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VARIABILITY ANALYSIS, HERITABILITY, GENETIC ADVANCE AND CORRELATION AMONG 30 ELITE GENOTYPES OF CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

Chickpea (*Cicer arietinum L.*) is a vital legume globally, yet restricted genetic diversity and environmental stresses limit its yield. This study assesses the genetic variability, heritability, genetic advance, and correlation among 30 elite chickpea genotypes during the Rabi season of 2022-23 at ITM University, Gwalior. The genotypes were evaluated in a Randomized Block Design (RBD) with three replications to analyze traits such as days to 50% flowering, plant height, number of pods per plant, 100-seed weight, and yield per plant. Statistical analysis, including ANOVA, revealed significant differences among the genotypes. High heritability coupled with genetic advance was observed for traits like days to 50% flowering and number of pods per plant, indicating strong potential for selection. Correlation analysis highlighted positive relationships between early flowering and yield components like pod number, while a negative correlation was noted with seed weight. These findings suggest that genotypes with early flowering and a higher number of pods should be prioritized in breeding programs aimed at improving yield potential and adaptability to different environments.

***Keywords* :** Chickpea, Genetic variability, Heritability, Genetic advance, Correlation analysis

Introduction

Chickpea (*Cicer arietinum* L.) is the third most important pulse crop globally, with India being the largest producer, accounting for approximately 70 percent of global production. Despite its prominence, the productivity of chickpea is constrained by its narrow genetic variability, susceptibility to diseases, and environmental stress factors such as drought and heat. The success of any crop improvement program depends largely on the extent of genetic variability available in the germplasm. Genetic variability, heritability, and genetic advance are crucial for understanding the potential for selection and breeding.

In recent years, researchers have focused on identifying key traits contributing to yield, such as flowering time, pod number and seed weight, as these traits are influenced by both genetic and environmental factors. Heritability, coupled with genetic advance, provides insights into the potential genetic gain from selection. This study aims to assess genetic variability, heritability, genetic advance and correlation among 30 elite chickpea genotypes to identify traits that can be exploited to enhance yield and adaptability. The objectives of the study are as follows: To assess genetic variability among 30 chickpea genotypes, to evaluate heritability and genetic advance, to analyze the correlation coefficients between key traits contributing to yield.

Materials and Methods

The experiment was conducted at the Crop Research Centre, School of Agriculture, ITM University, Gwalior, during the *Rabi* 2022-23. Gwalior, situated in the central region of India, experiences a subtropical climate with hot summers and cold winters. The experimental soil was sandy loam, suitable for chickpea cultivation.

The experiment was laid out in a Randomized Block Design (RBD) with three replications. A total of 30 elite chickpea genotypes were evaluated. Each genotype was sown with a spacing of 30 cm between rows and 10 cm between plants, covering a net plot area of 405 m². Recommended agronomic practices, including NPK application at 20:40:40, were followed. The analysis for the undertaken research was based on the 11 key characters such as days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield, and yield per plant were recorded from five randomly selected plants per plot.

The data was subjected to Analysis of Variance (ANOVA) to test the significance of differences among genotypes. Variability parameters, including Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability, and genetic advance, were estimated using standard formulas (Burton and De Vane, 1953). Correlation coefficient was calculated to determine the relationship between traits contributing to yield.

Results

Significant differences ($p < 0.01$) were observed among the genotypes for most of the traits studied, indicating substantial genetic variability. The highest variability was recorded for days to 50% flowering, number of pods per plant, and 100-seed weight. Traits such as plant height and days to maturity exhibited moderate variability, while traits like pod length and number of seeds per pod showed lower variability (Table 1)

Coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated for all traits (Table 2). PCV values were generally higher than GCV, indicating environmental influence on trait expression. However, traits like the number of pods per plant and 100-seed weight exhibited high GCV and PCV, suggesting strong genetic control.

Heritability and Genetic Advance

Heritability estimates ranged from 63.12% (number of seeds per pod) to 99.11% (number of pods per plant) (Table 3). High heritability for traits such as days to flowering and number of pods per plant indicates that these traits are predominantly controlled by genetic factors. The genetic advance (GA) was highest for the number of pods per plant (45.23), indicating a high potential for improvement through selection.

