Research Article

Correlation and Path Coefficient Analysis for Agronomical Traits of Sorghum *[Sorghum bicolor (L.) Moench]* Genotypes Under Drought Stress Area

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Abstract

Ethiopia is the center of origin and domestication for sorghum with a wide range of collections from various agro-ecologies. However, there are many factors that hinder the production and productivity of sorghum. Drought is one of the most important factors that affect crop production worldwide and continues to be a challenge to plant breeders, despite many decades of research. The association of traits that may exist between or among sorghum characters is essential for breeders. Therefore, the present study is aimed to analyze and determine the traits having greater association with yield utilizing the correlation and path analysis for different traits of lowland Ethiopian sorghum genotypes. Therefore, the field experiment was conducted at Miesso to estimate the association of traits, and determine their direct and indirect effects on grain yield. The area represents dry lowlands where sorghum is predominantly grown by smallholder farmers. A set of 72 sorghum genotypes advanced from a pedigree breeding approach was used in this study. The experiment was laid out using Row-Column design with two replications during 2021 main cropping season. R statistical software was used to analyze the data. The analysis of variance indicated that there were significant variations among the tested genotypes for the studied traits. Grain yield had positive and highly significant correlation with panicle weight, panicle yield, stand count and grain filling rate at both genotypic and phenotypic levels. Grain yield had also negative and highly significantly correlation with days to flowering at both genotypic and phenotypic level and days to maturity at genotypic level. Path coefficient analysis indicated that grain filling rate exerted the highest positive direct effect on grain yield at both genotypic and phenotypic levels.

Keywords

Correlation, Path Coefficient, Chlorophyll Content Meter

1. Introduction

Sorghum is often cross pollinated, diploid crop species (2n=2x=20) which belongs to the Poaceae family. It is the stable food of poor and the most food-insecure people, living mainly in the semiarid tropics [2]. It remains a critical component of food security for more than 300 million in Africa [14] and it is a staple crop for more than 500 million people in 30 sub-Saharan African and Asian countries [16] while it is primarily grown as feed grain in the developed world.

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Ethiopia is the second largest sorghum producing country in Eastern Africa next to Sudan and from cereals the crop stands third in terms of productivity per hectare, after wheat and maize. Of the cereals, sorghum covers 15% of the total area and contributed 16% of the total grain production in Ethiopia [6]. It is an important food and the stover feed crop in the dry lowland areas, where moisture is limiting and it is often the only crop grown. The crop requires relatively less water than other important cereals such as maize and wheat. However, yield potential of the crop is significantly limited due to drought and heat stresses within the tropics and sub-tropics necessitating sorghum breeding for drought tolerance and better productivity [4]. In Ethiopia, many sorghum growing areas suffer from recurrent droughts due to shortage and uneven distribution of rainfall. In many regions of the country, the rain comes late or stops early making the crop growing period very short leading to crop failures. The irregular rain pattern, coupled with subsistence farming system has made areas of the country vulnerable to drought and low productivity, leading to severe malnutrition and hunger.

The success of breeding for developing drought tolerant varieties requires searching for possible correlation between agronomic, morphologic and physiological traits with grain yield. The study of associations among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. A positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. The path coefficient analysis allows partitioning of correlation coefficient into direct and indirect contributions (effects) of various traits towards dependent variable and thus helps in evaluating the cause-effect relationship as well as effective selection. Therefore, the present study is aimed to analyze and determine the traits having greater association with yield utilizing the correlation and path analysis for different traits in sorghum.

2. Materials and Methods

2.1. Description of the Study Area

The field experiment was conducted at Miesso, located in eastern Ethiopia, Oromia Region at 39°21'E longitude and 8°30'N latitude during the 2021 main cropping season. The altitude of Miesso is 1270 m.a.s.l. The area represents dry lowlands where sorghum is predominantly grown by small-holder farmers. The area also characterized by a semiarid climate with high rainfall variability and frequent drought events that affect crop productivity significantly. Long-term average maximum and minimum temperature of the area are 31.5°C and 16.2°C, respectively, and the total annual rainfall is about 571 mm. The study site has a bimodal rainfall distribution with very short rainfall season between March and May, and a main rainy season between end of June to September. Rainfall distributions are erratic and water scarcity is prevalent. The soil type of the experimental site is vertosol with a high clay content at the top 15cm [9]. The soil has a slightly basic pH (7.6–7.8) with relatively low organic matter content (0.9–1.5%).

