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## Characterization of chickpea (*Cicer arietinum* L.) elite germplasm for seed yield and quality under normal sown condition

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### Abstract

Present research work was carried out on 32 diverse genotypes of chickpea (*Cicer arietinum* L.) at the research farm of Faculty of agricultural Sciences and Allied industries, Rama University, Kanpur during rabi 2020-21 in RBD with 3 replications with an aim to estimate the genetic parameters of variability for yield, and quality attributing traits. ANOVA for almost all the traits varied significantly except seeds/pods (SPP). Highest genetic and phenotypic variance have been observed for days to Initial flowering (23.67 and 28.56) followed by DTM (19.46 and 23.54) and SI (g) (18.73 and 19.52). Similarly, GCV for almost all the traits have been found lower than the corresponding PCV except for the traits PHT (cm) (14.77). Highest value of GCV have been exhibited by SI (25.89) followed by DFI (25.67), SYP (20.32), SPP (16.77) and SB (16.45) while minimum GCV value have been recorded for the traits DTM (4.42). It reveals that selection of the individual genotypes on the basis of this phenological traits would be rewarding. High heritability couple with genetic advance has been found for SYP (g) (77.34) followed by PB (69.74), BY (g) (67.83), SB (66.18) and DFF (61.27). While PHT (cm), SI (g) and HI (%) have represented the moderate value of heritability. It represents that while doing phenotypic selection, maximum genetic gain could be achieved through the selection of these traits. It is the paramount important traits while going to select any individual plant from the variable population. In our study Seed index [SI (g)] (18.21%) has contributed more in total variability followed by BY (g) (16.36%), SYP (g) (11.67%), SB (9.87%), HI (9.32%) and DTM (8.11%) while rest of the traits under study exhibited very less contribution to the total variability. Average protein content (%) in each genotype have been recorded 18.23%. Maximum protein content (%) have been observed in Gori (24.57%), followed by UTRI CHANA (24.22%), Birsa Local (23.76%) and RADHA (22.57%). While minimum protein content% have been observed for ICC 495458 (13.26%) (Table 5, Fig 3). Our finding is in close agreement with Singh *et al.*, (2014) and Sharma *et al.*, (2013) on his study conducted on the nutritional analysis of released chickpea variety.

**Keywords:** Genetic variability, chickpea, GCV, PCV, heritability, protein%

### Introduction

Chickpea is a cool season food legume and belongs to Fabaceae family. It is a true diploid ( $2n = 2x = 16$ ) species, self-pollinated, with 738 Mbp genome size and contains 28269 genes. It is being grown worldwide, including the Indian subcontinent, Africa, Middle-East and Europe, etc. Eastern Region east of the Mediterranean Sea was the most accepted primary centre of origin. Thereafter, chickpea was dispersed to different regions across the globe, starting from its origins in the Mediterranean/Fertile Crescent and extending to Central Asia.

Chickpea is one of India's largest grown pulse crops, with an area of about 15.00 million hectares and production of 15.87 million tons with productivity of 1.05 tons/ha globally (FAOSTAT, 2021)<sup>[10]</sup>. Although there has been a slight rise in the chickpea cultivation area in India, from 8.39 million hectares in 2015-16 to 10.9 million hectares in 2021, production has experienced a remarkable change and escalated from 4.75 million tonnes in 1983-84 to a remarkable 11.91 million tons in 2020-21 (Figure 1.1) due to increased productivity (0.67 tonnes to 1.08 tonnes) from 1961 to 2021 (FAOSTAT 2021)<sup>[10]</sup>. In Uttar Pradesh 5.77 lakh ha. area is covered under chickpea cultivation with annual production and productivity of 4.75 lakh tonnes and 824 kg/ha respectively.

Fluctuating cropping ecology, rapidly increased world population, decreased cultivated area and shifting of chickpea cropping ecology from collar region to central and southern part of India, which is somewhat warmer than their traditionally growing region has aroused a serious

need to develop an early maturing, high yielding variety having high protein content and resistant to different level of biotic and abiotic stress.

