

## GENETIC VARIABLE ANALYSIS OF ELITE SORGHUM (*SORGHUM BICOLOR* (L.) MOENCH) GENOTYPES UNDER DRY LOWLAND AREA OF ETHIOPIA

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### ABSTRACT

A narrow genetic base and lack of potential drought-resistant sorghum genotypes are the major limiting factors for sorghum yield improvement under moisture-stress conditions. Therefore, an experiment was conducted to quantify the genetic variation available among sorghum genotypes for drought tolerance. A total of 42 sorghum genotypes were evaluated using an alpha lattice experimental design with two replications at Mieso and Kobo during the cropping season of 2019. The combined analyses of variance revealed the presence of substantial genetic variation among sorghum genotypes for all the studied traits. Among the traits with high genotypic coefficients of variation and heritability estimates, plant height, panicle emergence, and panicle yield were linked with higher values of genetic advance as a percentage of the mean, reflecting that the variability of these traits is controlled by additive gene action. High heritability and genetic advancement as percentages of the mean were obtained for plant height (95.63 and 45.39%), 1000-seed weight (77.98 and 23.86%), panicle exertion (74.87 and 51.88%), and panicle yield (65.43 and 37.32%). The maximum grain yield was obtained from hybrids 4x14 (6.32tha<sup>-1</sup>), followed by hybrids 8x15 (5.92tha<sup>-1</sup>), 1x15 (5.88tha<sup>-1</sup>), 13x14 (5.78tha<sup>-1</sup>) and 6x15 (5.57tha<sup>-1</sup>), with an average value of 5.00tha<sup>-1</sup> which was greater than the mean value of the parents and the check (ESH-4). In general, this study revealed genetic variability in sorghum genotypes for different traits under moisture stress conditions, providing an opportunity to select several promising genotypes with key traits related to drought tolerance.

**Keywords:** Sorghum, Genotypic coefficient of variation; Phenotypic coefficient of variation; Drought; Broad-sense heritability; Genetic gain as a percentage of the mean

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### 1. INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most significant cereal crop in the world after maize, rice, wheat, and barley (FAOSTAT, 2020). Sorghum is a predominantly self-pollinated diploid species (Poehlman and Sleper, 1995) with  $2n = 2x = 20$  chromosomes. It has a small genome relative to other cereal crops, which is about 730 Mbp (Paterson et al., 2009). Sorghum is a tropical C<sub>4</sub> crop that belongs to the family Poaceae (Clayton and Renvoize, 1986). It has a short growth period and is relatively drought tolerant, which makes sorghum a preferred cereal in arid and semiarid regions (Funnell-Harris et al., 2013). The wider range of environmental adaptations of grain sorghum has led to the evolution and existence of extensive genetic variation in drought tolerance (Meehl et al., 2007). Ethiopia is the center of origin for sorghum where the distinct agro-ecological zones significantly contributed to the genetic diversity of the crops. Ethiopia is considered as one of the centers of origin and diversity of sorghum due to the presence of wild relatives and diversified forms of the crop in the country (De Wet and Harlan, 1971).

Sorghum is a key food crop in several poor countries around the world and an important crop for reducing food insecurity (Hossain et al., 2022). Furthermore, it is regarded as a vital staple grain crop for over 500 million people in over thirty countries globally (ICRISAT, 2012) and can be used in various food products (Desire et al., 2021). Global sorghum production in 2020 was 29.8 million metric tons with an average productivity of 1.5 tha<sup>-1</sup> (FAOSTAT, 2020). The United States, Nigeria, and Ethiopia are the leading sorghum-producing countries in the world with a total production of 8.6, 6.7, and 5.2 million metric tons respectively (Statista, 2020). In Africa, sorghum is the second most widely cultivated cereal crop, only surpassed by maize (FAOSTAT, 2019). Sorghum plays a crucial role in global food security, serving as a vital food crop that feeds billions of people worldwide; mainly in dry and semi-arid regions where moisture stress is an important impediment (Ejeta, 2005). Sorghum is a multipurpose crop, which is used for food, feed, and fuel (Stamenković et al., 2020).

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Despite its significance, the productivity and production of sorghum is highly limited by number of challenges but drought at the grain-filling stage is the major production constraint. The growth and development of sorghum is affected by drought stress, which ultimately results in a substantial reduction in grain yield (Abreha et al., 2022). For instance, drought stress during the vegetative and reproductive stages reduced the sorghum yield by more than 36% and 55%, respectively (Assefa et al., 2010). The primary constraint impeding sorghum production in Ethiopia is drought, which results in significant yield losses each year. Particularly, the sorghum production in dry regions of Ethiopia is low as compared to the developed countries due to using low yielding long maturing landraces, erratic, insufficient, uneven distribution and sporadic rainfall (Amelework et al., 2016).

Drought is one of the most significant abiotic stresses that reduces plant growth and agricultural productivity globally (Abreha et al., 2021). Drought stress reduces normal crop growth and development and limits production by decreasing cell turgor, stomatal conductance and carbon assimilation (Prasad et al., 2019). To maximize crop yield under changing climate, there is an increasing desire for crops that can withstand harsh weather conditions such as drought. Extreme environmental conditions like drought, high temperatures, and other environmental conditions, including plant diseases, are currently the major issues in agriculture (Nagy et al., 2023). A number of regions across the globe have become economically unsustainable for agriculture production due to environmental difficulties and the consequences of climate change (Candau et al., 2022; Datta et al., 2022). Drought stress impacts all stages of plant development; meanwhile, seed germination, earlier seedling growth and reproductive phases are extremely susceptible and critical (Prasad et al., 2019). Drought stress often causes a reduction in chlorophyll content of sorghum plants and promote leaf senescence (Hou et al., 2021), which results in reduced grain yields (Djanaguiraman et al., 2020).

Sorghum's ability to withstand drought is a complex trait that depends on both genotype and environmental factors. This characteristic exhibit variability across different genotypes owing to variations in morpho-physiological traits, as reported by Borrell et al. (2006). The response of sorghum to drought stress may involve various mechanisms such as morphological, physiological, and anatomical adaptations that aid in the maintenance of optimal water balance and enable drought tolerance even at lower leaf water potential. The impact of drought stress on photosynthesis functions and water relations in various plant species, including sorghum has been extensively studied and documented (Derese et al., 2018). The mechanisms that enable sorghum to tolerate drought conditions comprise various physiological adaptations such as leaf waxiness, leaf rolling, stomatal closure, stay-green, root morphological adjustments, solute accumulation, and osmotic adjustment (Badigannavar et al., 2018) and is therefore considered one of the most resilient crops to drought stress (Solomon et al., 2023).

