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Assessment of genetic variability and trait performance in chickpea (*Cicer arietinum* L.) under diverse environmental conditions

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Abstract

The current investigation was carried out at the Seed Breeding Farm, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) to evaluate genetic variability, heritability, and genetic advance for key agronomic traits in chickpea across over a period of two years during the *Rabi* seasons of 2022-23 and 2023-24 and pooled analysis. Analysis of genotypic and phenotypic coefficients of variation (GCV and PCV) revealed considerable variability for several yield-contributing traits. High GCV and PCV were observed for seed yield per plant, hundred seed weight, and biological yield per plant, indicating a strong genetic base for these traits. Moderate variability was recorded for number of effective and total pods per plant, number of seeds per pod, and height at first fruiting node. In contrast, plant height, primary and secondary branches per plant, stem thickness, and harvest index showed moderate to low variability. Notably, genetic variability was most pronounced under very late sowing, highlighting enhanced expression of genetic differences under terminal heat stress. Broad-sense heritability estimates were generally high, especially for hundred seed weight, number of seeds per pod, and total number of pods per plant, all of which consistently exceeded 90%, indicating strong additive genetic control and selection efficiency. Traits such as seed yield per plant, biological yield, plant height, and days to flowering also recorded high heritability. Genetic advance as a percentage of mean (GAM) was highest for hundred seed weight, followed by seed yield and biological yield, demonstrating their potential for substantial improvement through selection. Moderate GAM values were observed for pod-related traits and plant height. These findings provide a strong foundation for targeted genetic improvement and climate-resilient chickpea breeding strategies.

Keywords: Chickpea, genetic variability, genetic advance as a percentage of mean, heritability, GCV, PCV

Introduction

Chickpea (*Cicer arietinum* L.), a vital member of the *Fabaceae* family, is among the earliest domesticated food legumes. Its origin is traced to the Fertile Crescent, particularly the region spanning southeastern Turkey and adjoining areas of Syria, where three closely related wild annual species *Cicer reticulatum*, *C. echinospermum*, and *C. bijugum* naturally occur (Maesen *et al.*, 2017) [31]. Of these, *C. reticulatum* is recognized as the closest progenitor of the cultivated chickpea, and its domestication is estimated to have occurred around 7000 BC (Sajja *et al.*, 2017; Pearman, 2005) [25, 19].

Chickpea germplasm is broadly classified into two distinct seed types: Kabuli, characterized by large, cream-colored seeds and prevalent in the Mediterranean and Eurasian regions; and Desi, distinguished by smaller, angular, and darker seeds and commonly grown in the Indian subcontinent and parts of Asia. These seed types are genetically divergent and are often classified into four geographic races: Mediterranean, Eurasian, Oriental, and Asian. Advances in molecular biology have further enhanced our understanding of chickpea's genetic landscape, especially following the sequencing of the chickpea genome, including both cultivated and wild relatives (Varshney *et al.*, 2013) [32], thereby accelerating molecular breeding and trait discovery efforts.

From a nutritional perspective, chickpea is a protein-rich, energy-dense legume that serves as a critical dietary component in many semi-arid and developing regions.

It is valued not only for its high protein content comprising 18 amino acids, including eight essential ones but also for its balanced composition of carbohydrates, dietary fibers, unsaturated fatty acids, vitamins, and bioactive compounds such as isoflavones (Wang *et al.*, 2021) [35]. Starch serves as the main carbohydrate reserve, followed by oligosaccharides and simple sugars such as glucose and sucrose. Despite its relatively low lipid content, chickpea contains significant quantities of nutritionally important fatty acids like linoleic and oleic acids. Moreover, it is an abundant source of macro-and micronutrients including potassium, calcium, magnesium, sodium, iron, zinc, and copper, all of which contribute to its role in mitigating global mineral deficiencies and improving food and nutritional security.

