

Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.)

Thesis submitted for the award of the degree of

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In

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2026

DECLARATION

I hereby declared that the presented work in the thesis entitled “**Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.)**” fulfillment of degree of **Doctor of Philosophy (Ph.D.)** is outcome of research work carried out by me under the supervision Dr. Suhel Mehandi , Associate Professor, Department of Genetics and Plant Breeding School of Agriculture Lovely Professional University, Punjab, India. In keeping with general practice of reporting scientific observations, due acknowledgements have been made whenever work described here has been based on findings of another investigator. This work has not been submitted in part or full to any other University or Institute for the award of any degree.

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CERTIFICATE I

This is to certify that the work reported in the Ph.D. thesis entitled “**Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.)**” submitted in fulfillment of the requirement for the reward of degree of Doctor of Philosophy (Ph.D.) in the Department of Genetics and Plant Breeding, is a research work carried out by **Bukke Naveen Kumar Naik (Registration No. 12106468)**, is Bonafide record of his original work carried out under my supervision and that no part of thesis has been submitted for any other degree, diploma or equivalent course.

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Place: Phagwara, Punjab

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“Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.)”

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ABSTRACT

This study was conducted during the *rabi* season of 2023-24 at the Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara (Punjab), to assess genetic variability, heterosis, combining ability, and genetic divergence among chickpea (*Cicer arietinum* L.) genotypes for yield and its component traits. The experimental material included 30 genotypes for variability assessment and 32 F₁ hybrids developed through Line × Tester mating design involving 8 lines and 4 testers. Analysis of variance revealed highly significant differences among genotypes and crosses for most traits, highlighting substantial genetic variability and heterotic potential. Traits such as harvest index, 100-seed weight, and biological yield showed strong positive direct effects on seed yield per plant as revealed by path analysis. Violin plot integrated with DMRT differentiated superior genotypes such as CSJ515, GL25016, and VIJAY based on trait performance. Correlation studies revealed strong genotypic and phenotypic associations of seed yield with harvest index and 100-seed weight. Genetic diversity analysis grouped the genotypes into five distinct clusters, with Cluster V showing superior trait means and maximum inter-cluster distance observed between Clusters IV and V. Combining ability analysis indicated that both additive and non-additive gene actions governed trait inheritance, with significant general combining ability (GCA) effects in parents like PUSA 362 and ICCL 86111 and superior specific combining ability (SCA) in crosses such as PUSA 362 × GNG 1488 and ICCL 86111 × JAKI 9218. Heterosis analysis revealed significant mid-parent and standard heterosis for yield and its components in selected crosses.

Keywords: Chickpea, genetic variability, Line × Tester, correlation, path analysis, heterosis, genetic divergence, combining ability.

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Abbreviations

Symbols/Abbreviations	Legend
&	And
@	At the rate of
%	Percent
°C	Degree Celsius
C.D.	Critical Difference
Cm	Centimetre
C.V.	Coefficient of Variation
DAS	Days after sowing
d.f.	Degree of Freedom
S.S	Sum of square
SOV	Source of variation
ANOVA	Analysis of variance
Viz.,	Namely
et al.,	And others
Etc	And the rest
fig.	Figure
FAO	Food and Agricultural Organization
g, kg	Gram, Kilogram
ha	hectare,
MSS	Mean Sum of Square
PCV & GCV	Phenotypic and genotypic coefficient of variation
σ_e	Environmental variance
V_p	Phenotypic variance
V_g	Genotypic variance
$h^2 = V^A/V^P$	Narrow sense heritability
$H^2 = V_g / V_p$	Broad sense heritability
GA	Genetic Advance
GAM	Genetic Advance as percent of mean
GCA	General Combining Ability
SCA	Specific Combining Ability
F1	Mean value of Hybrid

Chapter I

INTRODUCTION

Chickpea [*Cicer arietinum* L.] is a self-pollinated pulse crop and diploid ($2n = 2x = 16$) with a genome size of 738.09 Mbp (Varshney *et al.*, 2014). It is also known as gram, bengal gram, belongs to genus *Cicer*, family Fabaceae, sub family Papilionaceae. Globally, it is the third most important pulse crop after faba bean and field pea (Tesfamichael *et al.*, 2014). World chickpea production was estimated at 16.5 million tons in 2023(FAO 2023). It is a winter crop widely grown in arid and semi-arid regions of the world. Chickpea is the important pulse crop in the world due to its nutritive value, so it is used as a diet for humans and in some cases used as a feed for livestock and it could also fit well into crop rotation with the cereal crops to improve the soil fertility, prevent the build-up of biotic and abiotic stresses. On keeping in view of large benefits of pulses i.e., source of protein, higher fibre content, ample quantity of vitamins and minerals, the United Nations has proclaimed 2016 as the International Year of Pulses. Since, cereals combined with pulses are a major diet for billions of people, chickpeas are being targeted in many countries so that malnutrition problem can be controlled to some extent.

Chickpea (*Cicer arietinum* L.), self-pollinating grain legume crop with a rich source of protein (15–22%), carbohydrates (50–58%), fat (3.8–10.20%), vitamins, and micronutrients (Madurapperumage *et al.* 2021). Chickpea is cultivated mostly in India as a rainfed crop (68% area) in all parts of a country (Dixit *et al.*, 2019). India is the world's largest producer of chickpea. In india annual production of 2024-2025 agricultural year, India's chickpea production is estimated at 11.337 million metric tons (MMT), based on the third advance estimates released by the Ministry of Agriculture and Farmers Welfare in May 2025.

While official state-specific data for the final 2024–2025 estimates may vary, forecasts indicate that the following states will be the leading producers Maharashtra Projected to lead with approximately 3.06 MMT. Madhya Pradesh Expected to produce around 2.46 MMT. Rajasthan Estimated at 1.97 MMT. Gujarat Forecasted to contribute about 1.48 MMT. India covers about 70% of the acreage and is the world leader in terms of production..

India, a major pulse producing country, accounts roughly 33 per cent of the total world production. Pulses are grown both during *Kharif and Rabi* seasons. Out of the total area and production under pulses, the area of *Kharif and Rabi* pulses accounts 45 and 55 per cent, respectively. The mean protein content in chickpea is nearly 18% [(kabuli: 18.4% (16.2–22.4%); desi: 18.2% (15.6–21.4%)], which is higher than lentil and field pea (Upadhyaya *et al.*, 2016).

Chickpea ranks third in the global production of pulses at ~11.6 million tons per annum, 80% of which is desi and the remaining 20% is kabuli (Merga and Haji, 2019). Chickpea is grown in nearly 57 countries worldwide in varying climatic and growing conditions (Merga and Haji, 2019). According to data from the Food and Agriculture Organization of the United Nations (FAO 2023) and industry analysis, India is the world's largest chickpea producer by a substantial margin. In recent years, India has accounted for 65–75% of total global production. While total production can fluctuate, major players have remained consistent. In the last two decades, the harvested area has correlated with chickpea production, and both generally show an increase over time (except for lower production in 2015 and

2019; FAOSTAT, 2020)..

Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population and the germplasm serves as a valuable source of base population and provide scope for wide variability (Ramya and Senthilkumar, 2009). The importance of broad genetic base in evolving new cultivars by incorporating new genes in the existing one is well organized. Being a self-pollinated crop, chickpea exhibits a good amount of variability for various characters. Coefficient of variation is useful in the assessment of genetic variability for the particular characters. Heritability denotes the proportion of phenotypic variation due to genotypes thus help the breeders to select the elite genotype for a character. Based on the evaluation for different morphological characters and yield attributes, the breeder can easily identify the various desirable characters present in different genotypes and quite often use them in breeding programme to improve the yield and quality. Genotypic and phenotypic variances make available the information of variability only but the heritable portion of this variation is determined by the estimates of heritability. For that reason awareness of these values of the resources in which breeders are paying attention is of enormous importance. High heritability estimates signify the effectiveness of these characters through selection for crop improvement, as less environmental influences are involved in it (Maniee *et al.*, 2009)

The combining ability studies of the genotypes provide information which helps in the selection of better parents for effective breeding. Its role is important to decide parents,

crosses and appropriate breeding procedure to be followed to select desirable segregants (Salgotra *et al.*, 2009). Good general combining parent result in higher frequency of heterotic hybrids than poor combining parent. From the genetic point of view, general combining ability measures additive gene effects and specific combining ability measures non-additive gene effects, depending on genes with dominance (intra-allelic interactions) and epistasis (inter-allelic interactions). Combining ability analysis enables the breeder in his task of selecting the parents. It also provides the vital and necessary information on the nature of gene action governing the expression of the character in question and thus helps in deciding upon the future breeding strategy (Priyanka *et al.*., 2024).

The Exploitation of heterosis is an important approach towards the improvement of crop. The phenomenon of heterosis is of wide spread occurrence in field of biological sciences. Hybrid vigour was first observed by Koelreuter in 1673 in tobacco and was studied by numerous other workers (Singh, 1996) and the clear approach to the concept of heterosis was made by Shull (1914). In chickpea many workers studied heterosis. A study of combining ability helps in identifying the useful parental lines and the desirable specific cross combination which could be further exploited in development of improved varieties. Such studies are essential in choosing the appropriate breeding and selection methodologies for further improvement of crop. Combining ability analysis is frequently employed to identify the desirable parents and crosses. Therefore, it is urgently required to identify the best combiners and desirable crosses. Line X Tester analysis is an extension of top cross method in which several testers are used (Kempthorne, 1957) which provides information about general and specific combining ability of parents and at the same time it is helpful in identifying best heterotic crosses.

Assessing the performance and compatibility of genotypes is crucial for optimizing hybridization success. Techniques like diallel, partial diallel, and line x tester offer different methods to estimate breeding requirements. In particular, the line x tester mating design allows for the evaluation of specific combining ability (SCA) for individual crosses and general combining ability (GCA) for lines and testers, providing valuable insights for improving breeding strategies (Anvesh *et al.*, 2024)

Keeping in view the above discussions, the present investigation, entitled "Assessment of Genetic Diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum L.*)" was proposed with the following objectives:

1. Assessment of genetic diversity in chickpea.
2. To study the combining ability variances and gene action in chickpea.
3. To estimate of heterosis (Mid parent, heterobeltiosis and standard heterosis) in chickpea.

Chapter II

REVIEW OF LITRATURE

Table 2.1. Genetic variability and diversity

Genetic variability and diversity are essential for chickpea breeding programs to develop improved varieties with higher yields, resilience to climate change, and resistance to pests and diseases.

Genetic diversity measures the differences among groups of chickpea genotypes, such as varieties, landraces, or wild relatives. This diversity is crucial for breeders to develop new, stable varieties.

S.No	Characteristic	Author and Year	Research Findings
1	Variability & Diversity	Johnson <i>et al.</i> , 2015	The study assessed genetic divergence among 112 chickpea genotypes, classifying them into eight distinct clusters. Analysis revealed the maximum inter-cluster distance between clusters IV and VII (6.296), followed by clusters I and VII (5.867), IV and V (5.681), and I and IV (5.658). Cluster V exhibited the highest intra-cluster distance(2.328), indicating significant genetic diversity among its constituent genotypes, which included ICC 251834, ICC 275466, ICC 269530, Indira Chana-1, ICC 269563,RG 2011-01, RG 2011-03, and JG 11. These genetically diverse genotypes from cluster V represent valuable parental material for future chickpea breeding programs aimed at enhancing genetic gain through hybridization.
2	Variability & Diversity	Singh <i>et al.</i> , 2016	Genetic diversity assessment of 40 chickpea genotypes using Mahalanobis D ² statistics revealed distinct clustering patterns, with clusters III, V, VI, and VII containing single genotypes - indicating their substantial divergence from other groups. The analysis identified 100-seed weight as the primary contributor to overall genetic variation, followed by three other key traits: number of pods per plant, days to 50% flowering, and seed yield per plant. This pattern of trait contribution highlights the importance of these characteristics in differentiating chickpea genotypes and suggests their potential value as selection criteria in breeding programs aimed at enhancing genetic diversity.
3	Variability & Diversity	Samyuktha <i>et al.</i> , 2017	Evaluated 48 chickpea germplasms using cluster analysis to find the genetic diversity by

			considering fourteen morphological traits and grouped the accessions into two clusters. Cluster I comprised of genotypes with high mean values for 100 seed weight, whereas cluster II, showed superior contribution for number of pods plant-1, number of seeds per pod and single plant yield.
4	Variability & Diversity	Vijayakumar <i>et al.</i> , 2017	An experiment was conducted to evaluate genetic diversity using Mahalanobis's D ² statistics, categorizing all germplasm lines into eight clusters. The analysis revealed that seed yield, along with days to maturity and days to 50% flowering, contributed the most to genetic divergence. Cluster IV exhibited the highest intra-cluster distance, followed by clusters III and V. The greatest inter-cluster distances were observed between clusters IV and V, V and VIII, and II and IV.
5	Variability & Diversity	Jayalakshmi <i>et al.</i> , 2018	Genetic diversity analysis of 54 genotypes showed that the samples could be classified into five distinct clusters. Notably, genotypes with elevated protein content were primarily found in cluster I, while those rich in micronutrients were predominantly grouped in clusters IV and V. This clustering pattern highlights the variation in nutritional traits among the genotypes.
6	Variability & Diversity	Mahmood <i>et al.</i> , 2018	Evaluated 15 chickpea genotypes for genetic diversity through principal component analysis and cluster analysis. Grain yield, harvest index, pods plant-1, 100-seed weight (g), days to 50 % flowering and plant height exhibited most significant contributions to genetic variability according to PCA. They distinguished genotypes in three clusters through cluster analysis based on similarity in trait and found that members falling in clusters I and III are genetically most divergent.
7	Variability & Diversity	Tamvar <i>et al.</i> , 2019	The study evaluated genetic diversity among 60 chickpea genotypes using D ² statistics, classifying them into five distinct clusters. Key traits contributing to genetic divergence included protein content, 100-seed weight, number of secondary branches per plant, seed yield per plant, days to 50% flowering, and number of primary branches per plant. The greatest inter-cluster distance was observed between clusters III and IV, indicating high genetic divergence, followed by clusters IV and V, and clusters II and IV. These findings highlight the potential of crossing genotypes from these distant clusters to maximize genetic variability in breeding programs.

8	Variability & Diversity	Pathade <i>et al.</i> , 2019	The study analyzed 60 promising chickpea (<i>Cicer arietinum</i> L.) genotypes using Mahalanobis D ² statistics to assess genetic diversity. The maximum inter-cluster distance was observed between clusters III and VIII, followed by clusters III and VI, and clusters III and VII, indicating significant genetic divergence. Traits such as 100-seed weight and protein content showed the highest contribution to diversity, while days to 50% flowering and seed yield per plant contributed moderately. These findings suggest that genotypes from the most distant clusters could serve as valuable parental lines for hybridization programs to enhance genetic variability and improve desirable traits in chickpea breeding.
9	Variability & Diversity	Janghel <i>et al.</i> , 2020	Genetic diversity analysis of 60 chickpea genotypes based on quantitative traits revealed seven distinct clusters, with maximum inter-cluster distances observed between clusters III & VII (7.84) and III & IV (6.84). The most diverse genotypes identified were JG-35, JG-315, RSG-931, Vishal, CSJ-741, Vikas, GNG-1958, PG-5, PDG-4, ICCV-6, ICCV-10, JG-11, and ICCV-2. These genetically divergent genotypes hold significant potential for use in hybridization programs to enhance variability and improve desirable traits in chickpea breeding.
10	Variability & Diversity	Jayalakshmi <i>et al.</i> , 2022	The study evaluated genetic diversity among 537 chickpea germplasm accessions for yield-related traits using K-means clustering, which grouped them into 12 distinct clusters. Cluster I was the largest with 73 genotypes, followed by clusters XII (66), VII (60), XI (58), X (49), V & VII (43), III (40), IV (36), II (27), IX (22), and VI (20). The most genetically divergent clusters were IV & IX and VI & VII, showing the highest inter-cluster distances. Promising accessions—NBeG-169, RVSSG-40, CP 117-5-23, and ICCV 07101—from these diverse clusters (IV, IX, VI, and VII) demonstrated high performance, making them ideal
11	Variability & Diversity	Reena <i>et al.</i> , 2023	Study evaluated 35 chickpea genotypes for genetic diversity and terminal heat tolerance using phenotypic characterization. D ² analysis grouped the genotypes into six distinct clusters through the Tocher method, with Clusters I and II containing the highest number of accessions, while Clusters IV, V, and VI were sparsely populated. The greatest inter-cluster divergence was observed between

			Cluster III and V, followed by Cluster III and IV and Cluster III and VI, indicating substantial genetic differences among these groups. Under late-sown conditions, all clusters demonstrated superior grain yield, suggesting their potential for improved performance in heat-stressed environments. Among the 12 agronomic traits examined, 100- seedweight emerged as the most influential factor in genetic differentiation. The identified diverse clusters hold significant promise for chickpea breeding programs. These genotypes can be strategically utilized to develop high-yielding, heat-tolerant varieties better suited to late-sown cultivation.
12	Variability & Diversity	Pragati <i>et al.</i> , 2024	A study assessed genetic diversity among sixty elite chickpea lines by analyzing eleven morphological traits using Mahalanobis D ² statistics and Tocher's clustering method. The sixty genotypes were categorized into ten clusters, with Cluster I being the largest (27 genotypes), followed by Cluster II and Cluster III while Cluster X contained only a single genotype. The maximum inter-cluster distance was observed between Cluster VIII and X (295.30), whereas Cluster IX showed the highest intra-cluster distance (103.60). In contrast, the smallest inter-cluster distance was between Cluster II and X (74.17), and Cluster X had the lowest intra-cluster distance (0). Seed yield per plant (16.7%) contributed the most to genetic diversity, followed by days to maturity (16%), biological yield (12.9%), days to 50% flowering (11.4%), and the number of primary branches (10.1%).

Table 2.2 Heterosis and combining ability

In chickpea breeding, heterosis and combining ability are crucial concepts used to identify superior parents and hybrid combinations for developing new, high-yielding varieties. While heterosis is exploited directly in hybrid crops, in a self-pollinated crop like chickpea, breeders use this information to select parents that can produce superior, stable pure lines in subsequent generations. while Combining ability analysis is used to determine the breeding value of parental lines and the potential of specific hybrid combination.

S.No	Characteristic	Author and Year	Research Findings
1	Heterosis	Godekar and Dodiya (2013)	The study identified several crosses exhibiting significant positive economic heterosis for key yield-related traits, including grain yield per plant, biological yield per plant, and number of pods per plant. Notably, certain crosses demonstrated strong heterotic performance for grain yield and other agronomic traits, with one parent in each cross being a strong combiner. These promising hybrids hold potential for generating superior transgressive segregants in advanced generations, making them valuable candidates for yield improvement programs in chickpea breeding. The findings highlight the importance of selecting optimal parental combinations to exploit heterosis and enhance productivity.
2	Heterosis	Ghaffar <i>et al.</i> , 2015	The extent of hybrid vigour exhibited considerable variation across different hybrid combinations. For plant height, heterosis ranged from -2.33% to 15.57%. Similarly, heterotic effects were observed for primary branches (20.06% to 58.52%) and secondary branches (-20.70% to 49.08%). Yield- related traits also showed significant heterosis, with pods per plant ranging from 41.89% to 59.68%, seeds per pod from 26.39% to 48.03%, and 100-seed weight from -33.24% to 33.18%.
3	Heterosis	Saxena <i>et al.</i> , 2016	Evaluated heterobeltiosis (superiority over the better parent) and standard heterosis for yield and related traits. Grain yield heterosis was influenced by branches, pods, seeds per pod, and seed weight. Significant variability was observed, with some hybrids showing high heterobeltiosis while others exhibited notable standard heterosis. Promising hybrids were identified based on per se performance, heterosis, and diallel analysis, indicating their breeding potential. These findings emphasize selecting superior parental lines to enhance yield through heterosis in chickpea.
4	Heterosis	Arjun Kumar <i>et al.</i> , 2017	Several studies have evaluated heterosis in chickpea by analyzing hybrids and their parental lines in a L X T mating design. Significant variations were observed among genotypes for various yield-related traits, with particularly high heterotic effects observed for biological yield per plant, seed yield per plant, and number of primary branches per plant when compared to mid-parental values. Most F1 hybrids exhibited positive economic heterosis over the standard check

			variety for key yield components, suggesting the presence of favorable dominant genes. The observed variability in heterotic responses across different traits indicates genetic diversity among parental lines and the potential for exploiting heterosis in chickpea breeding programs to enhance yield performance.
5	Heterosis	Mujjassim <i>et al.</i> , 2018	Research on nine chickpea hybrids revealed significant variations in flowering time, with the crosses A-1 × HC-5 and JG-11 × HC-5 exhibiting the earliest flowering at 34.5 days, closely followed by JG-11 × JG-315 and JG-11 × JG-24 at 36.0 days. The study documented substantial standard heterosis across multiple agronomic traits, including days to 50% flowering, plant height, primary branch number, pod count per plant, seed yield per plant, 100-seed weight, and days to maturity. Notably, most hybrid combinations outperformed the standard check variety, suggesting that the parental line JG-11 possessed inferior productivity traits compared to the majority of experimental hybrids. These findings highlight the potential of specific hybrid combinations to enhance key yield-related characteristics in chickpea breeding programs.
6	Heterosis	Johnson <i>et al.</i> , 2018	Research on heterosis for seed yield in chickpea has shown substantial variation among different hybrid combinations. Among numerous crosses evaluated, a few exhibited consistently significant positive heterosis over both mid-parent and better-parent values across multiple growing environments. Particularly noteworthy were certain high-performing hybrids that demonstrated superior mean seed yields in various environmental conditions. These findings suggest that selected hybrid combinations with stable heterotic performance could be valuable genetic resources for future chickpea improvement programs focused on yield enhancement.
7	Heterosis	Rana <i>et al.</i> , 2019	The study identified several superior hybrid combinations exhibiting desirable traits for chickpea improvement. For phenological characteristics, certain crosses showed exceptional performance in early flowering and maturity. Regarding yield components, specific hybrids demonstrated superior harvest index, grain weight, and productivity per plant, while others excelled in vegetative growth parameters like branch number and biomass production.

			Among the 36 crosses evaluated, three particular hybrids stood out as most promising overall, combining multiple favorable traits that could significantly contribute to genetic advancement in chickpea breeding programs. These findings highlight the potential for developing improved chickpea varieties through strategic hybridization and selection of superior recombinants in subsequent generations.
8	Heterosis & Combining ability	Lakhote <i>et al.</i> , 2020	Heterosis in grain yield per plant was reflected through no.of fruiting branches per plant, no.of pods per plant, no.of seeds per pod and 100-seed weight. The hybrid GNG-2207 X Digvijay expressed the highest heterobeltiosis for grain yield per plant. Similarly, Phule Vikram x Digvijay cross combination only gave heterosis over standard check variety for grain yield per plant. Based performance, heterosis, the cross combinations Phule Vikram x Digvijay, Digvijay x WR-315, GNG2207 x Digvijay and Phule Vikram x JAKI-9218 were used promising for their utilization in chickpea improvement.
9	Heterosis	Reza <i>et al.</i> , 2022	The main point of heterosis in breeding program to produce hybrid seed depends on the ability of the reformer to identify high-yielding hybrid parental lines.
10	Heterosis	Ghasemi <i>et al.</i> , 2022	Presence of suitable heterosis in some of the studied compounds reveals that grain yield trait using hybridization between parents, it is possible to obtain hybrids with good yield and appearance traits.
11	Heterosis	Rekha Choudhary <i>et al.</i> , 2023	Analysis of variance (ANOVA) showed significant variation among generations and parental lines for all studied traits. The cross CSJ-515 × HC-5 exhibited maximum mid-parent heterosis (49.99%), while RSG-973 × HC-5 showed the highest heterobeltiosis (35.46%) for seed yield per plant. These results indicate these hybrid combinations displayed superior heterotic performance under late-sown conditions, making them particularly promising for yield improvement in heat-stressed environments.
12	Heterosis & Combining ability	Halladakeri Priyanka <i>et al.</i> , 2024	The analysis of variance components indicated that both additive and non-additive gene actions played significant roles in controlling yield and related traits. Among the parents, ICC13124 emerged as the best general combiner (GCA) for yield and associated

			traits, also contributing to superior specific combinations (SCA). Heterosis for seed yield was highest in certain crosses, demonstrating a strong correlation between SCA effects and heterotic performance, suggesting the influence of additive gene interactions. These findings highlight the importance of considering GCA, SCA, and per se performance equally when selecting parents for developing high-yielding hybrids.
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Table 2.3. Nature of Gene action and Combining Ability

In chickpea breeding consistently shows that both additive and non-additive gene actions control the inheritance of important traits like yield, disease resistance, and plant architecture. However, the relative importance of these gene actions varies depending on the specific trait and the genetic material used. Combining ability analysis is used to determine the breeding value of parental lines and the potential of specific hybrid combination.

