlation coefficients into direct and indirect effects on seed yield per plant, was performed according to the method developed by Dewey and Lu (1959). Genetic divergence among genotypes was assessed using Mahalanobis D^2 statistics as per Rao (1952) and the clustering of genotypes was done using Tocher's method to group genotypes into genetically divergent clusters.

All statistical computations were carried out

using R software (version 4.3.2). The agricolae package (version 4.4.1) de Mendiburu (2021), metan package Olivoto and Lucio (2020) and lavaan package Rosseel (2012) were used for ANOVA, correlation, path analysis and genetic divergence studies. The cluster, factoextra and AGHmatrix packages were employed for multivariate clustering and relationship matrix generation. Data visualization and diagnostics were supported using base R plotting functions and ggplot2. Additionally, Python-based network visualization of inter- and intra-cluster distances among chickpea genotypes was performed using the Network x package (Hagberg *et al.* 2008), with graphical rendering facilitated by Matplotlib (Hunter 2007), and data manipulation handled through Pandas (McKinney 2010).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance (ANOVA) results demonstrated substantial genetic variability among the 30 chickpea (*Cicer arietinum* L.) genotypes for all studied traits except primary branches per plant evaluated over two years. Genotypic effects were highly significant for nearly all measured characteristics. Traore *et al.* (2022) observed high genetic variation and significant differences among diverse chickpea lines for all traits examined. The detection of wide genetic variability is advantageous for chickpea breeding programs, as genetic diversity is the fundamental prerequisite for selection and genetic gain in crop improvement (Srivastava *et al.* 2022). Nandigam *et al.* (2025) reported highly significant genotype differences for yield and other traits with no significant seasonal effect, highlighting cases where chickpea genotypes maintain performance across years.

Violin plot visualization with DMRT analysis

The violin plot analysis, integrated with Duncan's Multiple Range Test (DMRT), provided a comprehensive visualization of the performance of 30 chickpea genotypes across 11 traits by illustrating their distribution, range and statistically significant groupings. For days to 50% flowering (DFF), early flowering genotypes like GNG1958, ICCL 86111 and VIJAY were clearly separated from late-flowering ones such as JG130 and JG24. In terms of days to maturity (DM), genotypes like JG130 showed significantly delayed maturity, while VIJAY and RSG963 were among the earliest. VIJAY and JG14

Table 1. List of genotypes with pedigree and developing institute

Genotype Number	Genotype Name	Pedigree	Origin Institute
1.	JAKI 9218	(ICCC 37 × GW 517) × ICCV 10	PDKV, Akola (Maharashtra)
2.	BGD 209	Pedigree not well-documented	IARI, New Delhi
3.	JKM 7	-	-
4.	CSJ 515	FG 712 × CSJ 146	RARI, Durgapura
5.	K850	Banda Local × Etah Bold	CSAUA&T, Kanpur
6.	IPCK02	Kabuli selection (Shubhra)	ICAR-IIPR, Kanpur
7.	IPCK28	Kabuli selection (Ujjawal)	ICAR-IIPR, Kanpur
8.	T39-1	-	ICRISAT, Patancheru
9.	GOKCE	Multi-parent kabuli breeding population	ICARDA / CRIFC, Turkey
10.	PUSA256	(JG 62 × 850-3/27) × (L 550 × H 208)	IARI, New Delhi
11.	RSG931	-	RARI, Durgapura
12.	IPC71	<i>C. arietinum</i> × <i>C. judaicum</i>	ICAR-IIPR, Kanpur
13.	JG35	JG 130 × ICC 11551	JNKVV, Jabalpur
14.	JG24	-	JNKVV, Jabalpur
15.	IPC04-1	Kabuli selection	ICAR-IIPR, Kanpur
16.	JG14	(GW 5/7 × P 327) × ICCV 83149	JNKVV, Jabalpur
17.	JG130	-	JNKVV, Jabalpur
18.	GNG1581	-	ARS, Sri Ganganagar
19.	RADHACHOTI-1	Local landrace selection	Regional (India)
20.	RSG963	RSG 524 × PDG 84-10	RARI, Durgapura
21.	HC5	-	CCS HAU, Hisar
22.	GNG1958	GNG 1365 × SAKI 9516	ARS, Sri Ganganagar
23.	KPG59	-	CSAUA&T, Kanpur
24.	BG212	Selection from landrace	IARI, New Delhi
25.	PUSA362	-	IARI, New Delhi
26.	DIGVIJAY	Phule G 9108 × Bheema	MPKV, Rahuri
27.	VIJAY	P 127 × Annigeri	MPKV, Rahuri
28.	GL25016	-	GAU, Gujarat
29.	ICCL 86111	-	ICRISAT, Patancheru
30.	GNG1488	-	ARS, Sri Ganganagar