Correlation Analysis

Correlation analysis was performed to determine the relationship between yield and other traits at both the genotypic and phenotypic levels. This analysis helps to identify the traits that significantly contribute to yield and can be used as selection criteria in breeding programs.

Genotypic Correlation Coefficients

The genotypic correlation coefficients provide insights into the genetic relationships between traits, excluding environmental influences. High genotypic correlations indicate that selection based on one trait will likely improve the correlated trait (Table 5)

The number of pods per plant showed a strong positive genotypic correlation with yield per plant ($r = 0.89$), indicating that selecting genotypes with more pods will likely result in higher yield. Days to 50% flowering had a moderate positive correlation with yield ($r = 0.42$) and number of pods per plant ($r = 0.54$). This suggests that early-flowering genotypes tend to produce more pods and higher yields. A negative correlation was observed between 100-seed weight and days to 50% flowering ($r = -0.34$), implying that early-flowering genotypes might have lighter seeds.

Phenotypic Correlation Coefficients

The phenotypic correlation coefficients include both genetic and environmental influences, offering a broader view of trait interactions as they appear in the field (Table 4)

At the phenotypic level, the number of pods per plant also showed a strong positive correlation with yield per plant ($r = 0.83$), although slightly lower than the genotypic correlation. Days to 50% flowering exhibited a moderate positive phenotypic correlation with yield per plant ($r = 0.38$) and number of pods per plant ($r = 0.46$), similar to genotypic correlations. A negative phenotypic correlation was observed between 100-seed weight and days to 50% flowering ($r = -0.29$), implying that earlier-flowering genotypes might have lower seed weight.

Discussion

Genetic Variability

The significant variation observed among the 30 chickpea genotypes for all traits suggests the presence of substantial genetic diversity within the population. This diversity provides a strong foundation for breeding programs aimed at improving specific traits. Days to 50% flowering showed considerable variability, which is crucial for selecting early-flowering genotypes that can escape drought conditions. The variability in plant height, number of pods per plant, and yield per plant was also substantial, which is important for yield improvement efforts. The high mean sum of squares for number of pods per plant (1452.15) and yield per plant (9.05) indicates that these traits exhibit substantial genetic variability, making them ideal candidates for selection in breeding programs. These results are consistent with previous findings by Singh *et al.* (2021), who also reported significant variability for days to flowering, plant height, and number of pods in chickpea. The broad variability observed in this study provides a valuable genetic base for future improvement efforts, aligning with findings from studies such as Malik *et al.* (2014).

Coefficients of Variation (GCV, PCV, ECV)

The estimates of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) provide insights into the extent of genetic and environmental influences on trait expression. Number of pods per plant had the highest GCV (39.25%) and PCV (39.31%), indicating strong genetic control and minimal environmental influence on this trait. This suggests that the number of pods is a stable trait that can be effectively improved through selection. For 100-seed weight, both GCV (30.79%) and PCV (32.37%) were high, indicating that this trait also exhibits substantial genetic variability with moderate environmental influence. This trait can be targeted in breeding programs for increased seed size. The relatively small difference between GCV and PCV for traits such as days to 50% flowering and plant height indicates that these traits are largely governed by genetic factors with limited environmental effects. The high GCV and PCV observed for yield-related traits are similar to results reported by Raju *et al.* (2017) and Banik *et al.* (2018), who found that traits like pod number and seed weight exhibited strong genetic control, making them reliable for selection in breeding programs. The small differences between GCV and PCV for most traits reflect limited environmental interference, aligning with findings from Jayalakshmi *et al.* (2019), who reported minimal environmental influence on traits like plant height and pods per plant in chickpea.

Heritability and Genetic Advance

Heritability estimates provide information on the degree to which a trait is inherited from one generation to the next, while genetic advance indicates the potential for improvement through selection. Days to 50% flowering exhibited high heritability (99%) and genetic advance (31.58), indicating that this trait is predominantly controlled by genetic factors and can be improved through direct selection. Breeding for early flowering genotypes can help develop chickpeas that can escape terminal droughts in rain-fed regions. The number of pods per plant had the highest heritability (99.11%) and genetic advance (45.23), suggesting that this trait is strongly influenced by genetics and has high potential for improvement. This makes it a key selection criterion for enhancing chickpea yield. 100-seed weight also showed high heritability (90%) and genetic advance (9.83), making it a promising trait for increasing seed size. Improving seed size can lead to increased market value and higher yield per plant. High heritability coupled with substantial genetic advance is indicative of strong genetic control over these traits, a finding consistent with previous studies such as those by Desai *et al.* (2015) and Kumar *et al.* (201), who reported similar results for chickpea. The high genetic advance for traits like number of pods per plant and seed weight confirms that selection for these traits will lead to rapid genetic improvement, as also noted by Srivastava *et al.* (2017).

