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Genetic Variability, Heritability and Genetic Advance for Agronomical Traits of Ethiopian Sorghum [Sorghum Bicolor (L.) Moench] Genotypes

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Ethiopia is the center of origin and domestication for sorghum with a wide range of sorghum collections for various agro ecologies. However, there are many factors that hinder the production and productivity of sorghum. Thus, the present study was to assess genetic variability of early and medium maturing lowland adapted landrace and improved sorghum genotypes to evaluate the performance of sorghum genotypes and identify promising lines for the dry lowland environments of Ethiopia. Alpha lattice design involving 110early and medium maturing sorghum genotypes were used in replicated twice at Meiso and Sheraro in 2016 cropping season. Results from combined analysis of variance over the two locations revealed that mean squares due to genotypes for almost all traits were highly significant ($P \leq 0.01$) i.e. for days to flowering, days to maturity, grain yield, panicle weight, hundred grain weight, panicle length, plant height and disease score in both locations. The significant mean squares due to genotypes indicated the existence of variation among the genotypes, which could be exploited for the improvement of respective traits. heritability for nine morpho-agronomic traits calculated ranged from 0.03 for grain yield to 0.93 for plant height at Meiso and from 0.02 for plant height to 0.19 for number of panicles per plot at Sheraro. The information generated in the present study will be useful for breeders who want to improve yield and yield-contributing traits of sorghum.

Key words: Agronomic traits, Ethiopian, Genetic variability, Heritability and Sorghum

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INTRODUCTION

In Ethiopia, sorghum is one of the major grain crops produced, and it is the third important crop in terms of both area coverage and volume of production among cereals [5]. It is adapted to a wide range of environment and hence can be produced in the high lands, intermediate altitudes and low land areas. The crop is widely produced more than any other crops, in the areas where there is moisture stress due to its ability of coping with harsh environment. In the country cereals comprise 80.78% (10 million ha) of the field crops of which sorghum accounts for 14.58%. Sorghum is grown in 12 of the 18 major agro-ecologies of Ethiopia [12]. These sorghum growing agro ecologies could be broadly categorized into lowlands (dry and wet, <1600m), intermediate altitude (1600-1900) with high rainfall, and highlands (>1900m).

Even though, Ethiopia is the center of origin and domestication for sorghum with a wide range of sorghum collections for various agro ecologies there are many factors that hinder the production and productivity of sorghum, the most economically important once are: lack of high yielding varieties adapted to the different agro-ecologies of the country, lack of improved varieties of diverse uses and use qualities, biotic stresses such as birds, insect pests, diseases, weeds especially striga, abiotic stresses mainly drought, poor soil fertility, post-harvest losses to pests and diseases, lack of modern tools like molecular markers that are very useful for germplasm enhancement and improvement etc. Therefore, the present study was going: i) to assess genetic variability of early and medium maturing lowland adapted landrace and improved sorghum genotypes. ii) to evaluate the performance of sorghum genotypes and identify promising lines for the dry lowland environments of Ethiopia.

MATERIALS AND METHODS

Description of Experimental Area

The field work was conducted at two locations i.e. Mieso research sub-station which is located 9°14′N, 40°45′E, and 1394 m.a.s.l.and Sheraro research sub-station which lies at 14.4N, 37.9 E, 1179 m.a.s.l. The area is characterized by having a soil type of vertisol with a pH of 6-7 for both areas. Mieso is a town located in the eastern Hararghe Zone of Oromia Region and Sheraro is a town found in the west Tigray administrative zone of Tigray region. Both Mieso and Sheraro are among the potential sorghum producing dry lowland areas in the country.

Experimental Materials used for the Study

The materials used for the present study comprises a total of 110 sorghum genotypes selected for morphological characterization and variability analyses (Table 1). The genotypes were early and medium maturing sorghum genotypes collected locally, developed through pedigree breeding and introduced from exotic sources.

Experimental Design and crop management

One hundred ten sorghum genotypes were characterized at two locations in the 2016 cropping season. The experiment was laid out in alpha lattice design with two replications. Each plot has two rows of 5m long with spacing of 0.75m and 0.15m inter and intra rows, respectively. Seed rates of 10kg/ha was used in drill and planting was done at the onset of the main rainy season at the respective testing environment. Fertilizer was applied at the rates 100kg/ha Urea and 100kg/ha DAP. Split application was used for Urea half of it at planting time and the remaining half at knee stage period. In addition to hand weeding and land preparation all other cultural practices were applied as per the recommendation for sorghum production at respective areas. The genotypes were phenotyped and the detail agronomic and morphological data were collected from both experimental sites.