Globally, chickpea was cultivated on approximately 14.8 million hectares in 2022-23, yielding 18.09 million metric tons with an average productivity of 1,222 kg/ha (Directorate of Pulses Development, 2024). India stands as the world's leading chickpea producer, accounting for more than 50% of global output. In 2023-24, India contributed 9.46 million metric tons harvested from 11.58 million hectares, with an average yield of 1,224 kg/ha. Within India, the state of Madhya Pradesh remains a major production hub, producing 3.18 million metric tons from 2.11 million hectares at a higher-than-average yield of 1,510 kg/ha (Project Coordinator's Report, AICRP on Rabi Pulses 2023-24). However, to ensure future self-sufficiency and meet the projected national demand by 2050, India must sustainably enhance chickpea productivity to 1,500-1,700 kg/ha over an estimated area of 10.5 million hectares (Jha *et al.*, 2022) [7].

The success of any breeding program largely depends on the presence and effective utilization of genetic variability in breeding populations. Genetic variability forms the cornerstone for selection, enabling the identification of superior genotypes and the development of high-yielding, climate-resilient cultivars. The nature and magnitude of variability influence the potential genetic gain achievable through selection. Moreover, understanding the inheritance of yield-related traits and their genetic architecture including additive, dominance, and epistatic effects is essential for optimizing breeding strategies (Anand *et al.*, 2024) [1].

It is also critical to partition phenotypic variance into its genetic and environmental components. Heritability estimates provide insights into the degree to which trait expression is governed by genetic factors versus environmental influences. When interpreted alongside genetic advance, heritability estimates become even more informative, as they offer predictive value regarding the potential for trait improvement across generations (Naz *et al.*, 2021; Parida *et al.*, 2018) [16, 18].

In this context, the present study aims to assess the extent of genetic variability, heritability, and genetic advance for yield and its associated traits in chickpea, thereby providing a foundational basis for strategic selection and crop improvement initiatives.

Materials and Methods

The present investigation was carried out at the Seed Breeding Farm, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) over a period of two years during the Rabi seasons of 2022-23 and 2023-24.

The research included 30 advanced breeding lines of chickpea sourced from AICRP on chickpea at JNKVV, Jabalpur, and ICRISAT, Patancheru, Hyderabad (as detailed in Table 1). The experimental design utilized was a Randomized Complete Block Design (RCBD), with each plot consisting of four rows, each measuring four meters in length. The distance between the rows and plants was set at 30 cm × 10 cm. To facilitate successful crop development the recommended agronomic and plant protection practices were followed. Data were recorded on fourteen quantitative traits to assess the genetic potential of the genotypes.

The characters studied included days to 50% flowering, days to maturity, plant height, height at first fruiting node, stem thickness, number of primary and secondary branches per plant, total and effective number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, and seed yield per plant.

The collected data were statistically analyzed to estimate genotypic and phenotypic coefficients of variation (GCV and PCV) following the method of Burton (1952) [3], while phenotypic and genotypic variances were estimated as per Burton and De Vane (1953) [4]. Broad-sense heritability (H^2) was calculated using the formula suggested by Hanson *et al.* (1956) [5], and the expected genetic advance (GA) was computed as per Johnson *et al.* (1955) [8].

Results and Discussion

Analysis of variance

Genetic variability estimates were assessed for fourteen traits across thirty chickpea genotypes evaluated under six different environmental conditions, including the pooled environment. The ANOVA revealed that the mean squares attributable to genotypic effects were highly significant within individual environments and across the pooled analysis for all the traits studied.

Coefficient of Variation (%)

To elucidate the magnitude and nature of variability among advanced chickpea breeding lines, genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated across three distinct environments (EI, EII, and EIII), as well as for the pooled dataset. Across all traits, PCV values consistently exceeded corresponding GCV values, underscoring the role of environmental factors in shaping phenotypic expression. However, the relatively narrow differential between PCV and GCV for most traits indicates that the observed variability is largely of genetic origin, with minimal environmental interference. Such a trend is suggestive of additive gene action, thereby favoring the effectiveness of early-generation phenotypic selection.

High GCV and PCV estimates were recorded for traits such as hundred seed weight, seed yield per plant, biological yield per plant, and number of effective pods per plant. These findings reflect substantial genetic diversity and reinforce the selection potential of these traits across diverse environments. Notably, hundred seed weight demonstrated consistently high variation across all conditions, implying a strong genetic basis and relative environmental stability. This trait thus emerges as a robust and reliable selection target for enhancing seed size and market-preferred attributes, corroborating earlier reports by Kumar *et al.* (2021) [11], Ningwal *et al.* (2023) [17], and Moulya *et al.* (2024) [13].

