Original Article

Genetic Variability and Yield Performance of Sorghum (*sorghum bicolor* L.) Genotypes Grown in Semi-Arid Ethiopia

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ABSTRACT

The objective of this study was to understand the genotypic and phenotypic variations, and yield performance of early maturing sorghum genotypes. The experiment was conducted using randomized complete block design with row column arrangement and three replications. Grain yield, phenological and other traits were recorded. The residual maximum likelihood (REML) combined analysis of variance across locations showed very highly significant (P≤0.0001) difference for grain yield among locations and significant (P≤0.05) among genotypes and highly significant (P≤0.0001) among interactions for most of the traits studied. The genotypes 12MW6251, 14MWLSDT7322, 14MWLSDT7201, Pipline2, 4MWLSDT7238, 14MWLSDT7234 and 14MWLSDT7176 had the highest in mean grain yield, panicle weight and panicle width from the tested genotypes in across locations. The high coefficients of phenotypic (PCV) and genotypic (GCV) variances were obtained for traits like panicle exertion, stay green, drought score base genetic background as well as the potential to respond entirely to select drought tolerant genotype for sorghum production in drought prone areas. The characters, which showed high heritability (H%) with high genetic advance as percentage of mean (GAM%) were grain filling rate, plant hieght, grain yield, panicle weight, panicle exertion and stay green. The positive associations among grain yield with panicle weight, panicle width and grain filling rate indicate that selecting positively associated panicle related traits would have a positive effect on grain yield. Genotypes 12MW6251, 14MWLSDT7238, Pipline2 and 14MWLSDT7201 were grouped in cluster VI and identified for early flowering and maturity, and highest in grain yield, panicle weight, panicle length, panicle width, panicle number, plant hieght and thousand seed weight.

Key words: Early maturing, Correlation, Cluster, Heritability, Spatial model

Introduction

Sorghum [**Sorghum bicolor** (L.) **Moench**] is grouped under C4 tropical crop (Zinzala **et al.**, 2018) which belongs to the family **Gramineae** (Harlan and De Wet, 1972). Sorghum is naturally self-pollinated plant with the degree of spontaneous cross pollination, in some conditions, reaching up to 20%, relying on panicle types. Sorghum is an indigenous crop to Ethiopia where it is grown in a wider area of adaptation ranging from hot, dry lowland, intermediate to the highland environments.

The global sorghum production is estimated to be 62.3 million tons from 42 million hectares of land (USDA, 2017). In Africa, sorghum production is 29.14 million tons from 26.03 hectares of land (USDA, 2017). In Ethiopia, it ranks third in area coverage, after maize and teff (CSA, 2017). In Ethiopia, sorghum accounts for 16.4% of the total annual cereal grain production (CSA, 2017). In Ethiopia, the area covered with sorghum is 1.9 million ha, and its total production is 4.8 million tons of grain (CSA, 2017). It is the major staple crop in the dry lowlands, which covers 66% of the total cultivated areas of the country and the national average productivity of sorghum in Ethiopia is 2.5 tons/ha (CSA, 2017). However, research has revealed that there is a potential to raise sorghum productivity from 3 to 6 tones/ha using improved varieties and production practices (Adugna **et al.**, 2007).

In the developing countries, sorghum is mainly grown as a food grain crop while in the developed world the majority of the grain produced is used for feeding animal (Rakshit **et al.**, 2014). Sorghum grain is preferred next to tef, a small cereal grain crop, used as injera (Fantaye and Hintsa, 2017). Although there is inconsistency in the grain quality depending on the end use product, larger seed size, white and light red types of sorghum grains are mostly preferred for the preparation of injera. The grain is also used for the preparation of local beverages. In addition, the stover is equally valued as the grain, which is used for animal feed, fuel wood and construction purposes (Mindaye, 2016).

In Ethiopia, the current rate of yield increase in sorghum is inadequate. In Ethiopia, drought happened in any stage of sorghum development with the high frequency of terminal stress in dry lowland areas. Genetic improvement is considered as an integral part of overcoming the challenges of drought in the dry lowlands of the country. A major challenges of sorghum production in the dry lowland parts of the country is lack of early maturing improved varieties that can escape drought or tolerant to stresses, such as drought and lack of stable varieties across environments (Fantaye and Hintsa, 2017). Development of an early maturing and/or varieties that can withstand terminal stress through introgression of stay-green trait are the two major strategies being implanted in the sorghum breeding in Ethiopia. Therefore, the objective of this study was to understand the genotypic and phenotypic variations, and yield performance of early maturing sorghum genotypes sown at three locations in the semi-arid conditions of Ethiopia.

Experimental

Materials and methods

Description of the study area

The field experiment was conducted during the 2017 main cropping season at three locations (Sheraro, Kobo and Shewarobit), representing the dry lowland areas of Ethiopia situated in the altitude range of 1179-1513 meter above sea-level (m.a.s.l), where sorghum

is widely grown. The detailed agro-ecological features of the locations are presented in Table 1.

Table 1. Agro-ecological features of the experimental locations

Location	Longitude	Latitude	Altitude in m.a.s.l	Soil type	Rainfall in mm	Minimum T°	Maximum T°
Shewarobit	39°, 93'E	10°, 35' N	1500	Vertisol	713.0	17.7	32.6
Kobo	39°, 38' E	12°, 09'N	1513	Vertisol	677.8	14.8	32.1
Sheraro	38°, 9' E	14°, 6' N	1179	Vertisol	615.0	20.4	33.7

Source: National metrology data of 2017 main cropping season, m.a.s.l=meters above sea level, T°= Temperature

Genetic materials

Planting materials (Table 2) used for the experiment comprised of fifty nine early maturing advanced sorghum genotypes, which were advanced from pedigree breeding at Melkassa Agricultural Research Center and one sorghum released variety (Melkam) as a standard check were used.

Table 2. Description of sorghum genotypes tested at three locations during 2017 main cropping season

No	Genotype	Pedigree	Seed source	Status
1	Melkam	WSV387	2016MS Breeder Seed Inc.	Standard check
2	14MWLSDT7060	Macia/76T1#23	2017MW Seed increase#2	Advanced genotype
3	12MW6251	WSV 387/76T1#23	2017MW Seed increase#3	Advanced genotype
4	14MWLSDT7410	ICSR24010/B-35	2017MW Seed increase#4	Advanced genotype
5	12MW6302	WSV 387/76T1#23	2017MW Seed increase#5	Advanced genotype
6	14MWLSDT7322	SDSL2690-2/76T1#23	2017MW Seed increase#6	Advanced genotype
7	14MWLSDT7395	MR812/76T1#23	2017MW Seed increase#7	Advanced genotype
8	14MWLSDT7400	WSV387/76T1#23	2017MW Seed increase#8	Advanced genotype
9	14MWLSDT7310	Teshale/B-35	2017MW Seed increase#9	Advanced genotype
10	13MWF6#6077	ICSR 24010/Brihan	2017MW Seed increase#10	Advanced genotype
11	14MWLSDT7325	SDSL2690-2/76T1#23	2017MW Seed increase#11	Advanced genotype
12	2005MI5069	M36121/P9402	2017MW Seed increase#12	Advanced genotype
13	14MWLSDT7196	WSV387/76T1#23	2017MW Seed increase#13	Advanced genotype
14	14MWLSDT7311	Teshale/B-35	2017MW Seed increase#14	Advanced genotype
15	14MWLSDT7157	WSV387/E-36-1	2017MW Seed increase#15	Advanced genotype
16	14MWLSDT7193	WSV387/E-36-1	2017MW Seed increase#16	Advanced genotype
17	14MWLSDT7332	SDSL2690-2/76T1#23	2017MW Seed increase#17	Advanced genotype
18	14MWLSDT7115	ICSR24010/B_35	2017MW Seed increase#18	Advanced genotype
19	14MWLSDT7176	WSV387/E-36-1	2017MW Seed increase#19	Advanced genotype
20	14MWLSDT7209	WSV387/76T1#23	2017MW Seed increase#20	Advanced genotype
21	12MW6440	LocalBulk(White)/SRN-39/76T1#23	2017MW Seed increase#21	Advanced genotype
22	14MWLSDT7201	WSV387/76T1#23	2017MW Seed increase#22	Advanced genotype
23	12MW6146	WSV 387/E-36-1	2017MW Seed increase#23	Advanced genotype
24	14MWLSDT7364	2005MI5060/B-35	2017MW Seed increase#24	Advanced genotype
25	Pipline 2	(Teshale/E-36-1)BC3F3	2017MW Seed increase#25	Advanced genotype
26	14MWLSDT7413	WSV387/E-36-1	2017MW Seed increase#26	Advanced genotype
27	13MWF6#6037	2001 MS 7007/SRN-39	2017MW Seed increase#27	Advanced genotype
28	14MWLSDT7207	WSV387/76T1#23	2017MW Seed increase#28	Advanced genotype
29	14MWLSDT7040	WSV387/76T1#23	2017MW Seed increase#29	Advanced genotype
30	14MWLSDT7036	WSV387/76T1#23	2017MW Seed increase#30	Advanced genotype
31	14MWLSDT7324	SDSL2690-2/76T1#23	2017MW Seed increase#31	Advanced genotype
32	12MW6243	WSV 387/76T1#23	2017MW Seed increase#32	Advanced genotype

