



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.1.125>

REVEALING THE GENETIC VARIABILITY AND CORRELATION STUDIES FOR PRODUCTIVITY TRAITS IN ADVANCED BREEDING LINES OF CHICKPEA (*CICER ARIETINUM* L.)

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(Date of Receiving-01-01-2024; Date of Acceptance-07-03-2024)

ABSTRACT

A breeding effort was carried to investigate genetic variability, heritability, predicted genetic advance and the association studies between seed yield, yield attributing traits and quality traits during *Rabi* 2022–2023 at ZARS, Kalaburagi, India. The study was taken up with 14 genotypes, which includes advanced breeding lines and released variety as checks were planted in three replications using randomized complete block design. Studies on genetic variability have shown that every character was unaffected by the environment to the same extent. The genotypic coefficient of variation was slightly lower than the phenotypic coefficient of variation indicating that the existing variation is not only by the genotypes but also to some extent by the environment. For the majority of the traits, high to moderate genetic advance was found in conjunction with high heritability. This indicates presence of additive gene action. Hence, breeders can exploit these traits through phenotypic selection. The number of branches and pods on a plant were two key traits that showed a significant association with seed yield whereas, swelling capacity, hydration capacity and cooking time are positively associated with 100 seed weight. Thus, breeders can exploit those traits influenced by additive gene action for further genetic improvement in chickpea and it is possible to develop chickpea genotypes with high yielding and less cooking time. Finally, this investigation should be repeated over years and locations to confirm future breeding program.

Key words : Advanced Breeding lines, Correlation, Genetic variability, Heritability, Yield attributing traits.

Introduction

Chickpea (*Cicer arietinum* L.) is a self-pollinated, diploid ($2n = 2x = 16$) species with a genome size of 738 Mb (Varshney *et al.*, 2018). Chickpea belongs to a family Fabaceae (Leguminosae). There are nine annual and nearly 34 perennial wild species reported in chickpea (Singh *et al.*, 2014). *Cicer arietinum* is the only annual species that is grown (Solanki *et al.*, 2022). Chickpea (*Cicer arietinum* L.) play an important role in both sustainable agriculture and food security. Particularly in areas with limited resources, its high protein content, essential amino acids, and capacity to fix atmospheric nitrogen make it an indispensable source of nutrition.

However, the potential of chickpea cultivation is often hindered by various biotic and abiotic stresses, leading to yield losses and compromising the quality of the harvested produce. The necessity to enhance both seed yield and quality traits in chickpea varieties has led to extensive breeding efforts. Chickpea is an ancient crop of modern times that occupied cultivable lands in nearly 50 countries around the world and accounts for more than 20 per cent of world pulse production, moreover, much of the world's chickpea supply (80-90%) comes from India. India ranks first in area (9.9 million ha) and production (11.9 million tonnes) of chickpea in the world, with a productivity of 1192 kg ha⁻¹ (Anonymous, 2022). In India, Karnataka

ranks fourth in the cultivation of chickpea with an area of 0.713 million ha, with a yearly production of 0.4 million tonnes and productivity of 733 kg ha⁻¹ (Anonymous, 2022).

Since breeding efforts mainly depend on the selection process, which in turn relies on the influence of genes on the characteristics found for improvement, the significance of heritability in the production of chickpea genotypes with high yielding cannot be understated. (Karthikeyan *et al.*, 2022). Heritability serves as a crucial indicator of the transferability of a characteristic from parents to their offspring, representing proportion of existing variation that is attributable to genes. A higher heritability value signifies the effectiveness of selection in enhancing a trait within a population. This metric is mathematically expressed as the ratio between genetic and phenotypic variance and is typically categorized as high (above 60%), medium (30-60%), or low (below 30%) by Kumar *et al.* (2019).

In cases where traits are complex and influenced by multiple genes, the selection process becomes complex due to the ambiguous inheritance patterns. For such traits, indirect selection becomes essential, where other traits closely associated with the target traits are selected instead. Several studies have utilized correlation analysis to establish connections between yield and its related

traits (Karthikeyan *et al.*, 2022 and Kumar *et al.*, 2019). While numerous studies have revealed heritability and correlations between yield and its contributing traits. Thus, the research focused on GCV, PCV and heritability in chickpea and also studies on examining the correlation association between seed yield and its contributing traits.

