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Genetic Variability and Correlation Study for Yield and Yield Attributes in Coloured Sorghum Genotypes

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ABSTRACT: The experiment was carried out at College of Agriculture Raichur, during *rabi* 2021 in an augmented design to valuate the variability and characters association among grain yield and yield attributes in 100-coloured sorghum genotypes along with four checks *viz.,* M 35-1, AKJ 1, Paiyur 2 and GS-23. High PCV and GCV were observed for grain yield per plant and neck of panicle followed by panicle weight, panicle width, panicle length, peduncle length and 100-grain weight. Similarly, high heritability coupled with high genetic advance as per cent of mean was observed for the characters *viz.*, plant height, peduncle length, neck of panicle, panicle length, panicle width, panicle weight, 100 grain weight and grain yield per plant which shows that the heritability is due to additive gene effects and selection will be effective for these characters. Significant and positive correlation of grain yield per plant was observed with the characters *viz.,* panicle weight, panicle width, plant height, days to 50 per cent flowering, days to maturity and 100-grain weight at both phenotypic and genotypic level. Among these characters panicle weight (r = 0.8796 and 0.9266) showed high magnitude of positive association at both level with grain yield compared to other characters. Path analysis study revealed that panicle weight had a high direct positive effect on grain yield per plant; panicle width, peduncle length, plant height, days to maturity and 100-grain weight were showed the low magnitude of positive direct effects on grain yield. As a result, the above mentioned characters will be used for selection for increasing grain yield in coloured sorghum genotypes.

Keywords: Coloured sorghum, Variability, Genotypes, Heritability and Correlation.

INTRODUCTION

Sorghum, popularly called as jowar, is “The King of coarse cereals”, “king of millets” or “Great Millet” and is the fifth-most significant cereal crop in the world in terms of production and consumption, behind rice, wheat, maize, and barely. The latin word "Sorgo," which means "Raising above," is the source of the English word "sorghum. It is also called as *jola, jowar, cholam* in India. It is referred to as a failsafe crop and the camel of crops due to its great photosynthetic efficiency, ability to withstand heat and drought, and other characteristics. As a result, it is regarded as a crucial staple crop in arid and semi-arid areas of the world (Anagholi *et al.,* 2000).

India produced 4.78 million metric tonnes of sorghum on an area of roughly 4.24 million ha, with a productivity of 1130 kg/h (2021). (Anon., 2022a). Karnataka grows it on 1.41 million ha, producing 1.13 million metric tonnes with a productivity of 974 kg/ha in 2021. (Anon., 2022b). Africa is where sorghum first originated. It is a often cross-pollinated, diploid (2n = 20), C4 grass plant species that is a member of the tribe "Andropogeneae" and family "Graminae." The five primary races of cultivated sorghum are *bicolor, durra, guinea, caudatum* and *kafi,* and there are eleven intermediate races as well.

In coloured sorghum, the seed colour ranges from varied white hues to various pink, orange, red, and even brown hues. Seed colour is also influence by thickness of Pericarp. The grain's phenolic profile, particularly the bran layer, is intimately connected to colour. Red sorghum is generally associated with a phenolic component that has somewhat high concentrations but is absent of tannin, which is desirable in the brewing industry. White sorghum has a slightly higher overall phenolic content than yellow sorghum, which is higher in flavanones. Because it has coloured testa and significant concentrations of condensed tannins, brown sorghum called as tannin sorghum. The phenol concentration of coloured sorghum is high, and it had a unique pigment called 3-deoxyanthocyanin that doesn't have a hydroxyl group in the third carbon position. Because it is more stable under high temperatures and an alkaline pH, the pigment has a strong potential for usage as a food colouring. Additionally, sorghum is high in dietary fibre and antioxidant activity, and it can provide gluten-free protein. The crop needs to be enhanced in terms of productivity, nutrition, and biochemical factors.

MATERIAL AND METHODS

At the College of Agriculture, Raicur the experiment was carried out during *rabi*, 2021. The experimental material entails the 100-coloured sorghum genotypes with different colours, which included exotic collections obtained from R.S. Paroda gene bank, ICRISAT, Patancheru. The four checks were used in the study are M 35-1, Paiyur 2, AKJ 1 and GS-23. The checks M 35-1 and GS 23 were obtained from ARS, Hagari, UAS, Raichur, AKJ 1 was obtained from RARS, Vijayapur, UAS, Dharwad and Paiyur 2 was obtained from ARS, Coimbatore. Table 1 lists all of the genotypes used in the investigation, in an augmented design at the College of Agriculture, Raichur, which receives an average of 658 mm of rainfall annually, represents various agroclimatic situations. So, 100 coloured sorghum genotypes together with four checks were sown during *rabi,* 2021, in four blocks, each block was 4 m in long, with regular rows and plant spacing of 45 cm and 15 cm, respectively.