Seed yield per plant showed particularly high variability under very late sown conditions, reflecting both its genetic responsiveness and environmental sensitivity. This dual nature suggests its relevance as a selection index in breeding programs targeting stress-prone or marginal environments, consistent with observations by Tsehaye *et al.* (2020) [30] and Raju *et al.* (2017) [23]. Likewise, biological yield per plant and number of total pods per plant exhibited moderate to high variability, highlighting their pivotal role in contributing to yield potential. These patterns align with findings from Pravalika *et al.* (2024) [22], Verma *et al.* (2023) [34], and Velpula *et al.* (2022) [33], emphasizing the utility of pod-related traits in chickpea improvement.

Moderate genetic variability was also observed for architectural traits such as plant height, number of primary and secondary branches per plant, and height at first fruiting node. The narrow PCV-GCV gap in these traits suggests a predominant influence of additive gene effects, rendering them amenable to improvement through direct selection. This is consistent with reports by Nagar and Karnawat (2023) [15], Shanmugam and Kalaimagal (2019) [26], and Prathyusha *et al.* (2024) [21].

Traits like number of seeds per pod, harvest index, stem thickness, and total number of pods per plant exhibited moderate variability across environments, indicating their potential for genetic gain through selection. In contrast, phenological traits such as days to 50% flowering and days to maturity displayed consistently low GCV and PCV values across all environments, pointing to their genetic stability and limited variability. These observations, in line with those of Hussain *et al.* (2017) [6], Kumar *et al.* (2018) [10], and Arora *et al.* (2018) [2], suggest their importance in maintaining phenological synchrony across variable agro-ecological zones, despite their restricted potential for direct improvement through selection.

Heritability (%) and Genetic Advance as percentage of mean (%)

The combined estimation of heritability in the broad sense (H^2) and genetic advance as a percentage of mean (GAM) offers critical insight into the proportion of transmissible genetic variance and the potential effectiveness of selection for complex traits. In the present study, high heritability estimates were observed for the majority of yield-related traits across all three environments (EI, EII, and EIII) as well as under pooled analysis (Table 1), highlighting the predominance of additive gene action and suggesting limited environmental interference in trait expression.

Among the traits, hundred seed weight, number of seeds per pod, and biological yield per plant consistently exhibited high heritability (>90%) across all environments, often exceeding 97% for hundred seed weight. These traits were also associated with high GAM values (>40%), underscoring their strong genetic control and additive variance. Such high estimates reflect the efficacy of direct phenotypic selection in early generations. The results are consistent with earlier findings by Munde *et al.* (2018) [14], Pithiya *et al.* (2019) [20], and Maring *et al.* (2024) [12], who similarly reported high heritability coupled with substantial genetic advance for these traits in chickpea under diverse environments.

Seed yield per plant, biological yield, number of effective pods per plant, and total number of pods per plant also displayed high heritability (>85%) and moderate to high GAM (25-50%), particularly in EII and EIII. This pattern indicates a substantial additive genetic component governing these traits, even under stress-prone environments such as late sowing (EIII). The stability of seed yield under terminal heat stress suggests the presence of genetically resilient genotypes with adaptive potential. These observations are in line with reports by Solanki *et al.* (2019) [27], Sriraj and Gurjar (2022) [28], and Ningwal *et al.* (2023) [17], who emphasized the role of additive variance in maintaining yield performance across varied agro-climatic zones.

Moderate heritability (50-70%) along with moderate GAM (15-30%) was noted for plant height, height at first fruiting node, and number of seeds per pod, suggesting these traits are under partial genetic control with modest environmental modulation. Although selection may be moderately effective, genetic gains for these traits will be comparatively lower than those with high H^2 and GAM. Similar conclusions were drawn by Srivastava *et al.* (2021) [29] who reported moderate heritability for these morphological and reproductive traits in chickpea.

In contrast, traits such as number of secondary branches per plant, stem thickness, harvest index, and days to maturity frequently exhibited low to moderate heritability (<50%) and lower GAM values, particularly under pooled conditions. This suggests a substantial influence of non-additive gene action or environmental variability, thus limiting their effectiveness for early-generation selection. These results are consistent with the findings of Rani *et al.* (2022) [24], and Kakaei and Farshadfar (2024) [9], who also reported limited genetic gains for phenological and physiological traits under heterogeneous environments.

