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Mapping genetic gains: Broad-Sense heritability and trait variability in sorghum *[Sorghum bicolor* (L.) Moench] at Arba Minch, South Ethiopia

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Abstract

Genetic variation is vital for the plant breeding program. Eighty-one sorghum genotypes were tested in a simple lattice design at Arba Minch Agricultural Research Center in the 2020and 2021main cropping seasons with the objectives of assessing variability, heritability and genetic advance as a percent of the mean and genetic advance. The analysis of variance revealed that there were statistically significant differences among the genotypes for most of the studied traits. In terms of mean value performance, the genotypes showed noticeable variability in grain yield ranging from 95.6kg/ha to 7793.3kg/ha. The higher range of genotypic coefficient of variation values (GCV) (9.2–39.0) and phenotypic coefficient of variation (PCV) (11.5–39.4) were perceived. Relatively high phenotypic coefficient of variation (PCV) values (>20%) were attained for head length, head diameter, plant height, and grain yield. Similarly, high genotypic coefficient of variation (GCV) values (>20%) were also obtained for head length, height, and grain yield. The higher heritability estimates (> 80%) were realized for plant height and grain yield. Grain yield (GY) (98.20%) and head diameters (HD) (3.40%) were the highest and lowest broad sense heritable (H^2) traits, respectively. The traits with the highest estimates of genotypic coefficient of variation, genetic progress as a percentage of the mean, and broad-sense heritability were GY (98.2%), plant height (81.4%), head length (78.5), days to 90% maturity (66.3) and days to 75% flowering (63.8). Because of their advanced heritable characteristics and high estimates of the genotypic coefficient of variation and genetic advance as a percentage of total genetic variation, these qualities are useful for selective breeding. Therefore, hybridization and selection of these genotypes for desired traits with high H^2 together with higher GCV and GAM (genetic advance as a percent of the mean) will be effective in developing superior sorghum cultivars. Further improvement of these genotypes for desired traits is an important criterion for the sorghum improvement program.

Keywords: Genetic advance; Heritability; Mean; Variability; Sorghum

1. Introduction

Sorghum [*Sorghum bicolor*(L.) Moench], a tropical cereal C4 plant, is the world's most important cereal crop [1]. It is a monocotyledon plant of tropical origin, belonging to the Poaceae family [2]. Sorghum is called a camel of crops due to its high tolerance to water and temperature stress and high photosynthesis efficiency; it is well thought-out and an important plant in arid and semi-arid regions [3]. The grain of sorghum is a major factor in the daily menu of millions of people while the stover is used to feed livestock [4]. Sorghum contributes 16.4% of the world's yearly cereal grain production, making Ethiopia the sixth-largest producer of the crop [5]. Sorghum is one of the most significant cereal crops grown in Ethiopia as a kind of food insurance, particularly in the lowland regions where the climate is characterized by unpredictable drought and irregular rainfall [6]. According to CSA (Central Statistical Agency of Ethiopia) [7], Ethiopia now has a 2.7 tons/ha national average sorghum productivity. When compared to the 3.63 t/ha reported in the USA and Europe, the sorghum grain yield in Africa is typically low (0.95-1.17t/ha) [8]. Sorghum is a native of Ethiopia and exhibits high genetic diversity, as shown by numerous local landrace collections [5, 9]. In semi-

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arid Africa, it is highly suited to a variety of environmental circumstances [10, 11]. It is primarily produced in midland and lowland areas of Ethiopia. Compared to most Ethiopian-grown crops, it performs better in hot and dry environments. Due to its drought tolerance, it is widely grown throughout the country and is the most important cereal crop in lowland areas.

It is crucial to comprehend genetic heterogeneity in the population if we want to develop the right qualities. Grain yield is a crucial and intricate feature that depends on several other variables. In the heterogeneous structure of a plant, most of the features are connected. The quality and extent of genetic variety, heritability, and genetic progress in the population, as well as the nature of the relationship between yield and its constituent parts, all influence the improvement in sorghum. This makes it possible to simultaneously select for a variety of yield-related traits [12]. According to Sharma *et al*. [13], sorghum as a whole has a high level of genetic diversity. A selection can be made for improvement and potential hybridization from a range of alternatives provided by acceptable variability. Information on agricultural trait associations, according to Binodh *et al.* [14], is crucial for efficient crop improvement selection. The interaction of many different elements leads to a plant's phenotype, and the effects of all the individual constituent factors are added together to produce the final yield. A trait's heritability plays a key role in determining how it reacts to selection. Heritability estimates help breeders allocate the resources needed to effectively choose desired traits and to obtain the most genetic benefit with the least amount of time and money [15]. In comparison to individual concerns about the parameters, estimates of heredity with genetic advancements are more reliable and significant [16]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) measure the degree of variability, which provides knowledge about the proportion of variance in various qualities. Due to the existence of some mutuality, it becomes challenging to identify the features that contribute to yield when additional traits are included in a study. Roychowdhury and Tah [17] asserts that GCV and PCV, which offer data on the relative amount of variation in the several examined variables, are used to measure the level of variability.

