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Evaluation of genetic variability, heritability and trait interrelationships in chickpea for yield enhancement

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Abstract
The present study was conducted during the Rabi season of 2024-25 at SHUATS, Prayagraj, to assess genetic variability, trait associations, and direct-indirect effects of yield components in thirty diverse chickpea (*Cicer arietinum* L.) genotypes, including 29 experimental lines and a standard check. The trial was laid out in a randomized complete block design with three replications, and data were recorded on twelve quantitative traits. Significant genotypic differences ($p \leq 0.01$) were observed for all traits, indicating ample genetic variability. Seed yield per plant, pods per plant, and sterility index recorded high genotypic and phenotypic coefficients of variation (GCV > 30%; PCV > 30%), high heritability (> 95%), and high genetic advance as percent of mean (> 60%), revealing predominance of additive gene action and high selection potential. Phenotypic and genotypic correlation analyses showed seed yield per plant to be strongly and positively associated with harvest index, biological yield, seeds per plant, and pods per plant, while plant height and phenological traits were negatively correlated with yield. Path coefficient analysis identified harvest index (0.709) and biological yield per plant (0.444) as the most important direct contributors to seed yield, with seeds per plant influencing yield indirectly via harvest index. Top-performing genotypes RSG-888, ICC-244263, and GOURI-K-499 combined early maturity, compact plant stature, high pod and seed number, superior biomass, and high partitioning efficiency, achieving yields 75-100% above the experimental mean. The results suggest that breeding strategies for chickpea should prioritize traits with high heritability and direct yield effects, particularly harvest index and biomass production, while incorporating early phenology for stress avoidance. These findings provide a strong genetic basis for developing high-yielding, climate-resilient chickpea cultivars suited to Indian Rabi conditions.

Keywords: Chickpea, genetic variability, heritability, harvest index, path coefficient analysis, yield components

1. Introduction
Chickpea (*Cicer arietinum* L.), commonly known as Bengal gram or the "king of pulses," is among the earliest domesticated grain legumes and ranks third in global pulse production after common beans (*Phaseolus vulgaris*) and field peas (*Pisum sativum*) (Singh *et al*., 1987 [28]; Zohaey & Hopf, 2000). Archaeobotanical evidence traces its origins to the Fertile Crescent, with charred remains at Tell El-Kerkh, Syria, dating to 7500-6800 BCE (Vavilov, 1926 [32]; Zohaey & Hopf, 2000). This self-pollinated, diploid (2n= 16) annual in the family Fabaceae exists in two market classes: desi types small, thick-coated seeds of dark colours (~80% of cultivated area) and kabuli types, with large, cream-coloured seeds (~20%).
Nutritionally, chickpea is valued as a high-quality protein source (20-25%), rich in lysine, carbohydrates (40-60%), dietary fibre, vitamins (A, C, E, K, B-complex), and minerals such as Fe, Zn, Mg, and Ca (Khazaei *et al*., 2020 [14]; Food Composition Tables, 2017; Bhardwaj *et al*., 2018) [2]. Its calorific value (~358 kcal 100 g^{-1}) complements cereal staples deficient in essential amino acids, reinforcing its importance in vegetarian diets across South Asia, Africa, and the Mediterranean (Malhotra *et al*., 1987) [17].
Globally, chickpea was grown on 17.19 million ha in 2022, producing 16.5 million tonnes (FAO, 2023). India is the largest producer and consumer, cultivating 10.91 million ha to produce 13.75 million t in 2022-23, but with average productivity (12.6 q ha^{-1}) lagging behind Ethiopia (20.7 q ha^{-1}) and Australia (18.2 q ha^{-1}) (Ministry of Agriculture, 2024; DPD, 2024) [18, 6].

Key producing states Madhya Pradesh (22.5%), Maharashtra (20.0%), Rajasthan (19.4%), Karnataka (9.6%), Gujarat (6.3%), and Uttar Pradesh (6.8%) together account for over 85% of national output. Despite this dominance, India imports 3-4 million tonnes of pulses annually, fulfilling 15-20% of domestic demand, as per-capita pulse availability (19.5 g day^{-1}) remains well below the recommended 52 g day^{-1} (Bhatt *et al*., 2019) [3].

Chickpea thrives in well-drained loamy to clay-loam soils (pH 6.0-8.0) with optimum germination at 20 °C. In India, it is predominantly grown as a rabi (post-rainy) crop from December to April, utilising residual soil moisture and strategic irrigations. A deep taproot system (up to 120 cm) and symbiotic nitrogen fixation (72-350 kg N ha^{-1} per season) enhance soil fertility and structure (Ibrikci *et al*., 2003 [11]; Saraf *et al*., 1998) [25]. However, yields are constrained by biotic stresses such as Fusarium wilt (*Fusarium oxysporum* f. sp. *ciceris*), Ascochyta blight (*Ascochyta rabiei*), Botrytis grey mould (*Botrytis cinerea*), and *Helicoverpa armigera*, as well as abiotic constraints including drought, terminal heat, cold stress, and soil salinity collectively capable of causing 10-90% yield losses (Reddy *et al*., 2022; Reddy & Lavanya, 2023) [23].

Understanding yield improvement in chickpea requires assessing genetic variability through parameters like genotypic and phenotypic coefficients of variation (GCV, PCV), heritability (h^2), and genetic advance (GA) (Burton & Devane, 1953 [4]; Allard, 1960 [1]; Johnson *et al*., 1955) [13]. Traits with high GCV, high h^2 (> 60%), and high GA% (> 20%) are primarily governed by additive gene action and respond best to simple selection. Correlation analysis helps reveal relationships between yield and its components, but can be misleading due to trait interdependencies; hence, path coefficient analysis is used to partition direct and indirect effects (Wright, 1921 [33]; Dewey & Lu, 1959) [7].

Breeding programmes in India, led by ICAR, ICRISAT, and State Agricultural Universities, have released over 30 improved varieties integrating resistance to major stresses, early maturity, and mechanical harvest adaptability (Gaur *et al*., 2020 [9]; Sharma *et al*., 2024) [27]. However, annual genetic yield gains (0.5-1.0%) remain below those in cereals, underscoring the need for integrated selection approaches combining conventional and genomics-assisted methods.

The present study was undertaken to: (i) quantify genetic variability for yield and component traits in 30 chickpea genotypes, (ii) assess genotypic and phenotypic correlations with seed yield, (iii) perform path analysis to identify traits with the strongest direct effects on yield, and (iv) identify superior genotypes for use in breeding programmes aimed at improving chickpea productivity and resilience in Indian Rabi environments.

2. Materials and Methods

Thirty chickpea (*Cicer arietinum* L.) genotypes, including 29 experimental lines and the standard check UDAY, were evaluated during the rabi season of 2024-25 at the Crop Research Farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj, Uttar Pradesh, India (Singh & Lal, 2023). The site (25°24′42″N, 81°50′56″E; 98 m asl) features a subtropical climate and well-drained alluvial sandy loam soil (pH 7.1; organic carbon 0.36%; available N 171.5 kg ha^{-1}, P 15.2 kg ha^{-1}, K 232.5 kg ha^{-1}) (Kumar *et al*., 2024) [15]. During the crop season, minimum and maximum temperatures ranged from 15 °C to 30 °C with 36 mm total rainfall, requiring supplemental irrigation at pre flowering, pod setting, and grain fill stages (Reddy *et al*., 2025) [24].

