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GENETIC VARIABILITY, CORRELATION ASSOCIATION WITH YIELD TRAITS IN SORGHUM (*Sorghum bicolor* (L.) Monech)

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ABSTRACT

An experiment was conducted during the Rabi season of 2023-2024 at ICAR-IIMR, Hyderabad, using an alpha lattice design to determine the relationships among grain yield and its contributing traits in sorghum (*Sorghum bicolor* (L.) Monech), involving 96 genotypes and 4 checks. A wide variation in yield and its contributing traits was observed, indicating a high level of genetic diversity among the evaluated genotypes. PCV is higher than GCV, indicating the presence of an environmental effect for all traits. Days to 50 per cent flowering, ear head length, plant height, total number of leaves, and 100-seed weight showed high heritability estimates and high genetic advance. The genotypic correlation revealed that ear head width, total number of leaves, 100-seed weight, days to 50 per cent flowering, leaf width, and leaf length were strongly and positively associated with grain yield per plant. The genotypic path coefficient analysis showed that ear head width had the strongest direct positive effect on grain yield per plant, followed by total number of leaves and 100-seed weight. ECO487180 (81.80g), ICO286163 (81.90g), ICO289472 (83.75g), and ICO352469 (87.35g) recorded the highest grain yield per plant among the studied landraces. Improving grain yield in rabi sorghum may be achieved by selecting taller plants with more green leaves, moderately long panicles and bold seeds.

INTRODUCTION

Sorghum (*Sorghum bicolor (L.) Monech*) is a key climate-resilient cereal crop. It provides food, animal feed, and raw materials for industry. Even though it is widely grown and adaptable, sorghum productivity often falls short of its potential. This highlights the urgent need for genetic improvement (Alemu and Legesse, 2025). With its remarkable adaptability across different agro-ecological zones, especially in semi-arid and moisture-stressed areas, sorghum is vital for food security in South Asia and sub-Saharan Africa (Alemu and Legesse, 2025). In 2022, global sorghum production reached 55.35 million tons, demonstrating its significant role in agricultural economies worldwide (Khan *et al.*, 2025). However, production is limited by a narrow genetic base and a lack of drought-adapted varieties, particularly in stress-prone areas (Begna, 2025). Sorghum naturally tolerates drought and heat. It can thrive under low-input conditions, making it a reliable crop for semi-arid regions and poor soils (Chadalavada *et al.*, 2021). Due to its resilience, nutritional value, and versatility, sorghum is increasingly seen not only as a traditional staple crop but also as an important resource for food and nutritional security amid rising challenges posed by climate change

and resource scarcity (Mwamahonje *et al.*, 2024). Tackling these issues requires understanding the genetic

diversity and genetic structure of economically important traits, especially those related to yield and adaptation. This knowledge can help develop effective breeding strategies (Begna and Begna., 2021). Grain yield is a complex trait influenced by many genes and environmental factors. Therefore, selecting based solely on yield can be unreliable (Kalpande *et al.*, 2022). Assessing genetic variability, heritability, and genetic gain for yield and its component traits is crucial. This assessment helps determine the contributions of genetic and environmental factors and identifies traits suitable for selection. Additionally, understanding trait relationships through correlation analysis can provide valuable insights into yield components and help develop efficient selection criteria (Chauhan and Pandey, 2021). Relying only on released varieties for yield improvement is often ineffective due to their narrow genetic base and the resulting yield plateau (Patil *et al.*, 2022). In contrast, traditional landraces provide valuable but underutilized genetic diversity. Estimating genetic parameters and analyzing trait associations with grain yield are essential for effective germplasm evaluation and breeding (Somu *et al.*, 2025). This study evaluates phenotypic diversity, genetic parameters, and trait interrelationships with grain yield in sorghum.

The current study aimed to evaluate phenotypic diversity and genetic differences among sorghum genotypes using quantitative traits. It sought to estimate variability parameters and heritability and analyze trait associations with grain yield. The goal was to identify promising traits and diverse parental lines for future sorghum improvement programs.

MATERIALS AND METHODS

Experimental material: A set of 96 genotypes, along with their 4 checks (CSV26R, CSV29R, M35-1 and PKV KRANTI), was used in the study. The list of genotypes used in this study is given in Table 2.