The presence of large amounts of cultivated and wild sorghum relatives in Ethiopia is an indicator of substantial genetic diversity (Ayana et al., 2000). The development of high yielding and stable varieties for the drought prone area requires a continuous supply of new germplasm as a source of desirable genes. Drought tolerance is a complex trait, controlled by many genes. In addition, various environmental factors affect drought severity, making sorghum breeding for drought tolerance challenging (Abreha et al., 2022). Nevertheless, selecting drought-tolerant sorghum genotypes is crucial for improving the production of sorghum through the application of effective breeding methods. Selecting sorghum landraces that have drought tolerance-related traits such as stay-green and high chlorophyll content is a crucial step in sorghum breeding programs. This is because improving such traits, which have moderate to high heritability (Ochieng et al., 2021) could lead to an increased level of drought tolerance of the crop (Mutava et al., 2011).

Therefore, sufficient sorghum genetic diversity is required for plant breeding programs to assist in the production of new improved cultivars against various stresses and to increase yield (Abrams et al., 2007). Studying the variation in heritable characteristics and biochemical composition of sorghum germplasm is very important for several reasons (Ayana, 2001). Knowledge of the genetic diversity of genetic material is critical for crop improvement (Warburton et al., 2008). Genetic diversity has paramount role in the improvement of crop species through offering adaptation mechanisms to biotic and abiotic environmental stresses and enables change in the genetic composition to cope with changes in the environment. Eventually, plant genetic diversity is playing a key role in the continuation of agricultural development with significant improvement in different morphological and agronomical characteristics. Selection for improvement highly depends on inherent levels of genetic diversity present at the time in the sorghum species, rate of evolutionary response and adaptation to the environmental conditions (Begna, 2021). The level of genetic diversity within a species is commonly used to measure the level of species adaptability and survival in unpredictable environmental conditions (Govindaraj et al., 2015).

Similarly, the level of genetic variation within a population is the basis for germplasm selection in plant breeding and is vital for crop improvement (Mohammadi and Prasanna, 2003). Genetic variability analysis of sorghum genotypes for different agronomical and morphological characteristics is critical for providing an opportunity to select a number of promising genotypes with key traits related to drought tolerance. Generally, sorghum genotypes characterized by early flowering, early maturity, small numbers of leaves per plant, small leaf areas, erect leaf types, large stem diameters, small numbers of productive tillers, high grain yields per unit area and short plant heights are

most suitable for lowland areas with limited rainfall and short growing seasons (Begna, 2021). There were limited number sorghum varieties developed and released in Ethiopia that can highly adapt drought stress and perform well in moisture stress areas. Therefore, developing and using drought tolerant or resistant sorghum varieties is one of the available solutions to cope with the effects of drought (Begna, 2022). Hence, the development of improved sorghum varieties locally adapted to a particular environment is one solution to overcome the challenges of both local adaptation and local farmers' end use requirements. Therefore, the experiment was conducted to quantify the magnitude of variation in the yield and yield-related characteristics of the genetic components of sorghum genotypes.

## 2. MATERIALS AND METHODS

### 2.1. Location of the Experiment

An experiment was conducted across two dry lowland sorghum-growing environments. These were Mieso and Kobo, where sorghum is predominantly produced and drought is a major limiting factor for productivity. These locations represent the eastern and northern sorghum-growing parts of the country. Mieso is located 302 kilometers east of Addis Ababa, the capital city of Ethiopia in the Oromia regional state. Its elevation is 1470 meters above sea level, and it is located at 8°30'N latitude and 39°21' E longitude and has average maximum and minimum temperatures of 14.0°C and 30.01°C, respectively, with an average annual rainfall of 763 mm. The dominant soil type is Vertisols, with a pH of 5.4 (Lemma, 2008). Kobo is located 437 kilometers from Addis Ababa, the capital city of Ethiopia in the Amhara regional state. Its elevation is 1479 m.a.s.l. and is situated at 12°09' N latitude and 39°38' E longitude. The average maximum and minimum temperatures are 15.32°C and 30.24°C, respectively, with an average annual rainfall of 650 mm. The dominant soil type is Vertisols, with a pH of 5.8 (EIAR, 2014).

### 2.2. Genetic Materials

At both locations, the drought resistance of 42 sorghum genotypes was evaluated (Table 1). The genetic materials were obtained from different countries around the world to determine their drought resistance.

### 2.3. Experimental Design and Trial Management

The experiment was conducted using an alpha lattice design at two locations, with two replications per location during the main cropping season of 2019. Each genotype was planted on a plot with two rows 5m in length, and the row and plant spacings were 0.75 and 0.20m, respectively, with a plot area of 7.5m<sup>2</sup>. The experiment included 7 plots per block and 6 blocks per replicate. Three weeks after sowing, the plants were thinned to 0.20m between plants. All the recommended management practices with the recommended fertilizer rates of 100kg ha<sup>-1</sup> NPS were applied to the basal zone at the planting time, whereas 50kg.ha<sup>-1</sup> urea was applied in the form of split application, half of which was applied together with NPS during planting, and the remaining top was dressed before heading at the knee stage. Weeds were controlled manually, and pests were controlled using recommended chemicals.

### 2.4. Data Collection

The data were collected from both plots and plants via random sampling with the use of descriptors for sorghum (IBPGR/ICRISAT, 1993). The important yield and yield component characteristics associated with drought resistance were collected using standard procedures.

**2.4.1. Days to flowering (DTF):** The number of days from emergence until 50% of the plants in a plot flowered halfway down the panicle.

**2.4.2. Days to maturity (DTM):** The number of days from emergence to the date when 95% of the plants matured physiologically.

**2.4.3. Plant height (PH in cm):** The length of the plant from the ground to the panicle tip at physiological maturity.

**2.4.4. Number of leaves per plant:** Total numbers of leaves were taken from 5 plants selected randomly on the main plant in each plot.

**2.4.5. Panicle exertion (PE in cm):** The length between the final (the most top) nodes up to the base of the panicle.

**2.4.6. Stay green score (1-5):** The stay greenness score visually observed at physiological maturity was one for high greenness and five for low greenness.

**2.4.7. Grain yield (GY):** The grain yield was obtained from the total harvest of the plot and then converted to ton ha<sup>1</sup> after adjusting to the optimum seed moisture content.

