Genetic Variability, Heritability and Genetic Advance for Agronomic Traits of Ethiopian Sorghum [*Sorghum bicolor* (L.) Moench] Landraces

Abstract

Sorghum (*Sorghum bicolor* L. Moench) is an important food security crop mainly in semi-arid and tropical parts of the African countries. Even though it is believed to be originated and domesticated in Ethiopia, sorghum production is inhibited by limited number of high yielding varieties. A field experiment was conducted at Assosa and Pawe Agricultural Research Centers during the 2019/20 cropping season with the objective of identifying sorghum landraces and breeding lines with high grain yield, study phenotypic and genotypic variability, heritability and genetic advance for yield and yield contributing traits. Forty two (42) sorghum land races and breeding lines were planted in RCBD design in row column arrangement with two replications. The result of analysis of variance revealed that there is a significant variation among the tested land races and breeding lines for all the evaluated characters. The highest yield of 3297Kg/ha was recorded for AScol19-Krm 124 followed by Ya036/1 with the mean yield of 3146kg/ha while the lowest grain yield of 817kg/ha was recorded for ETSCAs 10002-2-13-1 breeding line.Higher Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation values were scored for grain yield. High estimates of broad sense heritability were found in all plant characters under study. Highest heritability estimates (97.8) were found in grain yield. Values of genetic advance ranged between 21.94 for days to physiological maturity to 1934.46 for grain yield and the genetic gain (of the mean percent) was ranged from 11.48 for days to physiological maturity to 99.41 for grain yield. The greater extent of broad sense heritability together with higher genetic advance in characters studied showed the evidence that these traits were under the control of additive genetic effects which means undertaking selection in these land races and breeding lines should lead to a rapid enhancement of the traits studied.

Key words: Genetic gain, grain yield, selection, sorghum, coefficient of variation

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) locally known as 'Mashilla' in Ethiopia is the second most important dry land crop for semi-arid tropics. It is one of the most important grain crops grown worldwide, with Nigeria, Sudan, Ethiopia, Burkina Faso and Niger leading its production in Africa (FAO, 2016). In developing countries, about two third of sorghum grain produced is used for human consumption (Ejeta, 2005). In Ethiopia the crop is grown entirely by subsistence farmers. The primary purpose of sorghum production in developing country is to meet the need for food, feed, traditional brewing and construction purposes while it is used primarily as animal feed and in sugar, syrup, and molasses industry in developed countries (Dahlberg *et al.*, 2011). In addition to its contribution to food security, sorghum is widely adapted and can be grown in a broad range of environments. One of its strongest traits is its great adaptability to tropical and subtropical areas of the world where water availability and soil conditions are marginal for other grain crops such as maize (ICRISAT, 2009).

Sorghum is considered as one of the most important crops in Ethiopia and especially to the humid lowland and intermediate agro ecology of the country. It is the major stable food crop in the benishangul gumuz region, western and south western oromia region and some parts of the southern Nations and Nationalities of Ethiopia all of which engaged in Mixed farming (agro-pastoralist). In Ethiopia from about 88.52% of crop production distribution contributed by cereal crops, sorghum has the 4th most contributed crop (15.71%) to the production following Maize (28.75%), Teff (17.11%) and Wheat (15.86%) (CSA, 2020). The Benishangul gumuz region is blessed with the ample genetic diversities of sorghum crops and the farmers in the region is primarily depending on sorghum to meet its food demand.

Genetic variability is prerequisite in the existing population for varietal improvement. Loss of genetic variability leading to genetic erosion has led to greater emphasis on germplasm collection and characterization for present and future plant breeding programs (Prasanna, 2010). Ethiopia and Niger have abundant sorghum genetic diversity and are the largest sorghum producing countries in eastern and western Africa, respectively (Tesfaye *et al.,* 2008). Knowing the genetic diversity of a crop usually helps the breeder in choosing desirable parents for the breeding program and gene introgression from distantly related germplasm. The Ethiopian sorghum landraces are genetically diverse and provides opportunities for improvement through breeding (Bejiga *et al*, 2021).