Table 2. Analysis of variance of chickpea genotypes over two years

Traits	Replicate (df=2)	Treatments (df=29)	Environment (df=1)	Interactions	Total	Error (df=145)
DFF	1.62	10.08**	111.99**	3.04	24.26	3.98
DM	1.79	61.95**	223.17**	24.96	55.34	27.61
PB	0.01	0.59	12.18**	0.0085	2.44**	0.05
SB	0.02	0.78**	25.36**	0.01	5.08	0.17
PH	0.09	26.66**	10.36	3.93	3.68	15.84
NPP	0.53	28.47**	539.37**	0.39	108.24	8.68
SPP	0.01	0.40**	1.32**	0.02	0.28	0.09
HSW	0.58	201.35**	8.84**	0.05	2.02	1.34
BYP	0.35	12.68**	102.92**	9.20	24.40	5.97
HI	3.88	47.82**	4.71	1.66	3.16	4.88
SYP	0.13	3.67**	4.17**	0.59	1.12	0.36

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively.

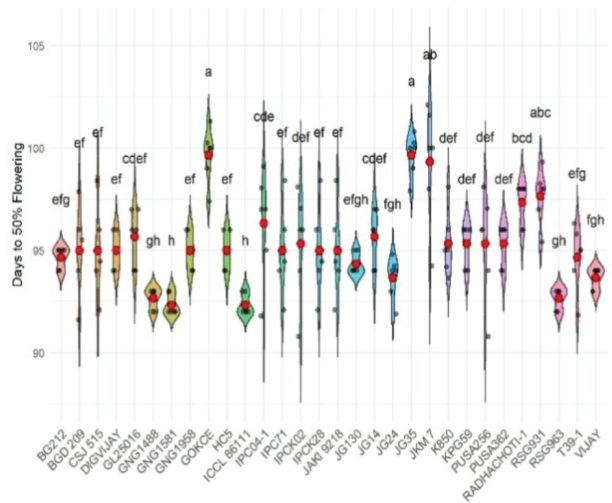
PB: primary branches; SB: secondary branches; NPP: number of pods per plant; DFF: days to 50% flowering; DM: days to maturity; HSW: hundred seed weight; HI: harvest index; SYP: seed yield per plant; PH: plant height; BYP: biological yield per plant.

recorded the highest number of primary branches, while IPC04-1 and JG35 were tallest in plant height, contrasting with short-statured genotypes like T39-1 and RSG963. GL25016 and GNG1581 produced

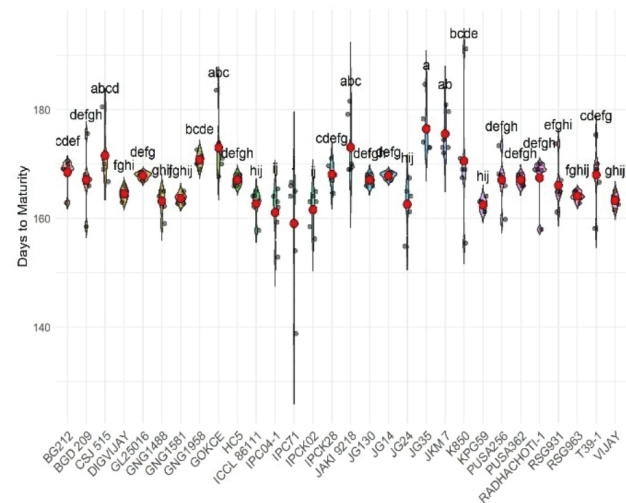
the highest number of pods per plant, whereas GOKCE and IPC04-1 had the least (Chetariya *et al.* 2023, Naik and Mehendi 2025). Seed size variation was prominent, with VIJAY, BGD209 and CSJ515

exhibiting the highest hundred seed weights, and IPC04-1 and T39-1 the lowest. CSJ515 and PUSA362 recorded the highest biological yield per plant, while IPC71 and IPC04-1 showed minimal biomass.

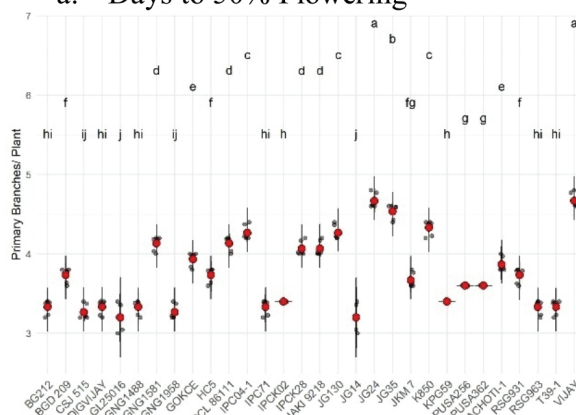
For seed yield per plant, CSJ515, GL25016 and PUSA256 were significantly superior, whereas JG14 and IPC04-1 performed the poorest. The harvest index (HI), a measure of resource-use efficiency, was



