

RESEARCH PAPER

Genetic Variability and Traits Association in Durum Wheat (*Triticum durum* L.) Genotypes in Sekota District, Wag-hemra, Ethiopia

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Paper No. 1114

Received: 11-03-2024

Revised: 20-05-2024

Accepted: 02-06-2024

ABSTRACT

The study was initiated with the objective of assessing genetic variability and trait association using 6×6 simple lattice design in Sekota district during main cropping season in 2021. Both plot and plant based data were collected and analysis following the simple lattice design guide. Analysis of variance (ANOVA) revealed the presence of significant differences among genotypes for days to heading, days to maturity, plant height, spike length, number of seeds per spike, thousand seed weight, biological yield, yield, harvest index and protein content. 4451.4 kg ha⁻¹ was the highest grain yield while the lowest was 2273.2 kg ha⁻¹ with a mean of 3092.12 kg ha⁻¹. 17 genotypes (50%) were higher yielder than average mean 3092.12 kg ha⁻¹. 4 genotypes (23.53%) were both high-yielder and relatively high in grain protein content. Moderate genotypic coefficient of variation coupled with high heritability and high genetic advance as a percentage of the mean were obtained for plant height, seeds per spike, biomass, grain yield and harvest index. Grain protein content had a low GCV, moderate heritability and low GAM, indicating a strong influence of environment on grain quality and less variation among genotypes in their grain protein content. Plant height, spike length, thousand kernel weight, biomass and harvest index had positive significant correlations with grain yield at both genotypic and phenotypic levels. Therefore, selection and hybridisation based on the desired traits could be possible for the improvement of durum wheat in the study area. For reliable results and recommendations, it is advisable to repeat the experiment for at least one more season over locations.

HIGHLIGHTS

- ① Durum wheat is among the most significant *Triticum* species with superior morphological inconsistency among landraces.
- ② The inconsistency and variety of traits exhibited among the genotypes, can serve in planning selection and crossing programs for durum wheat improvement.

Keywords: Durum wheat, Genetic variability, genetic parameter, protein content, pasta making

Durum wheat (*Triticum turgidum* L.) and bread wheat (*Triticum aestivum* L.) are two species grown mostly by smallholder farmers in Ethiopia (Tamene Mideksa *et al.* 2018). Durum wheat (*Triticum turgidum* L.) is an allotetraploid species with a

How to cite this article: Assefa, A., Alemayehu, T., Yirgal, K., Endale, Z., Hailmaryam, G. and Berihanu, T. (2024). Genetic Variability and Traits Association in Durum Wheat (*Triticum durum* L.) Genotypes in Sekota District, Wag-hemra, Ethiopia. *Int. J. Ag. Env. Biotech.*, 17(02): 101-117.

Source of Support: None; **Conflict of Interest:** None





total of 28 chromosomes ($2n = 4x = 28$), including a fully diploid chromosome (two genomes: AABB) in each parental species (Feldman, 2001). Ethiopia is considered one of the most diverse sources of durum wheat varieties (Vavilov, 1951). It grows widely in the highlands of Ethiopia, especially in the central, northwestern and northeastern regions of Ethiopia, at an altitude of 1,800 to 2,800 meters above sea level, including Shewa, Gojam, Gondar, Wello, Tigray, Hararghe, Arsi and Bale. The crop is more preferred due to its protein content and the protein content of durum wheat ranges from 11% to 16%, with optimal levels depending on the variety, environment and cultural practices industry requirements (Turnbull, 2001). For modern pasta production, durum wheat semolina must contain more than 14% protein (Landi and Guarneri, 1992). Selecting the best genotypes based on grain yield is generally difficult because grain yield is a complex, polygenic controlled quantitative trait that influenced by environmental variations and yield-related traits. The most important factor to consider in durum wheat selection is the degree of genotypic and phenotypic variability of the species (Acquaah, 2012). Any breeding program must fully understand the degree of genetic variation determined by the coefficient of genotypic variation and the coefficient of phenotypic variation in order to improve grain yield and associated traits. Knowledge of genetic variability, heritability of important agronomic traits, and the relationship between two traits or between different traits is essential for obtaining high-yielding varieties (Mohammed *et al.* 2012). In Wag-Hemra zone, wheat is one of food security crop and has versatile religious and traditional importance. The grain is used in different forms of food staffs *such as* bread, unleavened flat bread (*kitta*), leavened flat bread (*injera*), porridge, soup, roasted grain (*kollo*), cooked grain (*nifro*) and alcoholic beverages/drinks (*tella*) and the straw is an important material for livestock feed.

In Wag-hemra Zone, the area coverage, production and productivity of wheat was 8,174.47 ha, 12,085.36 t and 1.48 t ha⁻¹ in (CSA, 2017). The average productivity of the crop in the area (Wag hemra, Sekota) is very low even as compared to Amhara region (2.59 t ha⁻¹), national (2.76 t ha⁻¹) (CSA, 2019) and world (3.36 t ha⁻¹) averages (FAOSTAT, 2017).

The low productivity of the crop in wag hemra, sekota could may be due to lack of improved varieties (lack of improved varieties suited to the Wag-Hemra agro-ecology) and both biotic and abiotic factors are among the critical production constraints that need solved. Therefore, development of improved durum wheat varieties that give high yield and quality (relatively high protein content) through different breeding programs that suite to the prevailing growing environments is very required. Various studies on genetic variability, diversity and traits association on durum wheat have been conducted based on grain yield and yield- related traits at different regions of Ethiopia and reported existence of sufficient variations among tested genotypes for various traits (Worknesh *et al.* 2019; Zewdu *et al.* 2021; Addisu *et al.* 2021; Temesgen *et al.* 2022; Mulatu *et al.* 2023). However, information's on durum wheat variability studies are insufficient and there is no full information on the genetic variability and association of traits on durum wheat genotypes in Wag-Hemra administrative zone under Sekota District.

Therefore, this study was conducted to assess genetic variability and trait association among the durum wheat genotypes using multivariate analysis.

MATERIALS AND METHODS

Description of Experimental Location

The experiment was conducted at the Sekoat Dry Land Agricultural Research Site (Woleh) during 2021 (2013 E.C) *mehere* (main) cropping seasons in at the Wag- Hemra administrated Zone, in the north part of Ethiopia. The study site is located in Sekoat District North Wollo Zone of Amhara National Regional State (ANRS). It far 702 kilometers (km) far away from Addis Ababa (capital of Ethiopia). Specifically, the study site is situated in at a latitude of 12°52' 1° N and a longitude of 39° 05' 3° E with an elevation of 2101 m.a.s.). The annual minimum, maximum and mean temperatures of study area in 2021 were 12.32°, 28.55° and 20.43° respectively. The annual mean rainfall of the area was 786.1 mm. The dominant soil type is classified as cambisol. The general slope on the farm lands vary between 0 and 8 % but could normally be found on 0-25% slope range (Demlie and Shawel, 2016). Wheta, tef,

barly, filed pea, faba bean, sorghum check pea are some of the field crops grown the study area mostly by using local varieties.

Experimental Materials

The experiment was comprised of 34 newly advanced fixed lines and two checks (standard and local check durum wheat genotypes). The genotypes were obtained from Sirinka Agricultural Research Center (SARC), standard check from Mekelle Agricultural Research Center (SDARC) and local check from local farmers.