2.2. Experimental Materials

The experimental materials comprised of 72 different sorghum genotypes including three checks (Table 1.), which were released for moisture stress areas. The genotypes were obtained from Melkassa Agricultural Research Center (MARC). These genotypes were developed by the pedigree breeding method and with a subsequent selection of the derived segregating generation.

Table 1. List of sorghum genotypes used for the experiment.

Codes.	Genotypes	Pedigree	Seed Sources
G1	ETSC15437-2-2	14MILSDT7086/ "Gambella 1107"	MW21NVTSeedInc#1
G2	ETSC16087-23-1	235421/ICSTG2372	MW21NVTSeedInc#2
G3	ETSC16066-18-1	ETSL101851/Teshale	MW21NVTSeedInc#3
G4	ETSC16034-12-1	Argiti/ICSTG2372	MW21NVTSeedInc#4
G5	ETSC14573-5-4	Melkam/13sudanint10-1	MW21NVTSeedInc#5
G6	ETSC16091-10-1	235421/M204	MW21NVTSeedInc#6
G7	ETSC16032-4-1	05MW6073/M204	MW21NVTSeedInc#7
G8	ETSC15385-2-2	ETSC300301/Meko-1	MW21NVTSeedInc#8
G9	ETSC16034-10-1	Argiti/ICSTG2372	MW21NVTSeedInc#10
G10	ETSC15357-3-1	ICSV700/Meko-1	MW21NVTSeedInc#11

Codes.	Genotypes	Pedigree	Seed Sources
G11	ETSC14715-3-1	13MI5024/13sudanint13-2	MW21NVTSeedInc#12
G12	ETSC16005-9-1	14MWLSDT7310/M204	MW21NVTSeedInc#14
G13	ETSC15363-1-2	S35/ "Gambella 1107"	MW21NVTSeedInc#16
G14	ETSC14695-1-2	Debir/13sudanint27	MW21NVTSeedInc#17
G15	ETSC14225-4-2	"Gambella 1107"/S35	MW21NVTSeedInc#18
G16	ETSC16035-9-1	Argiti/B35 or 05MI5064/B35	MW21NVTSeedInc#19
G17	ETSC15312-3-1	Debir/(Hodem/Gobiye)	MW21NVTSeedInc#21
G18	ETSC17182-12-2	Local Bulk (White)/SRN39/E36-1/KariMatama1	MW21PYTSeedInc#22
G19	ETSC15363-1-2	WSV387/P-9403/ETSL101857	MW21NVTSeedInc#23
G20	ETSC17023-14-1	90BK4184/85MW5552/NTJ2	MW21PYTSeedInc#24
G21	ETSC17007-9-1	PGRCE6940/SAR24/Framida	MW21PYTSeedInc#25
G22	ETSC17240-8-1	(ICSV111/B35)/ICSV111/ "Gambella 1107"	MW21PYTSeedInc#26
G23	ETSC17268-7-1	MR812/B35/ "Gambella 1107"	MW21PYTSeedInc#27
G24	ETSC17073-6-2	(E-35-1)-4/CS3541derive5-4-2-1)/P9401/SRN39	MS20PYT#90
G25	ETSC17201-1-2	CR: 35: 5/ICSV-1005/76T1#23/ "Gambella 1107"	MW21PYTSeedInc#29
G26	ETSC17258-13-1	ICSR24010/B35/SRN39	MS20PYT#95
G27	ETSC14804-4-2	SILA/13sudanint10-1	MW21PYTSeedInc#20
G28	ETSC17285-5-2	PGRCE69420/87PW3173/SRN39	MW21PYTSeedInc#32
G29	ETSC15312-3-1	14MWLSDT7324/ICSTG2372	MW21NVTSeedInc#21
G30	ETSC17140-9-1	WSV387/P9403/B35/KariMatama1	MW21PYTSeedInc#34
G31	ETSC17006-8-1	PGRCE6940/SAR24/SRN39	MW21PYTSeedInc#35
G32	ETSC17158-3-2	ICSR24010/B35/ "Gambella 1107"	MW21PYTSeedInc#36
G33	ETSC17323-24-2	90BK4184/85MW5552/M-204	MW21PYTSeedInc#37
G34	ETSC17300-4-2	PGRCE6940/SAR24/SRN39	MS20PYT#221
G35	ETSC17296-3-1	PGRCE6940/SAR24/ "Gambella 1107"	MW21PYTSeedInc#39
G36	ETSC17298-4-1	PGRCE6940/SAR24/ETSL101848	MW21PYTSeedInc#40
G37	ETSC17213-3-2	IESV92084/E36-1/Melkam	MW21PYTSeedInc#42
G38	ETSC17142-9-3	WSV387/P9403/B35/ETSL100307	MW21PYTSeedInc#43
G39	ETSC17156-1-4	MR812/76T1#23/ETSL101865	MW21PYTSeedInc#44
G40	ETSC17301-10-2	PGRCE6940/SAR24/B35	MW21PYTSeedInc#45
G41	ETSC17268-5-3	MR812/B35/ "Gambella 1107"	MW21PYTSeedInc#46
G42	ETSC17298-5-2	PGRCE6940/SAR24/ETSL101848	MW21PYTSeedInc#47
G43	ETSC17186-2-1	Local Bulk /SRN39/76T1#23/ "Gambella 1107"	MW21PYTSeedInc#48
G44	ETSC17106-6-1	WSV387/P9403/E-36-1/M-204	MS20PYT#355
G45	ETSC17328-8-1	90BK4184/85MW5552/SRN39	MW21PYTSeedInc#50
G46	ETSC17268-5-1	MR812/B35/ "Gambella 1107"	MW21PYTSeedInc#51
G47	ETSC17194-3-1	Local Bulk (White)/SRN39/76T1#23/NTJ2	MW21PYTSeedInc#52
G48	ETSC17043-8-1	(E-35-1)-4/CS3541Drv.5-4-2-1)/P9401/ETSL10865	MW21PYTSeedInc#41
G49	ETSC17354-12-1	WSV387/P-9403/ETSL101857	MW21PYTSeedInc#54

