Journal of Animal & Plant Sciences, 35(1): 2025, Page: 221-236
ISSN (print): 1018-7081; ISSN (online): 2309-8694
https://doi.org/10.36899/JAPS.2025.1.0017

EVALUATION OF CHICKPEA (*Cicer arietinum* L.) GENOTYPES FOR GENETIC VARIABILITY AND MECHANIZATION POTENTIAL UNDER GANGETIC PLAINS

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ABSTRACT

Chickpea (*Cicer arietinum* L.), a vital pulse crop belonging to the Leguminosae family, is crucial for global food security. Urgent mechanization needs arise due to rising production costs and a workforce shift from agriculture. However, the mechanization of chickpea farming lags behind that of cereal crops, hindering its global expansion. India, with an annual production of 9.938 million tonnes, aims to enhance efficiency by developing chickpea varieties suitable for mechanized harvesting. The present study aimed to evaluate 43 chickpea genotypes for mechanical harvesting traits, yield components, and genetic diversity. Variability studies revealed ample variation, with high heritability in traits like first pod height, pods per plant, and seed index, suggesting additive gene action. Positive associations at both phenotypic and genotypic levels indicated the significance of these traits for seed yield improvement. Path analysis emphasized the positive influence of biological yield, harvest index, and first pod height on seed yield per plant. Traits such as first pod height in actual conditions, seed index, days to 50% flowering, and harvest index contributed significantly to genetic divergence. Cluster analysis identified promising genotypes (e.g., ICC 6811, ICC 13816) for hybridization, as they exhibited higher inter-cluster distances. Principal component analysis highlighted six principal components (PCs), with the PC1 and PC2 contributing the 40.7% of total variance. Promising genotypes for mechanical harvesting included ICC 12492, ICC 11627, ICC 440, ICC 2065, and ICC 1164, based on plant growth habit, plant height, first pod height, pods per plant, and seed yield. This study provides essential insights for future hybridization programs as well as trait introgression that make mechanical harvesting feasible.

Keywords: chickpea, mechanized harvesting, genetic diversity, hybridization.

INTRODUCTION

The imperative need for the mechanization of agricultural operations arises from escalating production costs and the shifting workforce dynamics, with a significant decline in agricultural employment observed globally (Anonymous, 2024). Figures from the World Bank indicate a noteworthy decrease in the agricultural workforce from 62.56% in 1991 to 41.49% in 2020 (FAO, 2023). Mechanization, by enhancing timeliness, precision in input application, and reducing input losses, contributes to increased production, productivity, and profitability in agriculture (Ramteke *et al*., 2012; Chowti and Saraswathi, 2024). Additionally, it facilitates value addition, the establishment of agro-processing enterprises, and safeguards produce from qualitative and quantitative damages (Pratap *et al*., 2016; Kuzbakova *et al*., 2022).

Chickpea (*Cicer arietinum* L.), an annual cool-season crop belonging to the Leguminosae family, holds considerable significance. Originating in the fertile crescent near Southeast Turkiye, and secondary centers in

India and Ethiopia, it has a diploid chromosome number of 2x=2n=16 and a genome size of approximately 738-Mb (Ladizinsky and Alder, 1976; Varshney *et al*., 2013; Sokolkova *et al*., 2020). India leads the world in chickpea production, contributing 65% of the global output, with Madhya Pradesh as the leading producer (FAO, 2023).

Despite its significance, the lack of mechanization remains a significant impediment to expanding chickpea cultivation in various nations (Dhimate *et al*., 2018; Singh *et al*., 2019). In India, the adoption of farm mechanization is gaining momentum to enhance productivity and reduce cultivation costs. This involves developing chickpea varieties suitable for mechanical harvesting or adapting existing equipment. The rising costs of manual harvesting and the challenges of timely labor availability further emphasize the need for mechanization in chickpea cultivation (Kouchakzadeh *et al*., 2022).

Current chickpea cultivars in India, however, fall short in terms of plant height, growth habit, and pod characteristics essential for mechanized harvesting. Literature suggests that traits like upright growth (Gaur, 2018; Dixit *et al*., 2019; Ahmad *et al*., 2023), uniform height of first pod (Kuzbakova *et al*., 2022), and strong stems are better suited for mechanization (Mewada *et al*., 2019; Patil *et al*., 2021). The creation of chickpea genotypes suited for mechanical harvesting is crucial for encouraging farmers to cultivate chickpeas. Specific chickpea genotypes exhibit plant geometries conducive to mechanized harvesting, and identifying these traits will enhance breeding programs aimed at improving yield and harvesting efficiency in mechanized agricultural systems (Munirathnam *et al*., 2015). The study aimed to evaluate chickpea genotypes for traits relevant to mechanical harvesting, yield components, and genetic diversity. The specific objectives were to assess genetic variability, heritability, and genetic advance, as well as to analyze the correlation and path coefficients among various traits, and to perform genetic divergence and principal component analysis to identify promising genotypes for breeding programs aimed at enhancing traits suitable for mechanized harvesting.

MATERIALS AND METHODS

Experimental site: The experimentation took place at an institutional 'AB' Block Farm, located in Kalyani-Simanta, Nadia, West Bengal, India. The agricultural landscape of the area corresponds to the Medium Gangetic New Alluvial plain of India. The experimental site is positioned at an altitude of 11.7 meters above Mean Sea Level (MSL), with precise geographical coordinates at 22 degrees 59 minutes 22.1 seconds North latitude and 88 degrees 25 minutes 33.3 seconds East longitude.

Climate: The region experiences a typical subtropical climate characterized by the consistent arrival of the Southwestern monsoon, typically occurring from June to October. Annual rainfall averages between 1500 mm to 2500 mm, with the majority falling during the three-month period from June to September. Various climatic variables such as maximum and minimum temperatures, relative humidity, and rainfall for the years 2021 and 2022 at the experimental site are outlined in Table 1.

Table 1: Meteorological data averaged on monthly basis recorded at the experimental site (*Rabi* 2021-22).

Month	Temperature (℃)		RH (%)		Total Rainfall (mm)	Bright Sunshine Hours
	Max.	Min.	Max.	Min.		
November	28.5	15.6	92.3	59.5	17.7	6.9
December	24.5	14.4	91.6	62.5	145.7	5.2
January	23.3	12.3	92.1	60	18.9	5.3
February	26.9	13.5	90.9	52.2	27.9	7
March	33.9	19.1	91.9	41.8	0	8.3
April	39.3	25.8	92.3	42.5	46	10

Experimental materials and method: The study was carried out during the rabi season of 2021-2022 using a randomized block design (RBD) with three replications. The biological samples comprised 43 different genotypes, including 2 control varieties, NBeG47 and Digvijay, sourced from the AICRP chickpea and ICRISAT (Table 2).

The spacing between individual plants within a row and between rows was set at 10 cm and 30 cm, respectively. The land was ploughed and levelled after harvesting of rice and divided into 86 plots, each plot of 3 rows being 4 m long. Fertilizer was applied in the ratio of 20 N: 40 P_2O_5: 20 K_2O kg/ha.

