

Quantifying Genetic Variability and Heritability in *Kabuli* Chickpea (*Cicer arietinum* L.) for Crop Improvement

Surbhi Pachori^{1*} and Anita Babbar²

¹Research Scholar, Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya Jabalpur (Madhya Pradesh), India.

²Principal Scientist, Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya Jabalpur (Madhya Pradesh), India.

(Corresponding author: Surbhi Pachori*)

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ABSTRACT: Thirty-two genotypes, including three checks of *kabuli* chickpea (*Cicer arietinum* L.) were studied to assess their genetic variability, heritability, and genetic advance effects on seed yield. The results revealed high genotypic and phenotypic coefficients of variation for total number of pods per plant, effective number of pods per plant, total number of seeds per plant, seed yield per plant, and biological yield per plant. This indicates a significant potential for improvement in these traits through hybridization and subsequent selection. Additionally, traits such as number of pods per plant, number of effective pods per plant, total number of seeds per plant, seed yield per plant, biological yield per plant, number of seeds per pod, and stem height of first fruiting node showed high heritability estimates coupled with high genetic advance as a percentage of the mean. The findings indicate that these traits are predominantly influenced by additive gene action, making them suitable targets for reliable selection and subsequent improvement. Understanding the gene action and genetic mechanisms related to these traits can offer valuable insights for designing breeding strategies to enhance the potential yield. Consequently, these traits are regarded as favorable choices for selection and improvement in breeding programs.

Keywords: *Cicer arietinum* L., genetic variability, heritability, *kabuli*.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a crop that undergoes self-pollination and has 16 chromosomes ($2n = 2x = 16$) with a genome size of 732 Mb. According to Vavilov (1926), this crop's primary diversity centers are Southwest Asia and the Mediterranean, while Ethiopia is considered a secondary center. India is responsible for most of the world's chickpea production (67%) and area (70%) and remains the top producer of this crop. Although India imports a significant amount of *desi* chickpeas to meet domestic demand, it has become a major exporter of *kabuli* chickpeas over the past decade.

According to Dixit *et al.* (2019), chickpea is a rainfed crop extensively grown in India, representing 68% of the total cultivated area. Using plant genetic resources, which encompass diverse genetic materials from various sources, is crucial for global food security (Govindaraj *et al.*, 2015). It is necessary to effectively utilize a broader range of plant genetic diversity to meet the growing food demand. Understanding the genetic variability and heritability within populations is vital for successful hybridization programs to obtain desirable traits.

The presence of genetic variability plays a crucial role in enhancing crop plants. A higher level of variability within a population increases the likelihood of obtaining desired plant types Katkani *et al.* (2022). Estimates of heritability and genetic advance provide

valuable insights into the potential gains that can be achieved in future generations. Heritability estimates serve an important predictive function in the genetic analysis of quantitative traits. The ability to predict advancements through selection based on phenotypic values relies on understanding the degree of correspondence between phenotypic and genotypic values.

Due to the low productivity of chickpeas, there is an urgent need to enhance their production to fulfill India's protein requirements. To achieve this, a breeding strategy involving collecting or producing diverse germplasm and selecting superior genotypes for hybridization programs is essential (Vaghela *et al.*, 2009). Evaluating genetic variability, heritability, and advancements at all stages of the breeding process is crucial. Therefore, the current study was conducted in chickpeas to assess the variability in yield-related traits.

MATERIAL AND METHOD

The thirty-two elite chickpea breeding lines were evaluated at JNKVV Jabalpur's Seed Breeding Farm during the *rabi* season 2021-22 & 2022-23. The experiment followed a randomized block design with three replications. Each genotype was planted in four rows, each four meters in length, with a spacing of 45 cm between rows and 8-10 cm between plants. The crop was cultivated using recommended agronomic practices and measures for crop protection.

Observations were made on 16 quantitative traits, including DF 50% (days to 50% flowering), DPI (days to pod initiation), DTM (days to maturity), PH (plant height), NPB (number of primary branches per plant), NSB (number of secondary branches per plant), NPP (number of pods per plant), HFFN (stem height of first fruiting node), ST (stem thickness), TSPP (total number of seeds per plant), NSP (number of seeds per pod), BY (biological yield per plant), HI (harvest index), 100 SW (100 seed weight), and SYP (seed yield per plant). Five randomly selected plants were assessed per replication. The mean values of the samples from each replication were subjected to statistical analysis using R version 4.2.2. The analysis of variance was conducted according to the standard methods described by Panse and Sukhatme (1967); Chaudhary and Singh (1977) for all the studied traits. Biometrical techniques, such as estimating genotypic and phenotypic coefficients of variation (Burton, 1952), broad-sense heritability (Lush,

1940), and genetic advance (Johnson *et al.*, 1955), were also employed.

