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Genetic Variability and Trait Heritability among Ethiopian Commercial Durum Wheat (*Triticum turgidum* ssp. durum L.) Varieties in Major Wheat-Producing Areas of Southern Ethiopia

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ABSTRACT

Wheat is one of the most important cereal crops worldwide and plays a vital role in global food security. Durum wheat (*Triticum turgidum* ssp. *durum*) is among the top ten globally cultivated crops and is recognized as a stress-tolerant and ancient cereal. A field experiment was conducted during the 2020 main cropping season at four locations to assess the genetic variability of durum wheat varieties. The primary objective of the study was to estimate heritability, genetic advance, and the extent of genetic variation for grain yield and its associated traits. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Quantitative data were collected on a plant and plot basis for sixteen agronomic and yield-related traits. Individual and combined analyses of variance for eleven traits revealed significant ($P < 0.05$) and highly significant ($P < 0.01$) differences among the tested varieties, indicating the presence of substantial genetic variability. Grain yield performance across the four locations exhibited a wide range of mean variation among varieties. Estimates of genotypic ($\sigma^2 g$) and phenotypic ($\sigma^2 p$) variances demonstrated considerable genetic and phenotypic variability for most traits. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for spike length, biological yield, and grain yield, suggesting that phenotypic expression reliably reflects genotypic performance and that selection based on phenotype would be effective for these traits. High heritability coupled with high genetic advance was recorded for biological yield (59%), spike length (50%), thousand seed weight (35.5%), and number of spikelets per spike (26%), indicating that these traits are predominantly governed by additive gene effects and can be improved through direct selection. Principal component analysis revealed that the first three principal components accounted for 77% of the total phenotypic variation, with PCA1 explaining 41%, PCA2 21%, and PCA3 15%. Traits such as days to heading, grain filling period, spike length, number of spikelets per spike, number of kernels per spike, and biological yield contributed most to PCA1 and played a major role in differentiating low- and high-yielding varieties. Overall, the study confirmed the existence of sufficient genetic variability among the tested durum wheat varieties, indicating substantial opportunities for genetic improvement through selection and further breeding programs.

Key words: Heritability; Genetic variability; Genetic advance; Principal component analysis; Eigenvalue.

1. INTRODUCTION

Durum wheat (*Triticum turgidum* ssp. *durum* L., 2n = 4x = 28) is a monocotyledonous crop belonging to the family Poaceae (Gramineae). It is among the ten most widely cultivated crops globally, with an annual production of approximately 37 million tons (Kabbaj et al., 2017). Ethiopia is a major producer of durum wheat in Sub-Saharan Africa, with a cultivated area of about 0.6 million hectares (Sall et al., 2019; FAOSTAT, 2015). Durum wheat is one of the oldest cultivated crops in Ethiopia and has been grown since ancient times, covering a substantial proportion of arable land. The country is recognized as a center of diversity for durum wheat, with more than 7,000 accessions conserved in the national gene bank, reflecting its high level of genetic diversity (Meles & Hailekiros, 2019; Feldman, 2001).

Genetic variability is the foundation of crop improvement programs, as it determines the potential for effective selection and genetic gain. As reported by Kumar (2013), the presence of genetic variability within a population reflects differences in genetic constitution and provides the basis for genetic improvement through selection. Falconer and Mackay (1996) defined variability as the occurrence of differences among individuals arising from genetic factors, environmental influences, or their interaction. When phenotypic differences are observed among individuals grown under identical environmental conditions, such variation is attributed solely to genetic causes and is referred to as genetic variation. According to Ali et al. (2008), selection for grain yield improvement can be effective only when sufficient genetic variation exists within the breeding material. Genetic variability among individuals within a population is therefore central to plant breeding, as effective management of diversity can lead to sustained genetic gain and buffer crop performance against environmental fluctuations.

Genetic variability within a population can be partitioned into heritable and non-heritable components using genetic parameters such as genotypic and phenotypic variances, genotypic and phenotypic coefficients of variation, heritability, and genetic advance. These parameters provide a scientific basis for selecting superior genotypes from existing populations (Kumar et al., 2013). Falconer and Mackay (1996) outlined three major approaches to assessing variability in breeding populations: (i) the use of simple statistical measures such as range, mean, variance, standard deviation, coefficient of variation, and standard error; (ii) estimation of variance components; and (iii) assessment of genetic diversity. The success of a breeding program largely depends on the magnitude of genetic variability present in the population and the extent to which economically important traits are heritable (Majumder et al., 2008). Therefore, for effective selection in durum wheat, breeders must thoroughly understand the genetic variability and heritability of key agronomic traits (Abinasa et al., 2011).