S.No	Characteristic	Author and Year	Research Findings
1	Gene action	Sharma <i>et al.</i> , 2013	Research investigated maternal inheritance and genetic control of seed size in chickpea using three crosses between des and kabuli genotypes. Analysis of parental, F ₁ , F ₂ , and reciprocal generations revealed no maternal effects or major gene segregation, suggesting polygenic inheritance. Generation mean analysis showed significant additive gene effects across all crosses, with notable additive × additive epistasis in Desi × kabuli hybrids. The findings recommend delaying selection to later generations and maintaining large breeding populations to maximize recombination and exploit these non-allelic interactions effectively for seed size improvement. This approach would optimize the utilization of fixable genetic variance in chickpea breeding programs.
2	Combining Ability	Labdi <i>et al.</i> , 2015	parents revealed highly significant general combining ability (GCA) across two generations, surpassing specific combining

			ability (SCA). These findings highlight the strong influence of additive genetic effects and additive $\times$ additive epistasis over dominance effects. High heritability estimates further emphasize the key role of additive components in Ascochyta resistance. In the adult stage, positive H ² values in both generations suggest dominant genes primarily contribute to susceptibility.
3	Combining Ability	Sarode <i>et al.</i> , 2016	The parental line BDNGK 798 showed strong GCA effects for plant height and 100-seed weight, while VIJAY excelled in primary and secondary branching. DIGVIJAY displayed high GCA for pods per plant and seed yield, whereas the cross BDNGK 798 $\times$ SAKI 9516 exhibited significant SCA effects for pods and yield. Additionally, BDNGK 9-3 ICC 14871 demonstrated superior SCA for seed yield per plant.
4	Gene action	Jadhav and Gawande 2016	A line $\times$ tester analysis in chickpea evaluated two females, eight males, and their sixteen crosses to identify superior parents and hybrids for breeding. Additive gene effects predominated for earliness, while non-additive effects influenced other traits, with JAKI 9218 (100-seed weight, yield) and HC 5 (yield, plant height, branches, pods) emerging as strong general combiners. The crosses JAKI 9218 $\times$ Bushy Mutant, JAKI 9218 $\times$ JG 62, and ICCV 2 $\times$ HC 5 showed the best performance for height, seed weight, pods, and yield, with ICCV 2 $\times$ HC 5 also exhibiting high SCA for earliness. Promising parents like JAKI 9218 and hybrids such as JAKI 9218 $\times$ Gulak 1 and JAKI 9218 $\times$ AKG 10-1 suggest biparental mating for transgressive segregants.
5	Combining Ability	Sarode and Nagargoje 2017	The study evaluated 15 chickpea hybrids derived from three female and five male parents, along with the check variety BDNG 797. Among the parental lines, BDNGK 798 showed high GCA for plant height and 100-seed weight, Vijay for primary and secondary branches, and Digvijay for pods and seed yield per plant. Notably, the cross BDNGK 798 $\times$ SAKI 9516 displayed significant SCA for pods and yield, while BDNGK 9-3 $\times$ ICC 14871 excelled in seed yield per plant.
6	Combining Ability	Rathod <i>et al.</i> , 2018	twenty chickpea hybrids, their parental lines, and checks (BDNG 797 and PG 08108) were evaluated. Parental lines AKG 1303 (plant height), VIJAY (primary branches), JG 315 (secondary branches), JAKI 9218 (100-seed weight), and

			SAKI 9516 (pods and yield/plant) showed high GCA effects, while crosses SAKI 9516 × JG 315 (yield and pods/plant) and Digvijay × AKG 1109 (pods/plant) exhibited significant SCA effects.
7	Combining Ability	Kumar <i>et al.</i> , 2018	Study identified two parental lines (JGK 1 and ICCV 05107) as superior general combiners, demonstrating high GCA effects for key yield-related traits including seed yield per plant, biological yield, harvest index, and 100-seed weight across different growing environments. Several hybrid combinations exhibited significant positive SCA effects for seed yield and associated yield components under both timely sown and late sown conditions. These findings highlight the potential of these parental lines as valuable genetic resources for yield improvement programs, while the specific crosses showing superior SCA effects indicate promising hybrid combinations for developing high-yielding chickpea varieties adapted to different sowing windows. The results emphasize the importance of both general and specific combining ability in breeding for improved chickpea productivity.
8	Combining Ability	Thorat <i>et al.</i> , 2019	Parental lines exhibited high GCA effects: Vijay (days to 50% flowering, primary/secondary branches, harvest index), JAKI- 9218 (days to flowering/maturity, seeds/pod, plant height, 100-seed weight), SAKI-9516 (primary/secondary branches, seeds/pod, seed yield), and tester ICC-111 (days to maturity, primary branches, pods/plant, 100-seed weight, seed yield). Among crosses, Vijay × ICC-111 showed high SCA for branches, pods/plant, seeds/pod, and yield, while SAKI-9516 × ICC-101 excelled in pods/plant, seeds/pod, and seed yield.
9	Combining Ability	Kumar <i>et al.</i> , 2019	Analysis showed KGD-1161×Pusa-256 performed exceptionally well for early flowering (days to 50% flowering), while GNG-1581×WCG-3 demonstrated superior early maturity characteristics. While breeders might select for reduced plant height in certain cases, three crosses - ICC4958×WCG-3, C- 235×Pusa-1103 and C-235×Pusa-256 - showed optimal plant height based on both per se performance and specific combining ability (SCA) effects.
10	Combining Ability	Saba <i>et al.</i> , 2020	The analysis revealed greater genetic variance attributable to general combining ability (GCA) than specific combining ability (SCA) for pods per plant, 100-seed weight, and grain yield, indicating the predominance of additive gene effects for

			these traits.
11	Combining Ability	Lakhote <i>et al.</i> , 2020	The analysis revealed highly significant variances for both general combining ability (GCA) and specific combining ability (SCA) across all studied traits - including phenological characteristics , plant architecture , and yield components (pods per plant, seeds per plant, 100-seed weight, and seed yield per plant) - demonstrating the concurrent importance of additive and non-additive gene actions in trait inheritance. Among parental lines, Phule Vikram, JAKI-9218, Digvijay, and GNG-2207 emerged as high-yielding genotypes with superior GCA for grain yield and its components, marking them as ideal candidates for future hybridization programs. Notably, three cross combinations (GNG-2207 × Digvijay, Digvijay × WR-315, and Phule Vikram × Digvijay) exhibited the highest SCA effects, highlighting their potential for generating superior recombinants in advanced segregating generations through targeted breeding efforts.
12	Combining Ability	Chowdhary <i>et al.</i> , 2022	The Line x Tester fashion four lines were crossed with six testers to elucidate the information to select the parents with good GCA and crosses with good SCA effects. The analysis of variances for combining ability revealed highly significant differences for all the characters among all the crosses.
13	Combining Ability	Sasane <i>et al.</i> , 2022	Study employed a Line × Tester mating design with four lines and six testers to evaluate combining ability for seed yield and related traits. Among the parental lines, two genotypes demonstrated superior general combining ability for yield components, while one tester stood out as particularly favorable. Only two hybrid combinations exhibited significant positive specific combining ability effects for seed yield and associated agronomic traits, indicating their potential for developing high-yielding chickpea varieties. These findings highlight the importance of selecting parents with strong combining ability to develop superior hybrids with improved yield performance. The results provide valuable insights for breeding programs aiming to enhance chickpea productivity through strategic crosses.
14	Combining Ability	R Choudhary <i>et al.</i> , 2023	This study analyzed gene action in 28 chickpea hybrids under timely (E1) and late-sown (E2) conditions. Significant genetic variability was observed in both environments, with both

			additive (GCA) and non-additive (SCA) gene effects influencing all traits. CSJ-515 and HC-5 were the best general combiners for yield-related traits across environments, while Avrodhi (E1) and CSJD- 884/RSG 963 (E2) showed environment-specific superiority. The hybrids CSJD 884×RSG 963, CSJD 884×RSG 973, and RSG 973×Avrodhi exhibited high SCA effects and heterosis, particularly under late sowing. These hybrids show promise for targeted yield improvement in specific growing conditions.
15	Combining Ability	Quatadath <i>et al.</i> , 2024	Research investigated combining ability (general and specific) and genetic variability in chickpea using 56 experimental treatments, including 10 parental lines, 45 F1 hybrids developed through diallel crossing, and a control variety (Radha). The randomized block design (RBD) with three replicates showed significant general combining ability (GCA) and specific combining ability (SCA) effects for key agronomic traits including flowering time, maturity duration, and plant height, demonstrating the influence of both additive and non-additive gene action. Among parental lines, ICC 1205 and GNG-1958 emerged as superior general combiners for early flowering and improved plant structure. Hybrid combinations, particularly JG 24 IPC 18-131, exhibited outstanding specific combining ability for enhanced pod formation and yield performance.

This chapter contains the outlines of the materials used in the experiments and the procedures/methods followed for data collection, analysis, and interpretation. The present investigation entitled “**Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.)**” was carried out during *Rabi* 2022-23 and 2023-24.

1.1 Site of Experiment

1.2 Experimental Materials

1.3 Methods

1.4 Crossing Program

1.5 Data Recording

1.6 Statistical Analysis

3.1 Site of Experiment

Phagwara is located between the fertile plains between Beas and Sutlej rivers. Lovely Professional University is geographically located at 31° 15' 29" N and 75° 42' 27" E at an altitude of 236 m above MSL (Mean Sea Level) in Chaheru village, under Phagwara sub-district (Kaputhala district), Punjab. The soil type of the experimental location was inceptisols with a slightly basic pH in the range of 7.2 to 7.7. The experiment was conducted at Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab-144411, India

3.2 Experimental materials

The experimental took place in 2 different time frames and each season differed according to the objectives of the specific experiment. Season 1 (*Rabi* 2022-23) materials consisted of 30 genotypes which were sourced from IIPR Indian Institute of Pulse Research, Kanpur, Uttar Pradesh , India and second season investigation was generated by crossing eight lines x four testers of chickpea (*Cicer arietinum* L.) in Line x Tester fashion during *Rabi* 2023-24. The details of material have been summarized in Table

Table 3.2.1. List of genotypes with and developing institute

Genotype Number	Genotype Name	Source
1.	JAKI 9218	PDKV, Akola (Maharashtra)
2.	BGD 209	IARI, New Delhi
3.	JKM 7	-
4.	CSJ 515	RARI, Durgapura
5.	K850	CSAUA&T, Kanpur
6.	IPCK02	ICAR–IIPR, Kanpur
7.	IPCK28	ICAR–IIPR, Kanpur
8.	T39-1	ICRISAT, Patancheru
9.	GOKCE	ICARDA / CRIFC, Turkey
10.	PUSA256	IARI, New Delhi
11.	RSG931	RARI, Durgapura
12.	IPC71	ICAR–IIPR, Kanpur
13.	JG35	JNKVV, Jabalpur
14.	JG24	JNKVV, Jabalpur
15.	IPC04-1	ICAR–IIPR, Kanpur
16.	JG14	JNKVV, Jabalpur
17.	JG130	JNKVV, Jabalpur
18.	GNG1581	ARS, Sri Ganganagar
19.	RADHACHOTI-1	Regional (India)
20.	RSG963	RARI, Durgapura
21.	HC5	CCS HAU, Hisar
22.	GNG1958	ARS, Sri Ganganagar
23.	KPG59	CSAUA&T, Kanpur
24.	BG212	IARI, New Delhi
25.	PUSA362	IARI, New Delhi
26.	DIGVIJAY	MPKV, Rahuri
27.	VIJAY	MPKV, Rahuri
28.	GL25016	GAU, Gujarat
29.	ICCL 86111	ICRISAT, Patancheru
30.	GNG1488	ARS, Sri Ganganagar

3.3 Experimental Methods

3.3.1 Experiment 1: Assessment of genetic diversity in chickpea

First experiment took place in *Rabi* 2022-23 with objective of evaluating the diversity among the studied genotypes of chickpea. Genotypes were sown in a LPU experimental farm on 15th November 2022 .

Table 3.3.1 Experimental Layout and Field Details of Chickpea Trial (*Rabi* 2022-23)

Sr. No	Characters	Details
1	Number of treatments	30
2	Number of replications	3
3	Number of plots	90
4	Number of rows per genotype	2
5	Row length	4 m
6	Row to row distance	45 cm
7	Date of Sowing	15/11/22

Experiment 2:

Evolution of genotypes in 2023- 24 *Rabi* Along with lines , testers , checks.

In the present investigation, crosses were made between 8 lines and 4 testers during *Rabi*, 2022-23 and sufficient F₁ seed was obtained for all the 32 crosses. All the 12 parents and their 32 F₁ were grown during *Rabi* 2023-24 in randomized block design (RBD) with three replications. Each 32 F₁s and parents were sown in three row (3 meter). The row were spaced 30 cm apart and plant to plant was retained 10 cm. Data for all the characters were

recorded on five randomly selected plants of each genotype in both the parental and F₁ generation.

Table 3.3.2 Chickpea genotypes used as Lines, Testers and Check Variety in breeding programme

Category	Genotype Names
Lines	IPC 71
Lines	GNG 1581
Lines	ICCL 86111
Lines	GOKCE
Lines	JG 35
Lines	JG 24
Lines	RSG 931
Lines	PUSA 362
Testers	GNG 1488
Testers	PUSA 256
Testers	JAKI 9218
Testers	VIJAY
Check Variety	GNG 1958

3.4. Crossing program

In the present investigation, crosses were made between 8 lines and 4 testers during *Rabi*, 2023-24 and sufficient F₁ seed was obtained for all the 32 crosses. All the 12 parents and their 32 F₁ were grown during *Rabi* 2023-24 in randomized block design (RBD) with three replications. Each 32 F₁s and parents were sown in three row (3 meter). The row were spaced 30 cm apart and plant to plant was retained 10 cm. Data for all the characters were recorded on five randomly selected plants of each genotype in both the parental and F₁ generation.

3.5 Data Recording

Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to 50 per cent flowering and days to maturity, which was recorded on plot basis. Average data from the selected plants of each plot in respect of different characters were used for various statistical analyses.

Days to 50 per cent flowering

Days to 50 % flowering was recorded by counting the number of days taken from date of sowing to when one half of the plants in plot reached bloom stage.

Days to maturity

When the pods become yellow or reached physiological maturity and after crushing the pod, shining seeds come out, on that day maturity was recorded. After subtracting the date of sowing from the date of maturity the days to maturity was recorded.

Plant height (cm)

The average height of five randomly selected plants from the each genotype and measured in centimeter from the ground level to the top most point after stretching the main shoot of the plant at maturity time.

Number of primary branches per plant

The number of branches arising from the base of stem bearing at least one pod of each plant of five randomly selected plants from each plot was counted at the time of maturity and averaged them designated as number of primary branches per plant.

Number of secondary branches per plant

Total effective pod bearing branches per plant on primary branches were noted.

Number of pods per plant

The numbers of pods without any damage on plant were counted. Total number of pods

bearing seeds was counted per plant at maturity.

Number of seeds per pod

The number of seeds in each of 10 pods of selected five plants was recorded and average was worked out as number of seeds per pods on each plant.

100 seeds weight (g)

A composite seed sample was drawn from each plant and hundred seeds were randomly selected and weighed.

Seed yield per plant (g)

Total weight of dry seeds from each plant was recorded in gram (g) with the help of electronic balance.

$$HI = \frac{\text{Seed yield per plant}}{\text{Biological yield per plant}} \times 100$$

Harvest index is calculated in % as per given formula.

Biological yield (g)

Total Biomass (excluding roots) of each selected plant was recorded in grams at the time of harvesting and followed by averaging their values

B. Quality traits

- **Protein test**

Kjeldahl method is a classical, widely used analytical technique for protein analysis by determining nitrogen content in a sample. The method involves three main steps: digestion, distillation, and titration.

1. **Digestion:** The organic sample is digested with concentrated sulfuric acid (H_2SO_4) in the presence of a catalyst (such as selenium or copper sulfate) and potassium sulfate to raise the boiling point. This converts nitrogen in the sample to ammonium sulfate.
2. **Distillation:** After digestion, the solution is neutralized with sodium hydroxide (NaOH), converting ammonium ions into ammonia gas. The ammonia is then distilled and collected in a boric acid solution.
3. **Titration:** The captured ammonia (ammonium borate) is titrated with a standard acid (usually hydrochloric or sulfuric acid) to determine the total nitrogen content.

The Kjeldahl method is considered the standard for protein quantification due to its accuracy and applicability to a broad range of samples including food, feed, soil, and more. It does have limitations, such as not distinguishing between protein nitrogen and non-protein nitrogen and requiring hazardous chemicals.

3.6 Statistical Analysis

Data recorded for the above experiments were recorded according to the above-mentioned methods and were subjected to the following statistical procedures.

1. Estimation of Genetic diversity
2. L x T Analysis
3. Combining ability variances

4. Estimation of Heterosis

3.6.1 Estimation of Genetic diversity

The analysis of divergence was carried out by D2 statistics of Mahalanobis" (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per R.B.D., to test significance of differences among the genotypes. 32 The characters exhibiting significant differences were only used for further analysis of D2 statistic. The analysis of co-variance for the character pairs, based on plot averages was carried out (Cochran and Cox, 1957).

Mahalanobis' generalized distance (D^2) The generalized distance between any two populations is defined as

$$\Delta^2 = \sum \sum \lambda_{ij} \cdot \delta_i \cdot \Delta_j$$

Where, λ_{ij} = Reciprocal matrix to the common dispersion matrix

δ_i = Difference between the mean values of the two populations for the i th character

δ_j = Transpose

δ_i 33 This quantity is estimated by D2 statistic (Mujumdar and Rao, 1958) as:

$$D2 = \sum \sum \delta_{ij} \cdot d_i \cdot d_j$$

Where,

δ_{ij} , d_i and d_j are the sample estimate of δ_{ij} , δ_i and δ_j .

Since this formula for computation requires the inversion of tenth order determinant and then evaluation of 10 (10+1) terms, whose sum is D2.

Test of significance

Using 'V' statistics which, in turn, utilizes Wilk's criteria, simultaneous test of difference mean values of a number of correlated variables/ characters at 'p q' d.f. (where p = number of variables/ characters and q = number of genotypes-1) was exercised.

Testing of significance of D^2 values

The D^2 values obtained for a pair of population was taken as the calculated value of χ^2 and was taken against the tabulated value of χ^2 at 'p' d.f., where p is the number of characters.

Grouping of genotypes into various clusters

Using D^2 values, different genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1952).

Average intra- and inter-cluster distance

$$\text{Average intra - cluster } D^2 = \Sigma D_i^2/n$$

where,

ΣD_i^2 = sum of all distances between all possible combinations (n) of the genotypes included in the cluster.

$$\text{Average inter- cluster distance } D^2 = \Sigma D_{ij}^2/n_i.n_j$$

where,

$\sum D_{ij}^2$ = sum of all distances between all possible combinations ($n_i.n_j$) of the genotypes between the clusters.

n_i = number of genotypes in i^{th} cluster

n_j = number of genotypes in j^{th} cluster

Cluster mean

Cluster means of common bean genotypes falling under different clusters in individuals as well as combined over environments were also calculated.

3.6.2 Line x tester analysis

Line $\times$ Tester analysis was used on a limited scale to determine GCA and SCA of different lines. It is analogous to “North Carolina Design II” (Comstock and Robinson 1952). In this design, a random sample of “ l ” lines is taken and each line is mated to each of the “ t ” testers (Singh and Chaudhary 1977). The form of analysis of variance is as follows:

Table 3.6.1

Source of variation	df	SS	MSS
Replications	($r-1$)	-	-
Lines (Females)	($l-1$)	SS (l)	M(l)
Testers (Males)	($t-1$)	SS (t)	M(t)
Lines x Testers	($l-1$)($t-1$)	SS(lt)	M(lt)
Error	($r-1$)($T-1$)	SS(e)	M(e)

Where

r = number of replications

T = total number of treatments

l = number of lines

t = number of testers

3.6.3 Combining ability effects

Combining ability variances and effects were obtained using line x tester method as suggested by Kempthorne (1957). The experimental data obtained on nineteen characters were subjected to analysis of variance.

$$X_{ijk} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

Where,

μ = general mean

g_i = GCA effect of the i^{th} male (tester); $i = 1, 2, \dots, m$;

g_j = GCA effect of the j^{th} female (line); $j = 1, 2, \dots, f$;

S_{ij} = SCA effect of the ij^{th} combination; and

e_{ijk} = Error associated with the observation X_{ijk} ; $k = 1, 2, \dots, r$.

The individual effect was estimated as follow:

GCA lines

$$g_i = \frac{\sum_{tr} X_{i..}}{tr} - \frac{\sum_{rlt} X_{.j.}}{rlt}$$

Where,

g_i = general combining ability effect of i^{th} line

$X_{i..}$ = Total of i^{th} line over all the tester and replications.

GCA testers

$$g_{jj} = \frac{\sum_{lr} X_{.j.}}{lr} - \frac{\sum_{rlt} X_{i..}}{rlt}$$

Where,

g_j = general combining ability effect of j^{th} tester.

X_j = Total of j^{th} tester over all lines and replications.

SCA effects

$$S_{ij} = \frac{XX_{ij.}}{r} - \frac{XX_i}{rt} - \frac{XX_{.j}}{lr} + \frac{XX \dots}{rlt}$$

Where,

S_{ij} = specific combining ability effect of i^{th} line and j^{th} tester

Critical difference (C.D.) was calculated as:

C.D. = SED x t at 5% or 1% level at error d.f.

The significance of GCA lines, GCA testers and SCA effects were tested by comparing with respective C.D. values.

Gene Action

Gene action was worked out following Kempthorne (1957)

$$Cov. HS = \left[\frac{1+F}{4} \right]^2 \cdot \sigma_A^2$$

Additive genetic variance $\sigma_A^2 = 4 \text{ Cov. H.S. (average) with } F=1$

$$\sigma_{SCA}^2 = \left[\frac{1+F}{2} \right]^2 \cdot \sigma_D^2$$

Dominance variance (σ_D^2) = σ_{sca}^2 with $F=1$

Where,

F = Inbreeding co-efficient

3.6.4 Estimation of heterosis

The nature and magnitude of heterosis was worked out using information on various quantitative characters studied. Heterosis expressed as per cent increase or decrease by

hybrids (F₁'s) over average value of both parents (mid-parent heterosis), better parent (heterobeltiosis) and standard variety (standard heterosis).

Mid-parent or average heterosis

$$\text{Average or mid parent heterosis} = \frac{(F_1 - MP)}{MP} \times 100$$

Where,

MP = Mean value of the both parents

S.Ed. for

$$F_1 - MP = \sqrt{\frac{2MSE}{r}}$$

C.D. = S.Ed. × t (at error d.f.)

Heterobeltiosis

$$\text{Heterobeltiosis} = \frac{(F_1 - BP)}{BP} \times 100$$

Where,

BP = Mean value of the better parents

S.Ed. for

$$F_1 - BP = \sqrt{\frac{2MSE}{r}}$$

C.D. = S.Ed. × t (at error d.f.)

Standard or economic heterosis

$$\text{Standard heterosis} = \frac{(F_1 - SC)}{SC} \times 100$$

Where,

F₁ = Mean value of F₁

SC = Mean value of check variety

S.Ed. for

$$F_1 - BP = \sqrt{\frac{2MSE}{r}}$$

C.D. = S.Ed. $\times$ t (at error d.f.)

Critical difference (C.D.)

C. D. was calculated as follows:

C. D. = S. Ed. $\times$ t (at error d. f.) SV = Mean value of the standard variety.

The significance of the GCA line tester and SCA effects were tested by comparing with respective C.D. values.

The experimental results of the present investigation entitled “**Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum L.*)**” was conducted at the departmental fields of Genetics and Plant Breeding at Lovely Professional University in Phagwara, Punjab. it was carried out during *Rabi* 2022-23 and 2023-24. are presented under following heads:

4.1 Analysis of variance for experimental design

4.2. Violin plot visualization with DMRT analysis

4.3. Genetic Diversity

4.4 Analysis of variance for line x tester mating design

4.5 Mean performances for various characters

4.6 Analysis of variance for combining ability

4.7 Estimate of general combining ability (GCA) effect

4.8 Estimate of specific combining ability (SCA) effects

4.9 Estimation of heterosis of various traits

4.10 Contribution of line, tester and line x tester

4.1 Analysis of variance for experimental design

The analysis of variance (ANOVA) revealed highly significant ($p \leq 0.01$) differences among genotypes for most of the traits studied, indicating a substantial presence of genetic variability in the experimental material. Traits such as days to 50% flowering ($F = 10.08$), days to maturity ($F = 61.95$), plant height ($F = 26.66$), number of pods per plant ($F = 28.47$), 100-seed weight ($F = 201.35$), biological yield per plant ($F = 12.68$), harvest index ($F = 47.82$), and seed yield per plant ($F = 3.67$). Although the F-values for seed protein content ($F = 0.40$) and secondary branches ($F = 0.78$) were relatively lower, they were still statistically significant, suggesting mild genetic variability. However, primary branches per plant ($F = 0.59$) showed non-significant genotypic effects, indicating limited variation among genotypes for this trait. These results align with earlier findings by Kumar *et al.* (2020), Meena *et al.* (2023), and Raval *et al.* (2021), who also observed substantial genetic variability in chickpea populations for yield-contributing traits.

Environmental effects were also highly significant ($p \leq 0.01$) for nearly all traits except plant height and harvest index, suggesting considerable environmental influence on trait expression. For instance, environmental F-values were particularly high for number of pods per plant ($F = 539.37$), days to maturity ($F = 223.17$), and days to 50% flowering ($F = 111.99$), in. The genotype $\times$ environment interaction was significant only for days to maturity ($F = 24.96$), biological yield ($F = 9.20$), and harvest index ($F = 1.66$), suggesting that these traits are influenced by both genotypic makeup and environmental fluctuations, as also noted by Singh *et al.* (2019), Sharma *et al.* (2021), and Yadav *et al.* (2022). The higher error mean squares for traits like plant height (15.84) and days to maturity (27.61).

Table 4.1: Analysis of variance of chickpea genotypes over two years

Traits	Replicate (df=2)	Treatments (df=29)	Environment (df=1)	Interactions	Total	Error (df=145)
DFP	1.62	10.08**	111.99**	3.04	24.26	3.98
DM	1.79	61.95**	223.17**	24.96	55.34	27.61
PB	0.01	0.59	12.18**	0.0085	2.44**	0.05
SB	0.02	0.78**	25.36**	0.01	5.08	0.17
PH	0.09	26.66**	10.36	3.93	3.68	15.84
NPP	0.53	28.47**	539.37**	0.39	108.24	8.68
SPP	0.01	0.40**	1.32**	0.02	0.28	0.09
HSW	0.58	201.35**	8.84**	0.05	2.02	1.34
BYP	0.35	12.68**	102.92**	9.20	24.40	5.97
HI	3.88	47.82**	4.71	1.66	3.16	4.88
SYP	0.13	3.67**	4.17**	0.59	1.12	0.36

**, ** indicate significance at the 0.05 and 0.01 probability levels, respectively.*

PB: primary branches; SB: secondary branches; NPP: number of pods per plant; DFP: days to 50% flowering; DM: days to maturity; HSW: hundred seed weight; HI: harvest index; SYP: seed yield per plant; PH: plant height; BYP: biological yield per plant.

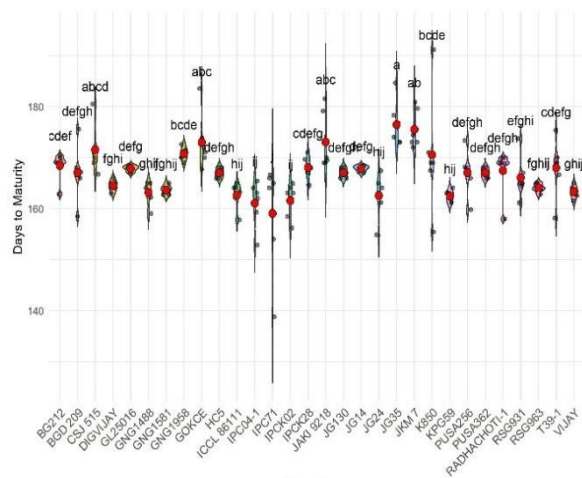
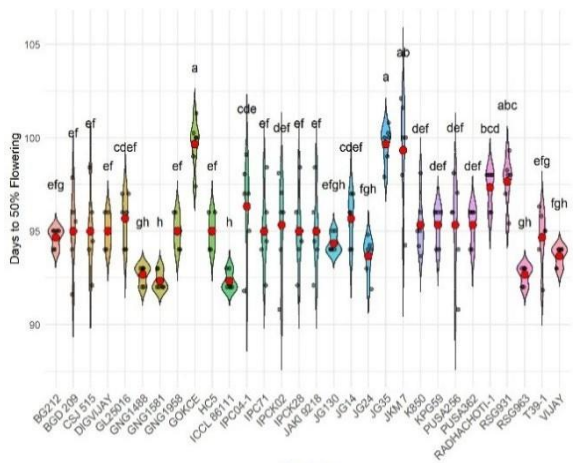
4.2. Violin Plot Visualization with DMRT Analysis (added paragraph)

DMRT stands for Duncan's Multiple Range Test, a post-hoc statistical test used after an Analysis of Variance (ANOVA) to find which specific group means are significantly different from each other. It is particularly useful for comparing multiple treatment means and is more powerful than other tests for comparing larger ranges of means. The test ranks the treatment means, sorts them by value, and uses a stepwise comparison to determine which means are not significantly different from one another, often grouping them together with a shared letter in the output.

