

Electronic Journal of Plant Breeding



Research Article

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

V. Santhiya¹, B. Selvi¹, D. Kavithamani^{1*} and A. Senthil²

¹Department of Millets, Center for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore – 641003, Tamil Nadu, India

²Department of Crop physiology, Tamil Nadu Agricultural University, Coimbatore – 641003, Tamil Nadu, India

*E-Mail: kavitharice@gmail.com

Abstract

Sorghum is one of the important coarse cereal crops being cultivated world-wide, especially in arid and semi-arid regions. Though the crop is cultivated widely, the production and productivity are still not as expected to its potential. To overcome this problem and to develop high yielding sorghum genotypes, it is highly essential to utilize the existing genetic variability prevalent among the germplasm accessions. In the present study, a set of 102 germplasm accessions were evaluated for 13 yields and their contributing traits to assess the variability and character association among them. The study clearly indicated the presence of a considerable level of variation for yield and its attributing traits among the genotypes. High PCV and GCV were observed for the traits viz., stem diameter, flag leaf length, flag leaf breadth, flag leaf area, the number of leaves, leaf length, leaf breadth, panicle length, panicle length of branches, test weight and grain yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for the traits viz., plant height, stem diameter, leaf length, leaf breadth, flag leaf length, flag leaf breadth, flag leaf area, panicle length, panicle length of branches, the number of leaves, the number of nodes per plant, days to 50 per cent flowering, test weight and grain yield per plant. Association studies revealed a positive and significant association of stem diameter, flag leaf length, flag leaf breadth, flag leaf area, panicle length and test weight on grain yield per plant. Path analysis revealed that test weight followed by days to 50 per cent flowering, panicle length, flag leaf length, flag leaf area and leaf breadth had a direct positive effect on grain yield per plant. Hence, from this study, it is suggested that the genotypes with high grain yield, test weight, flag leaf area and panicle length could be more promising to yield better hybrids in a further breeding programme.

Key words: sorghum, germplasm accessions, variability, association analysis, grain yield.

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench], “The King of coarse cereals” is a multipurpose crop that can be grown as food, feed and as fodder. In India, the area, production and productivity of sorghum is approximately 4.10 million hectares, 4.74 million metric tonnes and 1.16 metric tonnes per hectare, respectively (USDA, 2021). It is also called a camel of the desert because it produces a good yield under high temperature and low soil moisture. Sorghum is an often-cross pollinated crop and its inflorescence is

known as panicle or head. It can tolerate both droughts as well as water-logged conditions (Ali *et al.*, 2011). Clay loam soil type and warm day and night temperature are ideal for sorghum cultivation. It can grow in the pH range of 6.0 to 8.0. Physiologically, sorghum is a C₄ plant and has high photosynthetic efficiency, moderate water-use efficiency and low respiration rate (Arunkumar, 2013). The productivity of sorghum is so far lower than its potential (Gebregergs and Mekbib, 2020).

Plant genetic resources are essential components to meet the future food security needs of the world. Greater use of such diversity in sorghum breeding programs so as to develop cultivars with a broad genetic base will result in sustainable sorghum production (Karadi and Kajjidoni, 2019). The identification of trait-specific germplasm is key to the successful introgression of new diversity into the crop improvement programs (Upadhyaya *et al.*, 2019). Hence, sorghum germplasm accessions with high yielding performance are much needed for crop improvement. To achieve this, the available sorghum genetic variability could be effectively utilized in the breeding programme for its improvement.

Phenotypic selection of desirable characters with high GCV and PCV, high heritability coupled with high genetic advance is essential to acquire elite germplasm accessions for their deployment in successive breeding programmes. Yield is a complex trait and quantitative in nature. A positive or negative correlation between two traits is indispensable for plant breeder to develop new varieties with high yielding performance (Ezeaku and Mohammed, 2006).

The path coefficient analysis as suggested by Dewey and Lu (1959) was used to assess the cause-and-effect relationship through partitioning of the correlation coefficient into direct and indirect effects of traits towards the dependent variable. To bring about any improvement in any crop, the knowledge of the association of yield with other traits will be of immense help. Hence, this study is aimed to analyze and determine the traits having greater interrelationship with grain yield utilizing the correlation and path analysis (Khandelwal *et al.*, 2015). Thus, correlation and path analysis was greatly obliging for germplasm selection and crop enhancement programmes.

The present investigation was conducted to assess the variability and to study the association between the yield contributing traits in the available germplasm accessions, which in turn will be useful for the selection of valuable germplasm accession.

