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Correlation and Path Coefficient Analysis of Quantitative in Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes at Fedis, Eastern Ethiopia

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Abstract

The knowledge of the nature of inter relationship prevalent between contributory traits and grain yield is a pre-requisite to planning a meaningful crop improvement program. Therefore, the present study is aimed to determine the traits having a greater association with yield utilizing the correlation and path analysis for different traits of sorghum genotypes. Sixty-four sorghum genotypes including four standard checks were evaluated in an 8 ×8 simple lattice design at the Boko research site of Fedis Agricultural Research Center in the 2021 cropping season. Data on seventeen quantitative traits were collected. Correlation and path coefficient analyses were done by using SAS software. Grain yield showed positive and highly significant genotypic and phenotypic correlation with grain filling rate, leaf width, leaf area, panicle length, panicle width, head weight, thousand seed weight, and harvest index, and showed positive and significant association with biomass yield. This makes the work of plant breeders easy for improving both characters at once in the same direction. At genotypic and phenotypic levels, grain filling rate, harvest index, biomass yield, leaf area, thousand seed weight, and panicle weight had positive direct effects on grain yield. This implies any genetic improvement in those traits could improve grain yield. Leaf width, panicle length, and panicle width had positive genotypic correlation, but negative direct effects on grain yield. This implies that the indirect effects of other polygenic traits via those traits seem to be the cause of positive correlation and hence selection for yield should consider such important traits simultaneously.

Keywords: *Correlation, Path coefficient analysis, Sorghum*

1. Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], is the 5th most important cereal crop in the world after wheat, rice maize, and barley. It remains a critical component of food security for more than 300 million in Africa (Wagaw, 2019). It is a staple crop for more than 500 million people in 30 sub-Saharan African and Asian countries although it is primarily grown as feed grain in the developed countries (Mindaye *et al.*, 2016). Ethiopia is the third largest sorghum producer in Africa next to Nigeria and Sudan (FAO, 2021). Sorghum ranks third in area coverage, after maize and *teff* and it accounts for 15.71% of the total annual cereal (88.52%) grain production. The area covered with sorghum is 1.8 million ha, and its total

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production is 4.52 million tons, and the national average of sorghum productivity in Ethiopia is 2.69 t ha^{-1} (CSA, 2021) while 3-6 t ha^{-1} of yield is obtained by using improved sorghum varieties and management practices (Adugna *et al.*, 2005).

In Ethiopia, the various biotic factors (parasitic weed striga, diseases, and insect pests) and abiotic factors (drought and low soil fertility) contribute to the low productivity of sorghum (Asfaw, 2007). Particularly, in the lowland areas of Ethiopia including East Hararghe, the growing season is short; rainfall is also erratic and unreliable. Due to the limited number of early-maturing varieties which have good biomass yield in such areas, the late-maturing sorghum cultivars grown by farmers is frequently exposed to moisture stress at phases of growth that result in either low yield or total crop failure. Due to these problems, in the study area, the current sorghum production per unit area is not sufficient to meet the demand for human consumption, animal feed, fuel, and building material requirements of a rapidly growing population. The development of sorghum varieties for high yield with desirable traits helps in improving the food insecurity problem in the area.

The study of yield and yield components provides a basic framework for selecting useful characters in sorghum improvement programs. Grain yield is an important character that is polygenic in nature and significantly influenced by environmental conditions (Singh *et al.*, 2014). Most plant breeders are interested in maximizing selection efficiency that supports the identification of the best genotypes. Estimation of the correlation coefficient is useful in planning future breeding and provides a measure of association among traits, which could be useful as a selection guide. The path coefficient analysis enables us to determine the direct and indirect contribution of various traits toward yield. Correlation analysis provides information on associations among yield components. Path coefficient analysis permits the separation of the correlation coefficient into components of direct and indirect effects and measures the relative importance of each (Singh and Chaudhary, 1977; Sharma, 1998). Therefore, the study was conducted to study the association of quantitative traits among advanced sorghum genotypes in dryland areas.

2. Materials and Methods

2.1. Experimental Site

The study was conducted at the Boko research sub-site of Fedis Agricultural Research Center, East Hararghe Zone in 2021 cropping season. The area is situated at a distance of about 24 km away from Harar town in the southern direction. Fedis is located at the latitude of 09°07'N and longitude of 042°04'E, and an altitude of 1702 masl, with a prevalence of lowlands. The soil of the experimental site is black with sand clay loam surface soil texture that contains 8.20% organic matter, 0.13% total nitrogen, available phosphorus of 4.99 ppm, soil exchangeable potassium of 1.68 cmol(+)/kg, and a pH value of 8.26. The mean rainfall is about 801.3 mm for the last seven years. The mean maximum and minimum annual temperatures are 27.7 and 11.3°C, respectively for the last seven years (FARC, 2021).

