



ISSN Print: 2617-4693
 ISSN Online: 2617-4707
 IJABR 2023; SP-7(2): 212-217
www.biochemjournal.com
 Received: 20-05-2023
 Accepted: 25-08-2023

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Study of genetic variability parameters in Chick pea (*Cicer arietinum* L.) genotypes for yield and its components

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DOI: <https://doi.org/10.33545/26174693.2023.v7.i2Sc.215>

Abstract

The present study aimed to evaluate genetic variability and associations among 20 chickpea genotypes across two Rabi seasons, specifically in 2019-20 and 2020-2021. We employed a randomized block design for the assessment, with each genotype being replicated three times. We computed genetic variability parameters, including mean values, the range from maximum to minimum, and estimations of phenotypic coefficient of variation and genotypic coefficient of variation, which varied from moderate to high. Our investigation unveiled a substantial heritability in a broad sense, alongside significant genetic advances expressed as a percentage of the mean for these traits. This information holds significance in identifying the pivotal traits contributing to yield enhancement by exploring character associations and their direct and indirect effects on yield. Moreover, the analysis of variance indicated noteworthy differences among the genotypes for all the studied traits. In the initial year, significant disparities among the genotypes for all the studied characteristics were revealed, signifying considerable variability within the genotypes. For both phenotypic and genotypic coefficients of variation, biological yield per plant exhibited the highest values, while days to flower initiation displayed the highest heritability. The total number of pods per plant demonstrated the highest phenotypic and genotypic variance in both years. Additionally, genetic advancement as a percentage of the mean was most prominent for biological yield per plant. In the subsequent year, 100-seed weight exhibited the highest phenotypic and genotypic coefficients of variation, similar to the previous year. The total number of pods per plant displayed the highest phenotypic and genotypic variance, and the highest heritability in the broad sense was observed for the trait "Total number of pods per plant," with the genetic advance as a percentage of the mean being highest for 100-seed weight. Notably, the characteristics "Number of Effective Pods per plant" and "Number of pods per plant" demonstrated both high heritability and high genetic advancement as a percentage of the mean, indicating the presence of additive gene effects. Consequently, these traits can be effectively improved through selective breeding.

Keywords: Exhibited, additionally, genetic

Introduction

Scientifically designated as *Cicer arietinum* L., chickpea, commonly known as 'Bengal gram' or 'garbanzo,' holds a significant position as one of the most important grain legumes globally. It goes by various regional names such as chana, gram, and chhola. The term 'Cicer' originates from the Greek word 'kiros,' which is associated with the famous Roman family Cicero. Chickpea belongs to the Fabaceae family and has its origins in South East Turkey and Syria (Kumar and Abbo, 2001) [12].

The Latin term 'arietinum,' meaning 'ram,' alludes to the distinct shape of kabuli chickpea seeds, resembling a ram's head. Chickpea (*Cicer arietinum* L.) is an annual, self-pollinating crop with a diploid nature ($2n = 2x = 16$) and a genome size of 732 Mbp. It falls under the category of cool-season pulse crops and is cultivated in more than 44 countries worldwide, adapting to diverse agro-climatic conditions (Croser *et al.*, 2003; Abebe, T., Alamerew, S., & Tulu, L., 2017; Van der Maesen, 1987; Muehlbauer and Sarker, 2017; Singh *et al.*, 2018; FAOSTAT, 2004) [4, 33, 30, 15, 26].

In India, chickpea production covers approximately 9.44 million hectares of land, yielding around 10.13 million metric tons with a productivity rate of 1073 kg/ha. From a nutritional perspective, chickpea seeds have an average composition of 23% protein, 64% total carbohydrates (Comprising 47% starch and 6% soluble sugar), 5% fat, 6% crude fibre, and

2% ash (Jukanti *et al.*, 2012) ^[10]. Chickpea cultivation holds great importance due to its role in the diets of billions of people worldwide, particularly when combined with cereals. The timing of chickpea cultivation varies by region, with it being sown between September and November as a rabi crop in India, while northeastern Australia plants chickpeas in May/June and harvests from October to December. Chickpea varieties, such as Desi and Kabuli, have different maturity periods, with Desi varieties taking 95-105 days to reach physiological maturity, and Kabuli types requiring slightly longer, around 100-110 days. Chickpeas are considered a cool-season annual crop and thrive at optimal temperatures of approximately 27.5 °C, with a minimum of 16.6 °C and a maximum of 30.2 °C.

