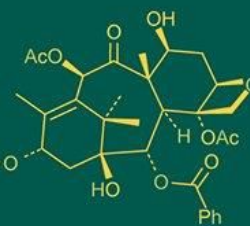


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Assessment of genetic variability, heritability, genetic advance and character association studies for yield and yield related traits in yellow sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract

Sorghum (*Sorghum bicolor* (L.) Moench), a climate-resilient C4 cereal, is essential for producing food and fodder in arid and semi-arid areas. Yellow pericarp genotypes, recognized for their elevated flavanone and phenolic levels, have undergone minimal genetic assessment. This research evaluated fifty two yellow sorghum genotypes in the Rabi 2024 season at ARS, Tandur, PJTAU, utilizing a randomized block design to examine genetic variability, heritability, among traits. Notable differences ($p < 0.01$) were detected among genotypes for every trait, signifying extensive genetic diversity. A high heritability was observed for days to 50% flowering (94.80%), days to maturity (94.10%), test weight (87.00%), and the number of grains per panicle (84.40%). Characteristics like test weight (GCV: 14.79%, PCV: 15.86%) and panicle width (GCV: 14.53%, PCV: 17.68%) exhibited significant genetic progress as a percentage of the mean (28.44% and 24.62%, respectively), indicating robust additive genetic influence. These results emphasize the promise of essential yield-influencing characteristics for selection, aiding the creation of high-yielding yellow sorghum varieties with enhanced yield and nutritional value for sustainable farming.

Keywords: Yellow sorghum, variability, heritability, genetic advance

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth most important cereal crop globally, following rice, wheat, maize, and barley in terms of production and utilization (FAO, 2021) [10]. Its remarkable resilience to drought, heat stress, and poor soils makes it particularly well-suited to arid and semi arid environments, earning it the nickname “camel of crops” Tari *et al.*, (2013) [22] and Prasad *et al.* (2019) [16]. As a C4 diploid species ($2n = 20$), sorghum plays a vital role as both a food and fodder crop, especially in regions such as Africa and India where it is extensively cultivated Reddy *et al.*, (2006) [17] and Upadhyaya *et al.*, (2017) [23]. Among sorghum grain types, yellow pericarp varieties stand out due to their elevated flavanone levels and moderately high total phenolic content compared to white sorghum, making them attractive candidates for nutritional improvement and biofortification Dykes and Rooney, (2006) [7] and Awika and Rooney, (2004) [2]. Despite these nutritional advantages, yellow sorghum types have received less attention in terms of genetic evaluation compared to pigmented types such as brown and black sorghum (Dykes and Rooney, 2007; Awika and Rooney, 2004) [2].

Understanding genetic variability is fundamental for crop improvement. Key agronomic traits such as grain yield, fodder biomass, and nutrient content must be evaluated to identify promising genotypes for selection and hybridization. Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance provide insights into trait variability, heritable potential, and scope for genetic gain through selection Falconer and Mackay, (1996) [9].

Given the increasing demand for nutritionally rich and climate-resilient cultivars, especially in marginal production environments, this study aims to quantify genetic variability in yellow sorghum germplasm for important agronomic and nutritional traits. Specifically, it estimates GCV, PCV, heritability, and genetic advance.

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By identifying traits with strong genetic influence and significant yield associations, the findings will support efficient selection strategies and contribute to the development of improved yellow sorghum varieties for sustainable agriculture and better nutrition.

2. Materials and Methods

The field experiment was conducted during the rabi season of 2024 at Agriculture Research Station (ARS), Tandur, PJTAU, Rajendranagar, Hyderabad India, under agro-climatic conditions suitable for sorghum cultivation. The experiment utilized a Randomized Block Design (RBD) and evaluated a total of 52 genotypes. Each block consisted of two rows, typically 3 to 4 meters in length, with a row spacing of approximately 45cm and a plant spacing of 10 to 15cm within rows. Standard agronomic practices, including appropriate irrigation, fertilization as per recommendations, and integrated pest management, were uniformly applied to ensure optimal crop performance. Data collection focused

on key agronomic and yield-related traits such as days to 50% flowering, days to maturity, plant height, number of leaves per plant, leaf length and width, panicle length and width, number of grains per panicle, 100 seed weight, grain yield per hectare, and fodder yield per hectare. observations were recorded from five randomly chosen plants per plot, and their mean values were used for statistical analysis. The collected data were subjected to analysis of variance (ANOVA) appropriate for the randomized block design. Genotypic and phenotypic variances, broad sense heritability, and genetic advance were computed to assess genetic variability and improvement potential, while correlation coefficients among traits were calculated to examine trait interrelationships. Correlation analysis reveals the degree and direction of association among traits allowing breeders to prioritize traits with genuine yield contributions. All statistical analyses were performed using INDOSTAT software version 9.1.

