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Genetic and path analysis of agronomic traits in Indonesian sorghum genotypes

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Abstract. *Nasution MA, Maulana Z, Alam M, Hanafi, Ulfa F, Abdullah A. 2025. Genetic and path analysis of agronomic traits in Indonesian sorghum genotypes. Biodiversitas 26: 5944-5954.* Sorghum (*Sorghum bicolor*) is a strategic cereal for food, feed, and bioenergy in tropical production systems, yet its improvement is constrained by limited characterization of genetic variability and yield-determining traits across local and commercial germplasms. This study evaluated eight contrasting genotypes under a randomized block design in Maros, South Sulawesi, to quantify genetic variation, heritability, and trait-yield relationships. Wide phenotypic divergence was observed, with grain yield ranging from 4.64 to 58.93 g per plant and plant height from 145.6 to 265.9 cm, reflecting substantial heterogeneity within the tested germplasm. High heritability estimates for grain yield (0.75), panicle dry weight (0.75), and thousand-grain weight (0.89) indicate strong additive genetic control and substantial prospects for early generation selection. Path analysis identified thousand-grain weight (direct effect = 0.713), panicle dry weight (0.442), and panicle width (0.304) as the major determinants of grain yield, confirming the central role of reproductive biomass in yield formation. In contrast, the number of nodes and leaves exhibited negative associations with grain yield, demonstrating a physiological trade-off between vegetative vigor and reproductive partitioning, which is consistent with earlier reports across cereals. Sugar content showed moderate heritability (0.68) and a limited direct influence on grain yield, reaffirming its relevance primarily for sweet sorghum improvement. Commercial varieties (Numbu, Kawali, and UPCA-S1) exhibited superior reproductive performance, whereas local genotypes (Watasolok and Okin) expressed adaptive attributes, including taller architecture and enhanced vegetative robustness. The complementary strengths of these groups underscore the potential of targeted hybridization coupled with selection for panicle- and seed-related traits to accelerate the development of high-yielding, climate-resilient sorghum cultivars in tropical environments.

Keywords: Breeding, genetic diversity, heritability, path analysis, sorghum

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is the fifth most significant cereal crop globally after wheat, rice, maize, and barley. The strategic significance of this crop is attributed to its nutritional composition, adaptability, and resilience to extreme conditions, including drought, nutrient-deficient soils, and elevated temperatures, thereby playing a crucial role in enhancing food security in arid and semiarid regions (Khalifa and Eltahir 2023; Mwamahonje et al. 2024). Sorghum has emerged as an alternative cereal resilient to climate change, which increasingly undermines the stability of primary food crop production. Besides being utilized as food and feed, sorghum possesses significant potential as a raw material for bioethanol production owing to its high biomass yield and sugar-laden stems (Guden et al. 2020; Umakanth et al. 2024).

In East Nusa Tenggara, Indonesia, sorghum is advocated to diversify food sources and exploit arid marginal regions. Nevertheless, its advancement has been obstructed by inadequate breeding programs, restricted access to adaptable superior varieties, and insufficient assessment of local germplasm (Senbetay and Belete 2020). This has led to reduced consumption and diminished focus on local varieties (Ariningsih et al. 2023). Indigenous genotypes typically exhibit resilience to both biotic and abiotic stressors, whereas commercial variants exhibit elevated productivity. The integration of the two offers the potential to generate novel varieties that are both high-yielding and adaptable (Kasule et al. 2024).

Sorghum, a C4 plant, exhibits high photosynthetic and water-use efficiencies, making it vital under climate change. The main challenge for breeders is to develop genotypes with stable yields across environments. Integrating conventional and modern tools, such as marker-assisted selection, QTL mapping, and high-throughput phenotyping, is essential (Hao et al. 2021; Mwamahonje et al. 2024). Success depends on genetic diversity and appropriate selection methods. Estimating genetic parameters variance, heritability, and genetic advance provides critical insights because traits with high heritability and advance are more responsive to selection (Fehr 1987; Allard 1999; Gebre et al. 2024).

Several studies have validated the genetic potential of sorghum. Panicle weight and thousand-grain weight exhibit high heritability, exceeding 90% (Baye et al. 2022), whereas plant height can reach up to 99% and grain yield approximately 76%, demonstrating significant genetic influence, especially in Ethiopia and Sudan (Gebregergs and Mekbib 2020; Gichile et al. 2022). Therefore, these characteristics may serve as markers for direct selection. Correlation analysis alone is inadequate because it fails to distinguish between the direct and indirect impacts of the features. Path analysis elucidates the role of each trait in yield (Dewey and Lu 1959; Burks et al. 2015; Fatimah et al. 2021; Wirnas et al. 2021).

Recent research in East Africa and India has demonstrated that panicle weight and width exert the most significant direct influence on grain yield, whereas plant height impacts yield more indirectly via biomass (Fuglie et al. 2024; Kasule et al. 2024; Mgendi 2024). The weight of 1,000 seeds reliably serves as a steady predictor of yield (Guden et al. 2020). Additional physiological and agronomic characteristics, including stem diameter (≥17 mm), leaf count (≥10), flag leaf area (≥209 cm²), and panicle diameter (≥49 mm), have also been suggested as selection criteria (Wirnas et al. 2021). Panicle length and plant height are critical factors that influence the yield of various cereals (Parimala et al. 2023; Saketh et al. 2023). Further evidence is provided by extensive genetic diversity (GCV 3.13-37.44; PCV 5.11-38.08), elevated heritability for panicle yield (97%), and substantial genetic advance (75.93%) (Gebregergs and Mekbib 2020).

Despite significant progress, research deficiencies continue to exist in Indonesia. To date, there has been no thorough assessment of local and commercial genotypes in standardized field settings, thus constraining the identification of essential features for selection in breeding programs. Bridging this gap is important to encourage the development of superior sorghum varieties tailored to Indonesia's tropical agroecosystems.

This study evaluated the genetic parameters of key agronomic traits in local and commercial sorghum genotypes, examined trait relationships through correlation and path analysis, and identified traits with direct effects on grain yield. The findings provide priority selection criteria for breeding high-yielding, adaptable sorghum varieties suited to tropical environments.

MATERIALS AND METHODS

Research location

This study was conducted at the Cereal Crop Assembly and Testing Center, division of the Agricultural Assembly and Modernization Agency (BRMP) under the Indonesian Ministry of Agriculture, located in the Maros District, South Sulawesi, Indonesia, altitude 60 m above sea level). The experiment was conducted during the planting season, and the planting began on March 14, 2024, until the research was completed in July 2024.

The research site is situated within lowland agroecosystem with a tropical monsoon climate (Am), receiving an average rainfall of about 71.2-156.5 mm per month during the research period. The soil type is classified as alluvial, with good drainage, a soil pH ranging from 5.8 to 6.3, and a moderate organic matter content. The field was irrigated using a surface irrigation system supported by pump wells around the site to ensure that the water availability remained stable. The land was plowed and harrowed, followed by leveling to optimize the uniformity of the planting and water distribution. Further details are shown in Figure 1.

Plant materials

The plant material comprises eight sorghum genotypes (*Sorghum bicolor*), which include four national varieties developed by the Agricultural Research and Development Agency under the Ministry of Agriculture of the Republic of Indonesia: Super-1, UPCA-S1, Numbu, and Kawali. Additionally, there are four local genotypes from the East Nusa Tenggara: Kuali, Watasolot, Okin, and Waiotan.

Experimental design

The experiment used a randomized block design with three repetitions. This design featured a single factor, which included four local and four national sorghum genotypes, resulting in 24 experimental units. Sorghum seeds were planted in plastic trays filled with a mixture of soil and compost. After 10 days, the seedlings were moved to beds measuring 200 cm × 100 cm, with a planting distance of 75 cm × 15 cm, resulting in 18 sorghum plants per plot. Organic fertilizer, in the form of manure and compost, was applied during soil preparation, while chemical fertilizers (Urea, SP-36, and KCl) were administered by dibbling twice: once at 2 weeks and again at 4 weeks post-planting. Weekly applications of insecticides, bactericides, acaricides, and fungicides were carried out following the recommended dosages. Sorghum plants were harvested when the seeds were mature and firm, the stems and leaves dried, and the seed heads remained intact. At this point, sorghum typically reaches physiological maturity, characterized by a seed moisture content of approximately 14%, hard and dry seeds, reduced chlorophyll in the leaves, and decreased seed dormancy (Oyier et al. 2017). To achieve higher starch, protein, and tannin levels, the main crop was harvested, whereas ratoon sorghum offered greater economic benefits and resource efficiency. However, the fat content in ratoon yields is lower than that in the main crop (Zhou et al. 2022).