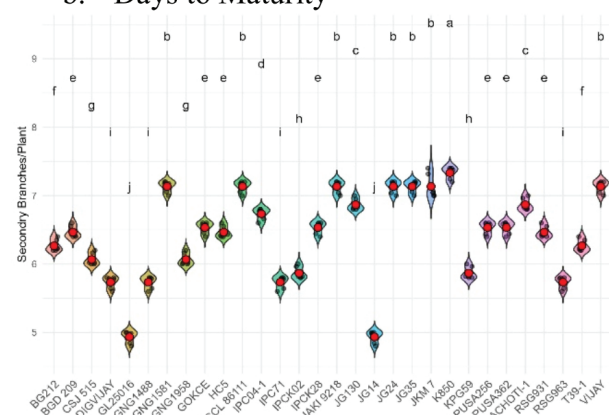
a. Days to 50% Flowering



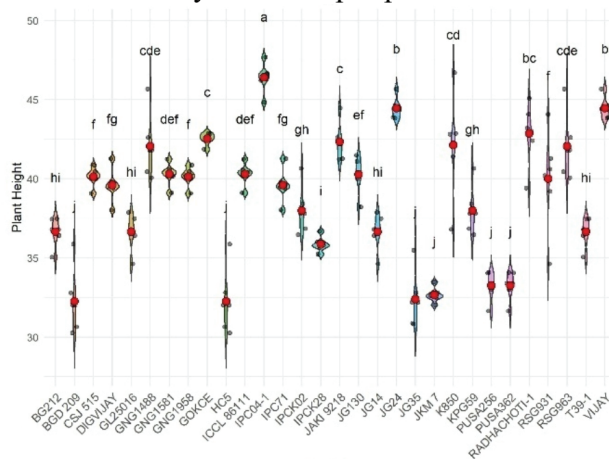
b. Days to Maturity



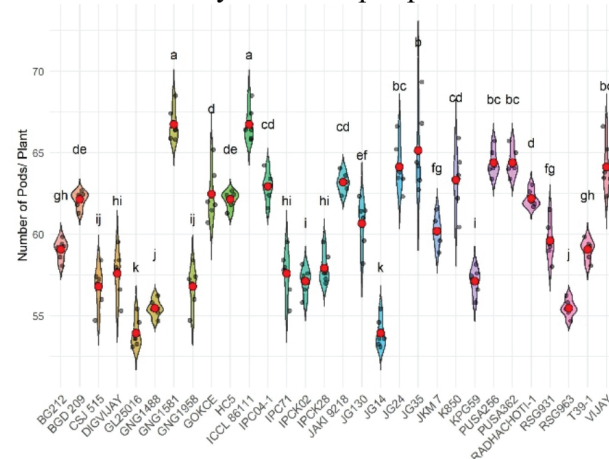
c. Primary branches per plant



d. Secondary branches per plant



e. Plant Height



f. Number of pods per plant

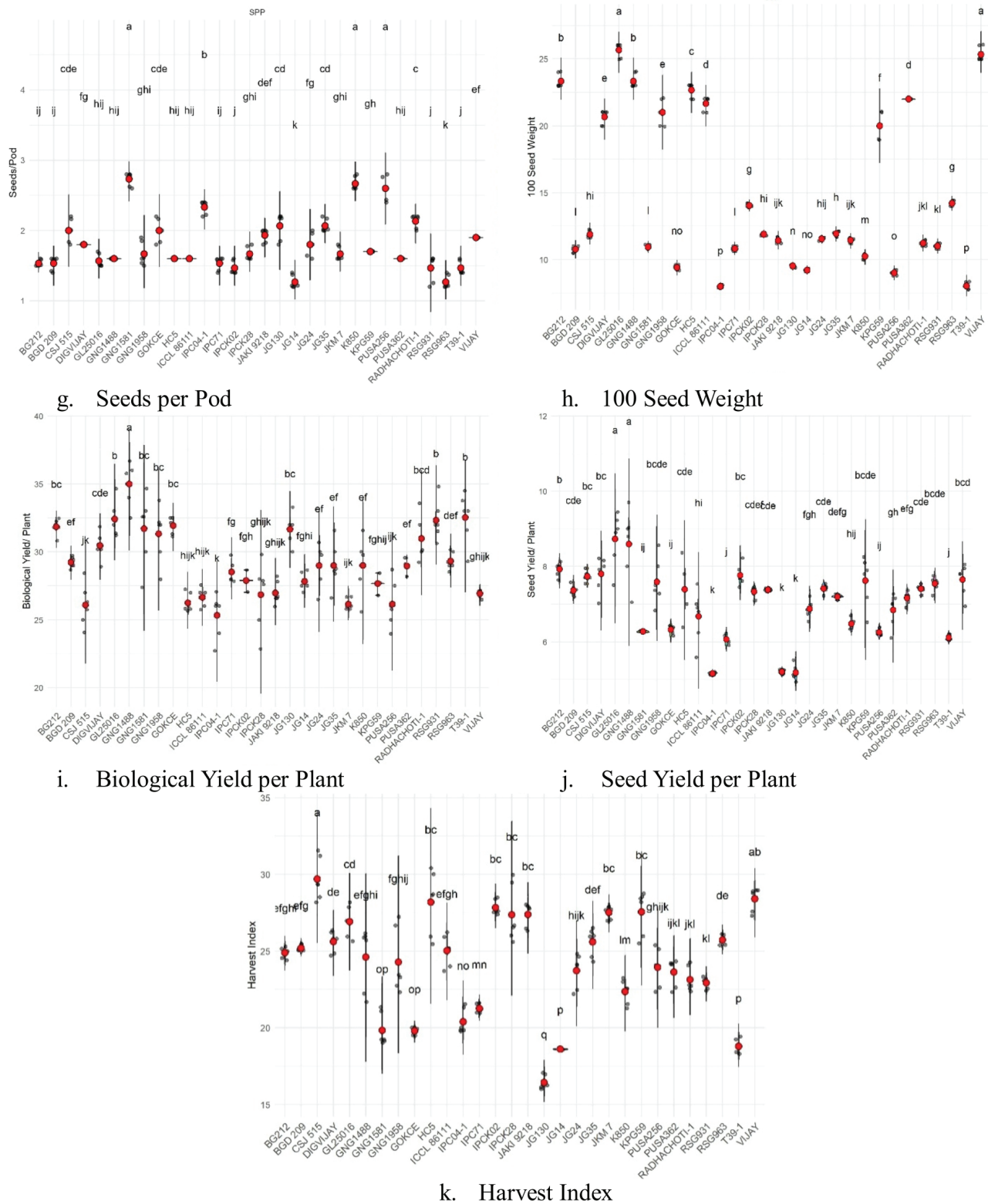


Fig. 1 (a-k). Violin plots illustrating the distribution of 30 chickpea genotypes of 11 traits [Red dots represent trait means, while vertical dispersion shows variability across replications. Alphabetic groupings above violins indicate significant differences among genotypes based on Duncan's Multiple Range Test (DMRT) at $p < 0.05$. Distinct violin colors represent genotypes categorized into clusters for visual comparison]

Table 3. Genotypic correlation of 11 traits of chickpea

Traits	DFF	DM	PB	SB	PH	NPP	SPP	HSW	BYP	HI	SYP
DFF	1.000	0.689**	0.042	0.120	-0.410*	0.077	0.258	-0.601**	-0.947**	0.161	-0.295
DM		1.000	0.211	0.746**	-0.995**	0.451*	0.381*	-0.341	-0.962**	0.611	0.150
PB			1.000	0.711**	0.252	0.811**	0.566**	-0.303	0.302	-0.301	-0.214
SB				1.000	-0.459**	0.799**	0.591**	-0.444*	0.249	-0.037	-0.010
PH					1.000	-0.128	0.035	-0.101	0.507**	-0.598**	-0.392
