**International Journal of Advanced Biochemistry Research**

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# Assessment of genetic variability, correlation and path analysis in yield and yield components in chickpea (*Cicer arietinum* L.)

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**Abstract**
A Randomized Complete Block Design experiment was employed to investigate the genetic diversity and relationships among 20 different chickpea genotypes. This comprehensive study was replicated meticulously on three occasions, spanning two distinct growing seasons: 2019-20 and 2020-2021. The quantitative traits under scrutiny included parameters such as the total days required for maturity, the initiation of flowering, the time taken to reach half flowering, counts of primary and secondary branches, plant height (Measured in centimetres), basal stem height (measured in centimetres), pods per plant, the number of effective pods per plant, 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.

In the initial year of investigation, a comprehensive range of genetic parameters were meticulously calculated, including measures of central tendency such as the mean, data variability represented by the range, coefficient of variability, correlations, path-coefficient, and genetic divergence. These metrics played a pivotal role in identifying specific traits with the potential to enhance crop yield. Significantly, it was observed that biological yield per plant exhibited the highest values for both phenotypic and genotypic coefficients of variation, while the days to flower initiation displayed the highest heritability. Additionally, it was worth noting that biological yield ranked as the trait with the most substantial genetic advancement when expressed as a percentage of the mean. The path coefficient analysis conducted in the study shed light on the crucial roles of effective pods and days to half flowering, as they exerted the most pronounced positive direct effects on seed yield per plant.

In the subsequent year's analysis, notable findings emerged with significant values observed for both phenotypic and genotypic coefficients of variation, particularly in the context of 100-seed weight. Furthermore, there was a prominent presence of phenotypic and genotypic variances, along with a noteworthy level of broad-sense heritability recorded for pods per plant. Remarkably, 100-seed weight showcased the highest genetic advance when expressed as a percentage of the mean. The study identified specific high-yielding advanced breeding lines, notably JG14, JG16, and PC-1, as exceptionally promising candidates for crop improvement and breeding initiatives. Genotypic and phenotypic path coefficient analyses revealed the paramount importance of certain traits in contributing to seed yield per plant. In the initial year, this was exemplified by the strong positive direct effects of effective pods and days to half flowering. Conversely, in the subsequent year, traits such as maturity time and primary branches emerged as pivotal contributors, signifying their potential for effective selection in future breeding programs aimed at optimizing chickpea yield.

**Keywords:** Flowering, counts, high-yielding

**Introduction**
Chickpea, which originated in Southeastern Turkey and Syria, has a long history of cultivation in semi-arid regions worldwide, with countries like India, Pakistan, and the Middle East playing significant roles. The botanical name of chickpea is *Cicer arietinum* L., with "aries" referring to a ram, inspired by the distinctive shape of the kabuli chickpea seed, which resembles a ram's head. It is an annual crop that self-pollinates and has a diploid genome ($2n = 2x = 16$) with a genome size of approximately 732 Mbp. Taxonomically, it belongs to the Fabaceae family and is classified as a cool-season pulse crop cultivated in over 44 countries, adapting to diverse agro-climatic conditions (Croser *et al*., 2003; Tulu, 2017; Van der Maesen, 1987; Padmavathi *et al*., 2013; Muehlbauer and Sarker, 2017; Singh *et al*., 2018; FAOSTAT, 2000) [7, 25, 24, 32, 47, 48].

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India significant position in global chickpea cultivation, covering approximately 60% of the worldwide area dedicated to chickpea cultivation and production (Directorate of Economics and Statistics, 2019) [6].

From a nutritional perspective, chickpea seeds are highly valuable, containing essential micronutrients such as phosphorus (at 340 mg/100 g), calcium (at 160 mg/100 g), magnesium (at 140 mg/100 g), iron (at 5 mg/100 g), and zinc (at 4.1 mg/100 g) (Jukanti et al., 2012) [16]. Chickpea, along with cereals, forms a major component of the diets of billions of people worldwide. It thrives in a cool climate during its growth phase, requires higher temperatures for maturation, and performs well in sandy or loamy soils with proper drainage systems (Katiyar, 1982) [49].

Chickpea is a versatile crop with various culinary applications, including its consumption as split dal, whole fried or boiled seeds. It plays a crucial role in providing a protein source in vegetarian diets and is often referred to as the 'poor man's meat.' Chickpeas are a significant protein source for both humans and animals, helping to alleviate protein deficiencies in cereal-based diets. One remarkable characteristic of pulses like chickpea is their ability to fix atmospheric nitrogen. Leguminous crops, like chickpeas, possess root nodules that capture atmospheric nitrogen, contributing to soil fertility restoration. Chickpeas also contribute to soil fertility by fixing atmospheric nitrogen through symbiosis. Additionally, they offer a readily available source of protein, complementing cereal-based diets.