Data collection and analysis

Measurements were taken of the dry seed weight per plant (seed yield per plant) and its components, including plant height (cm), stem diameter (mm), number of nodes, number of leaves, fresh plant weight (biomass, g), panicle width (cm), panicle length (cm), fresh panicle weight (g), dry panicle weight (g), Brix sugar content (%), and thousand-grain dry weight (g). All data were recorded and organized using Microsoft Excel 2019. Analysis of Variance (ANOVA) was performed according to the method of Gomez and Gomez (1984), and the post-hoc Honest Significant Difference test was conducted using PKBT-STAT version 3.2 (http://pbstat.com/pkbt-stat). Genetic and phenotypic variance analyses were performed based on the formula of Singh and Chaudhary (1979), heritability values were determined using the formulas of Fehr (1987) and Allard (1999), and genetic gain was calculated using the online application PBSTAT-PPB version 1.2 (http://www.pbstat.com/ppb/balanova.php). Correlation analysis was performed to assess the relationships between traits using the formulas and criteria of Gomez and Gomez (1984), while path analysis was carried out based on the method of Dewey and Lu (1959); both analyses were calculated using Jeffreys's Amazing Statistics Program (JASP) application.

RESULTS AND DISCUSSION

Analysis of variance in agronomic characters

Analysis of Variance (ANOVA) of the 12 agronomic traits of sorghum showed highly significant differences ($p<0.01$) among the eight genotypes (Table 1). The evaluated traits were Plant Height (PH), Stem Diameter (SD), Number of Nodes (NN), Number of Leaves (NL), Biomass (BI), Panicle Length (PL), Panicle Width (PW), Fresh Panicle weight (PF), Dry Panicle weight (PD), Brix sugar content (BR), Thousand-grain Weight (TW), and Grain Yield per plant (GY). The observed genetic diversity was substantial. Plant height varied between 145.60 and 265.93 cm, while GY ranged from 4.64 to 58.93 g, with an average of 32.14 g. These wide ranges indicate the presence of genotypes that can be used as parents in breeding programmes. Panicle traits, particularly PF and PD, also showed significant variation, underscoring their potential as reliable yield indicators. The accuracy of the measurements was high, as evidenced by the low error variance in traits, such as NL and TW, supporting precise heritability and genetic gain estimation.

Variance components and heritability

Analysis of Variance (ANOVA) of the 12 agronomic traits of sorghum showed significant genetic variation among the eight genotypes tested (Table 2). The parameters Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were used to assess genetic diversity. In general, most traits showed high heritability values (>60%), indicating that variation was influenced more by genetic factors than by the environment.

High GCV and PCV values were observed for yield-related traits: Plant Height (PH), Biomass (BI), Panicle Width (PW), Fresh Panicle weight (PF), Dry Panicle weight (PD), Brix sugar content (BR), and Grain Yield per plant (GY). Conversely, traits with moderate GCV-PCV values, such as Stem Diameter (SD), Number of Leaves (NL), Panicle Length (PL), and 1,000-grain weight (TW), indicated the presence of genetic diversity but were more influenced by the environment. The Number of Nodes (NN) showed the lowest variability (GCV = 9.60%; PCV = 12.18%); thus, its potential was limited. High heritability estimates were recorded for PH (0.96), BI (0.98), PW (0.88), PF (0.73), PD (0.75), TW (0.89), and GY (0.74), confirming strong genetic control.

Traits exhibiting moderate GCV-PCV values, including stem diameter, number of leaves, panicle length, and 1,000-grain weight, demonstrate some genetic diversity but are more susceptible to environmental influences. This implies that while genetic improvement is possible for these traits, environmental factors play a significant role in their expression, necessitating careful consideration of genotype-environment interactions in breeding strategies. The high heritability estimates for several traits, particularly plant height, biomass, panicle width, fresh and dry panicle weight, 1,000-grain weight, and grain yield per plant, further reinforce the strong genetic control over these characteristics. These high heritability values suggest that a large proportion of the observed phenotypic variation is due to genetic factors, and that selection based on these traits is likely to be effective in improving crop performance in subsequent generations.

Table 1. Analysis of variances for different morphological traits in sorghum

Traits	Genotype	Block/Rep	Residual	G. Mean	Range	CV (%)
Plant height (cm)	7095.68*	218.93 ^{ns}	98.03	219.67	145.60-265.93	4.51
Stem diameter (mm)	8.10*	0.02 ^{ns}	1.37	15.61	12.81-18.79	7.51
Number of nodes	5.31*	0.66 ^{ns}	2.80	12.38	10.93-15.27	3.62
Number of leaves	5.98*	0.43^{ns}	0.24	12.88	11.27-15.93	3.77
Biomass (g)	0.02*	0.02 ^{ns}	0.00	0.324	0.19-0.38	21.71
Panicle width (cm)	283.16*	3.09 ^{ns}	12.24	41.11	23.91-53.95	8.51
Panicle length (cm)	31.69*	1.42 ^{ns}	2.19	20.94	15.71-24.53	7.07
Fresh panicle weight (g)	1582.16*	125.60 ^{ns}	176.17	52.55	12.87-91.67	25.26
Dry panicle weight (g)	1343.76*	103.38 ^{ns}	131.45	44.33	8.39-81.40	25.86
Brix sugar content (%)	26.49*	2.36 ^{ns}	3.57	9.94	6.75-15.07	19.01
Thousand-grain weight (g)	25.02*	2.63 ^{ns}	0.10	22.39	3.20-42.50	14.38
Grain yield per plant (g)	717.78*	15.59 ^{ns}	71.67	32.14	4.64-58.93	26.34

Note: *: Significant ($p<0.01$), ns: Non significant

Table 2. Variance value components, coefficient of diversity, and heritability

Traits	σ2g	σ2e	σ^2p	GCV	PCV	H^{2}bs
Plant height (cm)	2,332.55	98.03	2,430.58	21.99	22.44	0.96
Stem diameter (mm)	1.70	0.20	1.90	10.55	11.15	0.89
Number of nodes	2.24	1.37	3.61	9.60	12.18	0.62
Number of leaves	1.91	0.24	2.15	10.74	11.39	0.89
Biomass (g)	0.01	0.004	0.01	25.16	25.16	0.98
Panicle width (cm)	90.31	12.24	102.55	23.12	24.63	0.88
Panicle length (cm)	9.83	2.19	12.02	14.98	16.56	0.82
Fresh panicle weight (g)	468.66	176.17	644.83	41.20	48.32	0.73
Dry panicle weight (g)	404.10	131.45	535.55	45.34	52.20	0.75
Brix sugar content (%)	7.64	3.57	11.21	27.80	33.68	0.68
Thousand-grain weight (g)	0.83	0.10	0.93	12.87	15.39	0.89
Grain yield per plant (g)	215.37	71.67	287.04	45.66	52.72	0.75

Note: σ2e: Environmental variance, σ2g: Genotypic variance, σ2p: Phenotypic variance, GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation, H^{2}bs: Broad-sense heritability

The average results of agronomic character observations

Table 3 shows the agronomic characteristics of the eight sorghum genotypes, consisting of four commercial varieties Super 1, UPCA-S1, Numbu, and Kawali) and four local varieties (Kuali, Watasolok, Okin, and Waiotan). Local genotypes showed stronger vegetative growth, with Waiotan and Watasolok exceeding 260 cm in height and Waiotan having more internodes (18.79), leaves (15.93), and the largest stem diameter (15.27 mm), indicating high biomass potential. Kuali was the shortest (145.60 cm) with thinner stem, favorable for lodging resistance. Meanwhile, commercial genotypes excelled in reproductive traits: Numbu led with the widest panicle (53.95 cm), highest PF (91.67 g), PD (81.40 g), Brix (15.07%), TW (40.87 g), and highest grain yield (294.67 g/plant). Okin followed in sugar content (13.46%), while Waiotan, despite tall growth, had the lowest yield (23.21 g/plant), showing vigor doesn't always mean higher productivity.

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Clear differences were observed in reproductive traits. Commercial genotypes generally excelled in traits directly related to yield. Numbu stood out with the widest panicle (53.95 cm), a fresh panicle weight of 91.67 g, and a dry panicle weight of 81.40 g, all of which contributed to its high grain yield. Kawali also had a relatively wide panicle (44.62 cm) and good dry panicle weight (57.20 g). Panicle length was relatively uniform among the genotypes, with Super 1 (24.53 cm) and Waiotan (24.39 cm) having the longest panicles, indicating that panicle length was not a major distinguishing factor among the varieties.