A higher degree of genetic variety within a species happens, and it is frequently used as a gauge of that species' capacity to adapt to a new environment. The kind and degree of genetic variability, heritability, and genetic progress in the base population affect how much the sorghum yield can be improved. Additionally, knowing the specifics of the relationship between yield and its constituent parts aids in the simultaneous selection of numerous features linked to yield improvement [12]. Regarding the significance of sorghum for ensuring food security in regions susceptible to drought, breeding initiatives in Ethiopia have placed a strong emphasis on the creation of early maturing varieties with sensible yields [11, 18]. Ethiopian Agricultural Research Centers and Universities have been creating and releasing early maturing sorghum varieties for lowland regions over the past fifty years [19, 20]. However, climate changes, diseases, and other factors challenged existing varieties in the production system. Plenty of studies have been done on the genetic diversity of the early maturing sorghum varieties to improve desirable qualities. Current and future climate change and variability direct breeders to estimate the degree and pattern of genetic variability present in the available germplasm. Breeders are also concerned about any potential associates between or among characters. Because there is some degree of dependency, it becomes challenging to identify the characters that contribute to yield when more characters are assessed in the study. The current study set out to calculate the genetic variances, heritability, and estimated genetic advancements in the genotypes of sorghum that were chosen.

2. Materials and Methods

2.1. Planting materials, experimental site, and experimental design

At the Arba Minch Agricultural Research Center in South Ethiopia during the major cropping seasons of 2020 and 2021, eighty-one sorghum genotypes were assessed including a standard check called melkam. The experimental location represents lowland sorghum farming conditions. Tables 1 and 2 contain descriptions of the experimental site and the sorghum genotypes, respectively. The experiment was done using a simple lattice design. Each genotype was planted on a 7.5m^2 plot (5m in length and 1.5m in width), with 0.15m and 0.75m between plants and rows, respectively. Urea (50 kg/ha) and NPS (100 kg/ha) were used as the recommended fertilizer applications. Half of the required Urea and all of the NPS were applied at planting, and the remaining half rate of Urea was top-dressed 40 days later.

Table 1 Topographic and climatic description of the test environment

Environment	Soil type	Altitude (masl)	Average rainfall	Temperature (^{0}C)		Geographical location	
				Min	Max	Latitude (N)	Longitude (E)
Arba Minch	Vertisol	1216	1000.0mm	16.0	37.0	06° 06'	37° 35'