NPP						1.000	0.747**	-0.273	0.583**	-0.349	-0.187
SPP							1.000	-0.478**	0.077	-0.546**	0.584**
HSW								1.000	0.404*	0.568**	0.756**
BYP									1.000	-0.257	0.101
HI										1.000	0.942**
SYP											1.000

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively.

Note: PB: primary branches; SB: secondary branches; NPP: number of pods per plant; DFF: days to 50% flowering; DM: days to maturity; HSW: hundred seed weight; HI: harvest index; SYP: seed yield per plant; PH: plant height; BYP: biological yield per plant.

Table 4. Phenotypic correlation of 11 traits of chickpea

Traits	DFF	DM	PB	SB	PH	NPP	SPP	HSW	BYP	HI	SYP
DFF	1.000	0.503**	-0.045	0.0009	-0.3182	-0.009	0.1521	-0.468**	-0.620**	0.091	-0.177
DM		1.000	0.093	0.442*	-0.590	0.219	0.236	-0.252	-0.542**	0.385*	0.122
PB			1.000	0.711*	0.25	0.746**	0.528**	-0.289	0.146	-0.266	-0.218
SB				1.000	-0.148	0.788**	0.574**	-0.397*	0.097	-0.05	-0.055
PH					1.000	-0.043	0.128	-0.077	0.271	-0.378	-0.23
NPP						1.000	0.660**	-0.234	0.233	-0.276	-0.200
SPP							1.000	-0.428*	0.024	-0.445*	0.485**
HSW								1.000	0.286	0.55	0.725**
BYP									1.000	-0.314	0.103
HI										1.000	0.908**
SYP											1.000

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively.