In terms of yield quality, the sugar content (Brix) showed an interesting pattern. Numbu had the highest sugar content (15.07%), followed by Okin (13.46%), making it a promising raw material for sweet sorghum-based bioethanol and functional foods. Other genotypes, such as Super 1, had moderate sugar content (10.22%), whereas Waiotan had the lowest (6.80%) and was more suitable for grain types. The 1,000 g Thousand Weight (TW) also confirmed Numbu's dominance (40.87 g), indicating a large seed size, followed by Okin (26.19 g), which is sufficient for seed quality. Grain Yield per plant (GY) is the main determinant of agronomic performance. Numbu clearly took the top position with a yield of 294.67 g per plant, far surpassing other genotypes. Kawali (188 g) and UPCA-S1 (178 g) were in the middle group, while Waiotan, despite its tall and leafy appearance, actually had the lowest grain yield (23.21 g/plant). This phenomenon shows that high vegetative vigor does not always translate to higher grain yield, because photosynthates in tall and leafy plants tend to be allocated to vegetative organs rather than the panicle.

Figure 2 shows the differences in performance between local and commercial sorghum genotypes based on 12 main agronomic traits: Plant Height (PH), Stem Diameter (SD), Number of Nodes (NN), Number of Leaves (LN), Biomass (BI), Panicle Width (PW), Panicle Length (PL), Fresh Panicle weight (PF), Dry Panicle weight (PD), sugar content/Brix (BR), 1,000 g Thousand Weight (TW), and Grain Yield per plant (GY). The dashed line representing local genotypes protrudes outward on vegetative parameters, particularly PH, SD, NN, and LN, indicating that local genotypes tend to have more vigorous vegetative growth, with taller plants, thicker stems, and more leaves and nodes. These characteristics provide advantages for local genotypes in biomass and forage production, but are not always accompanied by increased grain yield. In contrast, the solid line representing commercial genotypes stands out in terms of reproductive parameters, such as PW, PF, PD, TW, and especially GY. This pattern shows that commercial genotypes have wider and heavier panicles, larger seeds, and higher grain yields per plant than local genotypes. This difference underscores the fact that commercial genotypes are more targeted for grain productivity, making them more suitable for food and seed requirements. Meanwhile, sugar content (BR) appeared to be relatively balanced between the two groups, indicating that both local and commercial genotypes have the potential for use as sweet sorghum for bioethanol.

Table 3. Mean agronomic traits of eight local and commercial sorghum genotypes

Varietas	PH	SD	NN	LN	BI	PW	PL	PF	PD	BR	TW	GY
Super 1	263.80^{a}	12.40^{bc}	15.17^{bc}	12.67^{bcd}	0.32^{ab}	31.27^{de}	24.53^{a}	43.73^{bc}	33.33^{bc}	10.22^{abc}	23.41^{bc}	121.67^{bc}
UPCA-S1	157.13^{d}	11.40^{cd}	15.47^{abc}	11.80^{cd}	0.19^{b}	49.81^{ab}	18.88^{bc}	53.20^{b}	46.20^{b}	6.75^{c}	16.76^{cd}	178.00^{ab}
Numbu	246.60^{ab}	12.07^{bcd}	15.12^{bc}	12.60^{bcd}	0.46^{a}	53.95^{a}	19.00^{bc}	91.67^{a}	81.40^{a}	15.07^{a}	40.87^{a}	294.67^{a}
Kawali	191.33^{c}	13.00^{b}	16.22^{ab}	13.53^{b}	0.30^{ab}	44.62^{abc}	23.57^{a}	64.40^{ab}	57.20^{ab}	9.05^{bc}	24.61^{bc}	188.00^{ab}
Kuali	145.60^{d}	10.93^{d}	12.81^{c}	11.27^{d}	0.20^{b}	39.36^{cd}	18.87^{bc}	36.95^{bc}	33.00^{bc}	8.45^{bc}	19.08^{bc}	119.67^{bc}
Watasolok	257.80^{a}	11.67^{cd}	15.41^{abc}	12.33^{bcd}	0.38^{ab}	44.57^{abc}	22.56^{ab}	63.63^{ab}	51.47^{ab}	9.73^{abc}	19.80^{bc}	178.00^{ab}
Okin	229.13^{b}	12.27^{bc}	15.90^{abc}	12.93^{bc}	0.36^{ab}	41.41^{bc}	15.71^{c}	53.95^{ab}	43.67^{b}	13.46^{ab}	26.19^{b}	182.33^{ab}
Waiotan	265.93^{a}	15.27^{a}	18.79^{a}	15.93^{a}	0.38^{ab}	23.91^{e}	24.39^{a}	12.87^{c}	8.39^{c}	6.80^{c}	8.45^{d}	23.21^{c}
HSD 5%	28.64	1.29	3.39	1.40	0.20	10.12	4.29	38.4	33.17	5.47	9.32	122.46

Note: Values followed by the same letter within the same column are not significantly different according to the Honestly Significant Difference (HSD) test at the 5% significance level. PH: Plant Height (cm), SD: Stem Diameter, NN: Number of Nodes, LN: Number of Leaves, BI: Biomass (g), PW: Panicle Width (cm), PL: Panicle Length (cm), PF: Fresh Panicle weight (g), PD: Dry Panicle weight (g), BR: Brix sugar content (%), TW: Thousand-grain Weight (g), and GY: Grain Yield per plant (g)

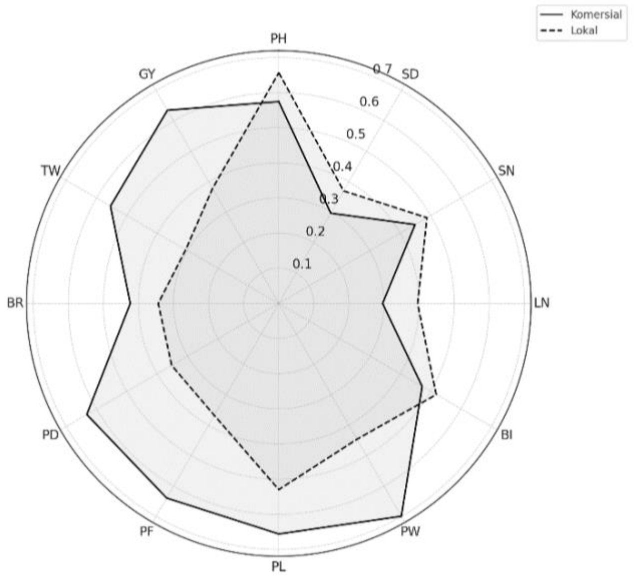

Figure 2. Comparison of local and commercial sorghum genotypes based on vegetative traits, reproductive traits, quality, and yield. PH: Plant Height (cm), SD: Stem Diameter (mm), NN: Number of Nodes, NL: Number of Leaves, BI: Biomass (g), PW: Panicle Width (cm), PL: Panicle Length (cm), PF: Fresh Panicle weight (g), PD: Dry Panicle weight (g), BR: Brix sugar content (%), TW: Thousand grain Weight (g), and GY: Grain Yield per plant (g)

Correlation analysis between characters

The Pearson correlation heatmap (Figure 3) provides an overview of the relationships between the 12 agronomic traits. Strong positive correlations were observed between panicle traits and Grain Yield per plant (GY). The panicle fresh weight (PF, r = 0.98), panicle dry weight (PD, r = 0.97), and panicle width (PW, r = 0.85) were closely associated with GY, confirming their direct contribution to yield. Therefore, genotypes with heavier and wider panicles tended to produce higher grain yields.

Plant height (PH) showed moderate correlations with PF and GY, indicating that taller plants can support larger panicles, but height alone is not a decisive determinant of yield. Similarly, Stem Diameter (SD) was positively correlated with PF and PD, suggesting its structural role in supporting assimilate allocation and grain filling. The Number of Nodes (NN) and Number of Leaves (NL) had weak correlations with GY but were strongly related to Biomass (BI), reflecting their role in photosynthetic capacity rather than direct yield contribution. Biomass was correlated with PF (r = 0.74) and PD (r = 0.70), indicating that greater vegetative mass can enhance reproductive allocation.

Brix sugar content (BR) showed modest positive correlations with PF and PD, but only a weak relationship with GY. This suggests that although sugar accumulation may support grain filling, it is not always predictive of grain yield in sorghum. Thousand-grain weight (TW), which represents seed size, was positively but weakly associated with GY, implying that yield in this population depended more on panicle biomass than on seed size.