Data Analysis and Procedures

SAS computer software [15] was employed to analyze different data structures collected from the two locations. Analysis of variance was performed for yield and other quantitative characters after the homogeneity test. Homogeneity of the error among the two locations were examined using Bartlett's test for each of the studied quantitative characters. For mean comparison, the means were separated using Duncan Multiple Range Test (DMRT) at 0.05 level of significant, according to the procedure described by Duncan [6] and Gomez and Gomez [9]. The combined analysis of variance was done for all traits, using the above mentioned software.

Analysis of variance was calculated using the following model:

$$Y_{ijk}=\mu+R_i+B_{ij}+T_k+e_{ijk}$$

Where, μ = General mean, R_i= (fixed) effect of Replicate i, B_{ij}= (random) effect of Block j within Replicate i, T_k= Effect of treatment k (this could be random or fixed).

Estimation of coefficients of variation

The phenotypic and genotypic variance and coefficients of variations were estimated as per the procedure suggested by Burton and De Vane [4] as follows:

Genotypic variance ($\sigma^2 g$) =Variation of the traits due to their genetic make-up.

$$\sigma^2 g = \frac{MSg - MS e}{r}$$

Table 1. List of sorghum genotypes used for morpho-agronomic characterization

No.	Genotypes	No.	Genotypes	No.	Genotypes	No.	Genotypes
1	Dekeba	29	IESV 23010DL	57	ETSL 100349	85	Yeju
2	Melkam	30	IESV 92045DL	58	ETSL 100714	86	ETSL 101701
3	Teshale	31	SILA	59	ETSL 101123	87	97 MW 6141
4	Meko	32	ETSL 101859	60	ETSL 101308	88	ETSL 100629
5	Gambella1107	33	ETSL 100318	61	ETSL 100459	89	PGRC/E 69475
6	2001 MS 7015	34	M204	62	ETSL 100549	90	03MW6058
7	ETSL 101846	35	99MW4023	63	ETSL 100540	91	04MW6043
8	Hormat	36	99MW4043	64	ETSL 100542	92	PGRC/E # 69447
9	ETSL 100279	37	01MS7013	65	ETSL 100664	93	PGRC/E 69391
10	ETSL 101867	38	01MS7033	66	ETSL 100636	94	PGRC/E 222885
11	ICSR 14	39	IESV 92168-DC	67	ETSL 100645	95	97 MW 6130
12	ICSR 50	40	03MW6049	68	ETSL 100583	96	No 30
13	S35	41	99MI5081	69	ETSL 101573	97	NTJ2
14	ICSTG 2372	42	PDL984931	70	ETSL 101492	98	Gobiye
15	ETSL 101862	43	ETSL 100122	71	Raya	99	Birmash
16	ETSL 101845	44	ETSL 100123	72	ETSL 101500	100	IESV 91104-DL
17	ETSL 101853	45	ETSL 100129	73	ETSL 101576	101	2002 BK 7042
18	IS 38399	46	ETSL 100132	74	ETSL 100872	102	97 MW 6113
19	IESV 92084-DL	47	ETSL 100133	75	ETSL 101565	103	No 253
20	05MW6028	48	ETSL 100134	76	ETSL 100354	104	Zengada-2
21	Wad Ahmed	49	ETSL 100144	77	ETSL 100346	105	Rufe
22	AG8	50	ETSL 100145	78	ETSL 100683	106	Tetron
23	Bashair	51	ETSL 100875	79	ETSL 100684	107	No 53
24	ICSR 56	52	ETSL 101293	80	ETSL 100666	108	2002 MW 6016
25	ICSR 93034	53	ETSL 100365	81	ETSL 100661	109	2003 MW 6120
26	ICSV 96143	54	ETSL 100351	82	04 MW 6043	110	97 MW 6128
27	ICSV 93041	55	ETSL 100352	83	ETSL 100638		
28	IESV 23005DL	56	ETSL 100355	84	ETSL 101507		

Where: MS_g = mean square due to genotypes,
MS_e = mean square due to error
r = the number of replication

Phenotypic Coefficient of variation(PCV),

$$PCV = \frac{\sqrt{\delta^2 p}}{\bar{x}} x100$$

Genotypic coefficient of variation(GCV),

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{x}} x100$$

Where, $\delta^2 g$ = Genotypic variance
$\delta^2 P$ = Phenotypic variance
$\bar{x}$ = Population mean of the character being evaluated

Estimation of heritability in broad-sense

Heritability in the broad sense for quantitative characters was computed using the formula suggested by Falconer [8]:

$$H = \frac{\delta^2 g}{\delta^2 p} x100$$

Where, H= heritability in the broad sense.