Observations Recorded: Observations were meticulously documented following the Distinctness, Uniformity, and Stability (DUS) guidelines (PPV and FRA, 2007; Sarao *et al*., 2009). For each plot in every replication, records were maintained for five randomly selected plants. Quantitative characters were comprehensively assessed, including days to 50% flowering (D50F), days to maturity (DTM), plant height

(PH), number of primary branches (PBR) and number of secondary branches (NSB), first pod height (FPH), seeds per pod (SPP), number of pods (NOP), seed index (SI), SPAD chlorophyll meter reading (SPAD), biological yield per plant (BYPP), seed yield per plant (SYPP), and harvest index (HI). Visual observations added another layer to the study, categorizing chickpea plants into five distinct forms—prostrate, spreading, semi-spreading, semi-erect, and erect based on the angle formed by the main stem (Bishnoi *et al.*, 2023). Further, the appropriateness of genotypes for mechanical harvesting and higher yield was assessed by examining traits such as plant growth habit, plant height, the height of the first pod from the ground measured both in upright condition (FPH) and actual plant growth condition (FPHAC), and seed yield per plant.

Table 2: Information regarding the genotypes used in the experiment.

Genotypes	Type	Origin	Province	Biological status
ICC 14595	Desi	India	Maharshtra	Landrace
ICC 1356	Desi	India	Uttar Pradesh	Landrace
ICC 11879	Kabuli	Turkey	Sakarya	Cultivar
ICC 8151	Kabuli	USA	-	Landrace
ICC 15518	Desi	Morocco	Fes	Breeding Line
ICC 8350	Intermediate	India	Maharastra	Landrace
ICC 18836	Kabuli	Syria	-	Unknown
ICC 15802	Kabuli	Syria	Damascus	Landrace
ICC 16261	Desi	Malawi	-	Landrace
ICC 5383	Desi	India	Bihar	Landrace
ICC 5434	Desi	India	Maharastra	Landrace
ICC 4093	Desi	Iran	Azerbaijan East	Landrace
ICC 14799	Desi	India	Uttar Pradesh	Landrace
ICC 16269	Desi	Malawi	Southern	Landrace
ICC 20265	Kabuli	Americas	-	Landrace
ICC 1098	Desi	Iran	Azerbaijan East	Landrace
ICC 5878	Desi	India	Uttar Pradesh	Landrace
ICC 708	Desi	India	Punjab	Landrace
ICC 10018	Desi	India	Odisha	Landrace
ICC 15762	Desi	Syria	Idlib	Landrace
ICC 3325	Desi	Cyprus	-	Landrace
ICC 1715	Desi	India	Uttar Pradesh	Landrace
ICC 13764	Kabuli	Iran	-	Landrace
ICC 12492	Kabuli	India	Andhra Pradesh	Breeding Line
ICC 4853	Intermediate	-	-	Intermediate
ICC 506	Desi	India	Andhra Pradesh	Landrace
ICC 8950	Desi	India	-	Landrace
ICC 12654	Desi	Ethiopia	Shewa	Landrace
ICC 1510	Desi	India	Uttar Pradesh	Landrace
ICC 12028	Desi	Mexico	-	Landrace
ICC 6811	Desi	Iran	-	Landrace
ICC 7323	Intermediate	Russian Federation	-	Landrace
ICC 11627	Desi	India	Punjab	Landrace
ICC 4918	Desi	India	Karnataka	Cultivar
ICC 1164	Desi	Nigeria	-	Landrace
ICC 2990	Desi	Iran	Hamadan	Landrace
ICC 440	Desi	India	Bihar	Landrace
ICC 15614	Desi	Tanzania	Shin Yanga	Landrace
ICC 13816	Kabuli	Russian Federation	-	Cultivar

Statistical and biometrical analysis

Genetic variation, correlation and path analysis: Analysis of variance (ANOVA) was conducted for a Randomized Complete Block Design comprising three replications. Genetic parameters were estimated following the method proposed by Johnson *et al.* (1955). Genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated according to the approach outlined by Burton and De Vane (1953). Broad-sense heritability (h^2) was estimated using the formula recommended by Hanson *et al*. (1956). Genetic advance was determined based on the method described by Johnson *et al*. (1955). Phenotypic and genotypic correlation coefficients for all pairs of ten traits were estimated as per the procedure outlined by Robinson *et al*. (1950). Path coefficient analysis was performed at the genotypic level following the methodology discussed by Dewey and Lu (1959). Path coefficient analysis involves the calculation of standardized partial regression coefficients, which allow the decomposition of correlation coefficients into direct and indirect effects of a set of independent variables on the dependent variable.

Genetic divergence- D square, PCA and cluster analysis: The dissimilarity (D^2) values between pairs of genotypes were influenced differently by the various component traits (Ryman *et al*., 2006). Each trait's relative contribution to the D^2 value was assessed and ranked on a scale from 1 to 14, corresponding to the number of traits considered in the study (14 in this case). Rank 1 indicated the trait with the greatest contribution, while Rank 14 denoted the least influential one. The frequency of each trait ranking first was tabulated, enabling the determination of its percentage contribution to the overall divergence. The analysis was performed using package 'biotools' in R (da Silva and da Silva, 2017).

Principal component analysis was carried out using the 'factoextra' package in R-Studio (Kassambara, 2016). Hierarchical clustering analysis was performed using the 'hClust' package, and intra- and inter-cluster distances were determined using the 'clv' and 'cluster' packages, following the guidelines outlined by Kassambara and Mundt (2017).

RESULTS

Analysis of variance: mean performance of genotypes and genetic variability: ANOVA revealed significant mean sum of squares for all the characters except the PBR (Table 3).

D50F ranged from 80 to 96 days, with a mean of 90.53 days. ICC 8151, ICC 16269, ICC 14799, and ICC 440 exhibited the maximum days for flowering (96 days), while Digvijay demonstrated the shortest duration (80 days). DTM varied between 119 and 132 days, with a mean of 127.34 days. The fastest maturing genotype was ICC 18836 (119 days), while ICC 4918, ICC 762, and ICC 440 required the longest time to mature (Table 4). Primary branches ranged from 2 to 5 and ICC 18836 and ICC 16261 displayed the highest PBR. Secondary branches ranged from 5.5 to 15, with ICC 20265 having the maximum and NBeG47 the minimum.

Table 3: Mean sum of squares from the analysis of variance for different character of chickpea.

Source of variation	DF	D50F	DTM	NPB	NSB	PH	FPH	FPHAC	NPP	NSPP	SI	SCMR	BYPP	SYPP	HI
Replication	2	0.41	10.46	0.42	2.35	8.21	0.22	1.41	658.71	0.35	1.10	46.07	404.73	50.88	505.59
Genotypes	42	18.17**	18.34**	0.46	5.89**	180.14**	29.51**	115.37**	2469.90**	0.28	69.01**	22.14**	1100.43**	312.24**	332.30**
Error	42	0.32	2.67	0.39	1.28	12.40	2.49	1.41	106.35	0.19	0.87	3.12	144.15	15.23	105.83

** Significant ($P \leq 0.01$); * Significant ($P \leq 0.05$).

(D50F) =Days to 50% flowering; (DTM) =Days to maturity; (NPB) = Number of Primary branches; (NSB) =Number of Secondary Branches; (PH)=Plant Height ;(FPH)=First Pod height; (FPHAC)=First Pod height in actual Condition; (NPP)=Number of pod per plant; (NSPP)=Number of seed per pod; (SI)=Seed Index; (SCMR)=SPAD Chlorophyll meter reading; (BYPP)=Biological Yield per Plant; (SY)=Seed Yield; (HI)=Harvest Index

Plant height ranged from 41 cm to 88 cm and CC 7323 attained the maximum PH while ICC 8950 exhibited the least.