Estimates of genetic variability combined with information on genetic and environmental effects provide reliable estimates of heritability and expected genetic gain in subsequent generations, expressed as genetic advance (Shukla et al., 2006). Heritability estimates indicate the proportion of phenotypic variation that is genetically controlled and thus transmissible to the next generation (Farshadfar and Estehghari, 2014). In crop improvement, only the genetic component of variation is of practical importance, as it determines the response to selection (Christiansen, 2002). High heritability of a trait indicates greater potential for transmission to subsequent generations (Ajmal et al., 2009). Heritability estimates are often used in conjunction with genetic advance to predict the expected improvement under selection pressure (Shukla et al., 2004). High heritability coupled with high genetic advance provides a clearer indication of the effectiveness of selection and suggests the predominance of additive gene action (Gashaw et al., 2007).

The genetic improvement of crops for both quantitative and qualitative traits requires reliable estimates of heritability to design efficient breeding programs (Akinwale et al., 2011). When heritability approaches 100%, genotypic variance equals phenotypic variance, and phenotypic performance becomes an accurate indicator of genotypic value (Johnson et al., 1955). However, high heritability alone does not guarantee effective genetic improvement; it must be accompanied by high genetic advance. Genetic advance represents the expected improvement in the mean genotypic value of selected individuals over the base population (Allard, 1960). Traits characterized by high heritability and high genetic advance are generally controlled by additive gene effects and can be effectively improved through selection (Mohammadi et al., 2011).

Despite Ethiopia's rich genetic resources of durum wheat, the widespread introduction of improved bread wheat varieties has contributed to the gradual replacement of locally adapted durum wheat landraces. According to Royo et al. (2009), this replacement has resulted in the erosion of genetically diverse, disease-resistant, and locally adapted durum wheat germplasm. Consequently, the production of indigenous durum wheat varieties has been declining, despite their substantial genetic variability and potential for improvement. This genetic diversity represents a valuable opportunity for selection and breeding to enhance durum wheat productivity and adaptability. Therefore, the present study was conducted to estimate heritability, genetic advance, and to evaluate the extent of genetic variability for grain yield and its contributing traits among Ethiopian commercial durum wheat varieties, with the aim of providing useful information for future breeding and genetic improvement programs.

2. MATERIALS AND METHODS

The field experiment was conducted at four distinct areas of Damote gale, Sodo zuria, Tambaro and Lemu districts of Southern Nation Nationalities People Region (SNNPR) in Ethiopia during main cropping season of July, 2020.

Treatments: The Nine Durum Wheat Varieties used for this study were Alemtena, Denbi, Donmatteo, Fetan, Mangudo, Wolde, Ude, Utuba, and Yerer.

Experimental design: The treatments were laid out in a randomized complete block design (RCBD) with three replications. The plot size was 1.2m width and 2.5m length with a gross area of $3m^2$.

Agronomic practice: The seed was drilled in rows spaced 20cm apart with a seed rate of 150kg/ha. The Experimental field has been ploughed, loosened and leveled to have a smooth seed bed for planting. Blended NPSB fertilizer 100kg/ha had been applied consistently to all plots when planting. Urea fertilizer as N source 150kg/ha applied in split where the first half during planting and the remained second half applied 35 days later on planted. Crop management practices such as cultivation, weeding, etc., are carried out during the crop growing period. Based on the objective to see the existence of variation and heritability between varieties different data were scored the plot, and plant bases.

Data collected: The data that scored the plot base were days to heading (HD), days to maturity (MD), grain filling period (GFP), biomass yield per plot (BM), grain yield per plot (GY), thousand seed weight (TSW) and harvest index (HI). Whereas, the parameters measured from plant bases such as, plant height in cm (PH), total number of tiller per plant (TNT), number of productive tillers per plant (NPTP), spike length (SL), number of spilets per spike (SPS), number of Kernels per spike (NKPS), and disease data. The collected data was organized by using Microsoft excel for analysis. Then, before conducting the combined ANOVA, normality of residual variance was checked for each location by grouping the varieties using the Shapro-Wilk (W) model to confirm the correctness of the result. Further confirmation, Bartlett's test was conducted to check the homogeneity of the residual variances across locations.

