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## Assessment of genetic variability in elite lines of chickpea for yield and its component traits

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### Abstract

The experimental material in the present study consisted of 60 germplasm lines of chickpea and four checks. These lines were evaluated in augmented design for variability, heritability and genetic advance during *rabi* 2021-22. The analysis of variance unveiled presence of significant variations among the genotypes for all twelve traits. The variability estimates calculated had higher PCV values over GCV. The highest PCV value was recorded for seed yield per plant. High PCV coupled with high GCV along with less difference in between GCV and PCV indicated the presence of wider adaptability for these traits in the genotypes studied and less influence of environment in the expression of traits. All the traits under investigation were found to be highly heritable, as majority of them showed high values of heritability (broad sense) estimates. Highest value of heritability estimate was recorded for seed yield per plant. High heritability coupled with high genetic advance as percent of mean indicated operation of additive gene action and the ample scope for improvement in these traits through simple selection.

**Keywords:** Chickpea, heritability, genetic variability, heritability, genetic advance

### 1. Introduction

The chickpea (*Cicer arietinum* L.,  $2n=2x=16$ , Fabaceae), which was one of the first grain legumes cultivated by humans (Pokorny *et al.*, 2015) [14], originated in Western Asia and has spread to India and other nations. Apart from being an affordable source of high-quality dietary proteins such as albumins and globulins, chickpea seeds also contain essential minerals like calcium, magnesium, potassium, and phosphorus as well as vitamins (thiamine, riboflavin, and niacin), unsaturated fatty acids (linoleic and oleic acids), dietary fibers and carbohydrates (Jimenez-Lopez *et al.*, 2020) [9]. India plays a significant role in chickpea production, accounting for approximately 70% of the global output. Madhya Pradesh, Uttar Pradesh, Maharashtra, Rajasthan, Gujarat, Andhra Pradesh, Karnataka, and Bihar are the primary states in India known for their prominent chickpea production.

Since a broad range of genetic diversity across parents is necessary for hybridization programmes, the morphological characterisation of germplasm is utilized to understand the genetic variance. Any effective hybridization programme must meet certain requirements in order to produce the desired Segregants, including the nature and extent of genetic diversity and heritability in a population as genetic and non-genetic variables. Being a self-pollinated plant chickpea lacks sufficient variability. Hence, vulnerability of current cultivars to different abiotic and biotic stresses are the main obstacles to increasing production (Parameshwarappa *et al.*, 2011 and Gaur *et al.*, 2012) [11, 8]. With numerous economically significant parameters, such as flowering time, grain weight, grain yield, etc., genetic variability studies in chickpea have been conducted. As a complex trait, the expression of yield is controlled by multiple related traits. In light of the aforementioned perspectives, the present experiment was designed to identify the morphological and genetic diversity in chickpea germplasm, followed by a path analysis for crop production.

### 2. Material and Methods

The present investigation was conducted during *rabi* 2021-22 at N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. The experimental material in the present study consisted of 60 germplasm lines of chickpea and four checks which were planted in augmented design *rabi* 2021-22. Plants were spaced 10-15 cm apart and rows were kept apart at 30 cm. To grow a healthy crop, the usual sets of practices for chickpea cultivation were used.

The observations were made on 12 traits *viz.* plant height, height of first pod bearing node, number of primary branches, pod length, number of pods per plant, number of seeds per pod, 100 seed weight, biological yield, seed yield, and harvest index from random samples of three visually healthy plants chosen at random from each row, each row representing a genotype of chickpea. However, traits like days to 50% flowering and days to maturity were recorded on row basis.

### 3. Statistical and genetic analysis

Means of the observations recorded for various traits were subjected to the following statistical analyses for drawing appropriate conclusion from the present investigation. The analysis of variance for each character was carried out for the augmented block design as method given by Federer (1956) [9].

Genotypic and phenotypic components of variance were calculated using following formulae (Burton, 1953) [5].

Phenotypic coefficient of variance (PCV %)

$$PCV [\%] = \frac{\sigma_{pi}}{x_i} \times 100$$

Genotypic coefficient of variance (GCV %)

$$GCV [\%] = \frac{\sigma_{gi}}{x_i} \times 100$$

Heritability coefficient ( $h^2$ ) was ratio of genotypic variance to phenotypic variance was calculated as follows (Allard 1960) [1].

$$h^2 = \sigma_{g^2} / \sigma_{p^2} \times 100$$

Genetic advance (GA) for each character studied was calculated as given by (Allard 1960) [1].

$$GA = h^2 KP$$

Were,

K = Selection differential which is equal to 2.06 at 5% intensity of selection.

Genetic advance as percent of mean (GAM)

$$GAM = GAXX100$$

Were,

X = general mean of the character

## 4. Result and Discussion

### 4.1 Analysis of variance

Knowing that chickpeas are an inbreeding and self-pollinating species, genetic variety is necessary to enhance quantitative attributes (Anbessa *et al.* 2006) [2]. The ANOVA for the studied characteristics showed that differences between genotypes were very significant ( $p < 0.01$ ) in the overall F tests. This showed that genotypes are diverse, that may be used in chickpea improvement programmes (Talekar *et al.* 2017) [19].