Table 1: List of genotypes used in present investigation and there country of origin.

Sr. No.	Genotypes	Country source	S. No	Genotypes	Country source
1.	IS522	Mexico	51	IS23955	Yemen
2.	IS2502	United states of America	52	IS24001	Yemen
3.	IS2582	United states of America	53	IS28056	Yemen
4.	IS2618	United states of America	54	IS28065	Yemen
5.	IS3579	Sudan	55	IS28074	Yemen
6.	IS3817	Mali	56	IS28172	Yemen
7.	IS6508	India	57	IS28015	Yemen
8.	IS7013	Sudan	58	IS28017	Yemen
9.	IS7527	Nigeria	59	IS28049	Yemen
10.	IS8222	Uganda	60	IS28050	Yemen
11.	IS8792	Zimbabwe	61	IS28217	Yemen
12.	IS9664	Sudan	62	IS28224	Yemen
13.	IS11180	Ethiopia	63	IS28230	Yemen
14.	IS12643	Ethiopia	64	IS28176	Yemen
15.	IS14897	Cameroon	65	IS28198	Yemen
16.	IS14904	Cameroon	66	IS28200	Yemen
17.	IS14905	Cameroon	67	IS28202	Yemen
18.	IS15098	Cameroon	68	IS28237	Yemen
19.	IS16006	Cameroon	69	IS28244	Yemen
20.	IS16169	Cameroon	70	IS28250	Yemen
21.	IS16202	Cameroon	71	IS28265	Yemen
22.	IS16310	Cameroon	72	IS28792	Yemen
23.	IS16316	Cameroon	73	IS28966	Yemen
24.	IS16398	Cameroon	74	IS29031	Yemen
25.	IS17591	Yemen	75	IS28982	Yemen
26.	IS18301	Niger	76	IS29012	Yemen
27.	IS18639	Nigeria	77	IS29013	Yemen
28.	IS18679	United states of America	78	IS29032	Yemen
29.	IS19298	Sudan	79	IS29033	Yemen
30.	IS19299	Sudan	80	IS29052	Yemen
31.	IS21868	Yemen	81	IS31706	Yemen
32.	IS22436	Sudan	82	IS30722	Cameroon
33.	IS22897	Sudan	83	IS30736	Cameroon
34.	IS22942	Sudan	84	IS30754	Cameroon
35.	IS19498	Sudan	85	IS30800	Cameroon
36.	IS20301	Niger	86	IS30802	Cameroon
37.	IS20842	United states of America	87	IS30781	Cameroon
38.	IS21835	Sudan	88	IS31906	Yemen
39.	IS23890	Yemen	89	IS32072	Yemen
40.	IS23916	Yemen	90	IS32165	Yemen
41.	IS40175	Mauritania	91	IS32185	Yemen
42.	IS22949	Sudan	92	IS33158	Cameroon
43.	IS22970	Sudan	93	IS33159	Cameroon
44.	IS23864	Yemen	94	IS33310	Cameroon
45.	IS23865	Yemen	95	IS33317	Cameroon
46.	IS28000	Yemen	96	IS33323	Cameroon
47.	IS28001	Yemen	97	IS33336	Cameroon
48.	IS28009	Yemen	98	IS33343	Cameroon
49.	IS28014	Yemen	99	IS34723	Cameroon
50.	IS23954	Yemen	100	IS35642	Chad

The whole range of advised practises and need-based plant protection techniques were employed to grow the healthy crop. Following the random selection of five plants from each genotype in each entry, the following observations were made for days to 50 per cent flowering (days), days to harvest (days), plant height, peduncle length, neck of panicle, panicle length and panicle width all these observation recorded in centimetre, panicle weight, 100 grain weight and grain yield per plant these observation recorded in gram. The

Analysis of Variance (ANOVA) was used to assess the variance components. A genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are used to quantify the degree of variability and reveal the relative amounts of variation in various traits. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was assessed by adopting the procedure suggested by Burton, 1952. The PCV and GCV estimates were categorised as high (>20%), medium (10-20%) and low (Sivasubramanian and Madhavamenon 1973). The heritability an important factor to estimate selection response (Hanson *et al.,* 1956) and genetic advance as per cent of mean (GAM) was calculated (Johnson *et al.,* 1955). To divide correlation coefficient as indirect and direct effects, a path co-efficient analysis along with correlation co-efficient analysis were performed. The formulas proposed by Dewey and Lu (1959) were used to calculate genotypic correlation coefficients. The proper correlation coefficient of the various component characters, as suggested by the Wright (1921) and refined by Dewey and Lu (1959), was used for the determination of the path coefficient indirect and direct effect of component characters to final grain yield. Data for each of these attributes was run through the INDOSTAT version 9.3 programme.