Genetic variability: Different statistical methods, including the evaluation of genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV), were utilized to measure the levels of heritable and non-heritable variations present in the investigated material. The categorization of GCV% and PCV% into Low (<10%), Medium (10-20%), and High (>20%) served as a crucial indicator of the variability magnitude. Notably, all traits exhibited higher PCV values compared to GCV. Low GCV values were identified for D50F (3.30), DTM (2.20), PBR (6.94), and SPAD (5.75). Moderate GCV was observed in the SBR (17.06), PH (14.70), FPH (12.92), and number of SPP (12.47). High GCV values were detected in FPHAC (41.27), number of pods per plant (36.22), SI (23.32), BYPP (36.82), SYPP (70.64), and HI (36.61).

Low PCV values were found in D50F (3.35), DTM (2.55), and SPAD (6.63). Moderate PCV was observed in PH (15.75) and FPH (14.06). High PCV was noted in the PBR (24.16), number of secondary branches (21.29), FPHAC (41.78), number of pods per plant (37.82), NSPP (28.88), SI (23.70), BYPP (42), SYPP (74.17), and HI (50.92).

Table 4: Variability in yield and its components for chickpea genotypes under study

SL No.	Traits	Max	Min	Mean	PCV%	GCV%	Heritability (bs)	GA	GAM%
1	D50F	96.00	80.00	90.53	3.35	3.30	96.50	6.05	6.68
2	DTM	132.00	119.00	127.34	2.55	2.20	74.51	4.98	3.91
3	NPB	5.00	2.00	2.70	24.16	6.94	8.24	0.11	4.10
4	NSB	15.00	5.50	8.89	21.29	17.06	64.26	2.51	28.18
5	PH	88.00	41.00	62.30	15.75	14.70	87.12	17.61	28.26
6	FPH	36.60	18.45	28.45	14.06	12.92	84.41	6.96	24.45
7	FPHAC	33.78	2.50	18.29	41.78	41.27	97.59	15.36	83.98
8	NPP	252.50	13.00	94.90	37.82	36.22	91.74	67.83	71.47
9	NSPP	2.50	1.00	1.70	28.88	12.47	18.63	0.19	11.08
10	SI	34.90	11.20	19.90	23.70	23.32	97.50	11.87	59.64
11	SCMR	60.77	45.50	53.58	6.63	5.75	75.24	5.51	10.28
12	BYPP	126.89	17.59	59.38	42.00	36.82	76.84	39.48	66.48
13	SYPP	74.67	2.18	17.25	74.17	70.64	90.70	23.91	138.58
14	HI	74.33	7.31	29.06	50.92	36.61	51.69	15.76	54.22

(D50F) =Days to 50% flowering; (DTM) =Days to maturity; (NPB) = Number of Primary branches; (NSB) =Number of Secondary Branches; (PH)=Plant Height ;(FPH)=First Pod height; (FPHAC)=First Pod height in actual Condition; (NPP)=Number of pod per plant; (NSPP)=Number of seed per pod; (SI)=Seed Index; (SCMR)=SPAD Chlorophyll meter reading; (BYPP)=Biological Yield per Plant; (SYPP)=Seed Yield per Plant; (HI)=Harvest Index; GA=Genetic Advance; GAM= Genetic advance as percent of mean; GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient of variation.

Table 5. Visual characterization of chickpea plant habit.

ICC 14595	Spreading	ICC 1715	Semi erect
ICC 1356	Spreading	ICC 13764	Semi erect
ICC 11879	Spreading	ICC 12492	Semi erect
ICC 8151	Spreading	ICC 4853	Semi erect
ICC 15518	Spreading	ICC 506	Semi erect
ICC 8350	Spreading	ICC 8950	Semi erect
ICC 18836	Spreading	ICC 12654	Semi erect
ICC 15802	Spreading	ICC 1510	Semi erect
ICC 16261	Spreading	ICC 12028	Semi erect
ICC 5383	Spreading	ICC 6811	Semi erect
ICC 5434	Prostrate	ICC 7323	Erect
ICC 4093	Semi spreading	ICC 11627	Erect
ICC 14799	Semi spreading	ICC 4918	Erect
ICC 16269	Semi spreading	ICC 762	Erect
ICC20265	Semi spreading	ICC 2990	Erect
ICC 1098	Semi spreading	ICC 440	Erect
ICC 5878	Semi spreading	ICC 15614	Erect
ICC 708	Semi spreading	ICC 13816	Erect
ICC 10018	Semi spreading	ICC 2065	Erect
ICC 15762	Semi spreading	ICC 1164	Erect
ICC 3325	Semi spreading	NBeG47 (check)	Erect
		Digvijay (check)	Semi erect

Heritability and genetic advance: Heritability (bs), represented by H^2 (bs), serves as an index for the transmission of traits from parents to their progeny, while genetic advance (GA) informs about genetic gain following selection on specific traits, removing the influence of the environment.

The study categorized heritability (bs) into Low (<40%), Medium (40-60%), High (61-80%), and Very High (>80%). Low heritability was observed in the NPB (8.24) and number of SPP (18.63). Traits with medium heritability included HI (51.69), while high heritability values were recorded for DTM (74.51), SBR (64.23), SPADs (75.24), BYPP (76.84). Very high heritability was noted in D50F (96.5), PH (87.12), FPH (84.41), FPHAC (97.59), NPP (91.74), SI (97.5), and SYPP (90.7).

The combination of heritability (H^2bs) and genetic advance revealed significant information for the selection of superior genotypes. High genetic advance was noticed in traits such as SBR (28.18), PH (28.26), FPH (24.45), FPH in actual condition (83.98), number of pods per plant (71.47), SI (59.64), BYPP (66.48), SYPP (138.58), and HI (54.22). Moderate genetic advance was observed in the SPP (11.08) and SPADs (10.28), while low genetic advance was noticed in D50F (6.68), DTM (3.91), and PBR (4.1).

Characterization of plants: The suitability of genotypes for mechanical harvesting with higher yield was identified with the help of characters viz., plant height (PH), the height of 1st pod from the ground in both in standard measurement protocol (FPH) and actual condition of the plant (FPHAC) and seed yield per plant (SYPP). Based on the plant architecture, the genotypes were categorized as Spreading, Semi-spreading, Semi-erect or Erect. The observation on 43 chickpea genotypes is displayed in Table 5.

Height of 1st pod above the ground level: The genotypes which showed 1st pod height above or around 30 cm are- ICC 15518 (34.45cm), ICC 8350 (30.83cm), ICC 15802 (29.5 cm), ICC 4093 (30.8cm), ICC20265 (29.48 cm), ICC 3325 (31.75cm), ICC 12492 (33.12cm), ICC 8950 (29.38cm), ICC 1510 (30 cm), ICC 6811 (29.05 cm), ICC 11627 (37.65 cm), ICC 1164 (32.77 cm), ICC 440 (35.43cm), ICC 2065 (33.05cm), ICC 5434 (30.8cm), NBeG47 (31.9 cm), Digvijay (32.05cm).

Height of 1st pod in actual condition of plant: The genotypes which showed above or around 30cm FPH in actual condition are ICC 12492 (30.37cm), ICC 1164 (31.58cm), ICC 11627 (31.75cm), ICC 762 (29.34cm), ICC 440 (32.29 cm), NBeG47 (30.35 cm), Digvijay (29.75cm).

