Morphological variability, heritability and genetic advancement in F2 sorghum lines

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Abstract. Evaluating genetic advancement is particularly important in sorghum breeding programs through selective processes. This study aimed to evaluate the morphological diversity and genetic parameters of 32 F2 sorghum genotypes, focusing on traits with high heritability and significant correlations with kernel weight per panicle. The research was conducted at the BPSI Cereals Experiment Station in Maros, South Sulawesi, from December 2023 to March 2024. A randomized block design with two replications was used to plant 32 genotypes (Gen-4 to Gen-64) in 4-meter rows with 70 cm x 20 cm spacing. Results The evaluation of 32 F2 sorghum genotypes revealed significant genetic advancements, particularly in traits with high heritability and positive correlations with kernel weight per panicle. Genotype Gen-48 exhibited the highest kernel weight per panicle, with notable plant height, stem diameter, panicle length, and biomass. Traits such as plant height, stem diameter, leaf angle, kernel weight per panicle, 100-kernel weight, panicle length, panicle width, panicle circumference, panicle weight, biomass, panicle density, and panicle length-width ratio demonstrated high heritability and genetic advance. In addition, it significantly correlates positively with grain yield, including plant height, stem diameter, leaf length, panicle length, panicle circumference, panicle width, panicle weight, weight of 100 kernels, and biomass.

1 Introduction

Global climate change over the past few decades has increasingly affected agriculture. These changes can significantly impact agricultural productivity, water availability, cropping patterns, and the overall balance of agricultural ecosystems. One of the main challenges in understanding the impact of climate on agriculture is its complexity. Climate change affects temperature and rainfall and can trigger changes in wind patterns, the distribution of pests and plant diseases, and seasonal patterns. Climate change presents formidable challenges to agricultural productivity, manifesting through severe weather events such as droughts, floods, and storms. These phenomena profoundly affect crop yields and agricultural stability

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[1]. There is an increase in air temperature because of El Niño in 2023 and the rise in greenhouse gas emissions. High air temperatures cause droughts, increasing crop failures and reducing food crop production [2, 3]. Farmers have identified drought-tolerant and short-maturing crop varieties as essential strategies for adapting to changing climate conditions and ensuring reliable harvests [4].

One of the prospectus food crops tolerant to climate fluctuations in Indonesia is sorghum. Sorghum has broad adaptability to various environmental stresses such as drought, high temperatures, and salinity [5-7]. Sorghum has a waxy layer on the epidermis of its stems and leaves that reduces cuticle conductance and increases water use efficiency during drought stress through an avoidance mechanism. It reduces high transpiration rates in drought conditions and increases root development to absorb water from deeper soil layers [8-11]. Sorghum can be used as food after rice, corn, wheat, and barley, and it is a staple food in semi-arid tropical regions of Africa, Asia, and Latin America [9]. Sorghum contains 4.40-21.10% protein, 55.60-75.20% starch, 21.20-30.20% amylose, 0.70-4.20% soluble sugar, 1.00-3.40% fiber, and 2.10-7.60% fat [13; 14]. Sorghum also offers an advantage with its ratoon system, allowing multiple harvests from a single planting, which reduces input costs [12].

The breeding of sorghum for food continues to meet national food needs and security. The breeding stages include crossing and selecting characters indicating high productivity and sorghum biomass [13]. Research showed that plant height, leaf number, leaf width, leaf chlorophyll, and stay-green traits positively correlate with sorghum yield [14]. Plant height and flowering age traits correlate significantly with food sorghum grain yield [15].

Comprehending heritability and genetic control is vital. Research demonstrates significant heritability estimates across various traits, highlighting the role of additive genetic effects and the potential for rapid improvement through selective breeding [16]. Selection effectiveness is achieved if the selection population has advantages over the base population. Genetic variability is an important parameter in the sorghum breeding process, providing information about genetic diversity within a population. High genetic variability facilitates obtaining superior sorghum genotypes [20, 21]. Several studies on genetic diversity in sorghum have shown high genotypic and phenotypic diversity in grain yield, panicle length, and plant height characteristics [19]. The highest genotypic and phenotypic variability coefficients are found in sorghum grain yield tolerant to anthracnose disease [18]. However, simply observing variability is insufficient for effective genotype selection, thus necessitating observations for heritability parameters.

