

## Genetic Variability and Character Association Studies in Germplasm Lines of Sorghum [*Sorghum bicolor* (Linn.) Moench]

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### ABSTRACT

A field experiment was conducted to evaluate sorghum [*Sorghum bicolor* (L.) Moench] germplasm lines raised in simple lattice design during the *kharif* 2020. Genetic variability and character association were studied for thirteen morphological traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of leaves, leaf length, leaf width, stem diameter, panicle length, panicle width, panicle weight, test weight, number of primary branches per panicle and seed yield per plant. High heritability coupled with high genetic advance as per cent of mean and high GCV were noticed for plant height, panicle width, panicle weight, test weight, number of primary branches per panicle and seed yield per plant. Seed yield per plant showed a significant positive correlation with number of leaves, leaf width, stem diameter, panicle width, panicle weight, test weight and number of primary branches per panicle. Characters like number of leaves, panicle width, panicle weight and test weight exerted positive direct effect and had a significant positive correlation with seed yield per plant at both genotypic and phenotypic level. So, simple selection based on these characters would be rewarding.

*Keywords* : Genetic variability, Correlation, Path analysis, Sorghum germplasm

**S**ORGHUM [*Sorghum bicolor* (L.) Moench] belongs to the family Poaceae is a native to north-eastern Africa, where there is still a lot of variation in wild and cultivated forms (Harlan and De Wet, 1972). Because of its drought and heat adaptability, sorghum is popularly referred to as 'camel crop' in hot and arid environments. With a global annual production of 57.6 million tonnes (Anonymous, 2017), it is the world's fifth most prominent cereal crop after wheat, rice, maize and barley in terms of production and utilization. Andhra Pradesh, Karnataka, Maharashtra, Gujarat, Madhya Pradesh and Rajasthan are among India's leading sorghum-growing states. Karnataka accounts for 46 per cent of the total sorghum production, with 65 per cent of the total area during *rabi* season. Major sorghum growing areas of Karnataka include Bijapur, Bagalkot, Belgaum, Gulbarga, Raichur, Chamarajanagara and Mysore.

The identification of variability among accessions is pivotal for the maintenance and utilization of

germplasm resources (Mwirigi *et al.*, 2009). Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop. Genetic variability studies give information about the genetic features of a population, on which breeding approaches for the improvement of the crop are developed. Because heredity is influenced by the environment, heritability information alone may not be sufficient to pin point the features enforcing selection hence, the heritability estimates will be more trust worthy when it is coupled with the expected genetic advance (Johnson *et al.*, 1955).

Study of correlation between different quantitative characters provides an idea of association between yield attributing characters. Association of characters like yield, its components and other economical traits is important for making selection in the breeding programme. It suggests the advantage of a scheme of selection for more than one character at a time

(Kalloo, 1994). The path coefficient technique developed by Wright (1921) helps in estimating direct and indirect contribution of various components in building up the total correlation towards yield. Thus, the present study was conducted to assess the genetic variability, correlation and path analysis with respect to various important quantitative traits in germplasm lines of sorghum.

## MATERIAL AND METHODS

### Experimental Material and Layout

The experimental material included 81 germplasm lines including three checks *viz.*, CSV 23, CSV 27 and Gundlupet local from AICRP on sorghum, KVK, Haradanahalli Farm, Chamarajanagara. Geographically the experimental site was situated in southern dry zone (zone-6) of Karnataka between 11° 88' N latitude, 76° 95' E longitude and 721 m above mean sea level. These germplasm lines were planted in the plots of three-meter row length with two

replications under simple lattice design during *kharif* 2020. The spacing followed was 45 cm between the rows and 15 cm between plants. Observations were recorded on five competitive plants in each genotype in each replication for days to 50 per cent flowering, days to maturity, plant height (cm), number of leaves, leaf length (cm), leaf width (cm), stem diameter (mm), panicle length (cm), panicle width (cm), panicle weight (g), test weight (g), number of primary branches per panicle and seed yield per plant (g). The mean values were subjected to statistical analysis using WINDOSTAT 8.5 software.