Chickpeas have gained attention in numerous countries as a strategy to combat malnutrition, and enhancing their genetics is crucial for improving both their productivity and nutritional value. The success of a breeding program relies significantly on the presence of genetic diversity within the breeding materials and the heritability of yield and quality traits as they are passed from one generation to the next.

Evaluations of genotypic and phenotypic coefficients of variation are essential for understanding how the environment influences different traits and what proportion of the observed variation can be attributed to genetic factors. The combination of heritability estimates and genetic advancements is crucial for predicting the specific outcomes of selecting the most suitable individuals for a given breeding program. In crop improvement efforts, the existence of substantial genetic diversity serves as a fundamental prerequisite. Parameters such as the phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance play a pivotal role in quantifying this diversity, thereby providing crucial insights into the genetic heterogeneity within the germplasm. This knowledge serves as a foundation for identifying promising genotypes capable of enhancing yield and other agronomic attributes. Heritability and genetic advance as a percentage of the mean represent invaluable tools within breeding programs, helping breeders assess the potential for improving various traits through selective breeding. The identification of chickpea genotypes characterized by high protein and micronutrient content, along with robust yield performance, holds paramount importance for future breeding endeavours. The primary aim of this study is to assess the extent of genetic diversity in both yield and quality traits in chickpeas, a critical step in the development of improved chickpea varieties with enhanced nutritional and yield characteristics.

Material and Methods

In this research, we conducted the cultivation of twenty distinct chickpea genotypes. These genotypes were sown in accordance with a Randomized Complete Block Design (RCBD) with three replications, spanning two distinct seasons: Season-I (2019-2020) and Season-II (2020-2021). Each genotype was assigned to a plot measuring 4 × 3 square meters, with a spacing of 0.50 meters between individual plots and 1 meter between blocks. We meticulously followed all recommended agronomic practices and essential plant protection measures throughout the cultivation process to ensure the optimal growth and development of the crop.

Our data collection for this study encompassed the careful observation and systematic recording of 14 quantitative traits. These traits encompassed various facets of chickpea

growth and yield, including flower initiation, the number of days required to reach 50 percent flowering, days to maturity, the count of primary branches per plant, the number of secondary branches per plant, plant height (Measured in centimetres), basal height (Measured in centimetres), total pod count per plant, total count of effective pods, seeds per pod, 100-seed weight (measured in grams), biological yield per plant (measured in grams), harvest index (Expressed as a percentage), and seed yield per plant (Measured in grams).

For the determination of protein content, mature seeds from each genotype within each replication were ground into a fine powder. A 0.2-gram sample of the powdered seeds underwent digestion with concentrated H₂SO₄ to quantify the nitrogen content, which was then expressed as a percentage. We conducted this analysis using the Micro-Kjeldahl digestion and distillation method. Our data analysis involved the execution of separate analyses of variance for each of the observed traits, following the recommended methodology. Genetic parameters, such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in a broad sense, and genetic advance, were calculated using established formulas. Additionally, we determined the mean and range for each trait. Heritability in a broad sense was estimated based on the method proposed by Lush in 1940, which assesses the contribution of genotypes to the overall variation in the studied traits.

Results and Discussion

The analysis of variance conducted for seed yield and its component traits, as outlined in Table 1, unequivocally highlights the profound significance of the mean sum of squares associated with genotypes for all the observed characteristics. This discovery underscores the presence of substantial genetic variability among the diverse genotypes with respect to all the traits under examination. In simpler terms, there exist noteworthy differences in these traits among the various chickpea genotypes, signifying the potential for genetic enhancement through selective breeding or other breeding methodologies. This genetic diversity among the genotypes constitutes a foundational requirement for crop improvement initiatives, serving as a reservoir of variability from which desirable traits can be selected and integrated into new cultivars to amplify crop performance and yield.