2.2. Plant materials, Experimental Design and Management

Sixty sorghum genotypes and four released varieties were used in this study (Table 1). All genotypes including Argiti and Melkam varieties were obtained from Melkassa Agricultural Research Center as Fedis 01 and Erer varieties were obtained from Fedis agricultural research center. Four released varieties (Fedis 01, Erer, Argiti, and Melkam) were used as standard checks. The field experiment was laid out in an 8×8 simple lattice design. The experimental plot consisted of 4 rows, 2.2 m length × 3 m width with 0.75 m × 0.2 m spacing between rows and plants, respectively. The gross and net plot sizes were 6.6 m^2 (3 m×2.2 m) and 3.3 m^2 (1.5 m×2.2 m), respectively. Seeds were sown by hand drilling at the rate of 12 kg ha^{-1} as per the recommendation for row planting in sorghum. Thinning was done two weeks after emergence to adjust between the plants. The recommended NPS fertilizer was applied at the rate of 100 kg ha^{-1} during planting and Urea fertilizer was applied as a top dressing of 50 kg ha^{-1} at the knee height stage. The field was kept free of weeds by hand weeding during the whole growing period and other cultural practices were carried out as per standard practices recommended for the study area.

2.3. Data Collection

Ten plants were carefully chosen aimlessly and marked for all plots before panicle emergency and, used as a sample for plant height, leaf number per plant, leaf length, leaf width, leaf area, panicle length, head weight, panicle width, and biomass yield. Plot base data (days to flowering, days to maturity, grain filling period, grain filling rate, stand count at harvest, thousand seed weight, grain yield, and harvest index) were collected following the sorghum descriptors (IBPGR, 1993).

Table 1: Description of Sorghum Genotypes used for the Study

No.	Genotype	Pedigree	No.	Genotype	Pedigree
1	ETSC16033-20-1	05MI5064/76T1#23	33	ETSC14225-4-2	Gambella1107/S35
2	ETSC16035-9-1	05MI5064/B35	34	ETSC15357-3-1	ICSV700/Meko-1
3	ETSC16034-10-1	05MI5064/ICSTG2372	35	ETSC16056-11-1	ICSV700/Melkam
4	ETSC16038-7-1	05MI5064/M-204	36	ETSC16059-4-1	ICSV93046/Meko-1
5	ETSC16027-14-1	05MW6073/76T1#23	37	ETSC16060-10-1	ICSV93046/Melkam
6	ETSC16032-11-1	05MW6073/M-204	38	ETSC16058-20-1	ICSV93046/Teshale
7	ETSC16026-7-1	06MW6015/M-204	39	ETSC14773-1-3	ICSV96143/13sudanint#11-3
8	ETSC14715-3-1	13MIF5#5024/13sudanint#13-2	40	ETSC16072-2-1	IS38266/Meko-1
9	ETSC15437-2-2	14MILSDT7086/Gambella1107	41	ETSC14799-3-1	Karimtama 1/13sudanint#10-1
10	ETSC16016-14-1	14MWLSDT7279/ICSTG2372	42	ETSC14325-4-1	Macia/S35
11	ETSC16020-1-1	14MWLSDT7279/M-204	43	ETSC 300003	Meko-1/SRN39/Meko-1
12	ETSC16002-17-1	14MWLSDT7310/B35	44	ETSC14573-5-4	Melkam/13sudanint#10-1
13	ETSC16001-20-1	14MWLSDT7310/ICSTG2372	45	ETSC14789-3-2	NTJ2/13sudanint#14
14	ETSC16005-35-1	14MWLSDT7310/M-204	46	ETSC15363-1-2	S35/Gambella1107
15	ETSC16006-3-1	14MWLSDT7324/ICSTG2372	47	ETSC14804-4-2	SILA/13sudanint#10-1
16	ETSC16011-2-1	14MWLSDT7401/ICSTG2372	48	05MW6073	Teshale/Gobiye
17	ETSC16079-12-1	16040/ICSTG2372	49	ETSC300080	Teshale/SRN39/Teshale
18	ETSC16087-23-1	235421/ICSTG2372	50	ETSC15376-1-2	WSV387/P9404/2372
19	ETSC16091-10-1	235421/M-204	51	ETSC15385-2-2	WSV387/P9405/Meko-1
20	ETSC16101-13-2	245056/M-204	52	ETSC17081	Debir/Gobiye///Debir
21	ETSC15367-6-1	A2267-2/2372	53	ETSC17029	Teshale/Framida///Teshale
22	ETSC15371-4-1	A2267-2/Meko-1	54	ETSC17084	Dekeba/Framida///Dekeba
23	ETSC15312-3-1	Debir/(Hodem/Gobiye)	55	ETSC17075	Debir/Birhan///Debir
24	ETSC14695-1-2	Debir/13sudanint#27	56	ETSC17086	Gambella1107/Birhan///Gambella1107
25	ETSC16045-15-1	ETSL101645-6/Melkam	57	ETSC17111	Wediaker/Birhan///Wediaker
26	ETSC16051-31-1	ETSL101649-6/Meko-1	58	ETSC16221	Melkam/B35///Melkam
27	ETSC16052-27-1	ETSL101649-6/Melkam	59	ETSC16216	Meko-1/B35///Meko-1
28	ETSC16065-1-1	ETSL101848/76T1#23	60	ETSC16212	Macia/B35///Macia
29	ETSC16062-27-1	ETSL101848/Teshale	61	Fedis 01	M-36121XP-9403
30	ETSC16068-2-1	ETSL101851/Melkam	62	Erer	3443-2-OPXP9403
31	ETSC16066-18-1	ETSL101851/Teshale	63	Argiti	WSV387XP-9403
32	ETSC16070-4-1	ETSL101853/Melkam	64	Melkam	WSV387