Data analysis: The collected data were organized using Microsoft Excel prior to statistical analysis. Before conducting combined analysis of variance (ANOVA), the normality of residuals for each location was tested using the Shapiro–Wilk (W) test. Homogeneity of error variances across locations was further examined using Bartlett's test. Analysis of variance was performed separately for each location, followed by combined ANOVA across locations using the General Linear Model (PROC GLM) procedure in SAS version 9.0. Mean separation was carried out using Fisher's Least Significant Difference (LSD) test at the 5% probability level. Variability components were estimated using appropriate statistical formulas, and principal component analysis (PCA) was conducted using Minitab version 17 software.

Variability component estimation: The phenotypic and genotypic variance and coefficient of variation estimated according to the methods suggested by Burton & Devane (1953).

Phenotypic and genotypic variability

Environmental Variance (δ^2e)

$$\delta^2 e = Mse$$

Genotypic Variance (δ^2g)

$$\delta^2 g = \frac{MSg - MSe}{r}$$

Where, r, number of replication; MSg, mean square due to genotypes; MSe, mean square error (environmental variance)

Phenotypic variance (δ^2p)

$$\delta^2 p = \delta^2 g + \delta^2 e$$

Where, δ^2g, genotypic variance; δ^2e, environmental variance (mean square of error). The phenotypic and genotypic coefficient of variation was calculated based on the formula driven by (Burton, 1952).

Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\delta^2 p} * 100}{\mu}$$

Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\delta^2 g} * 100}{\mu}$$

(Deshmukh et al., 1986) Classified PCV and GCV value as low (0 – 10%), moderate (10 – 20%) and high (>20%).

Broad sense heritability (H^2_b)

Broad sense heritability for all scored traits had been calculated by the ratio of genotypic variance to the total variance and expressed in percentage according to the technique suggested by (Falconer and Trudy, 1996).

$$H^2_b = \frac{\delta_g^2}{\delta_p^2} * 100$$

Where, H^2_b, heritability in the broad sense. Heritability values are classified based on percent magnitude scored (<40%) low heritability, value scored from 40 – 59% medium heritability, value scored from 60 -79% moderately high heritable and values greater than 80% regarded as very high heritability traits (Singh, 2001).

Genetic Advance (GA)

The expected genetic advances under selection assuming the selection intensity of 5% of the superior progeny have been estimated by the formula developed by (Allard, 1960).

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

Where, H^2_b, heritability in the broader sense; $\delta 2_P$, phenotypic standard deviation; GA, expected genetic advance; k, the standardized selection differential at 5% selection intensity (k = 2.063). Genetic advance a percent of the mean calculated to compare the extent of predicted advance of different traits under selection by the formula below:

$$GAM = \frac{GA * 100}{\mu}$$

Genetic advance as percent of mean was suggested as low (0 – 10%), moderate (10 – 20%) and high (>20%) as described by (Johnson et al., 1955).

3. RESULTS & DISCUSSION

The analysis of variance (ANOVA) for both individual locations and pooled data revealed significant ($P < 0.05$) and highly significant ($P < 0.01$) differences among the mean values of the evaluated durum wheat varieties. The presence of such significant differences indicates substantial genetic variability among the varieties, suggesting that the tested genotypes are genetically diverse and provide valuable opportunities for breeders to select desirable traits for genetic improvement.

Out of the sixteen agronomic, yield, and disease-related traits evaluated—including days to heading, grain filling period, plant height, spike length, number of spikelets per spike, number of kernels per spike, biomass yield, thousand seed weight, grain yield, harvest index, and yellow rust severity—several traits exhibited significant variation among varietal means. For those traits that showed significant differences in the combined ANOVA, genetic variability parameters, including genotypic variance (Vg), phenotypic variance (Vp), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2_{β}), genetic advance (GA), and genetic advance as a percentage of the mean (GAM), were estimated. In addition, principal component analysis (PCA) was performed to identify the traits that contributed most to the total variation among the durum wheat varieties.

Table 1. The analysis of variance result for the nine durum wheat varieties, the mean of each trait, and the Coefficient of variation

