

Original Research Article

Evaluation of Early Maturing Hybrids of Pearl millet in Arid Environment of Western Rajasthan

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Abstract

Pearl millet (*Pennisetum glaucum* L.) is a vital cereal in arid and semi-arid regions due to its tolerance to high temperature, moisture stress and poor soil fertility as well as its nutritional and fodder value. A study was conducted at ARS, Bikaner under AICRP on Pearl Millet to evaluate 23 pearl millet entries including five standard checks in the harsh agro-climatic conditions of western Rajasthan to identify early-maturing and high-yielding genotypes. The experiment, laid out in a randomized block design with three replications, recorded ten quantitative traits along with disease incidence. Significant variation was observed among genotypes for all traits indicating substantial genetic variability. High phenotypic and genotypic coefficients of variation were recorded for grain yield while moderate values were observed for dry fodder yield and panicle diameter. Most traits exhibited high heritability with grain yield and dry fodder yield showing both high heritability and genetic advance, suggesting predominance of additive gene action. Plant height, panicle length, panicle diameter and 1000-seed weight showed high heritability with moderate genetic advance. No incidence of major diseases was recorded, indicating overall genetic stability. The findings reveal considerable potential for selection and improvement of key traits and demonstrate the effectiveness of phenotypic selection in developing superior pearl millet genotypes adapted to arid environments.

Keywords: Pearl millet, genetic variability, heritability, genetic advance, grain yield, dry fodder yield, arid regions, phenotypic selection

Introduction

Pearl millet stands as a vital coarse cereal in the arid and semi-arid tropics. It is valued not only for its resilience under conditions of high temperature, low rainfall and poor soil fertility but also for its nutritional profile that is rich in energy, protein, dietary fiber and minerals such as iron and zinc (Gupta *et al.*, 2015; Hassan *et al.*, 2021; Karthik *et al.*, 2024). Furthermore, its versatility makes it suitable for both food and fodder. Within India, pearl millet holds a prominent position particularly in Rajasthan, Gujarat, Haryana, Maharashtra and parts of Uttar Pradesh (Satyavathi *et al.*, 2021). However, Western Rajasthan faces extreme agricultural constraints including variable rainfall, high evapo-transpiration, sandy soils and frequent heat and moisture stress (Singh, 2025). Despite these challenges, it remains a key crop in the region which is essential to local farming systems. Consequently, limited irrigation and poor soil health result in productivity levels that fall well below state and national averages (Singh, 2025; Yadav and Rai, 2013). Zone Ic (Bikaner, Jaisalmer and Churu districts) reported 4.23 lakh hectares of area, 2.44 lakh tonnes of production and a productivity of 537 kg/ha; in contrast, Rajasthan as a whole reported 3.52 lakh hectares of area, 53.73 lakh tonnes of production and 1234 kg/ha productivity during the same period (Anonymous, 2025). This stark productivity gap underscores the necessity for location-specific genotype selection (Yadav and Rai, 2013), as agro-climatic gradients reveal that western districts consistently lag behind the rest of the state.

All India Coordinated Research Project on Pearl Millet focuses on identifying high-yielding, stable and adapted genotypes for various agro-climatic zones to address these issues (Satyavathi *et al.*, 2021). Zone A1, representing the rainfed regions of Rajasthan, Haryana and Gujarat, exhibits notably low production and productivity. Beyond its grain value, the crop provides essential fodder for livestock and supports dietary diversity among resource-poor populations (Karthik *et al.*, 2024). Economically, it serves as a critical livelihood source for smallholders (Naorem *et al.*, 2023). The present investigation was conducted to identify promising early pearl millet entries suited to the harsh and arid environment of Zone A1 by comparing them with standard checks. Such evaluation is vital because genotypes that thrive in one environment may falter under the extreme moisture and heat stress characteristic of western Rajasthan. Therefore, testing in the target environment is essential to select genotypes with superior earliness, stability and yield.