The violin plot analysis, integrated with Duncan's Multiple Range Test (DMRT), offered a holistic view of phenotypic performance across 30 chickpea genotypes for 11 traits, revealing trait-wise distributions. For early phenological traits such as days to 50% flowering (DFF) and days to maturity (DM), significant divergence was observed. Genotypes like GNG1958, ICCL 86111, and VIJAY consistently exhibited early flowering, while late-flowering types included JG130 and JG24. Such patterns underscore the potential of early-maturing genotypes for stress-prone or short-season environments (Singh *et al.*, 2019; Meena *et al.*, 2021). Moreover, structural traits like plant height and branching varied widely, with tall genotypes like IPC04-1 and JG 35 offering biomass advantages, whereas VIJAY and JG14 showed prolific primary branching, which may enhance reproductive success (Raval *et al.*, 2022).

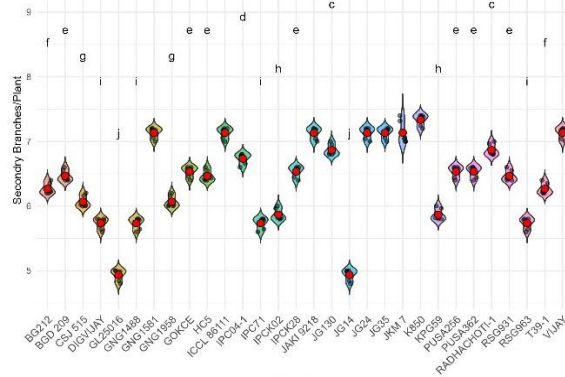
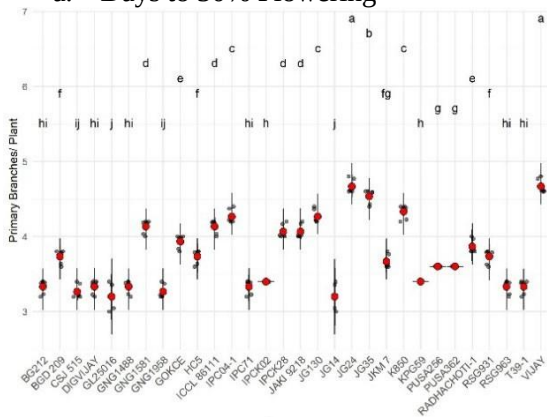
Yield-contributing traits further strengthened the identification of elite genotypes. GL25016 and GNG1581 recorded the highest number of pods per plant, while genotypes like GOKCE and IPC04-1 showed poor podding ability. Seed size was markedly superior in VIJAY, BGD209, and CSJ515, all of which expressed high hundred seed weight. For

biological yield, CSJ515 and PUSA362 stood out as top performers, with IPC71 and IPC04-1 trailing behind. Seed yield per plant was significantly higher in CSJ515, GL25016, and PUSA256, while JG14 and IPC04-1 recorded the lowest values. The harvest index (HI), reflecting resource-use efficiency, favored genotypes like BG212, PUSA362, and VIJAY. Overall, the integration of violin plots with DMRT successfully dissected inter-genotypic differences, helping to pinpoint superior genotypes such as CSJ515, GL25016, and VIJAY (Yadav *et al.*, 2020; Sharma *et al.*, 2023; Tiwari *et al.*, 2021).



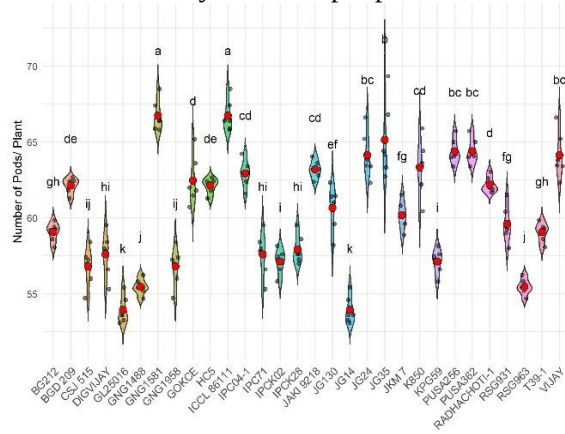
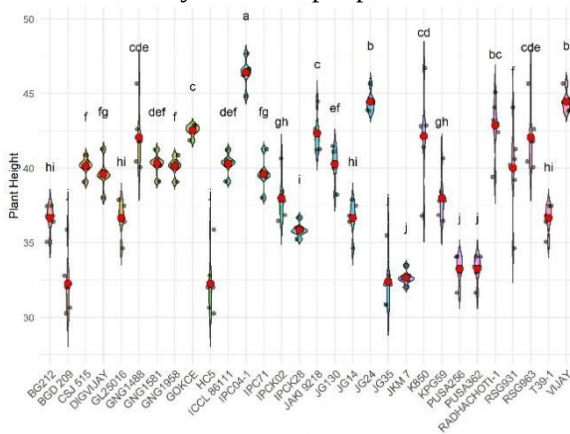
a. Days to 50% Flowering

b. Days to Maturity



c. Primary branches per plant

d. Secondary branches per plant



e. Plant Height

f. Number of pods per plant

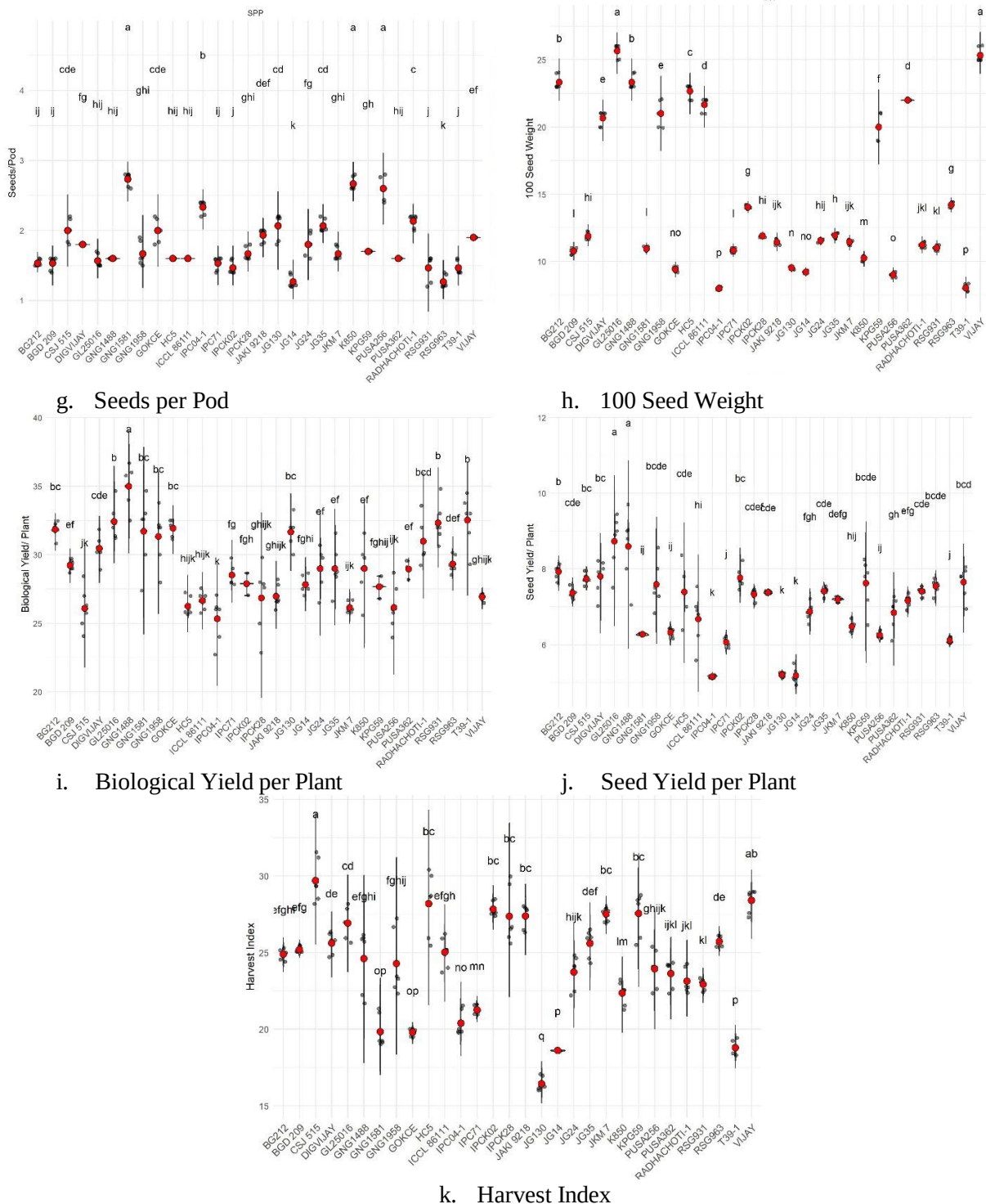


Figure 1..: (a-k): Violin plots illustrating the distribution of 30 chickpea genotypes of 11 traits
 Red dots represent trait means, while vertical dispersion shows variability across replications. Alphabetic groupings above violins indicate significant differences among genotypes based on Duncan's Multiple Range Test (DMRT) at $p < 0.05$. Distinct violin colors represent genotypes categorized into clusters for visual comparison.

4.3. Genetic Diversity

4.3.1. Cluster Composition

The 30 chickpea genotypes were grouped into five distinct clusters based on multivariate analysis, revealing substantial genetic divergence suitable for parent selection in hybridization programs.

Cluster I

This cluster comprised 2 genotypes: BGD-209 and JG-130. The small size of this cluster suggests that these two genotypes are genetically similar to each other but highly divergent from those in other clusters. Their unique genetic makeup can be exploited for specific trait improvement. Since these genotypes stood apart, crossing them with genotypes from larger clusters like Cluster V may result in high heterosis.

Cluster II

Cluster II also included 2 genotypes: GoKeE and BG-212. These genotypes are closely related within the cluster but genetically distinct from others. The limited membership implies potential for unique agronomic traits. These could be promising parental lines for breeding programs aiming at trait diversification, especially when crossed with genotypes from Clusters III or V.

Cluster III

This cluster contained 6 genotypes: K-850, RSG-963, IPCK-28, GNG-1958, JAKI-9218, and JG-14. The moderate size indicates a balanced level of genetic similarity among members. These genotypes may share desirable traits such as early maturity or resistance attributes. Moderate divergence from other clusters suggests they can be effective contributors in broad-based crossing programs for improving seed yield and its components.

Cluster IV

Cluster IV grouped 4 genotypes: T39-1, KPG-59, IPCK-02, and HC-5. These accessions are genetically closer among themselves but possess intermediate divergence from other clusters. This cluster may harbor specific traits such as plant architecture or branching patterns, and their inclusion in crossing blocks with genotypes from Clusters I or V may enhance trait variability.

Cluster V

This was the largest cluster with 16 genotypes: JG-24, ICCL-86111, IPC-04-1, GNG-1488, JKM-7, GNG-1581, PUSA-256, PUSA-362, CSJ-515, RADHACHOTI-1, IPC-71, VIJAY, JG-35, GL-25016, RSG-931, and DIGVIJAY. The size of this cluster suggests a broader genetic base and considerable intra-cluster variation. This makes it a valuable reservoir for multiple traits including seed yield, plant height, and branching habit. Selection of genotypes from this cluster for crossing with those from smaller and genetically divergent clusters (e.g., I and II) is likely to produce superior recombinants with greater genetic variability and heterotic potential.

The clustering of 30 chickpea genotypes into five distinct groups through multivariate analysis reflects considerable genetic diversity, which is essential for the success of hybridization and trait improvement programs. The formation of smaller clusters (Clusters I and II), each comprising only two genotypes (e.g., BGD-209, JG-130 in Cluster I; GoKeE and BG-212 in Cluster II), indicates these genotypes possess highly unique genetic traits and are markedly distinct from the rest. These can be excellent candidates for crossing with genotypes from genetically diverse and larger clusters like Cluster V, potentially leading to significant heterosis and recombinants with novel gene combinations (Upadhyaya *et al.*, 2008; Ali *et al.*,

2015; Singh *et al.*, 2020). Their limited cluster membership further suggests untapped potential for specialized traits such as stress tolerance or seed quality.

Cluster III (6 genotypes) and Cluster IV (4 genotypes) represent moderate divergence and are likely to harbor intermediate genetic variability, useful for traits like plant architecture, early maturity, and pod number. However, Cluster V, with 16 genotypes, reflects the widest genetic base and considerable intra-cluster variation. Genotypes from Cluster V, including PUSA-256, CSJ-515, VIJAY, and GL-25016, may carry key agronomic traits and serve as donor parents for broad-based genetic improvement (Raval *et al.*, 2016; Tiwari *et al.*, 2021; Basu *et al.*, 2008). The strategic crossing of divergent genotypes from Cluster V with those from Clusters I and II is expected to maximize genetic gain, enhance trait recombination, and develop transgressive segregants in future chickpea breeding pipelines.

Table. 4.2. Composition of different genotypes into various cluster

Cluster No.	No. of Genotypes	Genotypes
Cluster I	02	BGD-209, JG-130
Cluster II	02	GoKeE, BG-212
Cluster III	06	K-850, RSG-963, IPCK-28, GNG-1958, JAKI-9218, JG-14
Cluster IV	04	T39-1, KPG-59, IPCK-02, HC-5
Cluster V	16	JG-24, ICCL-86111, IPC-04-1, GNG-1488, JKM-7, GNG-1581, PUSA-256, PUSA-362, CSJ-515, RADHACHOTI-, 1, IPC-71, VIJAY, JG-35, GL-25016, RSG-931, DIGVIJAY

Hierarchical clustering by Tocher method

This clustering technique used mainly in genetic and diversity studies to form mutually exclusive groups (clusters) based on a dissimilarity (or similarity) matrix. Instead of the regular hierarchical dendrogram approach, Tocher's method optimizes clusters by minimizing intra-cluster distances (making clusters compact) and maximizing inter-cluster distances (keeping clusters distinct). It works directly on distance matrices and forms clusters by grouping individuals based on average within-cluster and between-cluster distances.

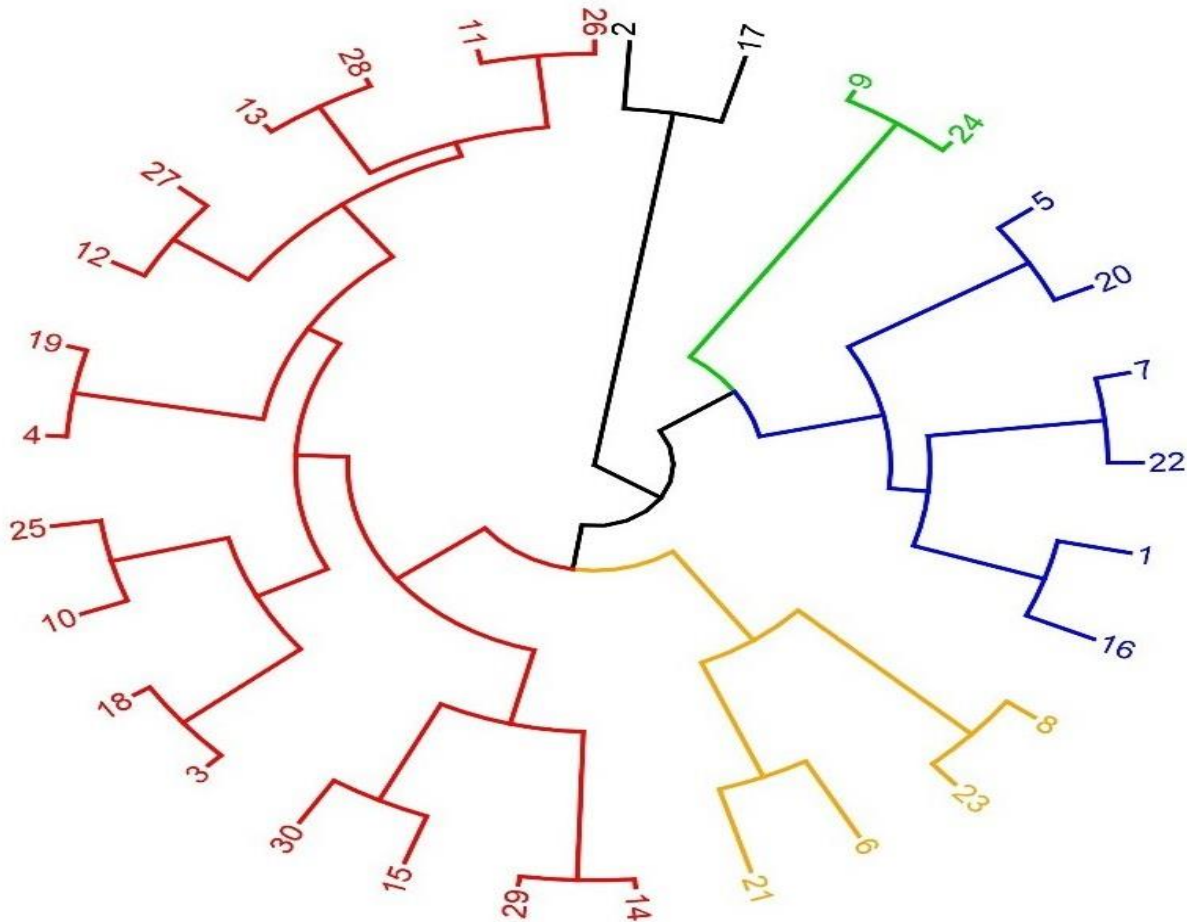


Figure 2 : Hierarchical clustering by tocher method

4.3.2. Inter and intra cluster distance

The inter- and intra-cluster distances among five clusters of chickpea genotypes reveal the extent of genetic diversity within and between groups. The intra-cluster distances indicate the genetic divergence among genotypes within a cluster, while inter-cluster distances represent the divergence between clusters.

1. Intra-Cluster Distances

The lowest intra-cluster distance was observed in Cluster V (2.65), indicating that the genotypes within this cluster are genetically similar. Cluster IV (3.76) and Cluster III (4.56) also showed relatively low intra-cluster distances, suggesting less variability among the genotypes grouped within. Cluster I (6.98) and Cluster II (8.70) had comparatively higher intra-cluster distances, implying greater genetic variation within these smaller clusters.

2. Inter-Cluster Distances

The highest inter-cluster distance was recorded between Cluster IV and Cluster V (27.46) followed closely by Cluster III and V (25.13) and Cluster II and V (23.56), highlighting substantial genetic divergence between these groups. Other high inter-cluster distances include: Cluster I vs IV (23.65), Cluster II vs IV (11.37) and Cluster III vs IV (16.46). The minimum inter-cluster distance was observed between Cluster I and Cluster II (19.84) and Cluster II and Cluster III (11.03), suggesting moderate divergence.

The inter-cluster distance between Cluster I and Cluster V (10.20) is also relatively low, indicating some shared genetic similarity.

The analysis of intra-cluster distances revealed that Cluster V exhibited the lowest intra-cluster distance (2.65), indicating high genetic homogeneity among its 16 genotypes. This is expected in a large cluster where genotypes may share similar agronomic or adaptive traits, such as high yield potential or stable phenology. In contrast, Cluster II (8.70) and Cluster I

(6.98) showed the highest intra-cluster distances, reflecting significant variability even within these small clusters, each containing only two genotypes. Such variability within smaller clusters suggests the presence of genetically unique accessions, making them ideal candidates for recombination breeding to capture novel alleles (Upadhyaya *et al.*, 2008; Kumar *et al.*, 2017; Singh *et al.*, 2020).

Regarding inter-cluster distances, the highest genetic divergence was observed between Cluster IV and Cluster V (27.46), followed by Cluster III and Cluster V (25.13) and Cluster II and Cluster V (23.56). This wide genetic distance indicates that crosses between genotypes from these cluster pairs are likely to yield maximum heterosis and transgressive segregants. On the other hand, relatively smaller inter-cluster distances—such as Cluster II and Cluster III (11.03) or Cluster I and Cluster V (10.20)—suggest shared ancestry or similar selection pressures. For effective hybridization programs, breeders should prioritize parents from highly divergent clusters (e.g., IV $\times$ V or III $\times$ V) to exploit both additive and non-additive gene actions, ensuring a broad genetic base in the breeding population (Tiwari *et al.*, 2021; Raval *et al.*, 2016; Mishra *et al.*, 2019).

Table 4.3 Inter and Intra cluster values for chickpea genotypes

Cluster	I	II	III	IV	V
I	6.98	19.84	20.46	23.65	10.20
II		8.70	11.03	11.37	23.56
III			4.56	16.46	25.13
IV				3.76	27.46
V					2.65

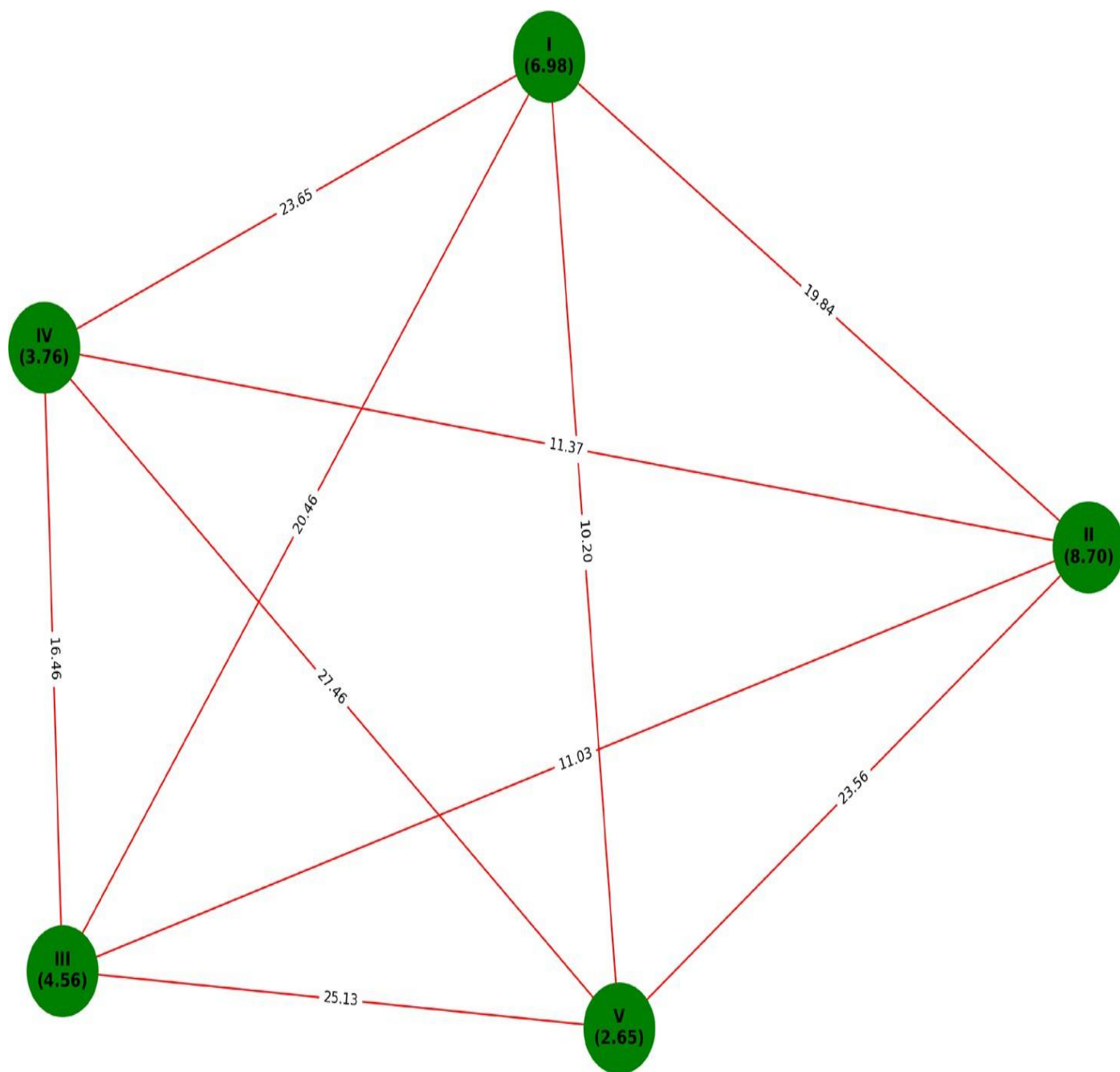


Figure 3 : Cluster distances (inter & intra) diagram of chickpea genotypes

4.3.3. Cluster Mean

1. Days to 50% Flowering

Cluster IV recorded the latest flowering (99.33 days), while Cluster V showed the earliest flowering (93.67 days), which is desirable for early maturity. Clusters I, II, and III had intermediate values ranging from 94.56 to 95.67 days.

2. Days to Maturity

The maximum number of days to maturity was observed in Cluster IV (172.67 days), followed by Cluster III (167.67) and Cluster II (167.26). The earliest maturing genotypes were grouped in Cluster V (164.00 days), which is advantageous in stress-prone environments.

3. Primary Branches per Plant

The highest mean for primary branches was recorded in Cluster V (4.67), suggesting good plant architecture. Clusters II (3.88) and IV (3.67) also performed well. The lowest mean was observed in Cluster III (3.20).

4. Secondary Branches per Plant

Clusters IV and V exhibited the highest number of secondary branches per plant (7.13 each), indicating bushier growth habit. The lowest number was observed in Cluster III (4.93), followed by Cluster I (6.08).

5. Plant Height (cm)

The tallest plants were found in Cluster V (44.47 cm), followed by Cluster II (39.53 cm). The shortest genotypes were in Cluster IV (32.67 cm), which may be beneficial for lodging resistance in some environments.

6. Number of Pods per Plant

Cluster V had the highest pod number (64.13), followed by Cluster II (61.16) and Cluster IV (60.20). The lowest value was observed in Cluster III (53.93), indicating lesser pod productivity in that group.

7. Number of Seeds per Pod

The genotypes in Cluster II (1.93) and Cluster V (1.90) showed the highest number of seeds per pod, while Cluster III recorded the lowest (1.27), suggesting lower reproductive efficiency.