Comparison between 1st pod height and 1st pod height in actual condition of plant: An investigation into the comparison between the first pod height measured conventionally in an upright position and the first pod height under natural conditions of plant growth revealed notable disparities. The conventional method of determining first pod height by holding the plant upright may not accurately reflect the true height of the first pod above the ground. Consequently, to provide a more accurate assessment, data regarding the height of the first pod above the ground under actual growth conditions were also incorporated (Figure 1).

Seed yield/plant: Genotypes that showed maximum yield on the basis of mean data obtained like- ICC 18836, ICC 1098, ICC5878, ICC 1164, NBeG47, Digvijay, ICC 3325 were found promising.

Figure 1. Comparison between 1st pod height and 1st pod height in actual condition.

Correlation and path analysis: Correlation analysis in chickpea genotypes revealed significant associations among traits influencing SYPP (Table 6). The number of pods per plant exhibited highly significant positive correlations with seed yield per plant, emphasizing its importance in yield enhancement. BYPP and HI also showed significant positive correlations, supporting their relevance in SYPP improvement. Traits such as PBR, SBR, number of SPP, and PH demonstrated significant correlations with SYPP, indicating their potential use in indirect selection.

Table 6: Correlation Coefficient analysis of yield and its attributing characters.

		D50F	DTM	NPB	^{NS}B	PH	FPH	FPHAC	NPP	SPP	SI	SCMR	BYPP	SYPP	HI
D50F	P	1**	0.3864**	0.0637^{NS}	0.1207^{NS}	0.0228	-0.1947^{NS}	-0.1594^{NS}	0.0604^{NS}	0.0736^{NS}	-0.1623^{NS}	-0.2452*	0.0489^{NS}	-0.1391^{NS}	-0.2365*
	G	1**	0.4611**	0.2506^{NS}	0.1453^{NS}	^{NS}0.0261^{NS}	-0.2124^{NS}	-0.1626^{NS}	0.0768^{NS}	0.188^{NS}	-0.1572^{NS}	-0.2786^{NS}	0.0782^{NS}	0.1461^{NS}	-0.3342*
DTM		P	1**	0.0266^{NS}	-0.1189^{NS}	0.022^{NS}	-0.0686^{NS}	0.189^{NS}	-0.0573^{NS}	0.0098^{NS}	-0.364**	-0.2818**	-0.1922^{NS}	-0.241*	-0.2503*
		G	1**	0.1981^{NS}	-0.1549^{NS}	0.0362^{NS}	-0.0817^{NS}	0.2247^{NS}	-0.0619^{NS}	-0.0750^{NS}	-0.427**	-0.3161*	-0.3631*	-0.265^{NS}	-0.2304^{NS}
NPB			P	1**	0.1583^{NS}	0.1437^{NS}	0.0373^{NS}	-0.1139^{NS}	0.0925^{NS}	0.1158	-0.2222*	-0.1868^{NS}	0.1902^{NS}	0.2137*	0.0449
			G	1**	0.3018*	0.6922**	0.5508**	-0.3397*	0.1342^{NS}	^{NS}2.6697**	-0.8452**	-0.7338**	0.6402**	0.6655**	^{NS}0.0048^{NS}
^{NS}B				P	1**	0.1444	0.019^{NS}	-0.2353*	0.4385**	-0.0049	-0.0716^{NS}	0.0886^{NS}	0.2758*	0.2843**	0.133^{NS}
				G	1**	^{NS}0.1838^{NS}	0.0099^{NS}	-0.2634^{NS}	0.5354**	^{NS}0.3547*	-0.113^{NS}	0.1275^{NS}	0.4295**	0.2869^{NS}	-0.0133^{NS}
PH					P	1**	0.8896**	0.4027**	0.1876^{NS}	-0.1057^{NS}	0.0866^{NS}	0.0068^{NS}	0.4246**	0.2572*	-0.0616^{NS}
					G	1**	0.9268**	0.4128**					0.5071**	0.278^{NS}	
									0.206^{NS}	-0.2699^{NS}	0.0806^{NS}	-0.037^{NS}			-0.0855^{NS}
FPH						P	1**	0.4844**	0.184^{NS}	-0.0797^{NS}	0.1591 ^{NS}	0.1135^{NS}	0.3846**	0.3124**	0.0189^{NS}
						G	1**	0.5056**	0.2258^{NS}	-0.1899^{NS}	0.1694^{NS}	0.0894^{NS}	0.4316**	0.3422*	0.0937^{NS}
FPHAC							P	1**	0.1309	-0.058^{NS}	-0.0002^{NS}	-0.013^{NS}	-0.1315^{NS}	0.1627^{NS}	0.214*
							G	1**	^{NS}0.1406^{NS}	-0.1764^{NS}	0.0011^{NS}	-0.0514^{NS}	-0.1779^{NS}	0.1753^{NS}	0.3351*
NPP								P	1**	0.0938^{NS}	-0.0464^{NS}	0.0554^{NS}	0.4558**	0.6369**	0.3549**
								G	1**	0.3777*	-0.0577^{NS}	0.0423^{NS}	0.5449**	0.6547**	0.4062**
^{NS}PP									P	1**	-0.3426**	0.0017^{NS}	-0.0026^{NS}	0.1299^{NS}	0.0557^{NS}
									G	1**	-0.8176**	0.0995^{NS}	-0.2172^{NS}	0.3574*	0.3908**
SI										P	1**	0.3285*	0.2208^{NS}	0.0507^{NS}	0.0228^{NS}
										G	1**	0.3285*	0.2208^{NS}	0.0507^{NS}	0.0228^{NS}
SCMR											P	1**	0.1052^{NS}	0.0436^{NS}	0.0397^{NS}
											G	1**	0.1161^{NS}	0.0156^{NS}	0.0552^{NS}
BYPP												P	1**	0.6111**	0.0119
												G	1**	0.7402**	^{NS}0.334*
SYPP													P	1**	0.7303**
													G	1**	0.8487**
HI														P	1**
														G	1**

*Significant at 5% probability level, ** highly significant at 1% probability level.

D50F showed positive genotypic correlations with BYPP, PH, and FPH, while SPAD chlorophyll meter value exhibited a negative correlation. DTM displayed negative correlations with SI and SPAD chlorophyll meter value. NPB showed significant negative correlations with SI and highly significant positive genotypic correlations with various traits, including PH and BYPP. SB displayed highly significant positive correlations with NPP and BYPP.

PH exhibited significant positive correlations with FPH, BYPP, and NPP. FPH showed significant positive correlations with FPH in actual condition, BYPP, and PH. NPP demonstrated highly significant positive correlations with BYPP, HI, and secondary branches, and a significant positive genotypic correlation with SPP. NSPP displayed highly significant negative correlations with SI and significant positive genotypic correlations with HI and primary branches. SI exhibited significant positive correlations with SPAD chlorophyll value and highly significant negative correlations with DTM, SI, and PBR at the genotypic level. SPAD showed significant negative correlations with DTM and NPB, along with significant positive correlations with SI.

BYPP displayed highly significant positive correlations with PH, FPH, NPP, and a significant positive genotypic correlation with primary branches. HI showed highly positive correlations with NPP and SYPP, along with significant negative correlations with D50F and DTM.