Overall, PF, PD, and PW emerged as the most reliable indicators of grain yield. Traits such as PH, SD, and BI contributed indirectly by supporting structural stability and photosynthesis. The weak correlations between NN, NL, and GY reinforce that excessive vegetative allocation is less beneficial for grain yield improvement.

Path analysis of traits on grain yield

Path analysis was conducted to evaluate the direct and indirect effects of the 12 agronomic traits on sorghum (GY) of sorghum (Table 4). The results showed varying contributions of reproductive, vegetative, and quality traits. The Thousand-grain Weight (TW, 0.713) had the greatest direct influence on GY, followed by the Dry Panicle weight (PD, 0.442), Panicle Width (PW, 0.304), and Fresh Panicle weight (PF, 0.171). These reproductive traits strongly contribute to yield. Vegetative traits showed smaller direct effects: Plant Height (PH, 0.194), Stem Diameter (SD, 0.330), and biomass (BI, -0.185).

Nevertheless, these traits contributed indirectly by increasing PF and PD. The Number of Nodes (NN, 0.096) and Leaves (NL, 0.087) had very slight direct effects and were negatively correlated with yield. Meanwhile, the Brix sugar content (BR, -0.325) had a negative direct effect on GY but showed a positive indirect contribution through PF, PD, and TW. Overall, reproductive traits related to panicle biomass (PF, PD, and PW) and grain size (TW) were the main determinants of grain yield per plant. Vegetative traits functioned as supporters, while NN and NL were negatively associated with productivity. BR is a more relevant quality indicator for sweet sorghum than a direct determinant of grain yield.

Discussion

The Coefficient of Variation (CV) further highlighted trait stability. NL (3.77%) and NN (3.62%) had low CVs values, indicating high stability, whereas GY (26.34%) and BI (21.71%) had high CVs values, suggesting their suitability for early selection. The lack of significant block effects confirmed that genetic, rather than environmental, factors were primarily responsible for the observed variation. Overall, these results suggest that traits such as PH, PF, PD, and GY are highly variable and heritable, offering significant opportunities for rapid selection. In contrast, Stable traits NL and NN support sorghum adaptation under stress. The stay-green phenotype, linked to root architecture, improves water uptake efficiency and sustains yield under drought and heat (Kamal et al. 2019; Menamo et al. 2023).

Table 4. Analysis of path coefficients showing the direct (bold) and indirect effects of character traits on seed yield per plant in eight sorghum genotypes

Traits	**PH**	**SD**	**NN**	**NL**	**BI**	**PW**	**PL**	**PF**	**PD**	**BR**	**TW**	**GY**
PH	**0.19**	0.61*	0.56**	0.58**	0.98**	-0.38 ^{ns}	0.46 ^{ns}	0.01 ^{ns}	-0.08 ^{ns}	0.37 ^{ns}	0.12 ^{ns}	-0.10 ^{ns}
SD	0.47*	**0.33**	0.98**	0.98**	0.38*	-0.51 ^{ns}	0.50 ^{ns}	-0.45 ^{ns}	-0.47 ^{ns}	-0.24 ^{ns}	-0.45 ^{ns}	-0.51 ^{ns}
NN	0.53**	0.76**	**0.1**	0.99**	0.50 ^{ns}	-0.69**	0.60*	-0.52*	-0.52 ^{ns}	-0.24 ^{ns}	-0.40 ^{ns}	-0.58*
NL	0.55**	0.78**	0.99**	**0.09**	0.54 ^{ns}	-0.65**	0.55*	-0.50 ^{ns}	-0.50*	-0.20 ^{ns}	-0.39 ^{ns}	-0.54*
BI	0.68**	0.10*	0.07 ^{ns}	0.35 ^{ns}	**-0.19**	0.02 ^{ns}	0.19 ^{ns}	0.40 ^{ns}	0.34^{ns}	0.92**	0.55 ^{ns}	0.32 ^{ns}
PW	-0.38 ^{ns}	-0.39 ^{ns}	-0.62**	-0.58**	-0.01 ^{ns}	**0.3**	-0.61*	0.92**	0.94**	0.50*	0.69**	0.95**
PL	0.41^{ns}	0.33 ^{ns}	0.48*	0.45*	0.06 ^{ns}	-0.44*	**0.07**	-0.43 ^{ns}	-0.43 ^{ns}	-0.53	-0.37 ^{ns}	-0.57 ^{ns}
PF	0.01 ^{ns}	-0.22 ^{ns}	-0.46*	-0.41 ^{ns}	0.33 ^{ns}	0.84**	-0.18**	**0.17**	0.10*	0.85*	0.95**	0.99**
PD	-0.07 ^{ns}	-0.23 ^{ns}	-0.46*	-0.41 ^{ns}	0.36 ^{ns}	0.86**	-0.22*	0.99**	**0.44**	0.80*	0.93**	.98**
BR	0.35 ^{ns}	-0.20 ^{ns}	-0.20 ^{ns}	-0.18 ^{ns}	0.40 ^{ns}	0.36 ^{ns}	-0.36**	0.50*	0.48*	**-0.33**	0.99**	0.87**
TW	0.11 ^{ns}	-0.28 ^{ns}	-0.34 ^{ns}	-0.32 ^{ns}	0.40 ^{ns}	0.63**	-0.39**	0.77**	0.79**	0.77**	**0.71****	0.95**
GY	-0.09 ^{ns}	-0.25 ^{ns}	-0.51*	-0.46*	0.28 ^{ns}	0.88**	-0.33 ^{ns}	0.98**	0.98**	0.51*	0.80**	**1**

Note: ns: Non-significant at α = 0.05, *: Significant at α = 0.05, **: Highly significant at α = 0.01, PH: Plant Height (cm), SD: Stem Diameter (mm), NN: Number of Nodes, NL: Number of Leaves, BI: Biomass (g), PW: Panicle Width (cm), PL: Panicle Length (cm), PF: Fresh Panicle weight (g), PD: Dry Panicle weight (g), BR: Brix sugar content (%), TW: Thousand-grain Weight (g), and GY: Grain Yield per plant (g)

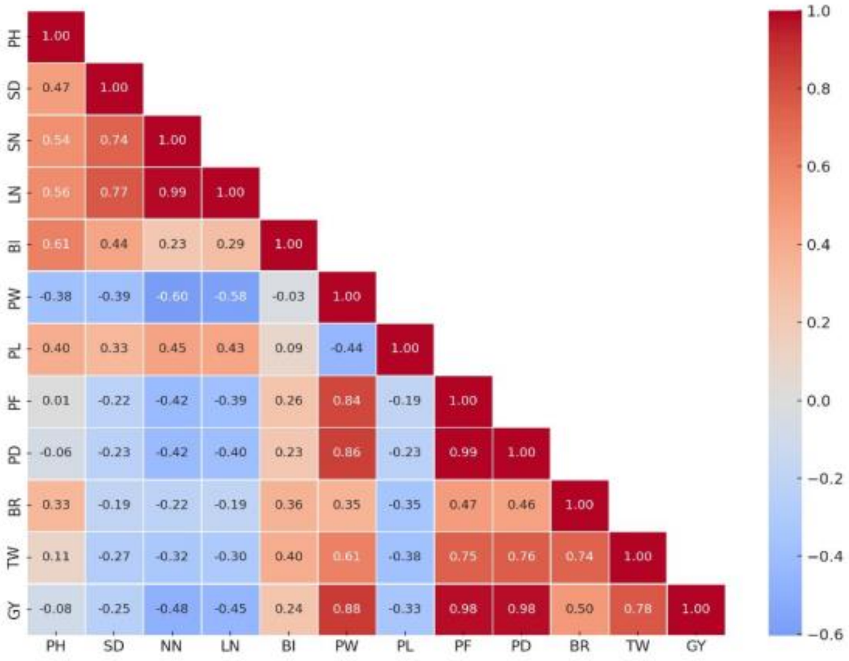

Figure 3. Pearson correlation heatmap matrix. PH: Plant Height (cm), SD: Stem Diameter, NN: Number of Nodes, LN: Number of Leaves, BI: Biomass (g), PW: Panicle Width (cm), PL: Panicle Length (cm), PF: Fresh Panicle weight (g), PD: Dry Panicle weight (g), BR: Brix sugar content (%), TW: Thousand-grain Weight (g), and GY: Grain Yield per plant (g)

The significant genotypic variation found in all traits highlights the vast genetic diversity of sorghum, which is vital for breeding. Traits such as PH, SD, and NL showed low CVs values, suggesting their stability. These traits are more reflective of adaptability than direct targets for yield improvement. Breeding approaches should utilize the genetic diversity of wild relatives and local lines to create modern varieties with improved yield, resistance, and adaptability. Molecular techniques, such as Marker-Assisted Selection (MAS), Genomic Selection (GS), and genome editing, enhance efficiency by introducing new variations and allowing precise gene modifications. The Green Revolution with semi-dwarf rice and wheat varieties increased crop yields through lodging resistance, nitrogen fertilizer efficiency, and the sd1 gene, which supports high productivity even under challenging conditions (Wu et al. 2018; Peng et al. 2021; Wang et al. 2021). Currently, integrating MAS and GS is crucial for accelerating the identification of superior traits in response to climate change (Saketh et al. 2023). Among the traits assessed, BR and TW were identified as important for the dual role of sorghum as both food and bioenergy.