$\left(\delta^{2} g\right)$ = Genotypic variance and

$\left(\delta^{2} p\right)$ = Phenotypic variance.

The genetic advance (GA) was calculated by the following formula [1]:

$$GA = K * \delta_{P} * H$$

Where, GA = expected genetic advance, δ_{p} =phenotypic standard deviation on mean basis, H= Heritability in broad sense, K =selection differential (where k = 2.06 at 5% selection intensity)

Genetic advance (as percent of mean) (GA) was computed by the following formula:

$$GA = \frac{GA}{\overline{X}} * 100$$

Where, $\overline{x}$ =population mean of the quantitative character, GA =genetic advance as percent of mean.

RESULTS AND DISCUSSION

Agronomic Traits of lowland adapted sorghum genotypes

The genetic diversity in the material used in a breeding programme is very important. In the present study results from combined analysis of variance over the two locations revealed that mean squares due to genotypes as well as location and genotypes x location interaction for almost all traits were highly significant ($P \leq 0.01$) i.e. for days to flowering, days to maturity, grain yield, panicle weight, hundred grain weight, panicle length, plant height and disease score in both locations (Table 2). These results are in conformity with findings of Mohammad *et al.* [13] who reported significant differences among genotypes of sorghum for economic yield, hundred grain weight and plant height. There were highly significant differences among genotypes in the means of two locations for all nine traits except number of panicles per plot. The significant mean squares due to genotypes indicated the existence of variation among the genotypes, which could be exploited for the improvement of respective traits.

All the genotypes displayed considerable amount of differences in their mean performance with respect to all the traits studied. Differences among the treatments in respect of all the characters studied were significant at 5 % and 1% level indicating the presence of sufficient amount of variability of these characters which provides ample scope for selection of superior and desirable genotypes for plant breeder for further genetic improvement. Kumar and Singh [11], Prabhakar[14] and Arunkumar *et al.*, [2] also observed the similar results. Table 3 showed the mean performance of the studied genotypes over two locations (Meiso and Sheraro). The highest grain yield (36.96 q ha-1) was observed for the ETSL 100459 followed by ETSL 101701(36.89 q ha-1), ETSL 100365 (36.85 q ha-1) and Teshale (35.58 q ha-1).Based on the results of the means of the two locations the accessions exhibited good variability in all the quantitative traits: the days to 50% flowering (66.25-82.75 days), days to maturity (106.75-124.75 days), plant height (130.25-275.2 cm), number of panicle per plot (24.5-70.5), panicle length (18.66-37.06 cm), panicle weight (800-2300gm), hundred grain weight 3.02-5.17gm), grain yield (10.38-36.95 q), showed wider range (Table 2).

Analysis of variance showed significant differences among sorghum genotypes for all nine morpho-agronomic traits at each location (Table 2). Moderate variability exists among the genotypes as was revealed by minimum and maximum values. A large proportion of sorghum genotypes gave reasonable yield and had earlier maturity at Sheraro than at Meiso. On average, the genotypes yielded about 13% higher and 10 days earlier in flowering at Sheraro compared to Meiso.

As shown in Table 4 some of the accessions identified superior for the different morphological characters are S35(106.75), ETSL 101507(107.5), Meko (107.75), ETSL 100351(109), ETSL 100346(109) and ETSL 101867(109.5) were for earliness, ETSL 100540 (275.2), ETSL 100349 (271.75), ETSL 101492 (269.9), ETSL 101293 (266.9) and Tetron (256.6) for plant height, ETSL 100346 (70.7), ETSL 100145(68), ETSL 101867(67), 01MS7033(67) and ETSL 100459 (67) for number of heads per plot, ETSL 100872(30.77), ETSL 101507(30.93), ETSL 100123(31.13), ETSL 100129(31.45) and ETSL 101492(37.07) for panicle length, Bashair (2250), ETSL 100122(2250), ETSL 100636(2250), ICSR 14(2300) and ETSL 100145(2300) for panicle weight, ETSL 100540(5.18), ICSR 93034(4.75), ETSL 100346(4.4), ETSL 100123(4.33) and ETSL 100129(4.33) for hundred grain weight, ETSL 100459(36.96), ETSL 101701(36.89), ETSL 100365(36.85), Teshale (35.58) and ETSL 100133(34) for grain yield (Table 4). Based on the results at both the locations, that there is great scope for improvement those plant traits by direct selection.