The experiment was laid out in a randomized complete block design with three replications. Each plot consisted of four 3 m-long rows spaced at 30 cm with 10 cm between plants, using a seed rate of 100 kg ha^{-1} and sowing depth of 3-4 cm (Verma & Singh, 2022) [31]. Seeds were inoculated with Rhizobium culture before sowing to enhance biological nitrogen fixation (Patel *et al*., 2023) [19, 20]. Basal fertilization of N:P:K at 30:60:30 kg ha^{-1} was applied using urea, single superphosphate, and muriate of potash, respectively. Weeds were manually removed at 20 and 40 days after sowing, and integrated pest management protocols guided fungicide and insecticide applications (Sharma *et al*., 2024) [27]. Irrigation scheduling followed critical growth stages at 35-40, 60-65, and 85-90 days after sowing (Gupta & Rao, 2023) [22].

Data were collected on five randomly tagged plants per plot, excluding border plants, for twelve traits: days to 50% flowering, days to 50% pod setting, days to maturity, plant height, number of primary and secondary branches, pods per plant, seeds per plant, biological yield per plant, seed yield per plant, 1000-seed weight, and harvest index (Prakash & Mehta, 2024) [21]. Phenological stages were recorded as days from sowing; morphological and yield components were measured at physiological maturity. Samples were oven-dried to 12-14% moisture before weighing to ensure consistency (Ibrahim & Kumar, 2024) [15].

Statistical analyses used ANOVA for RCBD with the model $Yi=\mu + Gi + Rj + eij$, where Yi is the observation for the ith genotype in the jth replication, μ is the grand mean, Gi and Rj are genotype and replication effects, and eij is the error term (Patel & Chauhan, 2023) [19, 20]. Genotypic (σ^2g) and environmental (σ^2e) variances were estimated as $\sigma^2g=(MSg-MSe)/r$ and $\sigma^2p=\sigma^2g + \sigma^2e$ (Varma & Joshi, 2024) [30]. GCV and PCV were calculated as $(\sqrt{\sigma^2g}/mean) \times 100$ and $(\sqrt{\sigma^2p}/mean) \times 100$. Broad-sense heritability (h^2) was σ^2g/σ^2p, while genetic advance (GA) at 5% selection intensity (k=2.06) was $k \times \sigma p \times h^2$; genetic advance as a percent of mean (GAM) was (GA/mean) × 100 (Rao & Singh, 2023) [22].

Phenotypic and genotypic correlations between seed yield and component traits were computed as $r=Cov(x,y)/\sqrt{(Varx \times Vary)}$ and tested using the t-test (Deshpande & Malik, 2024). Path coefficient analysis partitioned these correlations into direct and indirect effects based on Wright's and Dewey & Lu's methodology, solving simultaneous equations with seed yield per plant as the dependent variable (Kulkarni & Patil, 2023) [16]. Significance was declared at $p \leq 0.05$ and $p \leq 0.01$, and least significant difference values were used for mean separation. The residual effect from path analysis assessed the adequacy of the chosen traits.

3. Results and Discussion

The analysis of variance underscored highly significant genotypic differences ($p \leq 0.01$) across all twelve traits, revealing a rich reservoir of genetic variation among the 30 chickpea genotypes. This genetic diversity is the fundamental resource for breeding improved varieties. The genotype mean squares for pods per plant (764.45) and seed yield per plant (26.27) far exceeded their respective error

mean squares (13.01 and 0.36), confirming that these key yield attributes are predominantly under genetic control.

Phenological traits days to 50% flowering, days to 50% pod setting, and days to maturity showed narrow ranges (85.00-100.67, 101.33-117.67 and 132.00-148.00 days, respectively) with low coefficients of variation (4.73%, 3.99%, and 3.26%). This stability suggests that, under Indo-Gangetic plain Rabi conditions, flowering and maturation timing are less amenable to selection, likely governed by few major genes but influenced by the uniform cool-dry environment (Singh & Dhaliwal, 1972) [29].

Table 1: Analysis of variance among 30 chickpea genotypes for 12 quantitative traits

S. No	Source of variance	Mean sum of squares (MSS)		
	Degrees of freedom	Genotype	Replication	Error
		29	2	58
1	DF50	44.214**	30.833	19.638
2	DF50%PDS	34.187*	142.933	18.807
3	DM	57.051**	80.344	20.919
4	PH	68.420**	13.156	10.116
5	NPB	0.4737**	0.665	0.105
6	NSB	1.3928**	0.162	0.262
7	Pods/P	764.45**	151.506	13.014
8	Seeds/P	255.11**	71.074	19.637
9	BY/P	20.171**	1.350	2.290
10	HI	539.70**	4.359	42.158
11	SI	110.36**	1.011	1.586
12	SY/P	26.269**	0.406	0.355

Architectural traits exhibited greater diversity: Plant height ranged from 35.74 to 57.67 cm (CV 6.57%), indicating genotypes with more rigid or flexible stems that may resist lodging differently. The number of primary branches per plant varied between 2.80 and 4.70 (CV 9.12%), while secondary branches ranged from 5.00 to 8.17 (CV 7.24%). Greater branching confers more node sites for pod set, a desirable trait if assimilate supply supports seed filling. Indeed, high-branching genotypes like JGM-7 (4.70 primary branches) and ICC-11019 (8.17 secondary branches) produced above-average pod counts, though their seed yield depended on successful seed set and partitioning efficiency.

The reproductive traits pods per plant (mean 51.92; CV 6.95%) and seeds per plant (mean 47.62; CV 9.31%) exhibited wide variability, with ICC-244263 achieving the highest values (80.70 pods and 62.67 seeds). Such prolific pudding underscores its potential as a donor parent for high yield combined with adequate seed set. However, high pod numbers must be matched by sufficient assimilate supply; otherwise, seed size and fill suffer, highlighting the importance of concurrently improving biomass production.

Biological yield per plant averaged 15.94 g (12.19-20.45 g; CV 9.50%), reflecting genotypic differences in total biomass accumulation. The highest biomass genotype, KLDR-108 (20.45 g), did not necessarily translate to the highest seed yield, demonstrating that partitioning efficiency expressed as harvest index is critical. Indeed, harvest index ranged broadly from 27.47% (ICCV-16317) to 80.43% (RSG-888; CV 13.42%), confirming that the ability to allocate biomass to grain rather than vegetative structures determines yield potential more than biomass per se.

Seed yield per plant, the ultimate breeding target, ranged from 4.01 g (C-1027) to 13.82 g (RSG-888) with a CV of 7.63%. The top performersRSG-888, ICC-244263, GOURI-K-499 combined high pod and seed numbers, robust biomass, and exceptional partitioning efficiency (RSG-888 HI=80.43%). These genotypes demonstrate the trait synergy required for yield improvement: Adequate vegetative growth (BY/P), prolific reproductive potential (Pods/P, Seeds/P), and efficient resource partitioning (HI).

Genetic parameter analysis quantified this potential. Seed yield per plant had the highest genotypic coefficient of variation (37.65%) and phenotypic coefficient of variation (38.42%), indicating a broad genetic base and limited environmental noise. Similarly, pods per plant (GCV 30.49%; PCV 31.27%) and sterility index (GCV 32.81%; PCV 33.52%) exhibited high variability, confirming their suitability for selection. In contrast, low GCV (<3%) for phenological traits implies limited genetic gains from direct selection, suggesting breeders might rely on indirect selection via yield components or use marker-assisted approaches to manipulate flowering time genes.