Correlation Analysis

Genotypic Correlation

Genotypic correlations reveal the relationships between traits at the genetic level, free from environmental interference.

The number of pods per plant showed a strong positive genotypic correlation (r = 0.89) with yield per plant, making it a key trait for yield improvement. Genotypes with more pods tend to produce higher yields, highlighting the importance of this trait in breeding programs aimed at increasing productivity. Days to 50% flowering exhibited a moderate positive correlation with yield per plant (r = 0.42) and a negative correlation with 100-seed weight (r = -0.34). This indicates that earlier-flowering genotypes may have smaller seeds, suggesting a trade-off between early maturity and seed size. Breeders need to balance these traits based on the breeding objectives (e.g., early maturity for drought-prone areas versus larger seeds for market preference). The strong genotypic correlation between number of pods per plant and yield aligns with the findings of Reddy *et al.* (2021), who reported a similar positive correlation between pod number and yield in chickpea. The trade-off between days to flowering and 100-seed weight has also been observed in previous studies, such as those by Yadav *et al.* (2020), highlighting the challenge of balancing early maturity with seed size.

Phenotypic Correlation

Phenotypic correlations include both genetic and environmental influences, providing a more field-based perspective of trait interactions.

The number of pods per plant also showed a strong positive phenotypic correlation (r = 0.83) with yield per plant, confirming that this trait is a reliable indicator of yield performance in field conditions. Selecting for more pods can directly lead to higher yields. Days to 50% flowering had a moderate positive phenotypic correlation (r = 0.38) with yield per plant, but like the genotypic correlation, it showed a negative correlation with 100-seed weight (r = -0.29). This indicates that selecting for early flowering may lead to smaller seeds, a factor that should be considered in breeding programs depending on market demands. The strong phenotypic correlation between number of pods per plant and yield observed in this study is consistent with the results of Bharadwaj *et al.* (2019), who also found a strong positive relationship between these traits under field conditions. The negative correlation between days to flowering and 100-seed weight reflects the trade-offs often encountered in breeding programs, as noted by Ali *et al.* (2011), who suggested balancing these traits based on specific environmental and market requirements.

Conclusion

This study has identified early-flowering genotypes with a high number of pods as promising candidates for breeding programs aimed at enhancing chickpea yield. The high heritability and genetic advance for traits such as days to flowering and number of pods per plant suggest that these traits can be improved through selection. Future breeding efforts should focus on optimizing the balance between pod number and seed weight to maximize overall productivity. These findings contribute valuable insights for developing high-yielding, climate-resilient chickpea varieties.

Table 1 : Analysis of variance for 11 characters among 30 genotypes of chickpea

S.No.	Character	Mean sum of squares		
		Replications	Treatments	Error
		df=2	df=29	df=58
1	Days to flowering (DF)	27.54	712.76**	1.90
2	Days to maturity (DM)	99.60	165.4**	5.29
3	Plant height (PH)	27.09	253.99**	3.03
4	Number of primary branches (NPB)	0.52	4.70**	0.09
5	Number of secondary branches (NSB)	10.76	15.73**	0.35
6	Number of pods per plant (NP/P)	60.05	1452.15**	1.42
7	Pod length (PL)	0.11	0.27**	0.040
8	Number of seeds per pod (NS/P)	0.052	0.32**	0.052
9	100 -Seed weight (100SW)	39.46	78.26**	2.64
10	Biomass yield (BY)	71.77	98.25**	1.52
11	Yield per plant(YPP)	1.22	9.05**	0.23

(1% significance - **, 5% significance - *)

Table 2 : Estimates of GCV, PCV and ECV among 30 genotypes of chickpea

Trait	GCV	PCV	ECV
DF	20.75	20.84	1.85
DM	6.58	6.90	2.07
PH (cm)	16.02	16.31	3.05
NPB	28.54	29.41	7.08
NSB	20.31	21.00	5.33
NP/P	39.25	39.31	2.12
PL (cm)	16.35	20.03	11.65
NS/P	16.19	20.40	12.41
100SW	30.79	32.37	9.97
BY(g)	20.94	21.44	4.55
YPP(g)	19.72	20.48	5.53