Table 1: List of genotypes used

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	ICSV17214	16	ICSV 17240	31	ICSV 17257	46	PYPS7
2	ICSV 17215	17	ICSV 17241	32	ICSV 17258	47	PYPS10
3	ICSV 17217	18	ICSV 17242	33	ICSV 17259	48	PYPS11
4	ICSV 17220	19	ICSV 17243	34	ICSV 17260	49	PYPS13
5	ICSV 17222	20	ICSV 17244	35	ICSV 17261	50	PYPS14
6	ICSV 17225	21	ICSV 17245	36	ICSV 17262	51	N14
7	ICSV 17229	22	ICSV 17246	37	ICSV 17263	52	N15
8	ICSV 17230	23	ICSV 17247	38	ICSV 17264		
9	ICSV 17232	24	ICSV 17248	39	ICSV 17265		
10	ICSV 17233	25	ICSV 17250	40	ICSV 17266		
11	ICSV 17234	26	ICSV 17251	41	PYPS 1		
12	ICSV 17235	27	ICSV 17252	42	PYPS2		
13	ICSV 17236	28	ICSV 17253	43	PYPS4		
14	ICSV 17237	29	ICSV 17255	44	PYPS5		
15	ICSV 17238	30	ICSV 17256	45	PYPS6		

3. Results and Discussion

3.1 Analysis of variance

The statistical analysis was carried out according to the technique of Analysis of variance (ANOVA) for Randomized Block design which was studied for twelve traits (Table 4.1). The results obtained revealed that the genotypes included in the study had significant variation for all the traits indicating considerable amount of variation present in this material.

Table 2: Analysis of variance for yield and its components and nutritional traits in Sorghum

Sl no	Character	Mean sum of squire		
	Degree of freedom	Genotype	Replication	Error
1	Days to 50% flowering	71.32**	3.76	1.38
2	Days of maturity	72.30**	3.69	1.47
3	Plant height	928.53**	260.01	109.57
4	Number of leaves	5.77**	1.04	1.30
5	Leaf length	37.29**	2.31	7.22
6	Leaf width	1.04**	0.30	0.148
7	Panicle length	26.15**	17.29	8.01
8	Panicle width	14.54**	4.76	2
9	Number of grains per panicle	145590.84**	17194.39	8435.17
10	Test weight	0.45**	0.010	0.021
11	Fodder yield kg ^{ha} ⁻¹	1965211.10**	50158	180812.7
12	Grain yield kg ^{ha} ⁻¹	481079.15**	118847.5	49133.56

** Indicates significance at 1 per cent probability level

The results of the variance analysis are shown in Table2 , while the estimates for mean, variability, heritability, genetic advance for each trait are detailed in Table 3, Character association studies for each trait detailed in table 4

3.2 Mean, GCV, PCV, Heritability and Genetic Avance

Days to 50% flowering (DFF) is a critical trait that determines vegetative duration and aids in escaping terminal drought, thereby significantly influencing grain yield in sorghum. In the present study, the mean DFF among the sorghum lines was 71.1 days, with the earliest flowering observed in PYPS 11 (62.33 days) and the latest in ICSV 17263 (78.00 days), indicating substantial variability for this trait.Days to maturity (DM) influence the grain-filling period and total dry matter production. Extended maturity generally supports higher yields under non-stress environments (Vinoth *et al.*, 2021) ^[24]. The average maturity was 115.2 days, with the earliest maturing genotype being PYPS 11 (105.33 days) and the latest ICSV 17241 (121.00 days). Plant height (PH) is associated with both grain and fodder yield potential, contributing to lodging resistance and photosynthetic surface area. The mean plant height was 217.2 cm, ranging from 144.33 cm in ICSV 17263 to 235.33 cm in ICSV 17250 and ICSV 17260.