Table 5. Genotypic direct and indirect path coefficients of traits

Traits	DFF	DM	PB	SB	PH	NPP	SPP	HSW	BYP	HI
DFF	0.011	0.007	0.000	0.001	-0.004	0.001	0.003	-0.006	-0.014	0.002
DM	-0.007	-0.010	-0.002	-0.008	0.011	-0.005	-0.004	0.004	0.013	-0.006
PB	0.001	0.005	0.021	0.015	0.005	0.017	0.012	-0.007	0.007	-0.006
SB	-0.014	-0.088	-0.083	-0.117	0.054	-0.094	-0.069	0.052	-0.029	0.004
PH	-0.010	-0.026	0.006	-0.011	0.024	-0.003	0.001	-0.002	0.012	-0.014
NPP	0.009	0.051	0.092	0.091	-0.015	0.114	0.085	-0.031	0.066	-0.040
SPP	-0.017	-0.026	-0.038	-0.040	-0.002	-0.051	-0.068	0.032	-0.005	0.037
HSW	0.019	0.011	0.010	0.014	0.003	0.009	0.015	-0.032	-0.013	-0.018
BYP	-0.458	-0.429	0.103	0.085	0.172	0.198	0.026	0.138	0.340	-0.087
HI	0.172	0.655	-0.322	-0.040	-0.641	-0.374	-0.586	0.609	-0.276	1.071

Table 6. Phenotypic direct and indirect path coefficients of traits

Traits	DFF	DM	PB	SB	PH	NPP	SPP	HSW	BYP	HI
DFF	0.015	0.008	-0.001	0.000	-0.005	-0.0001	0.002	-0.007	-0.010	0.001
DM	-0.013	-0.026	-0.002	-0.011	0.015	-0.006	-0.006	0.007	0.014	-0.010
PB	-0.0004	0.001	0.008	0.006	0.002	0.006	0.005	-0.002	0.001	-0.002
SB	-0.0001	-0.030	-0.048	-0.067	0.010	-0.053	-0.039	0.027	-0.007	0.003
PH	-0.013	-0.024	0.010	-0.006	0.041	-0.002	0.005	-0.003	0.011	-0.016
NPP	-0.001	0.018	0.061	0.064	-0.004	0.082	0.054	-0.019	0.019	-0.023
SPP	-0.006	-0.010	-0.022	-0.024	-0.005	-0.027	-0.042	0.018	-0.001	0.019
HSW	-0.004	-0.002	-0.003	-0.004	-0.001	-0.002	-0.004	0.009	0.003	0.005
BYP	-0.251	-0.220	0.059	0.039	0.110	0.095	0.010	0.116	0.405	-0.127
HI	0.097	0.408	-0.282	-0.053	-0.400	-0.293	-0.471	0.582	-0.333	1.057

Table 7. Composition of different genotypes into various cluster

Cluster No.	No. of Genotypes	Genotypes
Cluster I	02	BGD-209, JG-130
Cluster II	02	GoKeE, BG-212
Cluster III	06	K-850, RSG-963, IPCK-28, GNG-1958, JAKI-9218, JG-14
Cluster IV	04	T39-1, KPG-59, IPCK-02, HC-5
Cluster V	16	JG-24, ICCL-86111, IPC-04-1, GNG-1488, JKM-7, GNG-1581, PUSA-256, PUSA-362, CSJ-515, RADHACHOTI-, 1, IPC-71, VIJAY, JG-35, GL-25016, RSG-931, DIGVIJAY

Table 8. Inter and Intra cluster values for chickpea genotypes

Cluster	I	II	III	IV	V
I	6.98	19.84	20.46	23.65	10.20
II		8.70	11.03	11.37	23.56
III			4.56	16.46	25.13
IV				3.76	27.46
V					2.65

highest in BG212, PUSA362, and VIJAY. Overall, the violin plots effectively highlighted significant genetic variability, clearly differentiating superior genotypes and trait combinations. Genotypes such as CSJ515, GL25016 and VIJAY consistently outperformed others across several traits, making them valuable candidates for yield-focused chickpea breeding programs (Singh *et al.* 2022, Hussain *et al.* 2025).

Correlation coefficient analysis

The correlation analysis revealed several important trait associations influencing seed yield and its components in chickpea, with stronger relationships generally observed at the genotypic level compared to the phenotypic level. This indicates that genetic linkages among traits are often masked by environmental variability [Table 3 & 4; Figure 2 & 3].

Days to 50% flowering exhibited a highly significant positive correlation with days to maturity at both the genotypic (0.689**) and phenotypic (0.503**) levels, suggesting that early-flowering genotypes tend to mature earlier (Kumar *et al.* 2023). However, DFF also showed highly significant negative correlations with hundred seed weight and biological yield per plant at both levels, though the strength of association was stronger genotypically (-0.601**, -0.947** respectively) than phenotypically (-0.468**, -0.620**) (Tengse *et al.* 2022, Dawane *et al.* 2020). Additionally, DFF was significantly and negatively correlated with plant height (-0.410*) at the genotypic level, while the phenotypic association was weaker and non-significant. Days to maturity (DM) showed a highly significant positive genotypic correlation with secondary branches (0.746**) and significant correlations with number of pods per plant (0.451*)

and seeds per pod (0.381*), indicating that later-maturing genotypes often exhibit higher vegetative and reproductive development (Vij and Singh 2021, Tiwari *et al.* 2021). At the phenotypic level, DM maintained a significant positive correlation with SB (0.442*) and harvest index (0.385*), though associations with NPP, SPP, seed yield (SYP) and PB were weak and non-significant. Notably, DM had highly significant negative genotypic correlations with PH (0.995**) and BYP (0.962**), consistent with the phenotypic trend where DM was significantly negatively correlated with BYP (0.542**) and non-significantly with PH and HSW (Eker 2022, Hailu *et al.* 2021).