Heritability is a genetic parameter used to measure the influence of genetics on character variation. Heritability indicates the extent to which genetic diversity contributes to phenotypic diversity within a population. Gebre et al. [23] reported that in the breeding of sorghum for feed, the highest heritability is observed in the components of the amylase enzyme, ash content, and iron in the kernel. This study aims to determine the genetic variability, heritability, genetic advancement, and character correlation of F2 generation sorghum genotypes.

2 Methodology

The research was conducted at the BPSI Cereals Experimental Station in Maros District, South Sulawesi, Indonesia, 5 meters above sea level (asl) from December 2023 to March 2024. The research site was at the coordinates stretch from 4°58'37"S-119°34'33"E. The study was conducted in a randomized block design with two replications. The treatments consisted of 32 F2 sorghum genotypes include: Gen-4, Gen-5, Gen-6, Gen-9, Gen-10, Gen-15, Gen-20, Gen-21, Gen-24, Gen-25, Gen-26, Gen-27, Gen-28, Gen-30, Gen-32, Gen-35, Gen-36, Gen-38, Gen-40, Gen-45, Gen-48, Gen-51, Gen-53, Gen-54, Gen-55, Gen-56, Gen-58, Gen-59, Gen-60, Gen-61, Gen-62, and Gen-64.

Each genotype was planted in two rows, each 4 meters long, with a planting distance of 70 cm x 20 cm. Two sorghum seeds were planted in each hole, treated with furadan to prevent pest attacks, and then covered with soil. Plant maintenance included weeding, watering, and hilling following the procedure issued by the Ministry of Agriculture, Indonesia. The first fertilization used 150 kg ha^{-1} of urea and 350 kg ha^{-1} of NPK 15:15:15 ten days after planting (dap). The second fertilization occurred when the plants were 35 daps with 200 kg ha^{-1} of urea.

Observation variables included plant height, stem diameter, leaf length, number of leaves, leaf width, leaf angle, panicle length, panicle width, panicle circumference, panicle weight, biomass, panicle density, and panicle length-to-width ratio, grain/kernel weight, and weight of 100 grains.

The data were analyzed using analysis of variance (ANOVA). Genetic variability, heritability, genetic advancement, and correlations were determined using the Rstudio software. Genotypic and phenotypic variation values were calculated based on variance analysis [21], as presented in Table 1.

Table 1. Sources of variance and components of analysis of variance and mean square estimates.

Varians	Degree of freedom	Mean square	Means square estimation (MSE)
Replication	r-1	MSr	$\sigma^2 e + g\sigma^2 r$
Genotype	g-1	MSg	$\sigma^2 e + r\sigma^2 g$
Error	(g-1)(r-1)	Mse	$\sigma^2 e$

Based on Table 1, the genotype and phenotype variability can be calculated using the formula:

$$\sigma^2 g=\frac{MSg\text{-}MSe}{r} \qquad \sigma^2 p=MSg+e/r \tag{1}$$

The standard deviation for genotypic variability is calculated using the formula:

$$\sigma\sigma^2 g = \sqrt{\frac{2}{r^2}\left(\frac{MSg^2}{dfg+2}+\frac{MSe^2}{dfe+2}\right)} \tag{2}$$

The standard deviation for phenotypic variability is calculated using the formula:

$$\sigma\sigma^2 p = \sqrt{\frac{2}{r^2}\left(\frac{MSg^2}{dfg+2}\right)} \tag{3}$$

where: $\sigma^2 g < 2\sigma_{\sigma 2g}$ = low; $\sigma^2 g \geq 2\sigma_{\sigma 2g}$ = high, and $\sigma 2p < 2\sigma_{\sigma 2p}$ = low, $\sigma^2 p \geq 2\sigma_{\sigma 2p}$ = high.

The values for broad-sense heritability (H^2) and genetic advancement (GA) are calculated using the formula by H. Jhonson in 1995[22] and J. Lush in 1940 [26].