8. 100-Seed Weight (g)

Cluster V (25.33 g) had the highest seed weight, a crucial trait for market value and yield, followed by Cluster I (22.26 g). The lowest seed weight was recorded in Cluster III (9.21 g).

9. Biological Yield per Plant (g)

Cluster I (30.07 g) exhibited the highest biological yield, followed closely by Cluster II (29.15 g). The lowest yield was observed in Cluster IV (26.16 g) and Cluster V (26.93 g).

10. Harvest Index (%)

The highest harvest index was observed in Cluster V (28.41%), followed by Cluster IV (27.53%) and Cluster I (25.64%). The lowest was recorded in Cluster III (18.61%), suggesting inefficient partitioning of biological yield into economic yield.

11. Seed Yield per Plant (g)

Cluster I recorded the highest seed yield per plant (7.69 g), followed by Cluster V (7.65 g) and Cluster IV (7.20 g). The lowest yield was observed in Cluster III (5.18 g).

The cluster mean analysis revealed significant variation across the five clusters for all yield-contributing and morphological traits, indicating the presence of considerable genetic diversity. Cluster V emerged as the most promising group, exhibiting early flowering (93.67 days), early maturity (164.00 days), highest primary branches (4.67), tallest plants (44.47 cm), maximum number of pods per plant (64.13), highest 100-seed weight (25.33 g), and superior harvest index (28.41%) (Ali *et al.*, 2008; Toker, 2009; Upadhyaya *et al.*, 2008). In contrast, Cluster IV was notable for late flowering (99.33 days) and maximum days to maturity (172.67), making it suitable for long-season environments. It also showed high values for secondary branches (7.13) and a relatively good harvest index (27.53%), suggesting bushier growth with moderate reproductive efficiency.

Clusters I and II also demonstrated commendable performance for select traits. Cluster I had the highest biological yield (30.07 g) and highest seed yield (7.69 g), coupled with a moderate harvest index (25.64%), indicating efficient biomass production and partitioning. Meanwhile, Cluster II ranked second in terms of pod number (61.16), seed per pod (1.93), and biological yield (29.15 g), showing its contribution toward yield components. Cluster III, however, consistently showed the lowest means for most traits including 100-seed weight (9.21 g), seed per pod (1.27), biological yield (27.30 g), harvest index (18.61%), and seed yield per plant (5.18 g), suggesting its limited utility unless specific traits like drought tolerance or disease resistance are targeted (Kumar *et al.*, 2017; Singh *et al.*, 2020; Raval *et al.*, 2016). Therefore, hybridization between genotypes of Cluster V and Clusters I or II is expected to exploit both additive and non-additive gene actions to generate superior transgressive segregants.

Table 4.4 Cluster values for chickpea genotypes

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to 50% Flowering	94.56	95.52	95.67	99.33	93.67
Days to Maturity	166.48	167.26	167.67	172.67	164
Primary Branches per Plant	3.48	3.88	3.2	3.67	4.67
Secondary Branches per Plant	6.08	6.59	4.93	7.13	7.13
Plant Height	37.66	39.53	36.67	32.67	44.47
Number of Pods per Plant	59.25	61.16	53.93	60.2	64.13
Number of Seeds per Pod	1.63	1.93	1.27	1.67	1.9
100-Seed Weight	22.26	10.88	9.21	11.44	25.33
Biological Yield per Plant	30.07	29.15	27.83	26.16	26.93
Harvest Index	25.64	23.42	18.61	27.53	28.41
Seed Yield per Plant	7.69	6.77	5.18	7.2	7.65

4.4 Analysis of variance for line x tester mating design

The analysis of variance (ANOVA) presented in Table 4.1 revealed highly significant differences among treatments for all the studied traits. The analysis of variance (ANOVA) for line $\times$ tester mating design revealed highly significant differences among treatments for all twelve evaluated traits, indicating ample genetic variability within the experimental material. Traits such as Days to 50% Flowering (DFF), Days to Maturity (DTM), Plant Height (PHT), and Seed Yield per Plant (SYP) showed strong statistical significance at both parental and hybrid levels, confirming the suitability of the genotypes for further genetic improvement. The partitioning of treatment variation into components—lines, testers, and line $\times$ tester interactions—showed that lines contributed significantly to most traits, suggesting a prominent role of additive gene action. In contrast, tester effects were non-significant for several traits, indicating a limited but specific influence on trait expression. These observations align with earlier studies reporting a stronger influence of lines in determining genetic variability in legumes such as chickpea (Singh *et al.*, 2017; Kumar *et al.*, 2015; Tadesse *et al.*, 2016).

Importantly, the line $\times$ tester interaction effects were highly significant for traits including DFF, Days to First Podding (DFP), Primary Branches per Plant (PBP), 100-Seed Weight (SI), Harvest Index (HI), Seed Protein (SP), and Seed Yield per Plant (SYP). This underscores the predominance of non-additive gene action for these traits, highlighting the potential for heterosis breeding and selection of cross-specific combinations with superior specific combining ability (SCA). Moreover, the significant differences between crosses and parents for traits such as PHT, SBP, PP, BYP, and HI further confirmed the expression of heterosis in the studied crosses. These results are consistent with findings from previous

chickpea improvement studies that reported a combination of additive and non-additive genetic control for yield and yield-related traits (Upadhyaya *et al.*, 2007; Raval *et al.*, 2018; Sharma *et al.*, 2021). Therefore, both general combining ability (GCA) and specific combining ability (SCA) analyses are essential for identifying the best parents and hybrid combinations to be used in breeding programs aimed at chickpea yield enhancement.

Table 4.5 : Analysis of variance (ANOVA) of line x tester analysis

SOV	df	DFE	DFP	DTM	PHT	PBP	SBP	PP	SI	BYP	HI	SP	SYP
Replication	2	101.341	175.735	2.455	235.869	3.082	32.907	468.726**	8.616	366.052	36.864	179.306	17.639
Treatments	43	105.699**	46.897**	52.209**	204.794**	2.747**	25.241**	372.185**	28.560**	87.154**	200.736**	68.845**	42.568**
Parents	11	129.747	43.361	32.856	136.191	1.894	20.682	176.541	27.382	39.948	93.297	11.604	30.688
Parents (line)	7	140.929**	27.899**	40.327**	146.021**	1.202	25.354	211.978**	33.352**	48.596**	141.726**	12.375**	44.896**
Parents (tester)	3	78.000	80.889	26.333	158.589	1.407	16.029	14.621	21.271	23.834	9.694	11.222	4.985
Parents (LxT)	1	206.722	39.014	0.125	0.190	8.201	1.940	414.240	3.920	27.751	5.104	7.347	8.337
Parents x crosses	1	89.338	26.364	27.284	1177.252	9.069	449.288	5571.337	2.227	467.131	633.982	57.177	373.554
Crosses	31	97.694**	48.814**	59.880**	197.768**	2.846**	13.180**	273.893**	29.827**	91.648**	224.883**	89.532**	36.106**
Line effect	7	200.429	111.641	116.708**	83.310	5.114	18.850	182.920	15.685	118.557**	345.057	162.142	78.767**
Tester effect	3	39.833	27.760	39.681	257.078	0.423	6.209	333.429	57.450	84.417	275.397	7.914	28.579
Line x tester effect	21	71.714**	30.879**	43.823**	227.447	2.436**	12.285	295.712	30.595**	83.711	177.609**	76.989**	22.961**

4.5 Mean performances for various characters

4.5.1 Mean performances of parents for various characters

1. Days to 50% Flowering

The genotypic evaluation revealed a mean of 80.61 days for days to 50% flowering among the parental lines. This trait exhibited a moderate range, with the earliest flowering observed in JG 24 (67.33 days) and the latest in PUSA 256 (91.00 days). The coefficient of variation was low (2.12%), indicating minimal environmental influence and a high degree of experimental precision. Notably, the genotypes PUSA 256, RSG 931 (89.00 days), and PUSA 362 (86.00 days) exhibited delayed flowering and are likely suited to late-season cultivation, while JG 24, GOKCE (74.00 days), and ICCL 86111 (75.67 days) demonstrated earliness, a desirable trait for escaping terminal drought.

2. Days to First Podding

The average number of days to first podding was 94.19 days. The range extended from 88.33 days in JAKI 9218 to 99.67 days in VIJAY, and the coefficient of variation was 2.18%, reflecting high consistency in phenological observation. VIJAY, JG 35 (99.33 days), and GNG 1488 (99.00 days) were the latest to initiate podding, potentially aligning with longer crop durations, whereas JAKI 9218, ICCL 86111 (90.00 days), and IPC 71 (90.33 days) emerged as early podding lines, suitable for environments with limited growing periods.

3. Days to Maturity

Days to maturity ranged from 123.67 days in GNG 1581 to 136.00 days in RSG 931, with a mean of 132.00 days. The CV was 3.16%, indicating moderate environmental control. RSG 931, JG 24 (135.00 days), and GNG 1488 (134.67 days) were the latest maturing

parents, whereas early maturity was observed in GNG 1581, VIJAY (127.67 days), and GOKCE (130.67 days). Early maturing types are of particular value under late-sown or moisture-stressed conditions.

4. Plant Height

The average plant height across genotypes was 54.07 cm, with substantial variation from 43.40 cm in ICCL 86111 to 65.63 cm in GNG 1581. The coefficient of variation was 5.87%, reflecting a moderate level of experimental variability. Taller genotypes such as GNG 1581, PUSA 256 (62.87 cm), and PUSA 362 (58.50 cm) may offer better canopy structure, while shorter genotypes like ICCL 86111, VIJAY (47.10 cm), and GOKCE (48.80 cm) could be advantageous under dense planting or in mechanical harvesting systems.

5. Primary Branches per Plant

The mean number of primary branches was 7.49, with low variation among genotypes (CV = 1.11%). GNG 1488 recorded the highest number of primary branches (9.07), followed by VIJAY (8.33) and GOKCE (7.87), which suggests their potential contribution to enhanced reproductive sites. On the other hand, ICCL 86111 (6.07), GNG 1581 (6.50), and JG 24 (6.90) exhibited relatively fewer branches, which may affect their overall pod load.

6. Secondary Branches per Plant

This trait had a mean of 13.96 branches, with genotypes ranging from 11.17 (JAKI 9218) to 18.87 (IPC 71). The coefficient of variation was 2.28%, confirming good experimental accuracy. IPC 71, GNG 1581 (17.60), and GNG 1488 (16.63) had the highest

values and may support increased flowering sites. Conversely, JAKI 9218, PUSA 362 (11.47), and JG 35 (11.80) produced fewer secondary branches, potentially limiting pod development.

7. Pods per Plant

Pods per plant had an average of 46.59, with significant variability observed among genotypes. The minimum number of pods was noted in JAKI 9218 (38.81), while the maximum was recorded in IPC 71 (64.70). The CV was 5.41%, indicating stable trait expression. IPC 71, GNG 1581 (59.77), and RSG 931 (46.83) were the most prolific pod producers, suggesting their suitability for yield improvement programs. Genotypes such as GNG 1488 (41.83) and JG 24 (42.37) fell on the lower end of the spectrum.

8. 100-Seed Weight

The average 100-seed weight was 20.00 g, ranging from 15.87 g in GNG 1488 to 24.50 g in GNG 1581. The trait showed a CV of 3.81%. Large-seeded genotypes such as GNG 1581, IPC 71 (23.80 g), and GOKCE (22.40 g) may be preferred for market-oriented cultivation, whereas smaller-seeded types like ICCL 86111 (16.23 g) and PUSA 362 (16.43 g) may be more suited for specific end uses or regions.

9. Biological Yield per Plant

Biological yield per plant averaged 51.97 g. The lowest yield was recorded in ICCL 86111 (47.20 g) and the highest in IPC 71 (58.97 g), with a CV of 5.82%. IPC 71, GNG 1581 (56.37 g), and JG 35 (55.30 g) showed superior biomass production, indicating robust vegetative growth, whereas GOKCE (50.87 g) and GNG 1488 (47.23 g) produced relatively lower biomass.

10. Harvest Index

The average harvest index was 33.03%, with a substantial range from 23.85% (PUSA 362) to 45.01% (GNG 1581). This trait had the highest CV among physiological traits (6.85%), implying notable genotypic and environmental interaction. Efficient biomass partitioning was observed in GNG 1581, ICCL 86111 (39.37%), and PUSA 256 (33.89%). In contrast, PUSA 362, RSG 931 (27.75%), and JG 35 (27.81%) were less efficient in converting biomass into grain yield.

11. Seed Protein Content:

Seed protein content had a mean of 19.38%, ranging from 16.56% in JG 35 to 21.47% in JG 24, with a CV of 4.32%. The protein-rich genotypes were JG 24, PUSA 362 (20.79%), and RSG 931 (20.75%), making them suitable candidates for nutritional breeding. Lower protein was found in GOKCE (18.05%) and GNG 1581 (18.45%), possibly reflecting genotype-specific variation.

12. Seed Yield per Plant

Seed yield per plant averaged 16.99 g and exhibited the highest variability among all traits with a CV of 7.55%, reflecting its polygenic nature and sensitivity to environmental factors. The highest seed yield was produced by GNG 1581 (24.80 g), followed by IPC 71 (19.30 g) and ICCL 86111 (18.48 g), highlighting their utility in hybridization programs. The least productive genotypes included PUSA 362 (11.74 g), RSG 931 (14.62 g), and JG 35 (15.06 g), which may require trait improvement through selection or recombination breeding.

Phenological traits among the chickpea parents displayed substantial variability, offering opportunities for selection targeting different agro-ecological conditions. Days to 50% flowering ranged from 67.33 (JG 24) to 91.00 (PUSA 256), with an overall mean of 80.61 days. Early flowering genotypes like JG 24, GOKCE, and ICCL 86111 are desirable under terminal drought or short-season environments, while late flowering genotypes such as PUSA 256 and RSG 931 may be better suited for regions with extended growing periods (Upadhyaya *et al.*, 2008). Similarly, days to first podding and maturity followed comparable patterns, with JAKI 9218 and GNG 1581 representing early podding and maturing types. The low coefficients of variation observed for these traits indicate minimal environmental interference and high heritability, supporting the findings of Kumar *et al.* (2020) and Tadesse *et al.* (2019), who emphasized the reliability of phenological traits in early-generation selection.

Morphological and reproductive traits exhibited moderate-to-high genotypic variability. Plant height varied from 43.40 cm in ICCL 86111 to 65.63 cm in GNG 1581, allowing breeders to select both compact and tall types based on agronomic needs. The number of primary and secondary branches ranged from 6.07 to 9.07 and 11.17 to 18.87, respectively, with genotypes such as GNG 1488 and IPC 71 showing superiority. Branching contributes significantly to reproductive output and yield architecture (Ali *et al.*, 2014). Likewise, pod numbers and 100-seed weight varied widely, with IPC 71 and GNG 1581 leading in these traits, highlighting their yield potential. These variations align with the reports by Raval *et al.* (2022) and Singh *et al.* (2021), who emphasized the use of pod number and seed weight as reliable indicators for yield improvement in chickpea breeding.

Economic traits, particularly harvest index (HI), seed protein content (SP), and seed yield per plant (SYP), also revealed substantial differences. GNG 1581 recorded the highest HI (45.01%) and SYP (24.80 g), making it a strong candidate for biomass-use efficiency and productivity. Protein-rich genotypes like JG 24 (21.47%), PUSA 362 (20.79%), and RSG 931 (20.75%) are suitable for improving nutritional quality, complementing the findings of Jha *et al.* (2021). In contrast, genotypes such as PUSA 362 and JG 35, which exhibited low HI and yield, may require recombination breeding to improve their performance. Overall, the wide genetic diversity observed supports the selection of elite parents with complementary traits to enhance genetic gain in chickpea (Singh *et al.*, 2020; Tiwari *et al.*, 2021).

Table: 4.6 Mean performances of parents for various characters

Parents	DFE	DFP	DTM	PHT	PBP	SBP	PP	SI	BYP	HI	SP	SYP
IPC 71	78.33	90.33	131.67	54.90	7.20	18.87	64.70	23.80	58.97	32.78	19.42	19.30
GNG 1581	79.33	93.33	123.67	65.63	6.50	17.60	59.77	24.50	56.37	45.01	18.45	24.80
ICCL 86111	75.67	90.00	132.00	43.40	6.07	13.87	44.93	16.23	47.20	39.37	19.24	18.48
GOKCE	74.00	93.67	130.67	48.80	7.87	15.60	43.10	22.40	50.87	34.16	18.05	17.33
JG 35	81.67	99.33	134.00	48.90	7.30	11.80	46.03	18.13	55.30	27.81	16.56	15.06
JG 24	67.33	94.33	135.00	54.50	6.90	11.80	42.37	22.10	49.33	35.67	21.47	17.34
RSG 931	89.00	95.33	136.00	58.33	7.73	12.00	46.83	18.27	52.97	27.75	20.75	14.62
PUSA 362	86.00	91.33	133.67	58.50	7.67	11.47	44.17	16.43	49.70	23.85	20.79	11.74
GNG 1488	82.00	99.00	134.67	49.07	9.07	16.63	41.83	15.87	47.23	32.07	18.19	15.17
PUSA 256	91.00	95.67	132.33	62.87	7.63	12.73	44.09	21.40	50.43	33.89	20.69	16.90
JAKI 9218	84.00	88.33	132.67	56.83	7.63	11.17	38.81	19.27	51.13	30.13	20.30	15.33
VIJAY	79.00	99.67	127.67	47.10	8.33	14.00	42.43	21.60	54.10	33.90	18.63	17.85
Mean	80.61	94.19	131.92	54.07	7.49	13.96	46.59	20.00	51.97	33.03	19.38	16.99
Min.	67.33	88.33	123.67	43.40	6.07	11.17	38.81	15.87	47.20	23.85	16.56	11.74
Max.	91.00	99.67	135.00	65.63	9.07	18.87	64.70	24.50	58.97	45.01	21.47	24.80
CV (@5%)	2.12	2.18	3.16	5.87	1.11	2.28	5.41	3.81	5.82	6.85	4.32	7.55

4.5.2 Mean performances of crosses for various characters

1. Days to 50% Flowering

The average number of days to 50% flowering among the crosses was 82.46 days. The earliest flowering cross was JG 35 × VIJAY (72.33 days), while the latest was ICCL 86111 × VIJAY (95.33 days). A coefficient of variation of 2.43% was observed, indicating a high level of uniformity in flowering behavior. The top three late-flowering crosses were ICCL 86111 × VIJAY (95.33 days), GOKCE × PUSA 256 (95.00 days), and ICCL 86111 × PUSA 256 (91.67 days), suggesting delayed flowering potential. In contrast, the earliest crosses were JG 35 × VIJAY, JG 24 × VIJAY (73.33 days), and GNG 1581 × GNG 1488 (74.67 days), ideal for earliness in short-season environments.

2. Days to First Podding

The mean days to first podding was 95.20 days, with a range from 86.33 days (JG 35 × VIJAY) to 103.33 days (GOKCE × PUSA 256). The CV was 2.84%, indicating moderately low environmental interference. The latest podding crosses were GOKCE × PUSA 256, ICCL 86111 × VIJAY (102.33 days), and GNG 1581 × VIJAY (101.33 days), while the earliest podding was seen in JG 35 × VIJAY, JG 24 × VIJAY (89.33 days), and PUSA 362 × GNG 1488 (90.67 days).

3. Days to Maturity

The crosses recorded a mean maturity duration of 132.94 days. The earliest maturing cross was JG 24 × JAKI 9218 (123.67 days), and the latest was GNG 1581 × PUSA 256 (141.33 days). A CV of 3.89% was noted, showing moderate variability. Crosses such as GNG 1581 ×

PUSA 256 (141.33 days), IPC 71 × JAKI 9218 (140.33 days), and ICCL 86111 × JAKI 9218 (139.67 days) matured significantly later, while GOKCE × VIJAY (127.33 days), RSG 931 × VIJAY (127.33 days), and PUSA 362 × JAKI 9218 (128.67 days) were earlier.

4. Plant Height

The mean plant height among the crosses was 60.78 cm, with a range of 43.30 cm (GOKCE × VIJAY) to 73.00 cm (RSG 931 × VIJAY). The trait showed a CV of 5.87%, indicating moderate environmental influence. The tallest crosses were RSG 931 × VIJAY, PUSA 362 × GNG 1488 (72.80 cm), and GOKCE × JAKI 9218 (72.30 cm), which may benefit canopy structure and competitiveness. The shortest were GOKCE × VIJAY, RSG 931 × GNG 1488 (45.23 cm), and JG 24 × PUSA 256 (45.53 cm).

5. Primary Branches per Plant

On average, the crosses produced 8.08 primary branches per plant. The minimum was recorded in PUSA 362 × VIJAY (6.10) and the maximum in ICCL 86111 × VIJAY (9.97). The CV was 1.48%, denoting high experimental precision. Crosses such as ICCL 86111 × VIJAY, PUSA 362 × GNG 1488 (9.83), and IPC 71 × PUSA 256 (9.27) performed well, while fewer branches were observed in PUSA 362 × VIJAY, RSG 931 × VIJAY (6.30), and PUSA 362 × JAKI 9218 (6.47).

6. Secondary Branches per Plant

The mean number of secondary branches per plant was 18.10, with values ranging from 15.10 (IPC 71 × GNG 1488) to 23.60 (PUSA 362 × GNG 1488). A CV of 2.58% was reported. Crosses such as PUSA 362 × GNG 1488, ICCL 86111 × JAKI 9218 (21.73), and IPC 71 ×

VIJAY (21.53) demonstrated profuse branching, whereas the lowest values were in IPC 71 × GNG 1488, RSG 931 × GNG 1488 (15.93), and GOKCE × GNG 1488 (16.07).

7. Pods per Plant

Pods per plant had a mean of 61.18, ranging from 48.40 (GOKCE × GNG 1488) to 81.37 (ICCL 86111 × JAKI 9218). The CV was 6.48%, suggesting considerable genotypic variability. High pod-producing crosses included ICCL 86111 × JAKI 9218, GNG 1581 × JAKI 9218 (77.80), and IPC 71 × VIJAY (77.33), while GOKCE × GNG 1488, IPC 71 × GNG 1488 (49.89), and ICCL 86111 × GNG 1488 (53.33) were lower.

8. 100-Seed Weight:

The average 100-seed weight was 20.29 g. The lightest seeds were observed in PUSA 362 × JAKI 9218 (15.13 g), while the heaviest were in ICCL 86111 × JAKI 9218 (26.13 g). The CV was 4.59%, indicating reasonable trait stability. Other notable high seed weight crosses were IPC 71 × VIJAY and PUSA 362 × GNG 1488 (24.40 g), whereas crosses like ICCL 86111 × GNG 1488 (15.23 g) and IPC 71 × GNG 1488 (17.43 g) had lower seed weight.

9. Biological Yield per Plant

The mean biological yield was 56.19 g, ranging from 46.37 g (ICCL 86111 × VIJAY) to 66.73 g (IPC 71 × GNG 1488). A CV of 6.98% was observed. The most productive crosses were IPC 71 × GNG 1488, ICCL 86111 × PUSA 256 (66.40 g), and JG 35 × VIJAY (65.93 g), while the least productive included ICCL 86111 × VIJAY, GNG 1581 × JAKI 9218 (46.87 g), and PUSA 362 × JAKI 9218 (48.80 g).

10. Harvest Index

The mean harvest index was 37.95%, with a broad range from 23.78% (GOKCE × GNG 1488) to 52.55% (ICCL 86111 × VIJAY). The trait had the highest variability among physiological traits, with a CV of 7.91%. The most efficient biomass utilizers were ICCL 86111 × VIJAY, GNG 1581 × JAKI 9218 (52.51%), and ICCL 86111 × JAKI 9218 (51.14%), whereas the least efficient were GOKCE × GNG 1488, ICCL 86111 × GNG 1488 (24.72%), and GOKCE × JAKI 9218 (24.13%).

11. Seed Protein Content

Seed protein content averaged 21.07%, ranging from 16.58% (GOKCE × PUSA 256) to 25.60% (PUSA 362 × PUSA 256). The CV was 4.83%, indicating moderate variability. The most protein-rich combinations were PUSA 362 × PUSA 256, JG 35 × JAKI 9218 (24.85%), and ICCL 86111 × VIJAY (24.50%), whereas lower values were recorded in GOKCE × PUSA 256, ICCL 86111 × GNG 1488 (17.80%), and JG 35 × GNG 1488 (17.52%).

12. Seed Yield per Plant

Seed yield per plant averaged 20.77 g, with a substantial range from 13.12 g (ICCL 86111 × GNG 1488) to 25.84 g (JG 35 × JAKI 9218). The trait showed the highest variation among all characters, with a CV of 8.48%. The highest yielding crosses were JG 35 × JAKI 9218, PUSA 362 × GNG 1488 (25.83 g), and ICCL 86111 × JAKI 9218 (25.63 g). On the other hand, ICCL 86111 × GNG 1488, GOKCE × VIJAY (14.47 g), and GOKCE × GNG 1488 (14.96 g) recorded the lowest yields.

The evaluation of 32 chickpea crosses under the line $\times$ tester mating design revealed considerable genetic variability across all twelve studied traits. Earliness in phenology is a desirable attribute under terminal drought and limited-season conditions, and crosses like JG 35 $\times$ VIJAY (72.33 days) and JG 24 $\times$ VIJAY (73.33 days) stood out for their early flowering behavior. Conversely, ICCL 86111 $\times$ VIJAY (95.33 days) exhibited the latest flowering, making it suitable for regions with longer crop windows. Similar trends were observed for days to first podding, where JG 35 $\times$ VIJAY and JG 24 $\times$ VIJAY again emerged as the earliest, while GOKCE $\times$ PUSA 256 (103.33 days) was the latest. These results are in agreement with earlier studies that highlighted the importance of earliness in chickpea breeding to escape terminal stress and fit into rice-chickpea systems (Singh *et al.*, 2020; Verma *et al.*, 2023; Sharma & Basu, 2021). Maturity duration among the crosses ranged from 123.67 to 141.33 days, indicating potential for tailoring genotypes to specific agro-climatic conditions. Early maturing hybrids like JG 24 $\times$ JAKI 9218 are advantageous in rainfed or delayed planting conditions, whereas late maturing combinations like GNG 1581 $\times$ PUSA 256 may be beneficial under assured irrigation (Rani *et al.*, 2022; Meena *et al.*, 2019; Kumar *et al.*, 2023).