Location and season: An experiment was conducted during the Rabi season of 2023-2024 at the ICAR-Indian Institute of Millets Research (ICAR-IIMR), situated at an altitude of 523 m above mean sea level, at 17.19°N and 78.23°E in Rajendranagar, Hyderabad, Telangana. The 96 genotypes and 4 checks were dibbled on 18th November 2023. Standard agronomic and plant protection practices were followed during the cropping season.

Layout and field design: The field trial was arranged using an Alpha Lattice design with two replications, following the method of Patterson and Williams (1976). Each replication consisted of 10 incomplete blocks (block size = 10), each containing 10 genotypes. To help control variation across the field, which is especially useful when testing many entries. Each genotype was planted in a two-row plot measuring 2 m, with a row spacing of 60 cm and a plant spacing of 15 cm within a row. Standard agronomic and plant protection practices were followed during the cropping season.

Traits Evaluated: Observations were recorded on nine traits, namely days to 50 per cent flowering (DFF), total number of leaves (TNL), leaf length (LL), leaf width (LW), plant height (PHT), ear head length (EHL), ear length width (EHW), 100 seed weight (HSW) and grain yield per plant (GYP). All the traits were evaluated following the methods described by Brown *et al.* (2006) and Reddy *et al.* (2013). Observations were taken from five randomly selected plants in each plot, apart from days to 50 per cent flowering and 100-seed weight. In every plot, at least 25 plants were grown, and five of those were tagged at random for detailed agronomic measurements.

Data were collected using the open-source Field Book app (version 6.2.2) on an Android device in digital format [https://play.google.com/store/search?q=field+book+appandc=apps] during field evaluations, ensuring real-time entry for each observation plot.

Statistical analysis and interpretation of data

Descriptive statistics and genetic parameters: The plot data for each trait were summarized by averaging across five plants per treatment and replication. These pooled mean values were then used for further statistical and biometrical analyses. Basic statistical parameters, such as the mean, range, and coefficient of variation, were calculated according to Steel *et al.* (1997). In addition, estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance expressed as a percentage of the mean were determined to assess genetic variability and selection potential in the material studied.

Analysis of variance: Before running the main analysis, we checked and transformed the data into R software to ensure the distribution met the normality assumption required for statistical testing. The experiment was completed using an alpha lattice design with two replications. Each replication comprised 10 incomplete blocks, each with 10 genotypes, for a total of 100 sorghum genotypes per block. The data were analysed using an analysis of variance suitable for an alpha-lattice design, employing the fixed-effects linear model.

$$Y\{ijk\} = mu + r_i + b_{j(i)} + g_k + e\{ijk\}$$

where $(Y\{ijk\})$ represents the observation of the $(k)^{th}$ genotype in the $(j)^{th}$ block of the $(i)^{th}$ replication, (mu) denotes the overall mean, (ri)

signifies the effect of the $(i)^{th}$ replication, (bj(i)) indicates the effect of the $(j)^{th}$ incomplete block within replication, (gk) is the fixed effect of the $(k)^{th}$ genotype, and (e{ijk}) is the random residual error. The ANOVA table included sources of variation attributable to replications, blocks within replications, genotypes, and error, with 1, 8, 99, and 91 degrees of freedom, respectively, for each trait. Mean squares for genotypes and blocks were tested against the residual mean square, and significance was determined at the 5% and 1% probability levels.

Genotypic and Phenotypic correlations: To explore how grain yield relates to its component traits, simple and genotypic correlation analyses were performed using the "variability" package in R software.

RESULTS AND DISCUSSION

Descriptive statistics and genetic variability parameters: Basic statistical and genetic parameters, including the mean, range, phenotypic and genotypic coefficients of variability, heritability and genetic advance as a percentage of the mean, are presented in Table 4. In this study, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits, suggesting that environmental factors exerted a noticeable influence on their expression. Similar findings were reported by Chauhan and Pandey (2021), who observed higher PCV than GCV values, indicating environmental effects on trait variability.

Analysis of variance: The analysis of variance showed highly significant differences (P < 0.001) among the studied sorghum genotypes for all traits (Table 3). These findings suggest that the observed differences among genotypes are likely due to genetic differences, reflecting substantial variation in the material and a relatively high level of diversity for the traits studied.