Experimental Design and Management

The field experiment was conducted in partially balanced simple lattice incomplete block design, 6 x 6 arrangements. The individual plot size was 4 rows of 2.5 meters (m) length with 0.2 m row spacing *i.e.* 0.8 m x 2.5 m = 2 meter square (m²) gross area and 2.5 m x 1.2 m = 3 m² net area. The distances between plots, blocks and replications were 0.5 m, 1 m and 1.5 m, respectively. The treatments (genotypes) were allocated to plots at random within each replication. Seed rate was calculated based on 150 kg ha⁻¹ basis.

Fertilizer was applied to all plots uniformly in the form of UREA (100 kilo gram (kg) UREA contains 46 % N) and NPSB fertilizers at the rates of 42 kilo gram per hectare (kg/ha) nitrogen (N) and 38 kg ha⁻¹ di phosphorus pento oxide (P₂O₅). All the NPSB fertilizer was applied by side dressing during planting, whereas urea was applied in two splits: half at the time of planting and the remaining half by top dressing at tillering stage after first weeding.

Data Collection and Measurement

The pre and post-harvest data on grain yield and yield related traits of durum wheat genotypes were collected on plot and plant basis following the data scoring standards of IBPGR the descriptors for wheat (IBPGR, 1985). The four central rows only were used for data collection. Five randomly taken plants from the four central rows of each plot (experimental unit) in each replication were used for plant based data collection. The averages of the five plants in each plot were used for statistical analysis for the traits recorded on a plant basis while and the whole two central rows' data were used for plot based data.

1. Data on plot basis

- 1. Days to heading (days):** The number of days was calculated by subtracting from sowing to a stage when 50% visual judgment of the plants in a plot produced spikes.
- 2. Days to maturity (days):** The number of days was calculated from sowing to 90% visual judgment of the heads attained physiological maturity in each plot and when grains are difficult to divide by thumb nail.
- 3. Thousand kernel weight (g):** The grain weight of 1000 seeds sampled at random from total grain harvested of the experimental plot were counted using electronic seed counter and weighted by using electronic sensitive balance and recorded; and adjusted with 12.5% moisture content.
- 4. Grain yield (g/plot):** The grain yield per plot (harvested, threshed and cleaned) was weighted using sensitive balance and then moisture of the grain yield seed was adjusted to 12.5% moisture level and converted to t/ha.
- 5. Grain protein content (%):** It was determined *via* Near Infrared Reflectance (NIR) Spectroscopy) at Debre Zeit Agricultural Research Center (DZARC) grain quality Laboratory following a standard procedure (AACC, 2000).
- 6. Biomass yield (g/plot):** The total biomass yield was recorded by weighing the total sun dried above ground biomass harvested from the two central rows and converted in to t/ha.
- 7. Harvest index (%):** It was estimated by dividing grain yield per plot to above ground biomass yield and multiplied by 100.

2. Data on plant basis

- 1. Plant height (cm):** It was measured in cm from ground level to the top of the spike excluding the oawns of five randomly taken plants from the middle four rows.
- 2. Spike length (cm):** The main spikes from the five sampled plants from the central two rows of each plot were measured in cm



and averaged to represent the spike length (excluding awns).

3. **Number of seed per Spike (No.):** The total number of grains/kernels in the main spike was counted at the time of harvest from five randomly taken plants and expressed as an average.

Statistical Data Analysis

1. Analysis of variance

Data entry and processing were carried out using Microsoft Excel (MS- Excel, 2010). The data collected for quantitative traits were subjected to analysis of variance (ANOVA) for simple lattice design using PROC LATTICE and PROC GLM procedures of SAS software version 9.2 (SAS Institute Inc, 2008) according to the procedures outlined by Gomez and Gomez (1984) after testing ANOVA assumptions and relative efficiency (RE) of design (simple lattice) over RCBD. The Mean square of traits that noted RE > 100% were taken from lattice, while RE < 100% was taken from GLM results. General linear model (GLM) is used to calculate the unadjusted block sum of squares, unadjusted treatment sum of squares, and intra-block error and handle relating one or several continuous dependent variables to one or several independent variables. Mean separations were carried out following the statistical significance of genotypes' mean squares using the Duncan Multiple Range Test (DMRT) at 5% and 1% significance levels to compare two genotypes' means. DMRT is used to compare a large number of treatments and computed for all possible pair comparisons than the least significance difference (LSD). Estimate of genetic parameters and correlations for the genotypes were continued based on statistical significance of genotypes' mean squares.

The statistical model for the simple lattice design:

$$P_{ijk} = \mu + gi + bk(j) + rj + eijk,$$

Where, P_{ijk} = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j ; μ = grand mean a constant common to all observations; gi = the effect of i^{th} genotype; $bk(j)$ = the effect of incomplete block k within replication j ;

rj = the effect of replication j ; and $eijk$ = the residual or effect of random error.

Estimation of Genetic Parameters

1. Estimation of phenotypic and genotypic variances

The total variance was partitioned into components due to genotype and environment. The phenotypic and genotypic variances of each trait were estimated from simple lattice and GLM analysis of variances.

The genotypic and environmental variances for different traits were computed as per the methods suggested by Burton and Devane (1953).

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

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

Then, the phenotypic variance was obtained from the sum of genotypic and environmental variances as:

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

Where: σ^2g = Genotypic variance; σ^2p = Phenotypic variance; σ^2e = Environmental variance; MSe = Error mean square (Environmental variance); MSg = Mean square due to genotypes; and r = Number of replications.

2. Coefficient of variation for the phenotypic and genotypic estimates

Coefficients of variations at Phenotypic and genotypic levels were estimated based on the method suggested by Burton and Devane (1953), and Deshmukh *et al.* (1986) using the following formula:

$$PCV(\%) = \frac{\sqrt{\sigma^2p}}{X} * 100$$

$$GCV(\%) = \frac{\sqrt{\sigma^2g}}{X} * 100$$

Where:

PCV = Phenotypic coefficient of variation (%);
 GCV = Genotypic coefficient of variation (%); σ^2p =

Phenotypic variance; σ^2g = genotypic variance and X = Grand mean.

Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) values were categorized as low (0-10%), moderate (10-20%) and high (20% and above) values as indicated by Burton and Devane (1953), and Sivasubramanian and Madhavamenon (1973).

3. Estimate of broad Sense heritability

Heritability specifies the proportion of the total variability that is due to genetic cause. Information on heritability provides the relative practicability of selection for a particular character. Different characters have different levels of heritability that can contribute for yield improvement in breeding programs. Broad sense heritability values on plot and plant basis were computed for all traits based on the formula adopted from Johnson *et al.* (1955), Allard (1960), Falconer and Mackay (1996) as follow:

$$H^2B(\%) = \frac{\sigma^2g}{\sigma^2p} * 100$$

Where: H^2B = Heritability in broad sense; σ^2p = Phenotypic variance; σ^2g = Genotypic variance.

Broad sense heritability estimates were classified as low (<30%), moderate (30 -60%) and high (> 60%) as given by Robinson *et al.* (1949) and Falconer and Mackay (1996).

4. Estimation of expected genetic advance

Although high heritability estimates have been found to be effective in the selection of superior genotypes on the basis of phenotypic performance, Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance are more useful in predicting the effect for selecting the best individual. The expected genetic advance for each trait at selection intensity of 5% was computed using the methodology given by Allard (1960) and Johnson *et al.* (1955) as;

$$GA = K * H^2B * \sigma p$$

Where: GA = Expected genetic advance under selection

K = the standardized selection differential constant at 5 % selection intensity ($K = 2.063$)

σp = Phenotypic standard deviation

H^2B = Heritability in broad sense.

The genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under selection, using the formula given by Robinson *et al.* (1949) as:

$$GAM(\%) = \frac{GA}{X} * 100$$

Where: GAM = Genetic advance as percent of mean; GA = Expected genetic advance under selection and X = Grand mean.

Genetic advance as percent of mean (GAM) was categorized as low (0-10%) moderate (10-20%: and high (20% and above) as given by Johnson *et al.* (1955) and Falconer and Mackay (1996).

Estimation of Correlation among yield and yield-related traits

1. Estimation of genotypic and phenotypic correlation

Phenotypic and genotypic correlation coefficients were computed from respective variance and covariance components based on the method described by Singh and Chaudhury (1996). Genotypic correlations were calculated by using genotypic variances and covariances while phenotypic correlations by using phenotypic variances and covariances.

The PROC CANDISC procedure in SAS software version 9.2 was used for phenotypic correlation and genotypic significance test. The levels of significance of correlation coefficients were determined from correlation table at the appropriate degrees of freedom and probability level (Gomez and Gomez, 1984). Phenotypic and genotypic correlation coefficients were computed from variance and covariance components based on the method described by Singh and Chaundry (1985).

$$r_{pxy} = \frac{\text{COV}_{pxy}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$



Where:

r_{pxy} = Phenotypic correlation coefficient between traits x and y

Cov_{pxy} = Phenotypic covariance between traits x and y

δ^2_{px} = Phenotypic variance of trait x

δ^2_{py} = Phenotypic variance of trait y .

$$r_{gxy} = \frac{cov_{gxy}}{\sqrt{\delta^2_{gx} \cdot \delta^2_{gy}}}$$

Where:

r_{gxy} = Genetic correlation coefficient between traits x and y

Cov_{gxy} = Genetic covariance for traits x and y

δ^2_{gx} = Genetic variance for trait x

δ^2_{gy} = Genotypic variance for trait y .

RESULTS AND DISCUSSION

Analysis of Variance

Analysis of variance (ANOVA) was calculated for ten (10) selected characters of the 36 case genotypes and the results are shown in Table 1. The of the ANOVA results showed that the genotypes showed significant differences ($P < 0.01$) in days to maturity, plant height and per seed, while there were significant ($P < 0.05$) differences in plant height, biomass, thousand kernel weight, grain yield and harvest rate, number of days to heading, spike length and grain protein content (Table 1). It implies that there was a large difference between the tested durum wheat genotypes. The presence of significant differences among the tested durum wheat genotypes justified the need to estimate further subsequent statistical analyses like genetic variability parameters and correlation coefficients for the genotypes, and it suggests that the genotypes were genetically diverse and that there was sufficient genetic variability in the materials used for this study. The presence of variation in durum wheat genotypes for different agronomic traits might give a chance to breeders to select genotypes depending on the objectives of the breeding activity. The presence of highly significant differences among durum wheat genotypes for yield and yield related

traits was also reported by different authors (Addisu *et al.* (2021), Mulatu *et al.* (2023), and Bantewalu *et al.* (2023).

Genotypes mean performance for phenology, growth, yield and yield related and quality traits

Days to heading ranged from 48 to 70 with a mean of 58 days (Appendix 1). Accordingly, genotype number 9 took the shortest (48) days to heading whereas genotype number 13 took longest (70) days to heading than the other durum wheat genotypes in the study area. A total of 18 (50%) genotypes were had heading date below the average mean. Similarly, Arega *et al.* (2010) reported variation in days to heading among on 44 durum wheat genotypes at north wollo (Geregera), Mohammed *et al.* (2011) also report variations in days to heading among 16 durum wheat genotypes at Sinana, South-eastern Ethiopia. Also in line with this, significant variation for days to heading (53-75.2 days) on 50 durum wheat genotype at Mao Komo, Benishangul Gumuz Regional State was reported by Addisu Dereje *et al.* (2021). The longest and the shortest days to maturity were recorded on genotype number 26 (144 days) and genotype number 36 (98 days) with a mean of 124.2 days, indicating that the tested genotypes were early to medium maturing category. In this study, the standard check variety (Wohabi) were early matured genotypes than the newly advanced (fixed line) and local check (farmer's variety). In this finding, only nine (25%) genotypes matured early than the average and both the standard and the local checks were including in the early categorize. Genotype number 21, 19, 29, 4, 31, 33, 34, 35, 32, and 36, were the genotypes that had maturity date below the grand mean. Only 4 (11.11%) genotypes were both early heading and early matured and this may be indicate early heading may not translate to early maturing.

With respect to plant height, the average mean was 83.56 cm (Appendix 1). In this regard, the longest and shortest plant height was recorded on standard check variety (115 cm) and genotype number 24 (44.7 cm), respectively with grand mean of 83 cm (Appendix Table 1). Similarly, variation in plant height (68-104 cm) on 104 durum wheat at Debrezeit and Dera was reported by Bantewalu *et al.* (2023). In line with this findings, variation in plant height

Table 1: Analysis of variance (ANOVA) for ten (10) selected traits of 36 durum wheat genotypes grown at Woleh (Sekota District) during the year 2021

Traits	Mean square values (MS)					RE to RCBD	R ²
	Rep	Block	Genotype	Error	CV		
DsH	37.55	12.02	62.54*	33.12	10.1	103.1	0.66
DsM	1.12	0.35	290.52**	13.32	3.02	108.2	0.95
Ph	20.58	22.85	240.93**	8.65	3.34	98.2	0.97
Sl	3.38	0.96	1.53*	0.71	14.36	96.2	0.71
Ss	4.75	1.41	59.55**	4.83	7.04	108	0.92
BM	25699	503177	5441559**	502312	7.94	106	0.92
TkW	0.22	7.86	40.46**	2.7	3.55	111	0.94
GY	19921	3487.6	586564**	31730	5.91	115.3	0.95
HI	2.34	15.83	103.06**	13.47	10.17	109	0.88
KPP	0.37	0.03	1.38*	0.62	6.47	100.61	0.69

Where Rep = replication, DsH = days to heading (no), DsM = days to maturity (no), Ph = plant height (cm), Sl = spike length (cm), Ss = seed per spike (no), BM = Biomass yield (kg ha⁻¹), TkW = 1000-kernel weight (gr), GY = grain yield (kg ha⁻¹), HI = harvest index (%), and KPP = Grain protein content (%), CV = coefficient of variation (%), RE to RCBD = relative efficiency over RCBD, R² = coefficient of determination, * and ** = significance at 5 and 1% level of probability.

with a mean of 87.54 cm was reported by Zewdu *et al.* (2021) on 100 durum wheat genotypes at Kellem Wollega zone of Oromia region. Spike length gave a mean value of 5.82 cm with the maximum (8.1 cm) and the minimum (4.3) spikelet length was on the genotype number 25 and genotype number 1 respectively. Similarly, to these findings, variation on spikelet length (5.3 up to 11.5 cm) with a mean of 8.6 cm on durum wheat was reported by Temesgen *et al.* (2022) on 420 durum wheat genotypes at Sinana and Chefa. Also, in line with this, Demeke *et al.* (2023) reports variation in spikelet length ranged from 6.72 up to 10.02 with a mean of 8.43 cm on 64 bread wheat genotype at Kulumsa. The maximum seed per spike (40) were found on genotype number 33 and the minimum (14.9) seed per spike on genotype 4 with a mean of 31.9. The mean biomass yield per hectare of 36 durum genotypes was 8916.7kg ha⁻¹ with the maximum (12532) on genotype 34 and the minimum (6050.0) on the genotype 4. Biomass variation on durum and bread wheat genotype was reported by Mohammed *et al.* (2011), Ahmed *et al.* (2017), Tilahun *et al.* (2021) and Mulatu *et al.* (2023). The maximum 1000-seed weight (54.54 gr) and the minimum (35.19 gr) was recorded on the genotype number 24 and 3 respectively with a mean of 43.51gram.