Estimation of broad sense-heritability of lowland adapted sorghum genotypes

An assessment of heritable and non-heritable

Table 2. Combined analysis of variance for nine morpho-agronomic traits of sorghum genotypes evaluated at Meiso and Sheraro, 2016

Traits	Mean squares			
	Genotype (df=109)	Location (df=1)	GxL (df=109)	Error (df=218)
Days to flowering	38.47**	102.1*	32.97*	24.75
Days to maturity	34.26**	4429**	21.62**	13.7
Plant height	3871**	276161**	3123**	2075
Number of panicles/plot	273^{ns}	6277.8**	281^{ns}	237
Panicle length	42.27**	190**	29.45**	15.88
Panicle weight	391219**	12022^{ns}	366839*	190610
Hundred grain weight	0.469**	950**	0.41*	0.21
Disease score	0.538**	8.18**	0.51*	0.324
Grain yield	128.76**	1056.85**	139.79**	123.8

*and ** = Significance and highly significance, respectively, ns= non- significance

Table 3. Mean performance of sorghum genotypes for nine morpho-agronomic traits evaluated at Meiso and Sheraro, 2016

Genotypes	Traits								
	DTF	DTM	PHT	NPPP	PAL	PAW	HGW	DS	YLD
1	74.00	114.50	198.80	66.25	29.50	1900.00	3.03	1.50	26.14
2	74.75	112.00	218.05	54.25	28.38	1800.00	3.80	1.25	23.58
3	74.75	113.00	240.10	61.25	25.35	1950.00	3.45	1.75	35.58
4	66.75	107.75	193.20	60.25	22.45	1700.00	4.00	1.25	27.40
5	76.50	115.25	179.95	64.25	18.95	2200.00	3.68	1.50	28.12
6	77.50	117.00	176.05	60.50	18.67	1700.00	3.90	1.00	24.37
7	74.75	111.00	198.35	51.50	27.03	1650.00	3.63	2.25	20.76
8	73.50	115.00	160.20	62.75	26.10	1850.00	3.63	1.25	33.94
9	71.50	110.00	215.10	56.50	27.40	1600.00	3.55	1.50	20.23
10	68.75	109.50	188.15	67.00	25.10	1650.00	3.85	1.25	19.95
11	72.25	111.50	206.15	62.50	23.52	2300.00	3.83	1.50	32.19
12	73.25	112.50	137.35	52.50	25.03	1600.00	3.28	1.25	22.01
13	66.25	106.75	150.60	57.75	23.30	1525.00	3.80	1.00	32.00
14	79.25	115.75	178.20	55.50	22.97	1775.00	4.05	1.00	24.82
15	75.00	110.75	188.10	54.00	23.83	1900.00	3.50	1.75	18.06
16	77.25	118.00	160.35	46.50	24.38	1650.00	3.30	1.25	28.59
17	72.50	115.50	241.90	55.00	25.48	1700.00	3.55	2.00	18.93
18	72.75	113.50	181.65	46.00	27.05	1300.00	3.53	1.25	32.72
19	76.50	118.00	244.25	37.25	25.32	1250.00	4.10	1.25	28.29
20	73.25	114.50	194.35	45.00	24.25	1600.00	3.83	1.00	25.66
21	74.25	114.75	196.25	59.25	24.77	1300.00	3.45	2.25	21.54
22	70.75	111.25	212.45	63.00	30.30	2000.00	3.88	1.50	21.32
23	74.25	113.25	176.00	64.25	26.38	2250.00	3.70	1.25	27.46
24	74.50	110.50	188.55	63.75	18.87	1950.00	4.00	1.25	21.91
25	77.25	115.25	202.90	48.00	22.95	2150.00	4.75	1.00	26.72
26	74.75	115.00	209.15	43.00	22.62	1500.00	3.98	1.25	26.62
27	76.25	112.25	247.75	56.00	30.50	1850.00	3.18	2.00	22.24
28	75.00	116.25	170.55	34.25	21.62	1850.00	3.48	1.25	21.52
29	74.25	111.50	180.40	55.25	25.27	1900.00	3.75	1.00	33.39
30	75.50	114.00	191.75	44.75	21.20	1650.00	4.13	1.25	19.55