The magnitude of variation at genetic level in a population and the heritability of desired traits are important aspects of any successful plant breeding activity. Adaptability and survival of any crop species against biotic and abiotic stress depends on genetic diversity (Fu and Somers, 2009) [12]. For selecting diverse and suitable genotypes heritability estimates coupled with genetic advance is more effective than heritability estimates alone in predicting genetic gain during selection. Heritability, which measures phenotypic variation due to genetic reasons, has a predictive role in crop breeding (Songsri *et al.* 2008) [29]. Yield of any crop plant is a very complex trait and it is governed by multiple gene. So direct selection for grain yield is sometimes not possible. Therefore, knowledge of interrelationship of the traits which have directly or indirectly effect of grain yield is prerequisite. In view of the above problem regarding the chickpea production a study has been conducted to screen the elite germplasm of chickpea and find out the diverse genotype having high yield and is suitable to produce stable yield performance under the stress environments.

### Materials and Methods

A set of 32 elite germplasm of chickpea (*Cicer arietinum* L.) which includes released varieties, exotic genotypes and local land races have been used in our present study. An experiment was conducted in RBD design with three replications during rabi 2020-21 at the Faculty of Agricultural Sciences and Allied Industries, Rama University, Mandhana, Kanpur. plant to plant distance was 10 cm and row to row 30 cm distance were maintained all the recommended agronomic practices were done time to time to raise the good crop.

Data on 12 quantitative traits *viz.*, Days to 50% flowering, Plant height, Primary branch/plant, Secondary branches/Plant, Days to initial flowering, Pods/ Plant, Seeds/ Pod, Days to maturity, 100 seed weight (g), Biological yield (g), Harvest index (%) and Seed yield per plant (g) have been recorded by randomly selecting and tagging the five competitive plants from each replication. Recorded data were compiled and have been subjected to statistical analysis such as ANOVA, heritability of traits under study (Burton and Devane, 1953) [6], Coefficient of variation (GCV, PCV) (Burton, 1952), estimation of heritability (Burton and De Vane, 1953) [6], genetic advance, correlation coefficient analysis (Al-Jibouri, *et al.*, 1958) [1] and path analysis (Dewey and Lu, 1959) [9] to extract the meaningful information regarding the magnitude of variation and relationship of major yield contributing traits.

### Results and Discussion

Analysis of variance of almost all the traits under study exhibited significant variation except for the traits Seeds/Pods (SPP) (Table 1.) Highest genetic and phenotypic variance have been observed for days to Initial flowering (23.67 and 28.56) followed by DTM (19.46 and 23.54) and SI (g) (18.73 and 19.52). While minimum value of genotypic as phenotypic variance have been observed for the trait PP (0.78) and PB (0.94). Its indicates that selection of diverse genotypes on the basis of these traits would be more rewarding. Our result was in agreement with findings of Jayalakshmi *et al.*, (2018) [14] for all the concerned biometrical traits under study, Jayalakshmi and Trivikrama Reddy (2018) [14] for protein

content, Raju *et al.*, (2017) [21] for days to 50% flowering, plant height and number of branches and secondary branches per plant. Similarly, Banik *et al.*, (2018) [3], Mohammed *et al.*, (2019) [18] and Mohan and Thiyagarajan (2019) [19] for days to maturity, Kumar *et al.*, (2018) [17] for number of pods per plant. Genotypic coefficient of variability is the measure of presence of amount of variability present among the individual genotypes for different traits under study. In our present study GCV for almost all the traits have been found lower than the corresponding PCV except for the traits PHT (cm) (14.77). Highest value of GCV have been exhibited by SI (25.89) followed by DFI (25.67), SYP (20.32), SPP (16.77) and SB (16.45) while minimum GVC value have been recorded for the traits DTM (4.42) (Table 1, Fig. 1). Similarly highest magnitude of PCV have been recorded DFI (31.04) followed by SI (27.55), SB (23.97), SPP (23.47) and SYP (g) (22.51). where as minimum PCV have been recorded for the traits DTM (5.49). our finding is in close agreement with the finding of Raju *et al.*, (2017) [21], Srivastava *et al.*, (2017) [30] and Mohammed *et al.*, (2019) [18].