Genetic variability for agronomic traits is a key component of breeding programs for broadening the gene pool of crops (Ramirez and Kelly, 1998). Morphological traits are conventional tools to analyze the genetic diversity (Prasanna, 2010). Morphological assays generally require neither sophisticated equipment nor preparatory procedures. Genetic enhancement in sorghum yield depends on the degree of genetic variability, heritability and genetic advance in the population as well as the nature of the correlation between yield and its components (Jimmy *et al.,* 2017). Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. The most important function of heritability in genetic studies of quantitative traits is its predictive role to indicate the reliability of phenotypic value as guide to breeding value (Falconer and Mackay, (1996). The extent of variability is measured by genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) which provides information about relative amount of variation in different characters.

A better understanding of the genetic diversity in sorghum would greatly contribute to crop improvement with a view to food security, quality and other important agronomic traits. Therefore, there is a need to evaluate the availability of genetic variability among sorghum accessions and identify the best accessions according to their performance. Dicko *et al.,* (2006) stated that the focus on identifying varieties that meet important traits in agricultural and nutrition necessities from the great diversity of sorghums is crucial to insure food security. With these all important points of genetic variability, this experiment was conducted with the objectives of identifying sorghum landraces and breeding lines with high grain yield, study phenotypic and genotypic variability and analyze the correlation of yield and yield contributing traits.

2. Material and Methods

2.1 The study area

The experiment was conducted at Assosa and Pawe Agricultural research centers during the 2020/21cropping season. Both Assosa Agricultural research center and Pawe Agricultural

Research centers were the federal research centers also serving as the only research centers in the Benishangul gumuz regional state. Assosa Agricultural research center is found at western parts of Ethiopia with $34^0$34’E latitude and $10^0$02’N longitude with the predominantly Nitosol soil type and the altitude of 1553 m.a.s. l. while Pawe Agricultural research center is found at north western part of Ethiopia with is located geographically between 36°20'-36° 32' longitude and 11°12'-11°21' latitude with an altitude of 1120 mean average see level.

2.2 Experimental Materials used for the Study

A total of 46 sorghum genotypes were used for this study which were selected for morphological characterization and variability analyses (Table 1). The genotypes were late and medium maturing sorghum genotypes collected locally and developed through pedigree breeding.

2.3 Experimental Design and crop management

The experiment was laid out in a row/column arrangement 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 both testing sites. Fertilizer was applied at the rates 50kg/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.

Data collection and Statistical analysis

The detail agronomic and morphological data were collected from both experimental sites.

The data were subjected to analysis of variance (ANOVA) suggested by using Genstat version 18 soft ware to assess the difference among the tested landraces. Mean separation was carried out using the least significant difference (LSD).

Table1: List of planting material used in the experiment both at Assosa and Pawe during 2019/20

Entry#	Genotype	Pedigree	Entry#	Genotype	Pedigree
1	ETSCAs 10001-1-1-1	Adukara /Meko	22	AScol19-As-2	AScol19-As-2
2	ETSCAs 10001-1-1-2	Adukara /Meko	23	AScol19-As-8	AScol19-As-8

3	ETSCAs 10001-1-4-1	Adukara /Meko	24	AScol19-Krm122	AScol19-Krm122
4	ETSCAs 10002-2-13-1	Adukara /Meko	25	AScol19-Kok001	AScol19-Kok001
5	ETSCAs 10003-3-32-1	Adukara /Meko	26	Mok 079/1	Mok 079/1
6	ETSCAs 10007-2-61-1	Adukara /Wetetbegunche	27	AScol19-As-6	AScol19-As-6
7	ETSCAs 10015-2-102-1	Assosa-1 /Wetetbegunche	28	AScol19-KA021/1	AScol19-KA021/1
8	ETSCAs 10015-2-103-1	Assosa-1 /Wetetbegunche	29	Ya 036/1	Ya 036/1
9	ETSCAs 10016-1-106-1	Assosa-1 /Melkam	30	Mok 079/2	Mok 079/2
10	ETSCAs 10016-1-106-2	Assosa-1 /Melkam	31	AScol19-JW127	AScol19-JW127
11	ETSCAs 10019-1-110-1	Assosa-1 /Meko	32	AScol19-BS 082/1	AScol19-BS 082/1
12	ETSCAs 10019-1-115-1	Assosa-1 /Meko	33	AScol19-Krm 124	AScol19-Krm 124
13	ETSCAs 10020-2-116-1	Assosa-1 /Meko	34	AScol19-As -14	AScol19-As -14
14	ETSCAs 10020-2-116-2	Assosa-1 /Meko	35	AScol19-AB126	AScol19-AB126
15	ETSCAs 10020-2-116-3	Assosa-1 /Meko	36	AScol19-As-1	AScol19-As-1
16	Y039-1	Y039-1	37	AScol19-SG 001	AScol19-SG 001
17	AScol19-JW128	AScol19-JW128	38	AScol19-As-13	AScol19-As-13
18	AScol19-Krm123	AScol19-Krm123	39	AScol19-SG 002	AScol19-SG 002
19	Assosa-1/1	Assosa-1/1	40	AScol19-As-5	AScol19-As-5
20	AScol19-As-7	AScol19-As-7	41	Assosa-1	Bambasi-9
21	AScol19-Al25	AScol19-Al25	42	Bonsa	97BK6129\85MW4138