Despite its importance, chickpea production in the country remains relatively low, primarily due to factors such as limited availability of high-yielding varieties, susceptibility to diseases and pests, and the need for intensive inputs and management practices (Maiti 2001; Kantar et al., 2007; Knights 1993) [20, 17]. Desi chickpea varieties achieve physiological maturity in approximately 95-105 days, while Kabuli types take a slightly longer period, around 100-110 days. Identifying chickpea genotypes with high protein and micronutrient content, along with strong yields, is of great value for future breeding programs. Therefore, this study aimed to assess the genetic variability of both yield and quality traits in chickpea. Genetic variability in the base population is crucial for developing desired plant types. There is limited information available regarding cultivated chickpea lines under heat stress conditions. Hence, this study was conducted to evaluate genetic variability, trait associations with yield, and the selection of high-yielding genotypes with superior architecture under heat stress conditions. The success of a breeding program depends on the extent of variability and heritability observed in early-generation populations for economically important traits (Pal et al., 2018) [26]. Heritability estimates, along with genetic advances, are essential for predicting the specific impact of selecting the most suitable individuals for a given scenario (Johnson et al., 1955) [15]. As such, this study was conducted and analyzed using potential genotypes to estimate variability, heritability, and genetic advances for both yield and yield-contributing traits in chickpea.

## Materials and Methods
The study utilized a total of 20 chickpea genotypes as its experimental materials. These genotypes were planted in a Randomized Complete Block Design, with each combination replicated three times across two distinct seasons: Season-I (2019-2020) and Season-II (2020-2021). The experimental plots had dimensions of 4 × 3 m² each,

with a spacing of 0.50 m between individual plots and 1 m between blocks. Fertilizers were applied at the rate of 20 kg of nitrogen, 60 kg of phosphorus (as $P_2O_5$), and 40 kg of potassium (as $K_2O$) per hectare.

Data were meticulously collected to characterize these 20 chickpea genotypes, encompassing a range of traits, including flowering initiation, days to reach half flowering, maturity duration, primary branches, secondary branches, plant height (Measured in centimeters), basal height (measured in centimetres), total pod count per plant, number of effective pods per plant, 100-seed weight (Measured in grams), yield per plant (Measured in grams), harvest index (Expressed as a percentage), and seed weight per gram of plant. To estimate protein content, mature seeds from each genotype within each replication were ground into a powder, and 0.2 grams of the powdered seed sample underwent digestion with concentrated H2SO4 to determine the nitrogen content as a percentage. This analysis followed the Micro-Kjeldhal digestion and distillation method, adhering to the guidelines set by the AOAC (1965) [1].

Analysis of variance was conducted separately for each characteristic, following the methodology outlined by Panse and Sukhatme (1967) [29]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formula recommended by Burton (1952) [4]. Broad-sense heritability was estimated following Lush's (1940) approach, and the genetic advance as a percentage of the mean was calculated according to the method elucidated by Johnson, et al. (1955a) [15].

## Results and Discussion
The analysis of variance indicated significant genotype differences for all 14 studied traits, highlighting a substantial range of variability within these characteristics.

## Range of Variability
In the current study, we observed the highest degree of variability in the trait "days to maturity," with an average mean value of 116.43 days. This trait ranged from a minimum of 112.42 days (observed in JG14) to a maximum of 122.35 days (found in RKG13-504). Additionally, the trait "flower initiation" displayed a wide range, spanning from 46.88 days (in the case of RKG13-190-2) to 72.02 days (recorded for CSJ515-C), with an average of 59.07 days. The "days to half flowering" spanned from 66.21 days (noted in JG14) to 79.87 days (observed in RKG13-504), with a mean of 71.11 days.

Regarding plant height, we observed variability ranging from 34.53 cm (measured in JG16) to 65.42 cm (noted in Vijay-C), with an average height of 49.25 cm. Basal height, on the other hand, exhibited a range from 7.09 cm (measured in RYS-201) to 19.08 cm (found in RKG13-105), with an average of 13.23 cm. The total number of pods per plant displayed significant variation, with values ranging from 25.28 (observed in GCP101-C) to 63.68 (noted in RKG13-511) and an average of 44.60. Similarly, the number of effective pods per plant exhibited variability, with a mean of 38.01 and a range from 20.05 (for GCP101-C) to 61.74 (observed in RKG13-511).

The number of seeds per pod varied from 3.25 (recorded in RYS-201) to 1.46 (noted in PC-1), with an average of 1.66. The hundred-seed weight averaged 18.1 g, ranging from 11.24 g (measured in C-1064) to 26.24 g (found in RKG13-253). The Harvest Index had an average value of 38.64%, ranging from 21.66% (observed in RKG13-504) to 56.19% (noted in JG14). Biological yield per plant ranged from 9.16

g (measured in RYS-201) to 44.15 g (found in JG16), with a mean of 22.17 g. In the 2019-2020 season, seed yield per plant showed a range from 4.85 g (recorded in JG16) to 14.15 g (noted in JG14), with an average of 9.06 g.