The highest grain yield per hectare was recorded from genotype number 8 (4451.4 kg ha⁻¹), while the lowest was obtained from genotype number

19 (2273.2 kg ha⁻¹) with a mean of 3092.12 kg ha⁻¹ (Appendix 1). Out of 34 newly advanced line genotypes included in the study excluding the local and standard checks, 17 genotypes (50%) were higher yielder than average mean (3092.12 kg ha⁻¹) and the standard check (3036.3 kg ha⁻¹). Genotype number 1, 2, 3, 6, 28, 10, 5, 14, 15, 21, 7, 8, 23, 27, 25, 26, and 29 are top yielder genotype than the average mean, standard and local checks and give a yield advantage up to 31.79 % over the standard checks and 36.26% over the local check. Similarly to this, grain yield variation on durum wheat genotype was reported by Zewdu *et al.* (2021) at Kellem Wollega zone of the Oromia region on 100 durum wheat genotype and Demeke *et al.* (2023) also reports yield variations on bread wheat at Kulumsa. Also in line with this, Worknesh *et al.* (2019) report yield variation on durum wheat genotypes ranged from 3515.25 to 7539.25 with a mean of 5788.98 kg ha⁻¹ at Debre Zeit and Chefe. 3.7 to 6.13 t ha⁻¹ yield variation on durum wheat was also reported by Bantewalu *et al.* (2023). Similarly with, Mohammed Abinasa *et al.* (2011) report yield variations in durum wheat ranged from 3202 to 4006.3 kg ha⁻¹ at Sinana, South-eastern Ethiopia on 16 durum wheat genotypes. Also, Arega *et al.* (2011) report yield variation in durum wheat ranged from 2.4 to 4.2 t ha⁻¹ with a mean of 3.2 t ha⁻¹ at north wollo (Geregera). Also in line with this, yield variation in wheat 26.5-43.8 q ha⁻¹ with a mean of 34.6 q ha⁻¹ was



reported by Ahmed *et al.* (2017) on 49 bread wheat genotypes at Jamma and Geregera.

The highest harvest index (48.33%) was recorded from genotype number 25 while the lowest harvest index was from genotype number 34 (18.49%), which indicates variability among the tested durum wheat genotypes in their efficiency in assimilating into grain yields.

Significant variation for grain protein content was observed on the tested genotype and ranged from 10.15 (genotype number 32) to 13.90 (genotype number 9) with a mean value of 12.58 % (Appendix 1). Out of 36 tested durum wheat genotypes, 11 genotypes, genotype number 9, 5, 24, 23, 22, 10, 19, 14, 28, 4, and 13 (30.55%) had relatively higher (> 13%) grain protein content than the average mean (12.56%) and this high grain protein content is importance in determining the pasta making quality (Delwiche, 2004). Out of 17 high-yielder genotypes, 4 genotypes (23.53%) were both high-yielder and relatively high in grain protein content. High yielders with high grain protein content suggested the chance of selecting high yielder and good quality (high in protein percentage) durum wheat genotypes to use as parents in the crossing program and could be selected for further breeding programs. In this study, genotypes that had a higher grain yield (4451 kg ha⁻¹, were had lower in grain protein content (12% and <). In argument to this work, variation (11.43 to 15.38%) in grain protein content in durum wheat was reported by Worknesh *et al.* (2019) at Debre Zeit and Chefe and variation on protein content (11.5 to 16.2%) with a mean of 13.4% was also reported by Temesgen *et al.* (2022) at Sinana and Chefe. Also in line with this, Arega *et al.* (2010) reports grain protein content differences among 44 durum wheat genotypes at south wollo (Geregera), Similarly, Mulatu *et al.* (2023) report grain protein content differences (10.7 to 16.8%) with a mean of 13.6% at Sinana and Selka among 49 durum wheat genotypes. The variation in grain protein content may be due to genetic differences among the tested durum wheat genotypes, environmental differences, or due to the interaction of genotypes by environment and other factors. Therefore, these high-yielding and high-grain protein content durum wheat genotypes could be selected for further breeding programs (stability testing over years and across locations) for the study area under rain-fed conditions.

Estimates of Variance Components

1. Phenotypic and genotypic variations

Estimated variance, PCV, GCV, broad heritability, developmental and genetic improvement percentage values for the traits studied are shown in Table 3. Differences were observed in various phenotypic and genotypic factors. For size, characters were used. The highest value of phenotypic variation was calculated in grain yield (309146.7) and the lowest value was calculated in protein content (1.006). The genotype was also high for grain yield (277417.04), while the genotype was low for grain protein (0.378). Environmental variation was also high for grain yield, biomass yield, days to maturity, days to maturity and harvest characteristics, indicating that environmental effects reflect phenotypic characteristics. These results are in close agreement with studies by Endashaw (2018), and Garome *et al.* (2022). GCV values ranged from 4.48% for protein content to 18.78% per harvest, while PCV values ranged from 7.98% for protein content to 21.42% per harvest (Table 2). Phenotypic and genotypic coefficients of variation were classified as low (<10%), medium (10-20%) and high (>20%) according to Burton and Devane (1953) and Sivasubramanian and Madhavamenon (1973). According to these classifications, the harvest rate had a high PCV, whereas the current study did not have a high GCV. This suggests that there were no significant differences in environmental factors between replicates and genotypes and/or that the interaction between genotypes and environment was not high between replicates throughout the study period. This result is related to the study of Gezahegn *et al.* (2015), in which no characters with high GCV were reported. Contrast to present findings, Dargicho *et al.* (2015) reported high PCV and GCV for 1000 kernel weight, biomass yield, harvest index and grain yield.

Moderate PCV values were recorded for days to heading (11.91%), plant height (13.37%), spikelet length (18.2%), seed per spike (17.79%), biomass yield (19.33%), 1000- kernel weight (10.67%), and grain yield (17.99 %) and this indicates that there were considerable variations among environmental factors between replications and genotypes since PCV is a combination of environmental, genetic and interaction variations.

The GCV values computed were moderate for traits plant height (12.89%), spikelet length (10.96%), seed per spike (16.4%), biomass yield (17.63%), and grain yield (17.03 %), and harvest index (18.78%). This suggests that the presence of sufficient variation among tested durum wheat genotypes and they show better response to selection. Similar to present findings, Garome *et al.* (2022) reported moderate GCV for biomass yield and grain yield. Also in line with this, Alemu *et al.* (2019) report moderate GCV for grain yield and harvest index on 30 durum wheat genotype at Kulumssa and Tongo. Similarly to this, moderate GCV for biological yield and spikelet length in durum wheat was reported by Worknesh *et al.* (2019) but contrast to this, high GCV for grain yield was reported by the same authors.