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} x\ 100 \tag{4}$$

$$GA = H^2 S; \qquad \%GA = \frac{GA}{x}\ x\ 100 \tag{5}$$

Where S is the selection differential and x is the population mean. The categorization of heritability values is as follows: $H^2 > 0.5$ (high), $0.2<H^2<0.5$ (medium), $H^2<0.2$ (low). Group of % GA is 0-10% (low), 10-20% (medium), >20% (high).

3 Results and discussion

3.1 Analysis of variance

The analysis of variance indicated that genotype significantly influences all observed variables except for leaf length, number of leaves, leaf width, and panicle width (Table 2). The non-significant influence of genotype on these variables is due to the substantial environmental impact [24]. These traits exhibit low genotypic variability but high phenotypic variability.

Table 2. Analysis of variance

Characters	Mean square (MS)		SE Mean	CV (%)
	Genotype	Error		
Plant height (PH)	3373.50**	174.30	9.33	7.30
Stem diameter (SD)	0.22**	0.04	0.15	9.10
Leaf length (LL)	101.72	64.35	5.67	9.60
Number of leafs (NBL)	7.71	4.85	1.56	15.60
Leaf width (LW)	1.58	0.75	0.61	10.50
Leaf angle (LA)	754.45**	33.51	4.09	11.40
Kernel weight per panicle (KW)	2112.82**	223.01	10.56	19.20
100 kernel weight (100KW)	0.59**	0.11	0.23	12.60
Panicle length (PL)	18.46**	1.91	0.98	5.40
Panicle width (PWI)	11.90	7.24	1.90	27.70
Panicle circumference (PC)	22.16**	1.74	0.93	6.40
Panicle weight (PWG)	3975.80**	180.80	9.51	11.50
Biomass (BIO)	120287.00**	5609.00	52.96	11.60
Panicle density (PD)	0.00**	0.00	0.02	19.80
Panicle length-width ratio (Ratio)	0.49**	0.13	0.25	12.60

**= significant at $P<0.01$, *= significant at $P<0.05$, CV= coefficient of variability

3.2 The Performance of Agronomic and Yield Components

The agronomic traits and grain yield performance of each tested genotype show significant variation (Table 3 and Table 4). This variation can be attributed to differences in genotypes and environmental influences. The study reveals that the plant height of the 32 tested sorghum genotypes ranges from 118.50 to 256.00 cm. The tallest plants are found in Gen-56, which is not significantly different from Gen-62 and Gen-54. Plant height is a trait primarily influenced by genetic factors [24].

Stem diameter is a crucial trait for selecting sorghum lines. The variation in stem diameter among the tested sorghum genotypes is due to genetic differences. According to Dailami et al. in 2011 [28], genetic factors significantly influence stem diameter during the vegetative phase. The size differences in stem diameter among sorghum genotypes depend on the interaction between genetic factors and environmental conditions, nutrient availability, and photosynthesis. The study shows that the stem diameter of the tested sorghum genotypes ranges from 1.64 to 3.01 cm, with the largest diameter found in Gen-60 (3.01 cm), which is not significantly different from Gen-4, Gen-6, Gen-25, Gen-26, and Gen-28.

Table 3. The performance of plant height, stem diameter, leaf width, leaf width and leaf angle of sorghum genotype.

