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## Genetic variability and character association studies among grain yield and yield component traits in red sorghum [*Sorghum bicolor* (L.) Moench]

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### Abstract

The present study was conducted with 68 red sorghum genotypes and four checks viz., CO 4, Paiyur 2, Usilampatti local and AURS 013 during *Rabi*, 2021 to assess the variability and character association among grain yield and yield component traits. This study clearly indicated the presence of a considerable level of variation among the genotypes. The data was observed for thirteen quantitative traits viz., days to 50% flowering, plant height, stem diameter, number of leaves, flag leaf length, flag leaf width, panicle length, panicle width, panicle weight, days to maturity, hundred seed weight, dry fodder yield per plant and grain yield per plant. High PCV and GCV were observed for panicle length, panicle width, panicle weight, hundred seed weight, dry fodder yield and grain yield per plant, which suggested the greater scope for selection of superior genotypes for these traits. Similarly, high heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, stem diameter, panicle width, panicle weight, hundred seed weight and dry fodder yield, which indicated that due to additive gene action, the selection may be effective. The traits viz., plant height, panicle width, panicle weight, hundred seed weight and dry fodder yield recorded significant and positive correlation with grain yield per plant. Path analysis study revealed that panicle weight had a high direct positive effect on grain yield per plant; days to 50% flowering and panicle width showed moderate positive whereas days to maturity showed moderate negative direct effect on grain yield per plant. As a result of this research, it is observed that the traits viz., panicle width, panicle weight, hundred seed weight and dry fodder yield exhibited a positive correlation and direct positive impact on grain yield per plant, which can be used for selection for increasing grain yield.

**Keywords:** Red sorghum, heritability, genetic advance, correlation, path analysis

### Introduction

Sorghum (*Sorghum bicolor* [L.] Moench) is a versatile and important grain cultivated throughout Asia and Africa for food, fodder, fuel, and fibre. Millions of people in tropical and semi-arid climate consume it in most of the days. It is the world's fifth most significant grain cereal and is an annual diploid crop species ( $2n = 2x = 20$ ) (Hariprasanna and Patil, 2015). Sorghum, a Poaceae family member with excellent photosynthetic efficiency, is a high-yielding, nutrient-efficient, and drought-tolerant crop (Kavipriya *et al.* 2019) [13]. It is an excellent carbon fixer in high-temperature, low-moisture settings since it is a C4 plant.

Globally sorghum is cultivated in 43.05 million hectares area with a production of 62.42 million tonnes and productivity of 1450 kg/ha during 2020-2021 (Anonymous, 2022) [2]. While in India, sorghum occupied an area of 4.38 million hectares with a production of 4.81 million tonnes and productivity of 1100 kg/ha during 2020-2021 (Anonymous, 2022) [2]. In Tamil Nadu, sorghum is grown as a rainfed crop and is cultivated in an area of 0.45 million hectares with a production and productivity of 0.47 million tonnes and 1048 kg/ha, respectively, during 2019-2020 (Agricultural Statistics at a Glance, 2020) [1].

Red sorghum is a nutrient-dense grain with a wide range of applications. It is high in vitamins, zinc (Zn) and iron (Fe). Sorghum is a preferred grain for optimal health, due to the high vitamin content. It contains much more fibre than other cereal grains such as barley and rice. Sorghum aids in the maintenance of calcium levels in the body because of its high magnesium (Mg) content (Katey Davidson *et al.* 2019). Of late, red sorghum grains are preferred by consumers after realizing the need of inclusion of millets in diet. In order to develop high yielding red sorghum varieties, as a preliminary attempt, a study was conducted to evaluate the available red sorghum genotypes in the Ramaiah gene bank of Department of Plant Genetic Resources, Tamil Nadu Agricultural University, Coimbatore along with known varieties viz.,

CO 4, Paiyur 2 and local collections *viz.*, Usilampatti local and AURS 013 (a local collection from Aruppukottai).