Table 3. Continues

31	77.75	112.50	159.30	42.75	25.37	1900.00	3.15	1.00	20.48
32	73.50	116.75	210.45	44.00	30.58	2100.00	3.30	1.50	22.15
33	77.75	117.25	224.35	51.50	24.43	1700.00	4.03	1.50	18.62
34	75.50	112.25	146.65	62.25	26.07	1800.00	3.55	1.25	20.81
35	77.50	117.25	156.50	44.50	26.73	1550.00	3.38	1.25	20.03
36	76.50	117.75	155.30	53.25	24.58	1600.00	3.35	1.75	22.43
37	81.50	116.75	166.55	53.50	20.13	2150.00	3.73	1.25	29.61
38	74.00	114.75	225.80	67.25	25.53	2000.00	3.75	2.00	27.74
39	71.25	112.25	182.90	52.75	22.65	1450.00	3.35	1.00	33.13
40	74.00	112.75	191.95	45.00	21.77	1250.00	3.60	1.75	14.09
41	73.50	112.75	175.10	49.25	25.60	1500.00	3.95	1.50	22.19
42	74.00	112.50	177.40	64.00	27.67	2150.00	3.50	1.75	28.93
43	72.75	113.75	200.80	48.75	27.43	2250.00	3.73	1.75	29.32
44	71.75	110.50	206.60	62.75	31.13	2025.00	4.33	2.00	27.70
45	73.50	111.25	244.55	57.50	31.45	2050.00	4.33	2.00	24.05
46	74.00	114.00	159.55	64.75	24.28	1800.00	4.00	2.00	22.01
47	67.75	112.50	180.90	62.00	22.98	2150.00	3.43	1.75	34.00
48	71.75	113.00	157.10	60.25	20.07	1750.00	3.65	1.75	25.91
49	72.50	111.50	255.95	44.50	27.50	1600.00	3.70	1.75	25.56
50	75.75	115.75	223.40	68.25	19.35	2300.00	3.63	2.00	31.79
51	75.00	113.75	208.95	48.25	26.72	1650.00	3.80	1.75	27.06
52	75.50	116.25	266.90	53.00	30.15	1750.00	3.50	1.75	22.07
53	71.75	111.00	232.15	61.50	27.77	1650.00	4.00	1.75	36.85
54	75.00	109.00	204.60	54.25	22.85	1600.00	3.93	1.75	24.50
55	73.50	111.00	184.70	58.25	26.55	1850.00	3.78	1.75	25.94
56	73.00	112.75	210.45	54.00	29.15	1800.00	3.70	1.50	29.49
57	73.50	111.00	271.75	53.25	26.02	2050.00	4.08	1.25	23.31
58	76.50	118.00	224.00	60.75	25.80	1950.00	4.03	1.25	30.42
59	75.00	116.00	174.35	43.50	23.08	2050.00	3.50	1.75	14.05
60	73.75	114.25	211.90	58.00	25.53	1400.00	3.35	2.00	26.70
61	73.50	114.25	172.90	67.25	22.95	2050.00	3.58	2.00	36.96
62	72.00	111.00	181.45	58.50	26.82	1700.00	4.05	2.00	27.00
63	74.75	114.25	275.20	62.00	30.10	2050.00	5.18	2.00	27.81
64	76.75	116.50	254.70	60.25	30.68	1550.00	3.93	2.25	19.76
65	72.50	110.25	186.80	44.50	21.48	1800.00	3.58	1.75	18.54
66	72.50	110.00	190.85	52.75	25.20	2250.00	3.53	2.25	28.80
67	73.00	114.00	173.80	65.75	21.62	1900.00	3.80	1.25	29.94
68	73.75	116.00	222.50	60.50	30.35	1500.00	3.53	1.75	33.32
69	72.25	113.00	175.70	51.50	25.48	1450.00	3.75	2.25	12.20
70	79.00	117.25	269.90	49.75	37.07	1100.00	3.13	1.75	22.29
71	75.50	114.75	174.95	63.50	22.05	2050.00	3.20	1.00	23.19
72	78.25	113.50	227.80	44.75	26.15	1400.00	3.65	1.25	20.71
73	80.50	114.25	192.65	57.75	21.57	2200.00	3.48	1.50	24.78
74	74.00	112.50	246.60	54.25	30.77	800.00	3.25	2.25	21.68
75	70.50	112.75	163.15	52.75	26.93	1300.00	4.15	1.50	31.23
76	70.50	112.75	130.25	63.25	23.12	1950.00	3.50	1.25	22.82
77	73.25	109.00	223.75	70.50	27.27	1550.00	4.40	2.00	28.58
78	72.50	112.25	207.50	55.00	23.56	1850.00	3.98	2.25	16.94