Genotype	**Plant height (cm)**	**Stem diameter (cm)**	**Leaf width (cm)**	**Leaf angle (^{0})**
Gen4	160.50fghi	2.75abc	9.25abcdef	32.50fg
Gen5	162.25fgh	2.41cdefgh	8.50bcdef	45.00cde
Gen6	217.50bcd	2.63abcd	10.25ab	40.00defg
Gen9	157.50fghij	1.64l	7.75ef	15.00h
Gen10	193.50de	2.18efghij	7.75ef	37.00defg
Gen15	118.50l	1.83jkl	7.75ef	42.50cdef
Gen20	227.00bc	2.55bcde	9.75abcd	42.50cdef
Gen21	138.00hijkl	1.90jkl	9.00abcdef	46.00cde
Gen24	131.00jkl	2.37cdefghi	9.50abcde	35.50efg
Gen25	139.50hijkl	2.78abc	9.50abcde	46.50cde
Gen26	140.00hijkl	2.94ab	10.75a	43.00cdef
Gen27	151.00ghijk	2.55bcde	8.75bcdef	43.00cdef
Gen28	144.50ghijkl	2.68abc	9.50abcde	40.00defg
Gen30	148.50ghijk	2.50cdef	8.50bcdef	41.50cdefg
Gen32	138.50hijkl	2.43cdefgh	8.75bcdef	52.00c
Gen35	171.00efg	2.42cdefgh	9.00abcdef	47.00cde
Gen36	227.50bc	2.24defghij	7.50f	47.50cd
Gen38	180.25ef	2.47cdefg	9.50abcde	74.50ab
Gen40	142.00hijkl	1.96ijkl	10.25ab	67.50b
Gen45	135.00ijkl	1.75kl	8.00def	70.50ab
Gen48	128.50kl	2.19efghij	8.25cdef	74.00ab
Gen51	223.25bc	2.15efghijk	9.65abcde	81.50a
Gen53	221.00bc	2.02hijkl	8.00def	72.00ab
Gen54	236.50abc	2.11fghijk	9.75abcd	81.00a
Gen55	224.00bc	2.13efghijk	8.25cdef	78.00ab
Gen56	256.00a	1.91jkl	8.25cdef	79.50a
Gen58	147.50ghijk	2.18efghij	7.75ef	76.50ab
Gen59	224.00bc	2.15efghijk	9.50abcde	13.00h
Gen60	215.50cd	3.01a	8.75bcdef	30.00g
Gen61	221.50bc	2.39cdefgh	10.00abc	52.50c
Gen62	243.00ab	2.47cdefg	9.00abcdef	41.50cdefg
Gen64	169.00efg	2.06ghijkl	8.50bcdef	17.50h
$Lsd_{\alpha=0.05}$	26.75	0.43	1.91	11.69

Note: The numbers followed by the same letter in the same column show no significant difference in the 5% LSD test.

Leaf area and leaf angle are key selection traits in sorghum because they play a crucial role in light interception and transmission, essential for photosynthesis. The architecture of the canopy, encompassing the dimensions, form, and alignment of shoot elements, impacts the attenuation of light within crop rows, thereby influencing light interception [29, 30]. The average leaf area of the tested sorghum genotypes ranges from 7.5 to 10.75 cm, and leaf angles range from 13.00 to 81.50 degrees. The widest leaf was found in genotype Gen-26, measuring 10.75 cm with a leaf angle of 43 degrees. The analysis shows that while the genotypic variability for leaf area was low, the variability for leaf angle was relatively high.