Heritability of the traits is an important selection parameter regarding the superior and variable genotypes from a diverse population. In plant breeding broad sense heritability is considered. Such traits having high heritability could be easily transfer to desired agronomic background to achieve the desired goal. In our present study highest heritability have been found for SYP (g) (77.34) followed by PB (69.74), BY (g) (67.83), SB (66.18) and DFF (61.27). while PHT (cm), SI (g) and HI (%) have represented the moderate value of heritability (Table 2.) (Fig 1.). while lowest range of heritability have been recorded for the traits SPP (21.56) and DTM (25.67). Our finding is in close agreement with the finding reported by Desai *et al.*, (2015) [8], Raju *et al.*, (2017) [21], Banik *et al.*, (2018) [3] and Singh *et al.*, (2018) [28].

Genetic advance (GA) measures the genotypic grain which we get from the phenotypic selection of a particular characters. It depends on selection intensity ( $i = 1.76$  at the 10% level), broad sense heritability ( $h^2$ ) of traits, and the phenotypic SD (standard deviation). Its highest value represents the maximum gain under selection while lowest value reveals about the low genetic gain under the phenotypic selection. In the current study maximum genetic gain have been recorded for the trait PP (21.98) followed by PB (14.45) and SYP (g) (11.83). It represents that while doing phenotypic selection, maximum genetic gain could be achieved through the selection of these traits. Where as minimum value of GA has been exhibited by the traits SB (1.98) while rest of the traits under study exhibited the lower range of GA (Genetic Advance). Means during phenotypic selection these traits would give very less genetic gain. Considering the same traits similar finding have been observed by Arshad *et al.* (2004) [2]; Gautam *et al.*, (2021) [13] on his research conducted on chickpea germplasm regarding the assessment of genetic variability under study. Highest value of genetic advance as percent of mean (GAM) have been recorded for the traits SYP (g) (37.51), followed by PP (27.36) and BY (21.67). Other traits under present study exhibited moderate range of GAM. While SPP (g), SI (g) and DFF, represented the lowest value of GAM (Table, Fig. 1).

Correlation coefficient estimates is the measure of association between any two traits. It determines the relationship between the traits and also tell whether any traits have positive or negative relationship between any two traits under selection.

Its value ranges from -1 to +1. Most of the major yield attributing traits have reflected positive and significant association with each other in the present study (Table 3.). Seed yield is the very complex quantitative traits and depends on many other characters. It is the paramount important traits while going to select any individual plant from the variable population. In our study Seed index [SI (g)] (18.21%) has contributed more in total variability followed by BY (g) (16.36%), SYP (g) (11.67%), SB (9.87%), HI (9.32%) and DTM (8.11%) while rest of the traits under study exhibited very less contribution to the total variability (Table 4., Fig. 2). Kumar *et al.*, (2018)<sup>[17]</sup> have also find the similar result on his experiment conducted on chickpea variability analysis. Our result is in close agreement with Dehal *et al.*, (2016)<sup>[7]</sup>, Tiwari *et al.*, (2016)<sup>[31]</sup>, Saroj *et al.*, (2013)<sup>[22]</sup> and Shafique *et al.*, (2016)<sup>[23]</sup>.

In present study protein content of elite chickpea germplasm have been estimated by Kjeldahl, J. (1883)<sup>[16]</sup> method. Average protein content (%) in each genotype have been recorded 18.23%. Maximum protein content (%) have been observed in Gori (24.57%), followed by UTRI CHANA (24.22%), Birsa Local (23.76%) and RADHA (22.57%).