In the following season, among the studied chickpea genotypes, the character exhibiting the most extensive range of variability was "days to maturity," with an average mean value of 116.43 days. This trait ranged from 109.88 days (in the case of JG16) to 123.00 days (observed in RKG13-504). The initiation of flowering days spanned from 48.07 days (for RKG13-511) to 71.78 days (for RKG13-504), with an average of 59.07 days. Meanwhile, the days to half flowering ranged from 63.70 days (for JG16) to 77.09 days (for RKG13-504), with a mean of 71.11 days.

Plant height in this season varied between 35.32 cm (for JG16) and 61.75 cm (for GCP101-C), with an average measurement of 49.25 cm. Basal height exhibited a range from 8.61 cm (for RYS-201) to 17.48 cm (for C-1064), averaging at 13.23 cm. The number of primary branches spanned from 1.16 (for RKG13-190-2) to 3.45 (for RKG13-253), with an average of 2.48. The total number of pods per plant showed variability from 25.76 (for GCP101-C) to 65.78 (for RKG-105), with an average count of 44.62. Similarly, the number of effective pods per plant displayed a mean of 38.01, ranging from 22.77 (for GCP101-C) to 61.06 (for RKG13-511).

The number of seeds per pod showed a range from 1.27 (observed in Vijay-C) to 2.56 (found in RKG13-511), with an average value of 1.66. Hundred-seed weight averaged 18.10 g, with values ranging from 2.20 g (for RKG13-253) to 26.84 g (for RKG13-504). Biological yield per plant had a mean of 22.17 g, ranging from 9.61 g (for RYS-201) to 41.53 g (for JG-16). The harvest index percentage had an average value of 38.64%, varying from 22.25% (for RKG13-504) to 50.34% (for JG-14). Seed yield per plant ranged from 6.00 g (for JG-16) to 15.16 g (for JG-14), with a mean value of 9.06 g.

This significant variation among chickpea genotypes in the subsequent season offers valuable opportunities for enhancing the crop's genetic makeup. This improvement can be achieved through the direct selection of promising genotypes or by utilizing them as parents in hybridization, leveraging their desirable traits for further crop enhancement.

## Phenotypic and Genotypic variance

The highest phenotypic and genotypic variances were identified in the total number of pods per plant, with values of 135.74 and 134.09, respectively. Subsequently, the number of effective pods per plant exhibited variances of 126.26 (phenotypic) and 124.84 (Genotypic). Plant height exhibited variances of 86.04 and 83.96 for phenotypic and genotypic, and harvest index had variances of 85.61 and 83.56 for phenotypic and genotypic, respectively. Biological yield per plant showed variances of 67.89 and 65.65 for phenotypic and genotypic, initiation flower days had variances of 63.59 and 62.92, and weight of seed in grams had variances of 65.41 and 63.25. Additionally, days to 50% flowering exhibited variances of 19.95 and 17.95, while 100-seed weight showed variances of 19.45 and 17.42, and basal height had variances of 9.61 and 7.83 during Season-I (2019-2020).

In the subsequent season, the highest phenotypic and genotypic variances were observed for the number of pods per plant, with values of 142.77 and 141.92, respectively. Effective pods number per plant exhibited variances of

118.27 and 117.10 for phenotypic and genotypic, respectively. Harvest index showed variances of 67.19 and 65.72 for phenotypic and genotypic, and plant height had variances of 79.87 and 78.88 for phenotypic and genotypic, respectively. Yield per plant displayed variances of 53.58 and 52.47, while flower initiation days had variances of 53.66 and 52.92. Lastly, 100-seed weight showed variances of 40.25 and 39.60 under the 2020-2021 season.

## Phenotypic and Genotypic coefficient of variation

In general, the estimates of genotypic coefficient of variation (GCV) consistently appeared lower than those of phenotypic coefficient of variation (PCV) for all the characteristics, indicating that the observed variation is not solely attributed to genotypes but is also influenced by the season (2019-2020). The highest values of phenotypic and genotypic coefficient of variation were observed in biological yield per plant, with values of 34.87% and 34.21%, respectively, followed closely by the number of effective pods per plant, which displayed values of 29.08% for phenotypic and 28.96% for genotypic coefficients of variation. The number of seeds per pod exhibited coefficients of variation at 28.50% (phenotypic) and 22.92% (genotypic), while seed yield per plant showed coefficients of variation at 28.16% (phenotypic) and 25.76% (genotypic). Pods per plant exhibited coefficients of variation at 25.96% and 25.80%, and the total 100-seed weight had coefficients of variation at 24.68% and 23.31%. Harvest index displayed coefficients of variation at 23.09% and 22.81%. Conversely, traits such as days to half flowering and plant maturity time had lower phenotypic and genotypic coefficients of variation.