33	12MW6420	LocalBulk(White)/SRN-39/E36-1	2017MW Seed increase#33	Advanced genotype
34	14MWLSDT7238	Macia/E-36-1	2017MW Seed increase#34	Advanced genotype
35	12MW6444	LocalBulk(White)/SRN-39/76T1#23	2017MW Seed increase#35	Advanced genotype
36	14MWLSDT7402	WSV387/76T1#23	2017MW Seed increase#36	Advanced genotype
37	14MWLSDT7234	Macia/E-36-1	2017MW Seed increase#37	Advanced genotype
38	12MW6471	IESV92084/E36-1	2017MW Seed increase#38	Advanced genotype
39	14MWLSDT7042	WSV387/76T1#23	2017MW Seed increase#39	Advanced genotype
40	14MWLSDT7033	WSV387/76T1#23	2017MW Seed increase#40	Advanced genotype
41	14MWLSDT7241	Macia/E-36-1	2017MW Seed increase#41	Advanced genotype
42	14MWLSDT7191	WSV387/E-36-1	2017MW Seed increase#42	Advanced genotype
43	2005MI5093	PGRCE22880/P9403	2017MW Seed increase#43	Advanced genotype
44	2401	(S35/B35)/S35	2017MW Seed increase#44	Advanced genotype
45	2004MW6197	SDSL-2690-2/SAR-39	2017MW Seed increase#45	Advanced genotype
46	2005MI5064	WSV387/P9403	2017MW Seed increase#46	Advanced genotype
47	2523	(ICSV111/B35)/ICSV111	2017MW Seed increase#47	Advanced genotype
48	04MW 6043	WSV387/Dabar	2017MW Seed increase#48	Advanced genotype
49	2005MI5057	WSV387/P9401	2017MW Seed increase#49	Advanced genotype
50	04MW 6079	SDSL2690-2/Dabar	2017MW Seed increase#50	Advanced genotype
51	14MWLSDT7202	WSV387/76T123	2017MW Seed increase#51	Advanced genotype
52	14MWLSDT7291	Macia/76T123	2017MW Seed increase#52	Advanced genotype
53	2001MS7036	PGRCE222878/ICSV708	2017MW Seed increase#53	Advanced genotype
54	90MW5319	85LPYT-224/(148/Framida)	2017MW Seed increase#57	Advanced genotype
55	99MW4047	((148/E-35-1)-4/CS3541derive5-4-2-1)/P9401	2017MW Seed increase#55	Advanced genotype
56	05MW6026	M36121/P9401	2017MW Seed increase#56	Advanced genotype
57	14MWLSDT7421	Macia/76T123	2017MW Seed increase#58	Advanced genotype
58	2003MW6053	ICSV112BF/SRN-39	2017MW Seed increase#59	Advanced genotype
59	2294	(S35/B35)/S35	2017MW Seed increase#60	Advanced genotype
60	2003MW6038	ICSV111/SRN-39	2017MW Seed increase#61	Advanced genotype

Experimental design and trial management

The trial was conducted using randomized complete block design with row column arrangement and three replications. The experimental plot consisted of 2 rows, each 5 m in length with 0.75 m between row spacing and 0.15 m between plants. The total area of each plot had a size of 7.5 m².

As per the recommendation for sorghum production in the lowland areas of Ethiopia, Di-ammonium phosphate (DAP) and urea were applied at the rate of 100 kg/ha and 50 kg/ha, respectively. Diammonium phosphate was applied by incorporating into the soil during planting of the seeds and urea was applied as side dressing at knee height stage (35 days) after planting of the seed. Thinning was done after three weeks of planting to maintain the space between plants and to balance the plant density. Other crop management practices were applied following the recommended practices.

Data collection and sampling techniques

Data were collected from the two rows for plot-based data and five randomly sampled plants for Plant based data following the descriptors for sorghum (IBPGR/ICRISAT, 1993). The details of the data collection were as follow:

Days to emergency: The number of days from planting to when 50% of plants started emergency.

Days to flowering: The number of days from emergence to when 50% of plants started flowering.

Days to maturity: The number of days from planting to the date when 95% of the plants matured physiologically.

Plant height (cm): Plant height was measured from five randomly sampled main plants from the two rows at 75% physiological maturity. The average height from the five plants was then recorded for the plot.

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

Panicle width (cm): The average width of individual panicle as measured panicle width measurement in the widest diameter of the panicle on five randomly selected plants per plot at maturity.

Panicle weight (g): The total weight of panicles per plot after harvest was measured.

Number of panicles: The total number of panicles per plot during harvest was counted.

Panicle yield (g): The yield was obtained by threshing the total number of panicles per plot during harvest.

Grain filling rate (kg/ha/day): It is the ratio of grain yield (kg/ha) to grain filling period and calculated as follows:

Grain filling rate (kg/ha/days) = $\dfrac{\text{Grain yield (kg/ha)}}{\text{Grain filling period (days)}}$

Thousand seed weight (TSW): Weight of 1000 seeds in gram that was measured from each plot after the moisture level adjusted to 10%.

Drought score: Tolerance to moisture deficit and scored as 1-5, 1=more tolerant, 2=mild drought tolerant, 3=moderate tolerant, 4=severe drought and 5=extreme drought.

Stay green: Level of greenness scored 1-5 after maturity, 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).

Panicle exersion: Score (1=well exserted more than 10cm between ligule of flag leaf to head base, 2=2-10cm exsertion, 3=less than 2 cm but ligule below the head base, 4=peduncle recurved but head is below the ligule and clearly exposed splitting the leaf sheath, 5=head covered by leaf sheath).

Data analysis

R software using spatial analysis and mixed model (Culllis *et al*., 1998; Gilmour *et al*., 1997) were used to analyze all the collected data from individual location and combined data over locations.

Analysis of data for each location and combined over location

Using the raw data collected on fifteen characters of sixty genotypes, which were grown at five locations, analysis of data using spatial and linear mixed and model of RCBD with row column arrangement was computed. Before pooling the data over locations, Bartlett's test of homogeneity of variance was adopted for most of the traits to determine the validity of the overall mixed analysis of the data of combined locations. This analysis revealed the homogeneity of error variance. Therefore, overall mixed analysis was done to determine the effects of the genotypes, locations and their first order interactions using mixed model. Genotypes were assumed to be fixed and environment effects random. Least significance difference was used to determine the significance of differences among the genotype means for each character. The model for spatial analysis is the same as the linear mixed model and is proposed by (Gilmour *et al.*, 1997).

$$y = X\tau + Zu + e$$

Where y is the observed outcomes, τ is the fixed effects (over all mean and genotype) and u is the random effects (replication, row and column effects). X is the design matrix associated with the fixed effects, Z is the design matrix associated with the random effects and e is the residual.