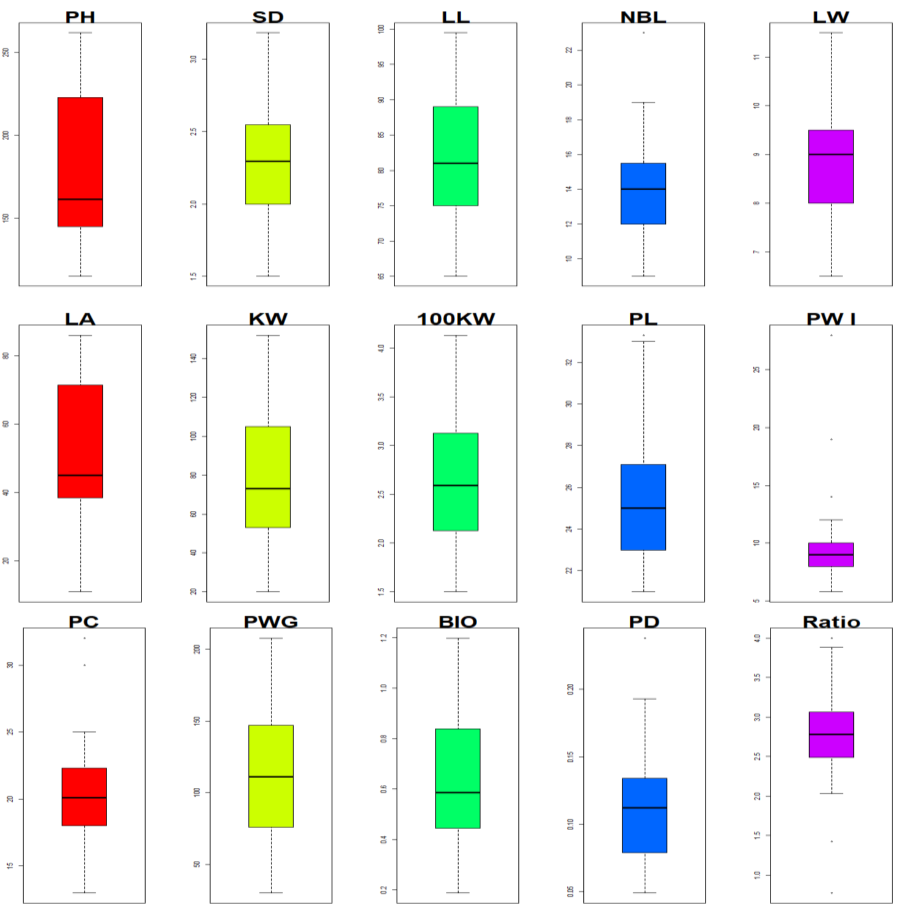


Figure 1. The boxplot of various agronomic traits and yield components of different sorghum genotypes visually represents the variability and distribution of these traits: PH= plant height, SD= stem diameter, LL= leaf length, NBL= number of leafs, LW= leaf width, LA= leaf angle, KW= kernel weight per penicle, 100KW= 100 kernel weight, PL= panicle length, PWI= panicle width, PC= panicle circumference, PWG= panicle weight, BIO= biomass, PD= panicle density, Ratio= ratio panicle length-width.

Panicle characteristics such as panicle length, weight of 100 grains, and biomass play significant roles in grain yield. The box plot in Figure 1 illustrates the variation in these yield components. Genetic variability analysis also shows that both genotype and phenotype diversity in these traits are relatively high. For instance, panicle length in sorghum genotypes ranges from 21.00 to 33.00 cm. The longest panicle is found in genotype Gen-4 (33.00 cm), significantly different from other sorghum genotypes except for Gen-5 (31.75 cm). Research by Maftuchah et al. in 2021 [24] similarly indicates diverse panicle lengths among sorghum genotypes, ranging from 23.92 to 47.75 cm, with high genetic and phenotypic variability. Variability in panicle length and panicle weight is attributed to higher genetic and phenotypic diversity compared to environmental variability [31].

Table 4. The performance of panicle length, 100 kernel weight, kernel weight, and biomass of sorghum genotype.