RESULTS AND DISCUSSION

The analysis of variance (Table 2) for days to 50 per cent flowering, days to mature, plant height, peduncle length, neck of panicle, panicle length, panicle width, panicle weight, 100-grain weight and grain yield per plant showed highly significant difference among the investigated genotypes at the ($P < 0.01$) level of significance.

Outcome suggests that the genotypes under test varied in their capacity to exhibit various features at the designated area. The wider range of mean in Table 3 indicates that sorghum production and productivity could be increased by using the greater genetic variability in the investigated genotypes as a source of breeding material for a character of interest and improvement for diverse aims. This suggests that the genotypes under test have seen greater genetic and phenotypic diversity. The results of Tariq *et al.* (2012); Abraha *et al.* (2015) respectively are in line with the current study reported all the characters had higher range of variability. Phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) (Table 3 and Fig. 1) values were high for grain yield per plant and neck of panicle followed by panicle weight, peduncle length, panicle length, panicle width and 100-grain weight. Present study indicated that the investigated material showed more variation for above mentioned characters.

The PCV and GCV values were moderate for plant height. Similar results of high PCV and GCV for panicle length, grain yield per plant and panicle weight reported by Swamy *et al.* (2018); Gebregergs and Mekbib (2020); Santhiya *et al.* (2021), grain yield per plant, panicle length and neck of the panicle by Kavipriya *et al.* (2020), for the character 100-grain weight, panicle width and panicle length by Mofokeng *et al.* (2019). The findings suggested that the investigated genotypes will have a larger and more effective chance of improving sorghum, if these aforementioned characters with high GCV and PCV are taken into account during selection and hybridization. Santhiya *et al.* (2021); Tamirat *et al.* (2021) reported moderate PCV and GCV for plant height. Days to mature and days to 50 per cent flowering revealed the lowest PCV and GCV values, which is consistent with the findings reported by Gebregergs and Mekbib (2020); Mulualem *et al.* (2018), which indicates less variation among the investigated genotypes for these two characters.

For characters such as peduncle length, panicle breadth, panicle length, and plant height, the PCV values were greater than their corresponding GCV values. It means that in addition to genes, the environment also has an impact on apparent variation. When comparing PCV and GCV, there was little difference in the characters' neck of panicle, 100-grain weight, panicle weight, days to 50% flowering, and days to mature, indicating that their genetic origins might be used to enhance breeding programme.

Characters such as 100-grain weight, panicle weight, plant height, peduncle length, panicle neck length, panicle breadth, days to mature and days to 50% flowering showed high heritability (Table 3 and Fig. 1). This suggests that selection for these characters could be successful because they had high heritability. The heritability for traits including days to 50% flowering, days to maturity, plant height, panicle length, and panicle weight was also reported by Khandelwal *et al.* (2015); days to 50 per cent flowering, days to mature, plant height, grain yield per plant, 100 grain weight (Badigannavar *et al.*, 2017; Endalemaw and Semahegn 2020; Gebregergs and Mekbib 2020; Kavipriya *et al.*, 2020; Santhiya *et al.,* 2021; Tamirat *et al.*, 2021), for panicle width (Endalemaw and Semahegn, 2020) and neck of the panicle (Kavipriya *et al.*, 2020).

GAM was ranged from 6.62% (days to mature) to 87.05% (grain yield per plant). According to Johnson *et al.* (1955), grain yield per plant, neck of panicle, panicle weight, panicle length, panicle width, peduncle length, 100 grain weight and plant height were classified under traits with high GAM. This indicates that these traits were under the control of additive gene action. So, these characters can be included in the sorghum breeding programme for its better improvement. Only two characters specifically days to 50% flowering (13.78%) and days to maturity (6.62%) were classified under moderate and low GAM, respectively, which shows the character is governed by non-additive genes and heterosis breeding may be useful. Similar results of high GAM for the character grain yield per plant and panicle length was reported by Santosh *et al.* (2014); grain yield per plant and plant height by Yaqoob *et al.* (2015); days to 50 per cent flowering and days to mature by Gebregergs and Mekbib (2020); Plant height, peduncle length, panicle weight, panicle length, panicle width, 100-grain weight and grain yield per plant all showed high heritability along with high GAM, demonstrating that the heritability are caused by additive gene effects and selection will be successful for these characters. Nyadanu and Dikera (2014) as well as others reported similar results.

A statistical measure called the correlation coefficient indicates the strength and magnitude of the relationship between any two variables that are only tangentially related. This connection is caused by linkage or pleiotropic gene activity, or more likely, by both. In plant breeding, correlation coefficient analysis evaluates the link between two characters and identifies character associations for enhancing yield and other economic characters. As a result of the association pattern between yield components, it is possible to choose the best genotypes from diverse populations based on a number of connected yield attributing characters. Table 4 displays phenotypic and genotypic correlation between various quantitative characters. The genotypic correlation was typically stronger than the phenotypic correlation, demonstrating an innate relationship between the numerous investigated characters.