Codes.	Genotypes	Pedigree	Seed Sources
G50	ETSC17272-3-1	MR812/B35/SRN39	MW21PYTSeedInc#55
G51	ETSC17321-4-2	(E-35-1)-4/CS3541Drv.5-4-2-1)/P9401/ETSL10865	MW21PYTSeedInc#56
G52	ETSC17350-3-1	WSV387/P-9403/M-204	MW21PYTSeedInc#57
G53	ETSC17115-5-1	WSV387/P9403/E-36-1/ETSL102496	MW21PYTSeedInc#58
G54	ETSC17093-3-1	WSV387/76T1#23/ "Gambella 1107"	MW21PYTSeedInc#59
G55	ETSC17213-1-1	IESV92084/E36-1/Melkam	MW21PYTSeedInc#60
G56	ETSC14203-5-2	Karimtama1/N-13	MW21PYTSeedInc#61
G57	ETSC17071-6-2	(E-35-1)-4/CS3541Drv.5-4-2-1)/P9401/ETSL10848	MW21PYTSeedInc#62
G58	ETSC17111-3-1	WSV387/P9403/E-36-1/NTJ2	MW21PYTSeedInc#63
G59	ETSC17360-18-2	WSV387/P-9403/ETSL101853	MW21PYTSeedInc#67
G60	ETSC17257-6-1	ICSR24010/B35/ETSL101857	MW21PYTSeedInc#68
G61	ETSC17258-3-2	ICSR24010/B35/SRN39	MW21PYTSeedInc#70
G62	ETSC17354-9-1	WSV387/P-9403/ETSL101857	MW21PYTSeedInc#73
G63	ETSC17129-6-1	SDSL2690-2/76T1#23/NTJ2	MW21PYTSeedInc#77
G64	ETSC17175-5-4	MR812/B35/ETSL102496	MW21PYTSeedInc#78
G65	ETSC17113-6-1	WSV387/P9403/E-36-1/ETSL101853	MW21PYTSeedInc#80
G66	ETSC17360-5-1	WSV387/P-9403/ETSL101853	MW21PYTSeedInc#82
G67	ETSC17172-4-4	MR812/B35/NTJ2	MW21PYTSeedInc#83
G68	ETSC17032-6-1	90BK4236/87PW3173/ETSL101857	MW21PYTSeedInc#84
G69	ETSC16001-6-1	14MWLSDT7310/ICSTG2372	MW21PYTSeedInc#85
G70	Melkam	WSV387	MW21Breeder Seed
G71	Argiti	WSV387/P9403	MW21Breeder Seed
G72	Tilahun	2005MI5060/E36-1	MW21Breeder Seed