Source: Gamo Zone Agriculture Office, South Ethiopia

Table 2 List of experimental genotypes and their status

S/N	Genotypes	Source	Status	S/N	Genotypes	Source	Status
1	ACC#220261	Melkessa	Accession	41	ETSL100576	Melkessa	Line
2	ACC#220270	Melkessa	Accession	42	IS38254	Melkessa	Line
3	ETSL100127	Melkessa	Line	43	ETSL100678	Melkessa	Line
4	ETSL101845	Melkessa	Line	44	ETSL100134	Melkessa	Line
5	ETSL102880	Melkessa	Line	45	ACC#220279	Melkessa	Accession
6	ETSL100544	Melkessa	Line	46	ACC#235811	Melkessa	Accession
7	ETSL101497	Melkessa	Line	47	ETSL102894	Melkessa	Line
8	ETSL101853	Melkessa	Line	48	ACC#220248	Melkessa	Accession
9	ETSL100120	Melkessa	Line	49	ETSL101074	Melkessa	Line
10	ETSL100661	Melkessa	Line	50	IS38428	Melkessa	Line
11	ACC#220278	Melkessa	Accession	51	ETSL101460	Melkessa	Line
12	ETSL101866	Melkessa	Line	52	ACC#235804	Melkessa	Accession
13	ETSL101843	Melkessa	Line	53	ETSL101492	Melkessa	Line
14	ACC#235807	Melkessa	Accession	54	ETSL100132	Melkessa	Line
15	ACC#220253	Melkessa	Accession	55	ACC#220241	Melkessa	Accession
16	ETSL102883	Melkessa	Line	56	ETSL100640a	Melkessa	Line
17	ETSL1005	Melkessa	Line	57	ACC#2202272	Melkessa	Accession
18	ETSL100920	Melkessa	Line	58	ETSL100066	Melkessa	Line
19	ETSL101846	Melkessa	Line	59	ACC#220247	Melkessa	Accession
20	ETSL101515	Melkessa	Line	60	ACC#211022	Melkessa	Accession
21	ETSL100016	Melkessa	Line	61	IS38313	Melkessa	Line
22	ETSL100875	Melkessa	Line	62	ETSL101123	Melkessa	Line
23	ETSL100666	Melkessa	Line	63	ETSL102882	Melkessa	Line
24	ACC#235810	Melkessa	Accession	64	ACC#235817	Melkessa	Accession
25	ACC#220252	Melkessa	Accession	65	ACC#220254	Melkessa	Accession
26	ETSL102881	Melkessa	Line	66	ETSL102889	Melkessa	Line
27	ETSL100129	Melkessa	Line	67	ETSL101456	Melkessa	Line
28	ETSL101561	Melkessa	Line	68	ETSL100346	Melkessa	Line
29	ETSL101860	Melkessa	Line	69	ACC#28547	Melkessa	Accession
30	ACC#220251	Melkessa	Accession	70	ETSL100683	Melkessa	Line

31	ACC#220255	Melkessa	Accession	71	ETSL101535	Melkessa	Line
32	ETSL100233	Melkessa	Line	72	MELKAM	Melkessa	Standard check
33	ETSL100684	Melkessa	Line	73	ETSL102888	Melkessa	Line
34	IS38341	Melkessa	Line	74	ETSL100311	Melkessa	Line
35	ETSL100859	Melkessa	Line	75	ETSL101510	Melkessa	Line
36	ETSL101855	Melkessa	Line	76	ETSL100352	Melkessa	Line
37	ETSL100640	Melkessa	Line	77	ACC#220274	Melkessa	Accession
38	ACC#220277	Melkessa	Accession	78	ETSL100667	Melkessa	Line
39	ACC#220240	Melkessa	Accession	79	ACC#220259	Melkessa	Accession
40	ETSL102892	Melkessa	Line	80	ACC#220266	Melkessa	Accession
				81	ETSL100973	Melkessa	Line

Source: Melkessa Agricultural Research Center, Ethiopia

2.2. Data collection and statistical analysis

Based on plants and plots, phenotypic data on quantitative parameters were collected. On a plot basis, the days to 75% flowering and the days to 90% maturity were recorded. The plant height, head length and head diameter were measured in cm on five randomly chosen plants per plot. The grain yield per plot was calculated and afterward converted to a hectare. The weight of a thousand seeds was determined by selecting 1000 seeds at random from a plot following threshing.

Genstat 18th edition and R-statistical software were used to compute the analysis of variance for the parameters under investigation. Genetic variance (σ^2g), phenotypic variance (σ^2p), and environmental variance (σ^2e) were used to estimate the coefficients of variation for the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and environmental coefficient of variation (ECV). The phenotypic and genotypic variances were assessed using the methods recommended by Burton and Devane [21].

2.3. Assessment of variance components

The phenotypic, genotypic, and environmental variances were computed according to the formula proposed by Singh and Chaudhury [22] as follows:

Genetic variance $(\sigma^2\mathrm{g}) = \frac{\mathrm{Mse-Mst}}{\mathrm{r}}$; Where, Mse= mean squares of error (environmental variance); Mst= mean squares due to treatment (genotype); r = the number of replications.

Phenotypic variance$(\sigma^2\mathrm{p}) = (\sigma^2\mathrm{g} + \sigma^2\mathrm{e})$; Where, $\sigma^2 e$= environmental variance.

$$\text{Environmental variance}(\sigma^2\mathrm{e}) = \ \mathrm{Mse}$$

Based on the analysis of variance, the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic advance (GA) were valued using the formula by Burton and Devane [21] as follows:

Phenotypic coefficients of variation (PCV) $= \frac{\sqrt{\sigma^2\mathrm{px}}}{\mathrm{x}} \times 100$; Where: σ^2px = phenotypic variance; x = phenotypic trait population means.

Genotypic coefficients of variation (GCV) $= \frac{\sqrt{\sigma^2\mathrm{gx}}}{\mathrm{x}} \times 100$; Where; σ^2gx = genotypic variance; x = phenotypic trait population means.