Range of Variability

In the initial season, specifically during the 2019-2020 sowing period, there was notable variation observed in the time it took for chickpea genotypes to reach maturity. The average duration was 116.43 days, ranging from 112.42 days (JG14) to 122.35 days (RKG13-504). Similarly, the time required for flower initiation spanned from 46.88 days (RKG13-190-2) to 72.02 days (CSJ515-C), with an average of 59.07 days. The days needed to achieve 50% flowering ranged from 66.21 days (JG14) to 79.87 days (RKG13-504), with an average of 71.11 days. Plant height displayed variability, ranging from 34.53 cm (JG16) to 65.42 cm (Vijay-C), averaging 49.25 cm, while basal height varied between 7.09 cm (RYS-201) and 19.08 cm (RKG13-105), with an average of 13.23 cm.

The number of pods per plant displayed a range, from 25.28 (GCP101-C) to 63.68 (RKG13-511), with an average of 44.60, while the count of effective pods per plant averaged 38.01, varying between 20.05 (GCP101-C) and 61.74

(RKG13-511). The number of seeds per pod exhibited a range from 3.25 (RYS-201) to 1.46 (PC-1), with an average value of 1.66. The hundred-seed weight averaged at 18.1 g, with values ranging from 11.24 (C-1064) to 26.24 g (RKG13-253). In contrast, the biological yield per plant averaged at 22.17 g, with a range spanning from 9.16 (RYS-201) to 44.15 g (JG16). The Harvest Index showed an average value of 38.64%, ranging from 21.66 (RKG13-504) to 56.19 (JG14). Lastly, seed yield per plant varied from 4.85 (JG16) to 14.15 (JG14), with an overall mean of 9.06.

In the subsequent season, among the genotypes under examination, the characteristic displaying the widest range of variation was still the number of days to maturity, with an average value of 116.43 days. This range extended from 123.00 (RKG13-504) to 109.88 (JG16) days. Similarly, other traits, such as the number of days to flower initiation, varied between 48.07 (RKG13-511) and 71.78 (RKG13-504) days, averaging 59.07 days. The duration for reaching 50% flowering spanned from 63.70 (JG16) to 77.09 (RKG13-504) days, with a mean of 71.11 days. Plant height measurements ranged from 35.32 cm (JG16) to 61.75 cm (GCP101-C), with an average height of 49.25 cm. Meanwhile, basal height was recorded between 8.61 cm (RYS-201) and 17.48 cm (C-1064), with an average of 13.23 cm. The number of primary branches varied from 1.16 (RKG13-190-2) to 3.45 (RKG13-253), with an average of 2.48. The total pod count per plant showed a range from 25.76 (GCP101-C) to 65.78 (RKG-105), with an average of 44.62. The count of effective pods per plant had an average of 38.01, spanning from 22.77 (GCP101-C) to 61.06 (RKG13-511). The number of seeds per pod ranged from 1.27 (Vijay-C) to 2.56 (RKG13-511), with an average value of 1.66. Hundred-seed weight averaged at 18.10 g, with values ranging from 2.20 (RKG13-253) to 26.84 g (RKG13-504). In terms of biological yield per plant, the mean was 22.17 g, with a range from 9.61 (RYS-201) to 41.53 g (JG-16). The Harvest Index displayed an average value of 38.64%, varying from 22.25 (RKG13-504) to 50.34 (JG-14). Finally, seed yield per plant ranged from 6.00 (JG-16) to 15.16 g (JG-14), with an average value of 9.06 g.

The diversity observed among the chickpea genotypes in this study presents significant opportunities for improving the crop through the direct selection of genotypes or by utilizing them as parental candidates in hybridization, capitalizing on their desirable characteristics.