2.3. Experimental Design and Procedures

The experiment was laid out in an incomplete block of 24 rows by 6 columns in 2 replications according to the commonly used procedure by the National Sorghum Research Program of Ethiopia. The experimental plots consist of 2 rows, each 5 m in length with 75 cm between rows and 15 cm between plants. The experiment was planted on the 11th of July, 2021. Seeds were sown manually by hand drilling at a rate of 10 kgha^{-1}. Thinning was done three weeks after the date of planting to maintain the recommended plant population. Fertilizer was applied at a rate of 100 kgha^{-1} Di Ammonium Phosphate (DAP) and 50 kgha^{-1} of Urea. DAP was applied at sowing while urea was applied at knee height stage (around 35 days after Planting). The field was maintained free of weeds through hand weeding while chemical sprays were made to control insect pests. Cypermethrin (22.5 g a.i. ha^{-1}) was sprayed 6 days after crop emergence to control shoot fly. Diazinon 48 EC, was applied 30 days after plantation to control fall army worm.

2.4. Data Collection

The data were collected both on plot and individual plant basis as per descriptor for sorghum [11].

2.4.1. Data Collection on Plant Basis

Plant height (cm): The average length of five randomly selected plants from the base of the plant to the tip of the panicle was taken at the time of maturity.

Panicle length (cm): The average length of five randomly selected plants from the base of the panicle to the tip was measured using barcode ruler.

Panicle weight (g): The average weight of five randomly selected panicles (un-threshed) / plot.

Panicle yield (g): The average yield of five randomly selected panicles (threshed) per plot.

2.4.2. Data Collection on Plot Basis

Days to 50% flowering (days): The number of days from emergence to the date at which 50% of the plants in a plot started flowering.

Days to 90% physiological maturity (days): The number of days from emergence to the stage where 90% of the plants in a plot reached at physiological maturity which was recognized by a black layer formed on the bottom of the kernel.

Grain filling period (days): The numbers of days from dates of 50% flowering to dates of 90% physiological maturity.

Grain filling rate (kg/ha/days): It is calculated as the ratio of grain yield (kg/ha) to grain filling period (days) as: Grain filling rate (kg/ha/days) = Grain yield / Grain filling period.

Stand count at harvest (No.): The total number of main plants in a plot was counted when 90% of the plants in a row mature physiologically.

Harvest index (HI %): Calculated as the ratio of dried grain weight adjusted to 12% moisture content to the dried total above ground biomass weight and multiplied by 100. A 5m row of each plot was harvested, above ground biomass (stem and leaves) was dried for 10 days and weighed. Then the panicles were harvested, dried, threshed and weighed to compute the harvest index.

Thousand seed weight (g): Collected as the weight of 1000 seeds and adjusted to 12.5% moisture level.

Grain yield (kg/ha): After harvesting, the panicles from each row were threshed, cleaned and weighed after adjusted to 12.5% moisture content. Then the raw grain yield (g/plot) was converted to total grain yield (kg/ha).

Stay-green score: Visual stay-green rating was done at physiological maturity using a scale of 1 to 5. Rating 1 indicates completely green normal size leaves (no leaf death), 2 = 25% of the leaves died, 3 = 26 to 50% of the leaves died, 4 = 51 to 75% are dead, 5 = 76 to 100% of the leaves and stem are dead (complete plant death).