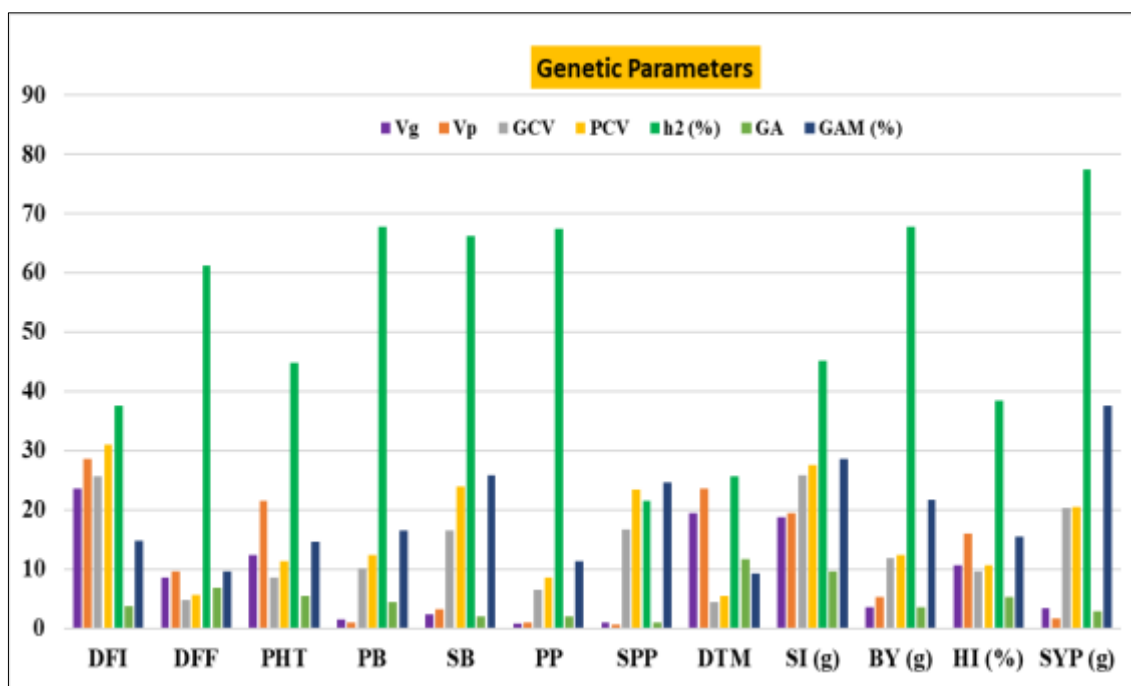
While minimum protein content% have been observed for ICC 495458 (13.26%) (Table 5. Fig 3). Our finding is in close agreement with Singh *et al.*, (2014)<sup>[27]</sup> and Sharma *et al.*, (2013)<sup>[24]</sup> on his study conducted on the nutritional analysis of released chickpea variety.

**Table 1:** Analysis of variance for 12 different quantitative characters in chickpea

Characters	Mean sum of squares		
	Replication (d.f.= 2)	Treatments (d.f.= 39)	Error (d.f.= 78)
DFI	19.825	104.51**	12.16
DFP	1.098	22.976**	0.89
PHT	10.87	38.92*	8.28
PB	3.43	1.45**	0.94
SB	2.11	1.06*	1.08
PP	1.43	0.99*	0.56
SPP	0.23	0.12	0.06
DTM	3.411	49.33**	2.11
SI (g)	1.78	55.11**	2.09
BY (g)	1.876	7.679**	1.56
HI (%)	4.67	29.419**	5.18
SYP (g)	3.856	3.456**	1.567

**Table 2:** Estimation of genetic variability parameters for different quantitative characters

Characters	Vg	Vp	GCV	PCV	h <sup>2</sup> (%)	GA	GAM (%)
DFI	23.67	28.56	25.67	31.04	37.62	3.76	14.83
DFP	8.67	9.54	4.76	5.73	61.27	6.87	9.56
PHT	12.45	16.44	14.77	11.37	44.76	5.43	14.63
PB	1.456	0.94	10.09	12.33	69.74	14.45	16.54
SB	2.452	3.26	16.45	23.97	66.18	1.98	12.76
PP	0.789	0.98	6.43	8.55	67.45	21.98	27.36
SPP	0.973	0.65	16.77	23.47	21.56	1.07	8.56
DTM	19.463	23.54	4.42	5.49	25.67	11.67	9.36
SI (g)	18.734	19.52	25.89	27.55	45.11	9.54	15.63
BY (g)	3.563	5.34	11.82	12.45	67.83	3.65	21.67
HI (%)	10.729	15.93	9.56	10.57	40.45	5.38	15.43
SYP (g)	3.45	1.72	20.32	22.518	77.34	11.83	37.51