Estimation of variance components

Environmental variance, genotypic variance and phenotypic variance was calculated based on formulas suggested by Burton and Devane, (1953).

Environmental variance (δ^2e) = error mean square.

$$\text{Genotypic variance } (\sigma^2 g) = \frac{MSg - MSe}{r}$$

$$\text{Phenotypic variance } (\delta^2 p) = \sigma^2 g + \delta^2 e / r$$

Where: MSg = mean sum square of genotype, MS_e = mean sum square of error and r = number of replications.

Estimation of phenotypic and genotypic coefficients of variation

Phenotypic and genotypic coefficients of variations were estimated using the equations suggested by Burton and Devane (1953).

$$\mathbf{PCV} = \frac{\sqrt{\sigma^2 p}}{x}\ \mathbf{X100}$$

$$\mathbf{GCV} = \frac{\sqrt{\sigma^2 g}}{x}\ \mathbf{X100}$$

Where: $\delta^2 p$= the phenotypic variance, $\delta^2 g$= the genotypic variance, X = the grand mean for the trait considered, Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV).

Estimation of heritability in broad-sense

Heritability in the broad sense for quantitative characters was computed using the formula suggested by (Falconer and Mackay,1996).

$$\mathbf{H^2} = \sigma 2g/\sigma 2p\ X\ 100$$; Where, H^2= heritability in the broad sense, $\delta^2 g$= the genotypic variance and $\delta^2 p$= the phenotypic variance.

Estimation of genetic advance and genetic advance as percent of mean

Genetic advance under selection represents improvement in a genotypic value in the selected population with the assumption that 5% of the genotypes were selected. The genetic advance (GA) for selection intensity (K) at 5% was calculated based on the method suggested by Johnson et al. (1955).

$$GA = K * \sqrt{}\ \delta^2 p * H^2$$

Where, $\delta^2 g$= genotypic variance, δ2p= phenotypic variance, K= Selection differential (K=2.06 at 5% selection intensity).

The genetic advance as percent of the mean (GAM) was calculated using the following equation.

$$\mathbf{GAM} = \frac{GA}{X}\ X\ 100$$

Where, GA=genetic advance and X = the grand mean for the trait considered.

Result and Discussion

Analysis of variance of the agro-morphological traits

The data of five quantitative traits were subjected to the analysis of variance using linear mixed models. The analysis of variance revealed that there were highly significant ($p<0.001$) differences among the tested genotypes for their Days to flowering, Days to Maturity, Plant height and grain yield, and also a significant ($p<0.05$) difference among the genotypes for the weight of their thousand seeds (Table 2). This indicates that there is an ample genetic diversity among the tested genotypes which pave the way for the improvement of sorghum crop in the breeding program. Highly significant differences among the quantitative traits in sorghum accessions under study and the qualitative diversity index values ranged from 31% for panicle shape and compactness to 84% of the glume color were also reported by Shegero *et al., (*2013).

Table2: The combined Analysis of variance (ANOVA) table for the agro-morphological traits of sorghum landraces evaluated at Assosa and Pawe during 2020.