Genetic parameters: The genetic parameters for the nine traits studied are presented in Table 4, and their graphical representation as percentages is shown in Figure 1. Highest GCV and PCV were recorded by grain yield per plant (27.88 and 37.35 respectively), followed by ear head length (23.92 and 25.03 respectively), 100-seed weight (17.05 and 18.81 respectively), plant height (13.91 and 14.85 respectively), total number of leaves (13.25 and 14.27 respectively), leaf width (9.02 and 10.46 respectively), and leaf length (7.73 and 8.73, respectively). For days to 50 per cent flowering, GCV was 10.00 and PCV was 10.18, whereas the values were (9.39 and 14.08, respectively), for ear head weight.

Heritability and genetic advance: The heritability of all traits ranged from 44.48 to 96.55. According to Gebre-Mariam and Mekbib (2020), broad-sense heritability is classified as low (<30%), moderate (30-60%) and high (>60%). High heritability was observed by days to 50 per cent flowering (96.55%), ear head length (91.34%), plant height (87.69%), total number of leaves (86.21%), 100-seed weight (82.12%), leaf length (78.39%) and leaf width (74.41%). The traits that exhibit high heritability can be improved through selection in the future. Ear head width (44.48%) and grain yield per plant (55.71%) exhibited moderate heritability and none of the traits exhibited low heritability.

Genetic advance as a percentage of the mean ranged from 12.9 in ear head weight to 47.09 in ear head length. High genetic advance as percentage of mean was recorded in ear head length (47.09), grain yield per plant (42.86), 100-seed weight (31.83), plant height (26.83), total number of leaves (25.34) and days to 50 per cent flowering (20.25). Leaf width (16.04), leaf length (14.09), and ear head weight (12.9) recorded moderate genetic advance as a percentage of the mean. High estimates of heritability, coupled with high genetic advance, were observed for days to 50 per cent flowering, ear head length, plant height, total number of leaves, and 100-seed weight. This indicates that there is scope to improve these traits through selection. Similar results were recorded by Chauhan and Pandey (2021).