Genetic advance (GA): The expected genetic advance for the different characters under selection was assessed as advised by Johnson et al. [23].

$\mathrm{GA} = \frac{\mathrm{K}\times\sqrt{\sigma^2\mathrm{p}}\times\sigma^2\mathrm{g}}{\sigma^2\mathrm{p}}$; Where: GA=expected genetic advance; $\sigma^2 p$ = phenotypic variance; $\sigma^2 g$ = genotypic variance; K = the selection differential (K = 2.06 at 5% selection intensity).

$\mathrm{GAM}(\%) = \frac{\mathrm{GA}}{\mathrm{x}} \times 100$; Where, GAM(%)= genetic advance as percent of mean; GA= genetic advance; x= grand mean of character.

$\text{Heritability } (\mathrm{H}^2) = \frac{\sigma^2\mathrm{gx}}{\sigma^2\mathrm{p}} \times 100$; Where, σ^2g = genotypic variance; σ^2p = phenotypic variance; H^2= broad sense heritability.

Evaluation of broad-sense heritability (H^2) and genetic advance as a percent of the mean (GAM) assuming selection intensity of 5% for individual analysis of variance was computed using the formula adopted from Johnson *et al*. [23]. The assessment of broad-sense heritability was classified according to Robinson *et al*. [24] as follows: 0 – 30% = low; 30 – 60% = moderate and > 60% is high and GAM: 0 – 10% = low; 10 – 20% = medium and > 20% is high.

3. Results and Discussion

The differences between the examined features were discerned and valued for a subsequent breeding effort. The majority of sorghum genotypes vary in head length, head diameter, plant height, blooming and maturity dates and grain production. The study's findings showed that the genotypes significantly varied for each trait under investigation. Genetic advance as a percent of the mean (GAM) ranged from 1.7% for head diameter to 146.1% for grain yield and heritability (H^2) ranged from 3.4% for head diameter to 98.2% for grain yield (Table 3 and Table 4). The findings show that the genotypes under test had various potentials for performing variable attributes. Other authors such as Amare *et al*. [25], and Gebregergs and Mekbib [26] also reported a comparable but significantly different genetic variability analysis of sorghum genotypes which is inline with the results of this study.

Genotypic variance (σ^2g), phenotypic variance (σ^2p), environmental variance (σ^2e), broad-sense heritability (H^2), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and GAM for yield and yield contributing traits of the sorghum genotypes are presented in Table 3 and Table 4. Predictable difference components for the recorded qualities revealed that the PCV was larger than the GCV, suggesting that the character's appearance was influenced by the environment. From the current study, GCV and PCV ranged from 0.04 and 0.12 for TSW to 39.4 and 39.0 for GY, respectively (Table 3). Gebregergs and Mekbib [26] also reported the existence of significant broad-based genetic diversity. Higher GCV and PCV values were seen for GY. The conclusion said that if these attributes are taken into account during selection and hybridization, tested genotypes will have an effective chance of improving sorghum for these traits. Amare *et al*. [25], Abraha *et al*. [27]), and Ranjith *et al*. [28] are a few other researchers who reported similar findings with this study. This shows that there is minimal investment required to develop these qualities to increase sorghum improvement because they give a small amount of heritable genetic (additive) component to the following generation. Ranjith *et al*. [28], and Gebregergs and Mekbib [26] also reported low GCV and PCV values for thousand seed weight (TSW) which is inline with the results of this study.

The outcome of the heritability assessment reveals that GY and PH had the highest in terms of heritability in general (98.2 and 81.4, respectively) while HD and TSW had the lowest heritabilities (3.4 and 36.0, respectively) (Table 4). The manifestation of an assured response to sorghum enhancement is represented by the heredity valuation [26]. The findings of other studies, for example, Ranjith *et al*. [28], and Gebregergs and Mekbib [26], reported similar results with the findings of current study.

In addition to strong broad-sense heritability, Johnson *et al*. [23] recommended that high heritability, a greater genotypic coefficient of variation, and genetic advance as a percent of the mean are relevant indicators for the sorghum development program. According to this hypothesis, these qualities are useful for selection to guarantee GY improvement in sorghum. According to the results of the current study, HD (3.4%) and TSW (36.0%) had poor broad sense heritability, while GY (98.2), PH (81.4%), HL (78.6%), DF (63.8%) and DTM (66.3%) had relatively high broad sense heritability. Because non-additive genetic effects on the phenotypic expression of characteristics are involved, it is difficult to assess the success of selection breeding by looking at the broad sense heritability value only. Similar findings in sorghum were reported by previous study [26].