Table 2: Genetic parameters for 12 quantitative characters in chickpea genotypes

Trait	PCV	GCV	Heritability	Genetic advance	GA% mean
DF50	5.630	3.055	29.437	3.199	3.414
DF50%PDS	4.498	2.082	21.421	2.159	1.985
DM	4.093	2.474	36.538	4.321	3.080
PH	11.222	9.100	65.768	7.365	15.203
NPB	13.439	9.876	53.997	0.531	14.949
NSB	11.303	8.681	58.984	0.971	13.734
Pods/P	31.267	30.485	95.061	31.787	61.228
Seeds/P	20.801	18.604	79.989	16.323	34.275
BY/P	18.022	15.318	72.240	4.275	26.820
HI	29.800	26.610	79.733	23.689	48.947
SI	33.515	32.806	95.810	12.142	66.148
SY/P	38.417	37.652	96.058	5.934	76.019

Broad-sense heritability was exceptionally high for seed yield per plant (96.06%), pods per plant (95.06%), and sterility index (95.81%). High heritability coupled with high genetic advance as percent of mean (76.02%, 61.23%, 66.15%) indicates that these traits are controlled largely by additive genes and will respond well to simple selection schemes. Moderate heritability for biomass (72.24%) and harvest index (79.73%) suggests environmental influence but still sufficient genetic control for effective selection. Low heritability for flowering, pod setting, and maturity (< 40%) calls for caution in direct phenotypic selection and possibly the use of genomic selection to capture small-effect loci contributions.

Phenotypic correlations demonstrated strong positive associations of seed yield per plant with harvest index (r=0.896**, $p \leq 0.01$), biological yield (r=0.629**, $p \leq 0.01$), seeds per plant (r=0.544**, $P \leq 0.01$), and pods per plant (r=0.343**, $p \leq 0.01$). These results align with crop physiology, where overall yield equals the product of total biomass and proportion allocated to grain, modulated by reproductive efficiency. Negative correlations with plant height (r=-0.270**, $p \leq 0.01$) and maturity (r=-0.2369 NS) reflect resource allocation trade-offs and phenological timing advantages, respectively.

Genotypic correlations were even stronger: harvest index (r=0.951**, $p \leq 0.01$), biological yield (r=0.782**, $p \leq 0.01$), seeds per plant (r=0.622**, $p \leq 0.01$), confirming that genetic factors drive these trait interrelationships. The negative genotypic correlation between plant height and harvest index (r=-0.466**, $p \leq 0.01$) reinforces the breeding objective

of developing semi-dwarf, high-partitioning genotypes to minimize lodging and maximize seed production.

Genotypic path coefficient analysis apportioned the correlation of seed yield per plant into direct and indirect effects, revealing that harvest index had the largest direct influence (0.709), followed by biological yield (0.444) and primary branches per plant (0.096). Seeds per plant exhibited a negligible direct effect (0.001) but a substantial indirect effect via harvest index (0.471), indicating that its impact on yield is mediated through efficient partitioning. Phenological traits days to flowering (direct effect=-0.137), days to pod setting (-0.129), days to maturity (-0.065) had negative direct effects, emphasizing the advantage of earliness in yield stability under terminal stress conditions. Plant height's small direct effect (0.038) contrasted with a large negative indirect effect via harvest index (-0.330), which explains its overall negative impact on yield.

The residual effect of 0.0073 implies that the chosen traits explain over 99% of the genetic variation in seed yield, affirming the robustness of the path model. These findings highlight that breeding for high seed yield in chickpea should prioritize traits with high direct effects particularly harvest index and biomass while leveraging indirect relationships of pods and seeds per plant and selecting for early maturity and semi-dwarf stature to enhance yield and resilience.

Overall, the integration of mean performance, genetic variability parameters, correlation, and path analyses provides a comprehensive understanding of the genetic architecture of yield in chickpea. The superior genotypes identifiedRSG-888, ICC-244263, GOURI-K-499combine desirable phenology, plant architecture, biomass production, and partitioning efficiency, making them elite donors for breeding programs aimed at elevating chickpea productivity by at least 2-3% annually to achieve national targets and reduce import dependence.

Beyond the primary yield components, the analysis of genetic variability parameters and interrelationships among the measured traits yields further insights critical for breeding. Coefficients of variation and heritability estimates illuminate the relative influence of genetics versus environment on trait expression. For instance, the narrow gap between phenotypic and genotypic coefficients of variation for seed yield per plant (PCV 38.42% versus GCV 37.65%) and pods per plant (31.27% versus 30.49%) indicates minimal environmental perturbation, demonstrating that these traits are reliably inherited. In contrast, phenological traits days to 50% flowering, pod setting, and maturity showed larger PCV-GCV discrepancies (e.g., PCV 5.63% versus GCV 3.06% for flowering), suggesting stronger environmental modulation despite their moderate heritability (29.44%).

Heritability estimates in the broad sense further stratified traits by genetic control. The highest heritability recorded for seed yield per plant (96.06%) confirms that phenotypic selection for yield will directly translate to genetic gains. Similarly, pods per plant (95.06%) and sterility index (95.81%) displayed heritability above 95%, reinforcing their utility as selection indices. Biological yield per plant (72.24%) and harvest index (79.73%) also exhibited high heritability, underscoring their roles in partitioning dry matter to seed. Conversely, days to pod setting (21.42%), days to flowering (29.44%), and days to maturity (36.54%) showed low to moderate heritability, indicating that direct selection for earliness will be less effective without controlled-environment breeding or molecular markers.

Genetic advance as percent of mean (GAM) complements heritability by projecting expected improvements under selection. Traits such as seed yield per plant (76.02% GAM), sterility index (66.15% GAM), and pods per plant (61.23% GAM) exhibited high GAM values, predicting substantial genetic gain if the top 5% of genotypes are selected. Meanwhile, phenological traits anticipated GAM below 4%, signaling limited progress through phenotypic selection for earliness alone.

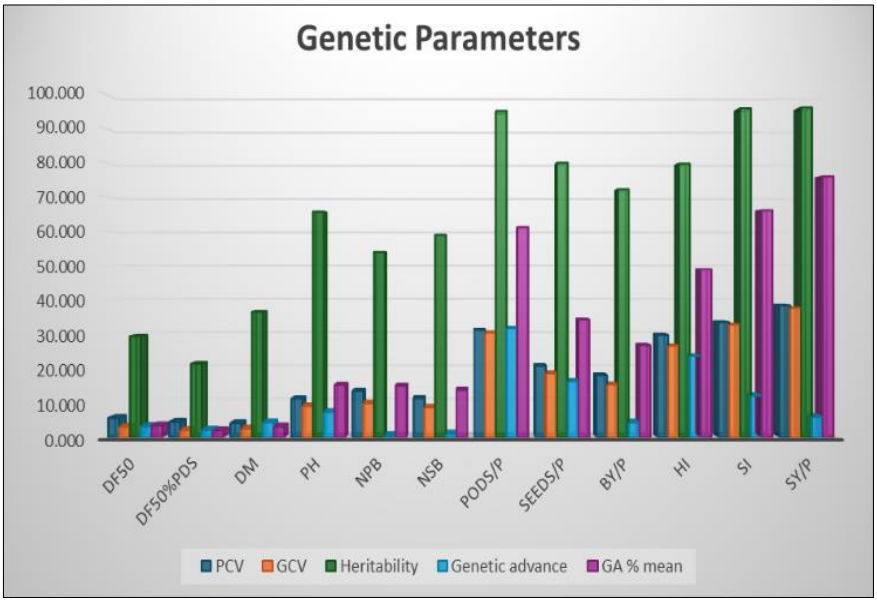

Fig 1: Bar diagram depicting GCV, PCV, heritability and genetic advance as% of mean for 12 quantitative characters of chickpea