Grain yield per plant exhibited significant positive correlation with panicle weight, plant height, days to 50 per cent flowering, panicle width, 100-grain weight and days to mature at both phenotypic and genotypic level. Tesso *et al.* (2011); Kavipriya *et al.* (2020); Endalemaw and Semahegn (2020) all reported similar findings (2020). Plant height is thought to have indirectly increased grain output because of the comparatively high direct contribution it makes to yield. According to Doggett (1988), number of nodes which corresponds to number of leaves that are created depends on the height of the plant. If adequately lighted, the more leaves have a higher potential for photosynthetic activity, leading to a higher yield.

Panicle weight showed a positive significant correlation with days to 50 per cent flowering, plant height and panicle width. Similar results are also obtained by Senbetay and Belete (2020). At the genotypic level, plant height had a positive and significant genotypic correlation with peduncle length, panicle length, panicle width and 100-grain weight. Similar results were also observed by Kalpande *et al.* (2014); Girish *et al.* (2016); Chauhan and Pandey (2021). Panicle weight showed positive significant correlation with days to 50 per cent flowering, plant height, 100-grain weight and panicle width. Like results are also obtained by Senbetay and Belete (2020); Suvarna *et al.* (2020); Chauhan and Pandey (2021).

The assessment of correlation alone may frequently be deceptive due to the mutual cancellation of component characters, so it is important to investigate the path co-efficient analysis, which considers the casual association in addition to the degree of relationship, because the mutual cancellation of component features can lead to estimation of correlation alone being frequently inaccurate. For this reason, the genotypic and phenotypic correlation was divided into direct and indirect effects to determine the relative relevance of the characters (Fig. 2 & Table 5).

At phenotypic and genotypic levels, six out of ten characters studied showed a positive and direct effect on grain yield. The character panicle weight showed a high magnitude of a positive direct effect on yield, but the remaining five characters, panicle width, peduncle length, plant height, days to maturity, and 100-grain weight were showed low magnitude of positive direct effects on grain yield. At both levels, six characters had a favourable direct impact on grain yield. The characters' panicle weight had a large direct impact on grain yield with a positive significant correlation, which showed their genuine relationship to one another and suggested that choosing these characters would increase grain yield.

The remaining characters like panicle length, neck of panicle and days to 50 per cent flowering showed negative direct effects of low magnitude on grain yield. The results are in agreement with Amare *et al.* (2015); Khandelwal *et al.* (2015); Zinzala *et al.* (2018). Residual effects were 0.324 and 0.185 at phenotypic and genotypic levels. These characters are important and can be employed in a strategic way to increase sorghum's grain yield.

Table 2: Analysis of variance for morphological, yield and yield attributing characters in coloured sorghum genotypes.

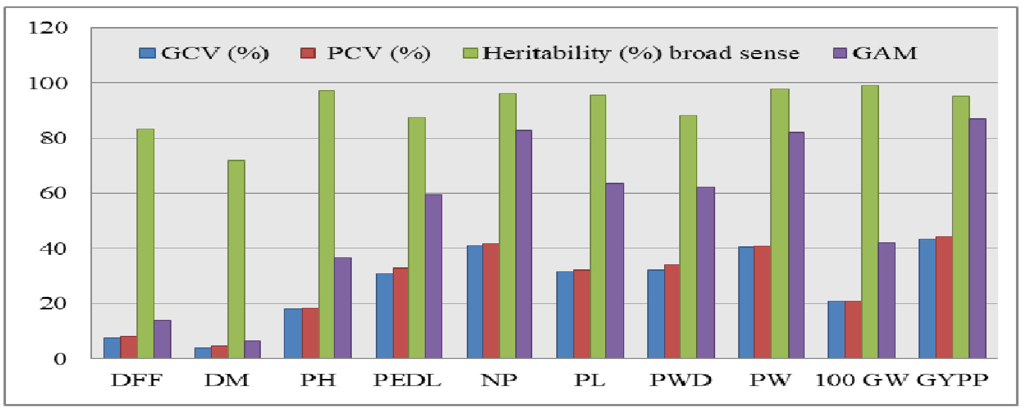
Source of variation	DF	DFF	DM	PH	PEDL	NP
Blocks	3	47.42	10	1323.94	110.05	22.31
Entries (checks + genotypes)	103	32.47 **	31.31 **	2560.43 **	346.36 **	94.02 **
Checks	3	85.42 **	152.67 **	3619.26 **	327.64 **	70.82 **
Genotypes	99	30.67 **	26.04 *	2480.46 **	341.33 **	91.58 **
Checks vs. Genotypes	1	51.64 **	188.83 **	7301.63 **	900.35 **	404.76 **
ERROR	9	4.58	6.67	63.6	37.75	3.14