2.4. Data Analysis

2.4.1. Phenotypic and Genotypic Correlation Coefficient (r)

Data analysis was subjected to SAS statistical package. Phenotypic and genotypic correlation coefficients between yield and yield-related traits were estimated using the standard method described by Singh and Chaudhary (1977).

$$r_{p_{xy}} = \frac{Cov_{p_{xy}}}{\sqrt{\sigma^2_{p_x} \sigma^2_{p_y}}}$$

where: $r_{p_{xy}}$ = Phenotypic correlation coefficient between character x and y

   $Cov_{p_{xy}}$ = Phenotypic covariance between characters x and y,

   $\sigma^2_{p_x}$ = Phenotypic variance for character x

   $\sigma^2_{p_y}$ = Phenotypic variance for character y

$$r_{g_{xy}} = \frac{Cov_{g_{xy}}}{\sqrt{\sigma^2_{g_x} \sigma^2_{g_y}}}$$

where: $r_{g_{xy}}$ = Genotypic correlation coefficient between character x and y

   $Cov_{g_{xy}}$ = Genotypic covariance between characters x and y

   $\sigma^2_{g_x}$ = Genotypic variance for character x

   $\sigma^2_{g_y}$ = Genotypic variance for character y

The calculated phenotypic correlation value was tested for its significance using a *t*-test:

$t = r_{ph}/SE\,(r_p)$

where, r_p = Phenotypic correlation,

   $SE\,(r_p)$ = Standard error of phenotypic correlation obtained using the following formula (Sharma, 1998).

$$SE\,(r_p) = \sqrt{\frac{1 - r^2 ph}{n - 2}}$$

where n = is the number of genotypes tested, r^2_{ph} = is the phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were tested for their significance by the formula described by Robertson (1959) as indicated below:

$t = r_{gxy} / SEr_{gxy}$

The calculated '*t*' value was compared with the tabulated '*t*' value at (n - 2) degree of freedom at a 5% level of significance. Where n is the number of genotypes.

$$SEr_{gxy} = \sqrt{\frac{1 - r^2 gxy}{h^2 x * h^2 y}}$$

where, h^2x = Heritability of trait x, h^2y = Heritability of trait y

2.4.2. Phenotypic and Genotypic Path Coefficient Analysis

Path coefficient analysis which refers to the estimation of direct and indirect effects of the yield attributing characters on yield was calculated based on the method used by Dewey and Lu (1959) as follows:

$$rij = pij + \Sigma rikpkj$$

where　　*rij* = Mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient.

　　　　Pij = component of direct effects of the independent character (i) on the dependent character (j) as measured by the path coefficient and,

　　　　Σrikpkj = summation of components of the indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k).

The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, was computed using the formula

$$1 = p^2R + \Sigma p \, ij \, rij$$

where p^2R is the residual effect, *P ij rij* = the product of the direct effect of any variable and its correlation coefficient with yield.

3. Results and Discussion

3.1. Phenotypic and Genotypic Correlation Coefficient

3.1.1. Phenotypic and Genotypic Association of Grain Yield with Yield-related Traits

The estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Table 2. Grain yield showed positive and highly significant genotypic and phenotypic correlation with grain filling rate (rg=0.82, rp=0.8), leaf width (rg=0.31, rp=0.3), leaf area (rg=0.28, rp=0.26), panicle length (rg=0.32, rp=0.29), panicle width (rg=0.35, rp=0.27), head weight (rg=0.45, rp=0.35), thousand seed weight (rg=0.29, rp=0.27) and harvest index (rg=0.9, rp=0.88). Grain yield also exhibited positive and significant genotypic and phenotypic correlation with biomass yield (rg=0.23, rp=0.21). This indicated the chance of simultaneous improvement of the grain yields with the associated traits.