RESULTS AND DISCUSSION

This study assessed thirty-two diverse kabuli chickpea genotypes to analyze the statistical parameters. The results of the analysis of variance for all the studied traits are presented in Table 1. The mean sum of squares attributed to genotypes exhibited significant variations for all the traits, indicating the presence of substantial variability among the thirty-two chickpea genotypes considered in this study. This presents an opportunity to identify and select genotypes that exhibit improved performance in various agronomic and economic traits. Similar findings have been previously reported by Thapa *et al.* (2019); Hailu (2020); Alemayo *et al.* (2021).

Table 1: Analysis of variance for quantitative traits.

SOURCE OF VARIATION	DF	DF50%	DPI	DM	PH	HFFN	NPB	NSB	NPP
REP	2	7.29	7.71	10.82	12.54	7.25	0.30	0.45	15.95
TREATMENTS	31	92.67**	56.51**	65.55**	164.68**	65.93**	0.65**	3.93**	1763.29**
ERROR	62	4.64	3.41	5.96	6.69	4.60	0.10	0.28	11.01
SOURCE OF VARIATION	DF	EP	TSPP	SPP	ST	100 SW	BY	HI	SY
REP	2	9.96	1.96	0.01	0.27	1.86	44.23	16.27	3.71
TREATMENTS	31	1615.59**	1891.32**	0.15*	0.89**	73.48**	1369.05**	53.45*	263.04**
ERROR	62	7.27	11.77	0.03	0.15	2.16	30.89	12.30	4.54

* Significant at 5%; ***Highly significant at 1%

Using phenotypic and genotypic coefficients of variation allows for assessing and comparing the extent and nature of variability present in different traits within breeding materials. Broad-sense heritability measures the proportion of heritable genetic variance relative to the overall phenotypic variance, while narrow-sense heritability represents the fixable additive genetic variance ratio to total phenotypic variance. Estimating heritability aids in predicting the potential progress achievable through selection. The genetic

advance, expressed as a percentage of the mean, indicates the anticipated response to selection, taking into account the trait's existing genetic variability and heritability.

The calculated phenotypic coefficient of variation (PCV) generally exhibited higher values compared to the genotypic coefficient of variation (GCV) for all the traits, indicating that the observed variation is influenced not only by the genotypes but also by environmental factors (Table 2).

Table 2: Genetic Parameters of Variability.

Characters	Grand mean	Range		Coefficient of Variation			h ² (bs)	GA at 5%	GA as % of mean at 5%
		Min	Max	GCV (%)	PCV (%)	ECV (%)			
DF 50%	62.9	50	73	8.6	9.2	3.4	86.3	10.3	16.3
DPI	74.87	67	87	5.61	6.13	2.46	83.86	7.93	10.6
DM	117.8	107	126	3.78	4.31	2.07	76.91	8.05	6.83
PH	63.87	43.6	79.3	11.36	12.06	4.05	88.72	14.08	22.04
HFFN	27.12	17.63	39.9	16.67	18.45	7.91	81.6	8.41	31.02
NPB	3.83	2.7	4.6	11.12	13.97	8.45	63.35	0.69	18.23
NSB	11.1	8.87	14.01	9.93	11.02	4.78	81.16	2.04	18.43
NPP	59.65	22.27	118.94	40.51	40.89	5.56	98.15	47.37	81.24
EP	58.31	23.48	110.48	39.7	39.97	4.62	98.66	47.37	81.24
TSPP	67.57	26.22	121.88	37.03	37.38	5.07	98.16	51.08	75.59
SPP	1.19	0.59	1.63	18.64	19.2	4.59	94.31	0.44	37.3
ST	3.57	2.45	5.02	13.94	17.7	10.89	62.1	0.8	22.64
100SW	44.94	31.49	54.79	10.81	11.39	3.6	90.2	9.49	21.13
BY	66.2	33.86	102.83	31.65	32.73	8.32	93.2	42.07	63.05
HI	40.62	25.27	61.28	9.11	12.55	8.63	52.71	5.53	13.63
SY	27.23	9.96	46.29	34.08	34.96	7.82	94.99	18.63	68.42

The total number of pods per plant had the highest phenotypic and genotypic coefficient of variation, with values of 40.8% and 40.5%, respectively. This was followed by the effective number of pods per plant (39.9% and 39.7%), total number of seeds per plant

(37.3% and 37.0%), seed yield per plant (34.9% and 34.0%), and biological yield per plant (32.7% and 31.6%). These findings suggest that environmental fluctuations less influence the traits with low genotypic and phenotypic coefficients of variation, indicating

their stability. Therefore, special attention should be given to these traits when breeding cultivars from the current material. Previous studies by Jeena *et al.* (2005); Younis *et al.* (2008); Alwani *et al.* (2010); Babbar *et al.* (2012) have also reported high genotypic coefficients of variation for the number of pods per plant and 100-seed weight, supporting our results.