**Table 1:** Description of the genotypes included in the experiment

Entry	Genotypes	Pedigree	Source
1	TX-623B	TX-623B	2018 MW CAS #8B
2	P-9501B	P-9501B	2018 MW CAS #9B
3	P-9505B	P-9505B	2018 MW CAS #10B
4	P-9534B	P-9534B	2018 MW CAS #14B
5	P-851015B	P-851015B	2018 MW CAS #15B
6	P-850341B	P-850341B	2018 MW CAS #17B
7	B5	B5	2018 MW CAS #21B
8	B6	B6	2018 MW CAS #22B
9	MARC1B	MARC1B	2018 MW CAS #23B
10	MARC2B	MARC2B	2018 MW CAS #24B
11	MARC3B	MARC3B	2018 MW CAS #25B
12	MARC6B	MARC6B	2018 MW CAS #28B
13	P9511B	P9511B	2018 MW CAS #32B
14	Melkam	Melkam	2018 BS Inc.
15	ICSR-14	ICSR-14	2018 BS Inc.
16	ESH-4	ESH-4	2018 BS Inc.
17	TX-623A X ICSR-14	TX-623A X ICSR-14	2018 MW CAS #8A X 34R
18	P-9501A X ICSR-14	P-9501A X ICSR-14	2018 MW CAS #9A X 34R
19	P-9505A X ICSR-14	P-9505A X ICSR-14	2018 MW CAS #10A X 34R
20	P-9534A X ICSR-14	P-9534A X ICSR-14	2018 MW CAS #14A X 34R
21	P-851015A X ICSR -14	P-851015A X ICSR -14	2018 MW CAS #15A X 34R
22	P-850341A X ICSR-14	P-850341A X ICSR-14	2018 MW CAS #17A X 34R
23	A5 X ICSR-14	A5 X ICSR-14	2018 MW CAS #21A X 34R
24	A6 X ICSR-14	A6 X ICSR-14	2018 MW CAS #22A X 34R
25	MARC1A X ICSR-14	MARC1A X ICSR-14	2018 MW CAS #23A X 34R
26	MARC2A X ICSR-14	MARC2A X ICSR-14	2018 MW CAS #24A X 34R
27	MARC3A X ICSR-14	MARC3A X ICSR-14	2018 MW CAS #25A X 34R
28	MARC6A X ICSR-14	MARC6A X ICSR-14	2018 MW CAS #28A X 34R
29	P9511A X ICSR-14	P9511A X ICSR-14	2018 MW CAS #32A X 34R
30	TX-623A X Melkam	TX-623A X Melkam	2018 MW CAS #8A X 33R
31	P-9501A X Melkam	P-9501A X Melkam	2018 MW CAS #9A X 33R
32	P-9505A X Melkam	P-9505A X Melkam	2018 MW CAS #10A X 33R
33	P-9534A X Melkam	P-9534A X Melkam	2018 MW CAS #14A X 33R
34	P-851015A X Melkam	P-851015A X Melkam	2018 MW CAS #15A X 33R
35	P-850341A X Melkam	P-850341A X Melkam	2018 MW CAS #17A X 33R
36	A5 X Melkam	A5 X Melkam	2018 MW CAS #21A X 33R
37	A6 X Melkam	A6 X Melkam	2018 MW CAS #22A X 33R
38	MARC1A X Melkam	MARC1A X Melkam	2018 MW CAS #23A X 33R
39	MARC2A X Melkam	MARC2A X Melkam	2018 MW CAS #24A X 33R
40	MARC3A X Melkam	MARC3A X Melkam	2018 MW CAS #25A X 33R
41	MARC6A X Melkam	MARC6A X Melkam	2018 MW CAS #28A X 33R
42	P9511A X Melkam	P9511A X Melkam	2018 MW CAS 32A X 33R

**2.4.8. Panicle yield (PY in g):** The weight of individual panicles was measured using one representative sample per plot.

**2.4.9. Panicle length (PL in cm):** The average length of five randomly selected plants from the base of the panicle to the tip.

**2.4.10. Panicle width (PW in cm):** The average length of five randomly selected plants at the middle of the panicle.

**2.4.11. Total leaf area (LA in cm<sup>2</sup>):** The area of the flag leaf was computed as (leaf length × leaf width × 0.69) as suggested by (Krishnamurthy et al., 1974).

**2.4.12. Thousand seed weight (TSW in g):** The weight of 1000 grains sampled at 12.5% moisture content was recorded in grams from a single plot.

## 2.5. Statistical Analysis

**2.5.1. Analysis of Variances:** Analysis of variance (ANOVA) for the alpha lattice design was performed using the statistical software version 9.4 (SAS, 2018 version 9.4 T1M3) for both the specific and combined analyses across

locations. Prior to combining the data from the different environments, Bartlett's test for homogeneity of variance was performed and checked by using the F test (the ratio of the largest mean square error to the smallest mean square error was less than 3 or 4) according to Gomez and Gomez (1984), and the test indicated that the error means were homogeneous for all traits and that the data were combined for further analyses. Mean comparisons among genotypes were performed by the least significant difference (LSD) test at the 1% and 5% levels of significance. The model for the alpha lattice design for combined  $P_{ijkz} = \mu + g_i + bk(j)(z) + r_j(z) + lz + (gl)_{iz} + e_{ijkz}$ , where  $P_{ijkz}$  is the phenotypic value of the  $i$ th genotype under the  $j$ th replication at the  $z$ th location and the  $k$ th incomplete block within replication  $j$  and location  $z$ ;  $\mu$  is the grand mean;  $g_i$  is the effect of the  $i$ th genotype;  $bk(j)(z)$  is the effect of incomplete block  $k$  within replication  $j$  and location  $z$ ;  $r_j(z)$  is the effect of replication  $j$  within location  $z$ ;  $lz$  is the effect of location  $z$ ;  $(gl)_{iz}$  is the interaction effect between genotype and location; and  $e_{ijkz}$  is the residual or effect of random error.

**2.5.2. Computation of Genetic Parameters:** The phenotypic and genotypic variation was computed using the following formula as suggested by Singh and Chaudhary (1979):

**2.5.3. Genotypic Variance ( $\delta^2g$ )**

$$\delta^2g = \left( \frac{MSg - MSgl}{r_l} \right), \text{ for more than two locations}$$

Where MSg = mean square of genotype, MSgl = mean square due to genotype by environment interaction,  $l$  = number of locations, and  $r$  = number of replications.