Materials and Methods

A set of 14 chickpea genotypes collected from Zonal Agricultural Research Station (ZARS), Kalaburagi, Karnataka, India which includes Advanced Breeding Lines and released varieties (Table 1) were evaluated for yield performance (kg/ha), variability and correlation studies during *Rabi* 2022-2023. The experiment was carried out at (ZARS), Kalaburagi. The site of experiment is situated in the North Eastern dry zone of Karnataka (Zone 2) located between 17.32° North latitude and 76.54° East longitude at a rise of 443 m higher than the mean sea level with an average rainfall of 34.80 mm. The weather during the crop grown period was recorded at a meteorological observatory in ZARS, Kalaburagi and is presented in supplementary 1. Each genotype was grown in four rows of four meters in length with 30 cm space between rows and 10 cm space between plants. A fertilizer dose of 20:50:0 NPK kg ha⁻¹ was applied to the crop as a basal application. The crop was grown in weed

Table 1 : Details of 14 chickpea genotypes obtained from AICRP scheme, ZARS, Kalaburagi.

| S. no. | Genotype | Parentage | Characteristic features |
|--------|-------------------|---|---|
| 1 | BGD 111-1 | JG-62 × ICC 12237//JG-62 | High yielding, wilt resistance, desi variety |
| 2 | GJG 1913 | PG 07104 × WR-315 | High yielding variety suitable for irrigated condition and mechanical harvesting |
| 3 | ICC 4958 | ICRISAT collection | Bold seeded, check variety for drought trail |
| 4 | KCD 20-03 | GG 2/ICC 1205 | High yielding, wilt resistance medium seed size desi genotype |
| 5 | KCD 20-8 | ICCV 93954//ICCV 93954// ICCV 96029/ICCV 93954 | High yielding, wilt resistance, medium seed size desi genotype |
| 6 | KCD 21-6 | NBeG-857 | High yielding, wilt resistance medium sized seeds. |
| 7 | KCD-11 | JG-11 × WR-315 | High yielding, wilt resistant desi genotype |
| 8 | KCD-134 | ICCV 03112 × ICCV 10 | High yielding, wilt resistant variety, suitable for irrigated condition |
| 9 | KCMH 20-17 | ICCV 10/ICCV 11601 | High yielding wilt resistant, medium sized seeds, suitable for mechanical harvest |
| 10 | KCMH-2 | GBM-2 × WR-315 | High yielding wilt resistant and suitable for mechanical harvest |
| 11 | GBM-2 | Mutant of Annigeri 1 | High yielding suitable for mechanical harvest (National / zonal check) |
| 12 | JG-11 | ICCV 93954 | High yielding wilt resistant desi variety (National check) |
| 13 | JG-14 | (GW 5/7 x P327) × ICCL83149 | Heat stress check |
| 14 | SA-1 | Annigeri-1 × WR-315 | High yielding, wilt resistance desi variety (MABC line)/Zonal & Regional Check. |

Supplementary 1 : Monthly meteorological data during the research period (2022-23) recorded at ZARS, Kalaburagi.

| Month | Temperature (°C) | | Relative humidity (%) | | Rainfall(mm) | No. of rainydays |
|----------------|------------------|--------------|-----------------------|--------------|--------------|------------------|
| | Max | Min | Morning | Afternoon | | |
| September 2022 | 30.92 | 23.35 | 84.10 | 82.49 | 115.2 | 11 |
| October 2022 | 30.89 | 21.52 | 77.85 | 78.35 | 128.4 | 8 |
| November 2022 | 31.30 | 18.70 | 57.49 | 87.51 | 0 | 0 |
| December 2022 | 30.29 | 17.27 | 78.00 | 73.33 | 0 | 0 |
| January 2023 | 30.40 | 15.69 | 66.89 | 45.56 | 0 | 0 |
| February 2023 | 32.73 | 18.41 | 63.65 | 58.85 | 0 | 0 |
| March 2023 | 34.90 | 21.84 | 57.07 | 24.81 | 0 | 0 |
| Average | 31.63 | 19.54 | 69.29 | 64.41 | 34.80 | 2.71 |

free through inter cultivation and manual weeding. In accordance with UAS, Raichur's recommended practice package, additional cultural techniques and plant protection measures were implemented to ensure a high-quality crop. At each entry in each replication, data were recorded on five randomly chosen plants. The GCV and PCV were calculated by the formulae given by Burton (1952). Broad sense heritability and predicted genetic advance were calculated as per Johnson *et al.* (1955). Phenotypic correlation coefficients were computed as per the methods suggested by Al-Jibouri *et al.* (1958). The statistical analysis on the individual character was carried out by WINDOSTAT software on the mean value of five randomly selected plants.