**Results and discussion**

Single location data analysis

The separate REML analysis of the 15 characters for sixty early maturing sorghum genotypes is presented in Table 3. The result of spatial analysis which is the variance component for grain yield at each site revealed highly significant difference between genotypes. This showed that at each location there were genetic diversity among genotypes for grain yield (Figure 1).

Genotypes were significantly different for days to flowering at each location (Table 3). This shows the observed numbers of days that genotypes spent to flower were statistically different at all locations. Genotypes were significant for days to maturity at Sheraro, Shewarobit, and Kobo (Table 3). This finding is in contrast to (Abiy and Firew, 2016), who indicated that genotypes were not significantly different for days to maturity at Shewarobit and Kobo, indicating the number of days that genotypes took to mature were similar. However, genotypes were not-significantly different for days to maturity at Kobo; show no genotypic effect for days to maturity.

Genotypes were significantly different at Shewarobit and Kobo but non-significant for grain filling period at Sheraro. This showed that genotypes took different period to fill their grain at both locations but not at Sheraro. Genotypes were significantly different for plant height, grain filling rate and 1000 seed weight at all locations. This indicates the performance of genotypes for plant height and grain filling rate are different in all locations.
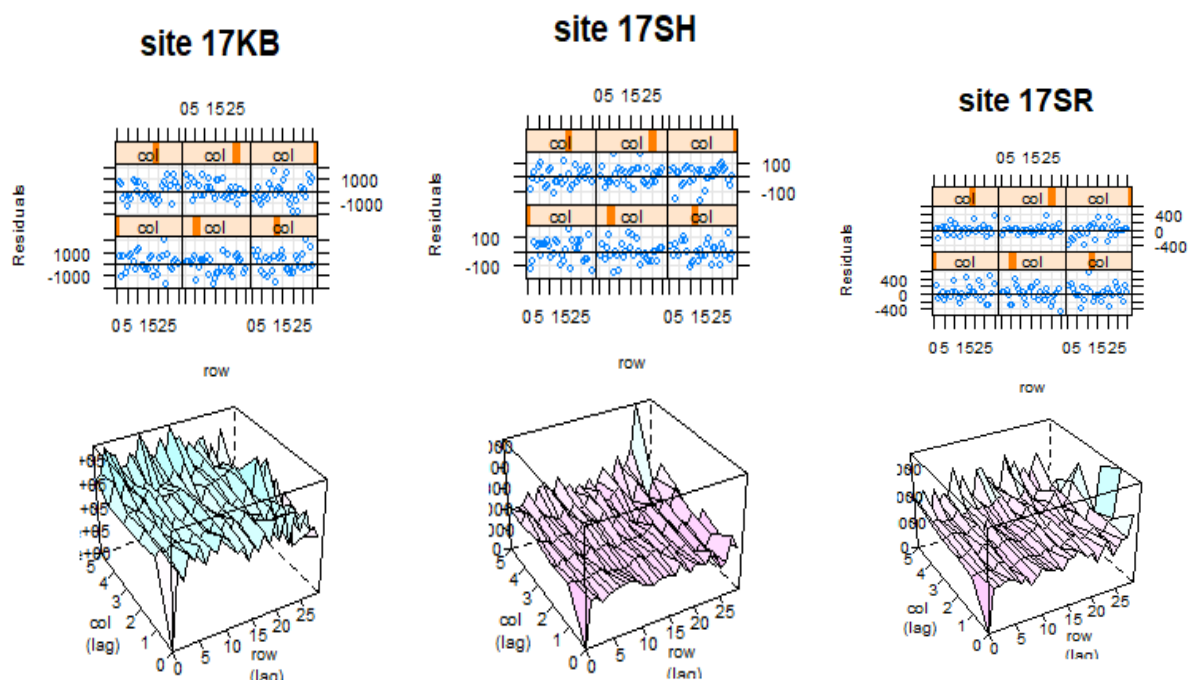
Figure 1. Spatial trend and spatially independent residuals from the spatial model for grain yield (kg/ha) in each location plotted against row and column positions

Note: 17KB= Kobo in 2017, 17SH= Sheraro in 2017, 17SR= Shewarobit in 2017

Table 3. Variance component estimation by REML and spatial model of early maturing sorghum genotypes for grain yield, phenological and other major traits tested at Kobo, Sheraro and Shewa Robit during 2017 main cropping season

	Site								
	SR			**KB**			**SH**		
Traits	**Genotype (df=59)**	**Replicate (df=2)**	**Error (df=118)**	**Genotype (df=59)**	**Replicate (df=2)**	**Error (df=118)**	**Genotype (df=59)**	**Replicate (df=2)**	**Error (df=118)**
DTE	0.08ns	0ns	0.79	0.01ns	0.01ns	0.19	0.03*	0.02ns	0.12
DTF	14***	0.56ns	5.87	18.1***	0.43ns	12.8	12.35***	0.0003ns	1.78
DTM	0.81**	0.15ns	1.18	2.13ns	0.001ns	12.1	6.52***	0.0001ns	6.83
GFP	9.92***	1.16ns	6.39	15.8**	0.84ns	20.1	6.33ns	0.001ns	35.4
GFR	501.9***	14.7ns	96.34	209***	1.01ns	32.64	317.4***	0.000012 ns	179.9
PHT	1117***	0.0001ns	37.3	732***	0.001ns	51	735***	0.55ns	68
GY	520310*	0.004*	41394.7	688377*	941.9ns	55189.6	244754*	0.0006*	57574.5
PWT	336386***	766ns	41246	506450***	0ns	24507	175877***	5284ns	48397
TSW	10.4***	0.001ns	2.8	13.09***	0.04ns	2.83	11.54***	0.0023ns	2.1
PN	29.81***	0.02ns	1.58	22.65***	0ns	11.82	37.34***	0.04ns	7.18
PL	3.54***	0.07ns	1.41	3.94***	0ns	1.04	1.91*	0.03ns	3.79
PW	0.8***	0.1ns	0.8	0.1ns	0ns	0.4	1*	0.9ns	3.1
PE	1.56***	0ns	0.16	0.72***	0ns	0.24	0.16***	0.01ns	0.11
DS	0.68***	0.01ns	0.36	0.27***	0ns	0.23	0.55***	0ns	0.21
STG	0.56***	0.02ns	0.3	0.4***	0ns	0.2	0.93***	0ns	0.2

Where REML=Restricted Maximum Likelihood, DTE=Days to Emergency, DTF=Days to flowering, DTM=Days to maturity, GFP=Grain filling period, GFR= Grain filling rate, PHT=Plant heght, PN= Panicle

number, PL= Panicle length, PW = Panicle width, PE = Panicle exersion, DS=Drought score, STG=Staygreen, PWT=Panicle weight, TSW=Thousand weight, *** = vary highly significant (P≤ 0.0001), ** = highly significant (P≤ 0.001), * = significant (P≤0.05) and [ns] = insignificant (P>0.05).

Combined analysis of data

The combined variance component estimation by REML of the fifteen characters for sixty early maturing sorghum genotypes is presented in Table 4.

The result showed that there were highly significant (P≤0.0001) differences among locations, and differences among the genotypes were significant (P≤0.05) for grain yield. This indicates that the high diversity of the growing conditions in the three locations and the small variability in the genotypes for grain yield performance. Significant effect of location on yield of sorghum varieties was reported by (Asfaw, 2007; Maposa *et al.*, 2010; Almeida *et al.*, 2014; Abiy and Firew, 2016; Lyle *et al.*, 2016). Furthermore, the GxE was also very highly significant (p≤ 0.0001), showing inconsistencies in the performance of sorghum genotypes across locations which shows difference in the response of sorghum genotypes at different environments. This outcome is in agreement with the findings of (Kenga *et al.*, 2003; Asfaw, 2007; Almeida *et al.*, 2014; Abiy and Firew, 2016).