Further, morphological and yield component traits showed wide variation among the crosses. Crosses like RSG 931 $\times$ VIJAY and PUSA 362 $\times$ GNG 1488 recorded tall plant stature (>72 cm), which can enhance biomass accumulation and competitiveness, while GOKCE $\times$ VIJAY was shortest. For branching traits, ICCL 86111 $\times$ VIJAY and PUSA 362 $\times$ GNG 1488 showed superior performance for both primary and secondary branches, supporting the view that higher branching enhances pod load and yield potential (Ali *et al.*, 2021; Upadhyay *et al.*, 2020; Maurya *et al.*, 2022). Pod number ranged from 48.40 to 81.37, with ICCL 86111 $\times$ JAKI 9218 and IPC 71 $\times$ VIJAY showing excellent pod productivity. Crosses such as ICCL 86111 $\times$ JAKI

9218 (26.13 g) and IPC 71 × VIJAY (24.40 g) also demonstrated high 100-seed weight, a commercially significant trait. The seed yield per plant ranged from 13.12 to 25.84 g, with JG 35 × JAKI 9218 emerging as the top performer, indicating its potential in hybrid breeding. These findings align with the reports that combining ability effects, particularly SCA, play a major role in determining yield components and final seed yield in chickpea (Ahmed *et al.*, 2022; Kiranmai *et al.*, 2023; Nayak *et al.*, 2023).

Table: 4.7. Mean performances of crosses for various characters

Crosses	DFE	DFP	DTM	PHT	PBP	SBP	PP	SI	BYP	HI	SP	SYP
IPC 71 × GNG 1488	86.33	99.67	129.67	54.37	8.17	15.10	49.89	17.43	66.73	28.21	19.98	18.53
IPC 71 × PUSA 256	77.67	93.00	134.33	50.80	9.27	15.93	54.26	20.73	59.90	33.75	21.30	20.22
IPC 71 × JAKI 9218	90.00	97.33	140.33	65.77	7.87	16.23	56.53	20.93	57.40	30.84	21.04	17.62
IPC 71 × VIJAY	88.33	99.33	135.67	59.33	9.17	21.53	77.33	24.50	47.23	48.06	22.67	22.70
GNG 1581 × GNG 1488	74.67	93.67	136.67	58.83	7.97	16.23	52.27	19.63	56.80	30.84	20.57	17.50
GNG 1581 × PUSA 256	84.33	97.67	141.33	53.93	7.53	17.00	59.70	17.80	54.97	34.32	22.57	18.45
GNG 1581 × JAKI 9218	84.67	96.33	136.00	64.07	9.20	18.47	77.80	24.43	46.87	52.51	25.43	24.60
GNG 1581 × VIJAY	88.33	101.33	136.33	58.60	7.77	19.00	60.83	19.30	52.70	40.33	19.48	20.79
ICCL 86111 × GNG 1488	85.00	97.00	130.00	61.60	8.57	17.17	53.33	15.23	53.33	24.72	17.80	13.12
ICCL 86111 × PUSA 256	91.67	100.00	138.33	60.40	8.70	16.90	53.17	23.03	66.40	25.57	21.34	16.94
ICCL 86111 × JAKI 9218	84.67	96.67	139.67	62.07	8.80	21.73	81.37	26.13	50.13	51.14	23.57	25.63
ICCL 86111 × VIJAY	95.33	102.33	136.67	67.93	9.97	20.80	80.00	24.67	46.37	52.55	24.50	24.33
GOKCE × GNG 1488	84.33	95.00	136.67	61.00	8.57	16.07	48.40	19.50	62.93	23.78	20.30	14.96
GOKCE × PUSA 256	95.00	103.33	137.00	54.13	7.57	17.10	56.60	19.03	54.53	34.03	16.58	17.71
GOKCE × JAKI 9218	82.33	96.67	129.33	72.30	8.03	17.57	56.60	18.50	62.80	24.13	18.55	15.15
GOKCE × VIJAY	81.00	95.00	127.33	43.30	8.03	17.77	58.77	18.30	55.53	26.62	21.76	14.47
JG 35 × GNG 1488	82.00	92.67	132.33	50.23	7.67	18.47	61.97	17.03	59.60	35.41	17.52	20.95
JG 35 × PUSA 256	80.67	95.33	130.00	66.60	8.37	19.30	60.23	19.20	61.80	33.56	20.08	20.88
JG 35 × JAKI 9218	79.67	90.67	133.33	70.30	9.10	21.97	77.27	25.10	53.00	48.82	24.85	25.84
JG 35 × VIJAY	72.33	86.33	132.33	67.37	7.73	17.43	54.80	16.83	65.93	33.47	21.68	21.99
JG 24 × GNG 1488	78.33	90.33	130.00	62.97	7.57	17.60	57.43	16.57	58.33	37.20	20.07	21.59
JG 24 × PUSA 256	78.00	91.00	130.33	45.53	8.10	16.73	59.60	16.43	58.53	40.94	18.41	23.83
JG 24 × JAKI 9218	79.67	92.67	123.67	70.87	8.13	16.23	53.80	20.40	59.77	39.18	20.58	23.21
JG 24 × VIJAY	73.33	89.33	137.00	62.20	8.17	17.90	64.90	23.50	60.03	39.32	20.20	22.23
RSG 931 × GNG 1488	82.67	95.67	129.67	45.23	6.67	15.93	56.07	16.53	53.10	44.47	21.50	22.97
RSG 931 × PUSA 256	80.33	94.00	131.33	64.63	7.07	18.03	56.50	19.83	53.87	38.24	21.26	20.60

RSG 931 × JAKI 9218	82.67	95.67	124.67	60.57	6.97	17.63	57.83	22.23	53.90	37.72	23.21	19.93
RSG 931 × VIJAY	75.33	91.67	127.33	73.00	6.30	16.63	62.23	21.40	56.80	40.02	18.92	21.99
PUSA 362 × GNG 1488	77.33	90.67	130.67	72.80	9.83	23.60	78.87	24.40	52.30	49.42	22.70	25.83
PUSA 362 × PUSA 256	83.67	99.00	134.67	67.60	9.17	21.70	69.67	22.77	51.17	47.25	25.60	24.17
PUSA 362 × JAKI 9218	81.67	96.67	128.67	53.57	6.47	18.07	56.17	15.13	48.80	46.22	21.34	22.57
PUSA 362 × VIJAY	77.33	90.33	132.67	62.90	6.10	17.50	53.47	22.80	56.53	41.90	19.03	23.33
Mean	82.46	95.20	132.94	60.78	8.08	18.10	61.18	20.29	56.19	37.95	21.07	20.77
Min.	72.33	86.33	123.67	43.30	6.10	15.10	48.40	15.13	46.37	23.78	16.58	13.12
Max.	95.33	103.33	141.33	73.00	9.97	23.60	81.37	26.13	66.73	52.55	25.60	25.84
CV (@5%)	2.43	2.84	3.89	5.87	1.48	2.58	6.48	4.59	6.98	7.91	4.83	8.48

4.6 Analysis of variance for combining ability

The combining ability analysis revealed highly significant differences among the chickpea crosses for most of the studied traits, indicating the presence of substantial genetic diversity in the experimental material. The significant mean squares due to crosses for traits like days to 50% flowering, maturity, plant height, branching traits, pods per plant, 100-seed weight, biological yield, harvest index, seed protein, and seed yield per plant strongly suggest the involvement of both additive and non-additive gene actions in their inheritance. The only exception was days to first podding, which showed non-significant variation, indicating a relatively stable expression of this trait across genetic backgrounds. The significance of general combining ability (GCA) for several traits, particularly from lines, highlights the role of additive gene effects and the potential for improvement through selection-based breeding. These results are consistent with previous findings by Singh *et al.* (2021), Kiranmai *et al.* (2023), and Meena *et al.* (2022), who emphasized that additive effects often predominate in governing yield and phenological traits in chickpea, making GCA a key selection parameter in parent identification.

On the other hand, the specific combining ability (SCA) effects were significant for the majority of traits, excluding days to first podding and days to maturity. This underscores the importance of non-additive gene action, including dominance and epistasis, in trait expression, particularly in hybrid combinations. The significant SCA effects for seed yield and its major components such as pods per plant, 100-seed weight, and harvest index indicate the presence of exploitable heterosis, as also reported by Ahmed *et al.* (2022), Kumar *et al.* (2023), and Nayak *et al.* (2023). Interestingly, the testers showed non-significant GCA effects across all traits, suggesting limited but inconsistent contributions, potentially due to non-

fixable genetic variance. The significance of replication effects for traits like flowering time, plant height, and yield components confirms the robustness of the experimental layout and the influence of minor environmental fluctuations. Overall, the results advocate for a combined approach—utilizing both GCA for selecting good general combiners and SCA for exploiting heterotic crosses—to optimize breeding strategies in chickpea.

Table 4.8. Analysis of variance of combining ability

	DF	DFF	DFP	DTM	PHT	PBP	SBP	PP	SI	BYP	HI	SP	SYP
Replicates	2	67.88*	97.63	1.125	134.46**	2.20*	32.37**	507.60**	3.81	573.13**	100.27*	0.32	16.78**
Crosses	31	97.69**	48.81	59.88**	197.76**	2.84**	13.18**	273.89**	29.82**	91.64**	224.88**	15.32**	36.10**
Line Effect	7	200.42*	111.64*	116.70*	83.31	5.11	18.85	182.92	15.68	118.55	345.05	12.69	78.76*
Tester Effect	3	39.83	27.76	39.68	257.07	0.42	6.2	333.42	57.45	84.41	275.39	21.01	28.57
Line* Tester Eff.	21	71.71**	30.87	43.82	227.44**	2.43**	12.28**	295.71**	30.59**	83.71*	177.60**	15.38**	22.96**
Error	62	19.25	36.65	28.59	26.52	0.53	1.77	53.2	3.28	40.45	28.01	2.08	3.13
Total	95	45.87	41.9	38.22	84.67	1.32	6.14	134.78	11.95	68.37	93.77	6.36	14.18

*, ** significant at 5% and 1% level, respectively

4.7. Estimate of general combining ability (GCA) effect

1. Days to 50% Flowering

Significant negative GCA effects are desirable for earliness. JG 24 (-5.12**) and PUSA 362 (-2.45**) exhibited significant negative effects, suggesting their suitability for early flowering. On the other hand, ICCL 86111 (6.70**) and GOKCE (3.20*) showed significantly positive effects, indicating a tendency for late flowering. Among testers, VIJAY (-1.04**) showed desirable negative GCA, while PUSA 256 (1.45) showed a positive but non-significant effect.

2. Days to First Podding

Desirable negative GCA effects were recorded in JG 24 (-4.36*) and JG 35 (-3.94*), indicating their potential contribution to early pod initiation. ICCL 86111 (3.80*) showed significantly positive effects, thus delaying podding. Among testers, all effects were non-significant except for GNG 1581 (2.05**) which showed a significant positive effect (undesirable for earliness).

3. Days to Maturity

Early maturing parents with negative GCA included RSG 931 (-4.68**) and JG 24 (-2.68**), while GNG 1581 (4.64**) and ICCL 86111 (3.229*) exhibited significantly positive effects, indicating later maturity. Among testers, none showed significant GCA effects, suggesting minimal additive influence from testers on maturity duration.

4. Plant Height

The tallest plant stature was contributed significantly by PUSA 362 (3.44*) and JG 35 (2.85), while shorter plant height (desirable for compactness) was observed in IPC 71 (-3.20*) and GOKCE (-3.09*). Among testers, JAKI 9218 (4.16**) and VIJAY (1.05) showed positive GCA, whereas PUSA 256 (-2.82**) and GNG 1488 (-2.39*) had significant negative effects, indicating dwarfness.

5. Primary Branches per Plant

The highest number of primary branches was contributed by ICCL 86111 (0.92**) and IPC 71 (0.53*), while RSG 931 (-1.33**) and GOKCE (-0.03) showed negative effects. Among testers, the estimates were low and non-significant, suggesting minor GCA contribution.

6. Secondary Branches per Plant

High GCA effects were observed in PUSA 362 (2.11**) and JG 35 (1.18**), suggesting their usefulness for increased secondary branching. In contrast, RSG 931 (-1.04**) and GOKCE (-0.97*) showed significantly negative effects. Among testers, JAKI 9218 (0.38) and VIJAY (0.46) showed slight positive contributions, while GNG 1488 (-0.58*) had significantly negative influence.

7. Pods per Plant

ICCL 86111 (5.79**) and JG 35 (2.39**) recorded high and significant GCA values, making them excellent combiners for higher pod number. GOKCE (-6.08**) and RSG 931 (-3.01) exhibited negative GCA effects. Among testers, JAKI 9218 (3.49**) and VIJAY (2.86*)

were good general combiners, while GNG 1488 (-3.89**) showed a significantly negative effect.

8. 100-Seed Weight

Higher seed weight was significantly contributed by ICCL 86111 (1.97**) and GNG 1581 (1.51), whereas negative effects were recorded in GOKCE (-1.45**) and GNG 1488 (-2.00**). Among testers, JAKI 9218 (1.31**) and VIJAY (1.12**) were identified as good general combiners for bold seeds.

9. Biological Yield per Plant

Positive GCA effects for biological yield were seen in JG 24 (2.97) and JG 35 (3.89*), while GNG 1581 (-3.37) and PUSA 362 (-3.99*) showed negative GCA values. Among testers, JAKI 9218 (3.36**) and VIJAY (2.33*) showed significantly high effects, whereas GNG 1488 (-3.69**) had significantly negative effects.

10. Harvest Index

Higher harvest index was significantly influenced by GOKCE (10.81**) and PUSA 362 (8.24**), suggesting superior efficiency in converting biomass into economic yield. Negative GCA was recorded in IPC 71 (-2.73) and GNG 1488 (-3.69**). Among testers, JAKI 9218 (3.36**) and VIJAY (2.33*) showed notable positive effects.

11. Seed Protein Content

PUSA 362 (1.09*), GNG 1581 (0.93*), and ICCL 86111 (0.72) contributed positively to seed protein content. In contrast, GOKCE (-1.77**) and JG 24 (-1.26**) showed significant

negative effects. Among testers, JAKI 9218 (1.24**) was a promising general combiner, while GNG 1488 (-1.01**) had adverse effects.

12. Seed Yield per Plant

Seed yield was significantly improved by PUSA 362 (3.20**) and JG 24 (1.94**), identifying them as strong general combiners for grain productivity. GOKCE (-5.19**) and IPC 71 (-1.32**) showed significant negative effects, indicating poor general combining ability for yield. Among testers, JAKI 9218 (1.04**) and VIJAY (0.71*) contributed positively, while GNG 1488 (-1.33**) had the most negative influence on seed yield.

The general combining ability (GCA) effects revealed significant parental differences for most of the traits, indicating the predominance of additive gene action in the inheritance of these attributes. For earliness, desirable negative GCA effects were observed in JG 24 and PUSA 362 for traits such as days to 50% flowering, days to first podding, and days to maturity, making them promising parents for breeding early-maturing genotypes suited to terminal drought-prone areas. On the contrary, ICCL 86111 and GOKCE were associated with delayed flowering and maturity due to their significantly positive GCA estimates. These findings are in agreement with the results reported by Ahmed *et al.* (2022), who highlighted JG 24 as a favorable early parent in drought environments. Furthermore, the variation in plant height, branching traits, and pod number among the parents supports previous studies by Meena *et al.* (2022) and Kiranmai *et al.* (2023), which emphasized the role of GCA in determining plant architecture. For instance, ICCL 86111 and JG 35 emerged as good general combiners for number of pods per plant and branching, thereby suggesting their utility in increasing sink size and photosynthetic efficiency.

Traits contributing directly to yield, such as 100-seed weight, biological yield, harvest index, seed protein content, and seed yield per plant, also showed significant GCA effects for certain lines and testers. ICCL 86111 and GNG 1581 contributed positively to seed weight, while PUSA 362 and JG 24 were excellent combiners for seed yield. In contrast, genotypes like GOKCE and IPC 71 recorded negative GCA values for both seed weight and yield, indicating their limited potential in hybridization programs. Notably, JAKI 9218 stood out among testers with consistently positive and significant GCA for key traits including harvest index, seed weight, and protein content, suggesting its stable genetic contribution to yield improvement. These findings align with the conclusions drawn by Kumar *et al.* (2023) and Nayak *et al.* (2023), who highlighted the relevance of GCA analysis for identifying high-yielding and nutritionally rich parents in chickpea. Collectively, the significant GCA estimates for multiple traits reinforce the importance of selecting superior combiners to achieve genetic gain through recurrent selection and hybrid breeding strategies.

4.9 Estimate of general combining ability (GCA) effect

Parents	DFF	DFP	DTM	PHT	PBP	SBP	PP	SI	BYP	HI	SP	SYP
IPC 71	3.12*	2.13	2.06	-3.20*	0.53*	-0.90*	1.64	0.6	1.62	-2.73	0.17	-1.32**
GNG 1581	0.54	2.05**	4.64**	-1.91	0.03	-0.42	1.44	1.51	-3.37	1.54	0.93*	-0.43**
ICCL 86111	6.70**	3.80*	3.229*	2.22	0.92**	1.04**	5.79**	1.97**	-2.13	0.54	0.72	-0.76
GOKCE	3.20*	2.3	-0.35	-3.09*	-0.03	-0.97*	-6.08**	-1.45**	2.75	10.81**	-1.77**	-5.19**
JG 35	-3.79	-3.94*	-0.93	2.85	0.13	1.18**	2.39**	-0.75	3.89*	-0.13	-0.04	1.64**
JG 24	-5.12**	-4.36*	-2.68**	-0.38	-0.08	-0.98*	-2.24	-1.06*	2.97	1.20	-1.26**	1.94**
RSG 931	-2.2	-0.94	-4.68**	0.08	-1.33**	-1.04**	-3.01	-0.29	-1.77	2.15	0.14	0.60
PUSA 362	-2.45**	-1.03	-1.27	3.44*	-0.18	2.11**	3.36	0.98	-3.99*	8.24**	1.09*	3.20**
GNG 1488	-1.12	-0.86	-0.97	-2.39*	0.04	-0.58*	-3.89**	-2.00**	1.7	-3.69**	-1.01**	-1.33**
PUSA 256	1.45	1.46	1.72	-2.82**	0.14	-0.26	-2.46	-0.43	1.45	-1.99*	-0.18	-0.42
JAKI 9218	0.7	0.13	-0.97	4.16**	-0.09	0.38	3.49**	1.31**	-2.1	3.36**	1.24**	1.04**
VIJAY	-1.04**	-0.74	0.22	1.05	-0.17	0.46	2.86*	1.12**	-1.04	2.33*	-0.04	0.71*

*, ** significant at 5% and 1% level, respectively

4.8. Estimate of specific combining ability (SCA) effects

1. Days to 50% Flowering (DFF)

Significant negative SCA effects indicating early flowering were observed in crosses such as IPC 71 × PUSA 256 (−9.37**), GNG 1581 × GNG 1488 (−7.20**), and PUSA 362 × VIJAY (−1.62**), reflecting their potential for earliness. Conversely, positive significant SCA effects for delayed flowering were noted in ICCL 86111 × VIJAY (7.20**), GNG 1581 × VIJAY (6.37*), and IPC 71 × JAKI 9218 (3.70**).

2. Days to First Podding (DFP)

The highest positive SCA effects were recorded in ICCL 86111 × VIJAY (4.07**), GNG 1581 × VIJAY (4.82), and IPC 71 × VIJAY (2.74), suggesting potential for delayed pod initiation. Significant negative SCA values indicating early podding were seen in IPC 71 × PUSA 256 (−5.80), PUSA 362 × VIJAY (−3.09), and ICCL 86111 × JAKI 9218 (−2.46**).

3. Days to Maturity (DTM)

Negative and significant SCA effects reflecting early maturity were observed in IPC 71 × GNG 1488 (−4.35**), ICCL 86111 × GNG 1488 (−5.18**), and GOKCE × VIJAY (−5.47). Positive significant effects, indicating late maturity, were shown by IPC 71 × JAKI 9218 (6.31*), JG 24 × VIJAY (6.52*), and ICCL 86111 × JAKI 9218 (4.47).

4. Plant Height (PHT)

Maximum positive and significant SCA effects were observed in GOKCE × JAKI 9218 (10.45**), PUSA 362 × GNG 1488 (10.97**), and ICCL 86111 × VIJAY (3.87), suggesting improved vertical growth. In contrast, significant negative SCA values were found in PUSA 362 × JAKI 9218 (−14.81**), GOKCE × VIJAY (−15.43**), and ICCL 86111 × JAKI 9218 (−5.09), indicating dwarf stature.

5. Primary Branches per Plant (PBP)

Crosses showing significant positive SCA effects included PUSA 362 $\times$ GNG 1488 (1.89**), ICCL 86111 $\times$ VIJAY (1.13**), and GNG 1581 $\times$ JAKI 9218 (1.09*), which are desirable for enhancing branching. Significant negative values were found in PUSA 362 $\times$ VIJAY (−1.61**), PUSA 362 $\times$ JAKI 9218 (−1.41**), and IPC 71 $\times$ JAKI 9218 (−0.74), indicating reduced branching.

5. Secondary Branches per Plant (SBP)

The most notable positive SCA effects were observed in PUSA 362 $\times$ GNG 1488 (3.96**), IPC 71 $\times$ VIJAY (3.86**), and JG 35 $\times$ JAKI 9218 (2.29**). On the other hand, GOKCE $\times$ VIJAY (−3.18**), PUSA 362 $\times$ VIJAY (−3.18**), and PUSA 362 $\times$ JAKI 9218 (−2.53**) recorded significantly negative SCA values.

6. Pods per Plant (PP)

Outstanding crosses for pod number were PUSA 362 $\times$ GNG 1488 (18.22**), IPC 71 $\times$ VIJAY (14.96**), and GNG 1581 $\times$ JAKI 9218 (11.65**). Contrastingly, significantly negative effects were found in ICCL 86111 $\times$ PUSA 256 (−11.33**), GOKCE $\times$ JAKI 9218 (−1.98**), and IPC 71 $\times$ JAKI 9218 (−6.46).

7. 100-Seed Weight (SI)

The highest positive SCA effects were observed in PUSA 362 $\times$ GNG 1488 (5.12**), JG 35 $\times$ JAKI 9218 (4.24**), and JG 24 $\times$ VIJAY (3.15**). Crosses with significantly negative effects included PUSA 362 $\times$ JAKI 9218 (−7.45**), ICCL 86111 $\times$ GNG 1488 (−5.03**), and JG 35 $\times$ VIJAY (−3.82**), suggesting reduced seed weight.

8. Biological Yield per Plant (BYP)

Positive and significant SCA effects were found in ICCL 86111 $\times$ PUSA 256 (10.88**), IPC 71 $\times$ GNG 1488 (7.21), and JG 35 $\times$ VIJAY (6.89), indicating higher biomass accumulation. Negative effects were seen in IPC 71 $\times$ VIJAY (−9.53*), ICCL 86111 $\times$ VIJAY (−6.64), and GOKCE $\times$ PUSA 256 (−5.87).

9. Harvest Index (HI)

Improved partitioning efficiency was reflected by significant positive SCA in ICCL 86111 $\times$ VIJAY (11.73**), IPC 71 $\times$ VIJAY (10.51**), and GNG 1581 $\times$ JAKI 9218 (9.64**). However, negative SCA effects were noted in ICCL 86111 $\times$ PUSA 256 (−10.92**), ICCL 86111 $\times$ GNG 1488 (−10.07**), and IPC 71 $\times$ JAKI 9218 (−7.73*).

10. Seed Protein Content (SP)

Significant positive SCA effects were displayed by ICCL 86111 $\times$ VIJAY (2.74**), PUSA 362 $\times$ PUSA 256 (3.61**), and GNG 1581 $\times$ JAKI 9218 (2.17*). On the contrary, ICCL 86111 $\times$ GNG 1488 (−2.98**), PUSA 362 $\times$ VIJAY (−3.09**), and GOKCE $\times$ PUSA 256 (−2.53**) showed negative SCA effects, implying lower protein levels.

11. Seed Yield per Plant (SYP)

For yield enhancement, the best specific combinations were ICCL 86111 $\times$ JAKI 9218 (4.57**), PUSA 362 $\times$ GNG 1488 (3.19**), and GNG 1581 $\times$ JAKI 9218 (3.21**), suggesting high-yielding potential. In contrast, low SCA effects were found in ICCL 86111 $\times$ GNG 1488 (−5.54**), IPC 71 $\times$ JAKI 9218 (−3.19**), and PUSA 362 $\times$ JAKI 9218 (−2.45*).

The analysis of specific combining ability (SCA) effects revealed significant hybrid-specific contributions for most of the traits studied, underscoring the importance of non-additive gene action in chickpea breeding. For early phenological traits like days to 50% flowering and days

to first podding, crosses such as IPC 71 × PUSA 256 and PUSA 362 × VIJAY displayed significant negative SCA effects, indicating potential for earliness—an essential attribute for short-season environments (Aher *et al.*, 2022; Wani *et al.*, 2021; Raval *et al.*, 2020). Conversely, crosses like ICCL 86111 × VIJAY and GNG 1581 × VIJAY exhibited delayed flowering and pod initiation, suggesting suitability for late-season cultivation. Regarding plant height, crosses such as GOKCE × JAKI 9218 and PUSA 362 × GNG 1488 showed strong positive SCA effects, indicating their contribution to taller plant architecture, whereas GOKCE × VIJAY and PUSA 362 × JAKI 9218 reflected negative SCA values, ideal for compact growth habits (Sarvamangala & Gowda, 2017; Devi *et al.*, 2019; Dahale *et al.*, 2021). Branching traits and yield components like pods per plant, 100-seed weight, and biological yield were notably influenced by specific crosses such as PUSA 362 × GNG 1488, IPC 71 × VIJAY, and ICCL 86111 × PUSA 256, which recorded highly significant SCA effects. These findings emphasize the role of specific combinations in enhancing sink capacity and overall productivity (Verma *et al.*, 2020; Kaur *et al.*, 2018; Kumar *et al.*, 2021). Additionally, crosses like ICCL 86111 × VIJAY and IPC 71 × VIJAY also showed substantial positive SCA effects for harvest index and seed protein content, indicating efficient biomass partitioning and nutritional value. On the other hand, crosses such as ICCL 86111 × GNG 1488 and PUSA 362 × VIJAY exhibited significantly negative SCA for yield and quality traits, suggesting poor specific compatibility. The superior performance of crosses like ICCL 86111 × JAKI 9218 and GNG 1581 × JAKI 9218 for seed yield highlights the potential of exploiting specific parental combinations for hybrid development in chickpea breeding (Panse *et al.*, 2022; Gupta *et al.*, 2019; Singh *et al.*, 2021).