Parameters	DH	GFP	PH	SL	SPS	KPS	BM	TSW	GY	HI	YR	Coefficient of variation
Alemtena	62^{e}	61^{ab}	68.1^{cd}	4.4^{e}	15^{cd}	52.1^{bc}	5.4^{cd}	35.1^{de}	2.4^{c}	45.6^{a}	10^{bcd}	37.0
Denbi	62.8^{de}	59.4^{abc}	72.5^{b}	5.3^{c}	15.7^{bcd}	53.6^{abc}	6.9^{b}	35.5^{d}	3.1^{b}	45.2^{a}	9.5^{cd}	33.2
Donmatteo	65^{bc}	61.2^{ab}	63.3^{e}	5.7^{b}	15.8^{bc}	46.6^{d}	5.3^{cd}	39.6^{bc}	2.4^{c}	46^{a}	9.5^{d}	32.4
Fetan	63.5^{cde}	59.5^{abc}	71.8^{b}	5.1^{c}	15.9^{b}	57.5^{a}	7.6^{a}	39.5^{d}	3.5^{a}	46.1^{a}	10^{cd}	29.5
Mangudo	66^{b}	58.9^{bc}	95.3^{a}	6^{b}	16.9^{a}	55.6^{ab}	7.3^{ab}	43^{a}	2.9^{b}	40.6^{bc}	15^{a}	29.5
Tesifaye	64.8^{bcd}	61.4^{ab}	67.9^{cd}	4.7^{de}	15.7^{bcd}	57.5^{a}	5.9^{c}	33^{e}	2.2^{d}	38.5^{c}	15.5^{a}	31.8
Ude	62.2^{e}	61^{ab}	71.3^{bc}	4.5^{e}	13^{e}	40.5^{e}	5.2^{d}	42.9^{a}	2.3^{cd}	44.7^{ab}	14^{ab}	34.9
Utuba	62.1^{e}	62.5^{a}	69.6^{bcd}	4.9^{cd}	15^{d}	45.7^{d}	4.9^{d}	41.4^{ab}	2^{e}	43.9^{ab}	9.5^{d}	32.6
Yerer	70.2^{a}	56.5^{c}	66.4^{de}	6.4^{a}	16.4^{ab}	49.2^{cd}	6^{c}	38.4^{c}	2.4^{cd}	37.6^{c}	11.5^{abc}	24.4

DH=days for heading, GFP=grain filling period, PH=plant height, SL=spike length, SPS=spikelet's per spike, KPS=kernel per spike; BM=biomass yield, TSW=thousand seed weight, GY=grain yield, HI=harvest index, YR=yellow rust

According to the mean performance results (Table 1), days to heading among the nine durum wheat varieties ranged from 62 days for the variety Alemtena to 70.2 days for Yerer. This wide range indicates the presence of substantial genetic diversity among the tested varieties for earliness and lateness traits. Such variability provides an opportunity for breeders to effectively select genotypes with early heading characteristics, which is particularly important in environments prone to terminal drought or short growing seasons. Most yield-contributing traits, including spike length, number of spikelets per spike, number of kernels per spike, and thousand seed weight, exhibited considerable variation among varieties. Due to this genetic variation, the tested varieties produced significantly different mean grain yields across locations. The highest grain yield (3.5 t ha^{-1}) was recorded for the variety Fetan, while the lowest yield (2.0 t ha^{-1}) was obtained from Utuba. Yellow rust severity also varied among the varieties, ranging from 9.5% for Denbi, Donmatteo, and Utuba to 15.5% for Wolde. Accordingly, Denbi, Donmatteo, and Utuba were identified as relatively resistant to yellow rust, whereas Wolde showed susceptibility to the disease. Traits governed by diverse genetic backgrounds, such as yield and disease resistance, deserve particular attention in breeding programs aimed at improving durum wheat productivity.

The coefficient of variation (CV) was interpreted as high (>20%), moderate (10–20%), or low (<10%). High CV values were observed across locations for varieties Alemtena, Ude, Denbi, Utuba, Donmatteo, Wolde, Fetan, and Mangudo, while a moderate CV was recorded for the variety Yerer. Based on the principle of adaptation, varieties with lower CV values are considered more stable and adaptable across a wider range of environments, whereas varieties with higher CV values tend to be better adapted to specific locations. Therefore, Yerer may be considered widely adaptable, while the remaining varieties appear to be specifically adapted. The mean grain yield across locations ranged from 2.0 t ha^{-1} for Utuba to 3.5 t ha^{-1} for Fetan. These findings are consistent with the report of Ganno et al. (2017), who observed wide variability in bread wheat, with days to heading ranging from 49 to 73.33 days and days to maturity from 87 to 118 days.

Estimation of Variance Components and Genetic Parameters: The genetic variability among the nine durum wheat varieties was assessed using phenotypic variance (σ^2p), genotypic variance (σ^2g), and environmental variance (σ^2e), as well as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (H^2), genetic advance (GA), and genetic advance as a percentage of the mean (GAM). Out of the sixteen traits evaluated, eleven traits that showed significant differences in the combined ANOVA were subjected to variability analysis, and the results are presented in Table 2.