Table 1. Mean values of 100 genotypes studied for nine traits during rabi season

Sr. No.	Genotypes	DFF	TNL	LL	LW	PHT	EHL	EHW	HSW	GYP
1.	EC0021380	77	8.1	62.95	7.90	212.4	15.30	4.70	3.75	50.70
2.	EC0105274	78	7.5	71.4	7.05	210	21.35	3.70	2.25	11.40
3.	EC0483852	65	7.9	86.5	5.40	266.3	27.80	4.95	3.35	41.40
4.	EC0485034	76	7.2	63.8	5.15	199.1	22.65	40	4.10	14.80
5.	EC0487174	79	10.9	75.4	7.65	320	12.55	6.65	4.75	67.40
6.	EC0487179	71	11.1	84.8	6.95	259.3	13.60	4.70	3.55	42.80
7.	EC0487180	78	8.7	78.4	6.85	219	12.30	6.50	3.65	81.80
8.	EC0487198	70	10.4	85.4	7.65	269	12.10	5.95	4.55	58.40
9.	EC0488206	80	8.4	78.65	6.80	289.4	31.40	3.80	3.45	25.60
10.	IC0121527	62	7.5	70.35	7.00	220.2	18.50	4.90	3.70	33.00
11.	IC0144869	63	8.5	75.8	7.35	222.6	23.35	5.75	3.15	59.75
12.	IC0240846	79	9.2	77.1	7.00	175.1	25.10	4.70	2.40	32.40
13.	IC0249714	62	8.7	66.75	7.25	230.9	11.95	5.95	4.00	52.30
14.	IC0285962	63	8.2	63.7	7.50	220	19.00	4.95	3.65	28.60
15.	IC0286051	61	8.9	64.65	7.10	191.1	28.25	5.20	3.50	36.30
16.	IC0286055	65	7.2	72.85	6.70	237.3	20.15	5.60	3.15	19.70
17.	IC0286061	68	7.9	76.5	7.40	228	18.20	5.55	3.80	43.05
18.	IC0286062	61	7.8	73.6	6.15	188	17.10	6.20	3.60	69.95
19.	IC0286063	62	6.3	71.65	6.70	189.3	18.65	6.35	3.55	58.45
22.	IC0286077	65	7.2	68.45	6.00	190.9	19.10	5.25	4.05	43.20
21.	IC0286087	57	7.3	66.85	7.90	198.2	15.80	6.05	3.40	38.60
22.	IC0286113	64	7.8	69.85	7.50	222.9	15.80	5.75	3.35	65.70
23.	IC0286132	60	8.8	63.20	6.20	218.1	19.80	6.45	3.65	56.90
24.	IC0286133	64	7.6	65.20	6.85	206.3	15.55	5.70	2.90	38.50
25.	IC0286163	68	8.5	64.10	8.00	181.5	11.35	6.85	3.45	81.90
26.	IC0286171	60	5.7	70.25	6.05	161.0	14.80	5.70	1.90	25.20
27.	IC0286179	78	8.7	69.30	7.40	209.2	14.45	6.00	3.30	61.50
28.	IC0286207	69	8.1	66.85	6.90	226.0	19.85	6.45	3.30	49.75
29.	IC0286214	64	7.4	68.75	7.65	182.3	15.40	6.20	3.80	54.40
30.	IC0286321	67	7.9	76.70	6.25	175.7	14.05	5.85	3.60	47.40
31.	IC0286325	65	7.5	66.90	7.50	149.5	13.80	6.50	2.85	49.15
32.	IC0286326	66	5.4	59.05	6.05	132.6	9.55	5.75	2.95	17.55
33.	IC0286327	57	6.4	71.55	4.95	207.7	25.65	4.95	3.05	23.60
34.	IC0286340	63	6.9	70.15	5.65	185.8	13.60	4.95	3.65	43.45
35.	IC0286384	59	8.3	68.80	7.30	194.0	21.30	5.95	3.25	38.60
36.	IC0286392	62	7.4	69.25	6.85	187.9	12.20	5.40	1.65	27.80
37.	IC0286402	65	8.1	75.15	7.45	205.6	16.65	5.05	4.15	29.50
38.	IC0286417	59	5.7	67.15	6.15	173.8	11.70	5.90	2.80	35.70
39.	IC0286435	81	8.3	64.55	8.10	206.7	11.35	5.95	3.95	72.05
40.	IC0286436	75	8.6	69.40	8.15	212.0	13.25	7.00	4.10	49.75
41.	IC0286437	82	8.2	62.20	7.40	171.0	12.05	5.75	3.85	50.00
42.	IC0286451	67	7.9	63.35	6.95	212.5	11.45	5.65	2.75	47.95
43.	IC0286469	68	6.6	62.00	6.40	212.0	14.20	5.40	2.95	26.95
44.	IC0286745	71	6.5	64.25	6.40	201.2	15.00	4.00	3.00	17.05
45.	IC0286747	67	8.8	64.55	6.80	208.7	12.75	5.20	3.60	34.20
46.	IC0286762	70	8.8	72.00	7.60	239.8	20.40	6.70	3.35	74.60
47.	IC0286764	67	8.1	74.65	7.80	220.3	17.85	5.75	3.55	45.00
48.	IC0286790	64	8.6	59.20	7.40	193.0	10.60	5.85	3.15	49.90
49.	IC0286876	67	5.3	54.60	6.45	157.2	14.30	5.55	3.30	36.05