Materials and Methods

The experimental material comprising 23 pearl millet entries (IHT 101 to IHT 123), including five standard checks, was evaluated at the Agricultural Research Station (ARS), Swami Keshwanand Rajasthan Agricultural University (SKRAU), Bikaner, Rajasthan. The trial was conducted in a Randomized Block Design (RBD) with three replications. Each entry was grown in a net plot measuring 4.0 m × 1.80 m, maintaining a crop geometry of 60 cm × 15 cm. The experimental site is characterized by sandy soil with an alkaline reaction (pH 8.0). The available nutrient status of the soil was very low in nitrogen (80 kg ha⁻¹), low in phosphorus (18 kg ha⁻¹) and medium in potassium (168 kg ha⁻¹). Recommended agronomic practices for the region were followed throughout the crop season. Basal doses of nitrogen and phosphorus were applied at sowing while the remaining nitrogen was supplied through top dressing at the appropriate crop growth stage.

Observations were recorded on ten quantitative characters, namely: days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), panicle diameter (cm), 1000-seed weight (g), population at harvest (number per net plot), seed set under bagging (%), grain yield (kg per net plot) and dry fodder yield (kg per net plot). Grain and fodder yields recorded on a net plot basis were converted to hectare yield using a conversion factor of 1388.89. In addition, the incidence of major pearl millet diseases, *viz.*, downy mildew, smut and ergot, was recorded under natural field conditions and expressed as percentage infection. The identity details of all entries are presented in Table 1. Genetic variability parameters were computed using standard biometrical procedures to evaluate the magnitude of variation available for selection and genetic improvement in pearl millet.

Statistical Analysis

The recorded data were subjected to statistical analysis to estimate mean performance and assess the extent of genetic variability among the hybrid entries. OPSTAT statistical software was used to analyze the recorded data at 1% and 5% level of significance.

1. Phenotype and genotype variability

The variability among genotypes was estimated using range, mean, standard error, phenotypic variance, genotypic variance and coefficients of variation. The variance components were computed following standard procedures and used to estimate phenotypic and genotypic coefficients of variation, heritability and genetic advance.

Genotypic variance (σ_g^2) was calculated as:

Table 1. Details of Pearl Millet Hybrids Tested under IHT (E) Trial of AICRP on Pearl Millet at ARS, Bikaner

Test Code	Project No.	Identity	Pedigree	Origin
IHT 101	MH 2887	Pusa Hybrid Bajra 2501	411A × PPMI 1327	ICAR-IARI, New Delhi
IHT 102	MH 2888	DHBH-24305	DHLB-14A × DHLBI-1035	ICAR-ICAR-AICRP-PM, Dhule
IHT 103	Check	PB1756	PSP91 × PP107	Crystal Crop Protection Ltd., Hyderabad
IHT 104	MH 2889	DHBH-24308	DHLB-36A × DHLBI-1035	ICAR-ICAR-AICRP-PM, Dhule
IHT 105	MH 2890	RHB 284	ICMA 02333 × RIB494	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 106	MH 2891	RHB 285	ICMA 04888 × RIB20K86	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 107	MH 2892	RHB 287	ICMA 99444 × RIB494	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 108	MH 2893	RHB 288	ICMA 93333 × RIB 3135-18	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 109	MH 2894	RHB 290	ICMA 98222 × RIB 15177	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 110	Check	RHB 223	ICMA 96666 × RIB 3135-18	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 111	MH 2895	RHB 292	ICMA 04999 × RIB15S076	ICAR-AICRP-PM, SKNAU, Jaipur
IHT 112	MH 2896	BHB 2501	ICMA 88004 × BIB-62	ICAR-AICRP-PM, SKRAU, Bikaner
IHT 113	MH 2897	BHB 2502	ICMA 98222 × BIB 23-1	ICAR-AICRP-PM, SKRAU, Bikaner
IHT 114	MH 2898	MPMH 52	ICMA 95222 × MIR 519-1	ICAR-AICRP-PM, PC Unit, Jodhpur
IHT 115	MH 2899	MPMH 53	ICMA 04999 × MIR 519-1	ICAR-AICRP-PM, PC Unit, Jodhpur
IHT 116	Check	HBB67 (Imp.)	ICMA 843-22 × H 77/833-2-202	ICAR-AICRP-PM, CCSHAU, Hisar
IHT 117	MH 2900	PA 9070	PSP 140 × PP 125	Crystal Crop Protection Ltd.
IHT 118	MH 2901	CZH 278	ICMA 04999 × CZI2022/7	ICAR-CAZRI, Jodhpur
IHT 119	MH 2902	CZH279	ICMA 843-22 × CZI2023/4	ICAR-CAZRI, Jodhpur
IHT 120	Check	MPMH35	ICMA1 94555 × MIR 1252	ICAR-AICRP-PM, PC Unit, Jodhpur
IHT 121	MH 2903	CZH 280	ICMA 083333 × CZI2023/4	ICAR-CAZRI, Jodhpur
IHT 122	Check	86M94	9PHGF39A × M444R	Pioneer Overseas Corp., Hyderabad
IHT 123	MH 2904	RVBH-2253	ICMA 97111 × 24110	ICAR-AICRP-PM, RVSKVV, Gwalior

$$\sigma_g^2 = (\text{MST} - \text{MSE})/r$$

where, MST = mean square due to treatments (genotypes), MSE = error mean square, and r = number of replications.