The mean performance of the varieties across the four locations revealed substantial variability, as reflected by the wide range values for each trait. For instance, days to heading varied from 62 days for Alemtena at Lemu to 70.2 days for Yerer at Tambaro, showing a difference of more than one week. Such variation allows classification of varieties into early- and late-maturing groups and may be attributed to inherent genetic differences and environmental effects. Similarly, plant height ranged from 55.8 cm for Donmatteo at Tambaro to 105 cm for Mangudo at Damote Gale, indicating large genetic and environmental influences on this trait. The differences observed between phenotypic variance (σ^2p) and genotypic variance (σ^2g) for the studied traits (Table 2) further confirmed the existence of exploitable genetic variability for improving durum wheat through selection and breeding.

Phenotypic and Genotypic Coefficients of Variation: The extent of variability within the population was measured using PCV and GCV. The PCV values ranged from as low as 8.2% for grain filling period to as high as 62% for grain yield. Similarly, GCV values ranged from 4.5% for grain filling period to 21% for grain yield. Traits such as grain filling period, days to heading, and plant height exhibited low GCV values, while grain filling period also showed low PCV. This indicates that environmental factors had a greater influence than genetic factors on the expression of these traits, suggesting limited potential for improvement through direct selection. These findings agree with Mesele et al. (2016), who reported low PCV and GCV values for days to heading, days to maturity, and grain filling period in bread wheat genotypes evaluated in northern Ethiopia.

In contrast, traits such as spike length, above-ground biomass (biological yield), and grain yield exhibited high PCV and GCV values. The high magnitude of both phenotypic and genotypic variability for these traits indicates the presence of substantial genetic variation and suggests good prospects for improving durum wheat yield through selection. High phenotypic expression in these traits is likely a reflection of underlying genetic variation, making phenotypic selection effective. This result is in line with the findings of Wolde et al. (2016), who stated that higher GCV values imply greater genetic variability and a higher likelihood of successful transmission of these traits to subsequent generations. Similarly, high PCV and GCV values reported for traits such as plant height, number of spikelets per spike, spike length, and biomass support the possibility of genetic improvement through selection and breeding, as also reported by Kifle et al. (2016) and Tesso et al. (2017).

Table 2. Variability parameters and estimated characters of nine durum wheat varieties for 11 traits

Trait	Range	Mean + SD	σ^2e	σ^2g	σ^2p	GCV%	PCV%	H^2b %	GA	GAM %
DH	62-70.2	64.3 +5.73	29.7	17.8	47.5	6.6	10.7	37.5	5.3	8.2
GFP	56.5-62.5	60.1 +6.66	17	7.17	24.17	4.5	8.22	30	3	5
PH	63.3-95.3	71.8 + 10.53	19.3	34.4	53.7	8.2	10.2	64	9.7	13.5
SL	4.4-6.4	5.2 + 0.83	0.2	1.7	1.9	25	26.5	89	2.6	50
SPS	13-16.9	15.5 + 2.24	0.9	4.6	5.5	13.8	15.1	84	4	26
KPS	40.5-57.5	50.9+ 9.72	4.2	35	39.2	11.6	12.3	41	5.3	10.4
BM	4.9-7.6	6.1 + 2.04	0.7	3.6	4.3	31.1	34	84	3.6	59
TSW	33-43	38.3 + 5.03	8.3	50.3	58.6	18.5	20	86	13.6	35.5
GY	2-3.5	2.6 + 0.87	2.3	0.3	2.6	21	62	11.5	0.38	14.6
HI	37.6-46.1	43.1 + 5.43	27.7	35.2	62.9	13.8	18.4	56	9.2	24.5
YR	9.5-15	11.6 + 4.8	0.30	1.7	2	11.2	12.2	85	2.5	21.5

NB: SD= standard deviation, σ^2e= environmental variance, $\sigma\ ^2g$= genotypic variance, σ 2p= phenotypic variance, GCV= genotypic coefficient of Variation, PCV= phenotypic coefficient of variation,H^2b= broad sense heritability, GA= genetic advance, GAM= genetic advance as percent of mean, DH= date of heading, GFP= grain filling period, PH= plant height, SL= spike length, SPS= spikelet's per spike, KPS= kernel per spike, BM= biomass yield in ton, TSW= thousand seed weight, GY= grain yield, HI= harvest index, YR= yellow rust.