50.	IC0287068	65	8.4	61.10	7.65	211.9	19.60	6.25	4.05	72.00
51.	IC0287445	68	6.6	68.40	7.30	156.1	11.35	6.20	2.70	28.40
52.	IC0287790	73	7.4	66.00	6.70	199.5	15.35	6.70	3.55	40.90
53.	IC0288257	76	8.3	74.50	7.65	179.0	14.00	6.50	3.90	64.80
54.	IC0288259	64	7.0	69.70	6.25	189.0	13.35	4.70	3.55	33.15
55.	IC0289468	88	9.0	71.40	6.85	247.6	15.65	5.15	3.40	67.30
56.	IC0289472	86	8.7	71.70	7.95	228.2	11.85	6.90	3.70	83.75
57.	IC0289639	72	7.5	64.75	6.45	180.5	12.50	5.50	2.05	31.60
58.	IC0289982	77	9.4	65.50	7.10	217.1	16.45	5.20	3.00	31.50
59.	IC0338975	72	9.1	70.30	8.45	215.0	21.00	6.60	4.00	59.20
60.	IC0344689	73	6.8	67.90	5.80	187.7	13.45	6.15	4.00	46.05
61.	IC0344697	70	5.9	60.60	7.20	146.4	20.85	4.15	2.10	28.50
62.	IC0352469	79	9.4	74.40	7.65	248.2	20.00	6.85	3.65	87.35
63.	IC0395722	66	8.3	67.10	7.00	209.2	18.90	5.80	3.25	58.80
64.	IC0395776	68	8.3	70.20	6.80	210.5	23.30	5.20	3.30	48.10
65.	IC0395816	68	7.5	82.25	7.95	172.0	15.90	6.95	4.40	73.05
66.	IC0415833	68	8.8	70.60	8.20	224.0	18.50	6.15	4.30	60.90
67.	IC0426744	62	8.7	81.70	6.90	231.5	11.20	5.45	3.75	53.10
68.	IC0436709	57	7.8	78.75	6.90	199.4	17.85	5.95	3.10	48.05
69.	IC0438340	67	7.6	66.00	7.25	223.0	20.55	5.95	3.70	41.55
70.	IC0446683	66	9.0	67.10	8.05	223.3	13.05	7.15	3.10	77.50
71.	IC0484376	73	5.6	52.30	6.45	140.1	22.90	4.65	1.65	19.40
72.	IC0484465	66	9.3	70.45	7.45	187.5	12.15	6.60	3.85	81.40
73.	IC0484870	66	7.8	66.75	7.25	201.9	19.05	5.35	3.05	49.45
74.	IC0484942	68	9.5	68.35	7.50	231.0	17.95	5.55	3.60	32.20
75.	IC0485069	68	7.7	71.35	6.90	202.8	21.00	6.30	3.35	38.25
76.	IC0485074	80	7.8	73.30	6.30	176.9	21.35	6.90	2.05	39.50
77.	IC0547997	62	6.8	72.75	7.50	186.6	17.70	4.40	3.90	33.10
78.	IC0547999	60	7.5	79.05	7.35	203.0	20.75	5.85	3.80	38.95
79.	IC0590880	56	6.5	68.10	7.45	167.6	19.90	4.60	1.85	24.15
80.	IC0590881	66	7.4	63.85	6.85	179.7	22.00	4.35	2.65	47.10
81.	IC0591745	72	7.1	67.60	7.45	170.8	22.90	5.60	2.20	35.30
82.	IC0594624	66	8.5	70.50	8.25	216.7	21.95	6.05	4.00	57.00
83.	IC0594626	67	7.3	73.95	7.50	221.5	21.05	5.15	3.10	32.40
84.	IC0595231	60	8.8	74.75	7.90	254.2	20.85	6.35	3.55	53.05
85.	IC0612159	70	8.6	62.35	6.15	193.2	15.75	4.35	2.65	45.35
86.	IC0612162	76	10.1	65.10	8.35	198.9	14.85	6.45	3.20	43.95
87.	IC0612164	86	8.1	65.80	6.60	195.9	16.50	6.10	4.30	54.10
88.	IC0621517	71	9.2	68.90	7.50	165.0	21.90	4.75	2.65	36.60
89.	IC0632067	75	9.7	72.05	8.85	211.8	17.65	6.40	3.95	59.25
90.	IC0632753	73	8.9	67.85	7.70	235.3	16.35	5.85	4.35	55.40
91.	IC0636718	78	9.6	70.45	7.05	255.3	22.95	4.80	3.75	25.75
92.	IC0636737	68	9.6	73.90	8.80	241.2	16.50	7.15	3.80	75.60
93.	IC0636738	69	9.0	74.75	8.20	231.9	17.60	6.25	4.20	27.70
94.	IC0636740	75	10.8	70.95	8.00	229.0	14.10	6.95	3.90	80.60
95.	IC0636743	66	8.9	70.30	7.80	221.0	12.05	6.40	3.90	66.80
96.	IC0638926	63	8.4	74.95	7.60	216.1	21.45	6.20	4.25	56.75
97.	CSV26R	61	8.5	67.25	7.25	201.7	19.55	6.15	3.80	49.80
98.	CSV29R	59	8.8	72.7	7.45	243.8	19.95	6.95	3.55	74.05
99.	M35-1	67	8.5	61.15	6.85	210.0	15.90	5.45	3.45	55.40
100.	PKVKRANTI	70	9.2	66.00	7.90	214.9	16.05	6.20	3.70	64.55