The variation in BR among the genotypes underscores the potential of sweet sorghum for biofuel production, whereas TW is closely linked to grain quality. Recent QTL studies have strengthened the genetic understanding of sweet sorghum as a biofuel crop, with key QTL identified for bioenergy traits and stalk sugar yield (de Souza et al. 2021). Genetic analyses further highlight the role of architectural and metabolic traits as well as agronomic variation among superior genotypes for bioethanol production (Yang et al. 2023; Nazli et al. 2024). In addition, sugar-regulating genes such as SbSWEET1A have been identified as potential molecular targets to enhance sugar accumulation (Xue et al. 2023). These findings highlight the extensive adaptive capacity of sorghum and its potential to improve both yield and quality (Kasule et al. 2024).

Nonetheless, trait expression is shaped by interactions between genetic composition and environmental factors. Variables such as water availability, temperature, and agricultural practices significantly affect the BR. Sorghum biomass production is influenced by water availability, temperature, and agricultural practices. Water scarcity causes drought stress, while high temperatures disrupt critical growth stages. Soil conservation practices and biochar improve fertility and water retention. The dynamics of sugar accumulation highlight the importance of adaptive management to support sorghum productivity and resilience (Tajudeen et al. 2022; Kundu and Kumar 2024). For example, a lack of water before flowering can decrease BR, whereas stress after flowering may enhance it (Emendack et al. 2018). Similarly, sorghum genotypes with green midribs yielded more juice and sugar, underscoring the strong connection between plant structure and sugar accumulation (Burks et al. 2015). In semi-arid tropical regions, there is a focus on water use efficiency and biomass production. Drought-resistant genotypes can sustain yield under stress, whereas those that efficiently accumulate sugar can achieve higher ethanol yields under heat stress (Kandhol et al. 2022; Irfan et al. 2023; Nazli et al. 2024; Ferioun et al. 2025). Conducting stability analyses using AMMI and GGE biplots is advantageous for identifying superior genotypes in different environments. The AMMI and GGE biplot models are effective in analyzing genotype × environment interactions, identifying stable and superior varieties such as G3, G10, and G14 (Wang et al. 2023; Rajesh-Kumar et al. 2025). The integration of multi-trait indices, including MTSI and Smith-Hazel index, strengthens the selection of high-yielding genotypes for sorghum breeding (Da Silva et al. 2021).

Phosphorus plays a role in enhancing plant growth and sugar accumulation through mycorrhizal symbiosis, which optimizes the absorption of essential nutrients from the soil (Yang et al. 2023; Pang et al. 2024). Genetic diversity in phosphorus tolerance offers a chance to select genotypes suitable for nutrient-poor soils, and the combination of nitrogen and phosphorus fertilization has been shown to significantly increase yield (Roy et al. 2021; Li et al. 2025). The integration of genetic diversity, key economic traits (BR, TW, and GY), environmental adaptation, and nutrient management underscores the importance of sorghum as a resilient and adaptable tropical crop. Advanced breeding techniques incorporating natural diversity, molecular tools, and environmental management are essential for developing improved sorghum varieties. These strategies will enhance food security, climate resilience, and sustainable bioenergy production in tropical regions.

BR showed moderate to high heritability (68%), reflecting a combination of genetic and environmental influences. The small difference between GCV and PCV in most traits confirms that environmental influence is relatively minor. The broad genetic diversity in PH, PF, PD, and GY suggests that these traits are promising primary selection criteria. These findings are consistent with those of Gebregergs et al. (2020) and Endalamaw and Adugna (2025), who emphasized that traits with high GCV are more responsive to direct selection. Traits with moderate GCV-PCV values (SD, NL, PL, TW) require multilocation testing before being established as reliable selection targets (Tolera et al. 2023). In contrast, the low diversity in NN restricts its application, except when associated with adaptive traits. The high heritability of reproductive traits (PF, PD, GY, BR, PW) highlights their potential as primary selection criteria (Maftuchah et al. 2021), whereas BR needs careful consideration due to its sensitivity to climatic and environmental conditions.

Therefore, multilocation evaluation is important to ensure consistent results and appropriate selection strategies (Habyarimana et al. 2020). A similar pattern has also been observed in other commodities: in tomatoes, reproductive traits with high heritability accelerate selection efficiency (Dwary et al. 2023), and in wheat, high heritability for grain yield and plant height provides opportunities for improving productivity (Ahmed et al. 2016). Even in forest trees and livestock, reproductive traits with high heritability have been proven to play a role in long-term adaptation under selection pressure (Caignard et al. 2018; Fathoni et al. 2022). High heritability in yield traits, such as GY, PH, and flowering time, confirms the dominance of genetic over environmental influences. This enables breeders to select with greater confidence that superior traits will be passed on to the next generation (Li et al. 2023; Kasule et al. 2024). Thus, major yield traits (PF, PD, and GY) can be prioritized for direct selection, whereas BR requires cross-environment selection strategies for greater accuracy. The development of genomic technologies has enhanced breeding effectiveness. The identification of genetic loci through Genome-Wide Association Studies (GWAS) enables the application of marker-assisted and genomic selection to accelerate breeding cycles and improve precision (Li et al. 2023; Kasule et al. 2024). The combination of GCV, PCV, and heritability results confirmed a strong genetic basis for the tested sorghum genotypes. The main yield traits, particularly PF, PD, and GY, are the most effective selection criteria for productivity improvement, whereas BR requires a multilocation selection approach to minimize environmental influence. Integrating genetic information with modern technology supports the acceleration of the development of more productive and adaptive sorghum varieties for dry tropical lands.

Local genotypes generally exhibit superior vegetative traits. Waiotan and Watasolok had Plant Heights (PH) exceeding 260 cm, and Waiotan had the largest Stem Diameter (SD, 15.27 mm). The Number of Leaves (NL) and Nodes (NN) was notably higher in the local varieties, with Watasolok and Waiotan being particularly prominent. These traits indicate robust growth vigor, which is crucial for biomass production as feed or bioenergy. According to Tolera et al. (2023), genotypes with strong vegetative vigor have the potential for dual-purpose applications.

However, excessive vegetative growth, although it reflects plant vigor and good nutrient uptake capacity, does not always result in higher seed yield. This is because more resources are allocated to stems and leaves rather than to reproductive organs, such as panicles, which directly contribute to seed yield (Boyles et al. 2019; Mwamahonje et al. 2024). Therefore, reproductive growth is very important to ensure optimal productivity. Numbu and Kawali had plant heights ranging from 240 to 260 cm, with slightly smaller stem diameters than the local varieties. This moderate size improves resistance to lodging, because overly tall plants are more susceptible to falling under strong winds or heavy rain. Mu et al. (2021) highlighted the need to balance vegetative vigor and stability to maintain sorghum productivity in tropical environments.

The most notable differences were observed in reproductive traits. Commercial genotypes consistently outperformed local genotypes in terms of Fresh Panicle weight (PF), Dry Panicle weight (PD), and Panicle Width (PW). For instance, Numbu recorded a PF of 91.67 g and a PD of 81.40 g, which were significantly higher than those of Watasolok (63.63 g) and Okin (53.95 g). Although Panicle Length (PL) was relatively uniform across the groups, with Waiotan and Super 1 showing nearly identical lengths, the overall yield components underscored the superiority of the commercial varieties. This is in line with Boyles et al. (2019), who found that modern sorghum varieties developed through intensive breeding typically have wider panicles, heavier weights, and more uniform grains, thereby boosting productivity.