The results agreed with the report of Tsegau and Tegegn (2020) who observed positive and highly significant phenotypic and genotypic correlation of grain yield with panicle length and panicle weight. A strong positive association of grain yield with panicle weight was reported by Deshmukh *et al*. (1986) and a strong correlation of yield with grain filling rate by Chalachew and Zigale (2020). Gebeyehu *et al*. (2019) observed positive and highly significant phenotypic and genotypic correlation of grain yield with leaf area, panicle weight, and harvest index and significant with biomass yield. Seetharam and Ganesamurthy (2013) reported that grain yield showed a positive and highly significant association with leaf width, panicle length, panicle width, and thousand seed weight.

3.1.2. Phenotypic and Genotypic Correlation Among Other Traits

The correlation coefficients were estimated between the component traits (Table 2). Days to maturity with grain filling rate, plant height, leaf length, and thousand seed weight showed positive and highly significant associations at the genotypic level; and showed positive and highly significant association with grain filling rate, plant height and leaf length, and positive and significant correlation with thousand seed weight at the phenotypic level. This result agreed with the findings of Prasad and Sridhar (2019) reported that days to maturity had positive and highly significant genotypic and phenotypic correlations with leaf length, leaf width, panicle width, and thousand seed weight. Tafere *et al*. (2018) reported that days to maturity had a positive and highly significant correlation with plant height and thousand seed weight

Grain filling rate with head weight and harvest index showed a positive and highly significant correlation both at genotypic and phenotypic levels. In addition, grain filling rate showed a significant and positive genotypic correlation with plant height and panicle width. Plant height had positive and highly significant genotypic and phenotypic associations with thousand seed weight and leaf length; and positive and significant with leaf length and thousand seed weight, respectively. Similarly, Firezer *et al*. (2020) reported that grain filling rate with harvest index, panicle weight, and thousand seed weight showed positive and highly significant genotypic and phenotypic associations. Tafere *et al*. (2018) reported that plant height had positive and highly significant genotypic and phenotypic correlation with thousand seed weights. Azimi *et al*. (2017) reported that plant height was positive and highly significant with leaf length and thousand seed weight for genotypic and phenotypic correlation.

Leaf number had a positive and highly significant association with leaf length, panicle wid,th and head weight, and a significant and positive correlation with leaf width and leaf area at the genotypic level. Whereas leaf number had a

Table 2: Estimates Genotypic (Below Diagonal) and Phenotypic (Above Diagonal) Correlation Coefficients for 17 Traits of 64 Sorghum Genotypes Evaluated at Fedis

Traits	DF	GFP	DM	GFR	PH	LN	LL	LW	LA	PL	PW	HW	BM	SCH	TSW	HI	GY
DF	**1.00**	0.27**	0.16	0.15	0.03	0.28**	0.05	0.05	-0.03	-0.04	0.08	0.01	-0.03	0.00	-0.03	0.01	-0.02
GFP	0.24*	**1.00**	0.75**	0.49**	0.33**	0.04	0.24**	0.06	-0.04	0.09	0.03	-0.02	0.09	0.15	0.23**	0.05	0.09
DM	0.18	0.81**	**1.00**	0.38**	0.37**	0.21**	0.36**	0.07	-0.05	0.05	0.13	0.05	0.07	0.11	0.17*	0.03	0.05
GFR	0.15	0.44**	0.40**	**1.00**	0.22**	0.06	-0.09	0.14	0.16	0.07	0.12	0.31**	0.06	0.04	-0.03	0.73**	0.80**
PH	0.05	0.37**	0.40**	0.25*	**1.00**	0.16	0.22*	0.03	0.04	0.10	-0.03	-0.06	0.12	0.01	0.29**	-0.09	-0.06
LN	0.34**	0.06	0.23	0.11	0.21	**1.00**	0.28**	0.15	0.13	-0.12	0.22**	0.17*	-0.10	0.01	0.12	0.17*	0.12
LL	0.06	0.38**	0.48**	-0.17	0.22*	0.34**	**1.00**	0.07	0.28**	0.01	0.20**	0.21**	0.01	0.09	0.09	0.09	0.08
LW	0.16	0.07	0.07	0.16	0.07	0.24*	0.09	**1.00**	0.61**	0.02	0.02	0.11	0.01	0.15	-0.05	0.17	0.30**
LA	0.03	0.05	0.04	0.12	0.04	0.23*	0.30**	0.7**	**1.00**	-0.03	0.08	0.17*	-0.05	0.04	0.04	0.19*	0.26**
PL	0.04	0.12	0.07	0.04	0.19	-0.07	0.07	0.06	0.04	**1.00**	-0.07	-0.04	0.94**	0.13	0.07	0.30**	0.29**
PW	0.17	0.05	0.17	0.20*	-0.03	0.30**	0.33**	-0.01	0.13	-0.16	**1.00**	0.78**	-0.07	0.08	0.16	0.23**	0.27**
HW	0.07	0.04	0.09	0.38**	-0.04	0.25**	0.30**	0.10	0.21	-0.10	0.84**	**1.00**	-0.03	0.11	0.18*	0.37**	0.35**
BM	0.04	0.12	0.07	0.04	0.19	-0.06	0.08	0.05	0.04	0.99**	-0.16	-0.10	**1.00**	0.17*	0.09	0.31**	0.21*
SCH	0.00	0.14	0.14	0.08	-0.03	-0.02	0.07	-0.13	-0.03	0.11	0.11	0.16	0.12	**1.00**	-0.09	0.08	0.13
TSW	0.12	0.35**	0.27**	-0.05	0.34**	0.23	0.14	0.03	0.03	0.05	0.13	0.16	0.04	0.19	**1.00**	0.13	0.27**
HI	0.04	0.07	0.07	0.81**	-0.13	0.22	0.05	0.17	0.15	0.33**	0.35**	0.47**	0.31**	0.12	0.18	**1.00**	0.88**
GY	0.02	0.13	0.10	0.82**	-0.08	0.19	0.06	0.31**	0.28**	0.32**	0.35**	0.45**	0.23*	0.17	0.29**	0.9**	**1.00**