MATERIALS AND METHODS

A field experiment was conducted to study the variability, correlation and path analysis of 102 sorghum germplasm accessions for 13 yields and their contributing traits at the Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *Summer*, 2021. Experimental material comprised of 50 accessions received from Department of Plant Genetic Resources, Tamil Nadu Agricultural University, Coimbatore, 22 accessions from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, 23 accessions from ICAR-Indian Institute of Millets Research (ICAR-IIMR), Hyderabad and seven checks from Department of Millets, Tamil Nadu Agricultural University, Coimbatore. The experimental design utilized for this study was Augmented block design II in which the checks were replicated and randomized into three blocks. Each germplasm accession was sown in a 4 m row with the spacing of 45 cm between rows and 15 cm between plants. Thirteen yield and its contributing traits *viz.*, plant height, stem diameter, leaf length, leaf breadth, flag leaf length, flag leaf breadth, flag leaf area, panicle length, number of leaves, test weight and grain yield per plant were recorded at the time of physiological maturity for five randomly selected plants per accession. Days to 50 per cent flowering and days to maturity were recorded on a row basis. Estimation of mean, range, ANOVA, variability parameters, correlation and path analysis was done by the TNAU-STAT software program (Manivannan, 2014).

Table 1. Mean performance of sorghum germplasm accessions for yield and its contributing traits.

Characters	Mean	Range		CV(%)
		Minimum	Maximum	
Plant height (cm)	216.34	140.45	330.90	5.32
Days to 50% flowering	62.63	46.00	87.00	6.38
Stem diameter (cm)	4.89	1.60	12.30	12.23
Flag leaf length (cm)	37.61	14.10	75.40	7.09
Flag leaf breadth (cm)	5.11	1.80	8.70	8.31
Flag leaf area (cm ²)	159.38	23.31	463.49	8.66
Number of leaves	9.57	5.00	15.00	10.53
Leaf length (cm)	65.81	22.70	95.70	7.37
Leaf breadth (cm)	7.56	3.20	12.10	5.60
Panicle length (cm)	18.25	7.50	45.80	12.77
Days to maturity	101.12	84.00	120.00	3.40
Test weight (g)	2.25	0.51	4.02	7.10
Grain yield per plant (g)	12.77	7.25	46.53	8.03

RESULTS AND DISCUSSION

The data recorded from all the 102 accessions were subjected to analysis of variance and it was found to be significant for all the traits involved in this study. Hence, it was further considered for the estimation of phenotypic variance, genotypic variance, heritability and genetic advance. Estimates of mean, range, standard error and standard deviation are given in **Table 1**.

Among the germplasm accessions, high PCV and GCV were observed for stem diameter (51.50 and 45.01), leaf breadth (25.49 and 24.55), flag leaf length (31.94 and 28.13), flag leaf breadth (33.93 and 26.67), flag leaf area (62.18 and 54.33), panicle length (46.15 and 40.71), the number of leaves (24.47 and 20.79), test weight (32.76 and 31.59) and grain yield per plant (54.53 and 48.46) (**Table 2**). Moderate PCV and GCV were observed for plant height (19.68 and 18.57), days to 50 per cent flowering (19.14 and 17.47) and days to maturity (11.03 and 10.22). Sheetal *et al.* (2021) also reported high PCV and GCV (20.16 and 20.85) for grain yield and moderate PCV and GCV (12.64 and 16.11) for plant height. Similar results were reported by Bejiga *et al.* (2021) and Shivaprasad *et al.* (2019). High PCV and moderate GCV (21.30 and 19.29) was observed for leaf length. In this study, the phenotypic coefficient of variance was quite superior to the genotypic coefficient of variance for each yield and its contributing traits, which show the influence of environmental factors over these characters.

Among the germplasm, high heritability coupled with high genetic advance as per cent of mean was observed for plant height (89.05 and 36.10), days to 50 per cent flowering (83.32 and 32.86), stem diameter (76.39 and 81.04), flag leaf length (77.54 and 51.02), flag leaf breadth

(61.76 and 43.17), flag leaf area (76.33 and 97.77), the number of leaves (72.20 and 36.40), leaf length (82.04 and 36.00), leaf breadth (92.77 and 48.71), panicle length (77.81 and 73.97), test weight (92.96 and 62.74) and grain yield per plant (78.98 and 88.72) (**Table 2**). These results clearly indicate that the variations observed among the germplasm accessions were due to additive gene action. This is in affirmation with the results of Bello *et al.* (2007) and Sheetal *et al.* (2021) who reported high heritability for plant height (61.50), days to 50 per cent flowering (67.20), panicle length (88.00) and grain yield per plant (93.5). A high level of additive gene effect is directly correlated with high breeding value. Hence, the selection of superior genotypes in an early generation is highly useful for the development of desired characters, which is to be exploited in a breeding programme. Days to maturity (85.78 and 19.50) showed high heritability with moderate genetic advance as per cent of mean, which revealed additive as well as non-additive gene action governing this trait. The selection of genotypes based on this character is limited.