Primary branches per plant showed highly significant and strong positive correlations with secondary branches per plant at both the genotypic (0.711**) and phenotypic (0.711**) levels (Tengse *et al.* 2022, Singh *et al.* 2021). Similarly, PB was positively and significantly associated with number of pods per plant ($rg = 0.811$, $rp = 0.746^{**}$) and seeds per pod ($rg = 0.566$, phenotypic $rp = 0.528^{**}$), indicating that well-branched plants tend to produce more pods and seeds (Dawane *et al.* 2020, Kumar *et al.* 2023). Secondary branches also demonstrated strong positive correlations with NPP ($rg = 0.799$, $rp = 0.788^{**}$) and SPP ($rg = 0.591^{**}$, $rp = 0.574^{**}$), emphasizing their role in enhancing reproductive output (Tiwari *et al.* 2021). However, SB was negatively associated with plant height ($rg = -0.459$) and hundred seed weight ($rg = -0.444$, $rp = -0.397^{**}$), suggesting a potential trade-off between branching intensity and resource allocation to vertical growth or seed size (Eker 2022, Mehendi and Mishra 2023).

Plant height showed a significant positive genotypic correlation with biological yield per plant (0.507), implying that taller plants accumulate more biomass. Conversely, PH had a strong negative correlation with harvest index (-0.598), indicating that increased vegetative growth may reduce partitioning efficiency to seeds (Hailu *et al.* 2021, Vij and Singh 2021).

Number of pods per plant had positive and highly significant correlations with SPP ($rg = 0.747$, $rp = 0.660^{**}$) and BYP ($rg = 0.583^{**}$, $rp = 0.233^{**}$),

Table 9. Cluster values for chickpea genotypes

Cluster/Traits	DFF	DM	PB	SB	PH	NPP	SPP	HSW	BYP	HI	SYP
I	94.56	166.48	3.48	6.08	37.66	59.25	1.63	22.26	30.07	25.64	7.69
II	95.52	167.26	3.88	6.59	39.53	61.16	1.93	10.88	29.15	23.42	6.77
III	95.67	167.67	3.20	4.93	36.67	53.93	1.27	9.21	27.83	18.61	5.18
IV	99.33	172.67	3.67	7.13	32.67	60.2	1.67	11.44	26.16	27.53	7.2
V	93.67	164.00	4.67	7.13	44.47	64.13	1.90	25.33	26.93	28.41	7.65

reaffirming pod number as a major yield contributor (Singh *et al.* 2022). However, its correlation with seed yield per plant (SYP) was weak and non-significant at both levels, suggesting that other traits mediate its influence on final yield. Seeds per pod displayed a moderate to strong positive correlation with SYP ($rg = 0.584$, $rp = 0.485^{**}$), though it was negatively associated with HSW ($rg = -0.478$, $rp = -0.428^{*}$) and HI ($rg = -0.546$, $rp = -0.445^{*}$), indicating possible trade-offs between seed number per pod and seed size or harvest efficiency (Kumar *et al.* 2023). Hundred seed weight exhibited a strong and highly significant positive correlation with seed yield ($rg = 0.756$, $rp = 0.725^{**}$) and harvest index ($rg = 0.568^{**}$, $rp = 0.550^{**}$). It also correlated positively with BYP at both levels, signifying that larger seeds are associated with greater biomass and yield potential (Dawane *et al.* 2020). Biological yield per plant (BYP) showed a moderate genotypic correlation with seed yield (0.101) and phenotypic correlation (0.103), both weak and non-significant, suggesting that high biomass alone is not sufficient for yield enhancement without efficient partitioning (Tiwari *et al.* 2021). The harvest index was very strongly correlated with seed yield per plant at both genotypic (0.942^{**}) and phenotypic levels (0.908^{**}), confirming HI as the most influential and reliable predictor of seed yield under the tested conditions (Eker 2022, Kumar *et al.* 2023). These findings emphasize the importance of traits such as pods per plant, seeds per pod, seed weight and harvest index in determining yield. Simultaneous improvement in branching pattern and efficient biomass partitioning can significantly enhance productivity in chickpea breeding programs (Singh *et al.* 2022, Hailu *et al.* 2021).

Path coefficient

Among the traits, harvest index exerted the strongest and most positive direct effect on seed yield per plant (1.071), indicating its predominant role as a direct determinant of yield (Kumar *et al.* 2023, Vij and Singh 2021) (Table 5 & 6). It was followed by biological yield per plant (0.340), which also contributed substantially and positively to seed yield. Number of seeds per pod (0.114), plant height (0.024), primary branches (0.021) and days to 50% flowering (0.011) showed relatively smaller but positive direct effects (Tengse *et al.* 2022).