### Materials and Methods

A field experiment was conducted to evaluate and study the association and cause of association of yield and yield contributing traits of 68 red sorghum germplasm accessions at Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *Rabi*, 2021. The experiment was laid out in an augmented block design I (ABD I) with 68 red sorghum genotypes and four checks. The checks were replicated five times. The red sorghum genotypes and checks were raised in two rows each. The crop production practices were followed as per the recommendation. The data on thirteen quantitative traits *viz.*, plant height, days to 50% flowering, flag leaf length, flag leaf width, number of leaves, stem diameter, panicle length, panicle width, panicle weight, days to maturity, hundred seed weight, dry fodder yield per plant and grain yield per plant were recorded on five randomly selected plants of all the genotypes including the germplasm accessions and checks. The estimation of mean, range (minimum and maximum) and variability parameters were done. Based on the classification of variability parameters, PCV and GCV and GAM were categorized into low (<10%), moderate (10-20%) and high (>20%) by Sivasubramanian and Madhavamenon (1973) and Johnson *et al.* (1955) respectively whereas  $h^2$  was categorized into low (<30%), moderate (30-60%) and high (>60%) by Johnson *et al.* (1955). The TNAU STAT software (Manivannan, 2014) was used to estimate analysis of variance (ANOVA) and association studies.

### Results and Discussion

Analysis of variance (Table 1) revealed significant mean sum of squares for the traits *viz.*, plant height, days to 50% flowering, stem diameter, panicle length, panicle width, panicle weight, days to maturity, hundred seed weight, dry fodder yield and grain yield per plant except for flag leaf length, flag leaf width and stem diameter which showed non-significant mean sum of squares with respect to checks, genotypes and checks vs genotypes. Significant differences among genotypes for all the traits studied, indicating thereby the presence of wide range of variability. Estimation of mean and range (maximum and minimum), variability parameters *viz.*, phenotypic variance (VP), genotypic variance (VG), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ), genetic advance (GA) and genetic advance as per cent mean (GAM) are given in the Table 2. In this study, PCV was superior to the GCV for yield and yield contributing traits, which shows the influence of environmental factors over these characters. Among the germplasm accessions, high PCV and GCV were observed for the traits *viz.*, panicle length, panicle width, panicle weight, hundred seed weight, dry fodder yield and grain yield per plant. Similarly, moderate PCV and GCV were observed for the traits *viz.*, plant height, days to 50% flowering, number of leaves and stem diameter. Subramanian *et al.* (2019) [25] reported high PCV and GCV for plant height, days to 50% flowering and number of leaves. Sheetal *et al.* (2021) [23] also reported high PCV and GCV for grain yield and moderate PCV and GCV for plant height. High PCV and GCV reported for panicle length, panicle weight and grain yield per plant; moderate PCV and GCV for days to 50%

flowering, plant height and panicle width as per Swamy *et al.* (2018) [26]. Similar results were reported by Bejiga *et al.* (2021) [4]. High amount of GCV and PCV suggested a greater scope for selection of superior genotypes for these traits.

Among the germplasm accessions, high heritability coupled with high genetic advance as per cent of mean was observed for the traits *viz.*, days to 50% flowering, stem diameter, panicle width, panicle weight, hundred seed weight and dry fodder yield. Similar results were reported by Shivaprasad *et al.* (2019) [24]. Bejiga *et al.* (2021) [4] reported high  $h^2$  with high GAM for days to 50% flowering, plant height, panicle length and grain yield per plant. This is in agreement with the reports by Sheetal *et al.* (2021) [23]. Goswami *et al.* (2020) [9] reported high PCV and GCV; high  $h^2$  with high GAM for panicle length, panicle width, dry fodder yield and grain yield per plant. These results clearly indicated that the variations observed among the germplasm accessions were due to additive gene action and the selection may be effective for the above mentioned traits.