Table 3: Estimates of Heritability and Genetic advance among 30 genotypes of chickpea

Trait	Heritability (Broad sense)	Genetic Advance	GA as % of Mean
DF	99.00	31.58	42.58
DM	91.20	14.35	12.95
PH (cm)	96.00	18.51	32.42
NPB	94.34	2.47	57.08
NSB	93.22	4.51	40.50
NP/P	99.11	45.23	80.74
PL (cm)	66.00	0.47	27.47
NS/P	63.12	0.49	26.60
100SW	90.00	9.83	60.34
BY(g)	95.05	11.43	42.17
YPP(g)	92.2	3.40	39.13

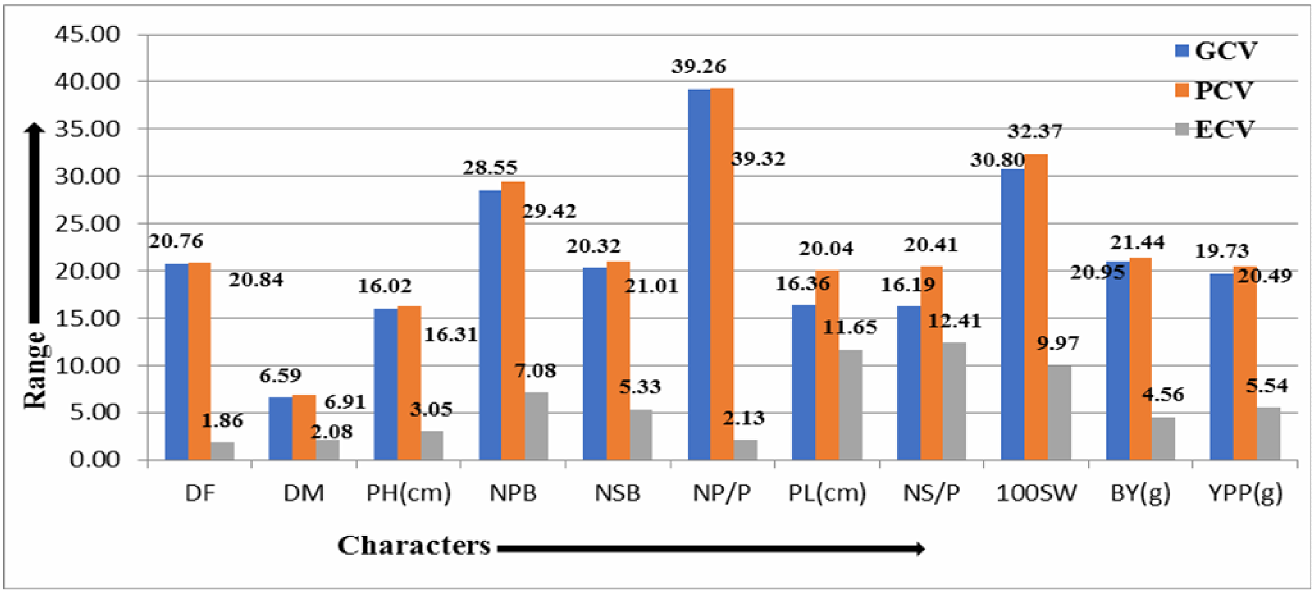

Fig. 1 : Graph representing GCV, PCV and ECV of 11 Characters

Table 4: Phenotypic Correlation Coefficients

Chara-cters	DF	DM	PH (cm)	NPB	NSB	NP/P	PL (cm)	NS/P	100SW	BY(g)	YPP(g)
DF	1	0.2501 *	0.6243**	-0.638**	0.3196**	0.8531**	0.2958 **	0.0125 NS	-0.2194 *	-0.3049 **	-0.168 NS
DM	0.2501 *	1	-0.0805 NS	-0.0988NS	0.0277NS	0.2072 NS	0.1599 NS	0.1083 NS	-0.2445 *	-0.1114 NS	0.1492 NS
PH (cm)	0.6243 **	-0.0805 NS	1	-0.6272**	0.1023NS	0.6278**	0.3969 **	0.0377 NS	0.2328 *	-0.2539 *	-0.2102 *
NPB	-0.638 **	-0.0988 NS	-0.6272**	1	0.2735**	-0.4161**	-0.3295 **	0.1365 NS	-0.1602 NS	0.391 **	0.0659 NS
NSB	0.3196 **	0.0277 NS	0.1023 NS	0.2735**	1	0.4892**	-0.0382 NS	0.1399 NS	-0.3358 **	0.331 **	-0.1978 NS
NP/P	0.8531 **	0.2072 NS	0.6278**	-0.4161**	0.4892**	1	0.2794 **	0.1402 NS	-0.2286 *	-0.2833 **	-0.1289 NS
PL (cm)	0.2958 **	0.1599 NS	0.3969**	-0.3295**	-0.0382NS	0.2794**	1	-0.1447 NS	0.3244 **	-0.2312 *	0.055 NS
NS/P	0.0125 NS	0.1083 NS	0.0377 NS	0.1365 NS	0.1399 NS	0.1402 NS	-0.1447 NS	1	-0.2708 **	0.0632 NS	-0.0222 NS
100SW	-0.2194 *	-0.2445 *	0.2328 *	-0.1602 NS	-0.3358 **	-0.2286 *	0.3244 **	-0.2708 **	1	0.0278 NS	0.317 **