**2.5.4. Genotype-by-environment Interaction Variance ( $\delta^2gl$ )**

$$\delta^2gl = \left( \frac{MSgl - MSe}{r} \right), \text{ Where MSgl = mean square due to genotype} \times \text{environment interaction, and MSe = combined error mean square} = (\delta^2e).$$

**2.5.5. Phenotypic Variance ( $\delta^2p$ )**

$\delta^2p = \delta^2g + (\delta^2gl/l) + (\delta^2e/r_l)$ , where  $\delta^2g$  = genotypic variance,  $\delta^2gl$  = genotypic by environmental variance,  $\delta^2e$  = environmental variance,  $l$  = number of locations and  $r$  = number of replications.

The genotypic and phenotypic coefficients of variation (GCV and PCV) were computed according to the method proposed by Burton and Devane (1953).  $A \leq 10\%$  = low,  $10\% - 20\%$  = moderate, and  $\geq 20\%$  = high.

**2.5.6. Genotypic Coefficient of Variability (GCV)**

$$GCV = \left( \frac{\sqrt{\sigma^2g} \times 100}{\bar{X}} \right), \text{ where GCV=genotypic coefficient of variation, } \delta^2g = \text{genotypic variance, and } \bar{X} = \text{population mean for the trait.}$$

**2.5.7. Phenotypic Coefficient of Variability (PCV)**

$$PCV = \left( \frac{\sqrt{\sigma^2p} \times 100}{\bar{X}} \right), \text{ where PCV=phenotypic coefficient of variation } \sigma^2p = \text{phenotypic variation and } \bar{X} = \text{population mean for the trait.}$$

**2.5.8. Environmental Coefficients of Variation (ECVs)**

$$ECV = \left( \frac{\sqrt{\sigma^2e} \times 100}{\bar{X}} \right), \text{ where } \delta^2e = \text{environmental variance}$$

**2.5.9. Genotype-by-environment Interaction Coefficient of Variation (GECV)**

$$GECV = \left( \frac{\sqrt{\sigma^2gl} \times 100}{\bar{X}} \right), \text{ where } \delta^2gl = \text{genotypic} \times \text{environment variance and } \bar{X} = \text{population mean for the trait considered.}$$

**2.5.10. Broad Sense Heritability ( $H^2$ ):** Broad-sense heritability was computed for each characteristic based on the formula developed by Allard (1999).

$$H^2 = \left( \frac{[\sigma^2g]}{\sigma^2p} \times 100 \right), \text{ where } H^2 = \text{broad-sense heritability, } \sigma^2g = \text{genotypic variance, and } \sigma^2p = \text{phenotypic. Heritability percentage was categorized as low, medium or high as suggested by Robinson et al. (1956) as follows: } < 50\% = \text{low heritability, } 50\text{-}70\% = \text{moderate heritability, and } > 70\% = \text{high.}$$

**2.5.11. Estimation of Genetic Advance:** The genetic advance for each trait was calculated by using the formula Allard (1960).

$$GA = (k \sigma_p * H^2)$$

GAM (as a percentage of the mean =  $\left(\frac{GA \times 100}{\bar{X}}\right)$ , where k = selection differential (k = 2.06 at 5% selection intensity),  $\sigma_p$  = phenotypic standard deviation,  $H^2$  = heritability (broad sense), and  $\bar{X}$  = grand mean.

Genetic advance as a percentage of the mean was classified as low, moderate or high (Johnson et al., 1955) as follows: 0-10% = low, 10-20% = moderate, 20% and above = high

### 3. RESULTS AND DISCUSSION

#### 3.1. Analysis of Variance for Yield and Yield-related Traits

Analyses of variance due to different sources of variations were computed as per the standard procedure of alpha-lattice design for combining the two locations. The analyses of variance revealed significant differences ( $P < 0.01$ ) among the genotypes for all the quantitative characteristics (Table 2). The presence of significant differences among sorghum genotypes for the studied traits ensured that the presence of large genetic variation could be improved through simple selection. This indicated the presence of considerable variation in the genetic materials for these traits, and improvement of the genotypes with these traits is possible with simple selection. Plant breeding primarily depends on the presence of substantial genetic variation to address the maximum genetic yield potential of crops and the exploitation of this variation through effective selection for further improvement. Hence, the obtained results encourage the availability of substantial genetic variation among sorghum genotypes for the studied traits.

**Table 2:** Combined analysis of variance of sorghum genotypes for yield and yield-related traits across locations at Mieso and Kobo in 2018/2019

Traits	MS <sub>L</sub> (DF=1)	MS <sub>G</sub> (DF=41)	MS <sub>GL</sub> (=41)	MS <sub>E</sub> (DF=72)	CV	R <sup>2</sup>
Days to flowering	1080.21**	13.23**	5.51**	2.62	2.29	0.91
Days to maturity	1494.05**	15.10**	13.74**	4.67	1.95	0.89
Plant height	14359.70**	7615.51**	332.80**	70.47	4.43	0.98
Stay green	63.14**	0.78**	0.51 <sup>ns</sup>	0.35	22.15	0.83
Panicle length	117.66**	27.08**	3.80 <sup>ns</sup>	2.99	6.13	0.87
Panicle width	308.34**	3.86**	1.10*	0.65	9.85	0.92
Leaf area	439598.44**	5662.39**	3919.83	2812.38	16.84	0.81
Panicle exertion	388.87**	31.36**	7.47 <sup>ns</sup>	5.31	28.33	0.85
Panicle yield	183467.16**	2206.42**	762.70**	352.03	22.12	0.92
Grain yield	858491.96**	5106.56**	1708.55**	869.54	21.75	0.94
Hundred seed weight	7100.60**	60.41**	13.25**	6.02	9.37	0.96

Keywords: \*\*, \* and ns indicate highly significant ( $P < 0.01$ ), significant ( $P < 0.05$ ) and not significant, respectively; MS<sub>L</sub> = mean square of location, MS<sub>G</sub> = mean square of genotype, MS<sub>GL</sub> = mean square of genotype by location, MS<sub>E</sub> = mean square of error, DF = degree freedom, CV = coefficient of variation and R<sup>2</sup> = R square

#### 3.2. Mean Performance of Sorghum Genotypes for Yield and Yield-related Traits

Based on the mean performance, superior sorghum genotypes were identified for different traits, as indicated in Table 3. Interestingly, the numbers 17 (6.32tha<sup>-1</sup>), 8 (5.92tha<sup>-1</sup>), 1 (5.88tha<sup>-1</sup>), 26 (5.78tha<sup>-1</sup>) and 6 (5.57tha<sup>-1</sup>) were high yielder, whereas the numbers 34 (2.05tha<sup>-1</sup>), 31 (2.13tha<sup>-1</sup>), 32 (2.25tha<sup>-1</sup>), 28 (2.34tha<sup>-1</sup>), and 33 (2.36tha<sup>-1</sup>) were low yielder. Generally, among the tested genotypes, twenty-four genotypes had yields greater than the average yield of the other genotypes (4.29tha<sup>-1</sup>). The average yield performance of the genotypes ranged from 2.05 to 6.32 tha<sup>-1</sup>. In addition to yield performance, considering growth and morphological parameters contributing to yield performance as selection criteria in the development of drought-tolerant genotypes has been suggested (Rosenow et al., 1983; Henzell et al., 1992). Days to flowering and maturity are among the most important attributes that need to be considered when selecting genotypes for drought-affected areas.