The quality traits varied. Okin, a local genotype, had a relatively high Brix sugar content (BR, 13.46%), whereas Numbu, a commercial genotype, had the highest value (15.07%). This indicates that both local and commercial genotypes could be valuable sources of sweet sorghum. A high sugar content is essential for expanding the use of sorghum in food and bioethanol production. These findings are consistent with those of Gebremedhn et al. (2020) and Endalamaw and Adugna (2025). This includes harvesting stages optimal for sugar yield and ethanol production, as indicated by studies that evaluate genotypes for traits such as brix content and bioethanol yield (Guden et al. 2020). The adoption of high-throughput phenotyping tools and rapid generation advancement methods also supports the development of varieties with desirable traits, such as increased yield and improved nutritional quality (Baloch et al. 2023; Mwamahonje et al. 2024). This approach can benefit from the country's rich agricultural diversity and can be tailored to specific environmental and socio-economic conditions (Sutiharni et al. 2024). The integration of both local and commercial genotypes in the production of sweet sorghum can maximize its potential for bioenergy and food applications.

The most significant trait distinguishing the two groups was seed yield per plant (GY). Numbu again led with 294.67 g per plant, significantly exceeding Okin, the top local performer, which yielded 182.33 g. This underscores the superior productivity of commercial varieties, mainly because the selection focused on yield components. According to Gebregergs et al. (2020), modern sorghum varieties undergo rigorous selection, resulting in enhanced yield stability and performance compared to landraces. Overall, the local and commercial genotypes demonstrated complementary strengths. Local varieties excel in vegetative vigor and specific quality traits, such as BR, whereas commercial varieties are superior in seed productivity and yield stability.

Consequently, crossbreeding these groups offers a promising strategy for creating new sorghum varieties that are both high yielding and of superior quality for food and bioenergy purposes. In this regard, breeding initiatives in Indonesia should not rely solely on commercial varieties, but should also utilize local germplasm as donor parents to enhance genetic diversity and adaptability in tropical dryland regions (Gebregergs et al. 2020; Endalamaw and Adugna 2025).

A comparison of key agronomic characteristics between local and commercial genotypes shows that the local genotype excels in PH, SD, and NN, while the commercial genotype performs better in PF, PD, TW, and GY. Both Okin (local) and Numbu (commercial) exhibit a high sugar content (BR), thus demonstrating shared benefits. Radar chart visualization helps to identify the relative strengths of each group, in accordance with the methods used in studies of sorghum diversity and breeding (Boyles et al. 2019; Endalamaw and Adugna 2025).

The significant positive correlation between panicle characteristics and GY underscores their role as key selection criteria. Kasule et al. (2024) reached similar conclusions, noting that PF and PD are vital for maintaining sorghum yield stability across various environments. In contrast, the weak correlations between vegetative traits and GY align with the finding that excessive vegetative growth redirects assimilation away from reproductive sinks (Tao et al. 2021

The moderate link between BR and GY highlights the dual-use potential of sorghum. Although BR is crucial for sweet sorghum and bioenergy production, it is less significant for enhancing grain yield. Habyarimana et al. (2020) observed that sugar-rich genotypes often compromise grain yield. Genomic research has shown that PF, PD, and TW are governed by Quantitative Trait Loci (QTLs) with high heritability, supporting their use in marker-assisted selection (Gebregergs et al. 2020; Vieira et al. 2025).

This correlation suggests that phenotypic selection should focus on panicle traits while maintaining supportive vegetative features. Combining high PF and PD with optimal PH and SD could maximize the yield potential. This approach is supported by genomic tools that identify stable Quantitative Trait Loci (QTLs) linked to yield traits. Future breeding strategies should combine phenotypic and genomic selection to boost sorghum production. Physiological indicators, such as biomass partitioning efficiency and sugar-use efficiency, can also be included to balance the improvements between grain and bioenergy sorghum types. Recent studies have highlighted that such integrative methods effectively ensure the adaptability and resilience of sorghum in tropical environments (Parikh et al. 2021).

In summary, the correlation analysis identified PF, PD, and PW as the most reliable predictors of GY. Supporting traits, such as PH, SD, and BI, contribute indirectly, whereas NN and NL are more indicative of photosynthetic vigor than yield potential. The limited role of BR in grain yield further emphasizes its relevance to sweet sorghum rather than grain types. These findings highlight the importance of combining phenotypic selection for panicle traits with genomic approaches to expedite the development of high-yielding, climate-resilient sorghum varieties suitable for tropical drylands.

These results confirm that reproductive traits, particularly TW, PD, PW, and PF, are the most reliable indicators of sorghum yield. The strong direct effects of these traits confirmed their role as primary selection criteria. These findings are consistent with those of Kasule et al. (2024), who reported fresh and dry panicle weights as the most consistent predictors of yield stability in tropical environments. Vieira et al. (2025) also emphasized that QTLs associated with panicle weight and grain size have high heritability, making them promising for marker-assisted selection. Conversely, vegetative traits (PH, SD, and BI) showed weak direct effects but contributed indirectly by improving panicle performance. Plant height and stem diameter play a role in plant stability; however, excessive biomass reduces yield because assimilates are allocated to vegetative tissues. Similar findings were reported by Parikh et al. (2021), who stated that optimal rather than maximal allocation of biomass is more important for increasing productivity.

The negative associations between NN, NL, and GY suggest a trade-off between vegetative and reproductive growth. Excess assimilation allocation to nodes and leaves reduces grain formation. Similar findings have been reported for maize and millet, where excessive vegetative vigor decreases the harvest index (Somu et al. 2024; Kumar et al. 2025). Brix sugar content (BR) has a negative direct effect on grain yield but a positive indirect contribution through panicle and grain traits. This confirmed that BR is more relevant as a quality trait for sweet sorghum and bioethanol than for grain yield. Habyarimana et al. (2020) also found a trade-off between sugar accumulation and grain productivity in sweet sorghum.

Nevertheless, BR integration remains important in dual-purpose sorghum breeding programs that use QTL markers for sugar accumulation (Gebregergs et al. 2020). The observed correlation further strengthens the importance of reproductive traits over vegetative traits in breeding strategies. Genomic prediction, when integrated with phenotypic selection for traits such as panicle weight (PF, PD) and grain size (TW), offers a promising pathway to accelerate the development of superior sorghum varieties. The use of genomic markers and high-throughput phenotyping enables efficient selection, while the strong correlation observed emphasizes that reproductive traits—rather than vegetative vigor are the primary determinants of yield stability in rainfed sorghum (Hao et al. 2021). Thus, combining phenotypic selection for PF, PD, and TW with genomic prediction offers a promising approach for expediting the development of superior varieties.

In conclusion, this study demonstrated that the tested sorghum genotypes have potential as parents in hybrid sorghum breeding programs. The complementary strengths of the local genotypes (Kuali, Watasolok, Okin, and Waiotan) and commercial varieties (Numbu, Kawali, Super 1, and UPCA-S1) show promise as parents for crossing. Cross-combinations, including Kuali × Numbu, Watasolok × Kawali, and Okin × Super 1, illustrate strategies for combining resistance with productivity. Traits such as plant height, panicle biomass, and grain yield are the main selection criteria for sorghum breeding programs.

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REFERENCES

Ahmed N, Chowdhry MA, Khaliq I, Maekawa M. 2016. The inheritance of yield and yield components of five wheat hybrid populations under drought. Indones J Agric Sci 8: 53-59. DOI: 10.21082/ijas.v8n2.2007.p53-59.

Allard RW. 1999. Principles of Plant Breeding. 2nd eds. John Wiley & Sons, Hoboken, New Jersey, USA.

Ariningsih E, Saliem HP, Nurhasanah A, Gunawan E, Agustian A, Saptana. 2023. Challenges and alternative solutions in developing sorghum to support food diversification in Indonesia. IOP Conf Ser: Earth Environ Sci 1153: 012032. DOI: 10.1088/1755-1315/1153/1/012032.

Baloch FS, Altaf MT, Liaqat W, Bedir M, Nadeem MA, Cömertpay G, Çoban N, Habyarimana E, Barutçular C, Cerit I, Ludidi N, Karaköy

T, Aasim M, Chung YS, Nawaz MA,Hatipoğlu R, Kökten K, Sun H-S. 2023. Recent advancements in the breeding of sorghum crop: Current status and future strategies for marker-assisted breeding. Front Genet 14: 1150616. DOI: 10.3389/fgene.2023.1150616.

Baye W, Xie Q, Xie P. 2022. Genetic architecture of grain yield-related traits in sorghum and maize. Intl J Mol Sci 23 (5): 2405. DOI: 10.3390/ijms23052405.