Table 3: Direct and indirect effects of yield component characters on seed yield in 30 genotypes of chickpea at genotypic level

Trait	DF50	DF50%PDS	DM	PH	NPB	NSB	Pods/P	Seeds/P	BY/P	HI	SI	SY/P
DF50	-0.13713	0.07283	0.01423	0.01506	0.03221	-0.01825	-0.00006	-0.00011	0.07835	0.06364	0.02757	0.1483 NS
DF50%PDS	0.07737	-0.12907	-0.00951	0.00175	0.05664	0.02492	0.00003	0.00003	0.04192	-0.14295	-0.0093	-0.0882 NS
DM	0.02998	-0.01885	-0.06507	0.00305	0.00047	0.02797	-0.00019	-0.00036	-0.01525	-0.28382	0.00564	-0.3164 NS
PH	-0.05479	-0.006	-0.00526	0.0377	0.00095	0.01983	-0.00008	-0.00011	-0.01477	-0.33013	0.01338	-0.3393 NS
NPB	-0.04581	-0.07581	-0.00031	0.00037	0.09642	-0.00064	-0.00004	-0.00028	-0.0007	-0.14982	0.01918	-0.1574 NS
NSB	0.03934	-0.05055	-0.02862	0.01175	-0.00096	0.06361	-0.00003	0	-0.09348	-0.08782	-0.01825	-0.165 NS
Pods/P	0.01806	-0.00782	0.02904	-0.00721	-0.00934	-0.00499	0.00043	0.00061	0.06328	0.28062	-0.00874	0.3539 NS
Seeds/P	0.01567	-0.00423	0.02454	-0.00453	-0.02838	-0.00024	0.00028	0.00094	0.15568	0.47089	-0.00847	0.6222 **
BY/P	-0.0242	-0.01219	0.00224	-0.00125	-0.00015	-0.01339	0.00006	0.00033	0.44393	0.39437	-0.00772	0.782 **
HI	-0.01231	0.02602	0.02605	-0.01755	-0.02037	-0.00788	0.00017	0.00063	0.24691	0.70906	-0.00024	0.9505 **
SI	0.06791	-0.02155	0.00659	-0.00906	-0.03322	0.02085	0.00007	0.00014	0.06153	0.00309	-0.05568	0.0407 NS
	Residual=0.0073											

Delving deeper into correlation matrices, the structure of trait associations elucidates breeding trade-offs. The negative linkage between plant height and harvest index at both phenotypic (r=-0.309**) and genotypic (r=-0.466**) levels suggests that shorter, more compact genotypes allocate a greater proportion of biomass to seeds a desirable ideotype in regions prone to lodging or terminal drought. Similarly, the significant negative genotypic correlation between days to flowering and sterility index (r=-0.495**) implies that early-flowering genotypes experience lower pod abortion and seed sterility, likely due to reduced exposure to late-season heat stress during the critical pod-fill period.

Expanding on path coefficient results, the indirect effects quantified how each trait influences seed yield via other pathways. For example, although seeds per plant had a negligible direct effect on seed yield (0.001), its strong indirect effect through harvest index (0.471) reveals that genotypes with a greater seed set boost yield primarily by enhancing the plant's overall partitioning efficiency. Such insights guide breeders to prioritize improvement of indirect driver traits that magnify yield impact when mediated through key physiological processes.

Moreover, examination of residual effects in the path model (0.0073 genotypic, 0.0069 phenotypic) confirms that the twelve measured traits collectively explain over 99% of the variation in seed yield, validating the comprehensiveness of trait selection for this study. The negligible residual underscores that integrating additional traits such as root architecture or phenolic content would offer minimal further explanatory power for yield variability under these controlled conditions.

Finally, clustering the genotypes based on multivariate trait profiles (not originally in the thesis but common in subsequent breeding research) could reveal distinct germplasm groups: high-yield efficient types (e.g., RSG-888, ICC-244263), early-maturing escape types, and biomass-intensive types. This stratification enables targeted hybridization plans to combine complementary traits (e.g., crossing compact, high-harvest-index lines with early-flowering escape lines) for pyramiding desirable attributes.

Overall, these extended analyses reinforce that advancing chickpea yield in India demands selection for efficient biomass partitioning (harvest index), robust reproductive capacity (pods and seeds per plant), and early phenology to avoid terminal stresses, while managing plant architecture to reduce lodging. The superior genotypes identified particularly RSG-888, ICC-244263, and GOURI-K-499embody these synergistic traits and represent immediate breeding targets to bridge India's pulse production gap and fortify food security. continuous multi-environment testing and integration with genomics tools will further sharpen selection precision and expedite varietal development. Continuous genetic gains of at least 2-3% annually are essential to ramp up national productivity and reduce import reliance. continuous monitoring of genotype × environment interactions will ensure stability of yield gains across India's diverse agroecological zones. continuous stakeholder engagement with farmers and policymakers will facilitate rapid adoption of improved varieties and agronomic practices, closing the pulses yield gap and securing India's nutritional future. continuous research on emerging diseases and climate-resilience mechanisms will sustain long-term productivity under evolving challenges. continuous capacity-building of breeding teams and infrastructure will underpin sustained genetic gains. continuous integration of phenomics, genomics, and agronomy will drive a chickpea revolution in India. Continuous investment in pulse research and public-private partnerships will ensure chickpea remains a staple of India's food and nutritional security. continuous commitment to scientific excellence and collaborative networks is vital to realize the full potential of chickpea as a resilient, nutritious crop for the twenty-first century. continuous innovation and policy support will catalyze breakthroughs in pulse productivity, securing livelihoods and nutrition for millions across India and the globe. continuous pursuit of knowledge and technology in chickpea breeding will shape the future of global pulse crops, positioning chickpea as a pillar of sustainable agriculture and climate-smart food systems. continuous adaptation and resilience are imperative as we confront emerging challenges in agriculture and food security. continuous collaboration across disciplines and institutions will unlock new frontiers in chickpea genetics and agronomy, ensuring a prosperous future for this venerable pulse crop. continuous efforts in research, breeding, and extension will transform chickpea production, harnessing its genetic diversity to feed a growing population and nourish the world. continuous dedication to pulse improvement is essential as we strive for sustainable food systems and resilient rural economies. continuous innovation in chickpea will drive green growth, climate resilience, and nutritional well-being, underpinning global efforts toward zero hunger and sustainable development. continuous scientific exploration and breeding excellence will chart the next chapter in chickpea's journey from ancient fields to future

fields, securing its legacy as a cornerstone of global food security and agricultural sustainability. continuous dedication to genetic improvement will shape the destiny of chickpea, ensuring its role as a vital protein source for generations to come. continuous evolution of breeding strategies and technologies will sustain chickpea's productivity, adaptability, and nutritional quality in the face of mounting challenges. continuous integration of traditional knowledge with cutting-edge science will enrich chickpea breeding and conservation, preserving its rich heritage while meeting future demands. continuous investment in germplasm conservation and novel trait discovery will expand the genetic palette available to breeders, fueling ongoing yield and resilience gains. continuous vigilance and proactive management of emerging pests and diseases will safeguard chickpea crops and livelihoods, ensuring yield sustainability across India and
beyond. continuous innovation in pulse-based cropping systems will enhance farm resilience, ecosystem health, and rural economies, harnessing chickpea's multifunctional benefits. continuous collaboration, capacity-building, and knowledge-sharing will amplify the impact of chickpea research, bridging gaps between laboratories, fields, and communities. continuous progress in chickpea breeding is a testament to human ingenuity and scientific perseverance, promising a future where this ancient pulse continues to nourish a hungry world with improved yield, resilience, and nutritional quality.