Source of variation	DF	PL	PWD	PW	TW	GYPP
Blocks	3	40.56	3.61	142.89	0.27	117.52
Entries (checks + genotypes)	103	57.74 **	9.8 **	807.11 **	1.28 **	593.85 **
Checks	3	3.21	0.65	520.21 **	1.13 **	359.64 **
Genotypes	99	56.71 **	8.86 **	815.89 **	1.04 **	590.68 **
Checks vs. Genotypes	1	324.01 **	129.66 **	798.72 **	25.36 **	1610.38 **
ERROR	9	2.3	0.94	16.5	0.1	25.56

** = Significant at 1 per cent; * = Significant at 5 per cent
DF = Degrees of freedom**; DFF** = Days to 50% flowering; **DM** = Days to mature; **PH** = Plant height (cm)
NP = Neck of panicle (cm); **PEDL** = Peduncle length (cm); **PWD** = Panicle width (cm); **PL** = Panicle length (cm)
100 GW =100 grain weight (g); **PW** = Panicle weight (g); **GYPP** = Grain yield per plant (g)

Table 3: Mean, range and genetic parameters for yield and yield attributing characters in coloured sorghum genotypes.

Sr. No.	Character	Co-efficient of variation		Heritability (%) broad sense	Genetic advance as per cent over mean (GAM)	Mean	Minimum	Maximum	Range
		Genotypic Coefficient of Variation GCV (%)	Phenotypic Coefficient of Variation PCV (%)						
1.	Days to 50 per cent flowering (days)	7.32	8.02	83.42	13.78	65.31	51	81	30
2.	Days to mature (days)	3.79	4.46	71.98	6.62	109.13	96	125	29
3.	Plant height (cm)	17.97	18.24	97.11	36.48	257.11	109.6	372.8	263.2
4.	Peduncle length (cm)	30.8	32.89	87.67	59.4	53.12	15	105	90
5.	Neck of panicle (cm)	40.96	41.77	96.14	82.73	21.67	3.6	55	51.4
6.	Panicle length (cm)	31.48	32.23	95.44	63.36	22	4.4	45.4	41
7.	Panicle width (cm)	32.09	34.16	88.22	62.08	8.18	3.2	15.2	12
8.	Panicle weight(g)	40.35	40.82	97.72	82.17	66.44	16.1	158	141.9
9.	100 Grain weight (g)	21.02	21.02	99	41.99	4.52	2.06	7.07	5.01
10.	Grain yield per plant (g)	43.32	44.42	95.13	87.05	52.25	9.58	120	110.42



DFF = Days to 50 per cent flowering; **DM** = Days to mature; **PH** = Plant height (cm); **PEDL** = Pednucle length (cm); **NP** = Neck of panicle (cm); **PL** = Panicle length (cm); **PWD** = Panicle width (cm); **PW** = Panicle weight (g); **100-GW**=100 Grain weight (g); **GYPP** = Grain yield per plant (g)

Fig. 1. Mean, range and genetic parameters for yield and yield attributing characters in coloured sorghum genotypes.