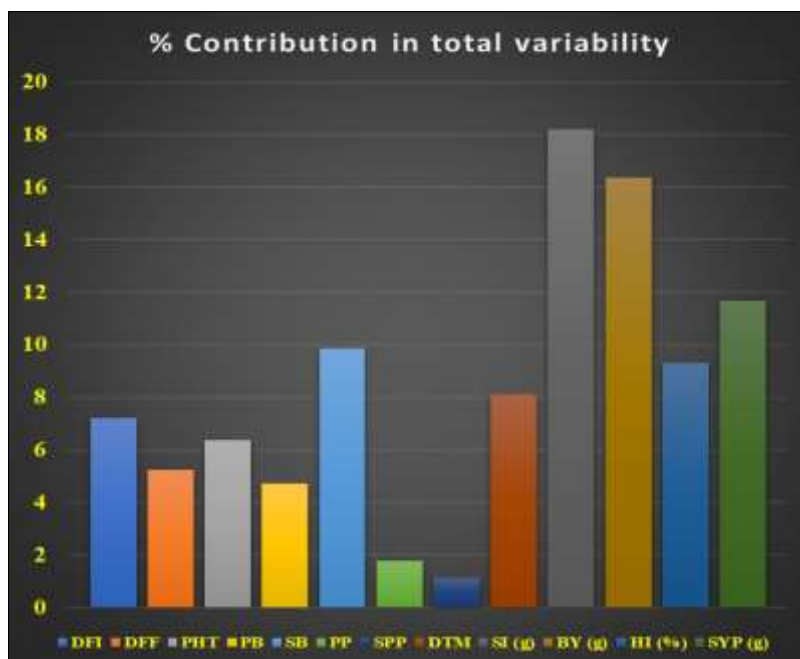
**Fig 1:** Genetic Parameter of variability of the traits under study

**Table 3:** Estimation of genotypic correlation for 12 yield component traits with seed yield in chickpea

Traits	Cor.	DFI	DFE	PHT (cm)	PB	SB	PPP	SPP	DTM	SI (g)	BY (g)	HI (%)	SYP (g)
DFI	r <sub>g</sub>	1.0000	0.5383**	0.2874	-0.4890*	0.1241	-0.5512**	0.0138	0.6561**	-0.6734**	-0.7434**	0.3299	-0.6734**
	r <sub>p</sub>	1.0000	0.0342	0.8732	-0.2565*	0.0763	0.0675	0.0252	0.0563	-0.2543*	-0.2674**	0.0062	-0.2510*
DFE	r <sub>g</sub>		1.0000	0.326	0.212	0.6732**	0.348	0.250	0.7375**	-0.433*	-0.516	0.038	0.549
	r <sub>p</sub>		1.0000	0.003	0.002	0.3032**	0.022	0.217	0.3505**	0.003	0.002	0.000	0.004
PHT	r <sub>g</sub>			1.0000	0.7383**	-0.216	0.6548**	0.316	0.1125	0.130	0.4120*	-0.073	0.146
	r <sub>p</sub>			1.0000	0.2183*	0.0010	0.0042	0.0027	0.0041	0.0503	0.3520**	0.1432	0.0061
PB	r <sub>g</sub>				1.0000	0.753**	0.623**	0.279	0.745**	0.221	0.4797*	0.5341**	0.7496**
	r <sub>p</sub>				1.0000	0.3453**	0.423**	0.146	0.574**	0.002	0.3197**	0.2501*	0.260*
SB	r <sub>g</sub>					1.0000	0.4286**	0.1379	0.5415**	0.1231	0.6397**	0.8207**	0.4114**
	r <sub>p</sub>					1.0000	0.2606*	0.0029	0.3415**	0.0145	0.3397**	0.5785**	0.5126**
PPP	r <sub>g</sub>						1.0000	0.1431	0.5327**	0.6432**	0.1453	0.1598	0.8641**
	r <sub>p</sub>						1.0000	0.0563	0.3927**	0.2533*	0.0057	0.0742	0.5641**
SPP	r <sub>g</sub>							1.0000	0.0452	0.1054	0.4414*	0.1227	-0.6890**
	r <sub>p</sub>							1.0000	0.0011	0.0178	0.5852**	0.1732	-0.2590*
DTM	r <sub>g</sub>								1.0000	-0.4889*	0.6732**	0.1506	0.6734**
	r <sub>p</sub>								1.0000	-0.3753**	0.3112**	0.4531**	0.3534**
SI (g)	r <sub>g</sub>									1.0000	0.1562	0.0384	0.0968
	r <sub>p</sub>									1.0000	0.0038	0.0004	0.0089
BY (g)	r <sub>g</sub>										1.0000	0.7974**	0.9631**
	r <sub>p</sub>										1.0000	0.2674*	0.2567*
HI (%)	r <sub>g</sub>											1.0000	0.9333**
	r <sub>p</sub>											1.0000	0.3673**
SYP (g)	r <sub>g</sub>												1.0000
	r <sub>p</sub>												1.0000