Drought tolerance score: This was recorded at the time of physiological maturity with a scale of 1 to 5 where 1 = poor, 2 = fair, 3 = good, 4 = very good and 5 = excellent.

Chlorophyll content of leaves: Leaf chlorophyll content was measured from five randomly selected plants per plot at flowering stage. Measurements were taken from two leaves per plant using a chlorophyll content meter (SPAD). The chlorophyll meter readings (SPAD values) were taken at the base of the leaf lamina of the second and fourth leaves from the top.

2.5. Data Analysis

2.5.1. Analysis of Variances (ANOVA)

The data were subjected to analysis of variance by using the R- statistical software version 4.3 [22]. The experimental design was described by the model: $y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + \varepsilon_{ijkl}$ where y_{ijkl}=the observation of ith treatment applied in the jth row and k^{th} column for l^{th} replication, μ is the grand mean effect, α_i is the ith treatment effect, β_j is the jth row effect, γ_k is the kth column effect, δ_l replication effect and ε_{ijkl} are uncorrelated random errors with zero mean and constant variance (δ^2).

Table 2. Analysis of Variance (ANOVA).

Source of Variations	Degrees of Freedom (DF)	Sum of Squares (SS)	Mean of Squares (MS)	F-Values
Rows	R-1	SSR	SSR/DFR	MSR/MSE
Columns	C-1	SSC	SSC/DFC	MSC/MSE
Treatments	Trt-1	SSTrt	SSTrt/DFTrt	MSTrt/MSE
Error	(RC-1) - (R-1) - (C-1) - (Trt-1)	SSE	SSE/DFE	
Total	R*C-1	SST		

DF = Degree Freedom, R = Rows, C = Columns, Trt = Treatments, DFE = Degree Freedom of Error, DFR = Degree Freedom of Rows, DFC = Degree Freedom of Columns, DFTrt = Degree Freedom of Treatments, SSR = Sum Squares of Rows, SSC = Sum Squares of Columns, SSTrt = Sum Squares of Treatments, SSE = Sum Squares of Error, SST = Sum Squares of Total, MSE = Mean Squares of Error, MSR = Mean Squares of Rows, MSC = Mean Squares of Columns, MSTrt = Mean Squares of Treatments.

2.5.2. Correlation Coefficients

Simple linear (Pearson) correlation coefficient was performed to understand the relationship among the agronomic traits studied [20]. The degree to which two variables vary together or the intensity of the association between two variables were measured by using correlation coefficient. The phenotypic and genotypic correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components by using covariance techniques as per [12].

$$r_p = \frac{Pcov_{xy}}{\sqrt{V_px.V_py}} \qquad (1)$$

$$r_g = \frac{Gcov_{xy}}{\sqrt{(V_g x.V_g y)}} \qquad (2)$$

Where: rp and rg = Phenotypic and genotypic correlation coefficient, Pcovxy = Phenotypic covariance between variables x and y, Vpx = Phenotypic variance of variable x and Vpy = Phenotypic variance of variable y. Gcovxy = Genotypic covariance between variables x and y, Vgx = Genotypic variance of variable x and Vgy = Genotypic variance of variable y.

2.5.3. Path Coefficient Analysis

By considering the phenotypic and genotypic correlation coefficients between traits, path coefficient analysis was carried out to know the direct and indirect effects of yield related traits on grain yield following the formula given by [8]. rij= pij+∑rik.pkj, 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, ∑rik pkj = summation of components of indirect effect of a given independent character (i) on the given independent character (j) via all other independent characters (k).

3. Results and Discussions

3.1. Genotypic and Phenotypic Correlation Coefficients

Improvement of a targeted trait cannot be achieved by direct selection of that particular trait, but also, indirect selection via other traits that are more heritable and easier to select. This selection strategy requires understanding the interrelationship of the characters among themselves and with the target character. In this experiment estimate of genotypic (rg) and phenotypic (rp) correlation coefficients between each pair of the studied traits are presented in Table 3. Genotypic correlation coefficient was found to be relatively higher in magnitude than their corresponding phenotypic correlation coefficient, except in a few cases, which clearly indicated the presence of inherent association among considered traits.