The result of the combined variance components showed that the total variation in yield was attributed to location (86.4%), genotype (1.9%) and GxE (10.9%) effects (Table 4). The largest proportion of the variance showed on grain yield performance was due to locations than other variances. Therefore, high percentage of the location component of variation is an indication that environment is the major factor that affect grain yield performance of sorghum genotypes in the dry lowland's areas of Ethiopia. Similar results of large location effects were also reported by (Akcuraet *et al.*, 2006; Asfaw, 2007, 2008; Hagos and Fetien, 2011; Shrestha *et al.*, 2012; Sewagegne *et al.*, 2013; Muez *et al.*, 2014; Dagnachew *et al.*, 2014; Vangge *et al.*, 2014; Abiy and Firew, 2016; Kinde *et al.*, 2016). The variance component due to GxE was 5.74 times higher than that of the genotypes. The highest magnitude of the interaction as compared to the genotype component revealed that the grain yield performance of sorghum genotypes across locations was different (Asfaw, 2007; Abiy and Firew, 2016), indicating inconsistencies in the performances of sorghum genotypes across environments. A significant GxE may be either a non-cross-over or cross-over type (Cornelius *et al.*, 1996). In the current study, the interaction was of cross-over type as the ranking of genotypes for grain yield changed at every location.

Significant differences among genotypes were found for days of flowering (P≤0.0001), grain filling period (P≤0.0001), grain filling rate (P≤0.05), plant height (P≤0.0001), date of maturity (P<0.05) and 1000 seed weight (P≤ 0.0001). These indicates the presence of the effect of genetic differences for these traits. Differences among locations were non-significant (P>0.05) for these traits except grain yield, indicating the absence of variation among locations for these traits which are independent of location effect in contrast to (Asfaw, 2007; Abiy and Firew, 2016; Kinde, 2016) who indicated that the large presence of variation among locations had high effect for these traits. Genotype by environment were significant for days of flowering (P≤0.001), grain filling period (P≤0.001), days to maturity (P≤0.001), grain filling rate (P≤0.0001), plant height (P≤0.0001) and 1000 seed weight (P≤0.0001) (Table 4). The highest magnitude of the interaction revealed inconsistencies of the performance of sorghum genotypes for these traits across locations were different.

Table 4. Variance component estimation by REML of early maturing sorghum genotypes for grain yield, phenological and other major traits tested at three locations during 2017 main cropping season

Traits	Genotype	Rep/Site	Estimate Site	Genotype:Site	Error
GY	61140*	76.11ns	2743000***	346000***	25870
DTE	0.04**	0.02**	1.42ns	0.01ns	0.43
DTF	10.48***	0.08ns	23.15ns	1.49**	8.41
DTM	0.55*	0.54ns	53.95ns	1.8**	9.95
GFP	6.61***	0.46ns	73.55ns	3.31**	19.62
GFR	65.51*	2.07ns	2098.39ns	256.85***	82.54
PHT	491.94***	0ns	1138.56ns	203.7***	41.91
PWT	42903.5*	574.9ns	1849005ns	261291.8***	33091
PN	7.3*	0.03ns	176.72ns	31.05***	5.48
PL	2.56***	0.01ns	4.31ns	0.7***	1.88
PW	0.28***	0.1ns	1.31ns	0.12*	1.06
PE	0.52***	0.00003ns	0.47ns	0.17***	0.15
DS	0.1*	0.0003ns	0.58ns	0.27***	0.241
STG	0.29***	0.002ns	0.24ns	0.19***	0.21
TSW	4.25***	0ns	7.03ns	7.24***	2.61

Where REML=Restricted Maximum Likelihood, DTE=Days to Emergency, DTF=Days to flowering, DTM=Days to maturity, GFP=Grain filling period, GFR=Grain filling rate, PHT=Plant height, PN= Panicle number, PL=Panicle length, PW=Panicle width, PE=Panicle exertion, DS=Drought score, STG=Stay green, PWT=Panicle weight, TSW=Thousand weight, *** =vary highly significant ($P \leq 0.0001$), ** = highly significant ($P \leq 0.001$), * = significant ($P \leq 0.05$) and ns = insignificant ($P>0.05$).

General and relative performance of the genotypes

Individual mean

Means for grain yield, phenolgical and other major traits of sixty early maturing advanced sorghum genotypes at Kobo, Sheraro and Shewa Robit is presented in Table 5. Individual location mean for grain yield was presented in Appendix Table A1, A2 and A3.

Shaorobit was the highest in grain yield and panicle weight with mean values of 5174.0 kg/ha and 4646 g, respectively, indicating that this environment is suitable for sorghum production, whereas Kobo were the poorest yielding environments with mean grain yields of 2832.1 kg/ha, (Table 5), revealing that this environment was not favorable for sorghum production.

Flowering days of genotypes at Shewarobit (72 days) and Sheraro (70 days) were statistically similar. At these two locations the required mean flowering days of genotypes were early than mean days of flowering at Kobo (80.7 days). This finding is like (Abiy, 2016) pointed out the flowering date of genotypes at Kobo was late. Compared to the overall location's maturity date, it was only at Kobo, had above the mean of the three locations maturity date (110.9 days). At Sheraro, the mean maturity days were lower than the grand mean (Table 5).

Average grain filling periods of genotypes at Sheraro (31 days) was short as compared to the other locations. This variation might be due to the differences in the amount of rain fall and temperature, (Table 5). The average grain filling rates of genotypes were 53.6 kg/day/ha at Kobo, 121.5 kg/day/ha at Sheraro and 130.8 kg/day/ha at Shaorobit (Table

5). The variation among means of grain filling rate of genotypes in each location was diverse. The grand mean grain filling rate of locations was 102 kg/day/ha, Shewarobit and Sheraro were the two locations that had faster grain filling rate than the rest one location. At Shewarobit, genotypes filled their grains at a faster rate than the genotypes in the other locations. At Kobo, grain filling rate was the poorest of all the locations.

The mean plant height of all the genotypes at the tested locations was 208.5 cm. Average height of genotypes at Kobo (189.0 cm), Sheraro (216.5 cm) and Shewarobit (220.1 cm) were different. The highest mean plant height of the genotypes was observed at Shewarobit, it is higher than the rest locations (Table 5). The lowest mean was observed at Kobo. This shows that drought is highly affected the performance of genotypes with plant height.

The mean 1000 seed weight of all the genotypes at the tested locations was 30.3 g. Average 1000 seed weight of genotypes at Kobo (31.6 g), Sheraro (29.3 g) and Shewarobit (30 g) were statistically similar, shows drought is not highly affected the performance of genotypes with seed weight.

At Kobo, drought was highly affected the performance of genotypes with plant hieght, grain yield, panicle weight, panicle length, panicle number, panicle width, panicle exersion, stay greenness and favored the genotypes to be late.

Table 5. Means for grain yield, phenolgical and other complex traits of 60 early maturing advanced sorghum genotypes at Kobo, Sheraro and Shewarobit during 2017 main cropping season

							Traits								
Locations	DTE	DTF	GFP	DTM	GFR	PHT	GY	PWT	TSW	PN	PL	PW	PE	DS	STG
Kobo	8	81	53	120	53.6	189	2831	3207	31.6309	45	19	14	3	4	3.9
Sheraro	4.8	70	31	101	122	216	3707	3864	29.2672	58	24	15	1	2	2.5
Shewarobit	7.1	72	40	112	131	220	5174	4646	29.9823	59	23	16	3	3	3.3

Where DTE=Days to Emergency, DTF=Days to flowering, DTM=Days to maturity, GFP=Grain filling period, GFR=Grain filling rate, PHT=Plant height, PN= Panicle number, PL=Panicle length, PW=Panicle width, PE=Panicle exersion, DS=Drought score, STG=Stay green, PWT=Panicle weight, TSW=Thousand weight.