The number of leaves per plant (NL) contributes to the crop's photosynthetic capacity, thereby influencing overall biomass accumulation (Vinoth *et al.*, 2024) ^[24]. Leaf number ranged from 10.67 leaves in ICSV 17234 to 16.33 in ICSV 17260, with a mean of 13.7.

Leaf length (LL) and leaf width (LW), as components of leaf area, influence light interception and dry matter production. In the present study, leaf length ranged from 41.00 cm in PYPS 6 to 58.33 cm in ICSV 17234, with an average of 51.9 cm. Leaf width varied from 4.00 cm in ICSV 17258 to 6.23 cm in ICSV 17217 and ICSV 17230, with an average of 4.9 cm. Panicle length (PL) and panicle width (PW) directly influence the number of grains per panicle and, consequently, the yield (Chibvongodze *et al.*, 2025) ^[4]. Panicle length ranged from 9.44 cm in ICSV 17253 to 21.20 cm in PYPS 2, with a mean of 16.3 cm, while panicle width varied from 9.11 cm in ICSV 17222 to 20.77 cm in ICSV 17261, averaging 13.9 cm.

The number of grains per panicle (NGP) is a direct component of grain yield. Higher grain numbers are

typically associated with well-filled, large panicles. In this study, NGP ranged from 777.33 in ICSV 17214 to 1803.82 in PYPS 13, with a mean of approximately 1,450 grains. Test weight (TW), or 100-grain weight, measures grain density and size, reflecting both yield potential and marketable quality. The test weight ranged from 1.96 g in ICSV 17220 to 3.73 g in ICSV 17256, with a mean of 2.6 g. Grain yield (GY) is the most critical trait in sorghum breeding, influenced by the interaction of several morphological and physiological components (Chibvongodze *et al.*, 2025) ^[4].

Yield across genotypes ranged from 3,214.68 kg ha⁻¹ in ICSV 17222 to 4498.60 kg ha⁻¹ in ICSV 17259, with a mean of 4031.1 kg ha⁻¹. Fodder yield (FY) is a crucial trait in dual-purpose sorghum varieties, as these provide both grain and biomass. It is generally positively correlated with plant height and leaf area. In this study, fodder yield ranged from 6015.67 kg ha⁻¹ in ICSV 17214 to 9296.88 kg ha⁻¹ in ICSV 17252, with an average of 8360.1 kg ha⁻¹.

Table 3: Estimates of mean, range, heritability and genetic advance for yield and yield contributing characters in advanced breeding lines

Characters	Mean	Range		Coefficient of variability		Heritability (%) broad sense	Genetic Advance as percent of mean (at 5%)
		Min.	Max.	GCV%	PCV%		
Days to 50% Flowering	71.55	61.60	78.00	6.93	6.75	94.80	13.53
Days of maturity	114.73	105.3	121.00	4.36	4.23	94.10	8.465
Plant height	214.86	144.33	235.33	9.10	7.69	71.40	13.38
Number of leaves	13.88	10.66	16.33	12.08	8.81	53.30	13.25
Leaf length in cm	51.51	41.00	57.66	8.06	6.14	58.10	9.60
Leaf width in cm	4.93	4.00	6.26	13.55	11.07	66.70	18.62
Panicle length in cm	16.77	9.43	28.33	22.35	14.66	43.00	19.80
Panicle width in cm	14.065	9.10	20.77	17.68	14.53	67.60	24.62
No of grains per panicle	1470.8	777.33	1803.6	15.82	14.53	84.40	27.51
Test weight	2.53	1.96	3.70	15.86	14.79	87.00	28.44
Fy kg ha ⁻¹	8313.1	6015.6	9296.6	10.59	9.277	76.70	16.73
Gy ha ⁻¹	4029.5	2307.6	4498.6	10.90	9.417	74.60	16.75

Days to 50% flowering (DFF) showed low PCV (6.93%) and GCV (6.75%), combined with high heritability (94.8%) and moderate GAM (13.53%), implying additive gene action and strong response to selection—aligning with findings of low heritability in heading and maturity traits in sorghum populations (Prasad and Sridhar (2019) ^[16] Days to maturity (DM) also exhibited low PCV (4.36%) and GCV (4.23%), high heritability (94.1%) but low GAM (8.47%), indicating limited selection gain despite high genetic control, as similarly reported for maturity traits in sorghum Mengistu *et al.* (2020) ^[15].