Genotype	Panicle length (cm)	100 kernel weight (g)	Kernel weight per panicle (g)	Biomass (g)
Gen4	33.30a	2.31ghijkl	88.00bcdef	677.00fghi
Gen5	31.75ab	2.68defghij	84.00cdefg	612.00ghij
Gen6	27.20defgh	3.44ab	133.00a	1136.00a
Gen9	23.70ijklmno	2.74cdefghi	28.50lm	381.00mnop
Gen10	30.10bc	3.14abcde	75.00efghi	566.00ijk
Gen15	26.75efgh	1.81l	51.00hijklm	238.00p
Gen20	27.25defgh	3.14abcde	137.00a	1022.50abc
Gen21	21.00o	2.38fghijkl	46.50ijklm	349.50nop
Gen24	23.55ijklmno	2.20hijkl	58.00fghijkl	494.00jklmn
Gen25	23.85ijklmn	2.15ijkl	59.00efghijkl	519.00jklm
Gen26	23.20jklmno	2.09ijkl	81.00efgh	600.00hij
Gen27	23.00jklmno	2.03jkl	62.00efghijk	472.00jklmn
Gen28	23.40ijklmno	1.99kl	63.00efghijk	532.00ijkl
Gen30	22.00lmno	2.07ijkl	40.00jklm	415.00lmno
Gen32	21.50no	1.96kl	43.00jklm	434.00klmno
Gen35	27.50cdefg	2.08ijkl	54.00ghijklm	446.00klmno
Gen36	24.50hijklm	3.01bcdef	115.50ab	943.00c
Gen38	24.75ghijkl	2.75cdefghi	83.00defg	1109.50ab
Gen40	22.00lmno	2.31ghijkl	24.00m	303.00op
Gen45	22.70klmno	2.72cdefghi	33.00klm	298.00op
Gen48	25.50fghij	3.33abcd	143.00a	603.00ghij
Gen51	26.00fghi	3.82a	80.00efgh	753.00efg
Gen53	25.50fghij	3.29abcd	89.00bcde	740.00efgh
Gen54	26.95efgh	3.10bcde	112.50abcd	879.00cde
Gen55	29.75bcd	2.93bcdefg	126.00a	960.00bc
Gen56	29.50bcde	2.83bcdefgh	81.00efgh	533.00ijkl
Gen58	23.50ijklmno	2.56efghijk	67.50efghij	491.50jklmn
Gen59	28.00cdef	3.04bcdef	77.00efghi	717.00fgh
Gen60	25.50fghij	3.46ab	123.50a	992.00abc
Gen61	23.00jklmno	3.39abc	84.00cdefg	773.00def
Gen62	25.00ghijk	2.84bcdefgh	114.00abc	913.00cd
Gen64	21.75mno	2.00jkl	54.00ghijklm	493.00jklmn
$Lsd_{\alpha=0.05}$	2.78	0.68	30.75	150.30

Note: The numbers followed by the same letter in the same column show no significant difference in the 5% LSD test.

Grain weight per panicle is crucial in selection processes, reflecting the potential yield per unit area from evaluated genotypes [29]. Genotypes significantly influence grain weight per panicle. On average, grain weights per panicle range from 24.00 to 143.00 g, with the highest recorded in sorghum genotype Gen-48 (143 g), not significantly different from genotypes Gen-6, Gen-20, Gen-36, Gen-54, Gen-55, Gen-60, and Gen-62. Grain yield relates to interactions among genetics, environmental factors, nutrient uptake, and plant growth stages [17]. Panicle length, grain weight, and panicle weight in sorghum are influenced by non-additive genetic effects [16] .

3.3 Genetic Variability and Heritability

Genetic variability indicates the extent of individual genetic influence within a population, whereas phenotypic variability results from the interaction between genetics and the environment. Table 5 presents the analysis of genetic and phenotypic variability. All observed traits show high genetic variability except for leaf length, number of leaves, leaf width, and panicle width. It explains that the tested sorghum genotypes exhibit considerable diversity within the population.

Table 5. Genotypic variance, phenotypic variance, error variance, standard deviation of genotypic variance, standard deviation of phenotypic variance of observed character.

Characters	σ^2g	σ^2p	σ^2e	$\sigma_{\sigma2g}$	$\sigma_{\sigma2p}$
Plant height (PH)	1599.60H	1773.87H	174.27	415.80	415.25
Stem diameter (SD)	0.09H	0.13H	0.04	0.03	0.03
Leaf length (LL)	18.69L	83.03H	0.04	14.82	12.52
Number of leaf (NBL)	1.43L	6.28H	4.85	1.12	0.95
Leaf width (LW)	0.42L	1.17H	0.75	0.22	0.20
Leaf angle (LA)	360.47H	393.98H	33.51	92.96	92.87
Kernel weight (KW)	944.91H	1167.92H	223.01	261.51	260.07
100 kernel weight (100KW)	0.24H	0.35H	0.11	0.07	0.07
Panicle length (PL)	8.27H	10.19H	1.91	2.28	2.27
Panicle width (PWI)	2.33L	9.57H	7.24	1.71	1.46
Panicle circumference (PC)	10.21H	11.95H	1.74	2.74	2.73
Panicle weight (PWG)	1897.54H	2078.30H	180.76	489.89	489.39
Biomass (BIO)	57338.73H	62947.85H	5609.12	14822.39	14806.31
Panicle density (PD)	0.01L	0.01L	0.05	0.03	0.03
Ratio pnicle length-width (Ratio)	0.18H	0.31H	0.13	0.06	0.06

Note: H= high, L= low, σ^2g= genotypic variance, σ^2p= phenotypic variance, $\sigma_{\sigma2g}$= standard deviation of genotypic variance, $\sigma_{\sigma2p}$= standard deviation of phenotypic variance.