Overall, traits such as hundred seed weight, seed yield per plant, biological yield, and number of pods per plant have emerged as highly promising for genetic improvement. Their consistently high heritability and substantial genetic advance across all environments reinforce the predominance of additive gene effects and suitability for selection-driven enhancement. Importantly, the robustness of these traits under late sowing and terminal heat stress (EIII) positions them as valuable targets for breeding climate-resilient genotypes. These findings align with the conclusions of Nagar and Karnawat (2023) [15], and Solanki *et al.* (2019) [27], underscoring the utility of such traits in enhancing both productivity and environmental adaptability in chickpea breeding programs.

Table 1: Analysis of Variance of yield and yield contributing traits

Environments	**Source of Variation**	**DF**	**Mean Sums of Squares**													
			DF50%	**DM**	**PH**	**HFFN**	**ST**	**NPBPP**	**NSBPP**	**TNPPP**	**NEPPP**	**NSPP**	**HSW**	**BY**	**HI**	**SYPP**
Timely Sown (Pooled E1 & E4)	Replicate	2	2.067	2.239	8.240	5.931	0.207*	0.082	7.0835*	9.405	6.024	0.001	0.476	7.370	0.411	2.144
	Environments	1	0.939	2.006	6.829	3.372***	0.008	0.000	0.020	0.350	1.713	0.000	0.863***	0.075	0.219	0.087
	Interactions	2	0.822	0.439	3.445	0.065	0.012	0.057	0.566	5.031	3.857	0.000	0.065	3.292	3.158	2.590
	Total	5	1.343	1.472’*	6.040	3.073	0.090	0.056	3.064	5.844	4.295	0.000	0.389	4.280	1.471	1.911
	Treatments	29	85.923***	34.605***	345.350***	78.215***	0.779***	0.943***	14.905***	594.822***	469.047***	0.226***	180.630***	359.385***	156.270***	89.526***
	Error	145	0.941	0.918	6.072	3.680	0.044	0.066	2.195	6.185	5.981	0.000	0.336	5.414	2.912	1.994
Late Sown (Pooled E2 & E5)	Replicate	2	1.239	1.172	2.864	2.352	0.027	0.004	0.001	10.358	3.085	0.001	0.102	3.362	0.047	0.392
	Environments	1	0.139	0.672	0.275	0.003	0.001	0.003	0.000	0.138	2.106	0.000	0.000	0.847	4.041	0.170
	Interactions	2	0.606	0.739	1.584	0.240	0.049	0.016	0.000	5.621	2.033	0.000	0.012	0.891	6.017	0.889
	Total	5	0.766	0.899	1.834	1.037	0.030	0.008	0.000	6.419	2.469	0.000	0.046	1.871	3.234	0.546
	Treatments	29	78.966***	39.338***	330.992***	82.009***	0.510***	0.921***	0.160***	373.244***	345.463***	0.1607***	164.919***	267.502***	150.024***	61.906***
	Error	145	1.161	1.349	6.625	3.149	0.050	0.065	0.001	6.865	4.665	0.001	0.325	3.082	1.989	1.092
Very Late Sown (Pooled E3 & E6)	Replicate	2	2.022	1.356	11.917	2.563	0.07475*	0.142	0.681	9.472	3.539	0.000	0.325	2.721	4.054	0.715
	Environments	1	1.089	0.800***	0.005	0.001	0.001	0.011	0.006	0.727	1.808	0.001***	0.273**	0.057	1.333	0.102
	Interactions	2	0.289	0.067	0.551	0.135	0.002	0.008	0.208	2.908	2.206	0.000	0.037	0.084	0.478	0.140
	Total	5	1.142	0.729	4.988	1.079	0.031	0.063	0.357	5.097	2.660	0.000	0.199	1.134	2.079	0.363
	Treatments	29	83.504***	67.422***	132.820***	36.349***	0.239***	0.840***	5.178***	193.025***	192.731***	0.086***	147.185***	102.645***	141.314***	26.404***
	Error	145	0.848	0.851	5.104	2.634	0.019	0.053	0.411	3.982	2.374	0.001	0.198	2.213	3.863	0.505
Overall Pooled Analysis	Replicate	2	5.172	8.893	21.226	9.084	0.249**	0.170	5.231*	21.946	11.004	0.002	0.747	11.904	2.572	2.853
	Environments	5	2025.40***	64918.8***	3880.4***	457.92***	13.048***	9.160***	862.843***	18608.8***	14336.8***	2.693***	79.291***	11337.7***	1374.824**	3211.91***
	Interactions	10	0.374	3.126	1.475	0.440	0.024	0.028	0.919	4.170	1.948	0.000	0.054	1.163	2.319	0.803
	Total	17	596.537***	64930.9***	1144.66***	136.012***	3.88166***	2.7305***	254.933***	5478.22***	4219.15***	0.792***	23.4406***	3336.72***	406.026***	945.490***
	Treatments	29	212.804***	3128.25***	670.018***	173.686***	1.21121***	2.3586***	18.0270***	820.847***	768.416***	0.371***	483.318***	540.498***	243.59***	134.128***
	Error	493	2.961	1423.541	13.421	4.130	0.052	0.074	1.462	25.024	17.878	0.007	0.791	14.270	14.578	3.627