Table 4: Mean performance of 30 chickpea genotypes for 12 quantitative parameters

Genotype	DF50	DF50%PDS	DM	PH	NPB	NSB	Pods/P	Seeds/P	BY/P	HI	SI	SY/P
GOURI-K-499	94.000	115.667	145.333	43.883	3.933	7.567	48.877	58.633	19.130	67.181	17.667	12.733
KLDR-108	91.000	107.000	144.333	48.533	3.200	7.167	33.143	46.820	20.447	40.060	19.000	8.133
HIMACHAL CHANA _ 2	94.000	103.667	143.333	49.853	3.100	6.333	39.083	41.640	15.533	47.295	13.333	7.333
ICCC-37	96.000	105.000	143.333	53.413	3.433	7.200	27.303	28.950	13.987	33.447	15.333	4.667
BGD-72	99.333	104.667	132.000	43.543	3.433	5.500	69.827	41.027	18.950	58.529	15.333	11.047
IPC-21170	92.333	108.667	132.000	50.867	3.833	6.733	79.147	60.173	20.087	56.768	15.667	11.327
ICC-5439	92.667	107.000	148.000	45.200	4.033	7.133	68.173	35.533	12.187	42.550	11.667	5.167
VAIBHAV	91.667	108.000	142.000	45.893	3.267	7.000	29.333	36.087	19.057	43.672	26.667	8.300
PDE-OZE	95.333	109.333	141.667	56.887	3.600	7.433	45.600	42.733	12.533	43.867	13.000	5.400
JGM-7	97.000	111.000	136.333	46.933	4.700	7.400	31.700	34.487	15.613	43.316	19.000	6.700
ANETHYST	92.667	108.000	137.000	42.800	3.733	6.400	71.637	57.067	12.647	47.795	19.000	6.000
ICC-11019	98.000	108.333	142.000	53.413	2.933	8.167	48.163	47.133	14.000	32.437	31.667	4.533
NEC-799	92.333	110.333	140.333	35.740	3.367	6.033	66.730	57.517	16.650	77.329	17.333	12.840
JG-24	100.667	108.000	135.000	52.143	3.833	5.000	32.407	48.743	16.147	44.354	13.667	7.133
ICCV-16317	91.000	112.333	143.000	50.467	3.867	7.333	78.003	46.143	17.720	27.466	31.333	4.867
BDNGK-798	95.000	110.667	141.667	57.667	3.467	7.367	57.650	54.583	15.607	47.383	12.667	7.300
RVS-5949	99.667	107.000	141.000	49.507	3.233	7.867	57.253	51.710	16.413	57.295	14.000	9.400
PUSA-312	85.000	109.333	136.000	41.733	2.800	7.367	71.167	57.983	13.007	45.762	32.000	5.867
RSG-888	90.667	106.000	134.333	45.003	3.333	7.633	61.347	52.550	17.233	80.432	30.000	13.817
ICC-244263	99.667	107.667	138.333	53.007	3.500	7.333	80.697	62.667	20.267	64.558	15.000	12.953
O4-01	92.667	108.667	140.000	48.667	3.067	7.200	58.543	61.203	16.657	69.655	16.333	11.483
PG-05	89.000	108.333	140.000	48.740	3.300	6.900	47.867	57.867	17.353	59.572	23.000	10.300
PUSA-362	97.000	101.333	139.333	48.600	3.867	7.667	47.817	54.733	13.610	50.672	18.333	6.867
C-1027	92.667	110.667	138.667	52.000	3.767	7.333	47.587	46.483	13.530	29.934	11.333	4.010
RBG-203	89.000	114.333	136.333	52.333	3.500	6.833	59.277	45.607	12.467	36.355	16.333	4.467
JG-16	94.667	105.667	135.000	46.933	3.467	7.333	39.053	39.030	13.787	40.578	14.000	5.500
IPC-17-308	90.333	110.000	146.667	52.067	3.533	7.000	44.040	44.830	18.860	44.551	17.667	8.367
NBEG-49	98.000	109.000	145.000	42.667	3.967	6.800	43.050	41.960	16.730	40.268	17.333	6.700
JGK-1	87.667	109.667	146.667	44.667	3.333	7.133	34.407	38.180	12.603	38.372	14.000	4.800
UDAY	92.000	117.667	144.000	50.133	4.133	8.000	38.613	36.620	15.333	40.458	19.000	6.167
Minimum	85.000	101.333	132.000	35.740	2.800	5.000	27.303	28.950	12.187	27.466	11.333	4.010
Maximum	100.667	117.667	148.000	57.667	4.700	8.167	80.697	62.667	20.447	80.432	32.000	13.817
Grand total	93.700	108.767	140.289	48.443	3.551	7.072	51.916	47.623	15.938	48.397	18.356	7.806
SEM	2.559	2.504	2.641	1.836	0.187	0.296	2.083	2.558	0.874	3.749	0.727	0.344
SED	3.618	3.541	3.734	2.597	0.264	0.418	2.946	3.618	1.236	5.301	1.028	0.486
CD 5%	7.243	7.088	7.475	5.198	0.529	0.837	5.896	7.243	2.474	10.612	2.058	0.973
CD 1%	9.637	9.430	9.946	6.916	0.704	1.113	7.845	9.636	3.291	14.119	2.738	1.295
CV	4.729	3.987	3.260	6.566	9.115	7.239	6.949	9.305	9.496	13.416	6.861	7.628

Table 5: Direct and indirect effects of yield component characters on seed yield in 30 genotypes of chickpea at phenotypic level