Plant height (PH) had low GCV (7.69%), low PCV (9.10%), high heritability (71.4%), and moderate GAM (13.38%). These values reflect moderate environmental influence and match general variability profiles in sorghum germplasm collections Goswami *et al.* (2020) ^[11] and Lata and Shailesh (2001) ^[13]. Number of leaves (NL) showed low GCV (8.81%) but moderate PCV (12.08%), with moderate heritability (53.3%) and GAM (13.25%), suggesting environmental effects limit direct selection, consistent with similar observations in other sorghum accessions by

Khandelwal *et al.* (2015) ^[12].

Leaf length (LL) exhibited low GCV (6.14%) and PCV (8.06%), moderate heritability (58.1%), and low GAM (9.60%), indicating minimal selection gain mirrored by patterns in leaf traits of diverse sorghum germplasm by Warkad *et al.*, (2025), Leaf width (LW) displayed moderate GCV (11.07%) and PCV (13.55%), moderate heritability (66.7%), and GAM (18.62%), suggesting moderate yield response potential through phenotypic selection aligning with observations of Chavan *et al.* (2007) ^[3]. Panicle length (PL) recorded high PCV (22.35%), intermediate GCV (14.66%), low heritability (43%), and moderate GAM (19.80%), pointing to strong environmental influence limiting direct genetic improvement—consistent with reports of limited selection potential for panicle length in sorghum (Santhiya *et al.* 2021) ^[18]. Panicle width (PW) had moderate variability (GCV: 14.53%, PCV: 17.68%), high heritability (67.6%), and high GAM (24.62%), indicating strong genetic control and high selection potential, consistent with sorghum studies by Chavan *et al.* (2007) ^[3].

Table 4: Phenotypic correlation coefficient analysis of yield and yield contributing characters

Character	DFF	DM	PH	NL	LL	LW	PL	PW	NGP	TW	Fykg ⁻¹	Gykg ⁻¹
DFF	1	0.98**	-0.127	-0.073	0.144	-0.063	0.09	0.31**	-0.234*	0.321*	0.073	0.158*
DM		1	-0.13	-0.063	0.1529	-0.0561	0.083	0.314**	-0.225*	0.321**	0.076	0.183*
PH			1	0.075	-0.003	0.247**	0.094	0.165*	0.169*	-0.026	0.450**	0.205*
NL				1	0.0852	0.360**	0.066	-0.153*	0.131	-0.114	0.199*	-0.372
LL					1	0.1523	-0.003	0.080	-0.1309	0.259**	-0.034	-0.190
LW						1	0.036	0.165*	0.239*	0.074	0.35**	-0.355
PL							1	0.084	0.015	-0.023	0.019	0.068
PW								1	-0.1	0.314**	0.307**	0.255*
NGP									1	-0.625**	0.363**	0.373**
TW										1	0.212**	0.287*
Fykg ⁻¹											1	0.657**
Gykg ⁻¹												1

Number of grains per panicle (NGP) exhibited moderate GCV (14.53%), PCV (15.82%), high heritability (84.4%), and high GAM (27.51%), denoting additive inheritance and excellent response to selection. This aligns with the reports of Sheetal *et al.* (2021) [19], where grain number per panicle showed high heritability (68%) in large germplasm sets. Test weight (TW) had GCV (14.79%), PCV (15.86%), high heritability (87.0%), and GAM (28.44%), suggesting strong additive genetic influence. This mirrors high heritability (83%) reported for 100 grain weight in sorghum germplasm by Prasad and Sridhar (2019) [16], Fodder yield (FY kgha-1) showed low GCV (9.28%) and moderate PCV (10.59%), high heritability (76.7%) and moderate GAM (16.73%), Grain yield (GY kgha-1) exhibited low GCV (9.42%), PCV (10.91%), moderate heritability (74.6%), and moderate GAM (16.75%) which aligns with the findings of Santhiya *et al.* (2021) [18].