Phenotypic and Genotypic variance

The analysis of phenotypic and genotypic variances for various traits in chickpea genotypes across two seasons (2019-2020 and 2020-2021) provides valuable insights into the extent of genetic variability within the population. In the 2019-2020 season, the total number of pods per plant exhibited the highest values for both phenotypic and genotypic variance, indicating significant genetic variability in this trait. This is a crucial finding, as the number of pods per plant is directly related to chickpea yield, and genetic variability in this trait offers opportunities for improving yield through selective breeding. Similarly, the number of effective pods per plant showed substantial variance, indicating genetic diversity in another important yield-related trait.

Other traits, such as the Harvest Index, plant height, biological yield per plant, days to flower initiation, and 100-seed weight, also displayed notable genetic variability. These traits encompass various aspects of chickpea growth, development, and yield, making them valuable targets for

breeding programs aimed at enhancing yield and quality. In the subsequent season (2020-2021), the pattern of high genetic variability continued, with the total number of pods per plant once again exhibiting the highest values for both phenotypic and genotypic variance. This consistency highlights the genetic diversity and stability of this trait across seasons. The number of effective pods per plant and plant height also maintained substantial variance, emphasizing their importance in chickpea breeding efforts. Additionally, traits related to flowering and maturity (days to flower initiation, days to 50% flowering) and seed-related traits (seed yield per plant, 100-seed weight) displayed significant genetic variability. These findings underscore the potential for selecting genotypes with desirable characteristics in these traits for further improvement.

Overall, the substantial genetic variances observed in these traits provide a solid foundation for chickpea breeding programs. Breeders can leverage this genetic diversity to select and develop improved chickpea varieties with enhanced yield, quality, and adaptability.

“Phenotypic and Genotypic Coefficient of Variation

The analysis of phenotypic and genotypic coefficient of variation (PCV and GCV) is crucial in understanding the extent of genetic variability within a population of chickpea genotypes. In the 2019-2020 season, it was observed that the PCV slightly exceeded the GCV for all traits, indicating that environmental factors had minimal influence on trait expression, and most of the variability was due to genetic factors. Some traits exhibited particularly high PCV and GCV values, indicating significant genetic variation. Biological yield per plant and the number of effective pods per plant had the highest values for both PCV and GCV, suggesting substantial genetic diversity for these traits. The number of seeds per pod and seed yield per plant also showed notable variability. These traits are essential for chickpea productivity, and their high genetic variability provides opportunities for improvement through breeding programs. The total number of pods per plant, 100-seed weight, and harvest index also exhibited considerable genetic variability, although slightly lower than the previous traits. In contrast, traits like days to 50% flowering and days to maturity showed lower PCV and GCV values, indicating that genetic variability for these traits was relatively limited. The positive and significant relationships observed between seed yield and traits such as the number of pods per plant, seed numbers, number of branches, and pods per plant highlight the importance of these traits in determining chickpea yield. These findings emphasize the potential for improving chickpea yield through selective breeding for traits that exhibit high genetic variability and positive correlations with yield. In the subsequent season (2020-2021), similar patterns were observed, with 100-seed weight, biological yield per plant, and seed yield per plant showing high PCV and GCV values, indicating significant genetic variability. The number of effective pods per plant also displayed notable variability. Once again, traits related to flowering and maturity (days to 50% flowering and days to maturity) exhibited lower PCV and GCV values, suggesting limited genetic variability for these traits.

These findings provide valuable insights for breeding programs, as traits with high genetic variability offer potential for improvement through selection and breeding efforts. The positive correlations between these traits and seed yield further support their significance in enhancing chickpea productivity.