Results and Discussion

The presence of genetic diversity is a prerequisite for crop improvement as it provides a wider range for selection of yield attributing characters. Thus, selection efficiency depends upon the nature, extent and magnitude of genetic variation present in the material and also the extent to which it is transferable to next generation. In plant breeding, the extent to which a phenotype is genetically determined is known from heritability values (Lourenco *et al.*, 2017). Broad sense heritability along with response to selection would be more valuable in predicting the success of choosing the best individuals (Johnson *et al.*, 1955). Hence, it is important to consider the predicted heritability along with predicted response as a tool in the selection programme for enhanced efficacy in choosing the best individuals.

Among the advanced breeding lines, highest range was registered for fifty percent flowering, 100 seed weight, plant height, pods per plant, cooking time and seed yield indicating the presence of genetic variability in the advanced lines as indicated in Table 2. Therefore, we can rely upon these lines in breeding programme for crop improvement.

Among all the traits, PCV was higher than the GCV indicating the influence of environmental effects in the trait expression to a certain extent. High phenotypic and genotypic coefficient of variation was registered for 100 seed weight, number of branches and pods per plant, hydration capacity and swelling capacity (Fig. 1). Mohammed *et al.* (2019) and Joshi *et al.* (2018) reported for 100 seed height, number of pods and branches per plant. Days to first and 50% flowering, days to vegetative phase, leaf area index, harvest index, plant height and cooking time recorded moderate PCV and GCV values. These results were similar with Shivkumar *et al.* (2013) for days to first and 50% flowering, Raju *et al.* (2017) and Desai *et al.* (2015) for days to vegetative phase, Kumar *et al.* (2019), Akanksha *et al.* (2016) for harvest index, Tsehaye *et al.* (2020) and Arora *et al.* (2018) for plant height and Tripathi *et al.* (2012), Saxena *et al.* (2013) for cooking time. Low PCV and GCV values were observed for days to reproductive phase and days to maturity. Similar results were showed by Malik *et al.* (2010) and Raju *et al.* (2017) for days to reproductive phase and Banik *et al.* (2018), Mohammed *et al.* (2019) and Mohan *et al.* (2019) for days to maturity.

Heritability estimates are considered in better understanding the inheritance of quantitative characters like seed yield and yield components. Similarly, predicted genetic advance is also a useful measure to predict gain in specified selection intensity. However, when it is combined along with heritability becomes more valuable to predict response to selection than the heritability estimates alone.

High heritability combined with high predicted genetic advance were registered for number of branches and pods per plant, hydration capacity, swelling capacity, cooking time, 100 seed weight, leaf area index, days to first and 50% flowering, days to vegetative phase and seed yield. Hence, these traits were controlled by additive gene action as shown in Table 2. Similar research findings