Association studies play a vital role in the assortment of better genotypes based on the correlated traits in a breeding programme (Swamy *et al.*, 2018). In this study, a simple correlation was worked out between 13 characters as presented in **Table 3**. The results revealed that plant height had a positive and significant correlation with days to 50 per cent flowering, stem diameter, number of leaves, leaf length, panicle length, and days to maturity while it had a negative and significant association with test weight. This result was in concordance with the findings of Gebreyohannes *et al.* (2018). Days 50 per cent flowering had a significant positive association with stem diameter, flag leaf length, number of leaves, leaf length,

Table 2. Variance estimates of yield and its contributing traits in sorghum germplasm accessions

Traits	PCV (%)	GCV (%)	h ² (%)	GAM (%)
Plant height	19.68	18.57	89.05	36.10
Days to 50% flowering	19.14	17.47	83.32	32.86
Stem diameter	51.50	45.01	76.39	81.04
Flag leaf length	31.94	28.13	77.54	51.02
Flag leaf breadth	33.93	26.67	61.76	43.17
Flag leaf area	62.18	54.33	76.33	97.77
Number of leaves	24.47	20.79	72.20	36.40
Leaf length	21.30	19.29	82.04	36.00
Leaf breadth	25.49	24.55	92.77	48.71
Panicle length	46.15	40.71	77.81	73.97
Days to maturity	11.03	10.22	85.78	19.50
Test weight	32.76	31.59	92.96	62.74
Grain yield per plant	54.53	48.46	78.98	88.72

PCV- Phenotypic coefficient of variation; GCV- Genotypic coefficient of variation; h² – heritability; GAM – Genetic advance as percent of mean

Table 3. Correlation for yield and its contributing traits in sorghum germplasm

	PH	DFF	SD	FLL	FLB	FLA	NOL	LL	LB	PL	DM	TW	GYPP
PH	1.000												
DFF	0.456**	1.000											
SD	0.271**	0.395**	1.000										
FLL	0.132	0.256**	0.454**	1.000									
FLB	0.003	0.133	0.488**	0.726**	1.000								
FLA	0.022	0.190*	0.492**	0.901**	0.926**	1.000							
NOL	0.326**	0.369**	0.526**	0.333**	0.330**	0.329**	1.000						
LL	0.284**	0.455**	0.362**	0.163*	0.120	0.119	0.319**	1.000					
LB	0.147	0.373**	0.517**	0.185*	0.425**	0.278**	0.380**	0.551**	1.000				
PL	0.280**	0.068	-0.016	0.041	-0.108	-0.019	0.039	0.095	-0.188*	1.000			
DM	0.464**	0.961**	0.372**	0.266**	0.116	0.183*	0.389**	0.437**	0.360**	0.062	1.000		
TW	-0.304**	-0.171*	0.276**	0.211*	0.262**	0.258**	0.111	0.009	0.142	-0.210*	-0.204**	1.000	
GYPP	-0.300**	-0.149	0.169*	0.293**	0.184*	0.273**	0.020	-0.006	0.011	0.163*	-0.188*	0.466**	1.000

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

PH-plant height; DFF- days to 50 per cent flowering; SD-stem diameter; FLL- flag leaf length; FLB-flag leaf breadth; FLA- flag leaf area; NOL- number of leaves; LL- leaf length; LB- leaf breadth; PL- panicle length; DM- days to maturity; TW-test weight; GYPP- grain yield per plant

leaf breadth, days to maturity and a negative association with test weight. Leaf breadth and days to maturity had significant and positive associations with leaf length. Leaf breadth had a significant and positive association with days to maturity and a negative correlation with panicle length. Panicle length had a significant and negative association with test weight. These results were comparable with that of Gebrie and Genet (2019), Shivaprasad *et al.* (2019), Senbetay and Belete (2020). Days to maturity had a significant and negative correlation with test weight. Grain yield had a significant and positive correlation with stem diameter, flag leaf length, flag leaf breadth, flag leaf area, panicle length and test weight while negative associations with plant height and days to maturity. In the same way, Pawar, (2017) reported a significant positive association between grain yield and flag leaf area. Similarly, Jimmy *et al.* (2017), Pawar, (2017), Deshmukh *et al.* (2018), Swamy (2018), Mengesha *et al.* (2019) and Mofokeng *et al.* (2019) reported a positive relationship involving grain yield and test weight. The positive correlation between stem diameter and grain yield was comparable with the findings of Shivaprasad *et al.* (2019) and Akatwijuka *et al.* (2019). Warkad *et al.* (2010) revealed a negative association between grain yield and days to maturity. Arunkumar *et al.* (2004) reported a positive and significant correlation between plant height and days to 50 per cent flowering.