Table 2. Analysis of variance for nine traits studied during Rabi season 2023-2024

SOV	df	DFF	TNL	LL	LW	PHT	EHL	EHW	HSW	GYP
Genotypes	99	92.16**	2.59**	71.81**	1.14**	1838.22**	35.91**	1.29**	0.80**	606.45**
Replications	1	206.04**	0.28	186.44**	1.19	23.67	1.05	0.53	0.09	725.42
Blocks	8	76.57**	1.50**	44.53*	0.22	935.46**	27.04**	1.18	0.50*	487.81
Error	91	3.39	0.38	16.06	0.27	229.82	3.28	0.7	0.15	284.68

** = Significant at 1% level. * = Significant at 5% level.

Table 3. Genetic parameters of nine traits studied during Rabi season 2023-2024

TRAIT	MEAN	RANGE	C.V. (%)	$h^2_{(bs)}$	GCV	PCV	GAM	CD (5%)
DFF	68.62	54-89	2.67	96.55	10.00	10.18	20.25	3.64
TNL	8.10	5-11.8	7.49	86.21	13.25	14.27	25.34	1.21
LL	69.56	46.9-93.6	5.74	78.39	8.73	14.09	14.09	7.93
LW	7.16	4.8-9.1	7.48	74.41	9.02	10.46	16.04	1.06
PHT	206.95	127.6-322.0	7.37	87.69	13.91	14.85	26.83	30.28
EHL	17.28	9.3-37.0	10.42	91.34	23.92	25.03	47.09	3.57
EHW	5.73	2.8-7.9	14.83	44.48	9.39	14.08	12.9	1.69
HSW	3.41	1.5-4.9	11.25	82.12	17.05	18.81	31.83	0.76
GYP	47.48	9.8-99.3	35.15	55.71	27.88	37.35	42.86	33.14

Table 4. Genotypic and Phenotypic Correlation matrix among nine traits studied during Rabi season 2023-2024

		DFF	TNL	LL	LW	PHT	EHL	EHW	HSW	GYP
DFF	G	1	0.338*	-0.024	0.15	0.179	-0.079	0.011	0.114	0.169
	P	1	0.307**	0.004	0.139	0.152	-0.089	0.004	0.091	0.148
TNL	G		1	0.366**	0.534**	0.653**	-0.034	0.319*	0.466**	0.523**
	P		1	0.318**	0.453**	0.594**	-0.028	0.287**	0.414**	0.444**
LL	G			1	0.111	0.491**	0.172	0.134	0.305*	0.207
	P			1	0.138	0.425**	0.150	0.148	0.242*	0.194
LW	G				1	0.239	-0.128	0.46**	0.322*	0.476**
	P				1	0.191	-0.094	0.387**	0.265**	0.401**
PHT	G					1	0.161	0.113	0.497**	0.296
	P					1	0.136	0.060	0.438**	0.223*
EHL	G						1	-0.345*	-0.134	-0.279
	P						1	-0.25**	-0.153	-0.217*
EHW	G							1	0.358**	0.705**
	P							1	0.329**	0.617**
HSW	G								1	0.471**
	P								1	0.425**
GYP	G									1
	P									1

** = Significant at 1% level. * = Significant at 5% level.

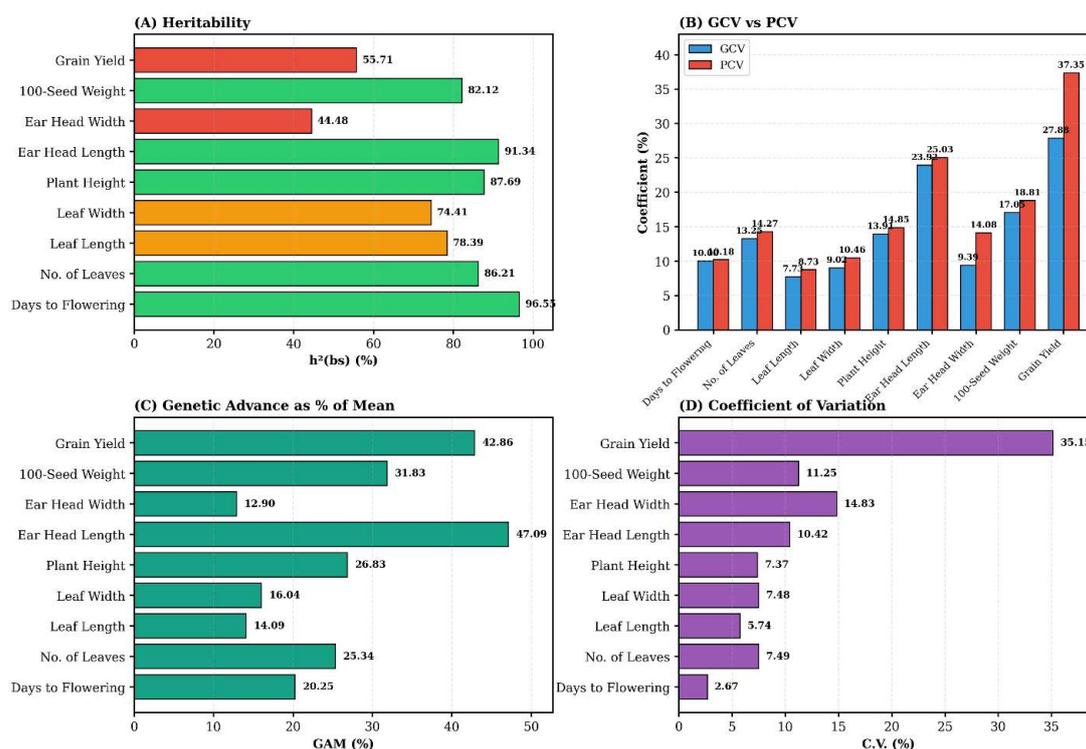**Genetic Variability Parameters for Nine Traits**