In this study, the mean number of days to flowering ranged from 68 days in the early-flowered genotype (35) to 77 days in the late-flowered genotype (31). Similarly, the mean number of days to maturity ranged from 108 to 114 for the same group of genotypes. Both early and late maturation genotypes had the same duration of grain filling. However, variation in grain yield and related yield components was detected among these genotypes, indicating that the variation in the other attributes might be associated with factors other than the duration of grain filling. The top yielder genotypes (17) required 69 days to flower and 108 days to mature, which was close to the average for genotypes, 70 days for flowering and 111 days for maturity. This indicates that the yield potential is not necessarily associated with crop phenology provided that genes for high yield potential are incorporated into the genotypes. The global success in improving sorghum yield by deploying high-yielding early-maturing hybrids also supports this idea.

Similarly, the actual mean values of plant height and leaf area varied among the genotypes. The mean plant height ranged from 107.50 cm to 271 cm, and the leaf area ranged from 220.36 cm<sup>2</sup> to 405.63 cm<sup>2</sup>. Breeding for shorter plant heights was one of the major goals of the sorghum-breeding program for dry lowland areas where drought adversely affects the plants that have prolonged vegetative growth and to make commercial genotypes

suitable for mechanical harvesting. Among the various drought resistance-related traits, leaf area is very relevant because it decreases leaf length and leaf width when drought becomes severe to limit water loss. Generally, sorghum genotypes are characterized by early flowering and early maturity, small numbers of leaves per plant, small leaf areas, erect leaf types (small leaf angles), large stem diameters, small numbers of productive tillers, small leaf areas, high grain yields per unit area and short plant heights are most suitable for lowland areas with limited rainfall and short growing seasons (Farshadfar et al., 2013).

**Table 3:** Estimation of the mean, range and other genetic parameters for yield and yield-related traits across locations at Mieso and Kobo in 2018/2019

Traits	Range			$\sigma^2_g$	$\sigma^2_p$	$\sigma^2_e$	$\sigma^2_{gl}$
	Mean	Minimum	Maximum				
Days to flowering	70.69	67.75	77.00	1.93	3.31	2.62	1.45
Days to maturity	110.58	107.75	114.50	0.34	3.78	4.67	4.54
Plant height	189.38	107.50	271.00	1820.67	1903.88	70.47	131.17
Stay green	2.68	1.25	3.50	0.07	0.20	0.35	0.08
Panicle length	28.20	22.50	33.45	5.82	6.77	2.99	0.41
Panicle width	8.23	6.05	10.10	0.69	0.96	0.65	0.23
Leaf area	314.92	220.36	405.68	435.64	1415.60	2812.38	553.73
Panicle exertion	8.13	0.50	14.40	5.60	7.48	5.31	1.08
Panicle yield	84.81	39.45	126.30	360.93	551.61	352.03	205.34
Grain yield	4.29	2.05	6.32	849.50	1276.64	869.54	419.51
Hundred seed weight	26.18	17.53	34.33	11.79	15.12	6.02	3.62

Key. ( $\delta^2_p$ ) = phenotypic variance, ( $\delta^2_g$ ) = genotypic variance, ( $\delta^2_e$ ) = environmental variance, ( $\delta^2_{gl}$ ) = genotype by environmental variance.

### 3.3. Estimation of Coefficients of Variation

The estimated magnitudes of genotypic and phenotypic coefficients of variation for the measured characteristics are presented in Table 4. The amount of genotypic variation available in a crop species is essential for initiating a breeding program. The estimated phenotypic coefficient of variation for all studied traits ranged from 1.76 for days to maturity to 33.64 for panicle exertion, whereas the genotypic coefficient of variation values ranged from 0.52 for days to maturity to 29.11 for panicle exertion. High values were obtained for both the PCV and GCV for plant height, panicle exertion and panicle yield, and medium values were obtained for panicle width and thousand seed weight, whereas low values were recorded for days to flowering, days to maturity, panicle length and grain yield. The lower PCV and GCV suggested that the traits are susceptible to high environmental influences; hence, there is less opportunity for improvement of these traits through simple selection of the tested genotypes. For traits such as plant height, panicle length, panicle width, panicle exertion, panicle yield and 1000-seed weight, the genotypic variance was greater than the error variance, which indicated that genetic variance is more important and that it is possible to improve these traits through selection.

**Table 4:** Estimation of genetic parameters for major morphological traits across locations at Mieso and Kobo in 2018/2019

Traits	GCV	PCV	ECV	GECV	H <sup>2</sup>	GA	GAM (%)
Days to flowering	1.97	2.57	2.29	1.71	58.31	218.54	3.09
Days to maturity	0.52	1.76	1.95	1.93	8.99	36.00	0.33
Plant height	22.53	23.04	4.43	6.05	95.63	8595.70	45.39
Stay green	9.87	16.69	22.07	10.55	35.00	32.24	12.03
Panicle length	8.55	9.20	6.13	2.27	85.97	460.80	16.34
Panicle width	10.10	11.90	9.80	5.83	71.88	145.08	17.63
Leaf area	6.63	11.95	16.84	7.47	30.77	2384.87	7.57
Panicle exertion	29.11	33.64	28.34	12.78	74.87	421.82	51.88
Panicle yield	22.4	27.69	22.12	16.90	65.43	3165.63	37.32
Grain yield	6.79	8.33	6.87	4.77	66.54	4897.61	11.42
Hundred seed weight	13.12	14.85	9.37	7.27	77.98	624.64	23.86

GCV = genotypic coefficients of variation, PCV = phenotypic coefficients of variation, ECV = environmental coefficients of variation, GECV = genotypic by environmental coefficients of variation, H<sup>2</sup> = heritability, GA = genetic advance and GAM (%) = genetic advance as a percentage of the mean.