Path Coefficient analysis

Direct Effects of Component Traits: Favorable direct effects on SYPP were observed for traits including DTM, NPB, NSB, FPH, FPHAC, NPP, NSPP, BYPP, and HI. Notably, HI, BYPP, FPH and NPP exhibited the strongest positive direct effects, underscoring their importance in enhancing SYPP. Conversely, negative direct effects were observed for D50F, PH, SI, and SPADs.

Indirect Effects of Component Traits: Positive and negative indirect effects were identified among various traits influencing SYPP in chickpea. For instance, D50F exhibited positive indirect effects through DTM, primary branches, secondary branches, NPP, NSPP, SI, SPAD, and BYPP, while showing negative indirect effects via PH, FPH, FPH in actual condition, and HI. Other traits, such as DTM, PBR, SBR, PH, FPH, FPH in actual condition, NPP, NSPP, SI, SPAD, BYPP, and HI, displayed intricate patterns of positive and negative indirect effects through different combinations of traits.

Table 7: Phenotypic path coefficient analysis for yield and its component characters in chickpea

	D50F	**DTM**	**NPB**	**NSB**	**PH**	**FPH**	**FPHAC**	**NPP**	**NSPP**	**SI**	**SCMR**	**BYPP**	**HI**
D50F	-0.00640	0.00782	0.00425	0.00234	-0.00310	-0.03346	-0.00957	0.00779	0.00547	0.00236	0.01092	0.02614	-0.15364
DTM	-0.00248	0.02024	0.00177	-0.00231	-0.00299	-0.01179	0.01134	-0.00739	0.00074	0.00529	0.01255	-0.10338	-0.16261
NPB	-0.00041	0.00053	0.06702	0.00307	-0.01954	0.00638	-0.00684	0.01194	0.00848	0.00323	0.00832	0.10235	0.02917
NSB	-0.00077	-0.00241	0.01061	0.01939	-0.01962	0.00327	-0.01413	0.05653	-0.00040	0.00104	-0.00394	0.14834	0.08640
PH	-0.00015	0.00045	0.00964	0.00280	-0.13590	0.15289	0.02418	0.02418	-0.00778	-0.00126	-0.00030	0.22837	-0.04002
FPH	0.00125	-0.00139	0.00249	0.00037	-0.12089	0.17188	0.02909	0.02372	-0.00588	-0.00231	-0.00506	0.20686	0.01228
FPHAC	0.00102	0.00382	-0.00763	-0.00456	-0.05473	0.08324	0.06006	0.01687	-0.00427	0.00000	0.00058	-0.07073	0.13903
NPP	-0.00039	-0.00116	0.00621	0.00850	-0.02550	0.03163	0.00786	0.12891	0.00691	0.00067	-0.00247	0.24515	0.23056
NSPP	-0.00048	0.00020	0.00771	-0.00010	0.01435	-0.01372	-0.00348	0.01209	0.07364	0.00497	-0.00008	-0.00134	0.03612
SI	0.00104	-0.00737	-0.01490	-0.00139	-0.01177	0.02736	-0.00001	-0.00598	-0.02523	-0.01453	-0.01309	0.10273	0.01533
SCMR	0.00157	-0.00570	-0.01252	0.00172	-0.00092	0.01951	-0.00078	0.00714	0.00013	-0.00427	-0.04454	0.05658	0.02579
BYPP	-0.00031	-0.00389	0.01275	0.00535	-0.05770	0.06610	-0.00790	0.05876	-0.00018	-0.00277	-0.00469	0.53785	0.00773
HI	0.00151	-0.00507	0.00301	0.00258	0.00837	0.00325	0.01285	0.04575	0.00410	-0.00034	-0.00177	0.00640	0.64966

Residual- 0.0635 (Diagonal value represents direct effect on seed yield/plant.)

Table 8: Genotypic path coefficient analysis for yield and its component characters in chickpea

	D50F	**DTM**	**NPB**	**NSB**	**PH**	**FPH**	**FPHAC**	**NPP**	**NSPP**	**SI**	**SCMR**	**BYPP**	**HI**
D50F	-0.01679	0.08508	0.02609	0.06087	-0.06111	-0.29374	-0.13985	-0.04068	0.00061	0.00341	0.03229	0.07032	-0.06075
DTM	-0.00774	0.18453	0.02063	-0.0649	-0.08481	-0.11298	0.19327	0.03278	-0.00023	0.00927	0.03663	-0.32643	-0.11041
NPB	-0.00421	0.03655	0.10412	0.12645	-1.62068	0.76161	-0.29225	-0.0711	0.00872	0.01835	0.08505	0.57551	0.27664
NSB	-0.00244	-0.02858	0.03142	0.41902	-0.43036	0.01365	-0.2266	-0.2837	0.00116	0.00245	-0.01478	0.38613	0.11929
PH	-0.00044	0.00668	0.07207	0.07702	-2.34144	1.28157	0.35512	-0.10916	-0.00088	-0.00175	0.00429	0.45585	0.11555
FPH	0.00357	-0.01508	0.05735	0.00414	-2.16998	1.38284	0.43492	-0.11966	-0.00062	-0.00368	-0.01036	0.38802	0.14225
FPHAC	0.00273	0.04146	-0.03537	-0.11037	-0.96655	0.69911	0.86027	-0.07451	-0.00058	-0.00002	0.00595	-0.15992	0.07289
NPP	-0.00129	-0.01141	0.01397	0.22435	-0.48236	0.31229	0.12097	-0.52987	0.00123	0.00125	-0.0049	0.48983	0.27217
NSPP	-0.00316	-0.01302	0.27797	0.14862	0.63205	-0.26263	-0.15175	-0.2001	0.00327	0.01775	-0.01153	-0.19523	0.14858
SI	0.00264	-0.0788	-0.088	-0.04734	-0.18867	0.23432	0.00097	0.03057	-0.00267	-0.02171	-0.03807	0.19851	0.02109
SCMR	0.00468	-0.05832	-0.07641	0.05343	0.08666	0.12361	-0.04418	-0.02241	0.00033	-0.00713	-0.1159	0.10438	0.0065
BYPP	-0.00131	-0.067	0.06665	0.17997	-1.18723	0.59685	-0.15303	-0.2887	-0.00071	-0.00479	-0.01346	0.89901	0.3077
HI	0.00245	-0.04901	0.06929	0.12024	-0.65083	0.47319	0.15083	-0.34691	0.00117	-0.0011	-0.00181	0.66543	0.41571

Residual - -0.0083 (Diagonal value represents direct effect on seed yield/plant.)

Favorable direct effects on SYPP were observed for DTM, PBR, NSB, FPH, FPH in actual condition, NSPP, BYPP, and HI. Notably, FPH, HI, BYPP, and FPH in actual condition exhibited the strongest positive direct effects. Negative direct effects were noted for D50F, PH, NPP, SI, and SPAD.

Genetic Divergence: The contribution of characters to genetic divergence was assessed using D square analysis, revealing that certain traits significantly impact diversity (Table 9). FPH in actual condition exhibited the highest contribution (31%) to genetic divergence, followed by SI (23%), D50F (15.5%), HI (8.6%), and NPP (6.6%). Further, other characters with varying contributions were BYPP, DTM, SPAD, PH, SYPP, SBR, SPP, FPH.