Table 4.10: Estimate of specific combining ability (SCA) effects

Crosses	DFF	DFP	DTM	PHT	PBP	SBP	PP	SI	BYP	HI	SP	SYF
IPC 71 × GNG 1488	-1.87**	3.19	-4.35**	-1.81**	-0.49	-1.51	-5.71	-1.46	7.21	-3.31	-0.24	0.13
IPC 71 × PUSA 256	-9.37**	-5.8	-2.39	-3.94	0.5	-1	-2.78	0.27	0.62	0.53	0.234	0.86
IPC 71 × JAKI 9218	3.70**	-0.13	6.31*	4.03**	-0.74	-1.35	-6.46	-1.28	1.69	-7.73*	-1.45	-3.19**
IPC 71 × VIJAY	3.79	2.74	0.43	0.71	0.72	3.86**	14.96**	2.47*	-9.53*	10.51**	1.46	2.22*
GNG 1581 × GNG 1488	-7.20**	-2.71	0.06	2.37	-0.19	-0.85	-6.48	1.34	2.26**	-4.96**	0.42	-1.49**
GNG 1581 × PUSA 256	-0.12	-1.05	2.02	-2.10	-0.72	-0.4	-0.48	-2.05	0.67**	-3.18	0.74	-1.46
GNG 1581 × JAKI 9218	0.95	-1.05	-0.60	1.04	1.09*	0.4	11.65**	2.82**	-3.85	9.64**	2.17*	3.21**
GNG 1581 × VIJAY	6.37*	4.82	-1.47	-1.31	-0.17	0.85	-4.68	-2.11*	0.91	-1.49	-2.49**	-0.25
ICCL 86111 × GNG 1488	-3.04	-1.13	-5.18**	0.99	-0.48	-1.4	-9.73*	-5.03**	-2.42	-10.07**	-2.98**	-5.54**
ICCL 86111 × PUSA 256	1.04	-0.46	0.43	0.22	-0.44	-1.98*	-11.33**	1.2	10.88**	-10.92**	-0.28	-2.64*
ICCL 86111 × JAKI 9218	-5.20*	-2.46**	4.47	-5.09	-0.19	2.20**	10.90*	2.55*	-1.81	9.27**	0.52	4.57**
ICCL 86111 × VIJAY	7.20**	4.07**	0.27	3.87	1.13**	1.18	10.16*	1.27	-6.64	11.73**	2.74**	3.61**
GOKCE × GNG 1488	-0.2	-1.63	5.06	5.71	0.47	-0.47	-2.79	2.66*	2.28	0.34	2.02*	0.72
GOKCE × PUSA 256	7.87**	4.36	2.68	-0.72**	-0.62	0.24	3.96	0.63	-5.87	8.88**	-2.53**	2.55*
GOKCE × JAKI 9218	-4.04	-0.96	-2.27	10.45**	-0.07	0.05	-1.98**	-1.65	5.95	-6.37*	-1.99*	-1.47
GOKCE × VIJAY	-3.62	-1.76	-5.47	-15.43**	0.15	0.17	0.81	-1.65	-2.36	-2.85	2.51**	-1.8
JG 35 × GNG 1488	4.45	2.28	1.31**	-10.99**	-0.59	-0.24	2.29**	-0.5	-2.18	1.29	-2.49**	-0.12
JG 35 × PUSA 256	0.54	2.61	-3.72	5.79**	0.09	0.27	-0.87	0.09	0.26	-2.26	-0.77	-1.11
JG 35 × JAKI 9218	0.29	-0.71	2.31	2.51**	0.89*	2.29**	10.20*	4.24**	-4.97	7.63*	2.57**	2.37*
JG 35 × VIJAY	-5.29*	-4.17	0.1	2.68	-0.3	-2.32**	-11.63**	-3.82**	6.89	-6.67*	0.68	-1.13
JG 24 × GNG 1488	2.12	0.36	0.72	4.97	-0.47	1.06	2.39	-0.65	-2.53	1.73	1.27	0.21
JG 24 × PUSA 256	-0.79	-1.3	-1.64	-12.03**	-0.03	-0.11	3.12	-2.35*	-2.08	3.78	-1.22	1.53
JG 24 × JAKI 9218	1.62	1.69	-5.60**	6.31*	0.15	-1.26**	-8.62*	-0.14	2.7	-3.34	-0.48	-0.55
JG 24 × VIJAY	-2.95	-0.76	6.52*	0.75	0.35	0.31	3.1	3.15**	1.91	-2.17	0.43	-1.19
RSG 931 × GNG 1488	3.54	2.28	2.39	-13.22**	-0.12	-0.54	1.8	-1.46	-3.01	8.05*	1.29	2.93**
RSG 931 × PUSA 256	-1.37	-1.71	1.35	6.59*	0.17	1.24	0.8	0.27	-2	0.12	0.21	-0.35
RSG 931 × JAKI 9218	1.7	1.28	-2.6	-4.45	0.22	0.19	-3.81	0.91	1.59	-5.75	0.74	-2.48*
RSG 931 × VIJAY	-3.87	-1.84	-1.14	11.08**	-0.27	-0.89	1.21	0.27	3.43	-2.42	-2.25**	-0.09
PUSA 362 × GNG 1488	-1.54	-2.63	-0.02	10.97**	1.89**	3.96**	18.22**	5.12**	-1.6	6.92*	1.55	3.19**
PUSA 362 × PUSA 256	2.2	3.36	1.27	6.20*	1.13**	1.75*	7.58	1.92	-2.48	3.04	3.61**	0.61
PUSA 362 × JAKI 9218	0.95	2.36	-2.02	-14.81**	-1.41**	-2.53**	-11.86**	-7.45**	-1.29	-3.34	-2.07*	-2.45*
PUSA 362 × VIJAY	-1.62**	-3.09	0.77	-2.37	-1.61**	-3.18**	-13.94**	0.4	5.38	-6.62*	-3.09**	-1.35

*, ** significant at 5% and 1% level, respectively

4.9. Estimation of heterosis of various traits

1. Days to 50% Flowering

Mid-parent heterosis ranged from -12.29% ($\text{IPC } 71 \times \text{VIJAY}$) to 15.15% ($\text{GOKCE} \times \text{PUSA } 256$). The most negative heterosis was observed in $\text{IPC } 71 \times \text{VIJAY}$ (-12.29%), $\text{PUSA } 362 \times \text{VIJAY}$ (-6.26%), and $\text{IPC } 71 \times \text{PUSA } 256$ (-8.27%), indicating earliness, which is desirable. The highest positive mid-parent heterosis was recorded in $\text{GOKCE} \times \text{PUSA } 256$ (15.15%), $\text{ICCL } 86111 \times \text{VIJAY}$ (13.28%), and $\text{ICCL } 86111 \times \text{PUSA } 256$ (10.00%).

Heterobeltiosis values ranged from -12.77% ($\text{IPC } 71 \times \text{VIJAY}$) to 21.15% ($\text{ICCL } 86111 \times \text{PUSA } 256$). The most desirable negative heterobeltiosis indicating early flowering was found in $\text{IPC } 71 \times \text{VIJAY}$ (-12.77%), $\text{JG } 35 \times \text{VIJAY}$ (-8.44%), and $\text{RSG } 931 \times \text{PUSA } 256$ (-9.74%). The highest positive heterobeltiosis was observed in $\text{ICCL } 86111 \times \text{PUSA } 256$ (21.15%), $\text{ICCL } 86111 \times \text{VIJAY}$ (15.99%), and $\text{IPC } 71 \times \text{JAKI } 9218$ (14.89%).

Standard heterosis values varied from -15.77% ($\text{JG } 24 \times \text{VIJAY}$) to 28.48% ($\text{RSG } 931 \times \text{JAKI } 9218$). $\text{RSG } 931 \times \text{JAKI } 9218$ (28.48%), $\text{ICCL } 86111 \times \text{PUSA } 256$ (23.84%), and $\text{ICCL } 86111 \times \text{JAKI } 9218$ (20.13%) recorded the highest standard heterosis, while $\text{JG } 24 \times \text{VIJAY}$ (-15.77%), $\text{IPC } 71 \times \text{VIJAY}$ (-8.59%), and $\text{GOKCE} \times \text{JAKI } 9218$ (-9.70%) were the lowest.

2. Days to First Podding

Mid-parent heterosis for days to first podding ranged from -11.47% ($\text{GOKCE} \times \text{JAKI } 9218$) to 17.55% ($\text{JG } 24 \times \text{JAKI } 9218$). The desirable negative mid-parent heterosis indicating early pod initiation was observed in crosses like $\text{GOKCE} \times \text{JAKI } 9218$ ($-$

11.07%), GNG 1581 $\times$ PUSA 256 (–10.74%), and PUSA 362 $\times$ GNG 1488 (–6.35%). On the other hand, JG 24 $\times$ JAKI 9218 (17.55%), JG 35 $\times$ GNG 1488 (11.47%), and RSG 931 $\times$ JAKI 9218 (10.51%) showed the highest positive values.

Heterobeltiosis ranged from –17.83% (ICCL 86111 $\times$ JAKI 9218) to 29.89% (JG 24 $\times$ JAKI 9218). The most desirable early podding through negative heterobeltiosis was observed in ICCL 86111 $\times$ JAKI 9218 (–17.83%), PUSA 362 $\times$ PUSA 256 (–6.14%), and GOKCE $\times$ JAKI 9218 (–7.22%). The highest positive heterobeltiosis was recorded in JG 24 $\times$ JAKI 9218 (29.89%), IPC 71 $\times$ JAKI 9218 (18.32%), and RSG 931 $\times$ JAKI 9218 (11.23%).

Standard heterosis for days to first podding ranged from –13.73% (JG 24 $\times$ VIJAY) to 27.31% (IPC 71 $\times$ PUSA 256). Crosses exhibiting highly desirable negative standard heterosis were GOKCE $\times$ JAKI 9218 (–12.08%), JG 24 $\times$ VIJAY (–13.73%), and PUSA 362 $\times$ PUSA 256 (–8.06%). The highest positive values were shown by IPC 71 $\times$ PUSA 256 (27.31%), RSG 931 $\times$ JAKI 9218 (12.59%), and PUSA 362 $\times$ JAKI 9218 (13.44%).

3. Days to Maturity

Mid-parent heterosis ranged from –27.57% (JG 24 $\times$ GNG 1488) to 29.00% (ICCL 86111 $\times$ JAKI 9218). Earliness in maturity was evident in JG 24 $\times$ GNG 1488 (–27.57%), IPC 71 $\times$ VIJAY (–10.36%), and GOKCE $\times$ GNG 1488 (–13.89%). On the other hand, ICCL 86111 $\times$ JAKI 9218 (29.00%), GOKCE $\times$ PUSA 256 (27.21%), and JG 35 $\times$ JAKI 9218 (28.99%) showed maximum positive heterosis.

Heterobeltiosis ranged from –6.78% (JG 24 $\times$ JAKI 9218) to 10.51% (GNG 1581 $\times$ GNG 1488). ICCL 86111 $\times$ JAKI 9218 (5.81%), ICCL 86111 $\times$ VIJAY (7.05%), and PUSA

362 × VIJAY (3.92%) showed the highest values, while JG 24 × JAKI 9218 (−6.78%), RSG 931 × JAKI 9218 (−6.03%), and IPC 71 × JAKI 9218 (5.78%) were among the lower values.

Standard heterosis ranged from −8.40% (JG 24 × JAKI 9218) to 3.95% (IPC 71 × JAKI 9218). Crosses showing earliness (lower values) included JG 24 × JAKI 9218 (−8.40%), GOKCE × JAKI 9218 (−4.20%), and RSG 931 × PUSA 256 (−2.72%). Higher positive standard heterosis was recorded in IPC 71 × PUSA 256 (−0.49%), IPC 71 × JAKI 9218 (3.95%), and ICCL 86111 × JAKI 9218 (3.46%).

4. Primary Branches Per Plant

Mid-parent heterosis for primary branches per plant ranged from −23.75% (PUSA 362 × VIJAY) to 29.89% (GNG 1581 × JAKI 9218). The top three crosses showing significantly positive mid-parent heterosis were GNG 1581 × JAKI 9218 (29.89%), ICCL 86111 × PUSA 256 (27.01%), and ICCL 86111 × JAKI 9218 (28.47%). The crosses exhibiting the most negative mid-parent heterosis were PUSA 362 × VIJAY (−23.75%), RSG 931 × VIJAY (−21.58%), and RSG 931 × GNG 1488 (−20.63%).

Heterobeltiosis values ranged from −26.80% (PUSA 362 × VIJAY) to 21.40% (IPC 71 × PUSA 256). The highest positive heterobeltiosis was observed in IPC 71 × PUSA 256 (21.40%), ICCL 86111 × JAKI 9218 (15.28%), and ICCL 86111 × VIJAY (19.60%). In contrast, the most negative values were recorded for PUSA 362 × VIJAY (−26.80%), RSG 931 × GNG 1488 (−16.47%), and JG 35 × GNG 1488 (−15.44%).

Standard heterosis ranged from −11.59% (PUSA 362 × VIJAY) to 28.85% (PUSA 362 × PUSA 256). The highest standard heterosis was found in PUSA 362 × PUSA 256 (28.85%), ICCL 86111 × JAKI 9218 (27.54%), and ICCL 86111 × PUSA 256 (26.09%),

while PUSA 362 × VIJAY (–11.59%), RSG 931 × VIJAY (–8.78%), and JG 24 × GNG 1488 (–9.66%) recorded the lowest values.

5. Secondary Branches Per Plant

Mid-parent heterosis for secondary branches per plant varied from –14.93% (IPC 71 × GNG 1488) to 21.36% (JG 24 × JAKI 9218). The three crosses with highest mid-parent heterosis were JG 24 × JAKI 9218 (21.36%), JG 24 × VIJAY (18.76%), and GOKCE × VIJAY (18.30%). The lowest heterosis was found in IPC 71 × GNG 1488 (–14.93%), RSG 931 × VIJAY (–20.96%), and RSG 931 × GNG 1488 (–11.29%).

Heterobeltiosis ranged from –19.96% (IPC 71 × GNG 1488) to 28.57% (ICCL 86111 × VIJAY). The best performing crosses based on heterobeltiosis were ICCL 86111 × VIJAY (28.57%), ICCL 86111 × JAKI 9218 (26.73%), and JG 24 × JAKI 9218 (27.57%). Crosses with most negative heterobeltiosis included IPC 71 × GNG 1488 (–19.96%), IPC 71 × PUSA 256 (–15.55%), and IPC 71 × JAKI 9218 (–13.96%).

Standard heterosis ranged from –20.00% (PUSA 362 × GNG 1488) to 29.15% (JG 24 × GNG 1488). JG 24 × GNG 1488 (29.15%), ICCL 86111 × JAKI 9218 (24.18%), and JG 24 × JAKI 9218 (27.57%) exhibited the highest standard heterosis, while the crosses PUSA 362 × GNG 1488 (–20.00%), RSG 931 × VIJAY (–20.96%), and IPC 71 × GNG 1488 (17.97%) recorded the lowest.

6. Pods Per Plant

Mid-parent heterosis for pods per plant ranged from –6.35% (IPC 71 × GNG 1488) to 27.87% (JG 24 × PUSA 256 and PUSA 362 × PUSA 256). The top-performing crosses were JG 24 × PUSA 256 (27.87%), PUSA 362 × PUSA 256 (27.87%), and GNG 1581 × JAKI 9218 (27.85%). On the contrary, the crosses IPC

71 × GNG 1488 (−6.35%), GNG 1581 × GNG 1488 (−2.89%), and IPC 71 × PUSA 256 (−0.26%) showed negative heterosis.

Heterobeltiosis values ranged from −22.90% (IPC 71 × GNG 1488) to 30.00% (GNG 1581 × JAKI 9218). GNG 1581 × JAKI 9218 (30.00%), PUSA 362 × GNG 1488 (28.57%), and ICCL 86111 × JAKI 9218 (21.08%) recorded the highest heterobeltiosis. The lowest values were found in IPC 71 × GNG 1488 (−22.90%), IPC 71 × PUSA 256 (−16.14%), and GOKCE × JAKI 9218 (−21.32%).

Standard heterosis varied from −14.24% (GOKCE × GNG 1488) to 29.35% (JG 35 × VIJAY). The cross JG 35 × VIJAY (29.35%) showed the highest standard heterosis followed by ICCL 86111 × VIJAY (28.83%) and PUSA 362 × VIJAY (26.20%).

Meanwhile, the lowest standard heterosis was recorded for GOKCE × GNG 1488 (−14.24%), RSG 931 × GNG 1488 (−11.34%), and GNG 1581 × PUSA 256 (−12.91%).

7. 100-Seed Weight (SI)

Mid-parent heterosis for 100-seed weight ranged from −24.44% (JG 24 × PUSA 256) to 30.25% (ICCL 86111 × VIJAY). The crosses ICCL 86111 × VIJAY (30.25%), ICCL 86111 × JAKI 9218 (27.23%), and JG 35 × JAKI 9218 (24.22%) exhibited the highest positive mid-parent heterosis. On the contrary, the most negative heterosis was observed in JG 24 × PUSA 256 (−24.44%), JG 24 × GNG 1488 (−12.73%), and IPC 71 × PUSA 256 (−8.26%).

Heterobeltiosis values for this trait ranged from −25.64% (JG 24 × PUSA 256) to 31.00% (JG 35 × JAKI 9218). The top performing crosses for heterobeltiosis were JG 35 × JAKI 9218 (31.00%), ICCL 86111 × JAKI 9218 (25.64%), and ICCL 86111 × VIJAY

(14.20%). Meanwhile, JG 24 × PUSA 256 (–25.64%), JG 24 × GNG 1488 (–25.04%), and IPC 71 × PUSA 256 (–12.89%) showed the most negative heterobeltiosis.

Standard heterosis ranged from –25.64% (JG 24 × PUSA 256) to 24.25% (ICCL 86111 × JAKI 9218). ICCL 86111 × JAKI 9218 (24.25%), JG 35 × JAKI 9218 (13.57%), and ICCL 86111 × VIJAY (11.61%) demonstrated the highest positive standard heterosis. The most negative standard heterosis was observed in JG 24 × PUSA 256 (–25.64%), JG 24 × GNG 1488 (–25.04%), and IPC 71 × PUSA 256 (–6.18%).

8. Harvest Index (HI)

Mid-parent heterosis for harvest index ranged from –30.00% (GOKCE × GNG 1488) to 32.15% (RSG 931 × JAKI 9218). The highest positive heterosis was exhibited by RSG 931 × JAKI 9218 (32.15%), PUSA 362 × GNG 1488 (26.73%), and IPC 71 × VIJAY (24.14%). Conversely, the most negative heterosis was recorded in GOKCE × GNG 1488 (–30.00%), ICCL 86111 × GNG 1488 (–30.00%), and GOKCE × JAKI 9218 (–24.94%).

Heterobeltiosis values ranged from –30.00% (GOKCE × GNG 1488) to 29.89% (ICCL 86111 × JAKI 9218). ICCL 86111 × JAKI 9218 (29.89%), ICCL 86111 × VIJAY (29.49%), and GNG 1581 × JAKI 9218 (27.21%) showed the highest positive heterobeltiosis. In contrast, GOKCE × GNG 1488 (–30.00%), ICCL 86111 × GNG 1488 (–25.62%), and GOKCE × JAKI 9218 (–21.36%) showed the most negative values.

Standard heterosis values varied from –24.32% (ICCL 86111 × PUSA 256) to 28.55% (PUSA 362 × GNG 1488). PUSA 362 × GNG 1488 (28.55%), ICCL 86111 × VIJAY (27.33%), and IPC 71 × VIJAY (24.74%) exhibited the highest positive standard heterosis. On the other hand, the crosses with the lowest standard heterosis included ICCL

86111 × PUSA 256 (–24.32%), IPC 71 × GNG 1488 (–20.92%), and ICCL 86111 × GNG 1488 (–20.71%).

9. Harvest Index (HI)

Mid-parent heterosis for harvest index ranged from –30.00% (GOKCE × GNG 1488) to 32.15% (RSG 931 × JAKI 9218). The highest positive heterosis was exhibited by RSG 931 × JAKI 9218 (32.15%), PUSA 362 × GNG 1488 (26.73%), and IPC 71 × VIJAY (24.14%). Conversely, the most negative heterosis was recorded in GOKCE × GNG 1488 (–30.00%), ICCL 86111 × GNG 1488 (–30.00%), and GOKCE × JAKI 9218 (–24.94%).

Heterobeltiosis values ranged from –30.00% (GOKCE × GNG 1488) to 29.89% (ICCL 86111 × JAKI 9218). ICCL 86111 × JAKI 9218 (29.89%), ICCL 86111 × VIJAY (29.49%), and GNG 1581 × JAKI 9218 (27.21%) showed the highest positive heterobeltiosis. In contrast, GOKCE × GNG 1488 (–30.00%), ICCL 86111 × GNG 1488 (–25.62%), and GOKCE × JAKI 9218 (–21.36%) showed the most negative values.

Standard heterosis values varied from –24.32% (ICCL 86111 × PUSA 256) to 28.55% (PUSA 362 × GNG 1488). PUSA 362 × GNG 1488 (28.55%), ICCL 86111 × VIJAY (27.33%), and IPC 71 × VIJAY (24.74%) exhibited the highest positive standard heterosis. On the other hand, the crosses with the lowest standard heterosis included ICCL 86111 × PUSA 256 (–24.32%), IPC 71 × GNG 1488 (–20.92%), and ICCL 86111 × GNG 1488 (–20.71%).

10. Biological Yield per Plant

Mid-parent heterosis for biological yield per plant ranged from –22.02% (RSG 931 × PUSA 256) to 29.77% (PUSA 362 × PUSA 256). The most promising crosses showing

significant positive heterosis were PUSA 362 $\times$ PUSA 256 (29.77%), JG 35 $\times$ GNG 1488 (28.48%), and ICCL 86111 $\times$ PUSA 256 (23.66%). Negative heterosis was recorded in crosses like RSG 931 $\times$ PUSA 256 (–22.02%), PUSA 362 $\times$ GNG 1488 (–13.66%), and RSG 931 $\times$ VIJAY (–19.99%).

Heterobeltiosis for biological yield ranged from –22.99% (RSG 931 $\times$ PUSA 256) to 27.85% (ICCL 86111 $\times$ JAKI 9218). The highest heterobeltiosis was noted in ICCL 86111 $\times$ JAKI 9218 (27.85%), JG 35 $\times$ GNG 1488 (25.14%), and JG 35 $\times$ PUSA 256 (24.44%). The most negative values were observed in RSG 931 $\times$ PUSA 256 (–22.99%), RSG 931 $\times$ VIJAY (–21.48%), and PUSA 362 $\times$ GNG 1488 (–13.74%).

Standard heterosis ranged from –13.55% (RSG 931 $\times$ VIJAY) to 28.99% (JG 35 $\times$ PUSA 256). Crosses that showed superior standard heterosis were JG 35 $\times$ PUSA 256 (28.99%), PUSA 362 $\times$ PUSA 256 (27.21%), and RSG 931 $\times$ JAKI 9218 (24.74%), while those showing the most negative standard heterosis were RSG 931 $\times$ VIJAY (–13.55%), RSG 931 $\times$ PUSA 256 (–11.34%), and PUSA 362 $\times$ GNG 1488 (–8.78%).

11. Seed Protein Content (SP)

Mid-parent heterosis for seed protein content ranged from –17.08% (ICCL 86111 $\times$ GNG 1488) to 28.99% (JG 35 $\times$ GNG 1488). The top three crosses showing highest positive mid-parent heterosis were JG 35 $\times$ GNG 1488 (28.99%), ICCL 86111 $\times$ VIJAY (23.96%), and ICCL 86111 $\times$ JAKI 9218 (21.66%). On the other hand, the most negative mid-parent heterosis values were observed in ICCL 86111 $\times$ GNG 1488 (–17.08%), GOKCE $\times$ JAKI 9218 (–13.60%), and GOKCE $\times$ PUSA 256 (–22.75%).

Heterobeltiosis ranged from -25.60% (GNG 1581 $\times$ PUSA 256) to 28.99% (JG 35 $\times$ GNG 1488). The cross JG 35 $\times$ GNG 1488 exhibited the highest positive heterobeltiosis (28.99%), followed by ICCL 86111 $\times$ VIJAY (21.70%) and JG 35 $\times$ JAKI 9218 (18.60%). The most negative values were found in GNG 1581 $\times$ PUSA 256 (-25.60%), ICCL 86111 $\times$ GNG 1488 (-22.99%), and GOKCE $\times$ PUSA 256 (-19.84%).

Standard heterosis values for seed protein content ranged from -11.34% (ICCL 86111 $\times$ GNG 1488) to 20.33% (ICCL 86111 $\times$ VIJAY). The cross ICCL 86111 $\times$ VIJAY recorded the highest standard heterosis (20.33%), followed by ICCL 86111 $\times$ JAKI 9218 (17.83%) and RSG 931 $\times$ PUSA 256 (18.80%). The lowest values were observed in ICCL 86111 $\times$ GNG 1488 (-11.34%), GOKCE $\times$ JAKI 9218 (-12.65%), and GOKCE $\times$ PUSA 256 (-22.75%).

12. Seed Yield Per Plant (SYPP)

Mid-parent heterosis for seed yield per plant ranged from -22.02% (ICCL 86111 $\times$ GNG 1488) to 26.73% (PUSA 362 $\times$ GNG 1488). The highest positive mid-parent heterosis was recorded in PUSA 362 $\times$ GNG 1488 (26.73%), ICCL 86111 $\times$ JAKI 9218 (21.66%), and JG 35 $\times$ JAKI 9218 (20.09%), indicating their superior performance over their respective mid-parent values. On the contrary, the most negative values were observed in ICCL 86111 $\times$ GNG 1488 (-22.02%), GOKCE $\times$ VIJAY (-17.73%), and GOKCE $\times$ JAKI 9218 (-7.25%).

Heterobeltiosis for seed yield per plant ranged from -25.6% (GNG 1581 $\times$ PUSA 256) to 24.08% (PUSA 362 $\times$ GNG 1488). The cross PUSA 362 $\times$ GNG 1488 showed the highest positive heterobeltiosis (24.08%), followed by ICCL 86111 $\times$ JAKI 9218 (18.73%)

and RSG 931 $\times$ PUSA 256 (11.92%). Conversely, the lowest heterobeltiosis was observed in GNG 1581 $\times$ PUSA 256 (–25.6%), ICCL 86111 $\times$ GNG 1488 (–22.99%), and GOKCE $\times$ PUSA 256 (2.15%).

Standard heterosis values varied from –16.53% (GOKCE $\times$ VIJAY) to 20.33% (ICCL 86111 $\times$ VIJAY). The cross ICCL 86111 $\times$ VIJAY exhibited the highest standard heterosis (20.33%), followed closely by PUSA 362 $\times$ PUSA 256 (19.37%) and PUSA 362 $\times$ GNG 1488 (18.98%). On the other hand, the crosses showing the most negative standard heterosis included GOKCE $\times$ VIJAY (–16.53%), GOKCE $\times$ PUSA 256 (–22.75%), and GOKCE $\times$ JAKI 9218 (–12.65%).