On the other hand, low GCV and PCV values (< 10%) were observed for days to heading (6.6%), days to maturity (9.47%), and grain protein content (4.48%). These low GCV value traits shows the absence of sufficient variation among tested durum wheat genotypes and indicates the need for creation of variability through different breeding methods like introduction, collection, hybridization, mutation *etc.* These results agreed with the findings of Arega *et al.* (2010), Mohammed *et al.* (2011), Ahmed *et al.* (2017), Yohannes *et al.* (2022), and Demeke *et al.* (2023) who reported low GCV for days to heading, days to maturity and low GCV for grain protein content was reported by Mulatu *et al.* (2017) and Worknesh *et al.* (2019). Low PCV values (< 10%) were for days to maturity (9.92%), and grain protein content (7.98%). This low PCV indicates that considerable environmental factors and low in variation in the genotype and required creation of variation using different breeding methods. But contrasting with this, moderate GCV and PCV for days to heading and days to maturity was reported by Bantewalu *et al.* (2023).

The magnitude of differences between PCV and GCV for days to heading (5.31), spikelet length (7.24), grain protein content (3.5), harvest index (2.64), biomass (1.7) and seed per spike (1.39) were relatively high as compared to other traits. This implies influence of environmental factors for the phenotypic expression of these traits were high. This may make it difficult or practically impossible to improve the characters by direct selection of high performing genotypes. Relatively a high difference

between PCV and GCV for harvest index, biomass on durum wheat was reported by Addisu *et al.* (2021) and Garome *et al.* (2022) on bread wheat.

In contrast, the differences between PCV and GCV values were narrow for days to maturity (0.45), plant height (0.48), 1000-kerenel weight (0.68), and grain yield (0.96). This minimum gap between PCV and GCV tells more of the phenotypic expression came from genotypic influences and also the environmental influence was less and their phenotypic expression would be a good indication of genetic potential and the effectiveness of selection of genotypes based on phenotypic performance of these traits. Thus, these characters could be used as direct selection criterion for crop improvement for studied area. In line with this, Zewdu *et al.* (2021), Temesgen *et al.* (2022) and Bantewalu *et al.* (2023) reports relatively narrow PCV and GCV difference on days to heading and days to maturity in durum wheat genotype.

2. Heritability and genetic advance

Broad heritability (H₂B) estimates ranged from 30.7% to 93% (plant height) in days (Table 2). Heritability can be classified as low (0-30%), medium (30-60%) and high (60% and above) Johnson *et al.* (1955) and Falconer and Mackay (1996). Considering this definition, medium and high values were observed for many features (Table 3). The highest heritability percentage was the number of days to maturity (91.2%), plant height (93%), seeds per spike (84.9%), biomass (83.1%), thousand grain weight (87.4%), grain yield was observed as (89.7%). and productivity (76.9%). Similarly, Zewdu *et al.* (2021), reported high value of heritability in broad sense for days to heading, plant height, spike length, biomass, harvest index and grain yield on 100 durum wheat genotypes at Kellem Wollega zone of Oromia region. Also in line with this findings, Addisu (2021) reported high value in broad sense for days to heading, spike length, and grain yield on durum wheat genotype at Benishangul Gumuz Regional Stat on 50 durum wheat genotype and Berhanu *et al.* (2017) reported high value of heritability for days to heading, days to maturity, and plant height on 49 tested bread wheat genotypes. But contrasting with this, low heritability value for grain yield was reported by Mohammed *et al.* (2011), and Temesgen *et al.* (2022) and low heritability for

Table 2: Range, mean, and variability components for 10 studied traits of 36 durum wheat genotypes tested at Woleh (Sekota District) during 2021

Traits	Min	Max	Mean	SE	$\delta^2 p$	$\delta^2 g$	$\delta^2 e$	GCV	PCV	HB ²	GA	GAM (5%)
DsH	46	77	58.02	4.06	47.83	14.7	33.12	6.6	11.91	0.307	4.38	7.54
DsM	98.5	144	124.2	2.58	151.92	138.6	13.32	9.47	9.92	0.912	23.16	18.64
Pl	64.7	115	83.56	2.07	124.79	116.14	8.65	12.89	13.37	0.93	21.41	25.63
Sl	4.3	8.1	5.82	0.59	1.13	0.41	0.71	10.96	18.2	0.363	0.79	13.62
Ss	14.9	40	31.9	1.55	32.19	27.36	4.84	16.4	17.79	0.849	9.93	31.13
BM	6050	12532.1	8916.26	501.15	2971936	2469623.2	502312	17.63	19.33	0.831	2951.06	33.09
TkW	35.12	54.54	43.51	1.16	21.58	18.88	2.7	9.99	10.67	0.874	8.37	19.24
GY	2273.2	4451.27	3092.13	125.95	309146.7	277417.04	31729.7	17.03	17.99	0.897	1027.82	33.24
HI	18.48	48.33	35.64	2.56	58.27	44.8	13.47	18.78	21.42	0.769	12.09	33.92
KPP	10.15	13.9	12.58	0.56	1.006	0.378	0.63	4.48	7.98	0.375	0.77	6.16

Where Min = Minimum, Max = Maximum, SE = standard error to the mean, $\delta^2 p$ = phenotypic variance, $\delta^2 g$ = genotypic variance, $\delta^2 e$ = environmental variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, HB² = heritability in broad sense, GA = genetic advance, GAM = genetic advance as the percentage of the mean, DsH = days to heading (no), DsM = days to maturity (no), Pl = plant height (cm), Sl = spike length (cm), Ss = seed per spike (no), BM = Biomass yield (kg ha⁻¹), TkW = 1000-kernel weight (gr), GY = grain yield (kg ha⁻¹), HI = harvest index (%), and KPP = grain protein content (%).

biomass was done by Mulatu *et al.* (2023). High heritability values indicate a high level of genetic variance as component to total variance or variation observed was mainly under genetic control; were less influenced by the environmental factors in their expression and existence of heritable/inherent potential difference among the traits included in this study. But contrasting with this, Ahmed *et al.* (2017) reported low heritability value in broad sense for biomass, grain yield, and harvest index on 49 bread wheat genotypes at Jamma and Geregera.

Moderate heritability values were recorded for days to heading (30.7%), spike length (36.3 and grain protein content (37.5%). Similar moderate heritability value for grain protein content were also reported by Temesgen *et al.* (2022), on 420 durum wheat genotype at Sinana and chefa, Alemayehu *et al.* (2019) on 64 durum wheat genotype at Debre-Zeite, and also Berhanu *et al.* (2017) were reported moderate heritability value for spike length. In this result, low heritability value was not recorded in any trait. But contrasting with this, Worknesh *et al.* (2019) reported high heritability value for grain protein content.

The estimated genetic advance as percent of the mean for the traits is presented in Table 2. Genetic advance as percent of the mean (GAM) ranged from 6.16% for grain protein content to 33.92 % harvest index, indicating that selecting the top 5% of the

base population could result in an advance of 6.16 % (grain protein content) to 33.92% (harvest index) percent over the respective population mean.