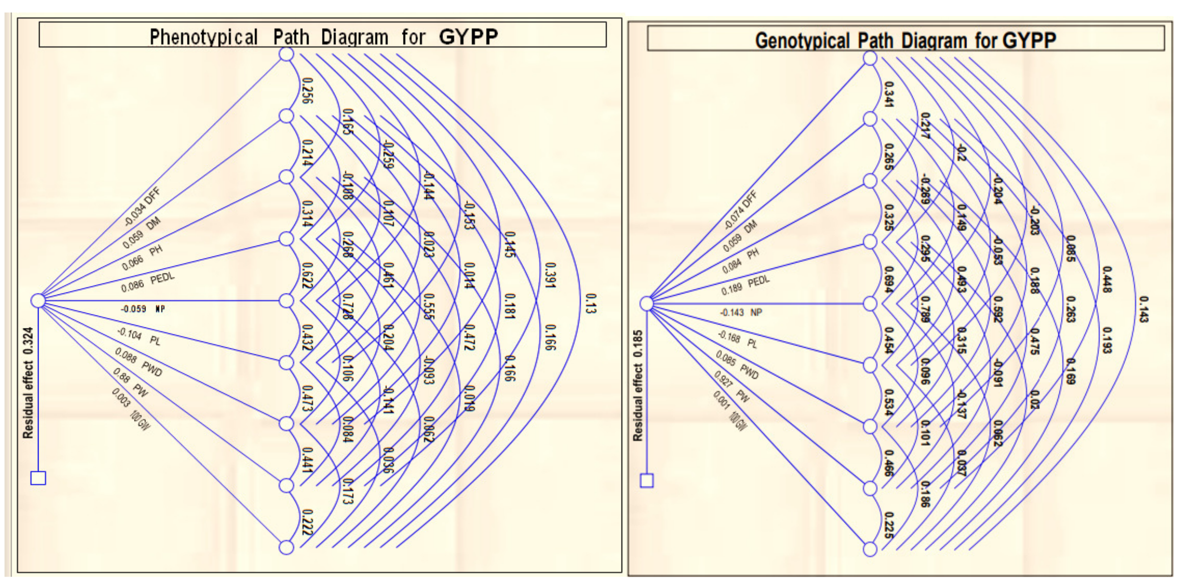


Fig. 2. Phenotypic and Genotypic path coefficient diagram showing influence of characters on grain yield per plant (GYPP) in coloured sorghum genotypes.

Table 4: Phenotypic and genotypic correlation coefficients for yield and yield attributing characters.

Character		DFF	DM	PH	PEDL	NP	PL	PWD	PW	100GW	GYPP
DFF	**P**	**1**	0.255**	0.165	-0.259**	-0.144	-0.153	0.145	0.391**	0.130	0.351**
	G		0.341**	0.217*	0.200*	-0.204*	-0.203*	0.085	0.448**	0.143	0.413**
DM	**P**		**1**	0.213*	-0.108	0.107	0.023	0.014	0.181	0.166	0.208*
	G			0.265**	-0.269**	0.149	-0.053	0.188*	0.263**	0.193*	0.253**
PH	**P**			**1**	0.313**	0.268**	0.461**	0.555**	0.472**	0.166	0.501**
	G				0.325**	0.296**	0.493**	0.592**	0.475**	0.169	0.511**
PEDL	**P**				**1**	0.621**	0.728**	0.204*	-0.093	0.020	-0.067
	G					0.694**	0.789**	0.315**	-0.091	0.020	-0.074
NP	**P**					**1**	0.431**	0.106	-0.141	0.062	-0.136
	G						0.454**	0.096	-0.137	0.062	-0.158
PL	**P**						**1**	0.473**	0.084	0.036	0.086
	G							0.534**	0.101	0.037	0.109
PWD	**P**							**1**	0.441**	0.173	0.470**
	G								0.466**	0.186*	0.528**
PW	**P**								**1**	0.222*	0.939**
	G									0.225*	0.974**
TW	**P**									**1**	0.224*
	G										0.230*
GYPP	**P**										**1**

** = Significant at 1 per cent; * = Significant at 5 per cent; **DF**= Degrees of freedom; **DFF** = Days to 50% flowering; **DM** = Days to mature
PH= Plant height (cm); **NP**= Neck of panicle (cm); **PEDL=** Peduncle length (cm); **PWD**=Panicle width (cm); **PL**= Panicle length (cm)
100 GW=100 grain weight (g); **PW**=Panicle weight (g); **GYPP=** Grain yield per plant (g)

Table 5: Phenotypic and genotypic path coefficient analysis of different yield attributing characters on grain yield.

Character		DFF	DM	PH	PEDL	NP	PL	PWD	PW	TW	GYPP
DFF	**P**	**-0.0343**	-0.0088	-0.0057	0.0089	0.0049	0.0052	-0.0050	-0.0134	-0.0045	0.3513**
	G	**-0.0742**	-0.0253	-0.0161	0.0149	0.0152	0.0151	-0.0063	-0.0333	-0.0106	0.4126**
DM	**P**	0.0151	**0.0591**	0.0126	-0.0064	0.0063	0.0014	0.0008	0.0107	0.0098	0.2076*
	G	0.0203	**0.0594**	0.0157	-0.0160	0.0088	-0.0031	0.0112	0.0156	0.0114	0.2527**
PH	**P**	0.0109	0.0142	**0.0662**	0.0208	0.0177	0.0305	0.0368	0.0313	0.0110	0.5011**
	G	0.0183	0.0224	**0.0843**	0.0274	0.0249	0.0416	0.0499	0.0400	0.0142	0.5110**
PEDL	**P**	-0.0222	-0.0093	0.0269	**0.0857**	0.0533	0.0624	0.0175	-0.0080	0.0017	-0.0672
	G	-0.0379	-0.0509	0.0616	**0.1893**	0.1314	0.1493	0.0596	-0.0173	0.0037	-0.0742
NP	**P**	0.0085	-0.0063	-0.0157	-0.0365	**-0.0587**	-0.0253	-0.0062	0.0083	-0.0036	-0.1359
	G	0.0293	-0.0214	-0.0424	-0.0995	**-0.1434**	-0.0650	-0.0138	0.0196	-0.0089	-0.1579
PL	**P**	0.0159	-0.0024	-0.0480	-0.0758	-0.0449	**-0.1041**	-0.0493	-0.0087	-0.0037	0.0856
	G	0.0341	0.0088	-0.0827	-0.1324	-0.0761	**-0.1678**	-0.0895	-0.0169	-0.0061	0.1087
PWD	**P**	0.0127	0.0012	0.0487	0.0179	0.0093	0.0415	**0.0878**	0.0387	0.0152	0.4708**
	G	0.0072	0.0159	0.0502	0.0267	0.0082	0.0453	**0.0848**	0.0395	0.0158	0.5278**
PW	**P**	0.3443	0.1593	0.4155	-0.0818	-0.1241	0.0738	0.3879	**0.8796**	0.1954	0.9391**
	G	0.4154	0.2436	0.4401	-0.0846	-0.1269	0.0933	0.4316	**0.9266**	0.2088	0.9743**
TW	**P**	0.0004	0.0005	0.0005	0.0001	0.0002	0.0001	0.0005	0.0007	**0.0031**	0.2244*
	G	0.0002	0.0002	0.0002	0.0000	0.0001	0.0000	0.0002	0.0003	**0.0013**	0.2297*