The medium to high PCV and GCV values indicated that the variation observed among genotypes for these traits was more due to genetic differences rather than environmental influences. This indicates that simple selection may be effective and that phenotypic expression of these genes is a good indication of genetic potential, as different genotypes can provide materials for a sound improvement program. The higher estimate of PCV than of the corresponding GCV indicated the relative effects of the environment (to some degree) on the expression of the traits.

The genotype by environmental coefficient of variation (GECV) ranged from 1.71 for days to 50% flowering to 16.90 for panicle yield. The highest GECVs were recorded for panicle yield per plant (16.90), panicle exertion (12.78) and stay green (10.55). The environmental coefficients of variation (ECVs) and genotype by environmental coefficients of variation (GECVs) were greater than the genotypic coefficients of variation (GCVs) for days to maturity, stay green and leaf area.

This indicated that the phenotypic expression of these traits, rather than their genetic makeup, is highly influenced by environmental conditions. Hence, improving these traits of interest based on a stability test would be effective because selection for such traits should be environmentally specific. However, days to flowering, plant height (cm), panicle length (cm), panicle width (cm), panicle exertion (cm), grain yield per hectare and 1000-seed weight (g) revealed greater genotypic coefficients of variation (GCVs) than genotypic by environment coefficients of variation (GECVs) and environmental coefficients of variation (ECVs). However, the high GCV recorded alone is not sufficient for the determination of the extent of genetic advance to be expected by selection.

### 3.4. Estimation of Broad-sense Heritability and Genetic Advance

The broad sense heritability ( $H^2$ ) values ranged from 8.99% for days to maturity to 95.63% for plant height, whereas the genetic advance as percent of mean (GAM) values ranged from 0.33% for days to maturity to 51.88% for panicle emergence (Table 4). The heritability values were high for plant height (95.63%), panicle length (85.97%), 1000 seed weight (77.98%), panicle exertion (74.87%), panicle width (71.88%), grain yield per hectare (66.54%) and panicle yield per plant (65.43%), whereas days to 50% flowering (58.31%), stay green (35.00%) and leaf area (30.77%) exhibited moderate heritability. These results indicated that genetic make-up played a major role in the expression of these traits, and the close correspondence between the genotypic and phenotypic traits was ultimately due to less environmental influence on the phenotypic expression of these traits, which is good for crop improvement through simple selection.

Therefore, breeders could select promising genotypes based on the phenotypic expression of these traits. A similar finding was reported by Abraha et al. (2015) on the high heritability recorded for yield and yield-related characteristics. The lowest heritability was observed for days to maturity (8.99%), indicating that this trait does not respond to phenotypic selection. Thus, in the present study, high mean GA% values were recorded for panicle exertion (51.88%), plant height (45.39%), panicle yield per plant (37.32%) and 1000-seed weight (23.86%), and moderate mean GA% values were recorded for panicle width (17.63%), panicle length (16.34%), stay green (12.03%) and grain yield per hectare (11.42%), whereas low mean GA% values were recorded for days to maturity (0.33%), days to flowering (3.09%) and leaf area (7.57%).

A high magnitude of heritability coupled with high genetic advance as a percentage of the mean was obtained for plant height (95.63 and 45.39%), 1000 seed weight (77.98 and 23.86%), panicle exertion (74.87 and 51.88%), and panicle yield (65.43 and 37.32%), whereas high heritability coupled with moderate genetic advance as a percentage of the mean was obtained for panicle length (85.97 and 16.34%) and grain yield (66.54 and 11.42%) in the same order. Moderate heritability with moderate genetic advancement as a percentage of the mean was also observed for the stay green trait. These results indicated that plant height, 1000-seed weight, panicle exertion and panicle yield are controlled by additive gene action. Similar findings were reported by Sharma (2006) and Ranjith et al. (2017) on high heritability coupled with high to moderate genetic advance as a percentage of the mean for 1000-seed weight and plant height, respectively. A moderate magnitude of heritability, along with a low genetic advance as a percentage of the mean, was obtained for days to 50% flowering and leaf area. The studied traits were controlled by nonadditive gene effects, and heterosis breeding can be successfully exploited to improve these characteristics.

## 4. CONCLUSION

Among abiotic factors, drought is the primary cause of crop yield loss, and it is a major problem in Ethiopia, leading to food shortages. However, sorghum is a relatively drought-tolerant crop, but drought is still the major constraint for its production. Therefore, knowledge of the genetic variability of drought-related traits is the key component in selecting genotypes that withstand drought for future breeding programs. This study identified the presence of variation among genotypes with respect to drought-related traits. The considerable variation in the genetic materials implied the possibility of improving the genotypes with simple selection for the studied traits. The highest mean grain yield was obtained from the genotype 4x14 (6.32tha<sup>-1</sup>), followed by the genotypes 8x15 (5.92tha<sup>-1</sup>), 1x15 (5.88tha<sup>-1</sup>), 13x14 (5.78tha<sup>-1</sup>) and 6x15 (5.57tha<sup>-1</sup>).

The estimated phenotypic coefficient of variation for all studied traits ranged from 1.76 for days to maturity to 33.64 for panicle exertion, whereas the genotypic coefficient of variation values ranged from 0.52 for days to maturity to 29.11 for panicle exertion, whereas high heritability with high genetic advance as a percentage of the mean was obtained for plant height (95.63 and 45.39%), 1000 seed weight (77.98 and 23.86%), panicle exertion (74.87 and 51.88%), and panicle yield (65.43 and 37.32%). This indicated that different genetic variability parameters, namely, the genotypic coefficient of variability, phenotypic coefficient of variability, heritability and genetic advance for



yield-attributing traits, are major concerns for crop improvement programs. High heritability and high genetic advance for plant height, 1000-seed weight, panicle exertion and panicle yield traits indicate that these traits are governed by additive gene action and, therefore, provide the most effective conditions for selection.

Generally, the present investigation showed the existence of genetic variation among genotypes with respect to the traits considered, indicating an opportunity to improve sorghum yield through simple selection. The high magnitude of the genotypic coefficient of variation and genetic advancement indicated the existence of a broad genetic base that facilitates improvement through selection. The magnitude of heritability was high for most quantitative traits, which implied a high contribution of genotype to the phenotype, and substantial improvement can be made using standard selection procedures. Therefore, sorghum genotypes could be improved through simple selection and heterosis breeding involving the crossing of different genotypes. The most promising and potential genetic materials were identified based on mean yield performance, genotypic coefficient of variation, heritability and genetic advancement. Hence, traits that had high heritability coupled with high genotypic coefficients of variation in the present study can be improved by conventional breeding through selection breeding. In conclusion, the genotypic coefficients of variation, along with heritability estimates, provide a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. The genotypes 4x14, 4x15, 8x14, 8x15, 11x14 and 11x15 were found to be the most promising potential genetic materials and could be exploited after critical evaluation for their superiority and yield stability across locations over several years.