Table 3 Mean, Range, estimates of components of variance, and coefficient of variation of the sorghum genotypes

Traits	Range	Mean	σ^2g	σ^2p	σ^2e	PCV (%)	GCV (%)	ECV (%)
DTF	56-100	71.4	43.3	67.8	24.6	11.5	9.2	7.0
DTM	91.0-144.0	123.0	83.5	125.8	42.4	9.1	7.4	5.3
HD(cm)	11.0-53.0	23.4	1.1	31.5	30.4	24.0	4.4	23.6
HL(cm)	10.0-55.0	26.4	64.5	82.0	17.5	34.3	30.4	15.9
PH(cm)	107.0-489.6	27.1	49.7	60.2	11.6	28.7	25.9	12.4
TSW(g)	1.0-3.0	1.8	19.0	11.4	15.2	0.12	0.04	0.08
GY(kg/ha)	95.6-7793.3	2157.6	71.7	72.4	9.7	39.4	39.0	0.45

σ^2g=genotypic variance; σ^2p= phenotypic variance; σ^2e= environmental variance; GCV=genotypic coefficient of variation; PCV= phenotypic coefficient of variation; ECV= environmental coefficient of variation; DTM=days to 90% maturity; DTF= days to 75% flowering; HD=head diameter; HL=head length; PH=plant height; TSW= 1000 seeds weight; GY= grain yield/ha

Table 4 Broad sense heritability (H^2), genetic advance (GA) and genetic advance as percent of the mean (GAM) of the sorghum genotypes

Traits	Broad-sense heritability (H^2)	Genetic advance (GA)	Genetic Advance as a percent of the mean (GAM)
DTF	63.8	10.8	15.2
DTM	66.3	15.3	12.5
HD	3.4	0.4	1.7
HL	78.6	14.7	55.6
PH	81.4	13.8	48.1
TSW	36.0	0.27	14.2
GY	98.2	23.7	14.1

DTM=days to 90% maturity, DTF= days to 75% flowering, HD=head diameter, HL=head length, PH=plant height, TSW=1000 seeds weight, GY= grain yield/ha

3.1. Genetic advance as a percent of the mean

Genetic advancement was categorized by researchers like Johnson et al. [23] as a percentage of the mean; values between 0 and 10% are considered low, 10 and 20% are considered moderate, and 20% and higher are considered high. GY (146.1), HL (55.6) and PH (48.1) were categorized as features with high GAM as a result. While the potency of the non-additive effect was limited, these qualities were more strongly influenced by the additive genetic effect. The outcome stated sorghum improvement program through a selection of these features is a suitable breeding approach for its advanced judgment of genetic advance as a percentage of the mean. Some researchers, such as Ranjith *et al*. [28], and Gebregergs and Mekbib [26], reported comparable findings. In terms of mean percentages, just one variable, HD (1.7), was categorized as having poor genetic advances.

4. Conclusion and recommendation

The current study's sorghum genotype testing revealed statistically significant variations that indicated the presence of a significant level of inconsistency. With high and moderate genotypic coefficient of variation and phenotypic coefficient of variation values for a trait of concentration for enhancement, it provides a favorable response for the efficacy of selection. The traits with the highest estimates of genotypic coefficient of variation, genetic progress as a percentage of the mean and broad-sense heritability were PH (81.4%), GY (98.2%), DTF (63.8), DTM (66.3) and HL (78.5). Because of their advanced heritable characteristics and high estimates of the genotypic coefficient of variation and genetic advance as a percentage of total genetic variation, these qualities are useful for selective breeding. Plant breeding is facing a challenge to feed the ever-increasing population with diminishing cultivable land. Current plant breeding has achieved some success in this regard. Nevertheless, it has resulted in genetic vulnerability because of the narrow genetic base of cultivated varieties in many crops. Therefore, there is a need for a paradigm shift in plant breeding focusing on diverse genetic resources. The genetic diversity of crop plants is the foundation for the sustainable development of new varieties. So there is a need to characterize the diverse genetic resources using different statistical tools and utilize them in the breeding program. Morphological data in conjunction with molecular data are used for the precise characterization of germplasm resources. With the advent of a high amount of molecular marker technologies, it is possible to characterize a larger number of germplasm with limited time and resources.

Compliance with ethical standards

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Disclosure of conflict of interest

The authors declare that they have no conflict of interest.

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