Note: * and ** = significant at 5% and 1% probability. DF = Days to flowering, GFP = Grain Filling Period, DM = Days to Maturity, GFR = Grain Filling Rate, and PH = Plant Height. LN=Leaf Number per plant, LL= Leaf Length, LW= Leaf Width, LA=Leaf Area, PL = Panicle Length, PW= Panicle Width, HW= Head Weight, SCH=Stand Count at Harvest, TSW=Thousand Seed Weight, BM= Biomass yield, GY= Grain Yield and HI=Harvest Index.

positive and highly significant correlation with leaf length and panicle width and; a significant and positive correlation with harvest index at the phenotypic level. Leaf width had a positive and highly significant correlation with leaf area both at genotypic and phenotypic levels. Leaf length had a positive and highly significant correlation with leaf area, panicle width, and head weight both at genotypic and phenotypic levels. Leaf area had a positive and significant phenotypic correlation with head weight and harvest index. This result is in line with, Prasad and Sridhar (2019) reported that leaf width had a positive and highly significant genotypic and phenotypic correlation with thousand seed weight and, leaf number per plant had a positive and highly significant genotypic and phenotypic correlation with leaf area, leaf length, leaf width, panicle width, and thousand seed weight.

Panicle length had a positive and highly significant genotypic and phenotypic association with biomass yield and harvest index. Panicle width had a positive and highly significant correlation with head weight and harvest index both at genotypic and phenotypic levels. Head weight showed positive and highly significant genotypic and phenotypic correlation with harvest index. In addition, head weight showed a positive and significant correlation with thousand seed weights at the phenotypic level. Biomass yield showed positive and highly significant genotypic and phenotypic correlation with harvest index. In addition, biomass yield had a positive and significant phenotypic association with stand count at harvest. Similarly, Khadakabhavi *et al.* (2017) reported high significant and positive significant associations of panicle length with panicle weight for genotypic and phenotypic correlation. Chalachew *et al.* (2017) observed a positive correlation of harvest index with panicle weight.

Genotypic correlation coefficients were relatively higher in magnitude than that phenotypic correlation coefficient in most cases, which indicated the presence of inherent association among considered traits. But, in some cases, the phenotypic correlation values were higher than the genotypic correlation values suggesting the importance of environmental effects. This is in agreement with the findings of Khandelwal *et al.* (2015). The association revealed the positive association between all possible pairs of traits suggesting the possibility of correlated response to selection so that with the improvement of one trait, there will be an improvement in the other positively correlated trait. This is because a positive genetic correlation between two desirable traits makes the work of plant breeders easy for improving both traits simultaneously. For instance, grain filling rate, leaf width, leaf area, panicle length, panicle width, head weight, thousand seed weight, harvest index, and biomass yield were beneficial traits that can be simultaneously selected for improvement in the current population. But, a negative correlation between two desirable traits may hamper attaining the simultaneous improvement of those traits along with each other.

3.2. Path Coefficient Analysis

3.2.1. Genotypic Direct and Indirect Effects of Traits on Yield

The genotypic path coefficient analysis showed that the highest positive direct effect on grain yield was exerted by grain filling rate (0.542) followed by harvest index (0.355), biomass yield (0.263), leaf area (0.251), and thousand seed weight (0.238). However, panicle length (-0.143), panicle width (-0.059), and leaf width (-0.103) had negative direct effects on grain yield while head weight (0.065) exerted negligible positive direct effects on grain yield (Table 3). Lenka and Mishra (1973) categorized the direct and indirect effects into negligible (0.00-0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-1.00), and very high (>1.00).