Table 3. Continues

79	76.00	112.75	172.95	56.75	26.15	2050.00	4.20	1.75	27.60
80	76.25	112.75	232.40	53.25	21.32	1800.00	4.15	1.25	26.96
81	73.50	118.00	186.25	45.75	25.07	1950.00	3.90	1.75	19.05
82	78.00	117.75	220.80	53.75	23.30	2050.00	3.90	1.00	33.74
83	79.25	117.50	209.00	45.75	21.98	2000.00	3.90	1.25	23.91
84	76.50	107.50	241.85	46.25	30.93	1700.00	3.55	1.75	14.58
85	71.50	110.75	142.10	60.75	22.78	1700.00	3.60	1.00	23.81
86	74.00	113.00	175.60	62.25	22.55	1950.00	3.45	1.75	36.89
87	76.75	113.25	191.30	57.75	27.37	1600.00	3.20	2.00	22.30
88	71.50	113.50	211.15	60.50	24.30	2100.00	4.03	1.50	33.98
89	76.75	115.50	183.00	52.75	21.50	1800.00	3.83	1.00	32.80
90	71.25	110.00	182.75	52.25	30.37	1700.00	3.80	1.50	26.04
91	71.25	110.25	153.10	41.00	26.83	1500.00	3.55	1.50	26.15
92	74.00	113.25	203.60	57.00	20.05	2050.00	3.25	1.00	29.63
93	75.75	114.50	203.30	51.25	22.10	2050.00	3.20	1.25	28.12
94	78.00	116.75	165.60	46.00	24.25	1400.00	3.88	1.25	27.25
95	72.00	113.25	168.40	53.50	24.10	1300.00	3.50	1.25	26.34
96	82.75	121.25	168.00	24.50	28.57	1350.00	3.35	1.50	10.38
97	74.00	111.50	204.55	55.50	28.00	2100.00	3.88	1.75	27.15
98	73.00	111.50	172.50	55.75	24.70	1600.00	3.85	1.50	18.70
99	77.75	113.75	153.85	62.00	27.82	1350.00	3.50	1.00	20.03
100	75.75	117.50	201.45	46.75	24.07	1850.00	3.25	1.25	13.20
101	82.00	119.75	205.05	50.75	23.57	1050.00	3.60	1.75	20.80
102	79.50	114.00	191.00	43.50	25.58	1500.00	3.50	1.25	18.21
103	76.75	115.75	180.25	48.75	29.13	1750.00	3.60	1.25	24.80
104	77.75	114.75	188.55	48.75	24.80	1750.00	3.60	2.00	27.95
105	71.25	113.75	196.10	52.00	23.27	950.00	3.23	1.25	14.94
106	81.25	119.00	256.60	49.00	27.27	1450.00	4.20	1.25	24.28
107	81.00	118.00	225.25	49.75	27.67	1200.00	3.48	1.25	30.38
108	76.25	115.75	202.80	63.00	28.57	1550.00	4.00	1.75	30.13
109	77.25	115.50	175.00	39.75	29.30	1450.00	3.13	1.50	26.66
110	82.75	124.75	174.10	35.75	23.93	1100.00	3.33	1.00	17.10
Mean	**74.75**	**113.83**	**196.60**	**54.07**	**25.38**	**1736.14**	**3.70**	**1.53**	**25.06**
Min	**66.25**	**106.75**	**130.25**	**24.5**	**18.66**	**800**	**3.02**	**1.00**	**10.38**
Max	**82.75**	**124.75**	**275.2**	**70.5**	**37.06**	**2300**	**5.17**	**2.25**	**36.95**
$LSD_{0.05}$	**6.9**	**5.1**	**63.48**	**21.46**	**5.5**	**608.45**	**0.63**	**0.79**	**15.7**
CV (%)	**6.6**	**3.2**	**23.17**	**28.5**	**15.7**	**25.14**	**12.3**	**37**	**14.4**