Combined mean

The mean for grain yield, phenological and other major traits of the 60 early maturing genotypes for combined location is presented in Table 6. The mean grain yield over all the locations and genotypes was 3035 kg/ha; with genotype mean grain yield ranging from 2085 kg/ha (13MWF6#6077) to 3655.7 kg/ha (12MW6251), indicating wide difference in yield potential across locations (Table 6). The lowest yielding genotype is 13MWF6#6077 (2085 kg/ha) and is mainly attributed to the high moisture stress occurred, during the study period, which is similar to the finding of (Menezes *et al.,* 2015). However, they were significantly different with all the genotypes. The genotypes 12MW6251, 14MWLSDT7322, 14MWLSDT7201, Pipline2, 4MWLSDT7238, 14MWLSDT7234 and 14MWLSDT7176 had highest in mean grain yield, panicle weight and panicle width from the tested genotypes.

Earliness indicates the response of genotypes that escape from moisture stress condition. The earliness traits (days to flowering, grain filling period and days to physiological maturity) enables them to flower, grain fill and mature early. That is why days to flowering and maturity are of the most important attributes that need to be considered in selecting genotypes for drought affected areas. In this study, number of days to flowering ranged from 66 to 81 days and number of days to maturity ranged from 112 to 118 days. The five

early genotypes (90MW5319, 2401, 2523 and 2294) were statistically significant different with the check. However, the three genotypes (14MWLSDT7325, 14MWLSDT7191 and 14MWLSDT7115) were late flowering, maturity and low yielding in contrast with Ludlow and Muchow (1990) reported late flowering varieties tend to offer yield higher than early flowering ones. Early flowering and maturing genotypes consist of adapting the crop cycle to water availability and evaporative demand, usually by reducing its duration, thereby reducing the total demand for water and withstand terminal stress (Tardieu, 2013). Flowering time is the most critical factor to optimize adaptation, hence grain yield, in environments differing in water availability and distribution during the growing season (Richards, 2006).

Plant height is a complex trait, it is being affected by environmental conditions and management practices. (Butler *et al.,* 2005; Al-Temimi *et al.,* 2013) reports indicated that plant height is directly linked to the productive potential of plant in terms of grain yield since it represents a good storage organ for photosynthetic metabolites. Therefore, significant reduction in plant height was noticed due to water stress; however, tolerant cultivars attained more plant height. Plant height plays a major role in the acceptance of varieties by users (farmers) in the study areas, with preference being given to tall plants, which can serve a dual purpose as food and feed. In plant height, there were a significant difference and statistical different between genotypes and check. Mean plant height ranged from 138 cm to 254.4 cm with average of 208.5 cm (Table 6). Most of the genotypes were significantly difference from the check, indicating the wide difference in plant height across locations. The check is small in stature as compared to most of the genotypes.

Mean thousand seed weight ranged from 24.9 g to 36.4 g with average of 30.3 g (Table 6). Most of the genotypes were statistically similar with the check. Genotypes 2005MI5057, 14MWLSDT7322, 2005MI5069 and 14MWLSDT7193 were the highest 1000 seed weight from the tested genotypes. Genotypes that had the maximum 1000 seed weight indicated post flowering drought tolerance. Hence, traits associated with post-flowering drought tolerance include improved longer grain filling period, stay-green and seed weight (Borrell *et al.,* 2000b; Burke *et al.,* 2010; Van Oosterom *et al.,* 1996). Drought stress during seed development shortens the seed filling period (Younesi and Moradi, 2009) which results earlier maturation of the seeds (Meckel *et al.,* 1984).

Table 6. Combined means for grain yield, phenolgical and other major traits of sixty early maturing sorghum genotypes by mixed model tested at Kobo, Sheraro and Shewarobit during 2017 main cropping season

No	Genotype Name	DTE	DTF	GFP	DTM	GFR	PHT	GY	PWT	TSW	PN	PL	PW	PE	DS	STG
1	Melkam	7	78	41.6	115	73.7	154.6	2918.7	3010.6	32.7	34.5	27.9	14.9	3.1	3.2	3.9
2	14MWLSDT7060	7	78	41.4	115	73.8	167.2	3296.0	3121.6	30.5	36.0	20.9	15.1	2.8	3.0	3.1
3	12MW6251	7	78	41.7	115	86.2	195.6	3655.7	3477.6	33.0	43.5	22.6	14.9	3.6	3.2	3.0
4	14MWLSDT7410	7	80	40.2	116	65.5	200.9	2752.0	3027.7	28.4	41.7	28.7	15.3	4.0	3.8	3.1
5	12MW6302	7	80	39.5	115	81.9	140.7	2969.7	3026.4	27.0	45.1	24.5	14.6	2.1	3.8	4.2
6	14MWLSDT7322	7	81	39.0	115	76.5	230.9	3452.3	2724.0	33.6	41.9	20.2	14.4	2.1	3.5	3.2
7	14MWLSDT7395	7	72	48.4	116	50.5	163.7	2884.3	2594.0	29.7	41.4	24.1	14.6	1.0	3.1	2.4
8	14MWLSDT7400	7	76	42.4	113	70.4	180.6	2726.0	3363.1	29.3	46.0	23.0	14.9	3.5	3.8	4.3
9	14MWLSDT7310	7	80	41.6	116	68.2	220.5	2968.3	2760.8	29.7	48.2	21.5	15.0	1.9	3.7	3.9
10	13MWF6#6077	7	79	41.7	116	47.0	129.0	2085.0	2702.5	22.4	44.7	24.7	14.2	2.4	2.9	3.0
11	14MWLSDT7325	7	82	38.4	116	67.7	219.3	2752.0	2650.5	31.6	43.8	21.1	14.5	2.0	3.4	3.7
12	2005MI5069	7	80	39.9	115	63.7	179.7	3227.7	2737.7	32.8	32.6	21.0	14.4	3.8	3.5	3.8
13	14MWLSDT7196	7	77	41.9	114	89.7	178.5	3245.0	4024.1	30.3	45.7	22.2	15.4	4.1	3.8	4.0