Source of variation	**DF**	**Yld**	**DTF**	**DTM**	**PHT**	**TSW**
Rep	1	7837	64.38	28.34	257	7.46
Genotype	41	1843731**	1105.03**	298.56**	26732**	254.33**
Site	1	234468465**	19200.1**	70561.01**	0	0
Genotype.Site	41	2380107**	155.25**	102.14**	0	0
Residual	83	40479	55.13	38.25	2517	12.58

Crop phenology and plant growth

Days to flowering ranged from 82.2 for a land race AScol19-Krm122 to 155 days for landrace AScol19-As-6 with a mean of 135.62 days. The days to maturity ranged from 169 for variety Bonsa to 199.2 for variety Assosa-1 with a mean of 191.15 days (Table 3). Hailegebrial et al. (2019) stated that in areas where rain fall is limited, early maturity is the most required characters of a crop grown by farmers. But in areas with high and long rain duration this is not a problem. Intermediate and humid low land agro ecology is characterized by long duration and high intensity rain fall which favors the growing of medium to late maturing sorghum varieties. Similar to this, most of the sorghum produced in the study area by the farmers is long maturing land races best suited to the high rain fall and high temperature as well. The high yielding land races flowers and matures lately while the low yielder ones are early maturing genotypes (Table 3). So, Assosa, pawe and similar agro-ecologies of Ethiopia suits the long maturing sorghum varieties while early maturing varieties flower early on the season and devastated by rain as well as by diseases especially grain mold and anthracnose. In contrary to this, the dry lowland agro-ecology favors the growing of early maturing sorghum variety to escape drought and erratic rain fall which may occur at different growth stages. Geremew et al. (2004) also reported that in dry lowland areas, the growing period is short, and highly erratic dry spells may occur at vegetative and grain formation stages of crop growth; therefore, the genotype cultured in these areas should be early maturing.

The Plant height was ranged from 144.7 cm for land race AScol19-Krm123 to 484.7cm for land race AScol19-JW128 with a mean of 350.5cm (Table 3). Farmers prefer landraces with taller plant height because it serves as a fire wood, shelter or housing, fencing material, for animal feed. However, some of the landraces with taller plant height gave lower grain yield than landraces that had medium plant height due to some unwanted traits and has a wild type characters as of loose head structure and susceptible to lodging. Therefore, landraces with reasonable plant height and medium to taller plant heights are better suited in humid lowland and intermediate agro-ecologies. In line with this, Amare et al. (2019) reported that plant biomass is a vital trait to sorghum growing farmers and the taller plant height is preferred primarily.

Yield and Yield component

From the current study, the high yield was recorded for the land race AScol19-Krm 124 with the score of 3297kg^{-ha} followed by land race Ya036/1, Mok079/1 and AScol19-BS 082/1 , which scores 3148 kg^{-ha} , 3055 kg^{-ha} and 3063kg^{-ha} respectively while the lowest grain yield was recorded for genotype ETSCAs 10002-2-13-1 which scores 817kg^{-ha} followed by land races AScol19-AB126 and AScol19-Al25 with the average grain yield score of 826 kg^{-ha} and 968kg^{-ha} (table 3) respectively.

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Table3: Mean values of grain yield and other agronomic traits of 40 sorghum landraces and two standard checks grown at Assosa and Pawe, 2020.

Genotype	YLD	DTF	DTM	PHT	TGW
AScol19-AB126	826	145.8	181.2	416.5	15
AScol19-Al25	968	130.2	185.2	376	15.5
AScol19-As -14	2488	146.8	194.2	398	29.75
AScol19-As-1	2457	151.2	195.8	419.5	38.1
AScol19-As-13	2027	147	197.8	389.7	33.8
AScol19-As-2	2298	145.8	194.5	399.5	32.25
AScol19-As-5	2342	147	198.8	415	34.8