As shown in Table 2, moderate phenotypic and genotypic coefficients of variation were recorded for traits such as number of kernels per spike, number of spikelets per spike, harvest index, thousand seed weight, and yellow rust severity. Moderate phenotypic coefficient of variation was also observed for days to heading and plant height. These findings are consistent with the reports of Kumar et al. (2010) and Baranwal et al. (2012), who evaluated wheat genotypes across locations and reported moderate variability for most of these traits.

Estimation of heritability and expected genetic advance: The results of the present study revealed that broad-sense heritability (H^2) estimates ranged from 11.5% for grain yield to 89% for spike length. Heritability is an important parameter for selecting effective population improvement strategies (Abinasa et al., 2011). Traits with high heritability values are particularly suitable for breeding methods based on direct phenotypic selection and short selection cycles, such as mass selection and simple recurrent selection (Acquaah, 2007). Furthermore, Ganno et al. (2017) reported that selection for traits with high heritability (>80%) is relatively straightforward due to the close correspondence between genotype and phenotype, resulting from minimal environmental influence.

Based on standard heritability classifications, low heritability was observed for grain yield (11.5%), grain filling period (30%), and days to heading (37.5%). Improvement of these traits through direct selection may be difficult due to strong environmental effects and possible non-additive gene action. Medium heritability estimates were recorded for number of kernels per spike (41%) and harvest index (56%), indicating that these complex traits are controlled by multiple genes. Plant height exhibited moderately high heritability (64%). Very high heritability estimates were recorded for spike length (89%), thousand seed weight (86%), biological yield (84%), number of spikelets per spike (84%), and yellow rust resistance (85%) (Table 2). These results indicate that environmental influence on these traits is relatively low and that the observed variation is mainly governed by additive gene effects. Consequently, selection efficiency and genetic gain for these traits are expected to be high. These findings are in agreement with Royo (2009), who reported very high heritability for days to heading, days to maturity, and plant height in bread wheat. Similarly, Chandrababu and Sharma (1999) noted that high heritability values indicate reliable identification of superior genotypes based on phenotypic expression.

Genetic advance as a percentage of the mean (GAM) is a critical parameter for assessing the effectiveness of selection and predicting genetic improvement. Heritability alone does not adequately estimate the expected gain from selection; therefore, heritability estimates should be considered alongside genetic advance. Genetic advance refers to the expected improvement in genotypic value of a population after one cycle of selection at a given selection intensity (Singh, 2001; Hamdi et al., 2003). In the present study, high GAM values (at 5% selection intensity) were observed for biomass yield (59%), spike length (50%), thousand seed weight (35.5%), number of spikelets per spike (26%), harvest index (24.5%), and yellow rust resistance (21.5%). Moderate GAM values were recorded for grain yield (14.6%), plant height (13.5%), and number of kernels per spike (10.5%). Low GAM values were observed for grain filling period (5%) and days to heading (8.2%). These results are in agreement with Awale et al. (2013), who reported moderate to high GAM values for spikelets per spike, kernels per spike, thousand seed weight, and harvest index in durum wheat. Similar findings were also reported in bread wheat by Regasa (2012).

Traits that exhibit high heritability coupled with high genetic advance are generally governed by additive gene effects and are amenable to effective selection, particularly in early generations (Dutamo et al., 2015). In the present study, biological yield, spike length, thousand seed weight, and number of spikelets per spike showed both high heritability and high GAM, indicating that these traits are predominantly controlled by additive genes. Therefore, phenotypic selection for these traits would be effective and could lead to rapid genetic improvement of durum wheat varieties. These findings are coinciding with reports by Ganno et al. (2017) and Eid (2009).