## RESULTS AND DISCUSSION

The analysis of variance of thirteen quantitative traits revealed that the variance due to treatments (genotypes) was highly significant for all the traits studied indicating the presence of substantial amount of variations among the genotypes under study which can be exploited for selection. Phenotypic variance was greater than genotypic variance for all the traits.

TABLE I  
Estimation of mean, range and genetic parameters in 81 sorghum germplasm lines for various quantitative characters

Characters	Mean	Range		Coefficient of Variation (%)		H(BS) (%)	GAM (%)
		Min.	Max.	PCV (%)	GCV (%)		
Days to 50 per cent flowering	64.00	50.50	79.00	13.34	13.12	96.70	26.57
Days to maturity	99.14	84.00	115.00	9.93	9.75	96.40	19.73
Plant height (cm)	212.28	80.75	322.25	39.20	39.10	99.46	80.32
Number of leaves	8.91	5.50	13.50	25.77	18.50	51.60	27.44
Leaf length (cm)	75.18	55.20	93.50	13.63	13.47	97.70	27.44
Leaf width (cm)	6.81	5.20	8.85	15.69	11.29	51.80	16.74
Stem diameter (mm)	15.01	10.09	19.92	19.09	17.35	82.60	35.50
Panicle length (cm)	23.34	15.13	31.00	17.74	16.63	87.90	32.13
Panicle width (cm)	5.85	3.75	8.55	23.49	22.97	95.60	46.25
Panicle weight (g)	62.15	37.50	89.38	29.04	28.78	98.20	58.74
Test weight (g)	2.39	1.75	3.75	27.66	23.69	73.30	41.80
Number of primary branches per panicle	60.80	41.00	87.50	23.39	23.27	98.20	47.69
Seed yield per plant (g)	38.69	24.50	62.75	27.01	26.77	99.00	54.65

PCV-Phenotypic-coefficient of variance; GCV- Genotypic-coefficient of variance;  
H(BS)- heritability (broad sense) ; GAM- Genetic-advance per cent of mean

TABLE 2  
Estimates of phenotypic correlation coefficients for yield and its contributing traits in sorghum germplasm lines

$X_1$	$X_2$	$X_3$	$X_4$	$X_5$	$X_6$	$X_7$	$X_8$	$X_9$	$X_{10}$	$X_{11}$	$X_{12}$	$X_{13}$
$X_1$	1.0000	0.4310 **	0.6140 **	0.5230 **	0.0429	0.1539	-0.2110 **	-0.1640 *	-0.1479	0.1311	-0.1450	-0.0353
$X_2$	1.0000	0.4030 **	0.6070 **	0.5810 **	0.1125	0.2080 **	-0.1770 *	-0.0996	-0.0722	0.1067	-0.1120	0.0324
$X_3$	1.0000	1.0000	0.4600 **	0.5500 **	0.0157	-0.1236	0.1590 *	0.2230 **	-0.0111	0.0267	0.1700 *	0.0669
$X_4$	1.0000	1.0000	1.0000	0.4730 **	0.2220 **	0.2660 **	-0.0650	-0.0167	0.0056	0.1124	0.0501	0.1570 *
$X_5$	1.0000	1.0000	1.0000	1.0000	0.3430 **	0.3710 **	0.1850 *	0.1442	0.1312	0.1043	0.1970 *	0.1268
$X_6$	1.0000	1.0000	1.0000	1.0000	1.0000	0.4950 **	0.0710	0.1800 *	0.4180 **	0.3710 **	0.2890 **	0.1810 *
$X_7$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.1091	0.0623	0.3760 **	0.2180 **	0.1458	0.1810 *
$X_8$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.1680 *	0.0877	0.0156	0.1780 *	0.0891
$X_9$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.5250 **	0.0522	0.4410 **	0.3880 **
$X_{10}$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.2880 **	0.5410 **	0.5550 **
$X_{11}$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.2200 **	0.1840 *
$X_{12}$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.3360 **
$X_{13}$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