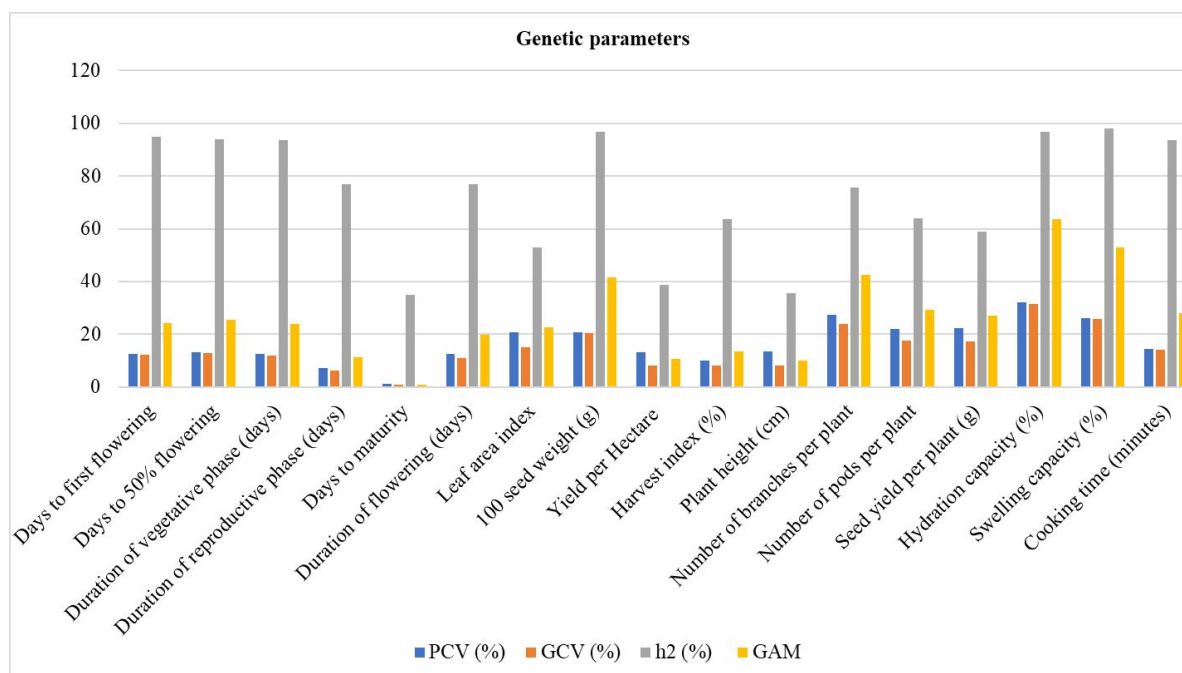


Fig. 1 : Estimation of coefficient of variation (PCV and GCV), heritability and genetic advance for 17 characters in chickpea for yield and yield attributing traits.

Table 2 : Estimation of genetic variability parameters in chickpea for yield and yield attributing traits.

| S. no. | Characters | Coefficient of variation | | h ² (%) (Broad sense) | GAM (5%) |
|--------|---------------------------------------|--------------------------|---------|----------------------------------|----------|
| | | PCV (%) | GCV (%) | | |
| 1 | Days to first flowering | 12.36 | 12.04 | 94.81 | 24.1 |
| 2 | Days to 50% flowering | 13.13 | 12.72 | 93.9 | 25.4 |
| 3 | Duration of vegetative phase (days) | 12.34 | 11.93 | 93.5 | 23.8 |
| 4 | Duration of reproductive phase (days) | 7.1 | 6.22 | 76.93 | 11.2 |
| 5 | Days to maturity | 1.27 | 0.75 | 35.01 | 0.91 |
| 6 | Duration of flowering (days) | 12.49 | 10.95 | 76.93 | 19.8 |
| 7 | Leaf area index | 20.75 | 15.1 | 52.97 | 22.6 |
| 8 | 100 seed weight (g) | 20.84 | 20.5 | 96.76 | 41.5 |
| 9 | Seed yield (Kg/ha) | 13.1 | 8.16 | 38.81 | 10.5 |
| 10 | Harvest index (%) | 10.12 | 8.07 | 63.61 | 13.3 |
| 11 | Plant height (cm) | 13.45 | 8.01 | 35.48 | 9.83 |
| 12 | Number of branches per plant | 27.34 | 23.77 | 75.53 | 42.6 |
| 13 | Number of pods per plant | 22.09 | 17.67 | 64.02 | 29.1 |
| 14 | Seed yield per plant (g) | 22.32 | 17.12 | 58.82 | 27 |
| 15 | Hydration capacity (%) | 31.97 | 31.43 | 96.7 | 63.7 |
| 16 | Swelling capacity (%) | 26.15 | 25.91 | 98.17 | 52.9 |
| 17 | Cooking time (minutes) | 14.48 | 14.01 | 93.68 | 27.9 |

were reported by Tripathi *et al.* (2012), Saxena *et al.* (2013) for hydration capacity, swelling capacity and cooking time. Anand *et al.* (2019), Awol *et al.* (2019) reported similar results for seed yield, number of branches and pods per plant. High heritability with moderate response to selection was observed for days taken to reproductive phase and flowering, plant height and harvest

index. Therefore, these characters were dominated by both additive and non-additive gene action. Raju *et al.* (2017) reported similar findings for days to flowering and reproductive phase. Tsehaye *et al.* (2020), Anand *et al.* (2019) reported for plant height and harvest index. High heritability with low predicted genetic advance was observed for days to maturity, indicating that this trait is

Table 3 : Estimation of phenotypic correlation coefficients for yield and yield attributing traits of chickpea genotypes.