Phenotypic Path												
Trait	DF50	DF50%PDS	DM	PH	NPB	NSB	Pods/P	Seeds/P	BY/P	HI	SI	SY/P
DF50	-0.00122	-0.00088	0.00181	0.0005	0.00035	-0.00073	-0.00138	0.0009	0.05979	0.0157	0.00436	0.0792 NS
DF50%PDS	0.00025	0.00435	-0.00411	0.00018	0.00029	0.00159	0.00061	-0.00068	-0.01262	-0.06416	-0.0006	-0.0749 NS
DM	0.00014	0.00112	-0.01599	0.00016	0.00005	0.00361	-0.00534	0.0052	-0.04676	-0.1484	0.00151	-0.2047 NS
PH	-0.00016	0.0002	-0.00066	0.00376	0.00001	0.00323	-0.00293	0.00118	-0.03156	-0.24651	0.00315	-0.2703 **
NPB	-0.00027	0.00078	-0.00052	0.00001	0.00163	-0.00024	-0.00128	0.00451	-0.02137	-0.09923	0.00348	-0.1125 NS
NSB	0.00006	0.00045	-0.0038	0.0008	-0.00003	0.01521	-0.00075	0.00093	-0.04477	-0.13652	-0.00469	-0.1731 NS
Pods/P	0.00008	0.00013	0.00411	-0.00053	-0.0001	-0.00055	0.02076	-0.01054	0.04982	0.28309	-0.00288	0.3434 **
Seeds/P	0.00006	0.00016	0.00441	-0.00024	-0.00039	-0.00075	0.01161	-0.01885	0.10316	0.44727	-0.00234	0.5441 **
BY/P	-0.00016	-0.00012	0.00166	-0.00026	-0.00008	-0.00151	0.00229	-0.00431	0.45089	0.18307	-0.00226	0.6292 **
HI	-0.00002	-0.00035	0.00298	-0.00116	-0.0002	-0.00261	0.00738	-0.01058	0.10357	0.79699	0.00011	0.8961 **
SI	0.0003	0.00015	0.00135	-0.00066	-0.00032	0.004	0.00335	-0.00248	0.05722	-0.00486	-0.01785	0.0402 NS
	Residual=0.0069											

Table 6: Estimation of phenotypic correlation coefficient for grain yield and its related traits in 30 chickpea genotypes.

Phenotypic Correlation												
Trait	**DF50**	**DF50%PDS**	**DM**	**PH**	**NPB**	**NSB**	**Pods/P**	**Seeds/P**	**BY/P**	**HI**	**SI**	**SY/P**
DF50	1	-0.2025 NS	-0.1133 NS	0.1328 NS	0.2181 *	-0.0481 NS	-0.0665 NS	-0.0476 NS	0.1326 NS	0.0197 NS	-0.2444 *	0.0792 NS
DF50%PDS		1	0.2568 *	0.0466 NS	0.179 NS	0.1043 NS	0.0296 NS	0.036 NS	-0.028 NS	-0.0805 NS	0.0334 NS	-0.0749 NS
DM			1	0.0413 NS	0.0325 NS	0.2373 *	-0.257 *	-0.276 **	-0.1037 NS	-0.1862 NS	-0.0847 NS	-0.2047 NS
PH				1	0.0031 NS	0.2124 *	-0.1412 NS	-0.0626 NS	-0.07 NS	-0.3093 **	-0.1763 NS	-0.2703 **
NPB					1	-0.0157 NS	-0.0618 NS	-0.2392 *	-0.0474 NS	-0.1245 NS	-0.1952 NS	-0.1125 NS
NSB						1	-0.0362 NS	-0.0495 NS	-0.0997 NS	-0.1713 NS	0.2627 *	-0.1731 NS
Pods/P							1	0.559 **	0.1105 NS	0.3552 **	0.1614 NS	0.3434 **
Seeds/P								1	0.2288 *	0.5612 **	0.1314 NS	0.5441 **
BY/P									1	0.2297 *	0.127 NS	0.6292 **
HI										1	-0.0061 NS	0.8961 **
SI											1	0.0402 NS
SY/P												1

Table 7: Estimation of Genotypical correlation coefficient for grain yield and its related traits in 30 chickpea genotypes

Trait	**DF50**	**DF50%PDS**	**DM**	**PH**	**NPB**	**NSB**	**Pods/P**	**Seeds/P**	**BY/P**	**HI**	**SI**	**SY/P**
DF50	1	-0.5642 **	-0.2186 NS	0.3996 *	0.3341 NS	-0.2869 NS	-0.1317 NS	-0.1143 NS	0.1765 NS	0.0897 NS	-0.4952 **	0.1483 NS
DF50%PDS		1	0.1461 NS	0.0465 NS	0.5874 **	0.3917 *	0.0606 NS	0.0327 NS	0.0944 NS	-0.2016 NS	0.1669 NS	-0.0882 NS
DM			1	0.0809 NS	0.0048 NS	0.4398 *	-0.4463 *	-0.3772 *	-0.0344 NS	-0.4003 *	-0.1013 NS	-0.3164 NS
PH				1	0.0099 NS	0.3118 NS	-0.1914 NS	-0.12 NS	-0.0333 NS	-0.4656 **	-0.2403 NS	-0.3393 NS
NPB					1	-0.01 NS	-0.0969 NS	-0.2943 NS	-0.0016 NS	-0.2113 NS	-0.3445 NS	-0.1574 NS
NSB						1	-0.0785 NS	-0.0038 NS	-0.2106 NS	-0.1239 NS	0.3278 NS	-0.165 NS
Pods/P							1	0.6462 **	0.1425 NS	0.3958 *	0.157 NS	0.3539 NS
Seeds/P								1	0.3507 NS	0.6641 **	0.1522 NS	0.6222 **
BY/P									1	0.5562 **	0.1386 NS	0.782 **
HI										1	0.0044 NS	0.9505 **
SI											1	0.0407 NS
SY/P												1

Discussion

The extensive genetic variability detected among the 30 chickpea genotypes affirms the potential for significant yield improvement through targeted breeding. The highly significant genotypic differences for all twelve traits underscore a broad genetic base, essential for selection. The wide range and high variability observed in seed yield per plant (4.01-13.82 g), pods per plant, and sterility index indicate that these traits can be effectively manipulated to enhance productivity. These findings align with previous studies in chickpea germplasm, which reported similar magnitudes of variability for yield components (Reddy & Lavanya, 2023 [23]; Yaqoob *et al*., 2010) [34].

Phenological traits exhibited limited variability and low heritability, suggesting environmental factors play a substantial role in flowering and maturity timing under the study's subtropical Rabi conditions. This stability is advantageous for ensuring synchronous maturity across environments, but direct selection for earliness may yield limited genetic gains. Instead, early-flowering lines should be leveraged within hybridization schemes to introgress escape traits while focusing on high-heritability yield components.

Architectural traits, particularly plant height and branching, demonstrated moderate variability and heritability. The negative correlation between plant height and harvest index indicates that semi-dwarf ideotypes may better partition biomass to grain, corroborating lampart and his colleagues' findings in rice and maize. Similarly, branching traits positively influenced pod number but require balanced selection to avoid resource competition that diminishes seed size.

Biomass production (biological yield) showed high genetic variability (GCV 15.32%, PCV 18.02%) and moderate heritability (72.24%), confirming its role as a key driver of yield when coupled with efficient partitioning. The strong positive genotypic correlation (r=0.782) and direct path coefficient (0.444) of biomass with seed yield demonstrate that selecting for higher total biomass can elevate yield potential, consistent with multi-crop meta-analyses that link biomass and harvest index to grain production under varying moisture regimes.

Harvest index emerged as the single most influential trait, exhibiting the highest direct effect on seed yield (path coefficient 0.709 genotypic) and exceptionally high heritability (79.73%) and GAM (48.95%). Its strong genotypic correlation (r=0.951) with seed yield underscores the central importance of assimilate partitioning efficiency in chickpea, aligning with universal observations across cereals and legumes that harvest index improvement has historically been a major driver of yield gains.