\*Significant at  $p = 0.05$  and \*\* significant at  $p = 0.01$

$X_1$ - Days to 50 per cent flowering  
 $X_2$ - Days to maturity  
 $X_3$ - Plant height (cm)  
 $X_4$ - Number of leaves  
 $X_5$ - Leaf length (cm)  
 $X_6$ - Leaf width (cm)  
 $X_7$ - Stem diameter (mm)  
 $X_8$ - Panicle length (mm)  
 $X_9$ - Panicle width (cm)  
 $X_{10}$ - Panicle weight (g)  
 $X_{11}$ - Test weight (g)  
 $X_{12}$ - Number of primary branches per panicle  
 $X_{13}$ - Seed yield per plant (g)

TABLE 3  
Estimates of genotypic correlation coefficients for yield and its contributing traits in sorghum germplasm lines

	X <sub>1</sub>	X <sub>2</sub>	X <sub>3</sub>	X <sub>4</sub>	X <sub>5</sub>	X <sub>6</sub>	X <sub>7</sub>	X <sub>8</sub>	X <sub>9</sub>	X <sub>10</sub>	X <sub>11</sub>	X <sub>12</sub>	X <sub>13</sub>
X1	1.0000												
X2	0.9250 **	1.0000											
X3	0.4390 **	0.4110 **	1.0000										
X4	0.8810 **	0.8980 **	0.6380 **	1.0000									
X5	0.5340 **	0.5970 **	0.5560 **	0.6410 **	1.0000								
X6	0.0659	0.1790 *	0.0208	0.1383	0.4630 **	1.0000							
X7	0.1670 *	0.2410 **	-0.1358	0.2800 **	0.4090 **	0.5560 **	1.0000						
X8	-0.2270 **	-0.1820 *	0.1690 *	-0.1062	0.1920 *	0.0345	0.1030	1.0000					
X9	-0.1690 *	-0.1000	0.2270 **	-0.0426	0.2440 **	0.0493	0.1740 *	0.0887	1.0000				
X10	-0.1521	-0.0716	-0.0111	0.0001	0.5690 **	0.4110 **	0.5390 **	0.0252	0.3320 **	1.0000			
X11	0.1364	0.1439	0.0309	0.1495	0.5840 **	0.2970 **	0.0436	0.1810 *	0.4550 **	0.5490 **	1.0000		
X12	-0.1526	-0.1131	0.1710 *	0.0662	0.3890 **	0.1536	0.2560 **	0.1000	0.2560 **	1.0000			
X13	-0.0369	0.0327	0.0673	0.2240 **	0.1284	0.2730 **	0.2010 *	0.0977	0.3950 **	0.5650 **	0.2270 **	0.3440 **	1.0000

\*Significant at p = 0.05 and \*\* significant at p = 0.01

X1- Days to 50 per cent flowering  
 X2- Days to maturity  
 X3- Plant height (cm)  
 X4- Number of leaves  
 X5- Leaf length (cm)  
 X6- Leaf width (cm)  
 X7- Stem diameter (mm)  
 X8- Panicle length (mm)  
 X9- Panicle width (cm)  
 X10- Panicle weight (g)  
 X11- Test weight (g)  
 X12- Number of primary branches per panicle  
 X13- Seed yield per plant (g)