Heritability (Broad Sense)

Broad-sense heritability is a valuable metric for assessing the extent to which genotypes contribute to the overall variation in traits. The effectiveness of selection for a specific trait largely depends on a high heritability estimate. Burton proposed that a combination of the Genotypic Coefficient of Variation (GCV) and heritability estimates provides the most accurate insight into the potential progress achievable through selection. In the first season, certain traits, such as days to flower initiation (98.94) and the number of effective pods per plant (98.87), displayed high heritability in the broad sense. However, basal height and seeds per pod exhibited low heritability among the fourteen quantitative characters. In the second season (2020-2021), the Total number of effective pods exhibited high heritability (99.01%), while the number of seeds per pod and number of primary branches showed low heritability. This low heritability may be attributed to the influence of

additive gene action, suggesting that phenotypic selection could be effective for these traits. Conversely, days to maturity showed high heritability but low genetic advance, possibly due to the effect of non-additive genetic variance, indicating that selection in this regard may not yield significant improvements. Similar findings were observed for other traits, including plant height, days to 50% flowering, number of pods per plant, 100-seed weight, seed yield per plant, number of branches per plant, and protein content. Traits with high heritability are typically influenced primarily by additive gene action and can be improved through individual plant selection. In this study, a comprehensive evaluation of broad-sense heritability considered various gene expressions, both additive and non-additive, providing a more informed basis for potential improvements in the studied traits.

Genetic advance as a percentage of the mean

Table 1: Genetic parameters of variability during season-I (2019-2020)

Trait	GM	Range		Variance		Coefficient of		h ² (B) %	GA	GA as % of mean
		Min.	Max.	Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)			
FI	59.07	46.88	72.02	63.59	62.92	13.34	13.27	98.94	16.25	27.19
F 50%	71.11	66.21	79.87	19.95	17.95	6.22	5.90	87.99	8.28	11.15
DM	116.43	112.42	122.35	10.76	8.97	2.78	2.54	83.33	5.63	4.78
PH	49.25	34.53	65.42	86.04	83.96	18.30	18.07	97.58	18.64	36.78
BH	13.23	7.09	19.08	9.61	7.83	22.33	20.16	81.52	5.20	37.50
PB	2.488	1.20	3.41	0.27	0.22	21.65	19.647	82.29	0.88	36.71
SB	7.31	5.75	9.85	1.98	1.62	18.07	16.36	81.92	2.37	30.50
TNPPP	44.60	25.28	63.68	135.74	134.09	25.96	25.80	98.78	23.71	52.84
TNEP	38.01	20.05	61.74	126.26	124.84	29.08	28.96	98.87	22.88	59.23
SPP	1.66	3.25	1.46	0.26	0.17	28.50	22.92	64.66	0.68	37.97
100SW	18.10	11.24	26.24	19.42	17.33	24.68	23.31	89.19	8.09	45.36
BY(g)	22.17	9.16	44.155	67.89	65.65	34.87	34.21	96.55	16.38	69.37
HI(%)	38.64	21.66	56.19	85.61	83.56	23.09	22.81	97.59	18.60	46.42
SYPP	9.06	4.85	14.15	6.87	5.75	28.16	25.76	83.67	4.51	48.55

Genetic advance, expressed as a percentage of the mean, was calculated and categorized into three groups: high (>20%), moderate (10-20%), and low (<10%), following Johnson's (1955) recommendations for all 14 characters (refer to Table 2). In this study, specific sowing conditions led to the highest genetic advance as a percentage of the mean for biological yield per plant (69.37%). Traits such as [mention the character name] exhibited a moderate genetic advance as a percentage of the mean (37.97%). In contrast, characters like days to maturity and days to 50% flowering displayed a low genetic advance as a percentage of the mean during the 2019-2020 season.

During the 2020-2021 season, the genetic advance as a percentage of the mean was highest for 100-seed weight (71.02%), with moderate genetic advance percentages reported for plant height (36.91%). Once again, characters

like days to 50% flowering and days to maturity recorded low genetic advance percentages. These findings suggest that characters with higher genetic advance percentages could benefit from selection pressure, as they may be influenced by additive gene action.

In the initial season of the experiment, biological yield per plant exhibited the highest phenotypic and genotypic coefficient of variation, while in the subsequent season, 100-seed weight displayed the highest phenotypic and genotypic coefficient of variation. Harvest index, number of seeds per pod, number of secondary branches, basal height, plant height, number of primary branches, and days to flower initiation showed moderate estimates of phenotypic and genotypic coefficient of variation in both seasons.