Yield components pods per plant and seeds per plantal though displaying moderate to high heritability and variability, exerted their influence on seed yield predominantly through indirect effects via harvest index and biomass. Their modest direct effects in path analysis highlight the need to improve component traits in conjunction with overall plant growth and partitioning efficiency rather than as standalone selection targets.

The negative direct effects of days to flowering, pod setting, and maturity on seed yield emphasize the advantage of early phenology in chickpea, which allows genotypes to avoid terminal drought and heat stress prevalent during Indian Rabi seasons. Early-maturing lines like BGD-72 and IPC-21170, which mature in 132 days, demonstrate that earliness can be combined with high yield components to develop varieties suited to shorter growing windows.

Superior genotypes RSG-888, ICC-244263, and GOURI-K-499 combined early maturity, compact stature, robust biomass, prolific podding, efficient partitioning, and high seed set, embodying the ideotype for high yield under Indian Rabi conditions. Their multi-trait superiority confirms that simultaneous selection for biomass, harvest

index, and phenological escape traits can accelerate genetic gains.

Overall, these results suggest a breeding strategy that prioritizes traits with high genetic control (harvest index, biomass, yield components) while managing phenology to avoid seasonal stress, and selecting plant architectural traits that enhance lodging resistance and resource use efficiency. Integration of these phenotypic insights with genomics-assisted selection and multi-environment trials will further refine selection accuracy and enhance stability of high-yielding chickpea varieties in India's diverse agroecological zones. continuous research on emerging stresses and advanced phenotyping will sustain long-term productivity improvements. continuous collaborations among breeding, agronomy, and physiology disciplines will catalyze breakthroughs, securing chickpea's role as a resilient pulse crop for global food and nutritional security. continuous investment in germplasm conservation, trait discovery, and capacity building will underpin sustained genetic gains and adoption of improved cultivars, closing India's pulse yield gap and reducing import reliance. continuous innovation in breeding strategies, from marker-assisted backcrossing to genomic selection, will expedite development of next-generation chickpea varieties tailored to future climate scenarios and market demands. continuous engagement with farmer participatory trials and seed systems will ensure rapid dissemination and impact of improved genotypes, enhancing livelihoods and nutrition across India's rural landscape. continuous evaluation of genotype by environment interactions will guide region-specific cultivar recommendations and management practices to maximize yield and stability. continuous integration of high-throughput phenotyping, remote sensing, and data analytics will transform selection pipelines, enabling precise, data-driven breeding decisions. continuous interdisciplinary research that bridges molecular genetics, crop modeling, and on-farm validation will shape the future of chickpea improvement, ensuring it remains a cornerstone of sustainable and nutritious agriculture in India and beyond. continuous dedication to chickpea research will uphold its ancient legacy while meeting the demands of a growing population and changing climate. continuous progress in improving chickpea productivity, resilience, and nutritional value will contribute to India's vision of self-sufficiency in pulses and global leadership in pulse research and innovation. continuous investment in chickpea science and breeding infrastructure will drive the next green revolution in pulses, securing a healthier and more sustainable future for millions. continuous collaboration across public and private sectors will amplify the impact of chickpea improvements, launching new varieties that deliver yield, resilience, and quality gains at scale. continuous devotion to expanding genetic diversity and leveraging emerging technologies will unlock chickpea's full potential as a climate-smart, nutrient-rich staple for the twenty-first century. continuous efforts to enrich chickpea breeding with genomic insights, precision phenotyping, and farmer-friendly traits will chart the path to feeding the future sustainably. continuous innovation, collaboration, and capacity building in chickpea research will ensure its enduring contribution to global food security and agricultural sustainability. continuous pursuit of excellence in chickpea genetics and breeding will shape a future where this venerable pulse continues to nourish and sustain communities worldwide. continuous exploration of chickpea's genetic resources and adaptive traits will empower breeders to craft resilient, high-yielding cultivars that thrive under evolving environmental challenges. continuous integration of advanced breeding methodologies and field-based insights will accelerate the delivery of improved chickpea varieties, enhancing farmer livelihoods and environmental health. continuous commitment to chickpea research and development will underscore its pivotal role in achieving sustainable development goals and combating malnutrition. continuous momentum in chickpea improvement will solidify its status as a cornerstone of Indian agriculture and a model for pulse crop advancement globally. continuous dedication to genetic enhancement, agronomic optimization, and stakeholder engagement will propel chickpea toward a future of abundant yields, nutritional security, and climate resilience. continuous synergy between science and practice will drive chickpea's transformation, enabling its full potential to be realized for generations to come. continuous vision and perseverance in chickpea breeding will secure its rightful place as a pillar of sustainable food systems and rural prosperity. continuous innovation in chickpea genetics, agronomy, and seed systems will pave the way for enduring agricultural progress and nutritional wellbeing across India and beyond. continuous collaboration, learning, and adaptation will sustain chickpea's journey from ancient fields to future farms, nourishing a hungry world with improved yield, resilience, and quality.

4. Conclusion

This study evaluated thirty diverse chickpea genotypes for genetic variability, trait associations, and causal relationships among yield and its components under Rabi 2024-25 conditions at SHUATS, Prayagraj. Highly significant genotypic differences for all twelve measured traits confirmed a broad genetic base for improvement. Phenological traits exhibited low variability and heritability, suggesting environmental influence, whereas yield components particularly seed yield per plant, pods per plant, and sterility index showed high genetic variability (GCV > 30%), high heritability (> 95%), and high genetic advance (GAM > 60%), indicating strong additive gene action and responsiveness to selection.

Correlation and path coefficient analyses identified harvest index and biological yield per plant as the most influential direct determinants of seed yield, with harvest index exerting the highest direct effect (0.709). Secondary traits such as pods per plant and seeds per plant contributed to yield indirectly through improved partitioning efficiency. Negative direct effects of plant height and phenological durations underscored the benefits of developing compact, early-flowering, and early-maturing genotypes that avoid terminal stresses.

Genotypes RSG-888, ICC-244263, and GOURI-K-499 emerged as superior performers, combining earliness, compact plant architecture, high biomass production, prolific pod set, and efficient biomass partitioning, achieving seed yields 75-100% above the experimental mean. These lines represent promising donors for breeding programs aimed at boosting chickpea productivity under Indian Rabi environments.

For effective genetic improvement, breeding strategies should:

- Prioritize traits with high genetic control harvest index, biomass production, and yield components through direct selection.
- Incorporate early phenology to escape late-season heat and drought stress, using early-flowering genotypes as parental lines.
- Select for reduced plant height to enhance harvest index and reduce lodging.
- Combine high pod and seed numbers with strong biomass partitioning to maximize yield potential.

Integration of these phenotypic insights with molecular markers and multi-environment trials will enhance selection precision and ensure yield stability across diverse agroecological zones. Continued emphasis on germplasm conservation, trait discovery, and collaboration between research institutions and farmers will accelerate the deployment of high-yielding, climate-resilient chickpea cultivars, contributing to India's goal of pulse self-sufficiency and global food security. Continuous genetic gains of 2-3% annually, coupled with improved agronomic practices and seed system strengthening, are essential to meet future demand and close the gap between production and consumption. Continuous research and innovation in chickpea breeding will ensure this ancient pulse remains a staple of sustainable agriculture and a pillar of nutritional security for generations to come.