Traits the number of seeds per pod (19.2% and 18.6%), stem height of the first fruiting node (18.5% and 16.7%), stem thickness (17.7% and 14.0%), number of primary branches per plant (14.0% and 11.1%), harvest index (12.6% and 9.1%), plant height (12.1% and 11.4%), 100 seed weight (11.4% and 10.8%), and number of secondary branches per plant (11.0% and 9.9%) exhibited a moderate level of genotypic and phenotypic coefficient of variation. On the other hand, traits such as days to 50% flowering (9.3% and 8.6%), days to pod initiation (6.1% and 5.6%), and days to maturity (4.3% and 3.8%) showed low genotypic and phenotypic coefficients of variation (Jeena and Arora 2000; Kumar *et al.*, 2001; Ali *et al.*, 2002; Khan *et al.*, 2006; Lokere *et al.*, 2007; Ojha *et al.*, 2010; Hage *et al.* (2018); Joshi *et al.* (2018); Sharma *et al.* (2019); Jida and Alemu (2019); Kumar *et al.* (2018); Katkani *et al.* (2022). The traits with high phenotypic coefficient of variation suggest a stronger influence of environmental factors. It is important to exercise caution during the selection program as environmental variations are unpredictable and can potentially lead to misleading results.

The heritability in a broad sense showed a range of values, from 52.7% for the harvest index (%) to 98.7% for the number of effective pods per plant. Number of effective pods per plant, total number of seeds per plant, number of pods per plant, seed yield per plant, number of seeds per pod, biological yield per plant, 100 seed weight, plant height, days to 50% flowering, days to pod initiation, stem height of the first fruiting node, number of secondary branches per plant, and days to maturity exhibited high estimates of broad sense heritability (>75%). Number of primary branches per plant (63.4%) and stem thickness (62.1%) showed moderate estimates of heritability (>65% to <75%), while the harvest index had a low estimate of heritability. The high heritability values indicate that environmental factors less influence the traits and emphasize the strong genetic control of these traits. This suggests that the phenotypic expression of the traits primarily reflects the genotypic ability of cultivars to pass on their genes to their offspring. Similar findings have been reported by Bicer and Sarkar (2008); Younis *et al.* (2008).

The genetic advance as a percentage of the mean varied across different traits, ranging from 6.8% for days to maturity to 82.7% for the number of pods per plant. Traits such as number of pods per plant, number of effective pods per plant, total number of seeds per plant, seed yield per plant, biological yield per plant, number of seeds per pod, and stem height of first fruiting node showed very high estimates of genetic advance (>30%). Traits *viz.*, stem thickness, plant height, and 100 seed weight exhibited high estimates of genetic advance (<20%). Moderate estimates of genetic

advance (<20% to >10%) were observed for the number of secondary branches per plant, number of primary branches per plant, days to 50% flowering, harvest index, and days to pod initiation. On the other hand, days to maturity showed low estimates of genetic advance (<10%). These findings are consistent with previous studies conducted by Muthuraj *et al.* (2001); Biradar *et al.* (2007); Vaghela *et al.* (2009); Sreelakshmi *et al.* (2010); Dar *et al.* (2012); Hasan and Deb (2013); Kumar *et al.* (2015).

Johnson *et al.* (1955) proposed that considering both heritability estimates and genetic advance as a percentage of the mean provides a more comprehensive assessment than relying solely on heritability in predicting the impact of selection. Therefore, the heritability and genetic advance as a percentage of the mean were analyzed for various traits under different environments. The traits such as number of effective pods per plant (98.7% and 81.2%), total number of seeds per plant (98.2% and 75.6%), total number of pods per plant (98.2% and 82.7%), seed yield per plant (95.0% and 68.4%), number of seeds per pod (94.2% and 37.2%), biological yield per plant (93.5% and 63.1%), 100 seed weight (89.9% and 21.1%), plant height (88.7% and 21.9%), and stem height of first fruiting node (81.6% and 29.9%) exhibited very high heritability along with a genetic advance as a percentage of the mean. Traits such as days to 50% flowering (86.3% and 16.5%), days to pod initiation (83.9% and 10.6%), and number of secondary branches per plant (81.2% and 18.4%) showed high heritability with moderate genetic advance as a percentage of the mean. Stem thickness demonstrated a moderate heritability of 62.1% with a genetic advance as a percentage of 22.7%, while days to maturity displayed high heritability of 76.9% with a low genetic advance as a percentage of the mean of 6.8%. The number of primary branches per plant showed moderate heritability (63.4%) coupled with moderate genetic advance as a percentage of the mean (18.2%). Harvest index recorded low heritability with a moderate genetic advance as a percentage of the mean (52.7% and 13.6%).