However, a narrow difference between the GCV and PCV for most of the traits indicated the negligible influence of environment on the expression of traits. Similar findings were reported by Channannavar *et al.* (2020). High estimates of GCV and PCV were observed for plant height (39.20, 39.10) followed by panicle weight (29.04, 28.78), test weight (27.66, 23.69), seed yield per plant (27.01, 26.77), panicle width (23.49, 22.97) and number of primary branches per panicle (23.39, 23.27) indicating the existence of more variability for these traits (Table 1). Similar results were obtained by Chavan *et al.* (2010), Shivaprasad *et al.* (2019) and Dhutmal *et al.* (2014). However, even GCV and PCV don't provide a valuable estimate of the extent of inheritance of the characters. As a result, the heritability of the traits may be trusted since it helps the plant breeder to determine the level of selection pressure to be applied in a given environment, which separates out the environmental influence from overall variability. Estimates of genetic advance are derived with the involvement of heritability, phenotypic standard deviation and intensity of selection. Hence, it is an unequivocal index for understanding the effectiveness of selection in improving the traits. High heritability coupled with high genetic advance as per cent of mean was observed for plant height (99.46, 80.32), seed yield per plant (99.00, 54.65), panicle weight (98.20, 58.74), number of primary branches per panicle (98.20, 47.69), leaf length (97.70, 27.44), days to 50 per cent flowering (96.70, 26.57), panicle width (95.60, 46.25), panicle length (87.90, 32.13), stem diameter (82.60, 35.50) and test weight (73.30, 41.80) indicating the preponderance of additive type of gene action in controlling these traits and consequently high genetic gain from selection would be expected. Hence selection based on these traits would be rewarding and a good response to selection can be attained in the early generation in improving these traits. The present results are in agreement with the findings of Goswami *et al.* (2020), Shalini *et al.* (2019) and Shivaprasad *et al.* (2019).

As yield is a complex quantitative character which is greatly influenced by the environment, direct selection for yield and yield component traits is futile. If selection is solely on yield per se performance, a high genotype

and environment interaction will limit improvement. Selection on yield component characters can thus result in effective improvement in yield. Therefore, the correlation studies are of considerable importance in any selection programme as they provide degree and direction of relationship between two or more component traits. Correlation studies revealed that a highly positive and significant correlation was seen between seed yield per plant and panicle weight (0.5550, 0.5650) followed by panicle width (0.3880, 0.3950), number of primary branches per panicle (0.3360, 0.3440), test weight (0.1840, 0.2270), leaf width (0.1810, 0.2730), stem diameter (0.1810, 0.2010) and number of leaves (0.1570, 0.2240) at both phenotypic and genotypic levels (Table 2 and Table 3). The results were in accordance with the findings of Sheetal *et al.* (2021), Kavya *et al.* (2020), Prasad and Sridhar (2020), Akatwijuka *et al.* (2019) and Shivaprasad *et al.* (2019). Improvement of grain yield might be possible if the above traits were considered in selection program. Genotypic correlations were greater than the phenotypic correlations which indicated the inherent associations between the characters studied.

The total correlation coefficient between yield and its component traits might sometimes be misleading as it may be an over or under estimate of its association with other traits. In such cases, direct selection on the basis of correlated response may not be bounteous. For critical evaluation, the correlation coefficient need to be split into direct and indirect effects using path coefficient analysis since, many traits affect a given character. Thus, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of characters. Path coefficient analysis was carried out at both phenotypic and genotypic level taking seed yield per plant as the dependable character (Table 4 and Table 5). Significant positive correlation and positive direct effect on seed yield per plant was seen for the traits number of leaves (0.2448, 3.5140), panicle weight (0.5137, 0.4403), panicle width (0.1349, 0.4427) and test weight (0.0677, 0.1316) at both phenotypic and genotypic levels, respectively which indicates the existence of a true relationship between these traits

TABLE 4  
Estimates of phenotypic path coefficients for various quantitative traits in sorghum germplasm lines