AScol19-As-6	2442	155	198.2	390.5	30.95
AScol19-As-7	2013	149	197.8	418.5	33.05
AScol19-As-8	2245	148	195	311.5	37.35
AScol19-BS 082/1	3063	143.8	198.8	420	34.15
AScol19-JW127	2449	127.5	184.5	429	22.35
AScol19-JW128	1301	136	193.2	484.7	22.45
AScol19-KA021/1	2778	152.8	199	381	30.5
AScol19-Kok001	1773	137.8	197.5	422.5	24.65
AScol19-Krm 124	3297	87.2	167.5	183.9	14.55
AScol19-Krm122	1082	82.2	168.2	202.8	11
AScol19-Krm123	1111	104.5	182.2	144.7	13.6
AScol19-SG 001	2103	153.5	197	366.5	30
AScol19-SG 002	2369	145.8	198.8	320	31.6
Assosa-1	2179	144.5	199.2	268.7	27.4
Assosa-1/1	2409	142.2	192.2	341	27.25
Bonsa	1216	97	169	193.7	13.5
ETSCAs 10001-1-1-1	1283	138	195	217.2	14.5
ETSCAs 10001-1-1-2	1663	140.2	189	303.5	26.85
ETSCAs 10001-1-4-1	1627	138	178.8	219	16.05
ETSCAs 10002-2-13-1	817	123	188.2	309	15
ETSCAs 10003-3-32-1	1408	136.8	190.8	328	13
ETSCAs 10007-2-61-1	2529	132.8	197.5	381	21.2
ETSCAs 10015-2-102-1	1251	115.2	181.8	327.5	14.4
ETSCAs 10015-2-103-1	1127	124.5	182	252.8	15.85
ETSCAs 10016-1-106-1	1116	139.5	188.2	360.7	16.7
ETSCAs 10016-1-106-2	1157	146.5	188.2	370	19
ETSCAs 10019-1-110-1	1370	135.2	197.5	414.5	21.8
ETSCAs 10019-1-115-1	1959	125.7	195.8	386	29.7
ETSCAs 10020-2-116-1	2442	138	198	400	32.4
ETSCAs 10020-2-116-2	1959	139.8	195.8	319	25.1
ETSCAs 10020-2-116-3	1851	137.5	190.8	348.5	22.8
Mok 079/1	3055	140.5	198	404.7	27.45
Mok 079/2	2365	140.2	196.8	470	26.95
Y039-1	2356	139.8	196.2	446.5	35.1
Ya 036/1	3146	144.2	194.2	368.5	29.95
Mean	1946	135.62	191.15	350.5	24.46
LSD	400.2	14.768	12.302	99.79	7.055
CV	10.3	5.5	3.2	14.3	14.5
P-value	<0.001	<0.001	<0.001	<0.001	<0.05

Phenotypic and genotypic variation for agronomic traits

The mean, phenotypic variance, genotypic variance and phenotypic and genotypic coefficient of variation for agronomic traits for the evaluated forty two (42) materials are presented in Table 4. Grain yield, plant height, and thousand grain weight score high phenotypic (δ2P) and genotypic (δ2g) variances. Phenotypic variance (δ2p) and phenotypic coefficient variation (PCV) were higher than their corresponding genotypic variance (δ2g) and genotypic coefficient of variation

(GCV), respectively for all the traits recorded in this study (Table 4). This indicates that the environment has greatly influenced the expression of these characters so that the traits evaluated across the two locations may have different scores resulting due to the environmental influence. Similar result was also reported by Bhagasara et al. (2017) which stated as the role of environment in the expression of characters that are demonstrated when phenotypic coefficient of variation (PCV) was slightly greater than corresponding genotypic coefficient of variation (GCV). Bejiga et al., (2021) also reported that the phenotypic variance (δ2p) and phenotypic coefficient variation (PCV) were higher than their corresponding genotypic variance (δ2g) and genotypic coefficient of variation (GCV) for the trait examined. High estimates of GCV and PCV were observed for grain yield (48.79, 49.34), thousand grain weight (44.94, 46.1) and plant height (31.39, 32.98) where as low GCV and PCV were noticed for days to maturity (5.96, 6.39) and days to 50% flowering (16.89, 17.33) (Table 4).

Phenotypic coefficient variation (PCV) and genotypic coefficient of variance (GCV) with values less than 10% are regarded as low, whereas values greater than 20% are considered as high and those between 10 – 20% are accounted medium (Deshmukh *et al.* 1986). Accordingly, higher PCV and GCV values were scored for grain yield (48.79%, 49.34%), thousand grain weights (44.94% and 46.1%) and plant height (31.39% and 32.98%) respectively while lower PCV value was scored for days to maturity (5.96%) (table 4). GCV measures the variability of any trait due to genetic factors so that higher GCV estimates of the genotypes showed large variation in phenotypic expression than the PCV estimates due to genetic factors (Jimmy *et al.* 2017).