Cluster analysis: Cluster analysis groups genotypes based on similarity, forming distinct clusters with related genotypes. The distance between clusters reflects their dissimilarity, with greater distances indicating higher variability. The 43 genotypes were grouped into four clusters: Cluster I (22 genotypes), Cluster II (13 genotypes), Cluster III (7 genotypes), and Cluster IV (1 genotype) (Table 10, Figure 2). The clustering pattern indicates substantial variability in the study population, enhancing the potential for diverse genetic traits.

Intra-Cluster and Inter-Cluster Distances: Maximum intra-cluster distance observed in Cluster II (5.035), followed by Cluster III (4.906), and Cluster I (3.694). Cluster IV has an intra-cluster distance of ‘0’ due to having only one genotype. Highest inter-cluster distance between Cluster I and Cluster IV (9.6319), followed by Cluster III and Cluster IV (9.0816), and others. Maximum genetic diversity is noted between Cluster I and Cluster IV, while Cluster I and Cluster II show lesser genetic diversity (Table 11).

Cluster Mean for Component Characters: In the case of D50F, it was observed that Cluster II demonstrated the highest mean duration of 91.6 days, while Cluster III and IV followed closely behind. Cluster I, however, exhibited the shortest mean duration of flowering. Conversely, in the examination of DTM, Cluster II showcased the highest mean duration of 129.7 days, with Clusters III and IV trailing behind, and Cluster I exhibiting the shortest duration. Similar analyses were conducted for other traits including PBR, SBR, PH, FPH, SPP, SI, SPAD, BYPP, SYPP, and harvest index (Table 12).

Principal Component Analysis (PCA) is a statistical technique that efficiently examines and summaries information in large data tables. In our study, PCA was applied to understand how 14 traits contributed to the overall variability among 43 genotypes.

PCA components and variance: The Scree plot (Fig 3) illustrated the percentage of variation by each Principal Component (PC). PC1 exhibited the highest variability (24.45%) with the highest Eigenvalue. The first six components contribute approximately 81.86% of the total variance. The six components (PC1 to PC6) and their respective contributions are as follows: PC1 (24.45%), PC2 (16.29%), PC3 (14.47%), PC4 (11.33%), PC5 (8.35%), and PC6 (7.86%).

Table 9: Contribution of different characters towards genetic divergence.

SL No.	Characters	Contribution towards divergence (%)
1	First pod height in actual condition	31
2	Seen index	23
3	Days to fifty percent flowering	15.5
4	Harvest index	8.6
5	NPP	6.6
6	Biological yield/plant	3.3
7	Days to maturity	2.3
8	SPAD chlorophyll meter reading	2.1
9	Plant height	2
10	Seed yield/plant	1.9
11	Number of secondary branches	1.1
12	Seed per pod	1
13	First pod height	1
14	Number of primary branches	0.6

Table 10. Distribution of genotypes in different clusters

Clusters	Number of genotypes	Genotypes
1	22	ICC 6811, ICC13816, ICC10018, ICC15762, ICC15802, ICC 708, ICC 1356, ICC12028, ICC 7323, ICC2990, ICC762, ICC14595, ICC 1715, ICC14799, ICC8950, ICC12654, ICC15614, ICC4853, ICC506, ICC16269, ICC13764, ICC 4918
1l	13	ICC 18836, ICC 16261, ICC 4093, ICC 1098, ICC 5878, ICC15518, ICC 8350, ICC 8151, ICC11879, ICC 5383, ICC 20265, ICC 3325, ICC 1510
1l1	7	NBeG47(Check), DIGVIJAY(Check), ICC 11627, ICC 2065, ICC 440, ICC 12492, ICC 1164
IV	1	ICC 5434

Table 11. Intra and inter cluster distances

Cluster	I	II	III	IV	No. of Genotypes	Name of Genotypes
L	3.69	5.09	5.44	9.63	22	ICC6811, ICC13816, ICC10018, ICC15762, ICC15802, ICC 708, ICC 1356, ICC12028, ICC 7323, ICC2990, ICC762, ICC14595, ICC1715, ICC14799, ICC8950, ICC12654, ICC15614, ICC4853, ICC506, ICC16269, ICC13764, ICC4918
Ll		5.03	5.97	8.84	13	ICC18836, ICC16261, ICC4093, ICC1098, ICC 5878, ICC15518, ICC8350, ICC8151, ICC11879, ICC5383, ICC20265, ICC3325, ICC1510
Lll			4.90	9.08	7	NBeG47(Ch), Digvijay (Ch), ICC11627, ICC 2065, ICC440, ICC12492, ICC1164
Lv				0	1	ICC5434

Table 12. Cluster means of different traits.

Cluster	D50F	DTM	NPB	NSB	PH	FPH	FPHAC	NPP	NSPP	SI	SCMR	BYPP	SYPP	HI
l	87.667	123.833	2.917	9.196	63.165	30.636	21.850	126.258	1.958	21.238	53.947	78.762	40.144	50.560
ll	91.600	129.700	2.766	8.118	78.464	34.404	30.836	82.250	1.500	20.915	53.553	57.727	14.622	25.770
lll	91.182	128.432	2.712	8.424	56.997	26.286	16.527	84.420	1.841	17.256	53.244	45.952	11.410	26.343
lV	90.300	125.900	2.533	10.155	65.395	28.940	13.767	105.475	1.350	24.433	54.133	78.158	17.681	23.802