Association studies are essential in the selection of better genotypes to improve grain yield based on the correlated traits in a breeding programme (Swamy *et al.* 2018) [26]. Grain yield is a complex trait governed by polygenic loci, which in turn depends upon many independent contributing characters. Simple correlation between thirteen traits is depicted in the Table 3. The traits *viz.*, plant height, panicle width, panicle weight, hundred seed weight and dry fodder yield recorded positive and significant correlation with grain yield per plant. A strong correlation of these traits with grain yield per plant indicated that simultaneous improvement of all the characters is possible. This is in agreement with the reports by Manickam and Vijendradas (1995) [15], Arunkumar *et al.* (2004) [3], Hundekar *et al.* (2016) [10], Swamy *et al.* (2018) [26] and Shivaprasad *et al.* (2019) [24].

Regarding inter correlations between different characters, plant height had a positive and significant correlation with flag leaf length, panicle width, panicle weight and dry fodder yield. Mofokeng *et al.* (2019) [17] reported that panicle width had a positive and significant correlation with plant height. Days to 50% flowering indicated positive and significant correlation with flag leaf length and days to maturity. Flag leaf length showed positive and significant correlation with the flag leaf width and days to maturity whereas flag leaf width indicated positive and significant correlation with dry fodder yield. Panicle length indicated positive and significant correlation with panicle width. Panicle width correlated with panicle weight and dry fodder yield in a positive and significant way. Panicle weight showed positive and significant correlation with hundred seed weight and dry fodder yield. Tesso *et al.* (2011) [27] reported that hundred seed weight showed positive correlation with panicle length. Gebreyohannes *et al.* (2018) [7] reported that plant height had a positive correlation with days to 50% flowering.

The nature of association between two variables is determined by analysing the path coefficient, which was used by Dewey and Lu (1959) [6] for plant selection. Kavaya *et al.* (2020) [14] defined this coefficient as the direct and indirect contribution of numerous independent variables to dependent variables. The phenotypic residual value (0.2828) indicated that the traits which are included in the phenotypic path analysis explained 71.72% of the variation in grain yield. The path coefficient analysis is shown in Table 4. In the present study, grain yield per plant was considered as dependent character

and other characters were taken as independent characters. The results revealed that panicle weight had a high direct positive effect on grain yield, this implies that highest panicle weight leads to increased grain yield. The trait viz., days to 50% flowering and panicle width had a moderate and direct positive effect on grain yield, whereas days to maturity showed moderate and direct negative effect on grain yield. When compared to the correlation, panicle weight show positive and significant effect; thus selection based on the panicle weight would be effective. This is in agreement with the reports by Deshmukh *et al.* (2018) [5] and Shivaprasad *et al.* (2019) [24]. Bejiga *et al.* (2021) [4] reported that days to 50% flowering, number of leaves and panicle width showed direct positive effect on grain yield except panicle length, which showed direct negative effect. They concluded that the above mentioned traits can be used for selection for increasing grain yield in red sorghum.

However, panicle width and dry fodder yield through panicle weight yielded high and positive indirect effect on grain yield. But both plant height and days to maturity showed moderate and positive indirect effect on grain yield through panicle weight and days to 50% flowering respectively. Thus, the present study indicated that the plant height, panicle weight,

panicle width, days to maturity and dry fodder yield are important characters in deciding the grain yield per plant. Hence these characters may be considered as selection indices in the breeding programme.

The traits viz., plant height, number of leaves, leaf breadth, panicle width and panicle weight showed a direct negative effect but days to 50% flowering and panicle length showed a direct positive effect on grain yield as per Gebrie and Genet (2019) [8]. This is in agreement with Shivaprasad *et al.* (2019) [24] and Senbetay and Belete (2020) [21]. According to the present study, comparison between association and nature of association studies revealed that the traits viz., panicle width, panicle weight, hundred seed weight and dry fodder yield exhibited a positive correlation and direct positive impact on grain yield per plant. As a result, the above mentioned traits will be used for selection for increasing grain yield in red sorghum.

Based on the present results, among the four checks, CO 4 is the best check with respect to yield. When compared to the best check and genotypes, the entries viz., IS 14775, IS 29630, 38 CS and IS 30536 are better than the best check (CO 4) with respect to yield. As a result, the above mentioned best genotypes can be used for further breeding programmes.