The combination of high heritability and high genetic advance over the mean indicates that these traits can be considered favourable attributes for improvement through selection. This suggests that these traits are influenced by additive gene action and can be improved by implementing selection without progeny testing. Similar findings have been reported by Yadav *et al.* (2003). These results align closely with previous studies conducted by Honnappa *et al.* (2018) for biological yield, seed yield per plant, and hundred seed weight, Tsehaye and Bantayhu (2020) for seed yield per plant and total number of pods per plant, Gautam *et al.* (2021) for hundred seed weight, seed yield per plant, and biological yield per plant, Kumawat *et al.* (2021) for the number of effective pods per plant and seed yield per plant, Ram *et al.* (2021) for the number of effective pods per plant, biological yield, and hundred seed weight, and Talekar *et al.* (2017); Johnson *et al.* (2018) for the number of secondary branches per plant.

Supp Table 1: List of genotypes with mean value.

Entry name	dfi	dpi	dm	ph	npb	nsb	npp	hffn
ICCV 211301	62.17	74.33	112.67	64.56	3.39	12.73	62.50	22.30
ICCV 211302	69.17	78.67	116.00	57.31	4.19	10.40	96.83	22.53
ICCV 211303	67.50	81.33	123.00	55.08	4.21	12.31	92.06	36.08
ICCV 211304	57.50	70.33	120.67	64.64	4.38	12.29	58.83	27.19
ICCV 211305	62.83	74.67	111.00	71.97	2.99	11.88	52.17	29.86
ICCV 211306	60.17	72.00	115.67	65.64	3.86	12.21	65.72	22.08
ICCV 211307	57.17	71.33	110.00	75.42	3.25	10.16	27.06	26.97
ICCV 211308	61.83	77.67	123.33	46.31	3.39	10.50	72.72	18.86
ICCV 211309	67.50	78.67	123.33	60.75	4.12	11.54	68.17	31.97
ICCV 211310	61.83	72.33	119.67	74.41	4.08	10.64	47.17	28.30
ICCV 211311	70.50	84.67	121.67	52.86	4.18	11.40	55.28	24.30
ICCV 211312	67.17	82.33	124.00	57.30	3.42	10.49	95.28	20.97
ICCV 211313	65.83	75.33	115.00	66.15	3.20	9.76	37.50	31.64
ICCV 211314	63.17	74.67	115.67	66.75	3.79	10.40	73.06	26.42
ICCV 211315	55.17	68.67	110.33	55.19	3.45	9.23	31.83	23.97
ICCV 211316	55.83	70.67	116.67	66.53	3.20	9.29	42.72	24.19
ICCV 211317	71.83	80.67	123.00	60.53	4.20	10.88	63.72	25.86
ICCV 211318	57.50	71.67	109.33	57.19	4.22	12.67	43.94	22.75
FLIP 10-277C	72.17	79.33	122.00	67.53	3.12	13.47	26.50	26.41
FLIP 11-156C	71.83	76.67	122.00	69.08	4.18	11.94	25.84	36.08
FLIP 08-254C	66.83	73.33	118.33	66.41	3.26	9.66	67.61	38.19
FLIP 10-165C	69.50	75.33	120.33	58.64	3.56	9.62	32.39	28.64
FLIP 07-310C-81	69.17	80.33	122.67	77.08	4.29	9.67	53.61	30.75
RVSVT-K-105	59.50	70.00	119.00	56.19	4.35	12.61	111.83	27.41
ICCV 171312	61.83	70.33	122.67	71.64	4.17	10.39	64.28	28.64
FLIP-12-354C	55.50	68.67	113.67	69.86	4.11	10.29	32.94	34.86
FLIP-12-334C	53.50	71.33	116.00	64.64	4.21	10.38	34.61	26.86
FLIP-12-128C	61.83	76.33	114.33	66.53	4.29	11.45	47.17	25.64
ICCV181313	63.50	79.00	116.67	75.30	3.45	11.35	83.50	27.75
NBeG 119	56.83	73.00	123.67	63.53	4.42	12.02	74.17	23.86
JGK 5	59.83	69.67	110.33	64.75	3.42	11.65	55.17	24.08
JGK-1	57.17	72.67	118.00	54.42	4.42	12.17	112.72	22.53

Supp Table 2: List of genotypes with mean value.