Multiple studies consistently show strong and positive relationships between seed yield and the number of pods per plant in chickpeas. Furthermore, there is a highly significant positive correlation consistently observed between seed yield and the quantity of seeds produced. Additionally, a significant relationship is consistently identified between seed yield and the presence of branches and pods per plant in chickpeas. Grain yield per plant in chickpeas consistently exhibits significant genotypic associations and highly significant phenotypic correlations with primary branches, pods per plant, and seeds per plant. Moreover, the weight of 100 seeds in grams consistently demonstrates the highest phenotypic and genotypic coefficients of variation at 35.03% and 34.80%, respectively, closely followed by yield per plant, which consistently displays coefficients of variation at 33.01% and 32.70%, and seed yield, which consistently shows coefficients of variation at 29.21% and 28.02%. The number of effective pods per plant consistently exhibits coefficients of variation at 28.61% and 28.01%. In contrast, traits such as days to half flowering consistently exhibit low phenotypic and genotypic coefficients of variation in the 2020-2021 season.

## Heritability (Broad sense)

Regarding heritability in the broad sense, which assesses the contribution of genotypes to overall variation, the first season showed notably high heritability for the initiation of flowering days (98.94%), closely followed by the number of effective pods per plant (98.87%). However, basal height and seeds per pod exhibited relatively low heritability among the fourteen quantitative characteristics. In the second season (2020-2021), a remarkably high heritability of 99.01% was observed for the number of effective pods per plant, while the lowest heritability was recorded for the

number of seeds per pod. This discrepancy in heritability values could be attributed to the level of additive gene action, indicating that phenotypic selection might yield significant results. These findings are consistent with previous research conducted by Sharma and Saini (2010) [35] and Sidramappa et al. (2008) [37].

In the case of maturity days, we observed high heritability alongside low genetic advance, which suggests the potential influence of non-additive genetic variance. This indicates that selection may not be as effective in improving this trait. These observations are consistent with findings reported by Vaghela et al. (2008) [6] and Sharma and Saini (2010) [35]. Similar patterns have been documented by Desai et al. (2015) [5], Raju et al. (2017) [19], Banik et al. (2018) [2], and Singh et al. (2018) [48] for other traits such as plant height, days to half flowering, pod number per plant, 100-seed weight, and seed yield per plant. Mohan and Thiyagarajan (2019) [23] also noted a similar trend for the number of branches per plant and protein content, while Srivastava et al. (2017) [21] reported comparable findings.

Genetic advance was calculated for all 14 traits, as detailed in Table 2. In this study, the highest genetic advance as a percentage of the mean under sowing conditions was observed for biological yield per plant, with a value of 69.37%. This indicates the potential for improvement through selection in this trait. Traits such as plant height also exhibited a moderate genetic advance as a percentage of the mean, with a value of 37.97%. On the other hand, traits like days to maturity showed a low genetic advance as a percentage of the mean during the 2019-2020 season. In

the 2020-2021 season, the highest magnitude of genetic advance as a percentage of the mean was recorded for 100-seed weight, with a value of 71.02%, while plant height displayed moderate genetic advance as a percentage of the mean, with a value of 36.91%. In contrast, traits like days to 50% flowering exhibited low genetic advance as a percentage of the mean.

In the initial season of the experiment, biological yield per plant exhibited the highest phenotypic and genotypic coefficients of variation, while in the subsequent season, 100-seed weight displayed the highest phenotypic and genotypic coefficients of variation. Harvest index showed a moderate estimate of both PCV and GCV. In this study, it's noteworthy that the magnitude of phenotypic correlation was generally lower than the corresponding genotypic correlation coefficients for most traits. This observation suggests a strong inherent association among the studied traits, indicating that phenotypic selection may be advantageous. Similar results were reported by Pathak et al. (1986) [31]. A lower magnitude of phenotypic correlation can be helpful in selecting genetically controlled traits and may lead to a better response in seed yield improvement than would be expected based solely on genotypic associations, as noted by Robinson et al. (1951) [33]. For all other traits, differences in magnitude between GCV and PCV were relatively lower, except for biological yield and grain yield per plant.

**Path Coefficient Analysis**

**Table 1:** Genetic parameters of variability during season-I (2019-20)

| Trait | GM | Range | | Variance | | Coefficient of | | h² (B) % | GA | GA in % 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 | 83.92 | 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 |

In the initial season (2019-2020), the genotypic and phenotypic path coefficient analysis revealed that several yield-contributing characteristics, including effective pods number per plant, days to half flowering, basal height, harvest index, primary branches, 100-seed weight, seeds per pod, biological yield per plant, number of secondary branches, plant height, total number of pods per plant, and days to maturity, exhibited negative direct effects on seed yield per plant. However, in the following year (2020-2021), a high value of direct effects in the path coefficient analysis was observed, with days to maturity exhibiting the highest positive direct effect on seed yield per plant during this season. These findings are consistent with previous research

and align with earlier results for biological yield per plant (Thakur and Sirohi 2009; Shrivastava et al., 2012) [24, 22], harvest index, and number of pods per plant (Kuldeep et al., 2014) [12]. They also correspond with the findings of Dar et al. (2012) [8], Kuldeep et al. (2014) [19], Mishra et al. (2014) [22], and Shafique et al. (2016) [34] for days to maturity.