**Table 1:** Analysis of variance of augmented block design for 13 quantitative traits in 68 genotypes of red sorghum

SV	df	PH	DFE	FLL	FLW	NOL	SD	PL	PW	PWt	DM	HSW	DFY	GYPP
Treatment	71	550.67**	46.12**	127.04	1.75	1.94	0.35**	34.83**	3.96**	54.84**	52.25**	0.34**	186.18**	24.54**
Checks	3	361.83**	198.58**	53.63	1.30	1.60	1.44**	83.48**	8.71**	24.47**	192.20**	1.31**	191.38**	35.60**
Genotypes	67	556.00**	39.68**	130.00	1.79	1.94	0.20**	27.19**	3.69**	52.35**	46.68**	0.28**	172.69**	24.34**
Checks vs Genotype	1	760.29**	19.61**	148.91	0.61	2.89	6.96**	400.56**	7.95**	313.09**	5.78**	1.27**	1074.50**	5.08**
Error	16	236.92	0.70	96.21	1.47	1.15	0.04	11.59	0.95	18.14	1.85	0.05	29.10	12.43

\*\* - Significance at 1% level; \* - Significance at 5% level

PH – plant height; DFE – days to 50% flowering; FLL – flag leaf length; FLW – flag leaf width; NOL – number of leaves; SD – stem diameter; PL – panicle length; PW – panicle width; PWt – panicle weight; DM – days to maturity; HSW – hundred seed weight; DFY – dry fodder yield per plant; GYPP – grain yield per plant.

**Table 2:** Mean performance and variance estimates of red sorghum germplasm accessions for yield and yield contributing traits.

Traits	Mean	Range		VP	VG	PCV (%)	GCV (%)	h <sup>2</sup> (%)	GA	GAM (%)
		Maximum	Minimum							
Plant height (cm)	133.13	168.3	80.25	556	319.08	17.71	13.42	57.39	27.88	20.94
Days to 50% flowering	53.68	72	45	39.68	38.98	11.74	11.63	98.24	12.75	23.75
Flag leaf length (cm)	54.15	75	31.28	130	33.79	21.05	10.73	25.99	6.10	11.27
Flag leaf width (cm)	5.84	7.9	3.2	1.79	0.32	22.90	9.68	17.88	0.49	8.43
Number of leaves	7.37	10	4	1.94	0.79	18.90	12.06	40.72	1.17	15.86
Stem diameter (cm)	2.39	3.7	1.8	0.2	0.16	18.72	16.74	80.00	0.74	30.85
Panicle length (cm)	17.62	29.1	10.6	27.19	15.6	29.59	22.41	57.37	6.16	34.97
Panicle width (cm)	6.44	12.72	3.5	3.69	2.74	29.85	25.72	74.25	2.94	45.66
Panicle weight (g)	25.69	42.5	15.2	52.35	34.21	28.16	22.76	65.35	9.74	37.91
Days to maturity	92.91	110	83	46.68	44.83	7.35	7.21	96.04	13.52	14.55
Hundred seed weight (g)	2.19	3.6	1.1	0.28	0.23	24.18	21.92	82.14	0.90	40.92
Dry fodder yield per plant (g)	46.41	67	29	172.69	143.59	28.31	25.82	83.15	22.51	48.50
Grain yield per plant (g)	16.88	34.75	9.75	24.34	11.91	29.23	20.44	48.93	4.97	29.46

VP = Phenotypic variance; VG = Genotypic variance; PCV = Phenotypic coefficient of variance; GCV = Genotypic coefficient of variation; h<sup>2</sup> = Heritability; GA = Genetic advance; GAM = Genetic advance as per cent mean.