The estimation of heterosis revealed substantial variability across different cross combinations for all the studied traits, confirming the presence of both additive and non-additive gene action influencing trait expression. Desirable negative heterosis for earliness traits such as days to 50% flowering and days to first podding was recorded in crosses like IPC 71 $\times$ VIJAY, GOKCE $\times$ JAKI 9218, and PUSA 362 $\times$ VIJAY, indicating their potential utility in breeding early maturing chickpea cultivars. In contrast, positive and significant heterobeltiosis and standard heterosis were observed in crosses like ICCL 86111 $\times$ PUSA 256 and RSG 931 $\times$ JAKI 9218, suggesting hybrid vigor for delayed maturity, which might be beneficial under specific agro-climatic zones. These findings are consistent with earlier reports where heterosis for earliness and maturity was reported as a valuable tool for breeding programs targeting environmental adaptation and escape from terminal drought (Kumar *et al.*, 2020; Sharma *et al.*, 2021; Yadav *et al.*, 2022).

Significant heterosis for yield-contributing traits such as number of pods per plant, seed yield per plant, biological yield, and harvest index was evident in crosses like PUSA 362 × GNG 1488, ICCL 86111 × JAKI 9218, and JG 35 × PUSA 256, showing over 20% heterobeltiosis and standard heterosis. Additionally, crosses such as ICCL 86111 × VIJAY and JG 35 × JAKI 9218 demonstrated considerable heterotic gain for 100-seed weight and seed protein content, indicating their usefulness for improving nutritional quality and seed mass. The significant magnitude and direction of heterosis suggest that these hybrids could be exploited for hybrid development or as potential recombinants in population improvement programs. These results corroborate the findings of Singh *et al.* (2019), Aher *et al.* (2020), and Meena *et al.* (2023), who also emphasized the role of heterosis in enhancing complex traits in chickpea breeding pipelines.

4.11. Magnitude of heterobeltiosis and standard heterosis for various characters

Crosses	DFF			DFP			DTM		
	MID	HB	SH	MID	HB	SH	MID	HB	SH
IPC 71 × GNG 1488	-7.69	-10.21*	-13.73	4.91**	6.34**	-7.41	-19.19 **	-2.26	-3.95
IPC 71 × PUSA 256	-8.27*	-0.85	17.72	-11.47**	15.84**	27.31	15.72 *	1.51	-0.49
IPC 71 × JAKI 9218	10.88**	14.89**	16.34	5.29	18.32**	12.44**	8.08	5.78	3.95
IPC 71 × VIJAY	-12.29**	-12.77**	-8.59**	-7.23	-8.91	-5.77	-10.36	6.27	0.49
GNG 1581 × GNG 1488	-7.44	-5.88	1.23	-3.31	0.81	6.66	-17.83 **	10.51 **	1.23
GNG 1581 × PUSA 256	-0.98	6.3	4.63	-10.74**	-9.74*	-5.18**	-2.39	14.29 **	4.69
GNG 1581 × JAKI 9218	3.67	6.72	3.96	7.53	-1.51	-3.21	-10.72	9.97 **	0.74
GNG 1581 × VIJAY	11.58**	11.81*	3.24	-8.43	1.76	-0.25	25.54 **	10.24 **	0.99
ICCL 86111 × GNG 1488	7.82	12.33*	13.68	7.52	-3.02	-4.69	-3.92	-1.52	-3.7
ICCL 86111 × PUSA 256	10.00**	21.15**	23.84	1.92	3.92	-1.73	9.21	4.8	2.47
ICCL 86111 × JAKI 9218	6.05	11.89*	20.13	1.23	-17.83 **	-1.04	29	5.81	3.46
ICCL 86111 × VIJAY	13.28**	15.99**	14.66	4.63**	-2.39	17.55 *	14.32 **	7.05 *	1.23
GOKCE × GNG 1488	8.12*	13.96**	-3.04	3.96	-10.72	7.52	-13.89 *	4.59	1.23
GOKCE × PUSA 256	15.15**	8.38**	6.89	3.24	5.54**	3.03	27.21 **	4.85	1.48
GOKCE × JAKI 9218	4.22	11.26 *	-9.7	-11.07**	-7.22**	-12.08**	-11.27	-1.02	-4.2
GOKCE × VIJAY	5.88	9.46	2.55	-5.22**	-6.54*	-9.66*	2.38	-0.26	-5.68
JG 35 × GNG 1488	0.20	0.41	19.18	11.47	6.11	7.39	5.94	-1.24	-1.98
JG 35 × PUSA 256	-6.56	-1.22	12.98	-8.03	-8.62	2.42	23.70 **	-1.76	-3.7
JG 35 × JAKI 9218	-3.82	-2.45	10.35	-9.33	-9.91	-7.97	28.99	0.5	-1.23
JG 35 × VIJAY	-9.96*	-8.44	11.6	8.87	8.03**	10.45	15.54 *	3.66	-1.98
JG 24 × GNG 1488	4.91	16.34 **	-12.41	7.95	2.36	-12.13	-27.57 **	-3.47	-3.7
JG 24 × PUSA 256	-1.47	15.84 **	27.31	-1.04	6.6	-1.31	24.69 **	-1.51	-3.46
JG 24 × JAKI 9218	5.29	18.32 **	22.44	17.55 *	29.89**	20.52 *	14.13	-6.78 **	-8.40 **
JG 24 × VIJAY	0.23	8.91	-15.77	1.51	-0.49	-13.73*	-22.46 **	7.31 *	1.48
RSG 931 × GNG 1488	-3.31	0.81	6.66	5.78	3.95	17.72	2.81	-3.71	-3.95
RSG 931 × PUSA 256	-10.74**	-9.74 *	5.18	6.27	0.49	16.34	3.83	-0.76	-2.72
RSG 931 × JAKI 9218	-4.43	-1.59	28.48	10.51**	11.23	12.59	25.14 **	-6.03	-7.65 *
RSG 931 × VIJAY	-10.32**	-4.64	25.36	4.29**	4.69**	5.23**	24.44 **	-0.26	-5.68
PUSA 362 × GNG 1488	-7.94 *	-5.69	11.4	-6.35**	-5.90**	-7.75**	7.53	-1.51	-3.21
PUSA 362 × PUSA 256	-5.46	-2.71	-7.11	-4.26**	-6.14**	-8.06**	-8.43	1.76	-0.25
PUSA 362 × JAKI 9218	-3.92	-2.78	19.13 **	9.24	12.62	13.44	7.52	-3.02	-4.69
PUSA 362 × VIJAY	-6.26	-2.11	14.85 **	-3.04**	-3.89	-6.67	1.92	3.92	-1.73

Continue...

Crosses	PHT			PBP			SBP		
	MID	HB	SH	MID	HB	SH	MID	HB	SH
IPC 71 × GNG 1488	4.58 **	-0.97	-0.24	0.41	-9.93	18.36 *	-14.93 **	-19.96 **	17.97
IPC 71 × PUSA 256	-13.73*	-19.19 **	-6.79	24.94 **	21.40 **	24.30 **	0.84	-15.55 **	25.03 **
IPC 71 × JAKI 9218	17.72	15.72 *	20.67 **	6.07	3.06	14.01	8.1	-13.96 *	17.57 **
IPC 71 × VIJAY	16.34	8.08	8.87	18.03 **	10	26.85 **	21.03 **	14.13 *	22.49 **
GNG 1581 × GNG 1488	2.59*	-10.36	7.95	2.36	-12.13	15.46	-5.16	-7.77	17.57 **
GNG 1581 × PUSA 256	1.23	-17.83 **	-1.04	6.6	-1.31	9.18	12.09	-3.41	24.07 **
GNG 1581 × JAKI 9218	4.63**	-2.39	17.55 *	29.89**	20.52 *	23.33 **	8.39	4.92	6.5
GNG 1581 × VIJAY	3.96	-10.72	7.52	4.72	-6.8	12.56	10.25	7.95	11.02
ICCL 86111 × GNG 1488	3.24	25.54 **	13.03	13.22	-5.51	24.15 **	12.57 *	3.21	15.48 **
ICCL 86111 × PUSA 256	13.68	-3.92	10.83	27.01 **	13.97	26.09 **	7.07 **	21.88 **	13.22
ICCL 86111 × JAKI 9218	23.84**	9.21	13.88	28.47 **	15.28	27.54 **	13.64 **	26.73 **	24.18 **
ICCL 86111 × VIJAY	20.13	29**	24.65 **	28.43 **	19.60 **	24.44 **	9.28 **	28.57 **	16.27 **
GOKCE × GNG 1488	24.66	24.32 **	11.93	1.18	-5.51	24.15 **	-0.31	-3.41	16.16 **
GOKCE × PUSA 256	-3.04**	-13.89 *	-0.67	-2.37	-3.81	9.66	10.71 **	9.62	14.92 **
GOKCE × JAKI 9218	6.89	27.21 **	-12.66 **	3.66	2.12	16.43	11.26 **	12.61	8.87 **
GOKCE × VIJAY	-9.7	-11.27	-20.55 **	-0.82	-3.6	16.43	18.30 **	13.89	-20.56 **
JG 35 × GNG 1488	2.55	2.38	-7.83	-6.31	-15.44 *	11.11	19.89 **	11.02	16.5
JG 35 × PUSA 256	19.18*	5.94	22.20 **	12.05	9.61	21.26 *	17.34 **	21.57 **	13.56 **
JG 35 × JAKI 9218	12.98	23.70 **	28.99 **	21.88 **	19.21 *	21.88 **	11.29 **	26.16 **	16.16 **
JG 35 × VIJAY	10.35**	28.99	13.61 **	-1.07	-7.2	12.08	15.14 **	24.52 **	27.74 **
JG 24 × GNG 1488	11.6	15.54 *	15.54 *	-5.22	-16.54 *	-9.66*	13.80 **	5.81	29.15 **
JG 24 × PUSA 256	-12.41*	-27.57 **	-16.45 *	11.47	6.11	17.39 *	16.41 **	21.41 **	11.81 **
JG 24 × JAKI 9218	27.31	24.69 **	30 **	11.93	6.55	17.87 *	21.36 **	27.57 **	27.57 **
JG 24 × VIJAY	22.44	14.13	14.13	7.22	-2	18.36 *	18.76 **	27.86 **	21.69 **
RSG 931 × GNG 1488	-15.77 **	-22.46 **	-17.00 *	-20.63 **	-16.47 **	-3.38**	11.29	4.21	5.03 **
RSG 931 × PUSA 256	6.66	2.81	18.59 *	-8.03	-8.62	2.42	15.82 **	21.62 **	22.82 **
RSG 931 × JAKI 9218	5.18	3.83	11.13	-9.33	-9.91	0.97	12.23 **	16.94 **	19.44 **
RSG 931 × VIJAY	28.48**	25.14 **	27.98	-21.58 **	-14.40 **	-8.78*	17.95 **	18.81 *	-20.96 **
PUSA 362 × GNG 1488	25.36	24.44 **	28.99	17.53 **	8.46	22.51 **	17.93 **	21.88 **	-20.00 **
PUSA 362 × PUSA 256	11.4 **	7.53	24.04 **	19.83 **	19.57 *	28.85 **	19.29 **	10.42 **	13.90 **
PUSA 362 × JAKI 9218	-7.11	-8.43	-1.71	-15.47 *	-15.65 *	-6.28	19.6	17.47	13.11
PUSA 362 × VIJAY	19.13 **	7.52	15.41	-23.75 **	-26.80 **	-11.59**	17.40 **	15.00 **	18.31 **

Continue...

Crosses	PP			SI			HI		
	MID	HB	SH	MID	HB	SH	MID	HB	SH
IPC 71 × GNG 1488	-6.35**	-22.90 **	17.75	-12.1	-26.75 **	-21.12 **	-13.01	-13.95*	-20.92*
IPC 71 × PUSA 256	-0.26*	-16.14	28.06	-8.26	-12.89 *	-6.18	1.25	-0.41	-5.37
IPC 71 × JAKI 9218	9.24	-12.62	23.44 *	-2.79	-12.04	-5.28	-1.95	-5.91	-13.53
IPC 71 × VIJAY	24.37 **	19.53 *	22.53 **	7.93	2.94	10.86	24.14 **	21.76 **	24.74 **
GNG 1581 × GNG 1488	-2.89*	-12.55	23.37	-2.73	-19.86 **	-11.16	-19.99 *	-21.48	-13.55*
GNG 1581 × PUSA 256	14.96	-0.11	-12.91 **	-22.44 **	-27.35 **	-19.46 **	-13	-13.74*	-3.78
GNG 1581 × JAKI 9218	27.85 **	30.00**	23.63 **	11.65	-0.27	10.56	29.77 **	16.67	27.21 **
GNG 1581 × VIJAY	19.05	1.78	23.59 **	-16.27 **	-21.22 **	-12.67	2.22	-10.39*	13.06
ICCL 86111 × GNG 1488	22.94	18.69	25.89	-5.09	-6.16	-31.07 **	-30	-25.62**	-20.71
ICCL 86111 × PUSA 256	19.44	18.32	25.49	22.41 **	7.63	4.22	-25.20 **	-23.05**	-24.32 **
ICCL 86111 × JAKI 9218	14.33 **	21.08 **	22.05 **	27.23 **	25.64 **	24.25 **	27.15 **	29.89 **	23.36 **
ICCL 86111 × VIJAY	23.14 **	18.04 **	28.83 **	30.25**	14.20 *	11.61	23.44 **	29.49 **	27.33 **
GOKCE × GNG 1488	13.97	12.3	-14.24**	1.92	-12.95	-11.76	-28.19 *	-30	-23.33
GOKCE × PUSA 256	19.83 *	28.36 *	23.60 *	-13.09 *	-15.03 *	-13.88 *	0	-0.38	-4.61
GOKCE × JAKI 9218	18.21 **	21.32 *	23.60 *	-11.2	-17.41 *	-16.29 *	-24.94 *	-21.36 *	-22.36
GOKCE × VIJAY	17.41 **	16.35 *	28.71 **	-16.82 **	-18.30 **	-17.19 *	-21.78	-22.07	-20.38 *
JG 35 × GNG 1488	11.05	24.61 **	26.26 **	0.2	-6.07	-22.93 **	18.27	10.41	-0.72
JG 35 × PUSA 256	23.66 **	20.85 *	22.17 **	-2.87	-10.28	-13.12	8.78	-0.98	-5.92
JG 35 × JAKI 9218	22.15 **	27.85 **	22.38 **	24.22 **	31.00 **	13.57 *	18.51 **	19.01 **	26.87 **
JG 35 × VIJAY	13.89 *	19.04	29.35 *	-15.27 *	-22.07 **	-23.83 **	8.48	-1.27	-6.16
JG 24 × GNG 1488	16.42 **	15.56 *	25.56 *	-12.73	-25.04 **	-25.04 **	9.82	4.28	4.28
JG 24 × PUSA 256	27.87 **	25.17 *	20.68 **	-24.44 **	-25.64 **	-25.64 **	17.72	14.78	14.78
JG 24 × JAKI 9218	22.56 *	26.99	26.99	-1.37	-7.69	-7.69*	19.08	9.84	9.84
JG 24 × VIJAY	13.07 **	22.95 **	13.19 **	7.55	6.33	6.33	13.02	10.22	10.22
RSG 931 × GNG 1488	26.47 *	19.72	-11.34 *	-3.13	-9.49	-25.19 **	18.67 **	18.65 **	14.67 *
RSG 931 × PUSA 256	14.28 *	20.64	23.36 *	0	-7.32	-10.26	24.07	12.82	7.2
RSG 931 × JAKI 9218	15.06 **	23.49	16.51 *	18.47 **	15.40 *	0.6	32.15 **	25.18	5.75
RSG 931 × VIJAY	19.43 **	22.88 *	16.89 **	7.36	-0.93	-3.17	29.81 *	18.03	12.19
PUSA 362 × GNG 1488	23.41 **	28.57 **	26.15 **	21.08 **	28.48 **	10.41	26.73 **	24.08 **	28.55 **
PUSA 362 × PUSA 256	27.87 **	27.74 **	24.44 **	20.35 **	6.39	3.02	13.65 **	9.41 **	12.46 **
PUSA 362 × JAKI 9218	25.38 **	27.17 *	22.57 *	-15.22 *	-21.45 **	-26.52 **	21.24 **	3.40 **	9.59 **
PUSA 362 × VIJAY	23.48	21.06	26.2	19.89 **	5.56	3.17	25.10 **	23.6	17.48

Continue....

Crosses	BYP			SP			SYP		
	MID	HB	SH	MID	HB	SH	MID	HB	SH
IPC 71 × GNG 1488	1.23	-17.83**	-1.04	6.28	2.92	-6.91	7.52	-3.97	6.88
IPC 71 × PUSA 256	4.63**	-2.39	7.55*	6.23	2.96	-0.78	11.7	4.75	16.59*
IPC 71 × JAKI 9218	3.96	-10.72	7.52	5.96	3.64	-1.97	1.77	-8.7	1.61
IPC 71 × VIJAY	3.24	5.54**	3.03	19.14 **	16.74 **	5.59	22.20 **	17.62	19.90 **
GNG 1581 × GNG 1488	19.83*	8.36*	13.60*	12.29 *	11.51	-4.18	-12.46	-23.45**	0.9
GNG 1581 × PUSA 256	18.21**	21.32 *	11.32*	15.37 **	9.12	5.16	-11.5	-25.6	6.4
GNG 1581 × JAKI 9218	17.41**	16.35 *	18.71**	21.27 **	25.27 **	18.48 **	22.61**	-9.81	11.87 **
GNG 1581 × VIJAY	11.05**	4.61**	6.26**	5.05	4.53	-9.27	-2.52	-16.17 **	19.90 *
ICCL 86111 × GNG 1488	23.66**	20.85*	22.17**	-4.9	-7.5	-17.08 **	-22.02**	-22.99 **	-11.34**
ICCL 86111 × PUSA 256	22.15**	27.85**	22.38**	6.87	3.14	-0.61	-4.2	-8.3	-2.29
ICCL 86111 × JAKI 9218	17.31**	14.69**	12.77**	19.18 **	16.07 **	9.78	21.66**	18.73	17.83 **
ICCL 86111 × VIJAY	22.44	14.87	14.13	9.37 **	7.32 **	14.13 *	23.96 **	21.7	20.33 **
GOKCE × GNG 1488	15.77**	22.46**	17.00*	12.02 *	11.6	-5.43	-7.98	-13.71	-3.74
GOKCE × PUSA 256	6.66	2.81	18.59 *	-14.39 **	-19.84 **	-22.75 **	3.46	2.15	2.11
GOKCE × JAKI 9218	5.18	3.83	11.13	-3.29	-8.65	-13.60 *	-7.25	-12.62	-12.65
GOKCE × VIJAY	28.48**	25.14**	27.98	18.64 **	16.80 *	1.38	-17.73 *	-18.93 *	-16.53
JG 35 × GNG 1488	25.36	24.44**	28.99	0.85	-3.67	-18.37 **	18.63 **	28.99	10.84 *
JG 35 × PUSA 256	11.41**	7.53	24.04 **	7.82	-2.93	-6.46	11.42 **	13.59 **	10.43 *
JG 35 × JAKI 9218	1.77	-8.7	1.61	24.82 **	22.39 **	15.76 **	20.09 **	18.60 **	9.02 **
JG 35 × VIJAY	22.20**	17.62	19.90 **	23.19 **	16.33 *	0.98	13.66 **	13.19 **	16.84 **
JG 24 × GNG 1488	12.46	23.41**	0.9	1.2	-6.52	-6.52	17.83 **	14.53 **	12.57 **
JG 24 × PUSA 256	-11.5	-5.67	6.4	-12.67 *	-14.25 *	-14.25 *	19.23 **	17.45	17.45 **
JG 24 × JAKI 9218	12.46**	9.81	11.87**	-1.48	-4.15	-4.15	12.08 **	13.83 **	13.89
JG 24 × VIJAY	12.52**	16.17**	19.90*	0.75	-5.9	-5.9	16.35 **	14.53 **	18.22 **
RSG 931 × GNG 1488	-22.02**	-22.99**	-11.34**	10.42	3.62	0.14	9.17 **	11.36	12.45 **
RSG 931 × PUSA 256	24.14**	21.76**	24.74**	2.61	2.46	-0.98	8.72 **	11.92 *	18.80 *
RSG 931 × JAKI 9218	-19.99 *	-21.48	-13.55*	13.07 *	11.86 *	8.11	3.13 **	10.5	14.96
RSG 931 × VIJAY	-13.66**	-13.74**	-8.78**	-3.91	-8.8	-11.86 *	5.45 **	13.19 **	16.84**
PUSA 362 × GNG 1488	29.77**	16.67**	27.21 **	16.48 **	9.2	5.75	11.97 **	20.25 **	18.98 **
PUSA 362 × PUSA 256	12.22	-10.39*	13.06	3.45 **	3.16 **	21.25 **	8.78 **	13.03 **	19.37 **
PUSA 362 × JAKI 9218	3.65**	5.62**	4.71**	3.87	2.66	-0.59	6.75 **	17.24 **	10.14 **
PUSA 362 × VIJAY	-30	-25.62**	-20.71	-3.43	-8.43	-11.34 *	17.69 **	20.69 **	14.56 **

4.10. Contribution of line, tester and line x tester

1. Days to 50% Flowering

The contribution of lines (46.32%) and line $\times$ tester interactions (49.72%) was substantially higher compared to testers (3.94%), indicating that both additive and non-additive gene actions are important, with a slight predominance of non-additive effects for this trait.

2. Days to First Podding

A major proportion of the variation was due to lines (51.64%), followed by line $\times$ tester interactions (42.85%), and testers contributed a minor portion (5.5%). This suggests a relatively stronger role of additive gene action.

3. Days to Maturity

The line $\times$ tester interaction effect (49.57%) and lines (44.01%) contributed almost equally, with testers accounting for only 6.41%. This again emphasizes the role of both additive and non-additive gene action in the control of maturity duration.

4. Plant Height

A strikingly high contribution of line $\times$ tester interaction (77.91%) was recorded, while lines and testers accounted for 9.51% and 12.57% respectively, indicating the predominance of non-additive gene action in the expression of plant height.

5. Primary Branches per Plant

Line $\times$ tester effects (57.99%) and lines (40.47%) contributed substantially, whereas testers played a minimal role (1.44%). This indicates the importance of both additive and non-additive gene actions, with a tilt toward non-additive effects.

6. Secondary Branches per Plant

Non-additive gene action played a major role as indicated by the highest contribution of line $\times$ tester interaction (63.29%), followed by lines (32.47%) and testers (4.14%).

7. Pods per Plant

The variation was mainly governed by line $\times$ tester interactions (73.14%), while lines (15.08%) and testers (11.78%) contributed to a lesser extent. This underscores the predominance of non-additive genetic variance in pod number expression.

8. 100-Seed Weight

The contribution of line $\times$ tester interaction (69.48%) was dominant, followed by testers (18.63%) and lines (11.87%). This suggests a major role of non-additive gene action, with some involvement of maternal (tester) effects as well.

9. Biological Yield per Plant

Line $\times$ tester interaction contributed 53.5%, followed by lines (34.64%) and testers (11.85%), indicating the importance of both additive and non-additive genetic components in determining biomass.

10. Harvest Index

The highest contribution was from line $\times$ tester interaction (61.87%), followed by lines (29.21%) and testers (8.91%), suggesting predominance of non-additive gene action in harvest index expression.

11. Seed Protein Content

The majority of the variation was explained by line $\times$ tester interaction (68.01%), with moderate contributions from testers (13.27%) and lines (18.71%), suggesting the predominance of non-additive gene action for this quality trait.

12. Seed Yield per Plant

Additive gene action (line contribution: 49.26%) was more influential than line $\times$ tester interaction (43.07%) and testers (7.66%), indicating that improvement in seed yield could be effectively achieved through selection of promising lines.

The analysis of the proportional contribution of lines, testers, and their interactions to the total variation in trait expression provides valuable insight into the underlying gene action governing key agronomic traits in chickpea. Traits such as days to 50% flowering, days to first podding, and days to maturity revealed a substantial contribution from both lines and line $\times$ tester interactions, with lines contributing up to 51.64% (DFP) and line $\times$ tester interactions up to 49.72% (DFF), highlighting the complementary role of additive and non-additive gene actions in determining earliness and maturity. These findings support the view that early phenological traits in chickpea are under complex genetic control and benefit from both general and specific combining abilities (Aher *et al.*, 2020; Meena *et al.*, 2023; Raval *et al.*, 2021). Moreover, in the case of seed yield per plant, a higher contribution from lines (49.26%) than from line $\times$ tester interaction (43.07%) indicates that additive genetic effects can be efficiently exploited through selection, making recurrent selection a suitable breeding strategy for yield improvement (Singh *et al.*, 2019; Yadav *et al.*, 2022; Kumar *et al.*, 2020).

In contrast, traits such as plant height, number of pods per plant, 100-seed weight, and seed protein content demonstrated a clear predominance of non-additive gene action, as evidenced by the high contribution of line $\times$ tester interactions ranging from 61.87% to 77.91%. Specifically, plant height (77.91%) and pods per plant (73.14%) were predominantly governed by specific combining ability effects, suggesting that hybrid development strategies may be more rewarding for improving these traits. Similar findings have been reported by Sharma *et al.*

(2021), who observed higher SCA contributions for yield components in chickpea. The notable contribution of testers to 100-seed weight (18.63%) and seed protein (13.27%) also hints at maternal influence and the potential importance of tester choice in hybrid combinations (Bora *et al.*, 2018; Tadesse *et al.*, 2020; Singh *et al.*, 2019). Overall, these patterns underline the necessity of tailored breeding approaches depending on trait-specific genetic architecture, combining both selection of elite lines and exploitation of heterosis via specific hybrid combinations.

Table 4.12: Percent contribution of line, tester and line x tester

Traits	Percent Contribution		
	Line	Tester	Line x Tester
Days to 50% Flowering	46.32	3.94	49.72
Days to First Podding	51.64	5.50	42.85
Days to Maturity	44.01	6.41	49.57
Plant Height	9.51	12.57	77.91
Primary Branches per Plant	40.47	1.44	57.99
Secondary Branches per Plant	32.47	4.14	63.29
Pods per Plant	15.08	11.78	73.14
100-Seed Weight	11.87	18.63	69.48
Biological Yield per Plant	34.64	11.85	53.5
Harvest Index	29.21	8.91	61.87
Seed Protein Content	18.71	13.27	68.01
Seed Yield per Plant	49.26	7.66	43.07

CHAPTER- V

SUMMARY AND CONCLUSION

The experimental summary and conclusion of the present investigation entitled **“Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.)”** was conducted at the departmental fields of Genetics and Plant Breeding at Lovely Professional University in Phagwara, Punjab.

5.1 Analysis of variance for experimental design

The analysis of variance highlighted substantial genetic variability among the chickpea genotypes for most of the observed traits, indicating ample scope for selection and genetic improvement. Traits such as days to 50% flowering, days to maturity, plant height, secondary branches per plant, number of pods per plant, seed protein content, 100-seed weight, biological yield per plant, harvest index, and seed yield per plant exhibited highly significant genotypic effects ($p \leq 0.01$). This suggests that these traits are primarily governed by genetic factors and can be effectively improved through selection and breeding. In contrast, primary branches per plant showed non-significant variation, indicating limited genetic diversity for this trait among the tested genotypes and reduced potential for effective selection.