Genetic advance as a percentage of the mean (GAM) was categorised as low (0-10%), moderate (10-20%) and high (20% and above) following Johnson *et al.* (1955) and Falconer and Mackay (1996). Based on this categorisation, low to high magnitudes of GAM were observed for different traits (Table 2). GAM was high for harvest index (33.92%), for grain yield (33.24%), biomass (33.09%), seed per spike (31.13%) and plant height (25.63%) indicating that these traits are controlled by additive gene action and direct selection for these traits is ideal for improvement. Similarly, Alemayehu *et al.* (2019) reported high GAM for the traits grain yield and above ground biomass. Also Worknesh *et al.* (2019) reported high GAM for grain yield, biological yield, plant height, and harvest index. In agreement with this findings, Alemu *et al.* (2019) reported high GAM for grain yield and harvest index on 30 bread wheat genotype at Asossa. In this study, moderate GAM was computed for days to maturity (18.64 %), spike length (13.62%), and thousand kernel weight (19.24%). The same moderate GAM results were reported by Berhanu *et al.* (2017) for days to maturity, spike length and thousand kernel weight. Low GAM was observed for heading (7.54%), and protein content (6.16%). In line with this, low GAM

for grain protein content was reported by Yohannes *et al.* (2020), Mulatu *et al.* (2023), Temesgen *et al.* (2022) and contrasting with this moderate GAM for grain protein content was reported by Alemayehu *et al.* (2019). This low GAM for the traits indicates these traits governed by non-additive gene action and direct selection for these traits is not effective.

In the present study, high heritability was associated with high GAM for traits plant height (93, 25.63), seed per spike (84.9, 31.13), biomass (83.133.09), grain yield (89.7, 33.24), and harvest index (76.9, 33.92) respectively (Table 2), suggesting the importance of additive gene action in the expression of these traits. This provides a chance for further improvement in advanced generations through direct selection. High estimates of heritability coupled with moderate GAM were observed for days to maturity (91.2, 18.64), and 1000-kernel weight (87.4, 19.24) respectively while moderate heritability with moderate genetic advance was noted for spike length (36.3, 13.62) respectively (Table 2). On the other hand, moderate heritability together with low genetic advance as percent of the mean were exhibited for protein content (37.5, 6.16) respectively. The presence of higher environmental factors along with non-additive gene action might be the possible causes for the lower values of heritability and GAM and it affects the direct selection of such traits via phenotypic expressions.

Correlation among yield and yield related traits

1. Correlations among traits

Estimating phenotypic and genotypic correlation coefficients among grain yield and yield related traits is important to utilize the available variability through indirect selection for high yield and other desirable traits improvement. The mean of genotypes traits was used for the correlation analysis. Assessment of the pair-wise associations among different traits revealed that some of the traits were positively correlated while others negatively correlated, indicating that improving or increasing specific trait had positive or negative influence on the other trait in such degree apparent from the correlation coefficients.

Grain yield had significant and positive correlation at genotypic and phenotypic level with plant height (0.38**), spike length (0.44**), seed per spike (0.5*), 1000-kernel weight (0.72**), biomass yield (0.89*), and harvest index (0.43*) (Table 3). This may indicate that genotypes of longer in plant height and spike, high in thousand kernel weight, biological yield, and harvest index had more grain yield than short in plant height and spike, low in thousand kernel weight, biomass yield, and harvest index. Therefore, any improvement of these traits would result in a substantial increment on grain yield. This

Table 3: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 10 traits in 36 durum wheat genotypes at Woleh (Sekota District) during 2021

Traits	DH	DM	PH	SL	Ss	TSW	BM	HI	GPC	GY
DH	1	0.90**	0.60**	0.38*	0.01ns	0.37**	-0.03ns	-0.25*	-0.22*	-0.13ns
DM	0.86**	1	0.37**	0.29*	0.04ns	-0.30*	0.02ns	-0.27*	-0.24*	-0.38*
PH	0.51**	0.6**	1	0.73**	0.12ns	0.05ns	0.56**	-0.14	-0.16ns	0.68*
SL	0.32**	0.16*	0.68**	1	0.03ns	0.14ns	0.60**	-0.23*	0.07ns	0.44*
SS	0.04ns	0.03ns	0.02ns	0.09ns	1	-0.18ns	0.11ns	0.52**	-0.01ns	0.50*
TSW	-0.62*	-0.11ns	0.08ns	0.07ns	-0.10ns	1	0.76**	0.28*	0.12ns	0.75**
BM	-0.01ns	0.06ns	0.52**	0.24**	-0.02ns	0.37**	1	-0.15ns	-0.03ns	0.89**
HI	-0.23*	-0.19ns	-0.12*	0.28**	0.58**	0.62**	-0.16*	1	-0.06ns	0.43**
GPC	-0.15ns	-0.23ns	-0.19*	0.10ns	0.13ns	0.02ns	-0.1ns	-0.04ns	1	-0.52*
GY	-0.09ns	0.01ns	0.49**	0.26*	0.11ns	0.72**	0.76**	0.36**	-0.49*	1

Where: **, *and ns; significant at 1%, 5% probability level and non-significant, respectively; DH = Days to heading (No.); DM = Days to maturity (No.); PH = Plant height; SL = Spike length; SS = Number of seed per spike; TKW = Thousand kernel weight; BM = Biomass; HI = Harvest index; GPC = Grain protein content; and GY = Grain yield.



result indicates that the traits like plant height, spike length, thousand kernel weight, biomass yield and harvest index could be exploited to increase grain yield in durum wheat genotypes. This positive significance correlation of such traits with grain yield suggested that simultaneous selection for these traits would improve grain yield and helps as indirect selection criteria and simultaneous improvement of these traits would be possible and The positive correlation of these characters with grain yield might result from the presence of strong linkage of genes or the characters may be the result of pleiotropic genes that control these characters in the same direction. This suggests a common genetic/physiological basis among these traits (Falconer, 1989). Similarly, Ahmed *et al.* (2017) reported a positive significance correlation of grain yield with plant height, 1000-kernel weight, biomass, and harvest index on genetic variability and character association in bread wheat Genotypes at Jamma and Geregera, Ethiopia. Also, in line with this, a significance correlation of grain yield with 1000-kernel weight and biological yield was reported by Sourour *et al.* (2018) on Correlation between agronomical and quality traits in durum wheat germplasm in semi-arid environment. In agreement with this, Worknesh *et al.* (2019) also reported a significance correlation of grain yield with plant height, biological yield, 1000- kernel weight, harvest index, number of seed per spike at both genotypic and phenotypic level on genetic variation for yield and quality traits of durum wheat genotype under water- logging condition in central highlands of Ethiopia. In line with this, Tigist *et al.* (2020) reported a significance correlation of grain yield with plant height, number of seed per spike, spike length, biological yield, harvest index and 1000-kernel weight at both genotypic and phenotypic level on genetic variability and association of traits in Ethiopian barley genotypes at Holetta, Central Ethiopia. Also in line with this, Demeke *et al.* (2023) reported positive and highly significant correlation of at Grain yield with plant height, number of seed per spike, biomass, and harvest index on both at the genotypic and phenotypic level on genetic variability and association of yield and yield component traits among introduced bread wheat genotypes at kulumsa, south east Ethiopia. Also in argument with this, Obsa *et al.* (2017) reported positive and

significant phenotype correlation of grain yield with biomass yield, 1000 grain weight, harvest index, plant height, and spike length on analysis of genetic variability among bread wheat genotypes for growth, yield and yield components in Bore District, Oromia Regional State.