Genetic parameters

The estimate of phenotypic (PCV %) and genotypic (GCV %) coefficients of variance are represented in Table 1. It is clear from all the observations that the phenotypic coefficient of variance was higher than corresponding genotypic coefficient of variance for all of the characters under study.

**Table 1:** Co-efficient of variance, heritability, genetic advance and genetic advance as percent of mean for different characters in chickpea genotypes

Sl. No	Trait	GCV	PCV	H <sup>2</sup> (BS)	GA	GAM
1	Days to 50% flowering	3.63	4.27	72.54	5.14	6.39
2	Days to maturity	4.39	4.48	95.91	11.21	8.87
3	Plant height (cm)	15.70	15.87	97.85	17.75	32.04
4	Height of first pod bearing node	20.68	20.78	98.96	12.70	42.43
5	Number of primary branches	20.91	21.06	98.58	1.00	42.82
6	Pod size	12.88	12.98	98.49	0.56	26.37
7	Number of pods per plant	38.05	38.19	99.24	21.39	78.19
8	Number of seeds per pod	14.45	14.56	98.43	0.39	29.57
9	100 seed weight	26.05	26.10	99.65	11.26	53.65
10	Biological yield	43.98	44.03	99.78	16.76	90.63
11	Seed yield	44.60	44.75	99.33	6.36	91.71
12	Harvest index	31.92	32.06	99.18	20.94	65.59

The seed yield was observed to have the highest phenotypic coefficient of variation and genotypic coefficient of variance followed by biological yield and number of pods per plant. This greater score indicates the potential for direct selection. Additionally, highest GCV for seed yield (44.60) followed by biological yield (43.98), number of pods per plant (38.05), harvest index (31.92), 100 seed weight (26.05), number of primary branches per plant (20.91), height of first pod bearing node (20.68). Moderate values of GCV were recorded for traits namely plant height (15.70), number of seeds per pod (14.45), pod size (12.88). While, low values of GCV were recorded for days to maturity (4.39) and days to 50% flowering (3.63). Comparing GCV and PCV values, less significant differences were found in all the traits suggested that the environment had little effect on the expression of the trait and that there was also a lot of variability. According to the findings, phenotypic-based selection for the

mentioned features may be fruitful for the enhancement of chickpeas. Low PCV and GCV values, however, suggest that simple selection is ineffective for enhancing any of these characteristics for days to 50% flowering or days to maturity. Singh *et al.* (2014) [17] observed a similar outcome and found that PCV and GCV estimates for days to 50% flowering and days to maturity were low. Even so, breeders have access to a wide range of cutting-edge genomic techniques for use in their breeding programmes for chickpeas. However, knowledge of genetic gain and heritability is necessary for selection processes. It is clear that parent's qualities are passed on to their offspring via heritability (Falconer, 1960) [7].

Knowledge of heritability and genetic advance aids in predicting gains in selection (Boghara *et al.* 2016) [4]. All the traits in the present experiment were highly heritable according to the Robinson *et al.* (1949) [15] scale since their

heritability values were more than 60%. Numerous researchers have found significant heredity for the number of seeds per plant, days to maturity, weight in hundred seeds, number of pods per plant, height of the plant, and seed production per plant (Thudi *et al.* 2014; Thakur *et al.* 2018; Parida *et al.* 2018) <sup>[21, 20, 12]</sup>. The environment seems to have less impact on the expression of characteristics, according to higher heritability estimates. As the traits are anticipated to be regulated by additive gene action, greater levels of heritability permit bigger benefits of selection. Genetic advance as a percentage of mean explains the expected gain when a simple selection for a trait is practiced. It is preferable to have greater genetic advance followed by higher heritability since these variables are often the ones that may be chosen to indirectly enhance the dependent variable.

Genetic advance as % mean (GAM) ranged from 6.39% for days to 50% flowering to 91.71% for number of seeds yield. For the majority of the traits with the exception of days to 50% flowering and days to maturity, both GAM and heritability were high. Waseem *et al.* (2014) <sup>[13]</sup> and Sharanappa *et al.* (2014) <sup>[16]</sup> reported strong heritability and high GAM for seed yield per plant and pods per plant in earlier literature. Different sets of germplasm might be the cause of such conflicting results. Due to the existence of additive gene action, the qualities with high heritability and high GAM may be enhanced by phenological selection with minimal effort (Parameshwarappa *et al.* 2009) <sup>[10]</sup>.

Traits *viz.* days to maturity and days to 50% flowering recorded with high heritability and low GAM, showed the dominance of non-additive gene effects and might be improved by population-level approaches. Anbessa *et al.* (2006) <sup>[2]</sup> and Singh *et al.* (2014) <sup>[17]</sup> found a similar conclusion for days to physiological maturity. Number of pods per plant, number of seeds per pod, biological yield, and seed yield all showed significant heritability along with high genetic progress as a percentage of mean. The findings of Srivastava *et al.* (2017) <sup>[18]</sup> and Aswathi *et al.* (2019) <sup>[3]</sup> are comparable to those of the current results.