Principal Component Analysis

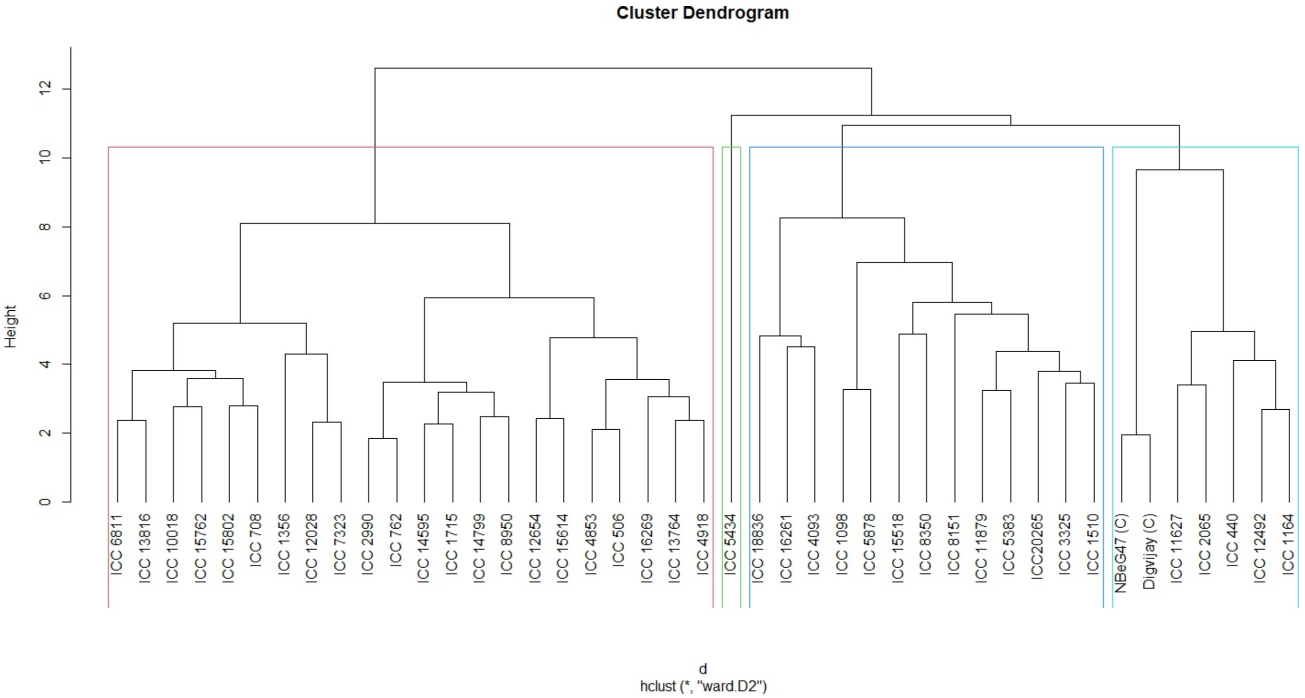

Figure 2. Cluster dendrogram displaying relationship between the species

Traits contribution to different PCs: Under PC1, SYPP, BYPP, NPP, FPH, PH, HI, and others contributed significantly to the variability. Similarly, SI, SPP, PBR, D50F, SPAD, DTM, and others had substantially contributed to PC2. In PC3, PH, DTM, FPH, FPHAC, HI, SPAD, and others showed prominent contributions. Further, in PC4, HI, FPHAC, SBR, D50F, SI, and others contributed maximally (Table 13).

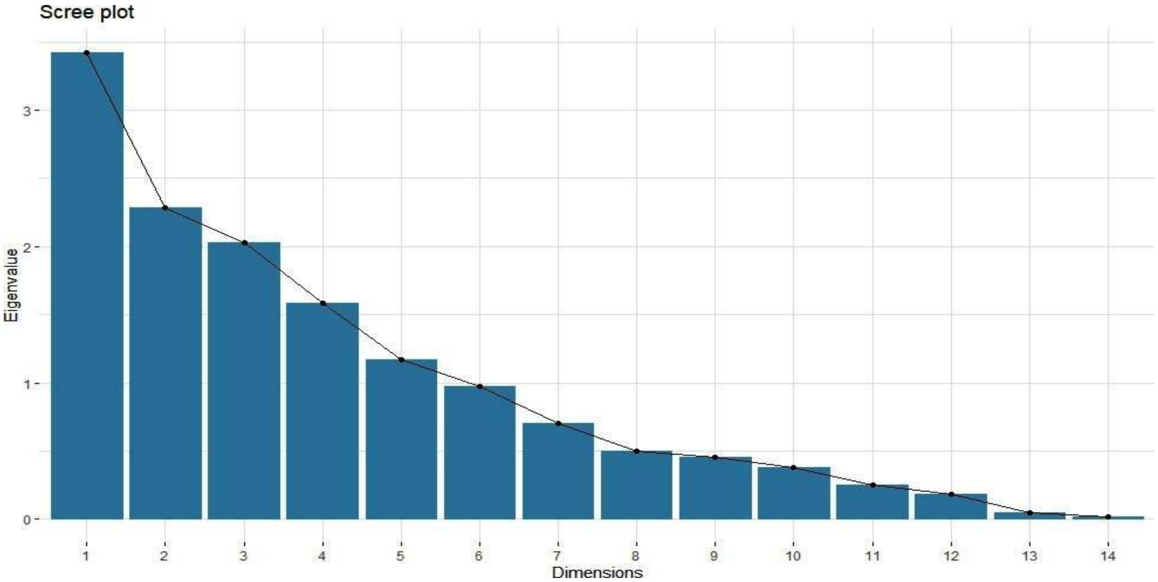

Figure 3. Scree plot from PCA analysis

Table 13. Importance of different components

Components	Eigen values	% of variance	Cumulative % of variance	Standard deviation
1	3.424	24.457	24.457	1.850
2	2.281	16.294	40.752	1.510
3	2.027	14.478	55.231	1.423
4	1.586	11.331	66.563	1.259
5	1.170	8.357	74.920	1.081
6	0.972	6.943	81.864	0.985
7	0.700	5.031	86.895	0.839
8	0.498	3.561	90.457	0.703
9	0.456	3.263	93.720	0.675
10	0.375	2.678	96.399	0.612
11	0.252	1.806	98.206	0.502
12	0.183	1.323	99.529	0.430
13	0.045	0.325	99.855	0.213
14	0.020	0.144	100.000	0.142

The results emphasize that traits related to yield (SYPP, BYPP, NPP) contributed the most to the variance in PC1. Hence, the genotypes belonging to PC1 are crucial for selection in chickpea breeding programs, particularly for yield improvement (Table 14). This aligns with findings from Jha *et al*. (2015).

In the PCA Biplot (Figure 4), PC1 and PC2 contributed the most to the total variability among the 14 components. The plot illustrates the relationship between these two principal components and their connection with other genotypes and variables. Genotypes situated close to the origin represent average values, closely associated genotypes are similar, while dissimilar genotypes are positioned further apart. Variables with minimal contribution are situated close to the X and Y axes, while variables with significant contributions are positioned farther from the axes for both PC1 and PC2. The angle formed between the lines of variables indicates their correlation, with a smaller angle signifying a stronger correlation. Diagonally opposite variables are negatively correlated with each other.

The examination of Principal components revealed distinct genotype contributions, elucidating pivotal associations within the dataset. Notably, ICC 1164, ICC 15518, and ICC 20265 emerged as prominent contributors to Principal Component 1, signifying their substantial influence on the underlying variability captured by this component (Table 15). Similarly, Principal Component 2 exhibited significant contributions from Digvijay (Check), ICC 1164, and NBeG47 (Check), suggesting their noteworthy roles in delineating the variation encapsulated within this dimension. Furthermore, Principal Component 3 showcased discernible contributions from ICC 2990, ICC 7323, and ICC 13764, underscoring their relevance in delineating additional variability within the dataset.

Table 14. Different traits contribution in different PCs in descending order.

	PC1	PC2	PC3	PC4	PC5	PC6
Traits	SYPP	SI	PH	HI	NPB	SPAD
	BYPP	NSPP	DTM	FPHAC	D50F	NSPP
	NPP	NPB	FPH	BYPP	NSPP	NSB
	FPH	D50F	FPHAC	NSB	NPP	NPB
	PH	SPAD	HI	D50F	DTM	SI
	HI	DTM	SPAD	SI	FPH	NPP
	NSB	NSB	D50F	NSPP	HI	BYPP
	DTM	FPH	NSB	SYPP	FPHAC	SYPP
	NPB	NPP	SYPP	PH	NSB	FPHAC
	FPHAC	FPHAC	SI	SPAD	PH	HI
	D50F	SYPP	NSPP	DTM	SPAD	DTM
	SI	PH	NPB	NPB	SI	FPH
	SPAD	BYPP	NPP	FPH	SYPP	PH
	NSPP	HI	BYPP	NPP	BYPP	D50F

Table 15. Principal components individual contribution- Top 3 genotypes.