BY(g)	-0.3049 **	-0.1114 NS	-0.2539 *	0.391 **	0.331 **	-0.2833 **	-0.2312 *	0.0632 NS	0.0278 NS	1	0.0659 NS
YPP(g)	-0.168 NS	0.1492 NS	-0.2102 *	0.0659 NS	-0.1978 NS	-0.1289 NS	0.055 NS	-0.0222 NS	0.317 **	0.0659 NS	1

Table 5: Genotypic Correlation Coefficients

Chara-cters	DF	DM	PH (cm)	NPB	NSB	NP/P	PL (cm)	NS/P	100SW	BY(g)	YPP(g)
DF	1	0.2654 NS	0.6383**	-0.6581**	0.3346 NS	0.8572**	0.3588 NS	0.0132 NS	-0.2378 NS	-0.312 NS	-0.1819 NS
DM	0.2654 NS	1	-0.0916 NS	-0.121 NS	0.0213 NS	0.2128 NS	0.1232 NS	0.164 NS	-0.2591 NS	-0.1409 NS	0.1262 NS
PH (cm)	0.6383**	-0.0916 NS	1	-0.6519**	0.1103 NS	0.6399**	0.5201 **	-0.0045 NS	0.2472 NS	-0.2593 NS	-0.2241 NS
NPB	-0.6581**	-0.121 NS	-0.6519**	1	0.3012 NS	-0.4282*	-0.4228 *	0.186 NS	-0.1515 NS	0.4185*	0.0741 NS
NSB	0.3346 NS	0.0213 NS	0.1103 NS	0.3012 NS	1	0.5047**	-0.0588 NS	0.1917 NS	-0.3526 NS	0.3318 NS	-0.2185 NS
NP/P	0.8572**	0.2128 NS	0.6399**	-0.4282*	0.5047 **	1	0.3417 NS	0.1684 NS	-0.2416 NS	-0.2921 NS	-0.139 NS
PL (cm)	0.3588 NS	0.1232 NS	0.5201**	-0.4228*	-0.0588 NS	0.3417 NS	1	-0.0043 NS	0.4051*	-0.3335 NS	0.0324 NS
NS/P	0.0132 NS	0.164 NS	-0.0045 NS	0.186 NS	0.1917 NS	0.1684 NS	-0.0043 NS	1	-0.3758*	0.0961 NS	-0.0381 NS
100SW	-0.2378 NS	-0.2591 NS	0.2472 NS	-0.1515 NS	-0.3526 NS	-0.2416 NS	0.4051*	-0.3758*	1	0.031 NS	0.3645*
BY(g)	-0.312 NS	-0.1409 NS	-0.2593 NS	0.4185*	0.3318 NS	-0.2921 NS	-0.3335 NS	0.0961 NS	0.031 NS	1	0.0611 NS
YPP(g)	-0.1819 NS	0.1262 NS	-0.2241 NS	0.0741 NS	-0.2185 NS	-0.139 NS	0.0324 NS	-0.0381 NS	0.3645 *	0.0611 NS	1

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