Heritability is the ratio of genetic variance to phenotypic variance within a population. This study employs broad-sense heritability, which describes the overall genetic influence on the phenotype of tested sorghum genotypes. Table 6 indicates that tested sorghum genotype traits with high genetic variability also exhibit high heritability values, whereas traits with low genetic variability show moderate heritability values. Traits with high heritability include plant height, stem diameter, leaf angle, kernel weight per panicle, 100 kernel weight, panicle length, panicle width, panicle circumference, panicle weight, biomass, panicle density, and panicle length-width ratio. Traits with moderate heritability include leaf length, number of leaves, leaf width, and panicle width.

Genetic advancement is a method used to predict changes in trait appearance within a population across each selection cycle. Genetic advancement percentage falls into three categories: high, moderate, and low (Table 6). Traits showing high genetic advancement percentages include plant height (43.67%), stem diameter (21.92%), leaf angle (74.54%), kernel weight per panicle (72.62%), 100 kernel weight (31.41%), panicle length (21.02%), panicle width (16.24%), panicle circumference (29.87%), panicle weight (74.50%), biomass (73.87%), panicle density (40.64%), and panicle length-width ratio (23.83%). Traits with moderate genetic advancement percentages include panicle width (16.24%), while traits with low genetic advancement percentages include leaf length (5.16%), number of leaves (8.42%), and leaf width (8.97%). Genetic advancement percentages for traits such as plant height, panicle length, panicle width, grain weight per panicle, 100-grain weight, and biomass. High genetic advancement is attributed to higher control of additive genes than non-additive genes. High heritability and genetic advancement facilitate the selection of superior sorghum genotypes [33;34].

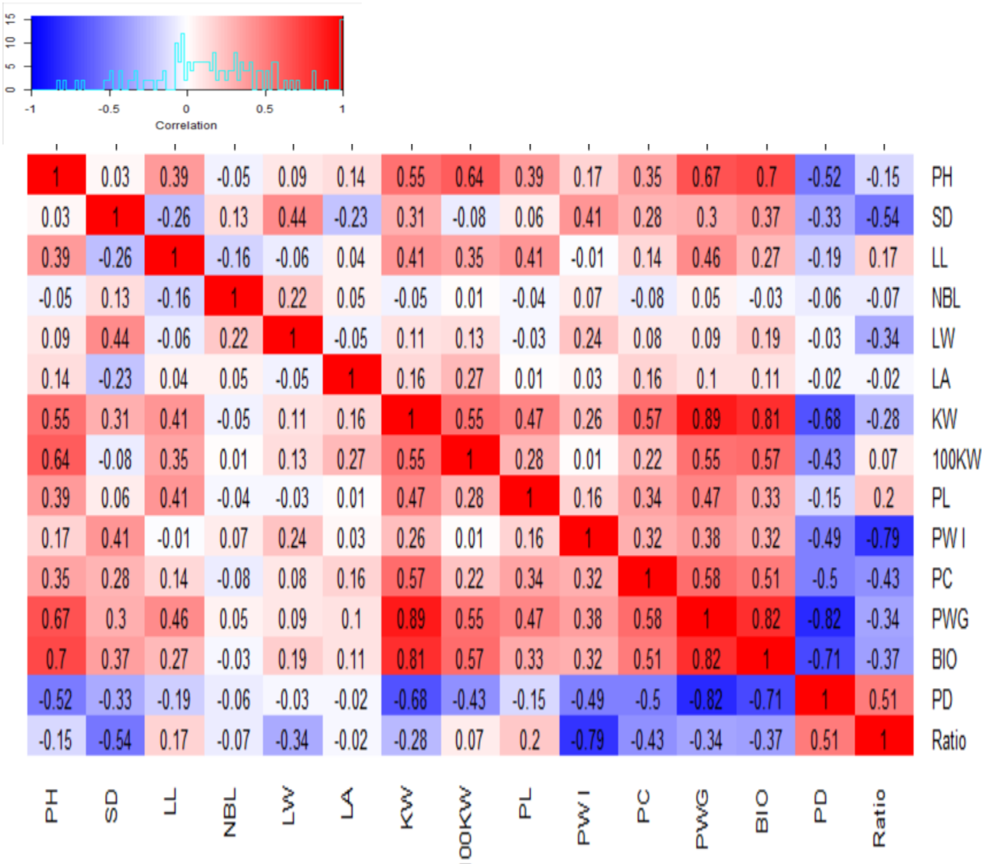
Table 6. Grand mean, heritability, genetic advances of observed character.