## 5. Conclusion

According to the results of the present study, traits days to maturity and days to 50% flowering recorded with high heritability and low GAM, showed the dominance of non-additive gene effects. While, the traits *viz.* seed yield, biological yield, number of pods per plant, harvest index, 100 seed weight, number of primary branches per plant and height of first pod bearing node showed high genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), and high heritability is coupled with genetic gain as a percent of mean.. High heritability coupled with high genetic advance as percent of mean for most of the traits indicates operation of additive gene action and the ample scope for improvement in these traits through simple selection.

## 6. References

- Allard RW. Principles of Plant Breeding. John Wiley and Sons, New York, c1960.
- Anbessa Y, Warkentin T, Vandenberg A, Bandara M. Heritability and predicted gain from selection in components of crop duration in divergent chickpea cross populations. *Euphytica*. 2006;152:1-8.
- Aswathi PV, Ganesamurthy K, Jayamani P. Genetic variability for morphological and biometrical traits in chickpea (*Cicer arietinum* L.). *Electronic Journal of Plant Breeding*. 2019;10(2):699-705.
- Boghara MC, Dhaduk HL, Kumar S, Parekh MJ, Patel NJ, Sharma R. Genetic divergence, path analysis and molecular diversity analysis in cluster bean (*Cyamopsis tetragonoloba* L. Taub.). *International Crop Production*. 2016;89:468-477.
- Burton GW. Quantitative Inheritance in Grasses. *Proc. 6th Int. Grassland Cong.* 1952;1:277-283.
- Federer WT. Augmented Block Design, Hawaii. *Planters Rec.* 1956;55:191-208.
- Falconer DS. Introduction to quantitative genetics. Oliver and Boyd, Edinburgh; c1960.
- Gaur PM, Jukanti AK, Varshney RK. Impact of genomic technologies on chickpea breeding strategies. *Agronomy Journal*. 2012;2:199-221.
- Jimenez-Lopez JC, Singh KB, Clemente A, Nelson MN, Ochatt S, Smith P. Legumes for global food security. *Frontiers in Plant Science*. 2020;11:926.
- Parameshwarappa SG, Palakshappa MG, Salimath PM, Parameshwarappa KG. Evaluation and characterization of germplasm accessions of sesame (*Sesamum indicum* L.) Karnataka. *Journal of Agricultural Science*. 2009;22:1084-1086.
- Parameshwarappa SG, Salimath PM, Upadhyaya HD, Patil SS, Kajjidoni ST. Genetic variability studies in minicore collections of chickpeas (*Cicer arietinum* L.) under different environments. *Indian Journal of Plant Genetic Resources*. 2011;24(1):43-48.
- Parida G, Saghf S, Eivazi A, Akbarzadeh A, Kavetsky T, Aliyeva I, *et al.* Study of genetic advance and broad sense heritability for grain yield and yield components of chickpea (*Cicer arietinum* L.) genotypes. *Advances in Biology & Earth Sciences*. 2018;3(1):5-12.
- Waseem M, Ali Q, Ali A, Samiullah TR, Ahmad S, Baloch DM, *et al.* Genetic analysis for various traits of *Cicer arietinum* under different spacing. *Life Science Journal*. 2014;11(12):14-21.
- Pokorny L, Riina R, Mairal M, Meseguer AS, Culshaw V, Cendoya J. Living on the edge: timing of Rand Flora disjunctions congruent with ongoing aridification in Africa. *Frontiers in Genetics*. 2015;6:154.
- Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. *Agronomy Journal*. 1949;41:353.
- Sharanappa SD, Kumar J, Meena HP, Bharadwaj C, Jagadeesh HM, Raghvendra KP, *et al.* Studies on heritability and genetic advance in Chickpea (*Cicer arietinum* L.). *Journal of Food Legumes*. 2014;27(1):71-73.
- Singh TP, Raiger HL, Kumari J, Singh A, Deshmukh PS. Evaluation of chickpea genotypes for variability in seed protein content and yield components under restricted soil moisture condition. *Indian Journal of Plant Physiology*. 2014;19(3):273-280.
- Srivastava S, Lavanya GR, Lal GM. Genetic variability and character association for seed yield in chickpea (*Cicer arietinum* L.). *Journal of Pharmacognosy and Phytochemistry*. 2017;6(4):748-750.
- Talekar SC, Viswanatha KP, Lohithaswa HC. Assessment of genetic variability, character association and path analysis in F2 segregating population for quantitative traits in Chickpea. *International Journal of*

- Current Microbiology and Applied Sciences. 2017;6(12):2184-2192.
20. Thakur NR, Toprope VN, Phanindra KS. Estimation of genetic variability, correlation and path analysis for yield and yield contributing traits in chickpea (*Cicer arietinum* L). Legume Research. 2018;7(2):2298-2304.
  21. Thudi M, Gaur PM, Krishnamurthy L, Mir RR, Kudapa H, Fikre A, *et al.* Genomics-assisted breeding for drought tolerance in chickpea. Functional Plant Biology. 2014;41(11):1178-1190.