The extent of genetic variability alone does not determine the effectiveness of selection for any trait but also the extent to which the trait will be inherited from one generation to the other generation does. From this study, higher heritability value was recorded for grain yield (97.8), thousand grain weight (95.05), days to 50% flowering (95.01) (Table 4). Robinson *et al.* (1949) stated that broad-sense heritability values greater than 60% are considered as high, 31 to 60% are moderate and 0 to 30% is considered as low. Based on this rating, high broad-sense heritability was recorded for all the traits evaluated in this experiment. Similarly to this findings, Bijiga *et al.*, (2021) also reported high broad sense heritability for grain yield, days to 50% flowering, days to maturity, plant height, head length, head width and kernel weight. According to Bello *et al.* (2007), the characters with high broad-sense heritability would have a positive response to selection. Traits that exhibit higher estimates of broad sense heritability indicated that they are under genetic control so that one can improve the variety through selection. If the broad sense heritability estimates is too low which means the trait has low probability to be inherited, it is difficult to improve the trait through selection. However, high heritability doesn't necessarily mean high genetic gain and by itself is not adequate to make enhancement during selection. Johnson *et al.,* (1955) stated that, the effectiveness of heritability is increased when it is used to estimate genetic advance. Thus the genetic advance has an added periphery over heritability as a guiding factor to breeders in selection program.

Table 4: components of variation for 42 sorghum land races and breeding lines evaluated at Assosa and Pawe, 2020

Character	**Range**	**Mean**	**δ^2p**	**σ^2g**	**δ^2e**	**PCV**	**GCV**
YLD	817-3297	1946	921865.5	901626	40479	49.34	48.79
DTF	82.2-155	135.62	552.515	524.95	55.13	17.33	16.89
DTM	167.5-199.2	191.15	149.28	130.155	38.25	6.39	5.96
PHT	144.7-484.7	350.5	13366	12107.5	2517	32.98	31.39
TGW	11-38.1	24.46	127.165	120.875	12.58	46.1	44.94

YLD= grain yield, DTF= Days to 50% flowering, DTM= Days to physiological maturity, PHT=Plant height, TGW= Thousand grain weight, δ^2p= phenotypic variance, σ^2g=genotypic variance, σ^2e=error variance, PCV= phenotypic coefficient of variation, GCV= Genotypic coefficient of variation

High (> 20) of genetic advance as a percent of mean was recorded for all agronomic traits under the study except days to physiological maturity. The genetic advance as percent of mean ranges from 11.48 for days to physiological maturity to 99.41 for grain yield. According to Johnson *et al.*, (1955) who classified genetic advance as percent of mean (GAM) values < 10% is low, 10 to 20% is moderate and > 20% is high, days to physiological maturity has moderate GAM score while grain yield, days to 50% flowering, plant height and thousand grain weight have high GAM score in this study (Table 5). This result implies that the improvement of these characters can be achieved via selection. Based on this result the improvement of days to physiological maturity in a genotypic value for the new population compared with the base population with one round of selection is not gratifying.

High estimate of heritability (97.8) and high GAM (99.41) was recorded for grain yield and similarly high heritability and GAM were recorded for Days to 50% flowering, plant height, and thousand grain weight (table 5). High heritability and high genetic advance as per cent of mean (GAM) was observed for grain yield of sorghum due to highly additive gene action (Jimmy et al. *(*2017). Similarly, high estimates of heritability are coupled with high genetic advance for grain yield and plant height. This indicates that the traits are highly heritable and one can improve these traits through crossing and selection. Therefore, hybridization and selection on these land races and breeding lines for a preferred trait with high heritability together with higher GCV and GAM were believed to be efficient for creating better sorghum cultivars.

Table 5: Broad sense heritability (H^2), Genetic advance (GA) and Genetic advance as a percent of Mean (GAM) for sorghum land races and breeding lines evaluated at Assosa and Pawe during 2020.

Traits	**H2**	**GA**	**GAM**
YLD	97.80	1934.46	99.41
DTF	95.01	46.01	33.92
DTM	87.19	21.94	11.48
PHT	90.58	215.74	61.55
TGW	95.05	22.08	23.23

YLD= grain yield, DTF= Days to 50% flowering, DTM= Days to physiological maturity, PHT=Plant height, TGW= Thousand grain weight

Summary and Conclusion

This study was conducted to explore the extent of genetic variability that exists among the evaluated land races and breeding lines. The result indicated that there is a wide genetic variation among the tested materials for all the five agronomic traits tested. This genetic variability among the land races and breeding lines enables the Plant breeder to improve the agronomic trait of interest like grain yield through hybridization and selection. At the humid lowland and intermediate agro-ecology especially, Benishangul gumuz region and western parts of Oromia regional state of Ethiopia, farmers prefer a sorghum variety that has a taller but manageable plant height to meet his/her biomass demand, medium to long maturing variety to match with longer rain duration accompanied by high grain yield.