On the other hand, grain yield had a negative-significant correlation at phenotypic and genotypic level with days to maturity (-0.38**) and grain protein content (0.52*). The result suggested that simultaneous selection for these traits would not improve grain yield. If the two desired traits are correlated negatively and are not controlled by similar or linked genes, simultaneous improvement is difficult through selection and then selection could be done separately. This suggests that selection for these traits would not improve grain yield rather may cause reduction. In line with this, a negative significance correlation of grain yield with grain protein content was reported by Sourour *et al.* (2018) and Worknesh *et al.* (2019). But in contrasting with this, a positive correlation of grain yield with days to maturity was reported by Demeke *et al.* (2023) and Addisu *et al.* (2021).

The grain yield related traits exhibited varying trends of phenotype and genotypic correlation among themselves. Days to heading had highly significant and positive correlations with days to maturity (0.86**), plant height (0.51**), spike length (0.32**) but negative and significant correlation with thousand kernel weight (-0.62*), harvest index (0.23*) (Table 3). In line with this, Obsa *et al.* (2017) reported that days to heading was associated positively and highly significantly with days to maturity, whereas positively and significantly correlated with biological yield, plant height, kernels per spike and spikelet per spike.

Days to maturity had strong positive correlation with days to heading (0.90**), plant height (0.06**), and spike length (0.16*) and this indicating that delays in maturity is associated with increase in, plant height, and spike length.

Plant height had significant positive correlations with days to heading (0.6**), days to maturity (0.37**), and spike length (0.68**), and biomass (0.52**) while significant negative association with harvest index (-0.12*), grain protein content (0.19*) (Table 3). Spike length showed significant

positive correlations with days to heading (0.38*), days to maturity (0.29*), plant height ($r_p = 0.73^{**}$) and biomass (0.24**) indicating, as spike length increases there would be a simultaneous increments of days to heading, days to maturity, plant height. But Spike length had highly significant negative phenotypic correlation with harvest index (-0.28*). Number of seeds per spike had highly significant positive correlation with harvest index (0.58**) while for the rest of traits there was no significant correlation, indicating a simultaneous increase in number of seeds per spike, days to heading, days to maturity, plant height, 1000-kernel weight, and grain protein and biological yield will be impossible. Thousand kernel weight had significant positive phenotypic correlation with biomass (0.37**) harvest index (0.62**) and hectoliter weight (0.72**), indicating a simultaneous increase in biomass, and harvest index together with 1000-kernel weight. But this trait had significant negative phenotypic correlation with days to heading (0.37**) and days to maturity (0.3*) (Table 3) and it implies, increase in thousand kernel weight decreases days to heading and days to maturity.

Biomass production was positively correlated with plant height (0.56**), ear length (0.60**) and thousand finger weight (0.76**) under poor growing and harvesting conditions ($r_p = -0.16^*$). While protein content is significantly correlated with plant height (-0.38*), it is not significant for dormancy at either phenotypic or genotypic level, and the magnitude of the genotypic correlation coefficient was greater than that of the phenotypic correlation coefficient. This suggests that the association is mainly due to genotypic and phenotypic factors that have little to do with environmental factors. However, the direction of the relationship was the same at both genotypic and phenotypic levels. A positive and significant relationship between grain yield and grain composition at the genotypic level seems to indicate interactions between traits, where genes that increase the growth of one trait also affect other traits. Therefore, traits that show a strong correlation with grain yield can be used as direct selection methods to determine genotypes for regional integration.

Generally, positive and significant association of pairs of traits justified the possibility of correlated response to selection. The negative correlations

may limite the simultaneous improvement of those traits. Based on this correlation result, grain yield had significant and positive both genotypic and phenotypic correlations with plant height, spike length, thousand kernel weight, biomass yield, and harvest index implying the possibility of correlated response to selection. Therefore, these traits could be used for indirect selection criteria during genotypes evaluation for the area.

CONCLUSIONS AND RECOMMENDATIONS

The analysis of variance revealed highly significant variations ($P < 0.01$) among the genotypes for most traits included in the study and it indicate the existence of sufficient variation among the tested durum wheat genotypes and possibility of improvement through selection. Genotype number 1, 2, 3, 5, 6, 7, 8, 10, 14, 15, 21, 23, 25, 26, 27, 28, and 29 are top yielder genotype than the average mean, the standard and the local checks and give a yield advantage up to 31.79 % over the standard checks and 36.26% over the local check. Out of 34 tested genotypes excluding the two checks, 11 genotypes, genotype number 4, 5, 9, 10, 13, 14, 19, 22, 23, 24, and 28 (30.55%) had relativity higher ($\geq 13\%$) grain protein content than the average mean (12.56%) and 4 genotypes (23.53%) were both high yielder and relatively high in grain protein content. High heritability value was observed for days to maturity, plant height, seed per spike, biomass, and grain yield and it may indicate a high level of genetic variance as the total variance or variation observed was mainly under genetic control; were less influenced by the environmental factors in their expression and existence of heritable difference among the traits included in this study. Among the traits included in these findings, plant height, seed per spike, biomass, grain yield, and harvest index were exhibited high GAM and suggesting the importance of additive gene action in the expression of these traits. Traits like plant height, seed per spike, biomass, grain yield, and harvest index offered moderate GCV, high heritability and high GAM while grain protein content had low GCV, moderate heritability and low GAM indicating that highly influence of environment on grain quality and less variation of genotypes in their grain protein



content and indicating creation of variation and selection of breeding methods to improve grain protein content.

Grain yield was significantly and positively correlated with plant height, spike length, thousand kernel weight, biomass, and harvest index at both genotypic and phenotypic levels. Generally, the information generated through this research shows the occurrence of genetic variability and traits association in the tested durum wheat genotypes. Therefore, it is recommended to use the top yielder and relatively high grain protein content genotypes for further breeding activity (including under regional variety trial or using them under crossing program). For reliable results and recommendation, it is advisable to repeat the experiment at least for one more season over locations for development of high yielder and good quality durum wheat variety.

ACKNOWLEDGMENTS

Heartily we acknowledge to Sirnka Agricultural Research Center for the aid of planting materials (seed).

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Appendix

Appendix 1: Mean values of 36 durum wheat genotypes at Woleh (Sekoat District) during 2021