DTF= days to flowering, DTM=days to maturity, PHT=plant height, NPPP= number of panicles per plot, PAL=panicle length, PAW=panicle weight, HGW=hundred grain weight, DS=disease score, GYD=grain yield qu/ha

components in the total variability observed is indispensable in adopting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The estimate of GCV and PCV alone is not much helpful in determining the heritable portion. The amount of advance to be expected from selection can be achieved by estimating heritability along with coefficient of variability. Burton also suggested that GCV and heritability estimate would give better information about the efficiency of selection [4] (Table 5).

The efficiency with which genotypic variability can be exploited by selection depends upon heritability of individual traits [3]. Effective selection can be achieved

Table 4. Mean of top five accessions over two locations in the lowland adapted sorghum genotypes

Characteristics	Mean	Five best entries and their pooled mean over two locations
Days to maturity	113.80	S35(106.75), ETSL 101507(107.5), Meko (107.75), ETSL 100351(109), ETSL 100346(109), ETSL 101867(109.5)
Plant height	196.6	ETSL 100540(275.2), ETSL 100349(271.75), ETSL 101492(269.9), ETSL 101293(266.9), Tetron(256.6)
Number of panicles/plot	54.10	ETSL 100346(70.7), ETSL 100145(68), ETSL 101867(67), 01MS7033(67), ETSL 100459(67)
Panicle length	25.37	ETSL 100872(30.77), ETSL 101507(30.93), ETSL 100123(31.13), ETSL 100129(31.45), ETSL 101492(37.07)
Panicle weight	1736	Bashair (2250), ETSL 100122(2250), ETSL 100636(2250), ICSR 14(2300), ETSL 100145(2300)
Hundred grain weight	3.70	ETSL 100540(5.18), ICSR 93034(4.75), ETSL 100346(4.4), ETSL 100123(4.33), ETSL 100129(4.33)
Grain yield	25.06	ETSL 100459(36.96), ETSL 101701(36.89), ETSL 100365(36.85), Teshale (35.58), ETSL 100133(34)

Table 5. Estimates of broad sense heritability (H^2), PCV, GCV, and genetic advance (GA) for nine morpho-agronomic traits of sorghum evaluated at Meiso and Sheraro, 2016

Traits	**Meiso**					**Sheraro**				
	GCV (%)	**PCV (%)**	**H^2**	**GA**	**GA (% of mean)**	**GCV (%)**	**PCV (%)**	**H^2**	**GA**	**GA (% of mean)**
DTF	3.97	7.09	0.31	3.45	4.58	3.16	7.53	0.18	2.03	2.74
DTM	3.08	3.71	0.69	6.18	5.28	1.27	4.22	0.09	0.88	0.79
PHT	21.80	22.62	0.93	74.23	43.27	3.82	28.52	0.02	2.33	1.05
NPPP	18.14	23.95	0.57	14.24	28.31	13.93	31.56	0.19	7.32	12.66
PAL	16.67	19.68	0.72	7.19	29.10	6.34	20.22	0.10	1.06	4.09
PAW	23.27	30.52	0.58	632.10	36.54	10.36	29.98	0.12	128.31	7.37
HGW	19.98	21.99	0.83	0.83	37.39	2.77	12.01	0.05	0.07	1.32
DS	28.41	35.54	0.64	0.65	46.80	9.52	45.28	0.04	0.07	4.13
YLD	7.36	41.22	0.03	0.64	2.70	10.58	44.51	0.06	1.38	5.18

DTF= days to flowering, DTM=days to maturity, PHT=plant height, NPPP= number of panicles per plot, PAL=panicle length, PAW=panicle weight, HGW=hundred grain weight, DS=disease score, GYD=grain yield, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, H^2=broad sense heritability, GA=genetic advance