The landrace Mok079/1 flowered and matured in 140.5 and 198 days respectively. It had 404.7cm plant height, 3055 kg/ha grain yield. Based on the scores of these agronomic traits the landrace Mok079/1 has the necessary agronomic distinctiveness to be doing well. As a result, this land race can be used in sorghum breeding programs as a source of genes for these traits. Generally, information generated from the current study should be used to find best sorghum breeding strategy for developing high yielding and medium to long maturing and higher crop stature sorghum lines for the intermediate and humid lowland agro-ecology of Ethiopia.

REFERENCE

Amare S, Adane G, Amare N, Habte N, Taye T, Alemu T, Tamirat B (2019). Performance evaluation of sorghum (*Sorghum bicolor* (L.) Moench) genotypes for grain yield and yield related traits in drought prone areas of Ethiopia. Advances in Crop Science and Technology 7(2):423.

Bello D, Kadams AM, Simon SY, Mashi DS (2007). Studies on genetic variability in cultivated sorghum (*Sorghum bicolor* (L.) Moench) cultivars of Adamawa state Nigeria. American-Eurasian Journal of Agricultural and Environmental Science 2(3):297-302.

Bhagasara VK, Ranwah BR, Meena BL, Rumana K (2017). Estimation of GCV, PCV, heritability and genetic gain for yield and its related components in sorghum [*Sorghum bicolor* (L.) Moench]. International Journal of Current Microbiology and Applied Sciences 6(5):1015-1024.

Burton GW, Devane EM (1953). Estimating heritability from replicated clonal material. Agronomy Journal 45:478-481.

CSA (Central Statistics Agency). (2015). Report onArea and Production of Crops Central Statistics Authority. Central Statistics Agency, Addis Ababa, Ethiopia

Dahlberg, J., Berenji, J., Sikora, V. and Latković. D .2011. Assessing sorghum [Sorghum bicolor (L.) Moench] germplasm for new traits: food, fuels & unique uses. Maydica 56:85-92.

Deshmukh SN, Basu MS, Reddy PS (1986). Genetic variability, character association and path coefficients and quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Science 56:816-821.

Dicko MH, Gruppen H, Traore AS, Voragen AGJ, van Berkel WJH (2006). Sorghum grain as human food in Africa: relevance of content of starch and amylase activities. African Journal of Biotechnology 5(5):384-395.

Ejeta, G. and Grenier, C., 2005. Sorghum and its weedy hybrids. *Crop ferality and volunteerisim. CRC Press, BocaRaton, FL*, pp.123-135.

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

Food and Agriculture Organization Crop Production Statistics (FAOSTAT)(2016). World Sorghum Production and Utilization. FAO, Rome.

Geremew G, Asfaw A, Taye T, Tesfaye T, Ketema B, Michael HS (2004). Development of sorghum varieties and hybrids for dryland areas.

Jimmy ML, Nzuve F, Flourence O, Manyasa E, Muthomi J (2017). Genetic variability, heritability, genetic advance and trait correlations in selected sorghum (*Sorghum bicolor* (L.) Moench) varieties. International Journal of Agronomy and Agricultural Research 11(5):47-56.

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

Johnson HW, Robinson JF, Comstock RE (1955). Estimation of genetic and environmental variability in soya bean. Agronomy Journal 7:314-318.

Prasanna, B.M., 2010. Phenotypic and molecular diversity of maize landraces: characterization and utilization. *The Indian Journal of Genetics and Plant Breeding*, 70:315- 327

Ramirez, P. and Kelly, J.D. 1998. Traits Related to Drought Resistance in Common Bean. *Euphytica*, 99, 127-136.http://dx.doi.org/10.1023/A:1018353200015.

Robinson HF, Comstock RE, Harvey PH (1949). Estimation of heritability and the degree of dominance in corn. Agronomy Journal 41(8):353-359.

Shegro A, Labuschagne MT, Geleta N, Van Biljon A (2013) Assessment of genetic diversity in sorghum using phenotypic markers. Cereal Res Commun. 41:509-518.

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

Tesfaye T, Issoufou K, Cecile G, Allison S, Patricia S, Jeff P, David M, Gurling B, Gebisa E (2008). The potential for crop-to wild gene flow in sorghum in Ethiopia and Niger geographic survey. Crop Science 48:1425-1431.