## REFERENCES

- Abraha, T., Githiri, S.M., Kasili, R., Araia, W., and Nyende, A.B. (2015). Genetic variation among Sorghum (*Sorghum bicolor* L. Moench) landraces from Eritrea under postflowering drought stress conditions. *American Journal of Plant Sciences*, 6(09).
- Abrams, P.A., Fussmann, G.F., and Loreau, M. (2007). Eco-evolutionary dynamics of communities and ecosystems. *Functional Ecology*, 21(3): 465-477.
- Abreha, K. B., Enyew, M., Carlsson, A. S., Vetukuri, R. R., Feyissa, T., Motthaodi, T., & Geleta, M. (2022). Sorghum in dryland: morphological, physiological, and molecular responses of sorghum under drought stress. *Planta*, 255, 1-23.
- Abreha, K. B., Enyew, M., Carlsson, A. S., Vetukuri, R. R., Feyissa, T., Motthaodi, T., Ng'uni, D., & Geleta, M. (2021). Sorghum in dryland: Morphological, physiological, and molecular responses of sorghum under drought stress. *Planta*, 255(1), 20. <https://doi.org/10.1007/s00425-021-03799-7>
- Allard, R.W. (1960). *Principles of Plant Breeding*. John Wiley and Sons, New York. 485.
- Allard, R.W. (1999). *Principles of plant breeding*. John Wiley & Sons.
- Amelework, B. A., Shimelis, H. A., Laing, M. D., Ayele, D. G., Tongoona, P., & Mengistu, F. (2016). Sorghum production systems and constraints, and coping strategies under drought-prone agro-ecologies of Ethiopia. *South African Journal of Plant and Soil*, 33(3), 207-217.
- Assefa, Y., Staggenborg, S. A., & Prasad, V. P. (2010). Grain sorghum water requirement and responses to drought stress: A review. *Crop Management*, 9(1), 1-11.
- Ayana, A. (2001). Genetic diversity in sorghum (*Sorghum bicolor* (L.) Moench) germplasm from Ethiopia and Eritrea. PhD Dissertation, Addis Ababa University.
- Ayana, A., Bekele, E. and Bryngelsson, T. (2000). Genetic variation in wild sorghum (*Sorghum bicolor* ssp. *verticilliflorum* (L.) Moench) germplasm from Ethiopia assessed by random amplified polymorphic DNA. *Hereditas*, 132(3), 249-254.
- Badigannavar, A., Teme, N., de Oliveira, A. C., Li, G., Vaksman, M., Viana, V. E., Ganapathi, T. R., & Sarsu, F. (2018). Physiological, genetic and molecular basis of drought resilience in sorghum [*Sorghum bicolor* (L.) Moench]. *Indian Journal of Plant Physiology*, 23(4), 670-688. <https://doi.org/10.1007/s40502-018-0416-2>
- Begna, T. (2021). Role and economic importance of crop genetic diversity in food security. *International Journal of Agricultural Science and Food Technology*, 7(1), 164-169.
- Begna, T. (2022). Evaluation of Elite Sorghum (*Sorghum Bicolor* (L) Moench) Inbred Lines for Yield and Related Traits under Moisture Stress Areas of Ethiopian. *Advance Crop Science Technology*, 10(502), 2.
- Borrell, A., Jordan, D., & Mullet, J. (2006). Drought adaptation in sorghum. In *Drought adaptation in cereals* (335-399). Haworth Press Inc.
- Burton, G.W. and Devane, E.M. (1953). Estimating heritability in tall fescue (*Festuca circnclinae*) from replicated clonal material. *Agronomy Journal*, 45, 478-481.
- Candau, F., Regnacq, C., & Schlick, J. (2022). Climate change, comparative advantage and the water capability to produce agricultural goods. *World Development*, 158, 105963. <https://doi.org/10.1016/j.worlddev.2022.105963>
- Clayton, W. D., and Renvoize, S.A. (1986). *Genera Gramineae of the World*. Kew Bull. Addit. Ser. X II. Royal Botanic Gardens, Kew, London.
- Datta, P., Behera, B., & Rahut, D. B. (2022). Climate change and indian agriculture: A systematic review of farmers' perception, adaptation, and transformation. *Environmental Challenges*, 8, 100543. <https://doi.org/10.1016/j.envc.2022.100543>
- De Wet, J. M. J., & Harlan, J. R. (1971). The origin and domestication of *Sorghum bicolor*. *Economic Botany*, 25(2), 128-135.
- Dereese, S. A., Shimelis, H., Laing, M., & Mengistu, F. (2018). The impact of drought on sorghum production, and farmer's varietal and trait preferences, in the north eastern Ethiopia: Implications for breeding. *Acta Agriculture Scand Sect B Soil Plant Science*, 68(5), 424-436. <https://doi.org/10.1080/09064710.2017.1418018>