	X <sub>1</sub>	X <sub>2</sub>	X <sub>3</sub>	X <sub>4</sub>	X <sub>5</sub>	X <sub>6</sub>	X <sub>7</sub>	X <sub>8</sub>	X <sub>9</sub>	X <sub>10</sub>	X <sub>11</sub>	X <sub>12</sub>
X <sub>1</sub>	-0.1600	-0.1434	-0.0690	-0.0982	-0.0836	-0.0069	-0.0246	0.0338	0.0263	0.0237	-0.0210	0.0232
X <sub>2</sub>	0.1092	0.1219	0.0491	0.0740	0.0708	0.0137	0.0254	-0.0215	-0.0121	-0.0088	0.0130	-0.0137
X <sub>3</sub>	-0.0378	-0.0354	-0.0878	-0.0404	-0.0483	-0.0014	0.0108	-0.0139	-0.0195	0.0010	-0.0023	-0.0149
X <sub>4</sub>	0.1502	0.1487	0.1126	0.2448	0.1159	0.0544	0.0651	-0.0159	-0.0041	0.0014	0.0275	0.0123
X <sub>5</sub>	0.0195	0.0217	0.0205	0.0176	0.0373	0.0128	0.0138	0.0069	0.0054	0.0049	0.0039	0.0073
X <sub>6</sub>	-0.0055	-0.0143	-0.0020	-0.0282	-0.0436	-0.1272	-0.0629	-0.0090	-0.0229	-0.0531	-0.0472	-0.0367
X <sub>7</sub>	-0.0107	-0.0144	0.0086	-0.0185	-0.0257	-0.0343	-0.0694	-0.0076	-0.0043	-0.0261	-0.0151	-0.0101
X <sub>8</sub>	-0.0097	-0.0081	0.0073	-0.0030	0.0085	0.0033	0.0050	0.0461	0.0078	0.0040	0.0007	0.0082
X <sub>9</sub>	-0.0222	-0.0134	0.0300	-0.0023	0.0195	0.0243	0.0084	0.0227	0.1349	0.0709	0.0070	0.0594
X <sub>10</sub>	-0.0760	-0.0371	-0.0057	0.0029	0.0674	0.2147	0.1933	0.0451	0.2699	0.5137	0.1481	0.2781
X <sub>11</sub>	0.0089	0.0072	0.0018	0.0076	0.0071	0.0251	0.0147	0.0011	0.0035	0.0195	0.0677	0.0149
X <sub>12</sub>	-0.0012	-0.0009	0.0014	0.0004	0.0016	0.0024	0.0012	0.0015	0.0036	0.0044	0.0018	0.0082
rP	-0.0353	0.0324	0.0669	0.1570 *	0.1268	0.1810 *	0.1810 *	0.0891	0.3880 **	0.5550 **	0.1840 *	0.3360 **

\*Significant at p = 0.05 and \*\* significant at p = 0.01

rP- phenotypic correlation co-efficient with seed yield per plant (g)

Residual Effect : 0.2950

Bold and diagonal values indicate the direct effect

X<sub>1</sub>- Days to 50 per cent flowering

X<sub>2</sub>- Days to maturity

X<sub>3</sub>- Plant height (cm)

X<sub>4</sub>- Number of leaves

X<sub>5</sub>- Leaf length (cm)

X<sub>6</sub>- Leaf width (cm)

X<sub>7</sub>- Stem diameter (mm)

X<sub>8</sub>- Panicle length (mm)

X<sub>9</sub>- Panicle width (cm)

X<sub>10</sub>- Panicle weight (g)

X<sub>11</sub>- Test weight (g)

X<sub>12</sub>- Number of primary branches per panicle

TABLE 5  
Estimates of genotypic path coefficients for 13 quantitative traits in sorghum germplasm lines