G#	HsD	DsM	Ph	sl	Ss	BM	TkW	GY	HI	KPC
1	57b-j	132c-f	72.9o-q	4.3h	32.8d-h	7950i-n	48.1b-d	3783b-d	47.59ab	12.5a-h
2	50.5g-j	133.5b-d	69p-r	5.3e-h	25.8k-n	7625j-o	47.8c-e	3242.9g-k	42.57a-f	12c-g
3	58b-j	125f-g	79.2l-n	5.5e-h	30g-k	8825g-j	35.2q	3114.3i-m	35.44f-j	11.45e-i
4	50.5g-j	116.5ij	66.9qr	4.4gh	14.9o	6050p	51.4ab	2426.7r-t	40.73b-g	13.5a-c
5	60a-i	126e-g	88.2e-i	7.1a-e	24mn	10350c-f	43.9f-j	3529d-h	34.08g-k	13.75ab
6	51f-j	128d-g	87.7f-i	5.6d-h	29.5g-k	9250g-i	41.6h-o	3175h-k	34.51g-j	12.05c-h
7	64a-d	130d-g	93c-f	6.2b-g	29.5g-k	10100d-g	42.6g-n	3658.8c-f	36.34f-j	12.85a-e
8	54c-j	123.5g-i	86.7g-j	5.4e-h	30g-k	10100d-g	48.1b-d	4451.4a	44.11a-d	12.85a-e
9	48j	118.5g-i	85.1j-l	5.3e-h	27.6i-m	8425h-l	48.9b-d	2768.1m-q	32.85h-k	13.9a
10	67ab	127d-g	80.9j-n	7.8a-c	34.8b-f	9775d-h	42.8i-m	3181.5h-l	32.56h-k	13.35a-c
11	63a-e	130.5d-g	77.2m-o	5.3e-h	37.1a-d	7075l-p	39.7m-o	2319.4t	33.20h-k	11.55d-h
12	59a-j	125f-g	69.7p-r	5.9d-h	35.6a-e	7050k-o	41j-o	2730n-s	38.88c-h	12.8a-f
13	70a	130d-g	90.7d-i	5.7d-h	27.2i-m	7650j-o	40.2l-o	2913.5k-o	38.08d-j	13.05a-d
14	58b-j	125f-g	66.8r	5.9d-h	30.7f-k	8775g-k	46.8c-f	3341.8f-j	38.03d-j	13.35a-c
Mean	58.02	124..20	83.56	5.82	31.9	8916.7	43.51	3092.12	35.63	12.58
DMRT (5%)	*	**	**	*	**	**	**	**	**	*
CV (%)	10.1	3.02	3.34	14.36	7.04	7.94	3.55	5.91	10.17	6.47

DsH = days to heading (no), DsM = days to maturity (no), Pl = plant height (cm), Sl = spike length (cm), Ss = seed per spike (no), BM = Biomass yield (kg ha⁻¹), TkW = 1000-kernel weight (gr), GY = grain yield (kg ha⁻¹), HI = harvest index (%), and KPP = grain protein content (%),* and ** significant at 1 and 5% level of probability.

Appendix 1: Mean values of 36 durum wheat genotypes at Woleh (Sekoat District) during 2021 (continued)

G#	HsD	DsM	Ph	sl	Ss	BM	TkW	GY	HI	KPC
15	61a-h	133b-e	67.3qr	5.4e-h	33.6c-g	9125f-i	40.9k-o	3489.5d-g	38.38d-i	12.45a-h
16	65.5a-c	138.5a-c	80.9k-n	5.5e-h	29.5g-k	8800g-k	40.8k-o	2829.3l-p	32.37h-k	12.25b-h
17	50h-j	126.5d-g	78.4m-o	5.6e-h	21.6n	7325l-p	44.6e-i	2979.5k-n	40.71b-g	12.75a-g
18	57.5b-j	140ab	86.6g-j	8ab	32.5e-h	6450op	43.3g-l	2455.1r-t	30.03d-j	12.65a-h
19	62.5a-f	141.5a	79.9k-n	5.6d-h	28.9h-l	6875m-p	41.6h-o	2273.2t	33.13h-k	13.35a-c
20	54e-j	133b-e	78.1m-o	5.8d-h	24.7l-n	8400h-l	40.4l-o	2683n-s	32.05h-k	12.55b-h
21	55c-j	118.5g-i	74.9n-p	5.7d-h	34.8b-f	7550k-o	49.5bc	3386.1e-i	45.22a-d	12.65a-h
22	62a-g	126e-g	85.4h-k	5.1f-h	32.9d-h	9300e-i	41.2j-o	2477.9p-t	26.74kl	13.45a-c
23	51.5e-j	124gh	86.2h-j	4.9f-h	31.5e-j	8125i-m	54.1a	3684c-f	45.27a-d	13.65ab
24	57b-j	129.5d-g	64.7r	5.8d-h	37.4a-c	8100i-m	54.5a	3016.8j-n	37.39e-h	13.7ab
25	62a-g	141a	94.1c-e	8.1a	31.7e-i	8450h-l	44.3f-j	4054.3b	48.33a	12.45a-h
26	59.5a-j	144a	81.1j-m	5.8d-h	32.9d-h	10125d-g	45.8d-g	3913.8bc	38.7c-h	12.25b-h
Mean	58.02	124..20	83.56	5.82	31.9	8916.7	43.51	3092.12	35.63	12.58
DMRT (5%)	*	**	**	*	**	**	**	**	**	*
CV (%)	10.1	3.02	3.34	14.36	7.04	7.94	3.55	5.91	10.17	6.47

DsH = days to heading (no), DsM = days to maturity (no), Pl = plant height (cm), Sl = spike length (cm), Ss = seed per spike (no), BM = Biomass yield (kg ha⁻¹), TkW = 1000-kernel weight (gr), GY = grain yield (kg ha⁻¹), HI= harvest index (%), and KPP = grain protein content (%),* and ** significant at 1 and 5% level of probability.

Appendix 1: Mean values of 36 durum wheat genotypes at Woleh (Sekoat District) during 2021 (continued)

G#	HsD	DsM	Ph	sl	Ss	BM	TkW	GY	HI	KPC
27	56.5b-j	124gh	92.6c-g	5.3e-h	38.2ab	11650a-c	41.4i-o	3578c-g	30.79jk	12.75a-g
28	54.5c-j	128d-g	76.6m-o	7.4a-d	28.8h-l	8900g-k	41.3i-o	3117.3i-m	35.05g-j	13.3a-c
29	48.5ij	116j	93.1c-f	6c-h	32.5e-h	10650b-e	44.7f-h	3729.8c-e	35.01g-j	12.7a-h
30	53.5d-j	123.5g-i	85.8h-k	5.6e-h	38.1ab	11125a-d	39.8m-o	2995.7j-n	27.09kl	11.15hi
31	54c-j	105.5k	96.2b-d	5.1f-h	35.1b-f	9000f-j	40.7k-o	2790.4m-q	31.16i-k	11.2g-i
32	63a-e	99l	97bc	5.7d-h	35.8a-e	12082.1a	39.5n-p	2600.1o-t	21.51lm	10.15i
33	60a-i	99.5l	102.2b	5.4e-h	40a	11825ab	38.7op	2400st	20.30m	11.25f-i
34	64.5a-d	100.5l	86.9g-j	5.8d-h	39.2ab	12532.1a	36.2pq	2317.8t	18.5m	12.45a-h
Local Check	63.5a-d	108k	91.4c-h	6.2b-g	39.2ab	8903.8g-k	41.7h-o	2873.3l-o	32.39h-k	12.75a-g
Wohabi	63.5a-d	98.5l	115a	6.3a-f	38.6ab	6692.3n-p	42.5h-n	3036.3i-n	45.73a-c	12.5a-h
Mean	58.02	124..20	83.56	5.82	31.9	8916.7	43.51	3092.12	35.63	12.58
DMRT (5%)	*	**	**	*	**	**	**	**	**	*
CV (%)	10.1	3.02	3.34	14.36	7.04	7.94	3.55	5.91	10.17	6.47

DsH = days to heading (no), DsM = days to maturity (no), Pl = plant height (cm), Sl = spike length (cm), Ss = seed per spike (no), BM = Biomass yield (kg ha⁻¹), TkW = 1000-kernel weight (gr), GY = grain yield (kg ha⁻¹), HI = harvest index (%), and KPP = grain protein content (%), * and ** significant at 1 and 5% level of probability.