The correlation analysis revealed that genotypic correlation coefficients were generally higher than their corresponding

phenotypic correlation coefficients for most characters. This suggests strong inherent associations among the studied traits and underscores the potential for rewarding phenotypic selection. A stronger genotypic correlation is advantageous when selecting for genetically controlled characters, as it can lead to a more favourable response in seed yield improvement compared to relying solely on phenotypic associations. Furthermore, for most characters, there was relatively little difference between genotypic and phenotypic variance in both seasons. This indicates that there was limited environmental influence on the expression

of these traits, emphasizing the genetic basis of these traits. Seasonal variance was negligible for some traits, suggesting minimal seasonal influence, while other traits showed a higher proportion of seasonal variance, indicating a greater influence of seasonal factors on those traits. This information highlights the varying degrees of sensitivity of different traits to seasonal changes. It's important to note that, in general, phenotypic variance should be higher in magnitude than genotypic variance, as it encompasses both genetic and environmental influences on trait expression.

Table 2: Genetic parameters of variability during season-II (2020-2021)

Trait	GM	Range		Variance		Coefficient of		h ² (B) %	GA	GA as % of mean
		Min.	Max.	Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)			
FI	59.07	48.07	71.78	53.66	52.92	12.40	12.31	98.60	14.80	25.19
F 50%	71.11	63.70	77.90	18.81	18.01	6.09	5.96	95.76	8.55	12.03
DM	116.43	109.88	123.00	12.55	11.82	3.04	2.90	90.97	6.64	5.70
PH	49.25	35.32	61.75	79.87	78.88	18.14	18.03	98.76	18.18	36.91
BH	13.23	17.48	8.61	6.86	5.81	19.79	18.22	84.78	4.57	34.57
PB	2.48	1.16	3.45	0.19	0.13	17.38	14.74	71.90	0.64	25.74
SB	7.31	5.20	9.76	2.15	1.82	20.03	18.45	84.84	2.56	35.01
TNPPP	44.62	25.76	65.88	142.77	141.92	26.77	26.69	99.40	24.46	54.83
TNEP	38.01	22.77	61.06	118.27	117.10	28.61	28.01	99.01	22.18	58.35
SPP	1.66	1.27	2.56	0.12	0.08	20.60	17.33	70.76	0.49	30.04
100SW	18.10	2.20	26.74	40.25	39.60	35.03	34.75	98.39	12.85	71.02
BY(g)	22.17	9.61	41.53	53.58	52.47	33.01	32.67	97.92	14.76	66.59
HI(%)	38.64	22.25	50.34	67.19	65.72	21.21	20.97	97.81	16.51	42.74
SYPP	9.06	6.00	15.16	7.01	6.45	29.21	28.02	92.00	5.01	55.36

Conclusion

The presence of genetic variability parameters is a crucial criterion for crop improvement. Based on the findings of this study, it can be concluded that high variability estimates were observed for all the studied traits. Specifically, in both seasons, the total number of pods per plant exhibited the highest levels of phenotypic and genotypic variance. Moreover, the maximum genetic advance as a percentage of the mean was observed for the number of effective pods per plant, whereas a low genetic advance as a percentage of the mean was recorded for the character days to maturity.

In the following season, the highest levels of phenotypic and genotypic coefficient of variation were recorded for 100-seed weight. Moderate estimates of phenotypic and genotypic coefficient of variation were observed for harvest index and the number of seeds per pod under both seasons. Additionally, the correlation analysis revealed that the genotypic and phenotypic correlation coefficients exhibited their lowest values for days to 50% flowering and days to maturity in both seasons.

The combination of high heritability and high genetic advance indicated that these characters can be improved through selection, as they are primarily under the control of additive gene effects. Therefore, it is important to consider both genetic variability and heritability when interpreting expected genetic advance to make informed decisions regarding the potential for improvement through selection. Genetic variability serves as a prerequisite for any breeding program, offering a plant breeder the opportunity to select high-yielding genotypes. This study aimed to gather

information on genetic variability for seedling parameters and their associations in chickpea, with the aim of suggesting seedling selection criteria for future breeding programs.

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