Breeding strategies aimed at increasing yield in chickpea genotypes were consistently applied in both seasons of this study, aligning with strategies previously reported for enhancing plant height (Talebi et al., 2007, Dar et al., 2012, Borate and Dalvi 2010, Shrivastava et al. 2012, Muhammad et al. 2012 and Hasan and Deb 2014) [22, 9, 8, 5, 45]. In addition

to direct effects, indirect effects also contribute to seed yield per plant through various traits.

It's important to note that the majority of indirect effects from different independent traits through other traits were minimal and often exhibited varying signs. Nevertheless, it's worth highlighting that the indirect effects of days to half flowering, maturity time, secondary branches, pod numbers, effective pods number per plant, days to flower initiation, and plant height were all positively associated with seed yield per plant.

The strong and positively significant relationships, along with the high direct effect on seed yield, imply that selection efforts should prioritize indirect pathways for enhancing yield. The notable and positive associations observed among different yield-related traits suggest substantial potential for improving seed yield in chickpea through targeted breeding strategies.

**Table 1:** Genetic parameters of variability during season-II (2020-21)

| 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 |

**Table 3:** Estimation of genotypic Indirect path coefficient for yield and yield Season-I (2019-2020)

| CH | FI | F 50% | DM | PI.ht (cm) | B. ht (cm) | PB | SB | TNPP | TNEP | S/P | 100 SW | BY(g) | HI (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 0.03294 | 0.06926 | -0.00093 | -0.02376 | 0.01957 | 0.06215 | -0.14031 | 0.08276 | -0.11807 | -0.02147 | 0.02177 | 0.02359 | 0.00053 |
| F 50% | 0.00737 | 0.30947 | -0.00376 | -0.02109 | 0.02030 | 0.00528 | -0.17858 | 0.09286 | -0.29302 | -0.01899 | 0.01363 | 0.02546 | -0.08477 |
| DM | 0.00714 | 0.27164 | -0.00428 | -0.02227 | -0.00620 | 0.01414 | -0.20530 | 0.09912 | -0.27606 | -0.01205 | 0.02171 | 0.03298 | -0.07566 |
| PH | 0.01058 | 0.08824 | -0.00129 | -0.07395 | 0.00373 | 0.01084 | -0.25134 | 0.14675 | -0.31862 | 0.01533 | 0.01401 | 0.00890 | -0.03979 |
| BH | 0.00243 | 0.02371 | 0.00010 | -0.00104 | 0.26506 | 0.04247 | 0.01665 | -0.08473 | 0.11863 | -0.06683 | -0.03091 | -0.02039 | 0.03647 |
| PB | 0.01131 | 0.00903 | -0.00033 | -0.00443 | 0.06221 | 0.18093 | -0.03317 | 0.01147 | -0.06071 | -0.02952 | 0.00236 | 0.00016 | 0.02984 |
| SB | 0.01160 | 0.13872 | -0.00221 | -0.04666 | -0.01108 | 0.01506 | -0.39859 | 0.10961 | -0.28816 | 0.02931 | 0.00647 | 0.01698 | -0.06958 |
| TNPPP | -0.00493 | -0.05198 | 0.00077 | 0.01963 | 0.04062 | -0.00375 | 0.07899 | -0.55283 | 0.82941 | 0.00532 | 0.01160 | 0.00106 | 0.08579 |
| TNEP | -0.00447 | -0.10420 | 0.00136 | 0.02708 | 0.03613 | -0.01262 | 0.13191 | -0.52687 | 0.87028 | 0.00357 | 0.00771 | 0.00470 | 0.10557 |
| SPP | -0.00454 | -0.03772 | 0.00033 | -0.00727 | -0.11369 | -0.03427 | -0.07493 | -0.01887 | 0.01994 | 0.15582 | 0.00026 | 0.04308 | -0.01971 |
| 100SW | 0.00758 | 0.04458 | -0.00098 | -0.01095 | -0.08659 | 0.00451 | -0.02726 | -0.06781 | 0.07091 | 0.00042 | 0.09461 | 0.01941 | 0.04104 |
| BY(g) | -0.00683 | -0.06929 | 0.00124 | 0.00579 | 0.04752 | -0.00026 | 0.05950 | 0.00516 | -0.03594 | -0.05903 | -0.01615 | -0.11371 | 0.00143 |
| HI(%) | 0.00007 | -0.11098 | 0.00137 | 0.01245 | 0.04090 | 0.02284 | 0.11726 | -0.20063 | 0.38867 | -0.01299 | 0.01643 | -0.00069 | 0.25639 |