No	Genotype															
14	14MWLSDT7311	7	78	42.1	116	67.4	234.9	2998.3	2913.1	29.6	51.0	21.0	14.3	1.3	4.1	3.5
15	14MWLSDT7157	7	78	40.9	114	79.9	205.6	3165.0	3044.5	33.6	46.8	21.5	14.7	2.3	3.1	3.2
16	14MWLSDT7193	7	69	47.3	111	66.6	155.5	3107.3	3341.0	35.7	41.6	20.0	15.0	3.4	3.4	4.2
17	14MWLSDT7332	7	79	41.6	116	78.3	168.1	3077.3	3757.0	32.6	47.0	17.6	14.5	4.1	3.1	3.4
18	14MWLSDT7115	7	82	41.1	118	61.1	203.8	2870.7	2859.4	30.1	40.1	24.6	14.5	3.9	3.6	2.5
19	14MWLSDT7176	7	73	46.5	115	80.6	189.6	3374.7	3668.2	35.3	44.3	23.5	15.3	2.1	3.3	3.6
20	14MWLSDT7209	7	78	41.3	115	81.4	194.7	2801.7	3366.1	31.4	44.9	21.2	14.4	1.7	2.6	2.2
21	12MW6440	7	78	40.6	114	74.1	183.3	3025.7	3216.4	31.0	38.8	22.8	14.7	4.2	3.9	4.0
22	14MWLSDT7201	7	78	41.1	114	83.5	190.9	3622.7	3633.4	34.3	43.5	21.6	14.8	2.2	3.4	3.8
23	12MW6146	8	78	40.7	114	67.1	149.2	2735.0	2754.1	31.0	35.9	24.7	14.7	2.3	2.7	3.3
24	14MWLSDT7364	7	78	41.8	115	81.0	187.5	3323.7	3184.5	33.7	46.0	22.5	14.8	2.0	3.7	3.6
25	Pipline2	7	73	44.6	113	85.3	205.4	3570.7	3735.3	33.4	48.2	21.5	15.8	2.4	3.4	3.8
26	14MWLSDT7413	8	77	42.2	114	83.1	179.2	3089.7	3763.8	29.6	47.6	21.2	14.5	2.9	3.3	3.3
27	13MWF6#6037	7	75	43.3	113	81.8	162.7	3327.7	3688.9	30.5	44.2	21.2	16.1	2.8	3.5	3.9
28	14MWLSDT7207	7	76	42.1	114	82.3	200.4	3040.7	3464.3	29.7	46.1	22.5	14.8	1.9	2.3	2.4
29	14MWLSDT7040	7	76	42.8	114	74.8	185.1	3233.7	3296.8	32.2	39.6	22.1	15.2	2.4	3.3	4.2
30	14MWLSDT7036	7	79	39.8	114	70.1	193.6	2924.7	3127.4	34.3	39.7	21.2	14.8	3.3	3.9	4.3
31	14MWLSDT7324	7	80	38.1	114	79.7	236.6	3042.3	3002.5	31.1	48.2	21.0	14.1	1.9	3.1	3.8
32	12MW6243	7	79	39.4	113	66.0	125.0	2572.3	3080.0	28.3	42.6	24.0	14.4	3.0	3.0	3.7
33	12MW6420	7	81	41.4	118	60.8	138.1	2785.0	2900.2	26.6	44.0	20.2	14.7	4.6	3.2	3.1
34	14MWLSDT7238	7	78	41.4	115	94.3	191.4	3640.0	3811.4	30.2	49.8	24.9	14.9	2.1	2.8	2.6
35	12MW6444	7	78	41.9	115	77.1	198.1	3151.0	3445.6	31.2	48.0	21.8	14.9	2.4	3.3	3.3
36	14MWLSDT7402	7	77	43.5	116	61.0	238.7	2751.0	3092.6	34.2	43.9	21.8	14.1	1.7	3.2	3.3
37	14MWLSDT7234	7	77	42.0	115	88.2	190.7	3487.3	3293.9	34.3	48.0	22.6	14.1	2.0	2.3	2.3
38	12MW6471	7	81	41.4	117	63.2	202.6	2614.7	3094.9	35.6	41.9	21.1	14.4	1.9	2.9	2.9
39	14MWLSDT7042	7	77	42.3	115	77.5	194.6	3159.7	3342.0	35.5	41.4	22.2	14.5	2.9	3.4	4.1
40	14MWLSDT7033	7	75	45.2	116	74.7	196.6	3197.7	4005.4	33.7	46.1	22.7	15.1	2.4	3.3	4.0
41	14MWLSDT7241	7	79	38.9	113	89.2	201.6	3240.7	3559.0	30.4	47.4	24.0	14.8	2.1	2.5	2.9
42	14MWLSDT7191	6	82	40.4	118	51.9	174.4	2399.7	2564.2	31.3	41.6	20.5	14.6	4.4	3.5	3.3
43	2005MI5093	7	78	40.3	114	79.3	207.8	3073.3	3478.2	30.2	46.8	19.8	14.1	1.9	3.8	3.9
44	2401	7	70	48.8	114	65.0	181.0	3185.7	3285.6	35.1	49.5	21.1	14.0	1.4	2.8	2.9
45	2004MW6197	7	78	41.0	115	65.4	169.3	3107.3	2647.9	33.9	37.9	21.5	14.1	2.3	4.1	3.7
46	2005MI5064	7	80	38.8	114	82.2	194.4	3214.3	2801.5	30.9	39.7	21.2	14.1	1.6	3.2	3.1
47	2523	7	70	48.7	114	53.4	157.4	2255.3	2757.2	31.4	45.5	21.9	14.0	3.9	3.5	3.2
48	04MW 6043	8	79	40.4	115	82.4	196.8	3038.0	3794.6	29.0	38.3	23.7	14.6	3.2	3.9	4.5
49	2005MI5057	7	76	42.4	114	79.1	199.8	3216.0	3399.9	33.9	44.7	24.2	14.6	2.1	3.2	3.6
50	04MW 6079	7	80	40.7	116	65.0	186.4	3131.7	2840.3	28.5	38.7	22.1	14.8	3.4	3.4	3.7
51	14MWLSDT7202	7	75	46.0	116	70.6	203.4	3000.3	3115.3	32.5	45.3	19.6	14.3	2.7	2.9	3.2
52	14MWLSDT7291	7	76	42.8	115	75.4	232.5	3125.3	3509.4	32.6	49.3	21.5	14.1	1.4	3.3	2.9
53	2001MS7036	7	74	46.3	115	54.8	204.2	2828.0	2601.1	29.8	46.5	25.3	13.9	1.3	3.5	3.3
54	90MW5319	7	68	50.0	113	71.4	171.4	3247.3	3388.7	31.7	47.9	21.5	14.8	1.7	2.8	3.0
55	99MW4047	7	77	41.0	113	64.6	134.9	3022.0	2565.9	30.7	37.5	22.2	14.2	2.8	3.4	3.6
56	05MW6026	7	75	42.6	112	74.0	201.8	2995.3	3210.4	33.3	48.8	21.7	14.3	1.9	2.6	3.2
57	14MWLSDT7421	7	75	43.3	114	70.9	205.7	3087.7	3018.6	34.7	46.2	20.8	13.9	2.1	3.1	3.0
58	2003MW6053	8	73	45.4	114	56.9	175.2	2590.3	2712.2	31.5	35.7	25.1	14.5	3.2	2.9	3.2
59	2294	7	66	53.0	115	63.3	167.5	3098.3	2977.8	33.6	46.0	20.7	14.7	1.4	3.2	2.9
60	2003MW6038	7	76	44.0	115	57.9	192.4	2622.7	2585.2	34.1	39.2	22.6	14.8	3.1	3.2	3.4
	Mean	7	77	42.5	115	72.2	187.0	3035.0	3165.3	31.6	43.6	22.3	14.6	2.6	3.3	3.4
	LSD at 5%	1	2.6	3.9	2.8	21	18.4	504.9	939.3	4.5	9.3	3.3	2.4	1.3	1.5	1.3

Where DTE=Days to Emergency, DTF=Days to flowering, DTM=Days to maturity, GFP=Grain filling period, GFR= Grain filling rate, PHT=Plant heght, PN= Panicle number, PL= Panicle length, PW = Panicle width, PE = Panicle exersion, DS=Drought score, STG=Staygreen, PWT=Panicle weight, TSW=Thousand weight, LSD = Least significance difference.

Phenotypic and genotypic variations

The genotypic coefficient of variation (GCV) for the characters varied from 1.52% for days to emergency to 31.28% for panicle exertion and the phenotypic coefficient of variation (PCV) for the characters varied from 2.83% for days to maturity to 42.16% for panicle exertion. In general, the PCV values were greater than the GCV values for all characters studied (Tables 2 & 3). This indicates that the high influence of environmental effect. According to (Deshmukh *et al.*, 1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are low and values between 10% and 20% to be medium. The high coefficients of phenotypic (PCV) and genotypic (GCV) variances were obtained for traits like panicle exertion, stay green, drought score base genetic background as well as the potential to respond entirely to select drought tolerant genotype for sorghum production in drought prone areas. Similar results were obtained by (Wu *et al.*, 2010; Kachapur *et al.*, 2009).

Moderate GCV and PCV estimates were observed for all characters except for days to emergency and maturity. The lowest PCV and GCV values were observed for days to emergency and maturity, which was in conformity with the findings of (Rani and Umakanth, 2012).

Heritability and genetic advance

Heritability estimates observed for the characters ranged from 18.71% (days to emergency) to 97.34% (plant hieght). The genotypes under study showed high broad sense heritability values for 10 characters (plant hieght, days to flowering, grain filling rate, grain yield, panicle weight, 1000 seed weight, panicle length, panicle number, stay green, panicle exertion), while other four characters had moderate heritability (Table 7).

According to (Singh *et al.*, 2011), if heritability of a character is very high, say 80% or more, selection for such characters could be easy. For a character with low heritability (<40%), selection may be considerably difficult or virtually impractical due to the masking effect of environment on the genotypic effects. Thus, in the present study, selection of genotypes based on grain yield and phenological traits would be more satisfactory to increase yield of sorghum genotypes.