Boyles RE, Brenton ZW, Kresovich S. 2019. Genetic and genomic resources of sorghum to connect genotype with phenotype in contrasting environments. Plant J 97: 19-39. DOI: 10.1111/tpj.14113.

Burks PS, Kaiser CM, Hawkins EM, Brown PJ. 2015. Genome-wide association for sugar yield in sweet sorghum. Crop Sci 55 (5): 2138-2148. DOI: 10.2135/cropsci2015.01.0057.

Caignard T, Delzon S, Bodénès C, Dencausse B, Kremer A. 2018. Heritability and genetic architecture of reproduction-related traits in a temperate oak species. Tree Genet Genomes 15 (1): 1. DOI: 10.1007/s11295-018-1309-2.

Da Silva KJ, Teodoro PE, da Silva MJ, Teodoro LPR, Cardoso MJ, de Paulo Campos Godinho V, Mota JH, Simon GA, Tardin FD, da Silva AR, Guedes FL, de Menezes CB. 2021. Identification of mega-environments for grain sorghum in Brazil using GGE biplot methodology. Agron J 113 (4): 3019-3030. DOI: 10.1002/agj2.20707.

De Souza VF, da Silva Pereira G, Pastina MM, da Costa Parrella RA, Simeone MLF, de Almeida Barros B, Noda RW, Silva LdaCE, de Magalhães JV, Schaffert RE, Garcia AAF, Damasceno CMB. 2021. QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. G3 11 (11): jkab314. DOI: 10.1093/g3journal/jkab314.

Dewey DR, Lu KH. 1959. Correlation and path analysis of components of crested wheatgrass seed production. Agron J 51 (9): 515-518. DOI: 10.2134/agronj1959.00021962005100090002x.

Dwary S, Dukpa P, Gaikwad M, Thapa U, Kumar P, Yeasmin S. 2023. Genetic variability, heritability and genetic advance studies in diverse genotypes of tomato (*Solanum lycopersicum* L.). Intl J Plant Soil Sci 35 (22): 441-446. DOI: 10.9734/ijpss/2023/v35i224152.

Emendack Y, Burke J, Laza H, Sanchez J, Hayes C. 2018. Abiotic stress effects on sorghum leaf dhurrin and soluble sugar contents throughout plant development. Crop Sci 58 (4): 1706-1716. DOI: 10.2135/cropsci2018.01.0059.

Endalamaw C, Adugna A. 2025. Analysis of sweet sorghum genotypes for biofuel and grain yield potential in the lowland region of Ethiopia: Genetic variation, heritability, and ethanol production. Agrosyst Geosci Environ 8 (2): e70118. DOI: 10.1002/agg2.70118.

Fathoni A, Boonkum W, Chankitisakul V, Duangjinda M. 2022. An appropriate genetic approach for improving reproductive traits in crossbred Thai-Holstein cattle under heat stress conditions. Vet Sci 9 (4): 163. DOI: 10.3390/vetsci9040163.

Fatimah S, Djunaedy A, Nurholis. 2021. Path analysis and preliminary yield trials of bambara groundnut (*Vigna subterranean* L. Verdc). in Madura DryLand, Indonesia. Sabrao J Breed Genet 53 (3): 417-434.

Fehr WR. 1987. Principles of Cultivar Development. McGraw-Hill, New York, US.

Ferioun M, Zouitane I, Bouhraoua S, Elouattassi Y, Belahcen D, Errabbani A, Louahlia S, Sayyed R, El Ghachtouli N. 2025. Applying microbial biostimulants and drought-tolerant genotypes to enhance barley growth and yield under drought stress. Front Plant Sci 15: 1494987. DOI: 10.3389/fpls.2024.1494987.

Fuglie K, Morgan S, Jelliffe J. 2024. World Agricultural Production, Resource Use, and Productivity, 1961-2020 (Report No. EIB-268). U.S. Department of Agriculture, Economic Research Service. DOI: 10.32747/2024.8327789.ers.

Gebre W, Mekbib F, Tirfessa A, Bekele A. 2024. Genetic diversity, association, and regression coefficient analyses of sorghum [*Sorghum bicolor* (L.) Monech] genotypes. Scientifica 2024 (1): 1611869. DOI: 10.1155/sci5/1611869.

Gebregergs G, Mekbib F. 2020. Estimation of genetic variability, heritability, and genetic advance in advanced lines for grain yield and yield components of sorghum [*Sorghum bicolor* (L.) Moench] at Humera, Western Tigray, Ethiopia. Cogent Food Agric 6 (1): 1764181. DOI: 10.1080/23311932.2020.1764181.

Gichile H. 2022. Review on breeding sorghum (*Sorghum bicolor* (L.) Moench) for nutritional quality improvement. Intl J Res Stud Agric Sci 8 (2): 13-19. DOI: 10.20431/2454-6224.0802002.

Gomez KA, Gomez AA. 1984. Statistical Procedures for Agricultural Research. 2nd eds. John Wiley & Sons, Hoboken, New Jersey, USA.

Guden B, Erdurmus C, Erdal S, Uzun B. 2020. Evaluation of sweet sorghum genotypes for bioethanol yield and related traits. Biofuels Bioprod Bioref 15 (2): 545-562. DOI: 10.1002/bbb.2169.

Habyarimana E, Lopez-Cruz M, Baloch FS. 2020. Genomic selection for the optimum index with dry biomass yield, dry mass fraction of fresh material, and plant height in biomass sorghum. Genes 11 (1): 61. DOI: 10.3390/genes11010061.

Hao H, Li Z, Leng C, Lu C, Luo H, Liu Y, Wu X, Liu Z, Shang L, Jing H-C. 2021. Sorghum breeding in the genomic era: Opportunities and challenges. Theor Appl Genet 134 (7): 1899-1924. DOI: 10.1007/s00122-021-03789-z.

Kumar SAH, Thomas UC, Al-Salman Y, Cano FJ, Stephen R, Pillai PS, Ghannoum O. 2025. Evaluation of yield-related morphological, physiological, agronomic, and nutrient uptake traits of grain sorghum varieties in the Kerala Region (India). Agronomy 15 (10): 2320. DOI: 10.3390/agronomy15102320.

Irfan M, Maqsood MA, ur Rehman H, Mahboob W, Sarwar N, Hafeez OBA, Hussain S, Ercisli S, Akhtar M, Aziz T. 2023. Silicon nutrition in plants under water-deficit conditions: Overview and prospects. Water 15 (4): 739. DOI: 10.3390/w15040739.

Kamal NM, Gorafi YSA, Abdelrahman M, Abdellatef E, Tsujimoto H. 2019. Stay-green trait: A prospective approach for yield potential, and drought and heat stress adaptation in globally important cereals. Intl J Mol Sci 20 (23): 5837. DOI: 10.3390/ijms20235837.

Kandhol N, Tripathi DK, Jain M. 2022. Nanoparticles as potential hallmarks of drought stress tolerance in plants. Physiol Plant 174 (2): e13665. DOI: 10.1111/ppl.13665.

Kasule F, Alladassi BME, Aru CJ, Adikini S, Biruma M, Ugen MA, Kakeeto R, Esuma W. 2024. Genetic diversity, population structure, and genome-wide association study of sorghum lines assembled for breeding in Uganda. Front Plant Sci 15: 1458179. DOI: 10.3389/fpls.2024.1458179.

Khalifa M, Eltahir EAB. 2023. Assessment of global sorghum production, tolerance, and climate risk. Front Sustain Food Syst 7: 1184373. DOI: 10.3389/fsufs.2023.1184373.

Kundu B, Kumar R. 2024. Enhancing crop resilience to climate change through biochar: A review. Intl J Environ Clim Change 14 (6): 170-184. DOI: 10.9734/ijecc/2024/v14i64219.

Li C, Mo X, Li S, Liu Y, Chen R, Yu S, Lin W, Wang Y, Hu Y. 2025. Response of agronomic traits and phosphorus uptake to soil P deficiency during rice cultivars improvement. Agronomy 15 (4): 983. DOI: 10.3390/agronomy15040983.

Li X, Wang J, Su M, Zhang M, Hu Y, Du J, Zhou H, Yang X, Zhang X, Jia H, Gao Z, Ye Z. 2023. Multiple-statistical genome-wide association analysis and genomic prediction of fruit aroma and agronomic traits in peaches. Hortic Res 10 (7): uhad117. DOI: 10.1093/hr/uhad117.

Maftuchah M, Febriana L, Sulistyawati S, Reswari HA, Septia ED. 2021. Morphological diversity and heritability of nine local sorghum (*Sorghum bicolor*) genotypes in East Java, Indonesia. Biodiversitas 22 (3): 1310-1316. DOI: 10.13057/biodiv/d220330.