The negative direct effects were observed for secondary branches (-0.117), days to maturity (-0.010), hundred seed weight (-0.032) and seeds per pod (-0.068), suggesting that their favorable

correlations with seed yield may be mediated through indirect pathways rather than direct influence (Tiwari *et al.* 2021, Singh *et al.* 2022). Days to 50% flowering exhibited negative indirect effects via BYP (-0.014) and HSW (-0.006), while maintaining positive indirect effects through HI (0.002) and SPP (0.003). Similarly, DM negatively influenced yield through SB (-0.008) and HI (-0.006), but positively through PH (0.011) and BYP (0.013) (Hailu *et al.* 2021).

Primary branches indirectly affected seed yield positively through NPP (0.017), SPP (0.012) and BYP (0.007) and negatively through HSW (-0.007) and HI (-0.006). Secondary branches, despite its negative direct effect, had positive indirect effects via PH (0.054) and HSW (0.052). PH influenced seed yield positively via BYP (0.012) and PB (0.006), though negatively through HI (-0.014) and DFF (-0.010) (Dawane *et al.* 2020). A strong positive indirect contribution was made by NPP through PB (0.092), SB (0.091) and SPP (0.085), while its negative influence came via HI (-0.040) and HSW (-0.031). SPP, though having a negative direct effect, showed positive indirect effects through HSW (0.032) and HI (0.037). HSW indirectly improved yield through DFF (0.019), SPP (0.015) and BYP (0.138). BYP, a critical component, exerted strong indirect effects via PH (0.172), NPP (0.198) and HSW (0.138), but was constrained by negative effects through DFF (-0.458) and DM (-0.429). The HI, in addition to its dominant direct role, also contributed positively through HSW (0.609) and DM (0.655), while being negatively influenced by PH (-0.641) and SPP (-0.586). The traits such as harvest index, biological yield per plant and seeds per pod emerged as key contributors to seed yield at the genotypic level, both through their direct and indirect pathways, underscoring their importance in chickpea yield improvement strategies (Kumar *et al.* 2023).

Genetic diversity

Cluster Composition

Using Mahalanobis D^2 statistics followed by Tocher's method of clustering, the 30 chickpea genotypes were grouped into five distinct clusters, indicating the presence of substantial genetic divergence [Table 7, Figure 4]. Cluster V was the largest, comprising 16 genotypes, including JG-24, ICCL-86111, PUSA-256, Digvijay and others, reflecting considerable intra-cluster variability (Kumar *et al.* 2023, Tiwari *et al.* 2021). Cluster III included six genotypes such as K-850, RSG-963 and