Grain filling rate and harvest index had exerted a high and positive direct effect on grain yield and it had a positive and high significant genotypic correlation. The moderate positive indirect effect of grain filling rate was exerted via harvest index, and the negligible indirect effect was exerted via biomass yield, head weight, and leaf width. Harvest index showed high positive indirect effects via grain filling rate and negligible positive indirect effects via leaf area, head weight, thousand seed weight, and biomass yield. Therefore, the genotypic correlation of these traits with grain yield was due to both direct and indirect effects. Biomass yield, thousand seed weight, and leaf area exerted moderate and positive direct effects on grain yield and it had positive and highly significant genotypic correlation with yield, except biomass yield showed positive and significant genotypic correlation with grain yield. Similarly, Girma *et al.* (2020) reported that harvest index and biomass yield highest positive direct effect on grain yield. Kumar *et al.* (2012) reported that thousand seed weights contributed a high direct positive effect on grain yield.

Table 3: Estimates of Direct (Bold Diagonal) and Indirect Effect (Off-Diagonal) at the Genotypic Level of Nine Traits on Grain Yield

Traits	GFR	LW	LA	PL	PW	HW	TSW	BM	HI	rg
GFR	**0.542**	-0.016	0.013	-0.017	-0.012	0.025	-0.012	0.011	0.287	0.82**
LW	0.086	**-0.103**	0.179	-0.009	-0.002	0.006	0.007	0.068	0.060	0.29**
LA	0.027	-0.073	**0.251**	-0.007	-0.008	0.014	0.012	0.011	0.053	0.28**
PL	0.064	-0.006	0.009	**-0.143**	0.009	-0.006	0.012	0.260	0.117	0.32**
PW	0.111	-0.003	0.034	0.023	**-0.059**	0.055	0.031	0.042	0.124	0.35**
HW	0.206	-0.010	0.053	0.014	-0.049	**0.065**	0.038	-0.026	0.160	0.45**
TSW	-0.027	-0.003	0.013	-0.007	-0.008	0.010	**0.238**	0.011	0.064	0.29**
BM	0.022	-0.027	0.010	-0.141	-0.009	-0.006	0.010	**0.263**	0.110	0.23*
HI	0.439	-0.017	0.038	-0.047	-0.021	0.029	0.043	0.081	**0.355**	0.90**

Note: * and ** = significant at 5% and 1% probability. GFR = Grain Filling Rate, LW= Leaf Width, LA=Leaf Area, PL = Panicle Length, PW=Panicle Width, HW= Head Weight, TSW=Thousand Seed Weight, BM= Biomass Yield, GY= Grain Yield and HI=Harvest Index. Residual= 0.32, rg = genotypic correlation with grain yield.

In this study, the magnitude of the direct effect and the genotypic correlation coefficients of grain filling rate, harvest index, leaf area, biomass yield, and thousand seed weight were near to similar. This justifies that the correlation explains the true associations and selection through these traits will be effective for sorghum yield improvement. High values of direct effects suggest that the true relationship and direct selection for these traits may also increase and give a better response for improvement of grain yield (Ali, 2012). Leaf width, panicle length, and panicle width exerted low negative direct effects on grain yield. These negative direct effects were counterbalanced by the positive indirect effects of grain yield. This result is in line with the report of Tsegau and Tegegn (2020) that panicle width negative genotypic direct effect on grain yield. The negative direct effect of leaf width and panicle length on grain yield has been reported in sorghum by Goswami *et al.* (2020).

The genotypic residual value (0.32) indicated that the traits which were included in the genotypic path analysis explained 68% of the variations in grain yield while some other factors which have not been considered here account for about 32% of the variation in grain yield. This indicates that the choice of yield-attributing traits in the study was good, even if other traits are also needed to justify grain yield per hectare.

3.2.2. Phenotypic Direct and Indirect Effects of Traits on Yield

The result of the phenotypic path analysis for the traits in the present study is presented in Table 4. Phenotypic path analysis showed that grain filling rate (0.470) exerted a high positive direct effect on grain yield followed by harvest index (0.424), biomass yield (0.315), leaf area (0.235), and thousand seed weight (0.216). Similarly, head weight exerted a low direct effect and a high positive phenotypic correlation with grain yield. Leaf width, panicle length, and panicle width showed a negative direct effect and a high positive phenotypic correlation with grain yield.

Grain filling rate, harvest index, and biomass exerted high and positive direct effects and significant positive phenotypic correlation with grain yield. Leaf area and thousand seed weight exerted a relatively high positive direct effect on grain yield. Head weight revealed a small positive direct effect on grain yield, and a positive indirect effect through grain filling rate and harvest index to grain yield, and a negligible positive indirect effect via leaf area, panicle length, and thousand seed weight. In general, the traits that exerted a high positive direct effect and their positive significant correlation coefficient with grain yield were known to affect grain yield in the favorable direction and need much consideration during the process of selection. This result is in agreement with the finding of Gebeyehu *et al.* (2019) reported that leaf area had a high positive direct effect on grain yield. Ambachew (2020) reported that harvest index, biomass yield, and thousand seed weight had a high positive direct effect on grain yield.