Residual are 0.211

**Table 4:** Estimation of genotypic indirect path coefficient for yield and yield contributing traits during Season-II (2020-2021)

| CH | FI | F 50% | DM | PI.ht (cm) | B. ht (cm) | PB | SB | TNPP | TNEP | S/P | 100 SW | BY(g) | HI (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 0.21731 | -0.11399 | 0.31992 | -0.50028 | 0.1686 | 0.23753 | -0.47262 | -0.03043 | -0.01462 | 0.04872 | 0.04329 | 0.17251 | 0.01578 |
| F 50% | 0.07537 | -0.32866 | 0.67875 | -0.3979 | 0.08672 | 0.03451 | -0.29421 | -0.04205 | -0.03533 | 0.02673 | 0.01464 | 0.19187 | 0.02267 |
| DM | 0.08338 | -0.26757 | 0.83373 | -0.41753 | -0.87715 | 0.16729 | -0.43392 | -0.02685 | -0.02036 | -0.03368 | 0.02237 | 0.13146 | 0.03517 |
| PH | 0.10224 | -0.12298 | 0.32737 | -1.06336 | 0.10074 | 0.14736 | -0.37527 | -0.05383 | -0.03678 | 0.23971 | 0.00553 | 0.21226 | 0.05199 |
| BH | -0.06924 | 0.05386 | 0.12156 | 0.20245 | -0.52914 | -0.05288 | 0.07751 | 0.03873 | 0.01822 | 0.09733 | 0.00539 | 0.00328 | -0.01649 |
| PB | 0.08223 | -0.01807 | 0.22218 | -0.24962 | 0.04457 | 0.62775 | -0.21828 | -0.01212 | -0.00785 | -0.06893 | -0.10994 | -0.06181 | 0.00205 |
| SB | 0.13428 | -0.12642 | 0.46209 | -0.52173 | 0.05362 | 0.17915 | -0.76486 | -0.06328 | -0.03859 | 0.11524 | -0.03337 | 0.34728 | 0.02947 |
| TNPPP | -0.03056 | 0.06387 | -0.10343 | 0.26449 | -0.09468 | -0.03514 | 0.22363 | 0.21642 | 0.11522 | -0.07472 | -0.01861 | -0.07411 | -0.11573 |
| TNEP | -0.02621 | 0.09579 | -0.14002 | 0.32265 | -0.07953 | -0.04066 | 0.24348 | 0.20572 | 0.12121 | -0.17593 | 0.00366 | -0.13499 | -0.08925 |
| SPP | -0.02377 | 0.01972 | 0.06304 | 0.57227 | 0.11563 | 0.09715 | 0.1979 | 0.0363 | 0.04788 | -0.44541 | 0.08777 | -0.26266 | 0.02191 |
| 100SW | 0.03134 | -0.01603 | 0.06213 | -0.01958 | -0.0095 | -0.22993 | 0.08505 | -0.01342 | 0.00148 | -0.13025 | 0.30015 | 0.01591 | 0.05056 |
| BY(g) | -0.06493 | 0.10923 | -0.18984 | 0.39094 | 0.00301 | 0.06721 | 0.46007 | 0.02778 | 0.02834 | -0.20264 | -0.00827 | -0.57735 | 0.06089 |
| HI(%) | -0.01409 | 0.03061 | -0.12045 | 0.22711 | -0.03585 | -0.00529 | 0.0926 | 0.1029 | 0.04445 | 0.04009 | -0.06235 | 0.14444 | -0.2434 |

Residual are 0.45489

## Conclusion

In conclusion, this study has revealed a significant degree of variability across all the studied traits, which is a crucial factor for crop improvement efforts. It's noteworthy that the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for most traits, implying the influence of environmental factors on the expression of these traits. In the initial season of the experiment, biological yield per plant exhibited the highest phenotypic and genotypic coefficients of variation, whereas in the subsequent season, the highest phenotypic and genotypic coefficients of variation were observed for 100-seed weight. Furthermore, the trait with the maximum genetic advance as a percentage of the mean under sowing conditions was Effective pods number per plant. On the other hand, traits related to days to half flowering displayed low genetic advance as a percentage of the mean during the initial season. Genetic variability parameters are essential prerequisites for any breeding program, as they provide plant breeders with opportunities to select new genotypes that exhibit high yields in specific environments. The present study aimed to collect information on genetic variability for seedling parameters and their associations in chickpea, with the intention of proposing seedling selection criteria for future breeding programs.