Phenotypic residual value = 0.324; Genotypic residual value = 0.185; *= Significant at 5 per cent; ** = Significant at 1 per cent
DF = Degrees of freedom; **DFF** = Days to 50% flowering; **DM** = Days to mature; **PH** = Plant height (cm); **NP** = Neck of panicle (cm)
PEDL = Peduncle length (cm); **PWD** =Panicle width (cm); **PL** = Panicle length (cm)
100 GW = 100 grain weight (g); **PW** = Panicle weight (g); **GYPP** = Grain yield per plant (g)

CONCLUSIONS

The present investigation revealed that the characters *viz*., panicle weight, days to maturity, plant height, panicle width and 100 grain weight had a direct positive effect and positive correlation on grain yield per plant. These characters panicle weight, grain yield per plant, panicle width and 100-grain weight also have high PCV and GCV coupled with high heritability and genetic advance as per cent of mean. Characters with high PCV and GCV coupled with high heritability and genetic advance as per cent of the mean will be of great utility in selecting the genotypes. Therefore, the aforesaid characters could be more promising to yield better hybrids in a further breeding programme and considered for selecting parental lines in a hybridization programme. In recent years coloured sorghum grain is gaining demand because of export potential for industrial use as red sorghum in brewing industries and yellow sorghum for weaning in baby foods.

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Conflict of Interest. None.

REFERENCES

Abraha, T., Githiri, S. M., Kasili, R., Araia, W. and Nyende, A. B. (2015). Genetic variation among sorghum (*Sorghum bicolor* L. Moench) landraces from Eritrea under post-flowering drought stress conditions. *American Journal of Plant Sciences*, *6*(09), 1410.

Amare, K., Zeleke, H. and Bultosa, G. (2015). Variability for yield, yield related traits and association among traits of sorghum (*Sorghum Bicolor* (L.) Moench) varieties in Wollo, Ethiopia. *Journal of Plant Breeding and Crop Science*, *7*(5), 125-133.

Anagholi, A., Kashiri, A. and Mokhtarpoor, H. (2000). The study of comparison between inside forage sorghum cultivars and speed feed hybrids. *Agricultural science and natural resources journal*, *7*(4), 73-83.

Badigannavar, A., Ashok Kumar, A., Girish, G. and Ganapathi, T. R. (2017). Characterization of post-rainy season grown indigenous and exotic germplasm lines of sorghum for morphological and yield traits. *Plant breeding and biotechnology*, *5*(2), 106-114.

Chauhan, P. and Pandey, P. K. (2021). Analytical Study on Correlation and Path Coefficient for Various Agronomical Traits in Sorghum [*Sorghum bicolor* (L.) Moench] in Tarai Region of Uttarakhand, India. *Indian Journal of Pure & Applied Biosciences, 9*(1), 436-441.

Dewey, D. R. and Lu, K. (1959). A correlation and path‐coefficient analysis of components of crested wheatgrass seed production 1. *Agronomy journal*, *51*(9), 515-518.

Doggett, H. (1988). Sorghum, 2nd edn. Tropical agricultural series.

Endalemaw, C. and Semahegn, Z. (2020). Genetic variability and yield performance of sorghum. *International Journal of Advanced Biological and Biomedical Research*, 8(2), 193-213.

Gebregergs, G. and 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 & Agriculture*, *6*(1), 1764181.

Girish, G., Kiran, S. B., Lokesh, R., Vikas, V., Kulkarni, V., Rachappa, V. and Talwar, A. M. (2016). Character association and path analysis in advanced breeding lines of rabi sorghum [*Sorghum bicolor* (L.) Moench]. *Journal of Applied and Natural Science*, *8*(1), 35-39.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. *Agronomy journal*, *48*(6), 268-272.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection 1. *Agronomy journal*, *47*(10), 477-483.