Table 4: Estimates of Direct (Bold Diagonal) and Indirect Effect (Off-Diagonal) at the Phenotypic Level of Nine Traits on Grain Yield

Traits	GFR	LW	LA	PL	P W	H W	TSW	BM	HI	rp
GFR	**0.470**	-0.011	0.012	-0.014	-0.011	0.035	-0.011	0.019	0.310	0.80**
LW	0.066	**-0.077**	0.143	-0.004	-0.002	0.013	0.006	0.082	0.072	0.30**
LA	0.024	-0.047	**0.235**	-0.010	-0.007	0.019	0.011	-0.028	0.064	0.26**
P L	0.033	-0.002	0.012	**-0.197**	0.016	-0.007	0.011	0.297	0.127	0.29**
P W	0.056	-0.002	0.019	0.033	**-0.093**	0.089	0.028	0.041	0.098	0.27**
H W	0.146	-0.008	0.040	0.012	-0.073	**0.114**	0.035	-0.073	0.157	0.35**
TSW	-0.024	-0.002	0.012	-0.010	-0.012	0.018	**0.216**	0.013	0.059	0.27**
BM	0.019	-0.020	-0.021	-0.185	-0.012	-0.026	0.009	**0.315**	0.132	0.21*
HI	0.343	-0.013	0.035	-0.059	-0.021	0.042	0.030	0.098	**0.424**	0.88**

Note: * and **=significant at 5% and 1% probability. GFR=Grain Filling Rate, LW=Leaf Width, LA=Leaf Area, PL=Panicle Length, PW=Panicle Width, HW=Head Weight, TSW=Thousand Seed Weight, BM=Biomass Yield, GY=Grain Yield and HI=Harvest Index. Residual= 0.36, rp= phenotypic correlation with grain yield.

Leaf width, panicle length, and panicle weight exerted negative direct effects on grain yield though it had positive and highly significant genotypic and phenotypic correlations with grain yield. This indicated that the positive correlation of these traits with grain yield was due to the positive indirect effect of the trait through other traits on grain yield. If the variable or trait has a positive correlation and the direct effect of the variable or trait is negative or negligible, the positive correlation of the trait is because of the indirect effects through other traits. In such conditions, it was suggested that the importance of considering indirect causal traits for simultaneous selection is necessary. Tafere *et al.* (2018) reported the negative phenotypic direct effect of panicle length on grain yield.

The phenotypic residual value (0.36) indicated that the traits which were included in the phenotypic path analysis explained 64% of the variations in grain yield while some other factors which have not been considered here account for about 36% of the variation in grain yield. This indicates that the choice of yield-attributing traits in the study was good, even if other traits are also needed to justify grain yield per hectare. It also gives a clue to go further study to find rest of traits contributed the rest of variation in grain yield.

4. Conclusion

Grain yield had positive and highly significant genotypic and phenotypic correlation with grain filling rate, leaf width, leaf area, panicle length, panicle width, head weight, thousand seed weight, and harvest index and; positive and significant with biomass yield. These traits rewarded a positive correlation towards yield. Thus, sorghum breeders should be given attention to those traits when selecting the best grain yield genotypes. Grain filling rate, harvest index, biomass yield, leaf area, thousand seed weight, and head weight had a positive direct effect on grain yield at genotypic and phenotypic levels. Direct selection of these important traits can improve sorghum yield. Panicle length, leaf width, and panicle width exerted a negative direct effect on grain yield at the genotypic and phenotypic levels. Therefore, much attention should be given to panicle length, leaf width, and panicle width as these traits are helpful via indirect selection to improve grain yield.

References

Ali, H.I., Mahmoud, K.M. and Amir, A.A. (2012). Estimation of Genetic Variability, Heritability and Genetic Advance in Grain Sorghum Population. *American Journal of Agricultural and Environmental Science*, 12(4), 414-422.

Ambachew, Tefera. (2020). Variability and Association Studies Among The Sorghum Genotypes For Seed Yield And Yield Related Traits Under Rainfed Condition of Ethiopia. *Journal of Genetics, Genomics and Plant Breeding*, 4(1), 9-19.

Asfaw, Adugna. (2007). Assessment of Yield Stability in Sorghum. *African Crop Science Journal*, 15(2), 83-92.

Azimi, A.M., Marker, S. and Bhattacharjee, I. (2017). Genotypic and Phenotypic Variability and Correlation Analysis For Yield and Its Components in Late Sown Wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(4), 167-173.

Chalachew, Endalamaw., Asfaw Adugna. and Hussein, Mohammed. (2017). Correlation and Path Coefficient Analysis Of Agronomic and Quality Traits in a Bioenergy Crop, Sweet Sorghum [*Sorghum bicolor* (L.) Moench]. *African Journal of Biotechnology*, 16(47), 2189-2200.

CSA (Central Statistical Agency). (2021). Agricultural Sample Survey: Report on Area and Production of Major Crops, Addis Ababa, Ethiopia.