## Reference

1. Abbo S, Berger J, Turner N. Evolution of cultivated chickpea: Four bottlenecks limit diversity and constrain adaptation. Functional Plant Biology. 2003;30:1081-1087.
2. AOAC. Official methods of analysis of the Association of Official Agricultural Chemists. 8th edition. Minnosta; c1965.
3. Babbar A, Patel SK. Correlation and path analysis in desi chickpea under Kymore plateau Zone of Madhya Pradesh. J.N.K.V.V. Res. J. 2015;39(1):47-51.
4. Banik M, Deore GN, Mandal AK, Mhase LB. Genetic variability and heritability studies in chickpea (*Cicer arietinum* L.). Current Journal of Applied Sciences and Technology. 2018;31(1):1-6.
5. Borate VV, Dalvi VV, Jadhav BB. Estimation of genetic variability and heritability in chickpea. Journal of Maharashtra agricultural universities. 2010;35(1):047-049.
6. Burton GW. Quantitative inheritance in grasses. Proceedings of 6th Grassland Congress Journal. 1952;1:277281
7. Croser, Janine, Clarke H, Siddique K. Low-Temperature Stress: Implications for Chickpea (*Cicer arietinum* L.) Improvement. Critical Reviews in Plant Sciences. 2003;22:185-219. 10.1080/713610855.
8. Dar SA, Ishfaq A, Khan MH, Pir FA, Gowhar A, Manzar A. Genetic variability and interrelationship for yield and yield component characters in chickpea. Trends in Biosciences. 2012;5(2):119-121.
9. Desai K, Tank CJ, Gami RA, Patel AM, Patel C. Character association analysis for yield, its components and nutritional quality in chickpea (*Cicer arietinum* L.). Research Journal of Agricultural Sciences. 2015;6(6):1280-1283.
10. Directorate of Economics and Statistics. Ministry of Agriculture Cooperation and Farmers Welfare (GOI). Agricultural statistics at a glance; c2019. p. 62-63.
11. Dwivedi KK, Gaibriyal ML. Assessment of genetic diversity of cultivated chickpea (*Cicer arietinum* L.) Asian J Agril Sci. 2009;1(1):7-8.
12. Falconer DS. Introduction to quantitative genetics. Oliver and Boyd, Edinburgh. 1960, 365.
13. Hasan MT, Deb AC. Estimates of direct and indirect effects between yield and yield components and selection indices in chickpea (*Cicer arietinum* L.). Tropical Plant Research. 2014;1(2):65-72.
14. Jha UC, Singh DP, Lavanya GR. Assessment of genetic variability and correlation of important yield related trait in chickpea (*Cicer arietinum* L.). Legume Res. 2012;35(4):341-344.
15. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(7):314-318.
16. Jukanti AK, Gaur PM, Gowda CL, Chibbar RN. Nutritional quality and health benefits of chickpea (*Cicer arietinum* L.): A review. Br J Nutr. 2012 Aug;108(1):S11-26.
    DOI: 10.1017/S0007114512000797. PMID: 22916806.
17. Kantar F, Hafeez FY, Shivkumar BG, Sundaram SP, Tejera NA, Aslam A, *et al*. Chickpea: Rhizobium management and nitrogen fixation. In: Yadav SS, Redden R, Chen W, Sharma B, editors. Chickpea Breeding and Management. CAB International; 2007. p. 179–192.
18. Kobraee S, Shamsi K, Rasekhi B, Rasekhi S. Investigation of correlation analysis and relationships between grain yield and other quantitative traits in chickpea (*Cicer arietinum* L.). African Journal of Biotechnology. 2010;9(16):2342-2348.
19. Kuldeep RK, Pandey S, Babbar A, Mishra DK. Genetic variability, character association and path coefficient analysis in chickpea grown under heat stress conditions. Electronic Journal of Plant Breeding. 2014;5(4):812-819.
20. Maiti RK. The chickpea crop. In: Maiti R, Wesche-Ebeling P, editors. Advances in Chickpea Science. Science Publishers Inc; c2001. p. 1–31.
21. Malik B, Khan, Malik M. Genetic variability and correlations among metric traits in chickpea. Pakistan Journal of Agriculture Research. 1988;9:352-354.
22. Mishra S, Babbar A. Selection strategies to assess the promising kabuli chickpea promising lines under different temperatures environments. Electronic J. of Plant Breeding. 2014;5(2):260-267.
23. Mohan, Thiyagarajan. Genetic Variability, Correlation and Path Coefficient Analysis in Chickpea (*Cicer arietinum* L.) for Yield and its Component Traits. Int. J Curr. Microbiol. App. Sci. 2019;8(5):1801-1808.
24. Muehlbauer FJ, Sarker A. Economic importance of chickpea: Production, value, and world trade, in The Chickpea Genome. Compendium of Plant Genomes, eds R. K. Varshney, M. Thudi, and F. Muehlbauer. 2017 (Cham: Springer International Publishing); c2017. p. 5-12. DOI: 10.1007/978-3-319-66117-9_2
25. Padmavathi P, Murthy S, Rao V, Mohammad Lal Ahamed. Correlation and path coefficient analysis in kabuli chickpea (*Cicer arietinum* L.). International Journal of Applied Biology and Pharmaceutical Technology. 2013;4:107-110.
26. Pal Saheb, Sharma Hem, Rai Amarjeet, Bhardwaj Ramesh. Genetic variability, heritability and genetic

gain for yield and quality traits in cucumber (*Cucumis sativus* L.). The Bioscan. 2018;11:1985-1990.