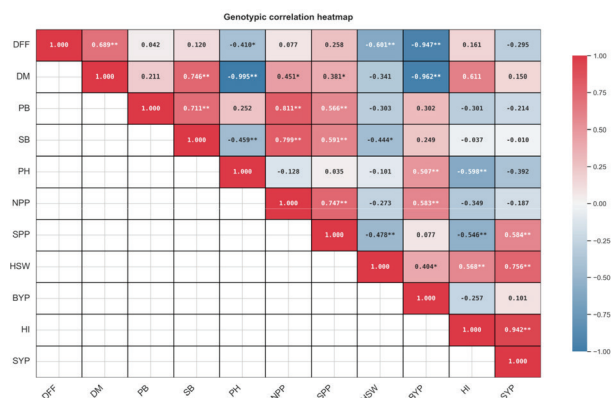


Fig. 2. Genotypic correlation heatmap of chickpea genotypes

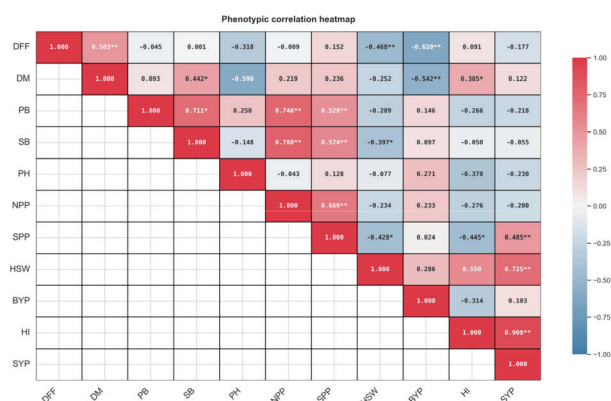


Fig. 3. Phenotypic correlation heatmap of chickpea genotypes

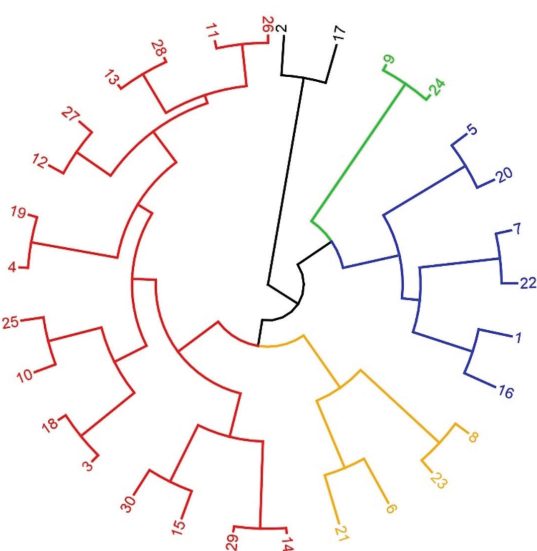


Fig. 4. Hierarchical clustering by tocher method

IPCK-28. Cluster IV was moderately sized with four genotypes, while Clusters I and II were the smallest, each consisting of two genotypes, indicating close genetic relatedness within those pairs. The genotypes grouped in solitary or small clusters suggest the presence of unique genetic backgrounds valuable for breeding programs (Hailu *et al.* 2021, Singh *et al.* 2022).

Inter and intra-cluster distance

The intra-cluster distances ranged from 2.65 to 8.70, with Cluster II (8.70) and Cluster I (6.98) showing the highest intra-cluster diversity, suggesting substantial variability within these clusters (Tiwari *et al.* 2021, Hailu *et al.* 2021). In contrast, Clusters III, IV and V had 4.56, 3.74 and 2.65 intra-cluster distances, respectively (Table 8 and Figure 5).

Regarding inter-cluster distances, the maximum genetic divergence was observed between Clusters IV and V (27.46), followed by Clusters III and V (25.13) and Clusters II and V (23.56). The minimum inter-cluster distance was between Clusters II and III (11.03) and Clusters II and IV (11.37), indicating moderate genetic relatedness among these groups (Kumar *et al.* 2023, Singh *et al.* 2022). The substantial distances between clusters suggest that crossing genotypes from distant clusters (IV and V) could result in high heterotic expression and transgressive segregants (Vij and Singh 2021, Singh *et al.* 2024).

Cluster mean

The cluster mean analysis for 11 quantitative traits revealed significant inter-cluster differences [Table 9]. Cluster V exhibited the highest values for

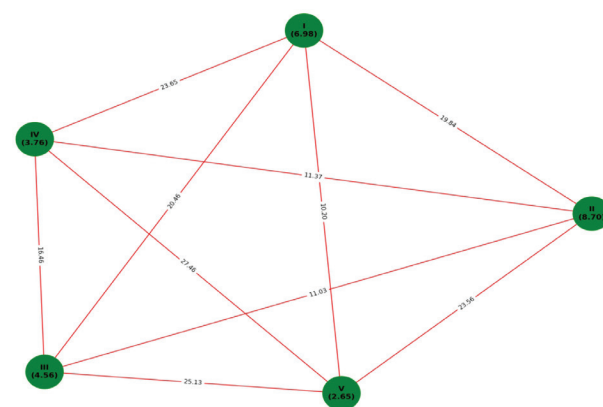


Fig. 5. Cluster distances (inter & intra) diagram of chickpea genotypes

key traits such as plant height (44.47 cm), number of pods per plant (64.13), hundred seed weight (25.33 g), harvest index (28.41%) and seed yield per plant (7.65 g), marking it as a promising source of high-yielding genotypes (Vij and Singh 2021, Kumar *et al.* 2023).

Cluster IV recorded the maximum days to 50% flowering (99.33) and days to maturity (172.67), making it suitable for long-duration types. Cluster I showed the highest biological yield per plant (30.07 g) and seed yield (7.69 g), suggesting a balance between biomass and productivity (Hailu *et al.* 2021, Praween *et al.* 2024). Conversely, Cluster III had the lowest cluster means for most traits, including hundred-seed weight (9.21 g) and seed yield per plant (5.18 g), indicating the presence of relatively low-performing genotypes. Cluster II, though small, maintained intermediate values across traits (Singh *et al.* 2022). The diversity analysis highlights wide genetic variation among the genotypes, with Cluster V emerging as the most desirable for yield attributes and Cluster IV for maturity traits. These findings can guide strategic parent selection in chickpea breeding programs aimed at combining early maturity with high yield potential (Kumar *et al.* 2023, Tiwari *et al.* 2021).

CONCLUSION

The harvest index exhibited the strongest positive direct effect on seed yield per plant, followed by biological yield, emphasizing their pivotal roles in yield determination. Genotypic correlation analyses highlighted that traits such as the number of pods per plant, seeds per pod and hundred seed weight were positively associated with seed yield, suggesting their utility as selection criteria in breeding programs. Cluster analysis using Mahalanobis D² statistics grouped the genotypes into five distinct clusters, with Cluster V comprising high-yielding genotypes characterized by superior plant height, pod number, seed weight and harvest index. These findings underscore the importance of integrating traits with strong direct and indirect effects on yield in selection strategies. For future chickpea improvement endeavors, breeders are advised to focus on genotypes exhibiting high harvest index and biological yield, coupled with favorable pod and seed characteristics, to enhance yield potential effectively.

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CONFLICT OF INTEREST

The authors declare no conflicts of interest.

Ethical issues: None

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