Phenotypic variance (σ_p^2) was estimated as:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

where, σ_e^2 = environmental (error) variance.

According to Singh and Chaudhary (1999), the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated using the following formulas:

$$\text{PCV} (\%) = (\sqrt{\sigma_p^2}/\bar{X}) \times 100$$

$$\text{GCV} (\%) = (\sqrt{\sigma_g^2}/\bar{X}) \times 100$$

where, $\bar{X}$ is the grand mean of the trait.

The values of GCV and PCV were classified as low (<10%), moderate (10–20%), and high (>20%) following the criteria suggested by Deshmukh *et al.* (1986).

2. Heritability, Genetic Advance and Genetic Advance as Percent of Mean

Heritability in the broad sense (h^2) was estimated for each trait according to Allard (1960) as:

$$h^2 (\%) = (\sigma_g^2/\sigma_p^2) \times 100$$

The expected genetic advance (GA) under selection was calculated following Johnson *et al.* (1955) assuming a selection intensity of 5%:

$$\text{GA} = k \times h^2 \times \sqrt{\sigma_p^2}$$

where, k = standardized selection differential (2.06 at 5% selection intensity), h^2 = heritability in broad sense, and $\sqrt{\sigma_p^2}$ = phenotypic standard deviation.

Genetic advance as percent of mean (GAM) was computed as:

$$\text{GAM} (\%) = (\text{GA}/\bar{X}) \times 100$$

where, GA = genetic advance and $\bar{X}$ = grand mean of the trait.

Results and Discussion

The ANOVA results are presented in Table 2. The mean sum of squares due to treatments are significant for all the characters studied, which revealed significant differences among the genotypes for all the traits studied. Significant genetic variability in breeding material is a prerequisite as it not only provides the basis for selection but also offers valuable information for identifying

diverse parents for use in hybridization programmes (Gupta *et al.*, 2015; Singh *et al.*, 2016; Basavaraj *et al.*, 2017). The mean performance is given in Table 3 for each character studied.

Per se performance

All the traits studied exhibited a wide range of variation, indicating substantial genetic diversity and ample scope for their improvement through selection.

1. Days to 50% flowering: The mean days to 50% flowering was 45.12 days with a range of 42.33 to 50.00 days. The earliest flowering genotype was HHB67 (Imp.) (check) (42.33 days) followed by CZH 278 (43.00 days) whereas RHB 223 (check) was the latest flowering genotype (50.00 days). Based on the critical difference (CD = 1.77 days), ten entries are at par with the earliest flowering entry.

2. Days to maturity: The overall mean for days to maturity was 74.99 days and varied from 72.00 to 79.00 days. HHB67 (Imp.) (check) matured earliest (72.00 days) whereas RHB 223 (check) matured latest (79.00 days). The difference between the earliest and latest maturing genotypes exceeded the CD value (2.18 days), indicating significant variation for maturity duration.

3. Plant height: Plant height ranged from 116.00 cm to 178.33 cm with a mean of 158.87 cm. The tallest genotype was RHB 292 (178.33 cm) followed by MPMH 52 (177.67 cm), while RHB 223 (check) was the shortest genotype (116.00 cm). Based on the critical difference (CD = 13.15 cm), six entries are at par with the tallest entry.

4. Panicle length: The mean panicle length was 23.48 cm, ranging from 20.67 to 26.67 cm. The longest panicles were recorded in MPMH 52 (26.67 cm) whereas DHBH-24305 (IHT 102) exhibited the shortest panicles (20.67 cm). Based on the critical difference (CD = 2.30 cm), seven entries are at par with the longest panicle.