The effectiveness of selection depends upon genetic advance of the character selected along with heritability. The characters, which showed high heritability (H%) with high genetic advance as percentage of mean (GAM %) were grain filling rate (81.60% and 66.65%), plant hieght (97.34% and 31.85%), grain yield (86.10% and 54.73%) and panicle weight (83.86% and 37.60%), panicle exertion(91.71% and 70.60%) and stay green (88.06 and 61.50%), respectively, which was in conformity with the findings of (Ali *et al.*, 2009). (Chalachew *et al.*, 2019) observed higher broad sense heritability value for days to flowering and higher heritability value coupled with high GAM% for grain yield. High heritability with high genetic advance indicates the control of additive gene and early selection may be effective for this character.

High heritability with moderate genetic advance were observed for days to flowering (93.28% and 16.99%), thousand seed weight (93.36% and 24.67%), panicle number (83.80% and 28.48%), panicle length (87.54% and 25.09%), respectively. Moderate heritability with high genetic advance were grain filling period (70.51% and 37.16%) and drought score (68.84% and 61.79%), respectively.

Moderate heritability with low genetic advance was observed for days to physiological maturity (53.57% and 8.40%), and low heritability with low genetic advance was observed for days to emergency (18.71 and 8.67%), respectively, which was similar to the results of (Chalachew *et al.*, 2019).

High GCV along with high heritability and genetic advance deliver well evidence than other parameters by itself. Based on the present study, plant height, grain yield, grain filling rate, panicle weight, panicle exertion and drought score are the most important quantitative traits for effective selection in sorghum genotypes. However, days to maturity and emergency showed less than 5%. A low GCV and GAM observed for these traits indicated that they were under high environmental influence and that selection for these traits would be ineffective.

According to (Jalata *et al.*, 2011) heritability in broad sense was high for all-important quantitative traits measured. High genetic advance was revealed from plant height, grain yield, grain filling rate, panicle weight, panicle exertion and drought score, this indicates that there is good capacity for crop improvement through early selection for grain yield and biomass production. High amount of genetic variability among the population indicated an increased opportunity for the selection of desirable genotypes as the variation is heritable one. This is an indication that most probably that heritability is due to genetic factor and selection could be effective in early generations for this trait and the possibility of improving sorghum yield through direct selection for grain yield and its components. The traits possessing low genetic advance with high heritability indicates that the presence of non-additive gene action, thus simple selection procedure in early segregating generations will not be effective for screening of the desirable traits.

Table 7. Variance components for 15 characters of sorghum genotypes

Traits	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	H (%)	GA	GAM(%)
DTE	0.41	0.01	0.40	9.62	1.52	18.71	57.51	8.67
DTF	21.62	13.11	8.51	6.26	4.87	93.28	1262.38	16.99
GFP	31.32	6.57	24.75	13.52	6.20	70.51	1537.53	37.16
DTM	9.88	1.12	8.75	2.83	0.96	53.57	931.64	8.40
GFR	445.64	147.12	298.52	20.70	11.90	81.60	6795.92	66.65
PHT	913.99	733.60	180.38	14.50	12.99	97.34	6640.87	31.85
GY	518561.22	211406.14	307155.09	18.45	11.78	86.10	213682.03	54.73
PWT	377467.65	138132.35	239335.30	15.73	9.52	83.86	146831.26	37.60
TSW	14.25	8.69	5.57	12.46	9.73	93.36	747.29	24.67
PN	36.78	13.42	23.36	11.27	6.81	83.80	1531.71	28.48
PL	5.21	2.28	2.93	10.30	6.82	87.54	556.23	25.09
PW	2.02	0.42	1.60	9.34	4.28	70.53	261.91	17.21
PE	0.98	0.54	0.44	42.16	31.28	91.71	236.50	70.60
DS	0.77	0.15	0.62	30.72	13.62	68.84	176.10	61.79
STG	0.87	0.39	0.48	28.89	19.36	88.06	198.02	61.50

Where DTE=Days to Emergency, DTF=Days to flowering, DTM=Days to maturity, GFP=Grain filling period, GFR=Grain filling rate, PHT=Plant heght, PN=Panicle number, PL=Panicle length, PW=Panicle width, PE=Panicle exertion, DS=Drought score, STG=Staygreen, PWT=Panicle weight, TSW=Thousand weight.

Phenotypic and genotypic correlations among characters

Phenotypic and genotypic correlations among characters are also presented in Table 8. Positive and significant correlations were observed between panicle weight, panicle width, grain filling rate and grain yield at phenotypic and genetic levels, showing the interrelationship of these traits. The positive associations among grain yield with panicle and panicle width, grain filling rate indicate that selecting for positively associated panicle related traits would have a positive effect on grain yield. This was further confirmed by (Chalachew *et al.*, 2017). On the other hand, grain yield had significant negative correlation with date of flowering and date of maturity at both levels. Positive and significant associations were observed between plant height, grain yield, panicle weight, panicle width, panicle number and panicle length at phenotypic correlation. Similar to the present study, (Tesso *et al.*, 2011) reported that grain yield was positively associated with thousand seed weight, panicle weight and panicle width among 200 sorghum accessions included in their studies. Days to 50% flowering, days to maturity, days to emergency, grain filling period were negatively correlated with grain filling rate, plant height, grain yield, panicle weight, panicle number, panicle length and panicle weight, but DTF and DTM characters were positively correlated with panicle exertion, drought score and stay green in phenotypic correlation, the rate senescence of determines the maintenance of quality flowers and seed set which agreed with the results of (ICRISAT, 2014). Furthermore, days to maturity had negative direct effect on grain yield at both levels, and their effect via other characters was also mostly negative. These negative correlations may help to select early maturing genotypes with high grain yield for moisture stressed areas where terminal drought is recurrent. Moreover, days to flowering was negatively correlated with such characters as panicle length, thousand seed weight which was similar to the results of (Chalachew *et al.*, 2017; Sowmy *et al.*, 2015). (Tesso *et al.*, 2011) also reported significant negative correlation between thousand seed weight and days to flowering. Plant height was positively correlated with panicle number and thousand seed weight; however, it was negatively associated with panicle exertion at phonotypic and genotypic level.

Positive and significant correlations were observed among panicle exertion, drought score and stay green at phenotypic and genetic levels. Panicle number, panicle length, grain yield, panicle weight, grain filling rate and plant height had negative correlations with panicle exertion, drought score and stay green at phenotypic levels. Delaying the onset of leaf senescence and reducing its rate offer an effective strategy for increasing grain production, fodder quality and grain crop residues particularly under water limited conditions as reported by (Borrell *et al.*, 2000). In Ethiopia, sorghum is growing mainly in moisture stressed areas. Stay green or non-senescence is an important trait associated with drought tolerance. It is indicated by maintenance of green stems and upper leaves when water is limiting during grain filling. Sorghum genotypes with the stay-green trait continue to fill their grains normally even under limited water or moisture stress conditions.

Genetic divergence and cluster mean analyses

The 90 genotypes were grouped into seven clusters as showed in Table 7. Cluster VIII and VII were found to be largest with 17 and 16 genotypes, respectively, and the cluster VII and VII were found to be the smallest cluster with three and four genotypes, respectively. Promising genotypes can be identified from the clusters based on the estimated cluster means recorded for each trait.