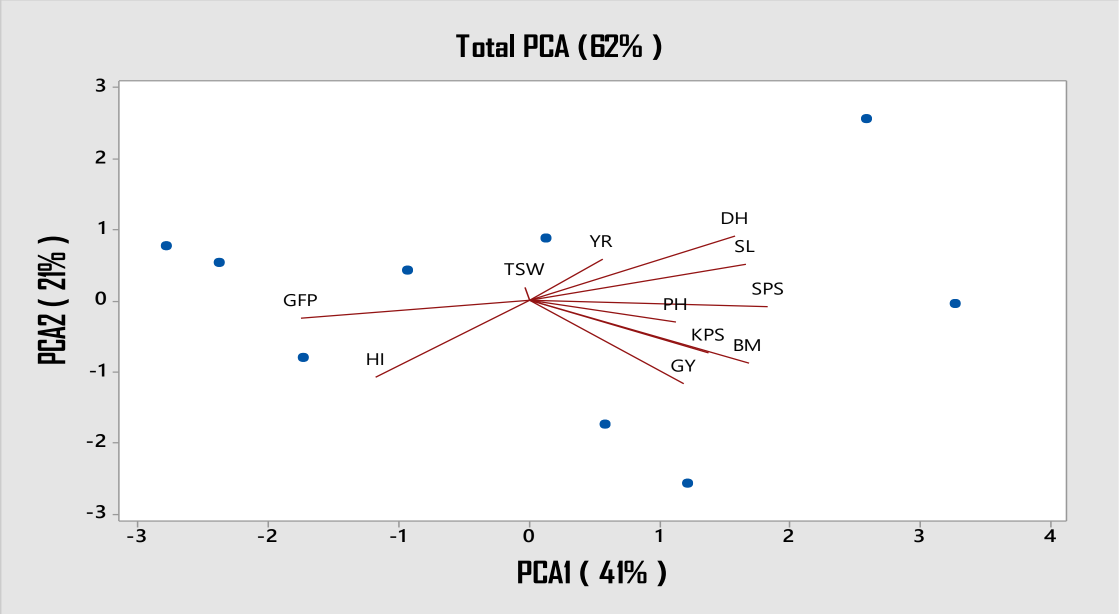

Figure 1. PCA Bi-plot for Quantitative data of Yield and Yield Related Traits

DH=days for heading, DM=days for maturity, GFP=grain filling period, PH=plant height, SL=spike length, TNT=total number of tiller, EFT=effective tiller number, SPS=spikelete's per spike, KPS=kernel per spike=BM=biomass yield, TSW=thousand seed weight, GY=grain yield, HI=harvest index, YR=yellow rust, LR=leaf rust, SR=stem rust

Phenotypic character-centered Principal Component Analyses (PCA): According to the criteria proposed by Kaiser (1961), principal components with eigenvalues greater than one are considered meaningful. Additionally, Johnson and Wichern (1992) suggested that principal components explaining more than 80% of the total variation should be retained. Principal component analysis is a powerful multivariate tool that extracts key components contributing to total variability and facilitates identification of important traits, thereby accelerating breeding programs. Each principal component explains a specific proportion of the total variance, with the first principal component contributing the most, followed by subsequent components (Das et al., 2017). In the present study, PCA results are presented in Table 3. Principal component analysis was performed using Minitab version 17 on all traits that exhibited significant variation ($P < 0.05$ and $P < 0.01$) in order to identify the major traits contributing to genetic diversity and to select potential donor traits for breeding.

For principal component (PC) analysis, an 11 × 9 data matrix was constructed using all measured traits. Among the eleven traits, three principal components with eigenvalues greater than one were retained. Accordingly, the first three principal components derived from the Euclidean similarity matrix explained a substantial proportion of the total variation. The first principal component (PCA1) had the highest eigenvalue (4.5) and accounted for 41% of the total variation. The second principal component (PCA2) had an eigenvalue of 2.3 and explained 21% of the variation, while the third principal component (PCA3) had an eigenvalue of 1.6 and contributed 15%. Together, these three components explained 77% of the total phenotypic variability among the nine tested durum wheat varieties.

The major contributing traits to PCA1 were days to heading, grain filling period, spike length, number of spikelets per spike, kernels per spike, and biological yield. These traits, grouped under the first principal component, were the most influential in discriminating high-yielding varieties and are therefore fundamental for identifying superior genotypes. PCA2 was mainly associated with days to heading, kernels per spike, biological yield, grain yield, and harvest index. The third principal component (PCA3) was primarily influenced by plant height, kernels per spike, and thousand-seed weight (Table 3).

As illustrated in Figure 1, the length and position of trait vectors indicate their relative contribution to total variation. Traits such as days to heading, spike length, spikelets per spike, biological yield, grain yield, grain filling period, and harvest index were positioned far from the origin, demonstrating their strong contribution to phenotypic variability. In contrast, thousand-seed weight, yellow rust, and plant height were located closer to the origin, indicating a relatively lower contribution. The ordination of the first axis was mainly associated with high seed weight, suggesting a shorter duration for dry matter accumulation and a higher harvest index. The second axis was largely dominated by early heading, longer spikes, higher spikelet number, taller plants, greater kernel number, higher biological yield, yellow rust resistance, and increased grain yield. Selection based on the first principal component would favor early heading, shorter grain filling duration, longer spikes, higher spikelet number, increased kernel number, and greater biological yield. Selection based on the second component would enhance harvest index and grain yield, whereas selection based on the third component would favor taller plants with heavier seeds.