5. Panicle diameter: Panicle diameter varied from 2.10 to 3.07 cm with a mean of 2.55 cm. The maximum panicle diameter was observed in BHB 2501 (3.07 cm), followed by PA 9070 (3.03 cm), while RHB 287 recorded the minimum diameter (2.10 cm). Based on the critical difference (CD = 0.32 cm), three entries are at par with the maximum panicle diameter.

6. 1000-seed weight: The average 1000-seed weight was 9.78 g and ranged from 7.87 to 11.33 g. The highest test weight was recorded in PB1756 (check) (11.33 g), followed by Pusa Hybrid Bajra 2501 (IHT 101) (11.03 g), whereas MPMH 52 and CZH 280 exhibited the lowest value (7.87 g). Based on the critical difference (CD = 1.01 g), six entries are at par with the highest test weight.

7. Population at harvest: The mean plant population at harvest was 72.38 plants per net plot, ranging from 67.00 to 77.33 plants. The highest population was observed in RHB 223 (IHT 110), BHB 2501 (IHT 112), and RHB 287 (IHT 107) (77.33 plants), while Pusa Hybrid Bajra 2501 (IHT 101) recorded the lowest population (67.00 plants).

8. Seed set under bagging: The mean seed set under bagging was 50.94%, with values ranging from 43.33% to 58.33%. The highest seed set was observed in DHBH-24305 (IHT 102) and CZH279 (IHT 119) (58.33%), while PB1756 (IHT 103) recorded the lowest seed set (43.33%).

9. Grain yield: Grain yield per net plot averaged 0.55 kg and ranged from 0.35 to 0.83 kg. The highest grain yield was recorded by Pusa Hybrid Bajra 2501 (0.83 kg), followed by BHB 2501, MPMH 53 and 86M94 (check) (0.75 kg each) and RHB 292 (0.72 kg). Based on the critical difference (CD = 0.15 kg plot⁻¹), the grain yields of BHB 2501, MPMH 53, 86M94 and RHB 292 were statistically at par with the highest yielding genotype. The lowest grain yield was observed in RHB 223 (check) (0.35 kg).

10. Dry fodder yield: Dry fodder yield ranged from 2.12 to 3.57 kg per net plot, with a mean of 2.54 kg. The highest dry fodder yield was recorded in MPMH 52 (3.57 kg), followed by RHB 223 (check) and MPMH 53 (3.27 kg each). RHB 223 and MPMH 53 were statistically at par with MPMH 52. The lowest fodder yield was observed in Pusa Hybrid Bajra 2501 (2.12 kg).

No incidence of downy mildew, smut or ergot was observed in any of the tested entries throughout the crop growth period under natural field conditions. Thus, all genotypes exhibited freedom from these major diseases during the course of experimentation.

Genetic variability parameters

Table 4 depicts the estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance (GA) and genetic advance as per cent of mean (GAM) for different characters studied in pearl millet.

Estimates of phenotypic coefficients of variation were higher than genotypic coefficient of variation, which depicts the environmental influence on characters. The high estimates of PCV and GCV were found for grain yield as 26.71 and 21.18, respectively. These findings are consistent with the results reported by Chaudhary *et al.* (2012), Gupta *et al.* (2015) and Ramya *et al.* (2022). Moderate estimates of PCV and GCV were recorded for dry fodder (17.30 and 14.00) and panicle diameter (12.65 and 10.05). Certain characters showed moderate estimates for PCV such as seed set under bagging (12.99), 1000-seed weight (11.50) and plant height

Table 2. Analysis of Variance (ANOVA)**Table 2: Analysis of variance (ANOVA)**

Source of Variation	Degree of Freedom	Characters									
		Days to 50% flowering	Days to maturity	Plant Height (cm.)	Panicle Length (cm.)	Panicle Diameter (cm.)	1000-Seed wt.(g)	Population at harvest/no. net plot	Seed set under bagging (%)	Grain Yield (kg/ net plot)	Dry Fodder Yield (kg/net plot)
Replication	2	0.04	0.08	0.12	0.14	0.1	0.12	0.05	0.12	0.01	0.014
Treatment	22	13.56**	12.83**	664.87**	12.02**	0.23**	3.04**	31.83**	49.11**	0.05**	0.445**
Error	44	1.15	1.74	63.43	1.93	0.04	0.37	23.59	41.16	0.01	0.067