Characters	Grand mean	H^2	GA	GA (%)
Plant height	179.16	0.90H	78.24	43.67H
Stem diameter	2.31	0.67H	0.51	21.92H
Leaf length	81.91	0.23M	4.22	5.16L
Number of leaf	13.95	0.23M	1.17	8.42L
Leaf width	8.91	0.36M	0.80	8.97L
Leaf angle	50.19	0.91H	37.41	74.54H
Kernel weight per panicle	78.44	0.81H	56.96	72.62H
100 kernel weight	2.67	0.69H	0.84	31.41H
Panicle length	25.40	0.81H	5.34	21.02H
Panicle width	9.55	0.24M	1.55	16.24M
Panicle circumference	20.37	0.85H	6.08	29.87H
Panicle weight	115.09	0.91H	85.74	74.50H
Biomass	637.34	0.91H	470.79	73.87H
Panicle density	0.11	0.62H	0.05	40.64H
Ratio panicle length-width	2.80	0.58H	0.67	23.83H

Note: H= high, M= medium, L= low, $\sigma^2 g$= genotypic variance, $\sigma^2 p$= phenotypic variance, $\sigma_{\sigma 2g}$= standard deviation of genotypic variance, $\sigma_{\sigma 2p}$= standard deviation of phenotypic variance.

3.4 Correlation of Observed Traits

Correlation is used in selection to determine the strength of relationships for each observed trait. The correlations among observed traits are presented in Figure 2. Traits that significantly correlate positively with grain weight per panicle include plant height (0.55), stem diameter (0.31), leaf length (0.41), panicle length (0.47), panicle circumference (0.57), panicle width (0.26), panicle weight (0.89), weight of 100 grains (0.55), and biomass (0.81). Rini et al. in 2022 [35] also found stem diameter, panicle diameter, and panicle length to correlate significantly positively with grain weight per panicle. According to Wirnas et al., (2021), traits that can predict high grain yield in sorghum are stem diameter, leaf count, flag leaf area, leaf greenness, and panicle diameter [36].



PH= plant height, SD= stem diameter, LL= leaf length, NBL= number of leafs, LW= leaf width, LA= leaf angle, KW= kernel weight per penicle, 100KW= 100 kernel weight, PL= panicle length, PWI= panicle width, PC= panicle circumference, PWG= panicle weight, BIO= biomass, PD= panicle density, Ratio= ratio panicle length-width.

Figure 2. Correlation among traits of sorghum genotypes

4 Conclusion

The evaluation of 32 F2 sorghum genotypes revealed significant genetic advancements, particularly in traits with high heritability and positive correlations with kernel weight per panicle. Genotype Gen-48 exhibited the highest kernel weight per panicle, with notable plant height, stem diameter, panicle length, and biomass. Traits such as plant height, stem diameter, leaf angle, kernel weight per panicle, 100-kernel weight, panicle length, panicle width, panicle circumference, panicle weight, biomass, panicle density, and panicle length-width ratio demonstrated high heritability and genetic advance. In addition, it significantly correlates positively with grain yield, including plant height, stem diameter, leaf length, panicle length, panicle circumference, panicle width, panicle weight, weight of 100 kernels, and biomass.

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