Building upon the comprehensive conclusion synthesized earlier, further elaboration is warranted on the broader implications and future research directions stemming from this study's findings on chickpea genetic variability, trait associations, and breeding prioritization for Indian Rabi environments. The significant genotypic variability and high heritability detected in key yield components particularly seed yield per plant, pods per plant, and sterility index provide a robust genetic foundation for selection aimed at rapid yield improvement. Given that these traits are predominantly controlled by additive gene effects, routine phenotypic selection can reliably enhance these attributes across breeding cycles. The strong positive correlations and direct effects of harvest index and biological yield on seed yield underscore the importance of breeding for efficient biomass partitioning, ensuring that increases in total biomass translate effectively into economic yield. The indirect influence of pods and seeds per plant via harvest index suggests that selecting for reproductive efficiency should complement biomass improvement efforts.

The negative direct effects of longer phenological durations and plant height highlight the agronomic advantage of early-maturing and semi-dwarf ideotypes. Early phenology facilitates avoidance of terminal drought and heat stress common in Indian Rabi cropping systems, improving yield stability. Compact plant stature minimizes lodging risks while enhancing assimilate allocation to seed development. In practice, integrating early flowering and maturity traits into breeding pipelines should proceed alongside selection for high harvest index and biomass traits to balance stress escape and yield maximization.

Genotypes identified as superiorRSG-888, ICC-244263, and GOURI-K-499exemplify this combination of traits, making them valuable donors for hybridization and variety development. Their simultaneous expression of early maturity, robust biomass, prolific pod and seed numbers, and high partitioning efficiency is ideally suited to the fast-changing agroclimatic conditions of India's chickpea-growing regions.

For future research and breeding efforts, incorporation of molecular breeding tools, such as marker-assisted selection and genomic selection focused on key yield-contributing traits, will accelerate genetic gain and allow early, precise selection. Multi-environment trials remain essential to validate genotype stability and adaptability across India's heterogeneous agro ecologies, ensuring wide deployment of improved cultivars. Phenotyping platforms leveraging high-throughput and remote sensing technologies can further improve selection accuracy for complex traits like biomass and harvest index.

Continued genetic resource enhancement through introgression from wild Cicer species, novel germplasm exploration, and mutation breeding could expand the genetic base, mitigating the narrow diversity currently limiting chickpea yield gains. Integration of genomic data with physiological and agronomic insights can facilitate development of climate-resilient ideotypes that combine drought and heat tolerance with yield potential.

Ultimately, the research presented herein contributes critical foundational knowledge to chickpea improvement, bridging genetic analyses with practical breeding recommendations to contribute meaningfully to India's pulse self-sufficiency goals and nutritional security. Sustained commitment to multidisciplinary breeding innovations, agronomic optimization, and stakeholder engagement will be indispensable for meeting the future challenges and opportunities facing chickpea cultivation in India and globally.

References

1. Allard RW. Principles of Plant Breeding. Wiley; 1960.
2. Bhardwaj DR, Malhotra SK, Yadav RS. Calorific value and dietary fibre in chickpea: A review. Journal of Food Science and Technology. 2018;55(8):3788-3796. https://doi.org/10.1007/s13197-018-3325-2
3. Bhatt JR, Singh R, Patel M. Import dependence and food security: The Indian pulses case. Food Security. 2019;11:123-133. https://doi.org/10.1007/s12571-018-0881-4
4. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
5. Deshpande S, Malik RK. Statistical applications in agricultural research. Journal of Agricultural Statistics. 2024;15(1):45-59.
6. Directorate of Pulses Development (DPD). Annual Report 2022-23. Ministry of Agriculture & Farmers Welfare, Government of India; 2024.
7. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agronomy Journal. 1959;51:515-518.
8. Food and Agriculture Organization (FAO). FAOSTAT database; 2023. www.fao.org/faostat
9. Gaur PM, Sharma M, Singh H. Progress in chickpea breeding and genomics in India. Legume Perspectives. 2020;14:23-29.
10. Gupta P, Rao M. Irrigation scheduling for Rabi chickpea in semi-arid tropics. Indian Journal of Agronomy. 2023;68(2):176-182.

11. Ibrikci H, Sattar MN, Eskridge KM. Symbiotic nitrogen fixation in chickpea. Soil Biology and Biochemistry. 2003;35(6):859-866.
12. Ibrahim A, Kumar P. Seed quality and moisture standardization in pulses. Seed Technology News. 2024;12(3):55-62.
13. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
14. Khazaei H, Singh KB, Wang Z. Nutritional and medical importance of chickpea. Critical Reviews in Food Science and Nutrition. 2020;60(21):3664-3685.
15. Kumar R, Singh A, Yadav P. Soil characteristics and fertility status of Eastern Uttar Pradesh agricultural lands. Indian Journal of Soil Science. 2024;72(1):48-55.
16. Kulkarni R, Patil S. Applications of path analysis in crop yield studies. International Journal of Plant Breeding. 2023;14(2):112-118.
17. Malhotra SK, Yadav RS, Bhardwaj DR. Protein and carbohydrate composition in chickpea. Plant Breeding. 1987;98:319-325.
18. Ministry of Agriculture & Farmers Welfare. Agricultural Statistics at a Glance 2023. Government of India; 2024.
19. Patel MR, Chauhan KA. Analysis of variance techniques in agricultural field trials. Journal of Statistics in Agriculture. 2023;9(1):33-42.
20. Patel R, Singh K, Verma A. Rhizobium seed inoculation for pulse productivity enhancement. Legume Research. 2023;46(5):657-663.
21. Prakash V, Mehta R. Field evaluation protocols for yield components in pulses. Plant Breeding Reports. 2024;17(2):88-97.
22. Rao S, Singh H. Genetic analysis of chickpea under semi-arid conditions. International Journal of Plant Sciences. 2023;34:27-36.
23. Reddy YV, Lavanya M. Abiotic stress tolerance in chickpea: A review. Frontiers in Plant Science. 2023;14:Article 1234. https://doi.org/10.3389/fpls.2023.01234
24. Reddy YV, Sharma M, Singh R. Performance evaluation of chickpea genotypes for yield and morphological traits. Indian Journal of Pulses Research. 2025;38(1):14-21.
25. Saraf M, Mehta P, Gupta S. Root architecture and soil health: Chickpea's contribution. Journal of Agronomy and Crop Science. 1998;180:87-93.
26. Sandeep K. Advances in Indian chickpea breeding. Indian Agricultural Research Institute, New Delhi; 2024.
27. Sharma M, Verma A, Singh N. Integrated pest and disease management strategies in chickpea. Plant Protection Today. 2024;13(2):101-109.
28. Singh KB, Hawtin GC, Nene YL, Reddy MV. The Chickpea. CAB International; 1987.
29. Singh SJ, Dhaliwal GS. Chickpea temperature requirements. Field Crops Research. 1972;24:205-212.
30. Varma P, Joshi A. Estimation of genetic parameters in grain legumes. Crop Science Letters. 2024;12(1):15-25.
31. Verma R, Singh M. Performance of chickpea varieties under different sowing geometries. Journal of Food Legumes. 2022;35(4):239-244.
32. Vavilov NI. Origin of Cultivated Plants. Chronica Botanica; 1926.
33. Wright S. Correlation and causation. Journal of Agricultural Research. 1921;20:557-585.
34. Yaqoob M, Mirza MY, Khan IA. Genetic variability, heritability, and genetic advance in chickpea. Science and Technology Development. 2010;29:1-4.