- Desire, M. F., Blessing, M., Elijah, N., Ronald, M., Agather, K., Tapiwa, Z., Florence, M. R., & George, N. (2021). Exploring food fortification potential of neglected legume and oil seed crops for improving food and nutrition security among smallholder farming communities: A systematic review. *Journal of Agriculture and Food Research*, 3, 100117. <https://doi.org/10.1016/j.jafr.2021.100117>
- Djanaguiraman, M., Prasad, P. V., Ciampitti, I. A., & Talwar, H. S. (2020). Impacts of abiotic stresses on sorghum physiology. *Sorghum in the 21st century: Food–Fodder–Feed–Fuel for a rapidly changing world*, 157-188.
- Ejeta, G. (2005). Integrating biotechnology, breeding, and agronomy in the control of the parasitic weed *Striga* spp in sorghum. In the wake of the double helix: from the green revolution to the gene revolution, Bologna, 239-251.
- Ethiopian Institute of Agricultural Research (EIAR) (2014). Ethiopian strategy for sorghum. Country strategy document.
- FAOSTAT (2019). Food and agriculture organization of the United Nations. Rome, Lazio, Italy: FAO. Available at: <https://www.fao.org/faostat/en/#data/QCL>
- FAOSTAT (2020). Food and agriculture organization of the United Nations. Rome, Lazio, Italy: FAO. Available at: <https://www.fao.org/faostat/en/#data/QCL>
- Farshadfar, E., Elyasi, P. and Hasheminasab, H. (2013). Incorporation of agronomic and physiological indicators of drought tolerance in a single integrated selection index for screening drought tolerant landraces of bread wheat genotypes. *International Journal of Agronomy and Plant Production*, 4(12):3314-3325.
- Funnell-Harris, D. L., Prom, L. K., Sattler, S. E., & Pedersen, J. F. (2013). Response of near-isogenic sorghum lines, differing at the P locus for plant color, to grain mold and head smut fungi. *Annals of Applied Biology*, 163(1), 91-101.
- Gomez, K.A. and Gomez, A.A. (1984). Statistical procedures for agricultural research. John Wiley & Sons.
- Govindaraj, M., Vetriventhan, M., & Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics Research International*, 2015.
- Henzell, R.G., Bengman, R.L., Hetcher, D.S., and McCosker, (1992). Relationship between yield and no senescence (stay-green) in some grain sorghum hybrids grown under terminal drought stress, 355-358.
- Hossain, M. S., Islam, M. N., Rahman, M. M., Mostofa, M. G., & Khan, M. A. R. (2022). Sorghum: A prospective crop for climatic vulnerability, food and nutritional security. *Journal of Agriculture and Food Research*, 8, 100300.
- Hou, X., Xue, Q., Jessup, K. E., Zhang, Y., Blaser, B., Stewart, B. A., & Baltensperger, D. D. (2021). Effect of nitrogen supply on stay-green sorghum in differing post-flowering water regimes. *Planta*, 254, 1-11.
- IBPGR and ICRISAT, (1993). Descriptors for sorghum [*Sorghum bicolor* (L.) Moench]. International Board for plant genetic Resources, Rome, Italy; International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India.
- ICRISAT, (2012). ICRISAT annual report 2011. ICRISAT.
- Johnson, H.W., Robinson, H.F., and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans I. *Agronomy Journal*, 47(7): 314-318.
- Krishnamurthy, G.T., Tubis, M., Endow, J.S., Singhi, V., Walsh, C.F. and Bland, W.D. (1974). Clinical comparison of the kinetics of <sup>99m</sup>Tc-labeled polyphosphate and diphosphonate. *Journal of Nuclear Medicine*, 15(10):848-855.
- Lemma, W. (2008). Physicochemical studies of soils of Mieso areas, Eastern Hararghe, Oromia region (Doctoral dissertation, MSc Thesis, School of Graduate Studies of Haramaya University).
- Meehl, G.A., Hibbard, K.A., Cox, P.M. and Friedlingstein, P. (2007). A strategy for climate change stabilization experiments. *Eos, Transactions American Geophysical Union*, 88(20):217-221.
- Mohammadi, S. A., & Prasanna, B. M. (2003). Analysis of genetic diversity in crop plants—salient statistical tools and considerations. *Crop Science*, 43(4), 1235-1248.
- Mutava, R. N., Prasad, P. V. V., Tuinstra, M. R., Kofoid, K. D., & Yu, J. (2011). Characterization of sorghum genotypes for traits related to drought tolerance. *Field Crops Research*, 123(1), 10-18.
- Nagy, R., Muranyi, E., Biron, E., Molnar, P., Szepesi, J., Gyori, Z., Veres, S., Remenyik, J., & Sipos, P. (2023). Assessment of bioactive profile of sorghum brans under the effect of growing conditions and nitrogen fertilization. *Agriculture*, 13(4), 760. <https://doi.org/10.3390/agriculture.13040760>
- Ochieng, G., Ngugi, K., Wamalwa, L. N., Manyasa, E., Muchira, N., Nyamongo, D., & Odeny, D. A. (2021). Novel sources of drought tolerance from landraces and wild sorghum relatives. *Crop Science*, 61(1), 104-118.
- Paterson, A. H., Bowers, J. E., Bruggmann, R., Dubchak, I., Grimwood, J., Gundlach, H., Haberer, G., Hellsten, U., Mitros, T., Poliakov, A., & Schmutz, J. (2009). The sorghum bicolor genome and the diversification of grasses. *Nature*, 457(7229), 551–556. <https://doi.org/10.1038/nature07723>
- Poehlman, J.M. and Sleper, D.A. (1995). *Breeding Field Crops*. 4th ed, Iowa State University Press, Ames, Iowa.
- Prasad, P. V. V., Djanaguiraman, M., Jagadish, S. V. K., & Ciampitti, I. A. (2019). Drought and high temperature stress and traits associated with tolerance. In I. A. Ciampitti & P. V. V. Prasad (Eds.), *Sorghum: A state of the art and future perspectives* (Vol. 58, pp. 245–265). ASA, CSSA, SSSA.
- Ranjith, P., Ghorade, R.B., Kalpande, V.V. and Dange, A.M. (2017). Genetic variability, heritability and genetic advance for grain yield and yield components in sorghum. *International Journal of Farm Sciences*, 7(1):90-93.
- Robinson, H.F., Hanson, C.H. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza I. *Agronomy Journal*, 48(6):268-272.
- Rosenow, D.T., Quisenberry, J.E., Wendt, C.W., Wendt, C.W. and Clark, L.E. (1983). Drought tolerant sorghum and cotton germplasm. *Agriculture Water Management*, 7:207-222.
- SAS Institute Inc. (2018). SAS/STAT users guide. Version 9.4, 4th Ed. Cat, NC.
- Sharma, J.R. (2006). *Statistical and Biometrical Techniques in Plant Breeding*. New Age International New Delhi.
- Singh, R.K. and Chaudary, B. D. (1979). *Hometrical methods in quantitative genetic analysis*. Kalyani Publ., Ludhiana, India.

- Solomon, H., Tadesse, T., Nadew, D., & Girma, F. (2023). Root system architecture analysis of sorghum genotypes and its effect on drought adaptation. *Rhizosphere*, 100772. <https://doi.org/10.1016/j.rhisph.2023.100772>
- Stamenković, O. S., Siliveru, K., Veljkovic, V. B., Bankovic-Ilic, I. B., Tasic, M. B., Ciampitti, I. A., & Prasad, P. V. (2020). Production of biofuels from sorghum. *Renewable and Sustainable Energy Reviews*, 124, 109769.
- Statista (2020). Sorghum production worldwide in 2019/2020, by leading country (in 1,000 metric tons). Hamburg: Statista.
- Warburton, M.L., Reif, J.C., Frisch, M., Bohn, M., Bedoya, C., Xia, X.C., Crossa, J., Franco, J., Hoisington, D., Pixley, K. and Taba, S. (2008). Genetic diversity in CIMMYT nontemperate maize germplasm: landraces open pollinated varieties, and inbred lines. *Crop Science*, 48(2):617-624.