Menamo T, Borrell AK, Mace E, Jordan DR, Tao Y, Hunt C, Kassahun B. 2023. Genetic dissection of root architecture in Ethiopian sorghum landraces. Theor Appl Genet 136 (10): 209. DOI: 10.1007/s00122-023-04457-0.

Mgendi G. 2024. Unlocking the potential of precision agriculture for sustainable farming. Discov Agric 2: 87. DOI: 10.1007/s44279-024-00078-3.

Mwamahonje A, Mdindikasi Z, Mchau D, Mwenda E, Sanga D, Garcia-Oliveira AL, Ojiewo CO. 2024. Advances in sorghum improvement for climate resilience in the global arid and semi-arid tropics: A review. Agronomy 14 (12): 3025. DOI: 10.3390/agronomy14123025.

Nazli RI, Aslankaciran C, Yang D, Liaqat W, Polat M, Cavdar AS, Tansi V, Baloch FS. 2024. Assessment of sweet sorghum genotypes for bioethanol production in semi-arid Mediterranean conditions. Agronomy 14 (11): 2626. DOI: 10.3390/agronomy14112626.

Oyier MO, Owuoche JO, Oyoo ME, Cheruiyot E, Mulianga B, Rono J. 2017. Effect of harvesting stage on sweet sorghum (*Sorghum bicolor* L.) genotypes in Western Kenya. Sci World J 2017 (1): 8249532. DOI: 10.1155/2017/8249532.

Pang F, Li Q, Solanki MK, Wang Z, Xing Y-X, Dong D-F. 2024. Soil phosphorus transformation and plant uptake driven by phosphate-solubilizing microorganisms. Front Microbiol 15: 1383813. DOI: 10.3389/fmicb.2024.1383813.

Parikh A, Brant EJ, Baloglu MC, Altpeter F. 2021. CRISPR/Cas-mediated genome editing in sorghum-Recent progress, challenges and prospects.

In Vitro Cell Dev Biol-Plant 57: 720-730. DOI: 10.1007/s11627-021-10215-y.

Parimala G, Raju CHD, Rao LVS, Umamaheswari K, Krishna K. 2023. Correlation and path coefficient analysis for yield, quality and their component traits in rice (*Oryza sativa* L.). Intl J Environ Clim Change 13 (10): 3782-3794. DOI: 10.9734/ijecc/2023/v13i103051.

Peng Y, Hu Y, Qian Q, Ren D. 2021. Progress and prospect of breeding utilization of green revolution gene SD1 in rice. Agriculture 11 (7): 611. DOI: 10.3390/agriculture11070611.

Rajesh-Kumar S, Anand G, Narayanan SL, Subramanian E, Mini ML. 2025. Delineation of genotype × environment interaction and identifying superior red sorghum [*Sorghum bicolor* L. Moench] genotypes via multi-trait-based stability selection methods. BMC Plant Biol 25 (1): 283. DOI: 10.1186/s12870-025-06188-4.

Roy S, Verma BC, Banerjee A, Kumar J, Ray US. 2021. Genetic diversity for drought and low phosphorus tolerance in rice (*Oryza sativa* L.) varieties and donors adapted to rainfed drought prone ecologies. Sci Rep 11: 13671. DOI: 10.1038/s41598-021-93325-2.

Saketh T, Shankar VG, Srinivas B, Hari Y. 2023. Correlation and path coefficient studies for grain yield and yield components in rice (*Oryza sativa* L.). Intl J Plant Soil Sci 35 (19): 1549-1558. DOI: 10.9734/ijpss/2023/v35i193700.

Senbetay T, Belete T. 2020. Genetic variability, heritability, genetic advance and trait associations in selected sorghum (*Sorghum bicolor* L. Moench) accessions in Ethiopia. J Biol Agric Healthc 10 (12): 1-8. DOI: 10.7176/jbah/10-12-01.

Singh RK, Chaudhary RD. 1979. Biometrical Methods in Quantitative Genetic Analysis. Book Haryana Agricultural University, Hissar, India.

Somu G, Meena N, Badigannavar A. 2024. Exploring genetic variability for morphological and yield contributing traits in sorghum (*Sorghum bicolor* (L.) Moench) germplasm from Southern India. Genet Resour Crop Evol 72: 5179-5194. DOI: 10.1007/s10722-024-02251-5.

Sutiharni S, Mariay IF, Andriyani LY, Tuhumena VL, Adlian A. 2024. Mapping the progress and direction of sustainable agriculture research in Indonesia: A bibliometric analysis perspective. West Sci Nat Technol 2 (1): 39-46. DOI: 10.58812/wsnt.v2i04.763.

Tajudeen TT, Omotayo A, Ogundele FO, Rathbun LC. 2022. The effect of climate change on food crop production in Lagos State. Foods 11 (24): 3987. DOI: 10.3390/foods11243987.

Tao Y, Trusov Y, Zhao X, Wang X, Cruickshank AW, Hunt C, Oosterom E J Van, Hathorn A, Liu G, Godwin ID, Botella JR, Mace ES, Jordan D R. 2021. Manipulating assimilate availability provides insight into the genes controlling grain size in sorghum. Plant J 108 (1): 231-243. DOI: 10.1111/tpj.15437.

Tolera B, Gedebo A, Tena E. 2023. Genetic diversity of sugarcane (*Saccharum* spp.) genotypes based on agro-morphological and biochemical traits. Cogent Food Agric 9 (1): 2254141. DOI: 10.1080/23311932.2023.2254141.

Umakanth AV, Paroha S, Kumar A, Ranganathan A, Swain D. 2024. Sweet sorghum for biofuel production in sub-tropical India. J Sci Res Rep 30 (4): 1-9. DOI: 10.9734/jsrr/2024/v30i41883.

Vieira RA, Nogueira APO, Fritsche-Neto R. 2025. Optimizing the selection of quantitative traits in plant breeding using simulation. Front Plant Sci 16: 1495662. DOI: 10.3389/fpls.2025.1495662.

Wang F, Yoshida H, Matsuoka M. 2021. Making the "Green Revolution" truly green: Improving crop nitrogen use efficiency. Plant Cell Physiol 62 (6): 942-947. DOI: 10.1093/pcp/pcab051.

Wang R, Wang H, Huang S, Zhao Y, Chen E, Li F, Qin L, Yang Y, Guan Y, Liu B, Zhang H. 2023. Assessment of yield performances for grain sorghum varieties by AMMI and GGE biplot analyses. Front Plant Sci 14: 1261323. DOI: 10.3389/fpls.2023.1261323.

Wirnas D, Oktanti N, Rahmi HN, Andriani D, Faturrahman, Rini EP, Marwiyah S, Trikoesoemaningtyas, Sopandie D. 2021. Genetic analysis for designing an ideotype of high-yielding sorghum based on existing line performance. Biodiversitas 22 (12): 5286-5292. DOI: 10.13057/biodiv/d221208.

Wu Z, Tang D, Liu K, Miao C, Zhuo X, Li Y, Tan X, Sun M, Luo Q, Cheng Z. 2018. Characterization of a new semi-dominant dwarf allele of SLR1 and its potential application in hybrid rice breeding. J Exp Bot 69 (20): 4703-4713. DOI: 10.1093/jxb/ery243.

Xue X, Beuchat G, Wang J, Yu Y-C, Moose S, Chen J, Chen L-Q. 2023. Sugar accumulation enhancement in sorghum stem is associated with reduced reproductive sink strength and increased phloem unloading activity. Front Plant Sci 14: 1233813. DOI: 10.3389/fpls.2023.1233813.

Yang L, Zhou Q, Sheng X, Chen X, Hua Y, Lin S, Luo Q, Yu B, Shao T, Wu Y, Chang J, Li Y, Tu M. 2023. Harnessing the genetic basis of sorghum biomass-related traits to facilitate bioenergy applications. Intl J Mol Sci 24 (19): 14549. DOI: 10.3390/ijms241914549.

Yang, S, Imran I, Ortas I. 2023. Impact of mycorrhiza on plant nutrition and food security. J Plant Nutr 46 (13): 3247-3272. DOI: 10.1080/01904167.2023.2192780.

Zhou Y, Huang J, Li Z, Wu Y, Zhang J, Zhang Y. 2022. Yield and quality in main and ratoon crops of grain sorghum under different nitrogen rates and planting densities. Front Plant Sci 12: 778663. DOI: 10.3389/fpls.2021.778663.