Principal Components	Genotypes
1	ICC 1164, ICC 15518, ICC 20265
2	Digvijay (Check), ICC 1164, NBeG47(Check)
3	ICC 2990, ICC 7323, ICC 13764
4	ICC 8151, ICC 15518, NBeG47(Ch)
5	ICC 18836, ICC 5434, ICC 16261
6	ICC 8350, ICC 18836, ICC 11879

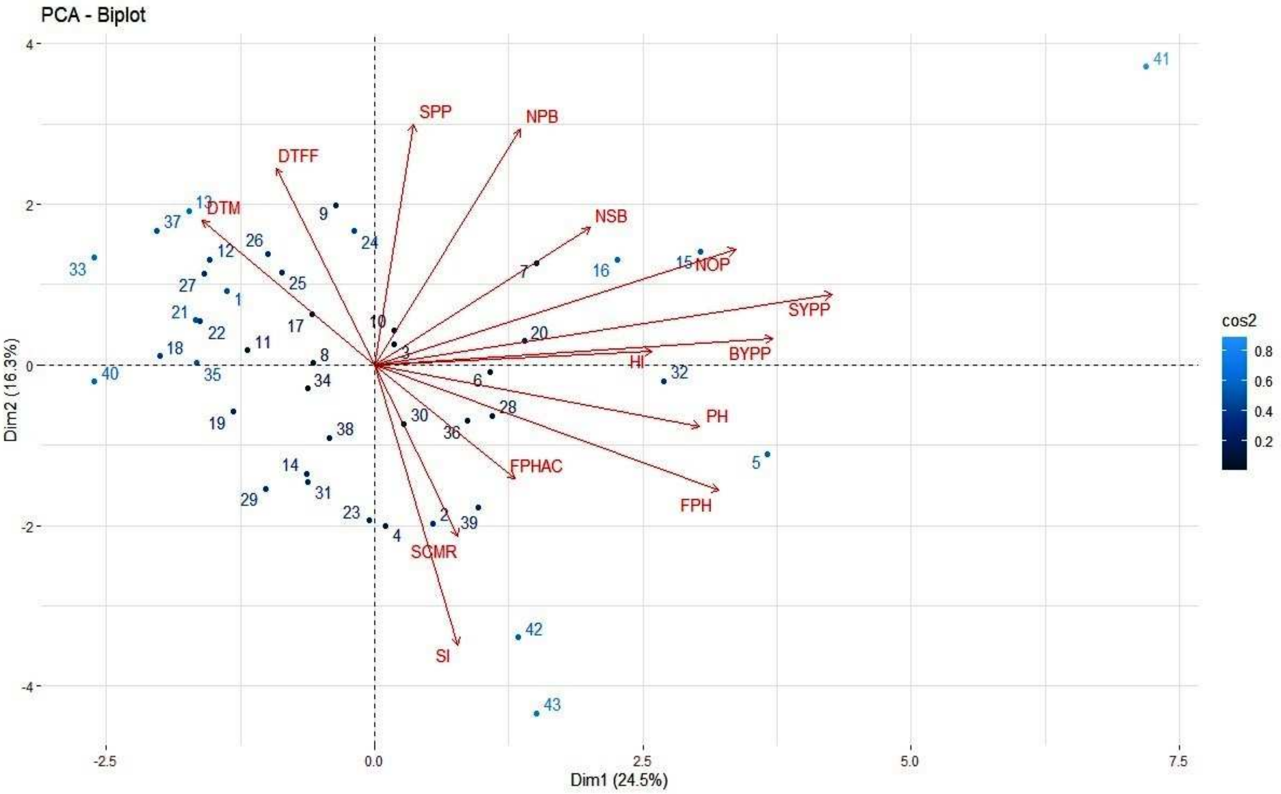

Figure 4. PCA biplot

DISCUSSION

The present experiment focused on the genetic study of chickpea to identify genotypes suitable for mechanical harvesting and exhibit higher yield. Analysis of variance revealed significant mean sum of squares for all the characters except the PBR. This suggests the presence of ample variability among the genotypes. For suitability of mechanical harvesting, observations indicate that the disparity between the measured first pod height and the height of the first pod under natural conditions is particularly pronounced in spreading-type genotypes. Conversely, this disparity is relatively comparable across erect-type genotypes. The maximum difference was observed between ICC 5434 (27.92 cm) whereas minimum in NBeG47.

Low GCV recorded for D50F and DTM were also reported by Takkuri *et al*. (2017). Moderate GCV for FPH found by Jayalakshmi *et al*. (2020). High PCV for seed yield per plant and number of pods per plant were also reported by Kanouni (2016), Chopdar *et al*. (2017), Akansha *et al*. (2017), and Raju and Lal (2021). Hotti and Sadhukhan (2018) observed analogous results for SYPP and SI, while Yadav *et al*. (2015) reported similarities for the PBR, NSB, NPP, and SI. Consistent findings for both high GCV and PCV were observed by Akansha *et al*. (2017) for the NPP and SYPP, Raju and Lal (2021) for SYPP and SI, and Datta *et al*. (2023) for BYPP, SI, and HI.

High heritability coupled with high genetic advance was found for FPHAC and NPP, PH, BYPP. High heritability for PH and D50F has been reported by Zali *et al*. (2011), and for SYPP by Gul *et al*. (2013) and Meena *et al*. (2014). High genetic advance values suggest the predominance of additive genes, making selection effective, as opposed to traits with low genetic advance, which are highly influenced by the environment and governed through non-additive gene action. Careful consideration of both heritability and genetic advance is essential for effective selection and improvement in chickpea traits. Further, examination of correlations among yield attributes highlighted significant associations. Path analysis under-scored the importance of traits like HI, BYPP, and FPH, suggesting their major contribution to yield enhancement. The indirect effect of component traits at genotypic level was comparable to phenotypic path analysis with slight variations in magnitudes. The low residual effect indicated that the essential independent variables were included in the analysis, signifying their responsibility for SYPP. Similar findings have been reported in literature (Babbar *et al*., 2015; Mewada *et al*., 2019), reinforcing the importance of traits like BYPP and HI for selection for seed yield in chickpea.

Genetic diversity, assessed through clustering, reveals distinct groups of genotypes. The choice of parents for future breeding programs should consider genetic distance, with genotypes from different clusters offering potential for creating robust genotypes with a broad genetic base. Based on cluster analysis, genotypes from Cluster I (e.g., ICC 6811, ICC 13816) can be prioritized for yield improvement. For the development of varieties suitable for mechanical harvesting, genotypes from Cluster II (e.g., ICC 18836, ICC 16261) with high mean values for FPH are recommended (Figure 2).

Conclusion: The research offers several avenues for future exploration, particularly in enhancing mechanical harvesting efficiency. Promising genotypes (ICC 1164, ICC 15518, ICC 20265) identified in this study can be further developed to improve their suitability for mechanical harvesting. Expanding the genotype pool will enhance the robustness of these findings. Developing markers for traits associated with mechanical harvestability, based on the promising genotypes from this study, will facilitate targeted breeding efforts. Future research should also explore additional physiological parameters and root architecture studies that are essential for creating new varieties optimized for machine harvesting.

Acknowledgements: The study was funded by Researchers Supporting Project number (RSPD2025R749), King Saud University, Riyadh, Saudi Arabia. The authors are thankful for the funds provided.

Author Contributions: Conceptualization- R.S., and M.H.; methodology- R.S. and P.K.S.; software and formal analysis- A.P.S.; S.M.;F.H.; investigation- S.M., H.K.S. and G.V.K..; resources, R.S.;A.M.; funding- W.E and Y.T. data curation; writing—original draft preparation- A.P.S.; writing—review and editing, P.K.S., R.S., W.E., Y.T., S.R.; all authors have read and agreed to this version of the manuscript.

Data Availability Statement: The authors confirm that the data supporting the findings of this study are available within the article.

Conflicts of Interest: The authors declare no conflicts of interest.

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