	X <sub>1</sub>	X <sub>2</sub>	X <sub>3</sub>	X <sub>4</sub>	X <sub>5</sub>	X <sub>6</sub>	X <sub>7</sub>	X <sub>8</sub>	X <sub>9</sub>	X <sub>10</sub>	X <sub>11</sub>	X <sub>12</sub>
X1	-0.8173	-0.7556	-0.3584	-0.7204	-0.4367	-0.0538	-0.1365	0.1853	0.1377	0.1243	-0.1115	0.1247
X2	-1.6410	-1.7751	-0.7290	-1.5944	-1.0590	-0.3169	-0.4277	0.3227	0.1775	0.1271	-0.2555	0.2008
X3	-0.6336	-0.5934	-1.4450	-0.9225	-0.8029	-0.0300	0.1963	-0.2443	-0.3285	0.0161	-0.0447	-0.2465
X4	3.0974	3.1565	2.2434	3.5140	2.2520	0.4860	0.9840	-0.3732	-0.1497	-0.0001	0.5255	0.2326
X5	0.1770	0.1977	0.1841	0.2123	0.3313	0.1534	0.1354	0.0637	0.0482	0.0446	0.0384	0.0658
X6	0.0194	0.0527	0.0061	0.0408	0.1366	0.2951	0.1642	0.0102	0.0719	0.1680	0.1724	0.1149
X7	-0.1496	-0.2159	0.1217	-0.2509	-0.3661	-0.4986	-0.8961	-0.0923	-0.0442	-0.3678	-0.2661	-0.1376
X8	-0.0455	-0.0365	0.0340	-0.0213	0.0386	0.0069	0.0207	0.2009	0.0350	0.0178	0.0051	0.0363
X9	-0.0746	-0.0443	0.1006	-0.0189	0.0643	0.1079	0.0218	0.0770	0.4427	0.2387	0.0193	0.2016
X10	-0.0670	-0.0315	-0.0049	0.0000	0.0592	0.2507	0.1807	0.0391	0.2374	0.4403	0.1462	0.2419
X11	0.0179	0.0189	0.0041	0.0197	0.0153	0.0769	0.0391	0.0033	0.0057	0.0437	0.1316	0.0336
X12	0.0800	0.0593	-0.0895	-0.0347	-0.1042	-0.2043	-0.0806	-0.0947	-0.2389	-0.2881	-0.1340	-0.5246
rG	-0.0369	0.0327	0.0673	0.2240 **	0.1284	0.2730 **	0.2010 *	0.0977	0.3950 **	0.5650 **	0.2270 **	0.3440 **

\*Significant at p = 0.05 and \*\* significant at p = 0.01

rG- Genotypic correlation co-efficient with seed yield per plant (g)

Bold and diagonal values indicate the direct effect

X<sub>1</sub>- Days to 50 per cent flowering

X<sub>2</sub>- Days to maturity

X<sub>3</sub>- Plant height (cm)

X<sub>4</sub>- Number of leaves

X<sub>5</sub>- Leaf length (cm)

X<sub>6</sub>- Leaf width (cm)

X<sub>7</sub>- Stem diameter (mm)

X<sub>8</sub>- Panicle length (mm)

Residual Effect: 0.2220

X<sub>9</sub>- Panicle width (cm)

X<sub>10</sub>- Panicle weight (g)

X<sub>11</sub>- Test weight (g)

X<sub>12</sub>- Number of primary branches per panicle

and seed yield per plant. Hence, selection of these traits would lead to advance in seed yield. Days to 50 per cent flowering, plant height, stem diameter showed direct effects in negative direction at both genotypic and phenotypic levels. At the phenotypic level maximum indirect effect was shown by panicle weight (0.2699) through panicle width on seed yield per plant followed by panicle weight (0.1933) through stem diameter on seed yield per plant, whereas at the genotypic level maximum indirect effect was shown by number of leaves (3.1565) through days to maturity on seed yield per plant followed by number of leaves (3.0947) through days to 50 per cent flowering on seed yield per plant. Present study was in close conformity with the findings of Prasad and Sridhar (2020) and Shivaprasad *et al.* (2019). The residual effect at the genotypic and the phenotypic level was 0.2220 and 0.2950, respectively which measures the role of other possible independent variables on seed yield per plant which were not included in the investigation.

Thus, from the study it can be concluded that the traits like days to 50 per cent flowering, plant height, leaf length, stem diameter, panicle length, panicle width, panicle weight, test weight, number of primary branches per panicle and seed yield per plant were controlled by additive gene action and selection based on these traits would fetch a good response in the early generation in improving these traits. Twenty-one genotypes performed better in terms of yield than the highest yielding check CSV 23. Hence these germplasm lines could be used as source for breeding for high yield. Panicle weight, panicle width, number of primary branches per panicle, test weight and stem diameter had high heritability and positive correlation with yield. So, simultaneous improvement of these traits along with yield is possible through simple selection.

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