Kalpande, H. V., Chavan, S. K., More, A. W., Patil, V. S. and Unche, P. B. (2014). Character association, genetic variability and component analysis in sweet sorghum [*Sorghum bicolor* (L. Moench)]. Journal of crop and weed, *10*(2), 108-110.

Kavipriya, C., Yuvaraja, A., Vanniarajan, C., Senthil, K. and Ramalingam, J. (2020). Genetic variability and multivariate analyses in coloured sorghum landraces (*Sorghum bicolor* (L.) Moench) of Tamil Nadu. *Electronic Journal of Plant Breeding*, *11*(02), 538-542.

Khandelwal, V., Shukla, M., Jodha, B. S., Nathawat, V. S. and Dashora, S. K. (2015). Genetic parameters and character association in sorghum (*Sorghum bicolor* (L.) Moench). *Indian Journal of Science and Technology*, *8*(22), 2-4.

Mofokeng, M. A., Shimelis, H., Laing, M. and Shargie, N. (2019). Genetic variability, heritability and genetic gain for quantitative traits in South African sorghum genotypes. *Australian Journal of Crop Science*, *13*(1), 1-10.

Mulualem, T., Alamrew, S., Tadesse, T. and Wegary, D. (2018). Genetic Variability, Heritability and Genetic advance for Agronomical Traits of Ethiopian Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes. *Academic Research Journal of Agricultural Science and Research, 6*(4), 251-259.

Nyadanu, D. and Dikera, E. (2014). Exploring variation, relationships and heritability of traits among selected accessions of sorghum (*Sorghum bicolor* L. Moench) in the Upper East region of Ghana. *Journal of plant breeding and Genetics*, *2*(3), 101-107.

Santhiya, V., Selvi, B., Kavithamani, D. and Senthil, A. (2021). Genetic variability and character association among grain yield and their component traits in sorghum [*Sorghum bicolor* (L.) Moench]. *Electronic Journal of Plant Breeding*, *12*(3), 788-793.

Santosh, K., Girish, G., Dharmaraj, P. S. and Lokesha, R., (2014). Genetic diversity analysis in germplasm lines of *rabi* sorghum [*Sorghum bicolor* (L.) Moench] based on quantitative traits. *International Journal of Plant Sciences*, *9*(1), 129-132.

Senbetay, T. and Belete, T. (2020). Genetic variability, heritability, genetic advance and trait associations in selected sorghum (*Sorghum bicolor* L. Moench) accessions in Ethiopia. *Journal of Biology, Agriculture and Healthcare*, *10*(12), 2020.

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, *60*(9-13), 1093-1096.

Suvarna, Salimath, P. M., Upadhyaya, H. D., Lokesha, R., Nidagundi, J. M., Patil, J. R. and Patil, A. (2020). Collection and characterisation of sorghum landraces from North Karnataka. *Journal of Pharmacognosy and Phytochemistry, 9*(1), 704-708.

Swamy, N., Biradar, B. D., Sajjanar, G. M., Ashwathama, V. H., Sajjan, A. S. and Biradar, A. P. (2018). Genetic variability and correlation studies for productivity traits in Rabi sorghum [*Sorghum bicolor* (L.) Moench]. *Journal of Pharmacognosy and Phytochemistry*, *7*(6), 1785-1788.

Tamirat, B., Berhanu, A. and Temesgen, T. (2021). Genetic variability and correlation of agronomic and malt quality traits in Ethiopian sorghum [*Sorghum bicolor* (L.) Moench] landraces at Sheraro, Northern Ethiopia. *African Journal of Plant Science*, *15*(7), 193-205.

Tariq, A. S., Akram, Z., Shabbir, G., Gulfraz, M., Khan, K. S., Iqbal, M. S. and Mahmood, T. (2012). Character association and inheritance studies of different sorghum genotypes for fodder yield and quality under irrigated and rainfed conditions. *African Journal of Biotechnology*, *11*(38), 9189-9195.

Tesso, T., Tirfessa, A. and Mohammed, H. (2011). Association between morphological traits and yield components in the durra sorghums of Ethiopia. *Hereditas*, *148*(3), 98-109.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Resources*, *20*, 557-585.

Yaqoob, M., Hussain, N. and Rashid, A. (2015). Genetic variability and heritability analysis for yield and morphological traits in sorghum (*Sorghum bicolor* L. Moench) genotypes. *Journal of Agricultural Research,* (03681157), *53*(3).

Zinzala, S., Davda, B. K., Modha, K. G. and Pathak, V. D. (2018). Studies on variability, correlation and path coefficient analysis in sorghum [*Sorghum bicolor* (L.) Moench]. *International Journal of Agriculture Sciences*, *10*(19), 7285-7287.

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