3.3 Character association studies for yield and yield related components

DFF: Days of 50% flowering, DM: Days of maturity, PH: Plant height in cm NL: No of leaves per plant, LL: Leaf length in cm, LW: leaf width in cm PL: Panicle length in cm, PW: Panicle width in cm, NGP: Number of grains per panicle, TW: Test weight in grams, Fodder yield kgha-1, grain yield kgha-1

In the present study, Days to 50% flowering (DFF) exhibited a strong positive correlation with days to maturity (0.98**), suggesting that genotypes flowering later also tend to mature later, which aligns with the expected physiological growth pattern in sorghum (Reddy *et al.*, 2006) [17]. It also showed significant positive associations with panicle width (0.31**) and test weight (0.321*), indicating that delayed flowering may contribute to enhanced grain filling and panicle structure.

However, DFF was negatively correlated with the number of grains per plant (-0.234*) Godbharle *et al.*, (2010). Similarly, days to maturity (DM) was positively associated with DFF (0.9138**), panicle width (0.314**), grain yield (0.1830*), and test weight (0.321**), Reddy *et al.*, (2006) [17]. Plant height showed significant positive correlations with fodder yield (0.45**), leaf width (0.247**), panicle width (0.165*), number of grains per plant (0.169*), and grain yield (0.2052*), indicating its contribution to biomass and productivity Deshmukh *et al.* (2021) [5]. Number of leaves had positive and significant correlations with leaf width (0.360**) and fodder yield (0.1993*), but negative associations with panicle width (-0.153*) Shivaprasad *et al.*, (2019) [20] and Lokesh & Biradar, (2021) [14]. Leaf length showed a significant positive correlation with test weight

(0.259**), Reddy *et al.*, (2006) [17]. Leaf width had strong positive correlations with panicle width (0.1651*), number of grains per plant (0.239*), and fodder yield (0.35**), * (Reddy *et al.*, 2006) [17].

Number of grains per plant had highly significant positive associations with fodder yield (0.3638**) and grain yield (0.3735**), but showed a strong negative correlation with test weight (-0.625**), indicating a trade-off between grain size and number Sheetal *et al.*, (2021) [19]. Test weight was positively correlated with grain yield (0.2876*), fodder yield (0.2121**), panicle width (0.314**), and leaf length (0.259**), while its negative relationship with number of grains (-0.625**) confirms the inverse link between seed size and number Santhiya *et al.*, (2021) [18]. Fodder yield had strong positive associations with grain yield (0.6577**), plant height (0.45**), leaf width (0.35**), panicle width (0.3070**), number of grains (0.3638**), and number of leaves (0.1993*), confirming its close link with vegetative biomass and productivity Ashwini & Kajjdoni, (2019a) [1]. Finally, grain yield showed strong positive correlations with fodder yield (0.6577**), number of grains per plant (0.3735**), test weight (0.2876*), and panicle width (0.255*), while being negatively associated with number of leaves (-0.3728) and leaf width (-0.3551), suggesting that an optimum leaf structure is necessary for enhanced yield performance.

4. Conclusion

The present study demonstrated substantial genetic variability among 52 yellow sorghum genotypes, with significant differences across all measured traits. High heritability and genetic advance for traits such as test weight, number of grains per panicle, and panicle width indicate the potential for effective improvement through selection. Correlation and path analyses further revealed that grain yield is positively influenced by traits like fodder yield, test weight, panicle width, and grain number, while excessive vegetative traits like leaf number and width may detract from yield potential. These results underscore the importance of integrating agronomic and physiological traits in selection indices. Ultimately, the identified high-performing genotypes and associated traits provide a valuable foundation for targeted breeding programs aimed at enhancing yield and nutritional quality in yellow sorghum for sustainable agricultural systems.

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7. Author's Contribution:

Akshay H V: Writing an original draft, Data curation, Formal analysis, Investigation, Software, Writing-review & editing. K Sujatha: Conceptualization, Data curation, Investigation, Methodology, Resources, Supervision, Validation, Visualization, Writing-review & editing. CH Anuradha: Writing-review. CV Sameer kumar: review & editing.

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