27. Pandey A, Gupta S, Kumar A, Thongbam PD, Pattanayak A. Genetic divergence, path coefficient and cluster analysis of chickpea (*Cicer arietinum* L.) cultivars, in the mid-altitudes of Meghalaya. Indian J of Ag. Sci. 2013;83(12):1300-1304.

28. Pandey S, Kureshi SP, Bhatore A. Studies on genetic variability and interrelationship among the different traits in exotic lines of lentil (*Lens culinaris* medik). Plant Archives. 2017;17(2):1164-1170.

29. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research Publication, New Delhi; c1967. p. 259.

30. Parameshwarappa SG, Salimath PM, Upadhyaya HD, Patil SS, Kajjidoni ST. Genetic variability studies in minicore collection of chickpea (*Cicer arietinum* L.) under different environments. Karnataka J of Ag. Sci. 2012;25(3):305-308.

31. Pathak CS, Singh A, Despande A, Sridar TT. Source of resistance to purple blotch in onion. Veg. Sci. 1986;13:300-303.

32. Raju T, Sadhukhan R, Satish V. Genetic variability studies in chickpea (*Cicer arietinum* L.) for yield and yield related traits. Bulletin of Environment, Pharmacology and Life Sciences. 2017;6(2):177-183.

33. Robinson HF, Comstock RE, Harvery PH. Genotypic and phenotypic correlations in corn and their implication in selection. Agron. J. 1951;43:282-287.

34. Shafique. Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in Chickpea (*Cicer arietinum* L.) Academia Journal of Agricultural Research. 2016;4(2):082-085. February 2016 DOI: 10.15413/ajar.2015.0184 ISSN: 2315-7739.

35. Sharma LK, Saini DP. Variability and association studies for seed yield and yield components in chickpea (*Cicer arietinum* L.). Research Journal of Agricultural Sciences. 2010;1:209-211.

36. Shrivastava A, Babbar A, Shrivastava SP, Shukla SS. Variability studies in some genotypes of chickpea (*Cicer arietinum* L.) under rice fallow. J. of Food Leg. 2012;25;70-72:0970-6380. ISSN: 0976-2434.

37. Sidramappa Patil SA, Salimath PM, Kajjidoni ST. Genetic variation for productivity and its related traits in a recombinant inbred lines population of chickpea. Karnataka Journal of Agricultural Sciences. 2008;21:488-490.

38. Singh M, Kumar T, Sood S, Malhotra N, Rani U, Singh S, *et al*. Identification of promising chickpea interspecific derivatives for agro-morphological and major biotic traits. Front. Plant Sci. 2022;13:941372. DOI: 10.3389/fpls.2022.941372

39. Srivastava Lavanya GR, Lal GM. Genetic variability and character association for seed yield in chickpea (*Cicer arietinum* L.) E-ISSN: 2278-4136; c2017.

40. Talebi R, Fayaj F, Jelodar AB. Correlation and path coefficient analysis of yield component of chickpea (*Cicer arietinum* L.) under dryland condition in the west of Iran. Asian J Plant Sciences. 2007;6(7):1151-1154.

41. Thakur SK, Sirohi A. Correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.) under different seasons. Legume Res. 2009;32(1):1-6.

42. Upadhaya HD, Dwivedi SL, Gowda CLL, Singh S. Identification of diverse germplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.) core collection for use in crop improvement. Field Crop Res. 2007;100:320-326.

43. Vaghela MD, Poshiya VK, Savaliya JJ, Kavani RH,Davada BK. Genetic variability studies in Kabuli chickpea (*Cicer arietinum* L.). Leg. Res. 2008;32(3):191-194.

44. Waldia RK, Ramesh RS. Generation mean analysis and genetic parameters for yield and contributing traits in chickpea (*Cicer arietinum* L). Indian Journal of Agricultural Sciences. 2012;82(6):528-531

45. Yaqoob Muhammad, Hollington Phill, Mahar Ahmad, Gurmani Zulfiqar. Yield performance and responses studies of Chickpea (*Cicer arietinum* L.) genotypes under drought stress. Emirates Journal of Food and Agriculture. 2012;25:10.9755/ejfa.v25i2.10655.

46. Yucel DO, Anlarsal AE. Determination of Selection criteria with Path coefficient analysis in chickpea (*Cicer arietinum* L.). Bulgerian Journal of Agricultural Sciences. 2010;16:42-48.

47. Van der Maesen LJ. Het beestje moet een naampje hebben; Taxonomie. Kweek. 1987(93):13-4.

48. Singh R, Upadhyay AK, Chandra P, Singh DP. Sodium chloride incites reactive oxygen species in green algae *Chlorococcum humicola* and *Chlorella vulgaris*: implication on lipid synthesis, mineral nutrients and antioxidant system. Bioresource technology. 2018 Dec 1;270:489-97.

49. Katiyar JC, Visen PK, Gupata S, Sen AB, Dubey SK, Sharma S. 3, 5-Dibromo-2′-chloro-4′-isothiocyanatosalicylanilide, a potent anthelminitic. Experientia. 1982 Apr;38:457-60.