Deshmukh, S.N., Basu, M.S. and Reddy, P.S. (1986). Genetic Variability, Character Association And Path Coefficients of Quantitative Traits in Virginia Bunch Varieties of Groundnut. *Indian Journal of Agricultural Sciences*, 56, 515-518.

Dewey, D.R. and Lu, K. (1959). A Correlation and Path Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy Journal*, 51(9), 515-518.

FAO (Food and Agriculture Organization). (2021). Food and Agriculture Data. Available at: http://www.fao.org/faostat/en/#data/QC. (Accessed on April 14, 2021).

Firezer Girma., Firew Mekbib., Taye Tadesse., Temesgen Menamo. and Kassahun Bantte. (2020). Phenotyping Sorghum [*Sorghum Bicolor* (L.) Moench] For Drought Tolerance With Special Emphasis To Root Angle. *African Journal of Agricultural Research*, 16(8), 1213-1222.

Gebeyehu Chala., Bulti Tesso. and Dagnachew Lule. (2019). Genetic Gain among Released Sorghum [*Sorghum bicolor* (L.) Moench] varieties in West Hararghe Zone. *Journal of Applied Biosciences*, 136, 13877-13886.

Girma Mengistu., Hussein Shimelis., Laing, M. Dagnachew Lule. and Mathew, I. (2020). Genetic Variability Among Ethiopian Sorghum Landrace Accessions For Major Agro-morphological Traits And Anthracnose Resistance. *Euphytica*, 216(7), 1-15.

Goswami, S.J., Patel, P.T., Gami, R.A., Patel, R.N. and Khatri, A.B. (2020). Correlation and Path Analysis Study Of Different Characters for Grain Yield and Fodder Purpose In Sorghum [*Sorghum bicolor* (L.) Moench]. *Electronic Journal of Plant Breeding*, 11(04), 1053-1061.

IBPGR. (1993). Descriptors for Sorghum [*Sorghum bicolor* (L.) Moench]. *International Board for Plant Genetic Resources,* Rome, Italy.

Khadakabhavi, S., Girish, G. and Yashoda, Y. (2017). Character Association and Path Analysis Studies in Germplasm Lines of Rabi Sorghum (*Sorghum bicolor* (L.) Moench). *Journal of Applied and Natural Science*, 9(1), 206-210.

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.

Kumar, N.V., Reddy, C.V.C.M. and Reddy, P.V.R.M. (2012). Study on Character Association in Rabi Sorghum (*Sorghum bicolor* (L). Moench). *Plant Archives*, 12(2), 1049-1051.

Lenka, D. and Mishra, B. (1973). Path Coefficient Analysis of Yield in Rice Varieties. *Indian Journal of Agricultural Science*, 43(4), 376.

Mindaye, T.T., Mace, E.S., Godwin, I.D. and Jordan, D.R. (2016). Heterosis in Locally Adapted Sorghum Genotypes and Potential of Hybrids for Increased Productivity In Contrasting Environments in Ethiopia. *The Crop Journal*, 4(6), 479-489.

Prasad, B.V. and Sridhar, V. (2019). Studies on Genetic Variability, Correlation and Path Analysis in Yellow Pericarp Sorghum [*Sorghum bicolor* (L.) Moench] genotypes. *International Journal of Current Microbiology and Applied Sciences*, 8(12), 367-373.

Robertson, A. (1959). The Sampling Variance of the Genetic Correlation Coefficient. *Biometrics*, 15(3), 469-485.

Seetharam, K. and Ganesamurthy, K. (2013). Characterization of Sorghum Genotypes for Yield and Other Agronomic Traits Through Genetic Variability and Diversity Analysis. *Electronic Journal of Plant Breeding*, 4(1), 1073-1079.

Sharma, J.R. (1998). *Statistical and Biometrical Techniques in Plant Breeding.* New Age International (P) limited, Publishers, New Delhi. P432

Singh, J., Prasad, L.C., Madakemohekar, A.H. and Bornare, S.S. (2014). Genetic Variability and Character Association in Diverse Genotypes Of Barley (Hordeum vulgare L.). *The bioscan*, 9(2), 759-761.

Singh, R.K. and Chaudhary, B.D. (1977). *Biometrical Methods in Quantitative Genetic,* Kalyani Publishers, New Delhi, Ludhiana, India, 318.

Tefere Mulualem., Sentayehu Alamrew., Taye Tadesse. and Dagne Wegary. (2018). Correlation and Path Coefficient Analysis for Agronomical Traits of Lowland Adapted Ethiopian Sorghum Genotypes [*Sorghum bicolor* (L.) Moench] Genotypes. *Greener Journal of Agricultural Sciences*, 8(15),155-159.

Tsegau Senbetay. and Tegegn Belete. (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), 1-8.

Wagaw, K. (2019). Review on Mechanisms of Drought Tolerance in Sorghum (*Sorghum bicolor* (L.) Moench) Basis and Breeding Methods. *Academic Research Journal of Agricultural Science and Research*, 7(2), 87-99.