3.2. Correlation of Grain Yield with Other Traits

Panicle length, panicle weight, panicle yield, stand count and grain filling rate showed positive and highly significant correlation with grain yield at genotypic level. Chlorophyll content, panicle weight, panicle yield, thousand seed weight and grain filling rate showed positive and highly significant correlation with grain yield at phenotypic level. The positive correlation of characters with grain yield could result from the presence of strong linkage of genes or the characters may

be the result of genes with pleiotropic effect that control these characters in the same direction. Selection of genotypes based on high mean values for these traits could be used to improve sorghum yield rather than selecting based on yield alone. Since drought tolerance is dependent on the timing and severity of the stress [15]. Therefore, introgression of these traits to adaptable and high yielding genotypes could have paramount importance for drought tolerance breeding.

Days to maturity and thousand seed weight showed negative correlation with grain yield at genotypic level. Days to flowering showed negative correlation with yield at genotypic and phenotypic level (Table 3). The negative correlation of these traits with grain yield suggested that the genotypes should be selected for low days to flowering as long days to flowering result in yield reduction. The negative correlation of days to flowering with grain yield indicated that early flowering genotypes had a chance to escape drought stress and thus; early flowering genotypes should be preferred during selection under stress condition.

3.3. Correlation Among Other Traits

The genotypic and phenotypic correlation of studied traits were presented in (Table 3). Days to flowering showed significant positive correlation with days to maturity and plant height and negative correlation with chlorophyll content, grain filling period, panicle length, harvest index and grain yield at both genotypic and phenotypic level. Similar relationships were recorded in other studies by [17]. Days to maturity exhibited positive and significant correlation with days to flowering, grain filling period and plant height at genotypic level. [1] similarly reported strong positive correlation between days to maturity and grain filling period. Days to maturity showed negative and significant correlation with panicle length, harvest index, grain yield and grain filling rate at genotypic level. At phenotypic level days to maturity showed positive correlation with days to flowering, grain filling period, plant height and thousand seed weight and negative correlation with panicle length, harvest index and grain filling rate. Grain filling period showed positive correlation with chlorophyll content, days to maturity and thousand seed weight and negative correlation with days to flowering and grain filling rate at both genotypic and phenotypic level.

Positive and significant genotypic correlation was observed for grain filling period, panicle length, panicle weight, panicle yield, thousand seed weight and harvest index with chlorophyll content. A previous study [19] reported similar findings. Grain filling period, thousand seed weight, harvest index and grain yield indicated negative significant correlation with chlorophyll content at phenotypic level. Chlorophyll content also showed negative correlation with days to maturity and days to flowering at genotypic and phenotypic level, respectively. Plant height showed positive correlation with thousand seed weight and negative correlation with

harvest index at both levels. Tall genotypes often produce smaller seeds, higher dry weight of leaves and stem, which are components of harvest index, and lower yield as compared to the short genotypes. This agreed with the findings by [5] that short genotypes have a higher harvest index and grain yield than tall genotypes. Harvest index showed significant negative correlation with days to flowering, days to maturity and plant height and positive correlation with chlorophyll content, panicle length, panicle weight and panicle yield at both genotypic and phenotypic level.

Grain yield showed positive and significant correlation with panicle length, panicle weight, panicle yield and grain filling rate at genotypic level. It also showed positive and significant correlation with chlorophyll content, panicle weight, panicle yield and grain filling rate at phenotypic lev-

el (Table 3). Similarly strong positive association of grain yield with panicle weight and panicle yield was reported by [21, 13, 7]. In sum, significant positive correlation among studied traits suggests that the traits could be improved simultaneously without any compensatory negative effects whereas the negative relationship between traits suggests that traits should be improved independently. The positive correlation of any pairs of traits of the present sorghum population indicated the possibility of correlated response to selection. In contrary to this, the negative correlation prevents the simultaneous improvement of those traits along with each other. [10, 18] also suggested that the negative association of traits was difficult or practically impossible to improve through a simultaneous selection of those traits.

Table 3. Estimates of genotypic correlation (above diagonal) and phenotypic correlation (below diagonal) of 72 sorghum genotypes studied at Miesso Agricultural Research Center during 2021 growing season.