The nature of the association between the two variables is determined by analyzing the path coefficient, which was

used by Dewey and Lu (1959) for plant selection. This coefficient measures the direct and indirect contribution of several independent traits to dependent traits Kavya *et al.* (2020). In this study, path coefficient analysis (Table 4) revealed that test weight had a high (0.341) direct positive effect on grain yield followed by days to 50 per cent flowering (0.301), panicle length (0.300), flag leaf length (0.290), flag leaf area (0.252) and leaf breadth (0.125). Similar results were obtained for days to 50 per cent flowering (Warkad *et al.*, 2010), panicle length, test weight (Arunkumar, 2013) and test weight (Shinde *et al.*, 2014). Direct negative effect on grain yield was observed for plant height (-0.291) and days to maturity (-0.428). These findings were parallel with the conclusions of Hundekar *et al.* (2016), Pawar, (2017) and Gebrie and Genet (2019). Flag leaf length had an indirect positive effect on grain yield through flag leaf area and flag leaf breadth. Likewise, days to 50 per cent flowering through days to maturity, flag leaf breadth through flag leaf length, flag leaf area through flag leaf length and flag leaf breadth and days to maturity through plant height, stem diameter and leaf length exhibited indirect positive effects.

The present investigation revealed that the characters viz., test weight, panicle length, flag leaf length and flag leaf area had a direct positive effect and positive correlation on grain yield per plant. These traits also have high PCV and GCV coupled with high heritability and genetic advance as per cent of mean. Traits with high PCV and

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

	PH	DFF	SD	FLL	FLB	FLA	NOL	LL	LB	PL	DM	TW	Correlation for GYPP
PH	-0.291	0.137	0.025	0.038	-0.001	0.006	-0.004	-0.009	0.018	0.084	-0.198	-0.104	-0.300**
DFF	-0.133	0.301	0.036	0.074	-0.053	0.048	-0.005	-0.015	0.047	0.020	-0.411	-0.058	-0.149
SD	-0.079	0.119	0.091	0.131	-0.194	0.124	-0.007	-0.012	0.065	-0.005	-0.159	0.094	0.169*
FLL	-0.038	0.077	0.041	0.290	-0.288	0.227	-0.004	-0.005	0.023	0.012	-0.114	0.072	0.293**
FLB	-0.001	0.040	0.045	0.210	-0.396	0.234	-0.004	-0.004	0.053	-0.033	-0.050	0.089	0.184*
FLA	-0.007	0.057	0.045	0.261	-0.367	0.252	-0.004	-0.004	0.035	-0.006	-0.078	0.088	0.273**
NOL	-0.095	0.111	0.048	0.096	-0.131	0.083	-0.013	-0.010	0.047	0.012	-0.166	0.038	0.020
LL	-0.083	0.137	0.033	0.047	-0.048	0.030	-0.004	-0.032	0.069	0.029	-0.187	0.003	-0.006
LB	-0.043	0.112	0.047	0.054	-0.169	0.070	-0.005	-0.018	0.125	-0.057	-0.154	0.048	0.011
PL	-0.081	0.021	-0.001	0.012	0.043	-0.005	-0.001	-0.003	-0.024	0.300	-0.027	-0.071	0.163
DM	-0.135	0.289	0.034	0.077	-0.046	0.046	-0.005	-0.014	0.045	0.019	-0.428	-0.070	-0.188*
TW	0.089	-0.052	0.025	0.061	-0.104	0.065	-0.001	0.000	0.018	-0.063	0.088	0.341	0.466**

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

PH-plant height; DFF- days to 50 per cent flowering; SD-stem diameter; FLL- flag leaf length; FLB-flag leaf breadth; FLA- flag leaf area; NOL- number of leaves; LL- leaf length; LB- leaf breadth; PL- panicle length; DM- days to maturity; TW-test weight; GYPP- grain yield per plant

GCV coupled with high heritability and genetic advance as per cent of the mean will be of great utility in selecting the germplasm accessions. Therefore, the aforesaid traits could be more promising to yield better hybrids in a further breeding programme and considered for selecting parental lines in a hybridization programme.

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