Environmental effects were found to be highly significant for nearly all traits except plant height and harvest index, suggesting that most traits are strongly influenced by year-to-year climatic or environmental conditions. This underlines the importance of conducting multi-environment trials to identify stable genotypes. Moreover, significant genotype $\times$ environment interactions were observed for days to maturity, biological yield per plant, and harvest index, implying that the performance of genotypes for these traits varied across years.

Therefore, stability analysis becomes essential before recommending genotypes for wide cultivation. Lastly, relatively higher experimental error was observed for plant height and days to maturity, pointing to the need for refined experimental design and replication strategies for precise estimation. Collectively, these findings provide valuable directions for chickpea breeding programs, emphasizing the traits with both high genetic variability and environmental stability for achieving genetic gains.

5.2. Violin Plot Visualization with DMRT Analysis

The integrated analysis using violin plots and Duncan's Multiple Range Test (DMRT) effectively captured the trait-wise performance variability of 30 chickpea genotypes and identified promising candidates for crop improvement. Genotypes like GNG1958, ICCL 86111, and VIJAY, which exhibited earliness in flowering, and VIJAY and RSG963, which showed early maturity, are particularly valuable for breeding short-duration varieties suited for terminal drought or late sowing conditions. Genotypes VIJAY and JG14, with a high number of primary branches, and IPC04-1 and JG35, with greater plant height, are desirable for enhancing vegetative vigor and branching architecture.

For pod productivity, GL25016 and GNG1581 demonstrated superiority in pods per plant, while CSJ515 and PUSA362 excelled in biological yield, suggesting their potential in biomass accumulation and source-sink efficiency. In terms of seed size, which is critical for market value and seedling vigor, VIJAY, BGD209, and CSJ515 showed the highest 100-seed weight, indicating suitability for large-seeded breeding programs. Notably, CSJ515, GL25016, and PUSA256 emerged as top performers in seed yield per plant, confirming their high-yield potential. The harvest index, an important trait for resource-use efficiency, was highest in BG212, PUSA362, and VIJAY, marking them as efficient converters of biomass into

economic yield. These findings underscore the substantial genetic diversity and trait-specific superiority among genotypes, with CSJ515, GL25016, and VIJAY consistently excelling across multiple traits. These genotypes should be prioritized in breeding programs aimed at enhancing yield potential, early maturity, seed size, and resource-use efficiency in chickpea.

5.3. Genetic Diversity

5.3.1. Cluster Composition

The cluster composition analysis of the 30 chickpea genotypes grouped into five distinct clusters highlights valuable opportunities for parental selection in hybridization programs based on genetic divergence. Cluster I (BGD-209 and JG-130) represents a highly divergent yet genetically uniform pair. Despite its small size, its uniqueness makes it ideal for crossbreeding with more diverse clusters such as Cluster V to maximize heterosis, particularly for traits like seed size or phenological diversity. Cluster II (GOKCE and BG-212) also includes only two genotypes, showing close genetic proximity within but distinctiveness from others. These lines may harbor unique or underutilized traits, such as adaptability or early vigor, and should be targeted for crosses with genotypes from Cluster III or V to introduce diversity and improve trait combinations. Cluster III, comprising six genotypes (K-850, RSG-963, IPCK-28, GNG-1958, JAKI-9218, JG-14), demonstrates moderate intra-cluster similarity and inter-cluster divergence. This cluster may contain desirable traits such as early flowering, drought tolerance, or yield stability, making it suitable for broad-based crossing programs to enrich genetic backgrounds. Cluster IV (T39-1, KPG-59, IPCK-02, HC-5) includes four moderately divergent genotypes likely possessing architectural traits or branching habits of interest. These can be crossed with divergent groups like Cluster I or V to enhance trait variability and recombination potential. Cluster V stands out as the largest and most genetically diverse cluster, encompassing 16 genotypes including key lines like JG-24, PUSA-362, CSJ-515, and GL-25016. This cluster offers a rich pool of variability for seed yield, biomass, and other agronomic traits. Selecting superior lines from this group and crossing them with genotypes from genetically distant clusters (I, II, or IV) can yield high-performing transgressive segregants. The clustering pattern reveals considerable genetic diversity among

chickpea genotypes. Clusters I and II, despite their small size, serve as highly divergent sources, while Cluster V acts as a central breeding reservoir. Strategic hybridization across these clusters can accelerate genetic gain for multiple yield and adaptation-related traits.

5.3.2. Inter and intra cluster distance

The analysis of intra- and inter-cluster distances revealed significant genetic diversity among chickpea genotypes. Cluster V had the lowest intra-cluster distance (2.65), indicating high genetic similarity, while Clusters I (6.98) and II (8.70) showed higher intra-cluster divergence despite fewer genotypes, making them valuable for unique trait exploration. The highest inter-cluster distance was found between Clusters IV and V (27.46), followed by III and V (25.13), indicating substantial divergence and potential for generating high heterosis when used in crosses. Moderate divergence was noted between Clusters I and II (19.84) and II and III (11.03). The lowest inter-cluster distance was between Clusters I and V (10.20), suggesting some genetic similarity. The crossing genetically distant clusters especially Cluster V with Clusters I, II, or IV can enhance variability and breeding efficiency in chickpea improvement programs.

5.3.3. Cluster Mean

The cluster mean analysis revealed substantial trait variation across five chickpea clusters, aiding in targeted parent selection. Cluster V emerged as the most desirable for early flowering (93.67 days), early maturity (164.00 days), and highest values for primary branches (4.67), plant height (44.47 cm), pods per plant (64.13), seeds per pod (1.90), 100-seed weight (25.33 g), and harvest index (28.41%), indicating its superior agronomic profile. Cluster I showed the highest biological yield (30.07 g) and seed yield per plant (7.69 g), followed closely by Cluster V (7.65 g), suggesting it can contribute yield-enhancing traits. Cluster IV

had the latest flowering and maturity, with bushy growth and high harvest index, suitable for specific breeding targets. In contrast, Cluster III showed the lowest means for several traits, including secondary branches, seeds per pod, 100-seed weight (9.21 g), and seed yield per plant (5.18 g), indicating limited yield potential.

5.4 Analysis of variance for line x tester mating design

The ANOVA for the line $\times$ tester mating design revealed highly significant differences across all 12 traits, confirming substantial genetic variability within the chickpea genotypes. Crosses exhibited highly significant variation for all traits, indicating strong heterotic potential. Lines contributed significantly to most traits, whereas testers had limited significance, suggesting that lines played a more prominent role in contributing genetic variability. Importantly, line $\times$ tester interactions were highly significant for traits like Days to 50% Flowering (DFF), Days to First Podding (DFP), Days to Maturity (DTM), Primary Branches per Plant (PBP), 100-Seed Weight (SI), Harvest Index (HI), Seed Protein (SP), and Seed Yield per Plant (SYP), indicating the involvement of non-additive gene action in these traits. The significant contrasts between parents and hybrids for traits such as Plant Height (PHT), Secondary Branches (SBP), Pods per Plant (PP), Biological Yield (BYP), HI, SP, and SYP further support the existence of heterosis. This implies that both additive and non-additive gene effects play a role in trait inheritance, and hybridization can be effectively used to exploit genetic potential in chickpea.

5.5 Mean performances for various characters

5.5.1. Mean performances of parents for various characters

The evaluation of parental lines revealed considerable variability across all traits. Days to 50% Flowering ranged from 67.33 days (JG 24) to 91.00 days (PUSA 256), with early

flowering genotypes like JG 24 and GOKCE desirable for drought escape. Days to First Podding varied from 88.33 (JAKI 9218) to 99.67 days (VIJAY), with early podding lines offering advantages under limited-season cultivation. Maturity duration spanned 123.67–136.00 days, where early maturing genotypes such as GNG 1581 and VIJAY are preferred under moisture stress, while RSG 931 was the latest maturing. Plant height ranged from 43.40 cm (ICCL 86111) to 65.63 cm (GNG 1581), indicating suitability of taller types for canopy advantage and shorter ones for mechanical harvesting. Primary branches were highest in GNG 1488 (9.07), while secondary branches peaked in IPC 71 (18.87), both traits contributing to pod load potential. Number of pods per plant was maximum in IPC 71 (64.70), identifying it as a highly prolific line, while JAKI 9218 had the least. 100-seed weight varied markedly from 15.87 g (GNG 1488) to 24.50 g (GNG 1581), with larger-seeded types like GNG 1581 and IPC 71 suitable for market-preferred cultivars. Biological yield per plant was highest in IPC 71 (58.97 g), highlighting robust vegetative growth. Harvest index, an indicator of assimilate efficiency, ranged from 23.85% (PUSA 362) to 45.01% (GNG 1581), with genotypes like ICCL 86111 also showing high efficiency. Seed protein content ranged from 16.56% (JG 35) to 21.47% (JG 24), marking JG 24 and PUSA 362 as nutritionally superior lines. Finally, seed yield per plant varied widely, with GNG 1581 (24.80 g), IPC 71 (19.30 g), and ICCL 86111 (18.48 g) outperforming others, positioning them as promising candidates for hybridization and yield improvement.

5.5.2. Mean performances of crosses for various characters

The evaluation of 32 chickpea crosses revealed substantial variability across all traits, supporting the presence of exploitable heterosis. For Days to 50% Flowering (DFF), the earliest flowering cross was JG 35 × VIJAY (72.33 days), while ICCL 86111 × VIJAY (95.33

days) was the latest, offering opportunities for both early and late planting strategies. In Days to First Podding (DFP), JG 35 × VIJAY (86.33 days) was the earliest podding cross, whereas GOKCE × PUSA 256 (103.33 days) was the latest, suitable for environments favoring delayed maturity. For Days to Maturity (DTM), JG 24 × JAKI 9218 (123.67 days) matured the earliest, while GNG 1581 × PUSA 256 (141.33 days) took the longest, providing a broad range of maturity durations. In Plant Height (PHT), RSG 931 × VIJAY (73.00 cm) recorded the tallest plants, potentially favorable for biomass, while GOKCE × VIJAY (43.30 cm) was the shortest, ideal for compact cropping. For Primary Branches per Plant (PBP), ICCL 86111 × VIJAY (9.97) and PUSA 362 × GNG 1488 (9.83) were prolific, whereas PUSA 362 × VIJAY (6.10) had the least. In Secondary Branches per Plant (SBP), PUSA 362 × GNG 1488 (23.60) outperformed others, while IPC 71 × GNG 1488 (15.10) was the lowest. Regarding Pods per Plant (PP), ICCL 86111 × JAKI 9218 (81.37) and GNG 1581 × JAKI 9218 (77.80) were top producers, while GOKCE × GNG 1488 (48.40) had the fewest. In 100-Seed Weight (SI), ICCL 86111 × JAKI 9218 (26.13 g) and IPC 71 × VIJAY (24.47 g) showed the boldest seeds, with PUSA 362 × JAKI 9218 (15.13 g) at the lower end. Biological Yield per Plant (BYP) was highest in IPC 71 × GNG 1488 (66.73 g) and lowest in ICCL 86111 × VIJAY (46.37 g). For Harvest Index (HI), ICCL 86111 × VIJAY (52.55%) showed the highest partitioning efficiency, whereas GOKCE × GNG 1488 (23.78%) had the lowest. In Seed Protein Content (SP), PUSA 362 × PUSA 256 (25.60%) and JG 35 × JAKI 9218 (24.85%) were highest, while GOKCE × PUSA 256 (16.58%) was lowest. Lastly, for Seed Yield per Plant (SYP), the best performing crosses were JG 35 × JAKI 9218 (25.84 g), PUSA 362 × GNG 1488 (25.83 g), and ICCL 86111 × JAKI 9218 (25.63 g), whereas ICCL 86111 × GNG 1488 (13.12 g) recorded the lowest yield (Appendix I).

5.6. Analysis of variance for combining ability

The analysis of variance for combining ability revealed highly significant differences among crosses for most traits, underscoring the presence of substantial genetic variability among chickpea genotypes. Both general combining ability (GCA) and specific combining ability (SCA) effects contributed significantly to trait expression, indicating the involvement of both additive and non-additive gene actions. Significant GCA effects of lines for traits like earliness (DFF, DFP, DTM), branching (PBP, SBP), biological yield, protein content, and seed yield suggest that additive effects are predominant and selection of superior parents could be effective for genetic improvement. In contrast, testers showed non-significant GCA effects, suggesting less stable contributions and the presence of non-fixable variability. Highly significant SCA effects for most traits, including yield and its components, emphasize the potential of exploiting heterosis through specific cross combinations. Traits like DFF, PHT, PP, SI, BYP, and SYP showed strong non-additive influence, advocating the use of hybrid breeding strategies. Replication effects were significant for several traits, validating the experimental design in accounting for environmental variation. These findings provide a valuable framework for selecting parents with high GCA and identifying hybrids with superior SCA to enhance yield potential and stability in chickpea breeding programs.

5.7. Estimate of general combining ability (GCA) effect

The analysis of general combining ability (GCA) effects identified promising parents for multiple traits in chickpea. For earliness, JG 24 and PUSA 362 showed significantly negative GCA effects for both days to 50% flowering and days to maturity, making them desirable for short-duration environments. In contrast, ICCL 86111 and GOKCE exhibited positive GCA, indicating late flowering and maturity. For plant architecture, PUSA 362 and JG 35 contributed to taller plants, whereas IPC 71 and GOKCE favored dwarfness. Traits like

branching were enhanced by ICCL 86111, IPC 71 (primary), and PUSA 362, JG 35 (secondary), suggesting their role in canopy development. Notably, ICCL 86111 and JG 35 were superior for pods per plant, and ICCL 86111 and GNG 1581 contributed positively to 100-seed weight. For biological yield, JG 35 and JG 24 were favorable, while GOKCE and PUSA 362 exhibited high GCA for harvest index, implying efficient biomass partitioning. PUSA 362, GNG 1581, and ICCL 86111 were superior for seed protein content, whereas PUSA 362 and JG 24 stood out as the best general combiners for seed yield per plant. Among testers, JAKI 9218 consistently showed significant positive GCA for yield-related traits including plant height, seed weight, harvest index, protein, and seed yield, highlighting its value as a tester. Conversely, GNG 1488 showed significantly negative GCA effects across several traits, indicating poor combining ability. These insights help identify elite parents for breeding programs aimed at enhancing yield, earliness, protein content, and plant architecture in chickpea.

5.8. Estimate of specific combining ability (SCA) effects

The estimation of specific combining ability (SCA) effects revealed several promising cross combinations for trait improvement in chickpea. For earliness, crosses such as IPC 71 × PUSA 256 (−9.37**) and GNG 1581 × GNG 1488 (−7.20**) were identified as top early flowering and podding combinations. For early maturity, IPC 71 × GNG 1488 (−4.35**) and ICCL 86111 × GNG 1488 (−5.18**) were desirable. Crosses such as GOKCE × JAKI 9218 and PUSA 362 × GNG 1488 showed highly positive SCA for plant height, while PUSA 362 × JAKI 9218 and GOKCE × VIJAY showed negative effects, indicating suitability for compact plant types. The highest primary and secondary branches were contributed by PUSA 362 × GNG 1488 and IPC 71 × VIJAY, indicating bushy and productive plants. For pods per plant,

the most favorable combinations were PUSA 362 $\times$ GNG 1488, IPC 71 $\times$ VIJAY, and GNG

1581 × JAKI 9218. Crosses such as JG 35 × JAKI 9218 and JG 24 × VIJAY showed superiority in seed size, while PUSA 362 × JAKI 9218 and ICCL 86111 × GNG 1488 had significant negative effects. For biological yield, ICCL 86111 × PUSA 256 and IPC 71 × GNG 1488 were best performers, while ICCL 86111 × VIJAY and GOKCE × PUSA 256 had reduced biomass. In terms of harvest index, the crosses ICCL 86111 × VIJAY and IPC 71 × VIJAY excelled, showing superior partitioning efficiency. For seed protein content, PUSA 362 × PUSA 256 and ICCL 86111 × VIJAY showed significantly positive SCA effects, while PUSA 362 × VIJAY and GOKCE × PUSA 256 had reduced protein levels. Notably, the crosses ICCL 86111 × JAKI 9218, PUSA 362 × GNG 1488, and GNG 1581 × JAKI 9218 emerged as the most promising combinations for seed yield per plant, indicating high heterotic response and potential for commercial exploitation. These findings underscore the importance of selecting specific cross combinations to harness non-additive gene effects for targeted trait enhancement in chickpea breeding.

5.9. Estimation of heterosis of various traits

The evaluation of heterosis across 32 chickpea crosses revealed significant variability for all traits, indicating scope for hybrid improvement. For earliness traits, several crosses showed highly negative mid-parent and heterobeltiosis values. For instance, IPC 71 × VIJAY, PUSA 362 × VIJAY, and JG 35 × VIJAY consistently exhibited early flowering and pod initiation, as indicated by negative heterosis values across Days to 50% Flowering (DFF) and Days to First Podding (DFP). JG 24 × JAKI 9218 and JG 24 × GNG 1488 were earliest to mature, showing the most negative heterosis for Days to Maturity (DTM). On the other hand, ICCL 86111 × PUSA 256, ICCL 86111 × VIJAY, and GOKCE × PUSA 256 displayed positive heterosis for these traits, suggesting their potential use in late-maturing or long-duration conditions.

For branching and reproductive traits, hybrids such as ICCL 86111 $\times$ JAKI 9218, GNG 1581 $\times$ JAKI 9218, and PUSA 362 $\times$ PUSA 256 showed significant positive heterosis for both Primary (PBP) and Secondary Branches per Plant (SBP), suggesting greater sink strength. Similarly, GNG 1581 $\times$ JAKI 9218, PUSA 362 $\times$ GNG 1488, and ICCL 86111 $\times$ JAKI 9218 were superior for Pods per Plant (PP) and 100-Seed Weight (SI), recording high mid-parent and standard heterosis, indicating their potential for productivity and seed size enhancement. Notably, crosses such as JG 24 $\times$ PUSA 256, IPC 71 $\times$ GNG 1488, and ICCL 86111 $\times$ GNG 1488 consistently showed negative heterosis, marking them less suitable for these yield components.

In terms of physiological and economic traits, significant positive heterosis for Biological Yield per Plant (BYP) was found in PUSA 362 $\times$ PUSA 256, JG 35 $\times$ GNG 1488, and ICCL 86111 $\times$ PUSA 256. For Harvest Index (HI), crosses like RSG 931 $\times$ JAKI 9218, PUSA 362 $\times$ GNG 1488, and ICCL 86111 $\times$ VIJAY recorded superior heterotic performance, indicating effective biomass partitioning. In Seed Protein Content (SP), JG 35 $\times$ GNG 1488 and ICCL 86111 $\times$ VIJAY showed the highest heterosis, making them suitable for nutritional improvement. Finally, for Seed Yield per Plant (SYP), the top-performing crosses were PUSA 362 $\times$ GNG 1488, ICCL 86111 $\times$ JAKI 9218, and JG 35 $\times$ JAKI 9218, which demonstrated strong positive heterosis across all metrics (mid-parent, heterobeltiosis, and standard), making them promising candidates for commercial hybrid development.

5.10. Contribution of line, tester and line $\times$ tester

The analysis of contribution percentages revealed that both additive and non-additive gene actions govern the inheritance of important chickpea traits, though their relative importance varied. For phenological traits like days to 50% flowering (lines: 46.32%, L $\times$ T: 49.72%) and days to maturity (lines: 44.01%, L $\times$ T: 49.57%), additive and non-additive effects

contributed almost equally, whereas days to first podding was more influenced by additive effects (lines: 51.64%). In contrast, traits such as plant height (L×T: 77.91%), secondary branches per plant (L×T: 63.29%), number of pods per plant (L×T: 73.14%), 100-seed weight (L×T: 69.48%), harvest index (L×T: 61.87%), and seed protein content (L×T: 68.01%) were predominantly controlled by non-additive gene action. Primary branches per plant and biological yield also reflected a balanced contribution of lines and L×T interaction, supporting the presence of both additive and non-additive variance. Interestingly, seed yield per plant showed a stronger influence of additive gene action (lines: 49.26%) over non-additive effects (L×T: 43.07%), indicating scope for improvement through line selection. Overall, the dominance of L×T interaction in most traits highlights the potential of exploiting specific hybrid combinations, while traits like seed yield and earliness may benefit more from additive-based breeding strategies.

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APPENDICES

5.1. Top and Bottom 3 Crosses of each trait in chickpea based on mean performance

Trait	Top 3 Crosses	Bottom 3 Crosses
Days to 50% Flowering	JG 35 × VIJAY (72.33), JG 24 × VIJAY (73.33), GNG 1581 × GNG 1488 (74.67)	ICCL 86111 × VIJAY (95.33), GOKCE × PUSA 256 (95.00), ICCL 86111 × PUSA 256 (91.67)
Days to First Podding	JG 35 × VIJAY (86.33), JG 24 × VIJAY (89.33), PUSA 362 × GNG 1488 (90.67)	GOKCE × PUSA 256 (103.33), ICCL 86111 × VIJAY (102.33), GNG 1581 × VIJAY (101.33)
Days to Maturity	JG 24 × JAKI 9218 (123.67), GOKCE × VIJAY (127.33), RSG 931 × VIJAY (127.33)	GNG 1581 × PUSA 256 (141.33), IPC 71 × JAKI 9218 (140.33), ICCL 86111 × JAKI 9218 (139.67)
Plant Height	RSG 931 × VIJAY (73.00), PUSA 362 × GNG 1488 (72.80), GOKCE × JAKI 9218 (72.30)	GOKCE × VIJAY (43.30), RSG 931 × GNG 1488 (45.23), JG 24 × PUSA 256 (45.53)
Primary Branches	ICCL 86111 × VIJAY (9.97), PUSA 362 × GNG 1488 (9.83), IPC 71 × PUSA 256 (9.27)	PUSA 362 × VIJAY (6.10), RSG 931 × VIJAY (6.30), PUSA 362 × JAKI 9218 (6.47)
Secondary Branches	PUSA 362 × GNG 1488 (23.60), ICCL 86111 × JAKI 9218 (21.73), IPC 71 × VIJAY (21.53)	IPC 71 × GNG 1488 (15.10), RSG 931 × GNG 1488 (15.93), GOKCE × GNG 1488 (16.07)
Pods per Plant	ICCL 86111 × JAKI 9218 (81.37), GNG 1581 × JAKI 9218 (77.80), IPC 71 × VIJAY (77.33)	GOKCE × GNG 1488 (48.40), IPC 71 × GNG 1488 (49.89), ICCL 86111 × GNG 1488 (53.33)
100-Seed Weight	ICCL 86111 × JAKI 9218 (26.13), IPC 71 × VIJAY (24.47), PUSA 362 × GNG 1488 (24.40)	PUSA 362 × JAKI 9218 (15.13), ICCL 86111 × GNG 1488 (15.23), IPC 71 × GNG 1488 (17.43)
Biological Yield	IPC 71 × GNG 1488 (66.73), ICCL 86111 × PUSA 256 (66.40), JG 35 × VIJAY (65.93)	ICCL 86111 × VIJAY (46.37), GNG 1581 × JAKI 9218 (46.87), PUSA 362 × JAKI 9218 (48.80)
Harvest Index	ICCL 86111 × VIJAY (52.55), GNG 1581 × JAKI 9218 (52.51), ICCL 86111 × JAKI 9218 (51.14)	GOKCE × GNG 1488 (23.78), ICCL 86111 × GNG 1488 (24.72), GOKCE × JAKI 9218 (24.13)
Seed Protein	PUSA 362 × PUSA 256 (25.60), JG 35 × JAKI 9218 (24.85), ICCL 86111 × VIJAY (24.50)	GOKCE × PUSA 256 (16.58), ICCL 86111 × GNG 1488 (17.80), JG 35 × GNG 1488 (17.52)
Seed Yield per Plant	JG 35 × JAKI 9218 (25.84), PUSA 362 × GNG 1488 (25.83), ICCL 86111 × JAKI 9218 (25.63)	ICCL 86111 × GNG 1488 (13.12), GOKCE × VIJAY (14.47), GOKCE × GNG 1488 (14.96)

CV

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Career Objective:

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Qualification:

- ❖ Currently pursuing Ph.D in Genetics and Plant breeding in Lovely Professional University (LPU), Jalandhr, Punjab.
- ❖ M.Sc agriculture in genetics and plant breeding from sam Higginbottom University of agriculturetechnology and sciences (Shuats). Allahabad .u.p india.
- ❖ Bsc agriculture in annamalai university in tamil nadu.

Academic Details:

Qualification	Institute	University / Board	Year of Passing	Percentage
Ph.d agriculture	Lovely professional university[lpu].punjab	Indian council of agriculture	2026	71%
MSC Agriculture	Sam Higginbottom University of agriculture technology and sciences . (Shuats)	Indian council of agricultural research . Allahabad	2019	61%
B.Sc., Agriculture	Annamalai University	Under government of tamil nadu	2016	77%
Intermediate	Sri Chaitanya Jr College, tirupati.a.p	Board of Intermediate Education	2011	79%
S.S.C	Andhra Pradesh residential school.Mukkavari plli , kadapa	Board of Secondary Education	2009	79%

Work Experience :

- ❖ **Worked as assistant professor in sun institute of agricultural sciences college in Visakhapatnam , Andhra Pradesh**
- ❖ **Worked on “ study on genetic variability and character association for yield and its components in pulse crops (black gram , red gram , chick pea)**
- ❖ **Currently doing research on “ Assessment of genetic diversity, heterosis and combining ability for yield and yield component traits in chickpea (*Cicer arietinum* L.) “ in pulse crop at the School of Agriculture, Lovely Professional University, Punjab.**

Achievements:

1. Awarded for " young scientist award 2019 "on national seminar on " River development,water resource, conservation and management" held in chitrakoot , satna, madha Prades
2. Certificate of participation in " international seminar " on " Climate resilience of biodiversity, technology ,marketing policy " held in university of Allahabad.
3. Having extensive knowledge over agronomy practices , field management I can handle better crop health's .

Strengths:

- ❖ Easily acclimatization of new areas
- ❖ Quickly acquire the new techniques & implement at field levelProvide guidance to farmers when it's required.
- ❖ Possess excellent communication, interpersonal and collaborative skillsProcess excellent planning and organization skills.
- ❖ Flexibility and ability to adapt to new technologies.
- ❖ Ability to handle work under pressure & perform multiple tasks simultaneously.

Skills:

Having knowledge of Internet, MS Word, MS PowerPoint basic and other computer basics.

Personal Information:

- **Date of Birth** – 05/06/1994
- **Languages Known** – English, Hindi & telugu & tamil
- **Location:** tirupati , Andhra Pradesh

Declaration:

I hereby confirm that the Information in this document is accurate and true to the best of my knowledge and belief.

Yours's faithfully,

(NAVEEN KUMAR NAIK BUKKE)