Traits	DTF	CHLc	DTM	SC	GFP	PH	PL	PW	PY	TSW	HI	GFR	GY
DTF	1	-0.66*	0.53**	-0.18ns	-0.55**	0.35**	-0.35**	-0.04ns	-0.08ns	0.09ns	-0.43**	0.05ns	-0.185*
CHLc	-0.36**	1	-0.51**	-0.07ns	0.19*	-0.15ns	0.32**	0.17*	0.34**	0.42**	0.41**	0.12ns	0.16ns
DTM	0.47**	-0.11ns	1	-0.36**	0.42**	0.30**	-0.33**	0.04ns	0.04ns	0.21ns	-0.41**	-0.32**	-0.182*
SC	-0.16*	0.07ns	-0.22**	1	-0.15ns	0.18ns	0.09ns	-0.26*	-0.4**	-0.4**	-0.33**	0.49**	0.46**
GFP	-0.46**	0.22**	0.55**	-0.03ns	1	-0.06ns	0.03ns	0.09ns	0.14ns	0.11ns	0.04ns	-0.38**	0.02ns
PH	0.27**	-0.05ns	0.30**	0.16ns	0.05ns	1	-0.14ns	0.06ns	0.06ns	0.26*	-0.46**	-0.03ns	0.08ns
PL	-0.19*	0.09ns	-0.20*	0.05ns	-0.02ns	-0.08ns	1	0.23**	-0.04ns	-0.24*	0.39**	0.14ns	0.182*
PW	-0.05ns	0.08ns	0.05ns	-0.11ns	0.06ns	0.07ns	0.31**	1	0.69**	0.09ns	0.61**	0.16ns	0.181*
PY	-0.03ns	0.16ns	0.04ns	-0.24**	0.08ns	0.05ns	0.22**	0.62**	1	0.36**	0.65**	0.17*	0.221**
TSW	-0.05ns	0.15ns	0.12ns	-0.24**	0.06ns	0.18*	-0.11ns	0.07ns	0.22**	1	-0.14ns	-0.24*	-0.27*
HI	-0.33**	0.27**	-0.30**	-0.19*	0.007ns	-0.32**	0.27**	0.42**	0.58**	-0.08ns	1	0.03ns	0.05ns
GFR	0.05ns	0.06ns	-0.25**	0.41**	-0.29**	0.02ns	0.13ns	0.18*	0.17*	-0.19*	0.06ns	1	0.949**
GY	-0.165*	0.197*	-0.07ns	0.42**	0.09ns	0.01ns	0.14ns	0.211*	0.204*	0.19*	0.07ns	0.885**	1

*and**, significant at P <0.05 and P<0.01, respectively. DTF = days to flowering, DTM = days to maturity, SC= stand count, CHLc= chlorophyll content, GFP = grain filling period, PH = plant height, PL = panicle length, PW = panicle weight, PY = panicle yield, HI = harvest index, GY = grain yield, GFR = grain filling rate and TSW = thousand seed weight.

3.4. Path Coefficient Analysis

Path coefficient analysis measures the direct and indirect contribution of independent variables on dependent variables [3]. It provides more information among variables than correlation coefficients analysis provides the direct effects of specific yield components on yield and indirect effects through other yield components. When the traits having direct positive effect on grain yield are selected for further improvement, the indirect one must be considered as they

have association with those characters in another way. In this experiment 8 traits were considered as causal variables at genotypic level while 7 traits were considered as casual variables at phenotypic level when grain yield is selected as dependent variable.

3.4.1. Genotypic Direct and Indirect Effects of Other Traits on Grain Yield

Genotypic path coefficient analysis revealed that grain filling rate (1.104) followed by days to maturity (0.427) exerted

the highest positive direct effect on grain yield (Table 4). Panicle length (0.009) was also exerted small magnitude of positive direct effect on grain yield whereas panicle yield (0.019) exerted medium positive direct effect on grain yield. Days to flowering (-0.472) exerted highest negative direct effect. Stand count (-0.281), panicle weight (-0.046) and thousand seed weight (-0.037) exerted average magnitude of negative direct effect. Positive indirect effect was exerted by panicle length, panicle weight, panicle yield and days to flowering through grain filling rate. The residual effect was 0.093, indicating that all the traits included in the study explained high percentage of variation in grain yield (90.75%), while other factors not included in the study can explain 9.25%.