Where, DTF: days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number of primary branches per plant, NSBPP: Number of secondary branches per plant, TNPPP: Total number of pods per plant, HFFN (cm): Height of first fruiting node, ST (mm): Stem thickness, NEPPP: Number of effective pods per plant, NSPP: Number of seeds per pod, HSW (g): 100 Seed weight, BY (g): Biological yield per plant, HI (%): Harvest index, SYPP (g): Seed yield per plant.

*** Significant at 0.1% level, **Significant at 1%, *Significant at 5%

Table 2: Traits with high heritability categorized by magnitude of genetic advance across environments

Condition	**EI**	**EII**	**EIII**	**Pooled Analysis**
High Heritability and high GA as% of mean	HSW	HSW, SYPP, BY	HSW, SYPP, BY, NEPPP	HSW
High Heritability and moderate GA as% of mean	PH, TNPPP, NEPPP, NSPP, BY, SYPP	PH, HFFN, TNPPP, NEPPP, NSPP	TNPPP	BY
High Heritability and low GA as% of mean	DTF, DM, PH, HFFN, ST, HI,	DTF, DM, HI,	DTF, DM, PH, NPBPP, NSPP, HI	DTF, PH, NEPP, NSPP

Where, DTF: days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NSBPP: Number of secondary branches per plant, TNPPP: Total number of pods per plant, HSW (g): NEPPP: Number of effective pods per plant, 100 Seed weight, BY (g): Biological yield per plant, HI (%): Harvest index, SYPP (g): Seed yield per plant.