Overall, principal component analysis proved to be an effective multivariate tool for differentiating durum wheat varieties and offers substantial benefits for future breeding programs by accelerating selection, reducing costs, and improving genetic gain. The present study revealed significant variability among durum wheat genotypes for the evaluated traits, indicating ample opportunities for genetic improvement through selection and breeding. These findings are consistent with earlier reports by Alemu et al. (2020) and Shabir et al. (2018).

Table 3. Eigenvalue, Percentage of variance, Cumulative variance, and coefficient of differentiations in each trait for three main components

PC	*Eigen value*	*Variance % for each PC*	*Cumulative* Variance % for each PC	*DH*	*GFP*	*PH*	*SL*	*SPS*	*KPS*	*BM*	*TSW*	*GY*	*HI*	*YR*
1	4.5	41	41	0.34	-0.38	0.24	0.36	0.40	0.31	0.36	-0.00	0.26	-0.25	0.12
2	2.3	21	62	0.39	-0.10	-0.12	0.21	-0.03	-0.31	-0.37	0.08	-0.50	-0.45	0.25
3	1.6	15	77	0.09	0.01	-0.49	-0.10	0.18	0.32	-0.08	-0.72	-0.09	-0.13	-0.20

DH=days for heading, DM=days for maturity, GFP=grain filling period, PH=plant height, SL=spike length, TNT=total number of tiller, EFT=effective tiller number, SPS=spikelet's per spike, KPS=kernel per spike=BM=biomass yield, TSW=thousand seed weight, GY=grain yield, HI=harvest index, YR=yellow rust, LR=leaf rust, SR=stem rust

4. CONCLUSION

The analysis of variance conducted on individual and pooled datasets revealed significant ($P < 0.05$) and highly significant ($P < 0.01$) differences among the evaluated durum wheat varieties, indicating the presence of substantial genetic variability. This genetic variability among the tested varieties provides a valuable opportunity for breeders to select superior genotypes for the improvement of desirable traits. Considerable differences in mean performance were observed among varieties for all studied traits, facilitating effective selection for yield enhancement in durum wheat. The average performance of the varieties across four locations for the eleven traits demonstrated wide variability, further confirming the existence of both genetic and environmental influences. Estimates of genetic and phenotypic variance components revealed appreciable genotypic (σ^2g) and phenotypic (σ^2p) variations for the majority of traits, indicating the availability of exploitable genetic variability among the durum wheat varieties. Traits such as spike length, biological yield, and grain yield exhibited high genotypic and phenotypic coefficients of variation (GCV and PCV), suggesting that phenotypic performance reliably reflects genetic potential and that selection based on these traits would be effective.

High heritability coupled with high genetic advance was observed for biological yield (59%), spike length (50%), thousand-seed weight (35.5%), and number of spikelets per spike (26%). The combination of high heritability and genetic advance indicates that these traits are predominantly governed by additive gene effect, implying that selection for these characters would result in rapid genetic improvement.

Principal component analysis further confirmed the presence of substantial variability among the nine tested durum wheat varieties. The first three principal components explained 77% of the total phenotypic variation, with PCA1 accounting for the largest share (41%), followed by PCA2 (21%) and PCA3 (15%). The major traits contributing to PCA1 included days to heading, grain filling period, spike length, number of spikelets per spike, kernels per spike, and biological yield. These traits were the most influential in discriminating high-yielding varieties and are therefore key selection criteria in durum wheat improvement programs. Overall, the study demonstrated significant genetic variability among the evaluated durum wheat varieties for all tested traits, revealed substantial opportunities for genetic improvement through effective selection and targeted breeding strategies.

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Conflict of interest

The authors declare that they have no conflicts of interest, competing financial interests or personal relationships that could have influenced the work reported in this paper.

Ethical approval

In this article, as per the plant regulations followed in the Areka Agricultural Research Center PO Box 79, In South Ethiopia Agricultural Research Institute, Ethiopia; the authors observed the genetic variability and trait heritability among Ethiopian Commercial Durum Wheat (*Triticum turgidum* ssp. durum L.) varieties in major wheat-producing areas of Southern Ethiopia. The ethical guidelines for plants & plant materials are followed in the study for observation, identification & experimentation.

Informed consent

Not applicable.

Data availability

All data supporting the findings of this study are embedded within the manuscript. Additional information may be made available from the corresponding author upon reasonable request.

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