Table 4. Estimates of direct (bold and underlined diagonal) and indirect effect (non-bold and off diagonal) of different traits on grain yield at genotypic level for sorghum genotypes.

Traits	DTF	DTM	SC	PL	PW	PY	TSW	GFR	r_g
DTF	-0.472	0.228	0.049	-0.003	0.002	0.001	-0.004	0.061	-0.185*
DTM	-0.252	0.427	0.093	-0.003	-0.002	0.001	-0.007	-0.352	-0.182*
SC	0.098	-0.145	-0.281	-0.003	0.008	0.056	0.020	0.713	0.461**
PL	0.164	-0.141	0.026	0.009	-0.009	0.001	0.009	0.156	0.182*
PW	0.019	0.018	0.073	0.002	-0.046	-0.002	-0.004	0.180	0.181*
PY	0.037	0.018	0.113	0.001	-0.026	0.019	-0.013	0.194	0.221**
TSW	-0.045	0.080	0.113	-0.001	-0.005	0.007	-0.037	-0.266	-0.271*
GFR	-0.026	-0.135	-0.155	0.001	-0.006	0.001	0.009	1.104	0.949**

3.4.2. Phenotypic Direct and Indirect Effects of Other Traits on Grain Yield

Phenotypic path coefficient analysis revealed that grain filling rate (0.879) exerted highest positive direct effect whereas, chlorophyll content (0.084), stand count (0.044), panicle weight (0.042) and panicle yield (0.022) exerted medium magnitude of positive direct effect on grain yield (Table 5). However, days to flowering (-0.177) and thousand seed weight (-0.039) exerted medium magnitude of negative direct effect and panicle weight, panicle yield, chlorophyll content and days to flowering exerted considerable amount of positive indirect effect on grain yield. The residual effect was 0.164, indicating all the traits included in the study explained high percentage of variation in grain yield (83.59%), while other factors not included in the study can explain 16.41%.

Table 5. Estimates of direct (bold and underlined diagonal) and indirect effect (non-bold and off diagonal) of different traits on grain yield at phenotypic level for sorghum genotypes.

Traits	DTF	CHLc.	SC	PW	PY	TSW	GFR	r_p
DTF	-0.177	-0.028	-0.007	0.001	0.001	-0.002	0.040	-0.165*
CHLc.	0.063	0.084	0.003	0.003	0.002	-0.006	0.050	0.197*
SC	0.027	0.006	0.044	-0.005	-0.008	0.009	0.349	0.42**
PW	0.001	0.006	0.005	0.042	0.007	-0.003	0.155	0.211*
PY	0.005	0.012	-0.010	0.026	0.022	-0.008	0.149	0.204*
TSW	-0.009	0.013	-0.011	0.003	0.005	-0.039	-0.164	0.19*
GFR	-0.008	0.004	0.018	0.007	0.002	0.007	0.879	0.885**

4. Summary and Conclusion

The relationship of different agronomic characters with each other and their relationship with yield is important. Grain yield showed positive and highly significant correlation with panicle length, panicle weight, panicle yield and grain filling rate at genotypic level whereas days to flowering and days to maturity showed significant negative correlation. At phenotypic level, chlorophyll content, panicle weight, panicle yield and grain filling rate showed significantly positive correlation with grain yield whereas days to flowering showed significant negative correlation. The positive correlations of all trait pairs in the studied sorghum genotypes indicated a possible correlation response to selection. In contrast, negative correlation prevents these characters from improving at the same time. Path coefficient analysis revealed that panicle weight, panicle yield and days to flowering showed positive indirect effect on grain yield through grain filling rate at both genotypic and phenotypic level.

Abbreviations

MARC   Melkassa Agricultural Research Center
ANOVA   Analysis of Variances

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Author Contributions

Ambesu Tiliye: Formal Analysis, Methodology, Software, writing – original draft, Writing – review & editing

Shimelis Alemayehu: Funding acquisition, Resources, Supervision, Visualization

Conflicts of Interest

The authors declare no conflicts of interest.

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Research Fields

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