Figure 1. Genetic parameters of nine traits studied during Rabi 2023-2024

Phenotypic and genotypic correlation analysis: The study revealed that genotypic correlation values were greater than phenotypic correlation values (Table 4), indicating that the association among traits was primarily due to genetic rather than environmental factors. Similar findings have been reported (Kavya *et al*., 2020; Rohila *et al*., 2020; Rajarajan *et al*., 2017; Amare *et al*., 2015; Mengesha *et al*., 2019; Gebre *et al*., 2024). The correlation analysis indicated that the trait "days to fifty per cent flowering" demonstrated a significant positive correlation with the total number of leaves. Additionally, the total number of leaves exhibited a significant positive correlation with leaf length, leaf width, plant height, ear head width, hundred seed weight and grain yield per plant. The trait leaf length also showed a significant positive correlation with both plant height and 100-seed weight. Furthermore, leaf width was significantly positively correlated with ear head width, 100-seed weight, and grain yield per plant. Plant height revealed a significant positive correlation with 100-seed weight. Similarly, ear head width showed a significant positive correlation with both 100-seed weight and grain yield per plant. The observed correlations among the above-mentioned traits were consistent at both phenotypic and genotypic levels, indicating a strong genetic basis for their association. Conversely, the trait ear head length exhibited a significant negative correlation with ear head width at the genotypic level, and a significant negative correlation with both ear head width and grain yield per plant at the genotypic level.

Overall, grain yield per plant is the resultant expression of several component traits. Correlation analysis revealed that grain yield per plant exhibited significant (1%) positive correlation with ear head width (0.705), leaf width (0.476), total number of leaves (0.532) and hundred seed weight (0.471) at the genotypic level, while at the phenotypic level it also showed a significant (1%) positive correlation with ear head width (0.617), leaf width (0.401), total number of leaves (0.444), hundred seed weight (0.425) and plant height (0.223) significant positive correlation at (5%). (Tilaye, 2022; Rajendra, 2023; Sureshbhai, 2021; Ngidi *et al.,* 2024; Senbetay and Belete, 2020; Thant *et al.,* 2021). The analysis of the results indicates that ear head width, leaf width, total number of leaves and plant height are the most critical factors. These traits show strong correlation coefficients and a significant direct impact on grain yield per plant.

CONCLUSION

In summary, the results indicate that the rabi sorghum landraces examined in this study exhibit considerable variation and high heritability for all the yield and yield-component traits. The PCV was greater than the GCV for all traits, indicating that the observed variation in the traits was influenced not only by genetic differences among plants but also by environmental factors. Days to 50 per cent flowering, ear head length, plant height, total number of leaves and 100-seed weight showed high heritability estimates and high genetic advance. The genotypic correlation analysis showed that several key traits, including ear head width, total number of leaves, 100-seed weight, days to 50 per cent flowering, leaf width and leaf length, were strongly and positively associated with grain yield per plant. These traits had a favourable direct influence on grain yield, suggesting their importance in selection for higher productivity. The genotypic path coefficient analysis showed that ear head width had the strongest direct positive effect on grain yield per plant, followed by total number of leaves and 100-seed weight. Selecting taller plants with more green leaves, medium-sized panicles and bold seeds may be effective for enhancing grain yield in rabi sorghum.

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