**Table 4:** Percent contribution of each traits towards total variability

Characters	% Contribution toward total variability
DFI	7.23
DFE	5.24
PHT	6.37
PB	4.73
SB	9.87
PP	1.78
SPP	1.13
DTM	8.11
SI (g)	18.21
BY (g)	16.36
HI (%)	9.32
SYP (g)	11.67

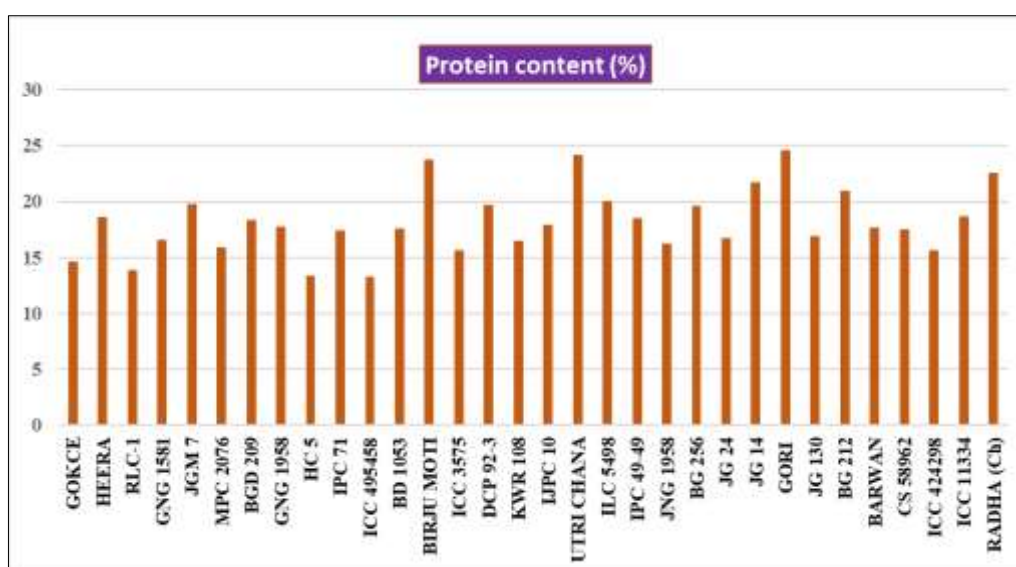


**Fig 2:** % Contribution of the characters to total variability



**Table 5:** Protein content (%) of the different genotypes

S. No.	Entry name	Protein content (%)	S. No.	Entry name	Protein content (%)
1	GOKCE	14.67	17	IJPC 10	17.94
2	HEERA	18.64	18	UTRI CHANA	24.22
3	RLC-1	13.85	19	ILC 5498	20.05
4	GNG 1581	16.55	20	IPC 49-49	18.49
5	JGM 7	19.76	21	JNG 1958	16.23
6	MPC 2076	15.93	22	BG 256	19.65
7	BGD 209	18.34	23	JG 24	16.74
8	GNG 1958	17.73	24	JG 14	21.72
9	HC 5	13.38	25	GORI	24.67
10	IPC 71	17.46	26	JG 130	16.89
11	ICC 495458	13.26	27	BG 212	20.95
12	BD 1053	17.56	28	BARWAN	17.65
13	Birsa Local	23.76	29	CS 58962	17.48
14	ICC 3575	15.65	30	ICC 424298	15.67
15	DCP 92-3	19.67	31	ICC 11334	18.73
16	KWR 108	16.49	32	RADHA (Ch)	22.57
Minimum protein content (%)					13.26
Maximum protein content (%)					24.57
Avegare protein content (%)					18.23

**Fig 3:** Protein percentage of all the genotypes under study**References**

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