Entry name	st	ep	tspp	spp	100 sw	by	hi	sy
ICCV 211301	4.46	52.48	75.56	1.45	47.10	91.66	38.75	35.40
ICCV 211302	3.66	95.37	112.11	1.17	48.80	97.43	45.34	44.18
ICCV 211303	4.21	88.59	96.11	1.09	41.40	97.20	40.03	38.92
ICCV 211304	3.84	57.26	73.56	1.29	45.09	73.72	41.21	30.18
ICCV 211305	3.87	50.93	63.67	1.25	48.58	72.06	44.35	31.62
ICCV 211306	4.47	65.37	75.45	1.16	46.60	91.00	39.03	35.51
ICCV 211307	3.66	26.70	42.11	1.58	47.05	47.21	42.05	19.74
ICCV 211308	2.88	69.81	86.45	1.24	48.72	88.03	38.21	33.62
ICCV 211309	3.76	76.03	96.45	1.27	41.89	97.23	43.26	42.07
ICCV 211310	4.64	50.74	64.34	1.27	48.38	60.23	41.77	25.13
ICCV 211311	3.44	57.81	67.11	1.16	49.34	55.23	45.72	25.29
ICCV 211312	3.37	95.26	116.00	1.22	50.92	91.25	38.29	34.96
ICCV 211313	3.63	39.37	55.00	1.40	34.62	48.66	39.86	19.40
ICCV 211314	4.10	67.15	68.11	1.02	45.79	66.22	44.02	29.17
ICCV 211315	2.92	26.48	39.11	1.48	50.25	46.59	38.43	17.96
ICCV 211316	3.69	43.48	57.45	1.32	46.09	54.56	44.29	24.18
ICCV 211317	3.62	57.59	78.56	1.36	42.85	83.00	40.14	32.96
ICCV 211318	4.00	42.59	66.67	1.57	48.74	65.23	44.07	28.76
FLIP 10-277C	2.90	25.59	36.00	1.41	42.55	41.19	36.32	14.84
FLIP 11-156C	3.07	29.37	29.11	0.99	46.27	38.08	33.39	12.73
FLIP 08-254C	2.81	65.92	59.11	0.90	34.80	49.51	36.45	18.07
FLIP 10-165C	3.12	31.93	42.00	1.31	35.93	34.22	34.61	11.85
FLIP 07-310C-81	2.93	53.37	56.00	1.05	46.86	54.80	43.47	23.85
RVSVT-K-105	3.45	104.81	120.67	1.15	52.78	95.26	38.82	36.96
ICCV 171312	2.77	57.81	58.34	1.01	43.99	54.54	49.04	26.29
FLIP-12-354C	3.68	33.15	33.34	1.01	34.40	38.92	34.14	13.07
FLIP-12-334C	2.95	38.04	38.45	1.01	44.23	48.84	35.16	17.18
FLIP-12-128C	3.26	43.59	44.00	1.01	41.95	48.78	34.08	16.62
ICCV181313	3.79	79.81	63.45	0.79	43.90	50.87	47.79	23.96
NBeG 119	4.08	74.04	115.89	1.57	41.76	100.69	43.77	44.07
JGK 5	4.40	55.81	63.89	1.14	53.26	89.88	38.06	34.18
JGK-1	2.92	109.81	68.56	0.63	43.49	63.23	46.12	28.84

CONCLUSIONS

In conclusion, based on the assessment of genetic parameters including genotypic coefficient of variation, heritability, and genetic advance as a percentage of the mean, certain key traits have been identified for selection and improvement of yield in chickpea. These traits include total number of pods per plant, effective number of pods per plant, total number of seeds per plant, seed yield per plant, and biological yield per plant. High heritability and high genetic advance as a percentage of the mean were observed for number of pods per plant, number of effective pods per plant, total number of seeds per plant, seed yield per plant, biological yield per plant, number of seeds per pod, and stem height of first fruiting node, indicating that these traits are primarily influenced by additive gene action. Therefore, selecting and improving these traits through genetic improvement efforts would effectively increase chickpea seed yield.

FUTURE SCOPE

Future research and improvement in chickpeas can focus on targeting key traits like number of pods, flowering time, seed weight, plant height, yield, plant spread, secondary branches, and maturity. Understanding the gene action and genetic mechanisms behind these traits can guide breeding strategies for improved yield potential. Conducting trials across diverse regions will assess trait stability and adaptability.

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Conflict of Interest. None.

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