Table 8. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 15 characters from 60 sorghum genotypes

Traits	DTE	DTF	GFP	DTM	GFR	PHT	GY	PWT	TSW	PN	PL	PW	PE	DS	STG
DTE	1	0.59**	0.70**	0.85**	0.47**	0.22**	-0.08	-0.12*	0.19**	-0.44**	-0.56**	0.19**	-0.52**	0.64**	0.44**
DTF	0.30*	1	0.36**	0.68**	0.51**	-0.15*	0.47**	0.44**	0.02	-0.53**	-0.49**	0.35**	0.37**	0.45**	0.31**
GFP	-0.16	0.85**	1	0.82**	-0.74**	-0.35**	-0.29**	-0.30**	0.30**	-0.54**	-0.57**	0.28**	-0.37**	0.55**	0.37**
DTM	0.26*	0.71**	-0.32*	1	0.63**	0.23**	0.22**	-0.25*	0.21**	-0.50**	-0.60**	0.23**	-0.53**	0.64**	0.40**
GFR	0.14	0.17	-0.30*	-0.12	1	0.43**	0.83**	0.77**	-0.16*	0.69**	0.50**	0.51**	-0.21**	-0.40**	-0.26**
PHT	0.06	0.26*	-0.15	0.30*	0.14	1	0.31**	0.29**	0.15*	0.44**	0.20**	0.18**	-0.29**	-0.12*	-0.28**
GY	0.07	-0.28*	0.20	-0.32*	0.86**	-0.01	1	0.90**	0.01	0.58**	0.28**	0.54**	0.05	-0.12*	-0.07
PWT	0.11	-0.16	0.13	-0.20	0.81**	-0.03	0.90**	1	-0.03	0.58**	0.31**	0.54**	0.05	-0.16*	-0.05
TSW	-0.15	-0.30*	0.24	-0.18	0.14	0.36*	0.28*	0.12	1	-0.23**	-0.34**	-0.11*	0.05	0.12*	0.16*
PN	-0.12	-0.02	0.01	0.11	0.16	0.28*	0.15	0.15	-0.14	1	0.42**	0.38**	-0.29**	-0.38**	-0.39**
PL	0.00	-0.09	0.08	-0.16	-0.10	-0.19	-0.08	-0.01	-0.34	-0.20	1	0.38**	-0.30**	-0.39**	-0.35**
PW	0.00	-0.18	0.15	-0.12	0.41*	-0.15	0.53**	0.65**	0.06	0.04	0.10	1	0.07	-0.01	-0.03
PE	0.02	0.19	-0.15	0.12	-0.02	-0.34*	-0.07	0.11	-0.11	-0.34*	-0.03	0.18	1	0.52**	0.46**
DS	-0.15	0.01	0.08	-0.04	-0.07	0.09	-0.04	0.06	0.06	-0.16	0.06	0.16	0.33*	1	0.56**
STG	-0.11	-0.03	-0.11	-0.34*	0.23	-0.22	0.25	0.31*	0.09	-0.28*	0.03	0.40*	0.37*	0.54**	1

Where DTE=Days to Emergency, DTF=Days to flowering, DTM=Days to maturity, GFP=Grain filling period, GFR=Grain filling rate, PHT=Plant heght, PN=Panicle number, PL=Panicle length, PW=Panicle width, PE = Panicle exersion, DS=Drought score, STG=Stay green, PWT=Panicle weight, TSW=Thousand seed weight, ** =highly significant (P≤ 0.001), * =significant (P≤0.05).

Table 9. Distribution of 60 sorghum genotypes in different clusters

Cluster	Number of genotypes	Genotypes				
Cluster-I	5	14MWLSDT7332	14MWLSDT7413	14MWLSDT7196	14MWLSDT7033	04MW 6043
Cluster-II	16	14MWLSDT7207	2005MI5093	2005MI5057	90MW5319	14MWLSDT7040
		2401	14MWLSDT7176	13MWF6#6037	14MWLSDT7193	14MWLSDT7042
		14MWLSDT7060	14MWLSDT7364	12MW6444	14MWLSDT7291	14MWLSDT7241
		14MWLSDT7234				
Cluster-III	17	12MW6440	05MW6026	Melkam	12MW6302	14MWLSDT7324
		14MWLSDT7421	14MWLSDT7410	14MWLSDT7402	14MWLSDT7036	14MWLSDT7202
		14MWLSDT7400	14MWLSDT7209	2294	12MW6243	12MW6471
		14MWLSDT7157	14MWLSDT7311			
Cluster-IV	6	2005MI5069	2005MI5064	04MW 6079	2004MW6197	99MW4047
		14MWLSDT7322				
Cluster-V	8	14MWLSDT7395	2001MS7036	14MWLSDT7115	12MW6420	14MWLSDT7325
		12MW6146	2003MW6053	14MWLSDT7310		
Cluster-VI	4	Pipline2	14MWLSDT7238	14MWLSDT7201	12MW6251	
Cluster-VII	3	13MWF6#6077	2523	14MWLSDT7191		

Table 10. The summary of cluster means of 15 quantitative traits for the sorghum genotypes based on data set

Traits	I	II	III	IV	V	VI	VII	Overall Mean
DTE	7.4	7.0	7.0	7.0	7.3	7.0	6.7	7.0
DTF	77.4	75.3	77.2	79.3	77.8	76.8	77.0	77.2
GFP	42.3	43.4	42.1	40.1	42.9	42.2	43.6	42.4
DTM	115.0	114.1	114.6	114.7	115.9	114.3	116.0	114.9
GFR	81.6	77.7	71.4	69.6	60.9	87.3	50.8	71.3
PHT	183.8	189.1	192.4	182.6	184.3	195.8	153.6	183.1
GY	3129.5	3224.4	2908.5	3192.6	2801.7	3622.3	2246.7	3017.9
PWT	3869.0	3404.2	3099.3	2719.6	2729.0	3664.4	2674.6	3165.7
TSW	31.0	32.7	31.8	31.7	30.0	32.7	28.4	31.2
PN	44.9	45.1	44.2	38.1	42.0	46.3	43.9	43.5
PL	21.5	22.0	22.5	21.4	23.3	22.7	22.4	22.2
PW	14.8	14.8	14.5	14.3	14.6	15.1	14.3	14.6
PE	3.3	2.2	2.5	2.7	2.5	2.6	3.6	2.8
DS	3.5	3.1	3.3	3.5	3.3	3.2	3.3	3.3
STG	3.8	3.4	3.5	3.5	3.2	3.3	3.2	3.4

Genotypes 12MW6251, 14MWLSDT7238, Pipline2 and 14MWLSDT7201 were grouped in cluster VI and identified for early flowering and maturity, and highest in grain yield, panicle weight, panicle length, panicle width, panicle number, plant hieght and thousand seed weight (Table 8).

Genotypes were grouped into seven clusters and the future breeding program utilizing the studied accessions is suggested to be based on the genetic analysis of the various traits to which clusters are predominant. Hence, for future breeding work it could be useful to select individual genotypes from these clusters by considering the special advantages of each cluster and the objectives of the breeding program.

Conclusions

Sorghum (***Sorghum bicolor***) is one of the major important cereal crops which the lives of millions of people depend and grows in areas where other major cereals marginally grown. However, drought becomes the major problem for sorghum production in Ethiopia especially in drought prone areas of the country which needs the development of drought tolerant or resistance varieties.

The spatial analysis for each location revealed that the genotypes were significantly different for grain yield. Shaorobit was the highest yielding environment, indicate this location is suitable for sorghum production, whereas Kobo was the poorest yielding location with mean grain yields. The genotypes 12MW6251, 14MWLSDT7322, 14MWLSDT7201, Pipline2, 4MWLSDT7238, 14MWLSDT7234 and 14MWLSDT7176 had highest in mean grain yield, panicle weight and panicle width from the tested genotypes in across locations.

The sorghum growing dry lowland areas of Ethiopian were various and contributed largely to the changes of genotypes yield performance over locations. Therefore, further study on the GXE effects and stability of early maturing sorghum genotypes is needed in multi locations for a number of years and location to determine the interaction effect of genotypes and select stable genotypes. Since the current study was conducted only for one

year, the work should be repeated at least for some more years to give sound conclusions and reliable recommendations. High amount of genetic variability among the population indicated an increased opportunity for the selection of desirable genotypes as the variation is heritable one. This is an indication that most probably that heritability is due to genetic factor and selection could be effective in early generations for this trait and the possibility of improving sorghum yield through direct selection for grain yield and its components.

The positive associations among grain yield with panicle and panicle width, grain filling rate indicate that selecting for positively associated panicle related traits would have a positive effect on grain yield.

Genotypes 12MW6251, 14MWLSDT7238, Pipline2 and 14MWLSDT7201 were grouped in a cluster and identified for early flowering and maturity, and highest in grain yield, panicle weight, panicle length, panicle width, panicle number, plant hieght and thousand seed weight. For future breeding work it could be useful to select individual genotypes from this cluster by considering the special advantages in earliness, biomass and grain yield

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