when heritability estimates are high. In addition, it gives an indication as to how a given trait or agronomic character will respond to selection [8]. In the present study broad sense heritability (H^2) for nine morpho-agronomic traits calculated using 110 sorghum genotypes ranged from 0.03 for grain yield to 0.93 for plant height at Meiso and from 0.02 for plant height to 0.19 for number of panicles per plot at Sheraro (Table 5). Results indicated that most characters were highly heritable at Meiso that showed heritability greater than 0.50, except days to flowering (0.31) and grain yield (0.03). Traits with high heritability (>0.60) at Meiso were days to maturity, plant height, panicle length, hundred grain weight and disease score. The high degree of heritability estimate for most of the traits suggested that the characters are under genotypic control. Similar result was also reported by Warkade*et al.*[16], whereas of all the traits at Sheraro showed low heritability. High heritability is always not an indication of high genetic gain characters which showed high heritability coupled with wider variability would be successfully improved by direct selection. The high heritability doesn't necessarily mean high genetic gain and alone is not sufficient to make improvement through selection. The utility of heritability is increased when it is used to estimate genetic advance [10]. Thus the genetic advance has an added edge over heritability as a guiding factor to breeders in selection programme.

SUMMARY AND CONCLUSIONS

The study was conducted with the overall objective of investigating to assess genetic variability of early and medium maturing lowland adapted landrace and improved sorghum genotypes. Significant differences among the tested genotypes were detected for different traits studied, which indicated that there are some promising inbred lines possessing of most important agronomic traits including yield and earliness, which will be used for future breeding program.

Therefore, some of the accessions identified superior for earliness are S35 (106.75), ETSL101507 (107.5), Meko (107.75), ETSL 100351(109), ETSL 100346(109) and ETSL 101867(109.5) whereas for grain yield are ETSL100459 (36.96), ETSL101701 (36.89), ETSL100365 (36.85), Teshale (35.58) and ETSL100133 (34). In general, information generated from the current study should be used to find best sorghum breeding strategy for developing high yielding and early maturing sorghum lines.

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REFERENCES

[1] Allard, R.W., (1960). Principles of Plant Breeding. John Willey and Sons, New York. 485p.

[2] Arunkumar B. Biradar, B.D and Salimath, P.M. 2004 Genetic variability and character association studies in Rabi sorghum. Karnataka J of Agril. Sci, 17 (3): 471 – 475.

[3] Bilgin, O., Korkut, K. Z., Baser, I. Dalioglu, O. Ozturk, I.T. Kahraman and Balkan, A. (2010) Variation and heritability for some semolina characteristics and grain yield and their relations in Durum Wheat (Triticum Durum Desf.).World Journal of Agriculture Sciences 6(3), 301-308

[4] Burton GW (1952) Quantitative inheritance of grasses. Proc. 6th International Grassland Congress 1: 227-283.

[5] CSA (Central Statistics Agency). (2015). Report on Area and Production of Crops Central Statistics Authority. Central Statistics Agency, Addis Ababa, Ethiopia.

[6] Duncans, D., (1955). Multiple range and Multiple F-tests. Biometrics, 11: 42.

[7] Falconer D.S., (1989). Introduction to quantitative genetics.3rded. Jhon Wiley and Sons, Inc.New York 438P.

[8] Falconer, D.S., Mackay, T.F.C. (1996). Introduction to Quantitative Genetics, 4th ed. Longman Group Ltd.

[9] Gomez, K. A. and Gomez, A. A. (1984). Statistical Procedures for Agricultural Research Second Edition, John Wiley and Sons, New York

[10] Johnson HW, HF Robinson and RE Comstock (1955) Estimate of genetic and environmental variability in soybean. Agro. J. 47: 314-318.

[11] Kumar R and Singh K.R (1986). Genetic variability, heritability and genetic advance in grain sorghum farm Sc: J C.S. Azad Univ., Kanpur, 1:1-2.

[12] Ministry of Agriculture and Rural development (MoARD), Federal Democratic Republic of Ethiopia (2009). Animal and Plant Health Regulatory Directorate, Crop Variety Register Issue No. 12 Addis Ababa, Ethiopia

[13] Muhammed, T., Shahid I. A. and Muhammed, I. (2007). Genetic variability and association for harvest index in sorghum under rain fed conditions. International Journal Agriculture Biology, Vol. 9, No. 3.

[14] Prabhakar(2003). genetic variability and correlation studies in F2 population of Rabi sorghum. J Maha. Agril. Univ., 28 (2): 202 – 203.

[15] SAS Institute, Inc. (2003). SAS proprietary Software. SAS Institute, Inc, CARY, NC, Canada.

[16] Warkad YN, NR Potdukhe, AM Dethe, PA Kahate and RR Kotgire (2008) Genetic variability, heritability and genetic advance for quantitative traits in sorghum germplasm. Agri. Sci. Digest 28(3): 202-205.