*, ** - Significant at 5% and 1% level of significance

Table 3. Mean Performance**Table 3: Mean performance**

Test Code	Identity	Days to 50% flowering	Days to maturity	Plant Height (cm.)	Panicle Length (cm.)	Panicle Diameter (cm.)	1000-Seed wt.(g)	Population at harvest/no. net plot	Seed set under bagging (%)	Grain Yield (kg/ net plot)	Dry Fodder Yield (kg/net plot)
IHT 101	Pusa Hybrid Bajra 2501	45.33	75.67	176.67	21.33	2.87	11.03	67.00	53.33	0.83	2.12
IHT 102	DHBH-24305	47.33	77.33	164.67	20.67	2.47	9.73	76.67	58.33	0.47	2.25
IHT 103	PB1756 (C)	43.67	73.00	155.00	22.00	2.53	11.33	77.00	43.33	0.58	2.20
IHT 104	DHBH-24308	48.00	78.00	161.67	22.00	2.63	9.93	71.33	55.00	0.46	2.63
IHT 105	RHB 284	44.00	74.00	148.33	24.00	2.57	9.17	68.67	53.33	0.44	2.28
IHT 106	RHB 285	43.33	74.00	167.00	23.33	2.47	9.07	72.00	48.33	0.55	2.43
IHT 107	RHB 287	43.67	73.67	158.33	22.67	2.10	8.47	77.33	46.67	0.45	2.80
IHT 108	RHB 288	44.00	73.67	174.33	24.67	2.33	10.63	73.33	51.67	0.55	2.75
IHT 109	RHB 290	47.67	77.67	152.67	22.33	2.90	10.63	77.00	53.33	0.52	2.50
IHT 110	RHB 223 (C)	50.00	79.00	116.00	21.00	2.17	10.13	77.33	51.67	0.35	3.27
IHT 111	RHB 292	44.67	74.33	178.33	24.00	2.73	10.30	71.67	46.67	0.72	2.43
IHT 112	BHB 2501	44.67	74.33	151.67	21.33	3.07	11.00	77.33	55.00	0.75	2.22
IHT 113	BHB 2502	44.33	74.33	151.67	22.33	2.63	9.63	71.67	48.33	0.46	2.35
IHT 114	MPMH 52	45.00	74.67	177.67	26.67	2.30	7.87	70.00	51.67	0.60	3.57
IHT 115	MPMH 53	44.00	74.00	173.33	26.00	2.63	8.40	68.33	48.33	0.75	3.27
IHT 116	HBB67 (Imp.) (C)	42.33	72.00	155.33	26.00	2.17	9.37	71.00	48.33	0.46	2.18
IHT 117	PA 9070	43.67	73.67	167.33	26.67	3.03	10.93	70.67	55.00	0.58	2.62
IHT 118	CZH 278	43.00	72.67	165.00	23.33	2.27	10.23	73.33	53.33	0.53	2.20
IHT 119	CZH279	43.33	73.33	159.67	25.00	2.20	9.87	68.33	58.33	0.59	2.35
IHT 120	MPMH35 (C)	48.67	78.33	145.67	21.00	2.87	10.70	72.00	50.00	0.43	2.57
IHT 121	CZH 280	45.33	75.33	141.67	26.33	2.57	7.87	70.33	46.67	0.50	2.23
IHT 122	86M94 (C)	43.33	73.33	172.67	22.00	2.43	9.40	72.00	50.00	0.75	2.72
IHT 123	RVBH-2253	48.33	78.33	139.33	25.33	2.63	9.17	70.33	45.00	0.42	2.43
Grand Mean		45.12	74.99	158.87	23.48	2.55	9.78	72.38	50.94	0.55	2.54
Range		42.33 - 50.00	72.00 - 79.00	116.00 - 178.33	20.67 - 26.67	2.10 - 3.07	7.87 - 11.33	67.00 - 77.33	43.33 - 58.33	0.35 - 0.83	2.12 - 3.57
C.D.		1.77	2.18	13.15	2.30	0.32	1.01	N/A	N/A	0.15	0.43
SE(m)		0.62	0.76	4.60	0.80	0.11	0.35	2.80	3.70	0.05	0.15
SE(d)		0.88	1.08	6.50	1.14	0.16	0.50	3.97	5.24	0.07	0.21
C.V. (%)		2.38	1.76	5.01	5.92	7.67	6.27	6.71	12.59	16.27	10.17

(10.23). These findings are in agreement with the reports of Singh *et al.* (2014a), Kumar *et al.* (2015), Sharma *et al.* (2018) and Ramya *et al.* (2022). Although these characters, along with the remaining characters studied, depicted low estimates for GCV.