Table 3: Parameters of Genetic Variability for different traits

Character	Environment	Grand mean	Range		Coefficient of variation (%)		h2 (bs) (%)	Genetic advance as percentage of mean at 5%
			Mini	Max	GCV	PCV		
DTF	EI	57.98	55.30	70.70	6.49	6.70	93.80	12.95
	EII	52.81	41.83	61.50	6.82	7.12	91.80	13.46
	EIII	47.38	37.83	55.00	7.83	8.07	94.20	15.66
	Pooled	52.72	42.17	61.00	6.48	7.25	79.70	11.91
DM	EI	110.07	104.50	118.00	2.15	2.32	85.90	4.11
	EII	95.39	88.50	101.50	2.64	2.91	82.40	4.93
	EIII	83.26	77.00	90.00	4.00	4.15	92.90	7.94
	Pooled	96.24	90.00	103.17	2.51	3.07	66.90	4.23
PH	EI	56.38	43.70	72.64	13.34	14.03	90.30	26.11
	EII	51.47	39.19	66.43	14.29	15.14	89.10	27.78
	EIII	41.95	31.50	48.56	11.00	12.25	80.70	20.35
	Pooled	49.93	39.44	60.96	12.10	14.15	73.10	21.30
HFFN	EI	26.71	17.69	33.77	13.19	15.02	77.10	23.87
	EII	24.48	16.56	33.47	14.81	16.49	80.70	27.40
	EIII	21.68	16.88	26.14	10.93	13.25	68.10	18.58
	Pooled	24.29	17.04	29.72	12.63	15.15	69.50	21.70
ST	EI	3.29	2.62	4.05	10.65	12.43	73.40	18.79
	EII	2.81	2.23	3.48	9.88	12.68	60.80	15.87
	EIII	2.44	1.90	2.78	7.85	9.68	65.80	13.13
	Pooled	2.85	2.35	3.33	8.92	12.00	55.30	13.67
NPBPP	EI	3.56	2.38	4.66	10.76	12.96	68.90	18.38
	EII	3.13	2.14	4.32	12.09	14.57	68.80	20.65
	EIII	2.85	2.02	4.03	12.73	15.08	71.20	22.13
	Pooled	3.18	2.18	4.34	11.22	14.13	63.00	18.34
NSBPP	EI	13.93	10.76	17.56	10.45	14.92	49.10	15.09
	EII	9.85	8.41	11.83	9.57	12.95	54.70	14.58
	EIII	7.04	5.12	8.78	12.66	15.60	65.90	21.17
	Pooled	10.27	8.71	12.57	9.34	15.02	38.60	11.96
TNPPP	EI	64.53	43.32	87.86	15.35	15.83	94.10	30.67
	EII	53.64	41.37	70.95	14.57	15.37	89.90	28.46
	EIII	32.88	25.43	49.07	17.07	18.12	88.80	33.13
	Pooled	50.35	38.33	65.24	13.21	16.53	63.90	21.74
NEPPP	EI	58.06	40.70	75.73	15.13	15.71	92.80	30.03
	EII	48.58	38.76	66.66	15.52	16.14	92.40	30.73
	EIII	30.30	22.75	45.47	18.59	19.27	93.00	36.94
	Pooled	45.65	35.56	61.50	14.15	16.91	70.00	24.38
NSPP	EI	1.38	1.04	1.92	14.09	14.17	98.90	28.85
	EII	1.15	0.90	1.53	14.16	14.34	97.60	28.83
	EIII	1.00	0.84	1.34	12.01	12.26	96.00	24.24
	Pooled	1.18	0.96	1.49	12.11	13.93	75.70	21.71
HSW	EI	26.97	17.68	38.54	20.32	20.44	98.90	41.64
	EII	25.96	17.04	37.60	20.18	20.28	99.00	41.36
	EIII	24.88	17.02	36.66	19.90	19.98	99.20	40.82
	Pooled	25.94	17.25	37.60	19.96	20.25	97.10	40.53
BY	EI	43.83	31.13	58.18	17.52	18.31	91.60	34.55
	EII	36.17	24.56	47.45	18.35	18.98	93.50	36.55
	EIII	19.30	13.78	28.61	21.20	22.55	88.30	41.04
	Pooled	33.10	23.76	42.81	16.34	19.93	67.20	27.58
HI	EI	49.13	40.65	57.70	10.29	10.86	89.80	20.09
	EII	41.24	32.59	51.57	12.05	12.52	92.50	23.87
	EIII	41.94	31.18	52.99	11.41	12.34	85.60	21.75
	Pooled	44.10	38.68	50.00	8.09	11.85	46.60	11.37
SYPP	EI	21.46	13.20	28.68	17.80	18.97	88.00	34.39
	EII	14.91	8.69	21.08	21.36	22.48	90.30	41.80
	EIII	8.11	5.38	12.76	25.63	27.09	89.50	49.97
	Pooled	14.83	9.49	19.35	18.16	22.25	66.70	30.55

Where, DTF: days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number of primary branches per plant, NSBPP: Number of secondary branches per plant, TNPPP: Total number of pods per plant, HFFN (cm): Height of first fruiting node, ST (mm): Stem thickness, NEPPP: Number of effective pods per plant, NSPP: Number of seeds per pod, HSW (g): 100 Seed weight, BY (g): Biological yield per plant, HI (%): Harvest index, SYPP (g): Seed yield per plant

Conclusion

Analysis of GCV and PCV across environments revealed substantial genetic variability, particularly for seed yield per plant, hundred seed weight, and biological yield. Among these, hundred seed weight consistently showed high heritability coupled with high genetic advance, indicating strong additive gene action and minimal environmental influence. These findings suggest that hundred seed weight is a reliable selection criterion for genetic improvement, while overall variability highlights the potential for effective selection in breeding programs aimed at enhancing chickpea productivity across diverse environments.

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