**Table 3:** Correlation for yield and yield contributing traits in red sorghum germplasm.

	PH	DFE	FLL	FLW	NOL	SD	PL	PW	PWt	DM	HSW	DFY	GYPP
PH	1.000												
DFE	0.117	1.000											
FLL	0.373**	0.307*	1.000										
FLW	0.139	0.212	0.245*	1.000									
NOL	-0.024	-0.196	0.066	0.099	1.000								
SD	0.061	0.185	-0.039	-0.133	0.053	1.000							
PL	0.175	0.207	0.211	-0.149	-0.034	0.121	1.000						

PW	0.384**	0.065	0.079	0.079	-0.150	0.068	0.306*	1.000						
PWt	0.347**	-0.088	0.080	0.023	0.020	0.085	0.209	0.444**	1.000					
DM	0.081	0.971**	0.294*	0.211	-0.183	0.150	0.187	0.016	-0.136	1.000				
HSW	0.093	-0.056	-0.068	0.011	0.210	-0.045	-0.113	0.071	0.228*	-0.121	1.000			
DFY	0.834**	0.091	0.177	0.236*	-0.035	0.081	0.113	0.363**	0.479**	0.053	0.103	1.000		
GYPP	0.409**	-0.028	0.049	0.098	-0.101	0.120	0.199	0.624**	0.914**	-0.097	0.242*	0.541**	1.000	

\*\* - Significance at 1% level; \* - Significance at 5% level

PH – plant height; DFF – days to 50% flowering; FLL – flag leaf length; FLW – flag leaf width; NOL – number of leaves; SD – stem diameter; PL – panicle length; PW – panicle width; PWt – panicle weight; DM – days to maturity; HSW – hundred seed weight; DFY – dry fodder yield per plant; GYPP – grain yield per plant.

**Table 4:** Path coefficient analysis indicating direct and indirect effects of characters on grain yield in red sorghum germplasm accessions.

	PH	DFF	FLL	FLW	NOL	SD	PL	PW	PWt	DM	HSW	DFY	GYPP
PH	-0.029	0.027	-0.013	0.009	0.002	0.003	-0.005	0.093	0.262	-0.020	0.004	0.074	0.409**
DFF	-0.003	0.230	-0.011	0.014	0.018	0.008	-0.006	0.016	-0.066	-0.234	-0.003	0.008	-0.028
FLL	-0.011	0.070	-0.035	0.016	-0.006	-0.002	-0.006	0.019	0.060	-0.071	-0.003	0.016	0.049
FLW	-0.004	0.049	-0.009	0.066	-0.009	-0.006	0.004	0.019	0.018	-0.051	0.001	0.021	0.098
NOL	0.001	-0.045	-0.002	0.007	-0.094	0.002	0.001	-0.036	0.015	0.044	0.010	-0.003	-0.101
SD	-0.002	0.042	0.001	-0.009	-0.005	0.045	-0.003	0.016	0.064	-0.036	-0.002	0.007	0.120
PL	-0.005	0.048	-0.007	-0.010	0.003	0.006	-0.027	0.074	0.158	-0.045	-0.005	0.010	0.199
PW	-0.011	0.015	-0.003	0.005	0.014	0.003	-0.008	0.243	0.335	-0.004	0.003	0.032	0.624**
PWt	-0.010	-0.020	-0.003	0.002	-0.002	0.004	-0.006	0.108	0.755	0.033	0.011	0.043	0.914**
DM	-0.002	0.223	-0.010	0.014	0.017	0.007	-0.005	0.004	-0.103	-0.241	-0.006	0.005	-0.097
HSW	-0.003	-0.013	0.002	0.001	-0.020	-0.002	0.003	0.017	0.172	0.029	0.046	0.009	0.242**
DFY	-0.024	0.021	-0.006	0.016	0.003	0.004	-0.003	0.088	0.362	-0.013	0.005	0.089	0.541**

Residual effect: 0.2828

\*\* - Significance at 1% level; \* - Significance at 5% level

(High = 0.30-0.99, Moderate = 0.20-0.29, Low = 0.10-0.19)

PH – plant height; DFF – days to 50% flowering; FLL – flag leaf length; FLW – flag leaf width; NOL – number of leaves; SD – stem diameter; PL – panicle length; PW – panicle width; PWt – panicle weight; DM – days to maturity; HSW – hundred seed weight; DFY – dry fodder yield per plant; GYPP – grain yield per plant.

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