Heritability is an important genetic parameter that measures the proportion of phenotypic variation attributable to genetic factors and indicates the likelihood of transmitting traits from parents to their offspring. Based on heritability estimates, traits are categorized as having low (<30%), moderate (30–60%) or high (>60%) heritability (Robinson *et al.*, 1949). Estimation of heritability assists plant breeders in identifying and selecting superior genotypes from genetically diverse populations. Traits exhibiting high heritability are generally less influenced by environmental factors and can be improved effectively through selection. In the present study, most of the traits exhibited high (62.89%–78.27%) heritability estimates. These results are in agreement

with previous findings reported by Kumar *et al.* (2015), Sharma *et al.* (2018), Bika and Shekhawat (2015), Yahaya (2015), Abdulhakeem *et al.* (2019) and Ramya *et al.* (2022) for related traits. Low heritability was recorded for the population at harvest per plot and seed set under bagging, indicating a greater influence of environmental factors on the expression of these traits. Similar findings were reported by Rama *et al.* (2005) and Kumar *et al.* (2016), as heritability is a good index of transmission of characters from parents to their progeny.

Genetic advance is an important parameter that indicates the expected improvement in a trait achieved through selection. In the present study, high heritability and genetic advance as percentage of mean (>20) was recorded for dry fodder yield and grain yield, indicating predominance of additive gene action for these characters. Traits displaying both high heritability and high genetic advance as a percentage of the mean are

Table 4. Genetic Variability Parameters

Characters	GCV	PCV	Heritability (%)	GA	GAM (%)
Days to 50% flowering	4.509	5.097	78.271	3.707	8.218
Days to maturity	2.565	3.109	68.061	3.269	4.359
Plant Height (cm.)	8.912	10.226	75.965	25.422	16.002
Panicle Length (cm.)	7.812	9.803	63.492	3.01	12.822
Panicle Diameter (cm.)	10.053	12.647	63.194	0.419	16.463
1000-Seed wt.(g)	9.639	11.496	70.302	1.628	16.648
Population at harvest/no. net plot	2.289	7.091	10.423	1.102	1.522
Seed set under bagging (%)	3.196	12.993	6.053	0.825	1.62
Dry Fodder Yield (kg/net plot)	13.996	17.3	65.458	0.592	23.327
Grain Yield (kg/ net plot)	21.18	26.708	62.892	0.192	34.602

primarily under additive gene control, rendering them highly reliable for direct phenotypic selection (Sangwan *et al.*, 2019). 1000-seed weight, panicle diameter, panicle length and plant height exhibited high heritability coupled with moderate genetic advance as percentage of mean. Similar results were reported by Lakshmana *et al.* (2003), Sumathi *et al.* (2010), Vinodhana *et al.* (2013), Kumar *et al.* (2014) and Basavaraj *et al.* (2017). Traits exhibiting high heritability alongside low genetic advance are often influenced by environmental fluctuations, necessitating more nuanced breeding approaches like heterosis or recurrent selection to achieve further gains (Ahmad *et al.*, 2018). Furthermore, the presence of high heritability coupled with significant genetic advance observed for key yield-related traits indicates that phenotypic selection will be particularly efficient for developing superior genotypes (Ayesha *et al.*, 2019; Subbulakshmi *et al.*, 2022).

Conclusion

The success of crop breeding programmes largely depends on the availability of genetic variability and the inheritance of desirable traits, while the analysis of genetic variation helps breeders formulate effective selection strategies for trait improvement. In the present study, the traits exhibited varying levels of variability, heritability and genetic advance as a percentage of the mean among the studied genotypes. Traits showing high values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicate a high level of genetic variability. High heritability values indicate that the traits under study are largely controlled by genetic factors and are less affected by environmental influences in their expression. The presence of high variability suggests the potential for effective selection and improvement of traits. Traits exhibiting high heritability along with high genetic advance as a percentage of the mean indicate the predominance of additive gene action, suggesting that these traits can be effectively improved through selection. In contrast, traits with moderate heritability and low genetic ad-

vance as a percentage of the mean are predominantly governed by non-additive gene action, implying that direct selection for these traits may be less effective.

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