| | DF | DFE | DVP | DRP | DM | DUF | LAI | HSW | HI | PH | BP | PP | YP |
|-----|----------|---------|-----------|----------|---------|----------|--------|----------|---------|---------|----------|---------|----|
| DF | 1 | | | | | | | | | | | | |
| DFE | 0.337* | 1 | | | | | | | | | | | |
| DVP | 0.991*** | 0.349* | 1 | | | | | | | | | | |
| DRP | -0.889** | -0.351* | -0.885*** | 1 | | | | | | | | | |
| DM | 0.441** | 0.369 | 0.448** | -0.299 | 1 | | | | | | | | |
| DUF | -0.878** | -0.320* | -0.872*** | 0.596 | -0.269 | 1 | | | | | | | |
| LAI | -0.349* | 0.075 | -0.356* | 0.336* | 0.018 | 0.358* | 1 | | | | | | |
| HSW | -0.456* | -0.282 | -0.442** | 0.288 | -0.358* | 0.214 | 0.165 | 1 | | | | | |
| HI | -0.390* | -0.258 | -0.394** | 0.409** | -0.368* | 0.405** | -0.060 | -0.064 | 1 | | | | |
| PH | 0.438** | 0.263 | 0.457** | -0.467** | 0.289 | -0.487** | -0.188 | 0.073 | 0.408** | 1 | | | |
| BP | 0.528** | 0.377* | 0.522** | -0.441** | 0.035 | -0.434** | -0.259 | -0.451** | -0.098 | 0.282* | 1 | | |
| PP | 0.302 | 0.074 | 0.296 | -0.163 | -0.042 | -0.101 | -0.079 | -0.367* | 0.381** | 0.311** | 0.636*** | 1 | |
| YP | 0.165 | 0.188 | 0.1624 | -0.111 | -0.135 | -0.098 | 0.003 | 0.0226 | 0.079 | 0.1353 | 0.582** | 0.840** | 1 |

Where,

DF :- Days to first flowering

DFE :- Days to 50% flowering

DVP :- Duration of vegetative phase (days)

DRP :- Duration of reproductive phase (days)

DM :- Days to maturity

DUF :- Duration of flowering (days)

LAI :- Leaf area index

HSW :- 100 seed weight (g)

HI :- Harvest index (%)

PH :- Plant height (cm)

BP :- Number of branches per plant

PP :- Number of pods per plant

YP :- Seed yield per plant (g)

influenced by non-additive gene action and Barad and Javia (2018), Karthikeyan *et al.* (2022) registered similar results.

The correlation coefficient is the measure of the degree of symmetrical association between two characters which helps us in understanding the nature and magnitude of association between yield and its attributing traits. It provides a better understanding of productivity traits, which helps the breeder during selection. A positive correlation between desirable traits is favourable to the plant breeder because it helps to improve both characters simultaneously. A negative association, on the other hand, will prevent the simultaneous expression of the two characters with high values by Navaselvakkumaran *et al.* (2019).

The number of pods (0.840) and branches per plant (0.582) had extremely significant and positive phenotypic correlation with seed yield, lines with more pods and more branches tend to have significantly higher seed yield per plant (Table 3). The correlation between days to first flowering (0.165), 50 per cent flowering (0.188), duration of vegetative phase (0.1624), leaf area index (0.003), 100 seed weight (0.0226), harvest index (0.079) and plant height (0.1353) recorded non-significant and positive phenotypic correlation with seed yield. The characters *viz.*, duration of the reproductive phase (-0.111), days to

maturity (-0.135) and duration of flowering (0.098) showed non-significant and had negative phenotypic correlation with seed yield. Similar findings for the seed yield per plant were reported by several other researchers and the seed yield per plant had a positive significant association with harvest index and number of pods per plant by Tare *et al.* (2023), Katkani *et al.* (2022), Kumawat *et al.* (2021) for number of branches and pod per plants. Kuldeep *et al.* (2014) for plant height, number of branches, number of pods per plant and 100 seed weight reported in chickpea. Anand *et al.* (2019) for days to 50 per cent flowering; Agrawal *et al.* (2018) for leaf area index; Rathod *et al.* (2020), Mohan *et al.* (2019) for 100 seed weight and Ali *et al.* (2010) showed negative correlation of days to flowering with seed yield.

Conclusion

The advanced breeding lines and varieties were evaluated during *Rabi* 2022-23 for productivity traits. High phenotypic and genotypic coefficient of variation was registered for 100 seed weight, number of branches and pods per plant, hydration capacity and swelling capacity. This is attributed to the dominance of additive gene action and possesses high selective value and thus, selection pressure could profitably be applied on these characters for crop improvement. High magnitude of GCV observed for grain yield indicates the presence of

wide variation to be allowed for further improvement by selection. Those traits, which showed high heritability combined with high genetic advance, we can rely upon these characters for crop improvement, as these traits were dominantly controlled by additive gene action. Correlation studies disclosed that number of pods (0.840) and branches per plant (0.582) had significant positive association with seed yield. Therefore, selection for these traits is expected to result in higher seed yield.

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