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Phenological, physiological, and agronomic trait variation and heritability in durum wheat (*Triticum turgidum* L. subspecies *durum* Desf) genotypes

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Durum wheat is the most commonly cultivated tetraploid wheat, accounting for approximately 8% of wheat production worldwide and 10% in Ethiopia. Variation in phenotypic traits indicates genetic diversity and allows genotype identification with desirable characteristics for breeding programs. This study examined the variation, heritability, and correlation of 11 durum wheat phenotypic traits, including days to maturity (DTM), chlorophyll content (CC), spike length (SPL), spikelets per spike (NSPS), grains per spike (NGS), and grain yield (GYD). Based on a simple lattice design, field trials were conducted using 169 durum wheat genotypes in Ethiopia. Various statistical analyses, including Analysis of variance (ANOVA), broad-sense heritability (h^2b), and correlation between traits, were conducted. The genotypic variance, environmental variance, and genotype-by-environment interaction were significant for 5 phenotypic and 4 physiological traits, respectively. The three components of phenotypic variance were highly significant (P < 0.01) for DTM and GYD, and both showed moderate heritability. Based on principal component analysis, three clusters were identified, with the first 2 principal components explaining 37.3% of the variance. This study revealed that early-maturing and high-yielding landraces suitable for cultivation in lowland areas exist in the crop's gene pool and can be used to develop early-maturing cultivars.

Key words: Durum wheat, genotype-by-environment interaction, genotypic variance, grain yield, heritability, landrace.

INTRODUCTION

Durum wheat *(Triticum turgidum* L. subspecies *durum* Desf.) belongs to the Triticeae tribe of the Gramineae

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family (Soreng et al., 2015). It arose in the eastern Mediterranean and replaced its ancestor *Triticum dicoccum* as the major cultivated allotetraploid (2n = 4x = 28, AABB) wheat (Ren et al., 2013). At present, it is the most commonly cultivated form of tetraploid wheat and is primarily produced for consumption in the form of pasta and semolina (Oliveira et al., 2012; Ceglar et al., 2021). It is a valuable source of energy, minerals, and bioactive compounds for human nutrition (Saini et al., 2021). According to Sall et al. (2019), durum wheat accounts for approximately 8% of global wheat production. Turkey and Canada are the 2 largest producers of durum wheat in the world (Martínez-Moreno et al., 2022), while Ethiopia is the largest producer in Sub-Saharan Africa (Mulugeta et al., 2022; Negisho et al., 2021).

The cultivation of durum wheat in Ethiopia dates back to 1000s of years, and the country has been considered as the crop's secondary center of genetic diversity (Vavilov, 1951; Harlan, 1969). However, recent studies revealed that Ethiopian durum wheat landraces represent a distinct group within the crop's global gene pool, making the secondary center of origin and domestication of durum wheat (Kabbaj et al., 2017). Durum wheat was the most commonly cultivated wheat in Ethiopia until the 1970s, and it contained a wide array of landraces. Its germplasms are currently conserved in the Ethiopian Biodiversity Institute (EBI) as well as several gene banks around the globe, such as The Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, International Maize and Wheat Improvement Center (CIMMYT), International Center for Agricultural Research in the Rural Areas (ICARDA), and United States Agency for International Development (USAID). Following the introduction of bread wheat (*Triticum aestivum*) in the early 1940s, the production of durum wheat gradually decreased and was overtaken by bread wheat in the 1970s (Lantican et al., 2005). The introduction of improved bread wheat to Ethiopia from international breeding programs and their wide adaptation with satisfactory GYDs leading to the replacement of durum wheat with bread wheat was the primary reason for the decline in durum wheat production over time. Currently, durum wheat accounts for about 10% of the total wheat production area in Ethiopia (Tadesse et al., 2022).

A majority of durum wheat production in Ethiopia is confined to marginal lands where small-scale farmers grow low-yielding landraces under rainfed conditions, averaging about 2 t/ha. Durum wheat is grown primarily on vertisols in rainfed conditions in Ethiopia and is locally known as "yekoticha sinde" in Amharic, which indicates its suitability for cultivation on soils containing heavy black clay.

About 5 million households produce bread and/or durum wheat in Ethiopia on an estimated land area of about 2 million hectares, producing a national average yield of about 3 t/ha (Central Statistical Agency (CSA), (2021). Hence, durum wheat cultivation covers about 0.2 million hectares in the country. In addition to its use for pasta and semolina, it has been used for making various types of food in Ethiopia, including bread and "kinche", a coarse porridge made from partially ground grains.

Due to limited improved cultivars adapted to marginal lands and their low abiotic stress tolerance levels (Bekele, 1984; Eticha et al., 2005), modern cultivars cover less than a quarter of the area under durum wheat cultivation Tesemma and Bechere (1998). Recent collaborations with ICARDA and the Borlaug Global Rust Initiative (BGRI) have improved the delivery of modern cultivars to Ethiopian farmers, but their adoption remains hampered by their low tolerance to abiotic stresses, such as droughts. In the last few years, more resources have been allocated to the production of wheat (both bread and durum wheat) in Ethiopia, and as a result, wheat production has increased. For example, wheat was produced on approximately 2 million hectares in 2022/23 with an estimated yield of 5.7 million tons, an increase of 3.3% from 2021/2022 Rachel (2022).

Further expanding durum wheat production and improving its productivity are among Ethiopia's top priorities. To accomplish this, phenotypic evaluation of durum wheat genetic resources cultivated in the country is of paramount importance. This is because variation in phenotypic traits is indicative of genetic diversity and allows the identification of genotypes with desirable characteristics, such as high GYD, that can be used in breeding programs. Genetic variation is one of the key factors in improving crop plants, including durum wheat. Plant breeders rely on genetic variation to select genotypes of interest for variety development.

Estimating the phenotypic and genotypic coefficients of variation, heritability, and genetic advance is essential to develop a breeding strategy to improve a complex trait such as GYD (Addisu and Shumet, 2015). Phenotypic coefficients of variation (PVC) and genotypic coefficients of variation (GVC) provide information on the relative magnitude of variation in different populations (Falconer, 1996), which is essential for the identification of desirable genotypes for cultivar development. Crop traits under strong genetic influence show high heritability and are amenable to a high rate of genetic advance (Abinasa et al., 2011; Mengistu et al., 2018). Heritability explains the relationship between phenotypic and genetic variance. Estimating the heritability of quantitative traits provides key information on the reliability of using phenotypic values to determine the genetic merits of populations for improvement (Falconer, 1996). A number of studies have been conducted on the relationship between yield-related traits of durum wheat and its heritability (Abinasa et al.. 2011; Tsegaye et al., 2012). A large number of phenotypic traits that include phenological traits of durum wheat were reported to have high heritability due to a relatively low influence of environmental factors on them (Abinasa et al., 2011; Mengistu et al., 2018; Tsegaye et al., 2012).

Table 1. Descriptive statistics, mean square values from the analysis of variance, and coefficient of variation for 11 phenotypic traits based on field trials of 169 durum wheat genotypes carried out at 2 locations.

Trait	Min	Max	Mean	GEN (df=168)	ENV (df=1)	GEN:ENV (df=168)	Error (df=288)
DTH	50	79	62.6	26.40	265.94***	29.09	27.63
DTF	55	84	67.8	26.75	228.5**	28.50	23.40
DTM	97	129	111.4	5.95**	101000***	6.50***	4.51
CC	19.9	63.1	46.8	91.70***	0.18	0.07	35.70
NET	3	11	6.1	1.89	40.76	1.86	1.60
PH	50	110	79.0	364.4***	29.00	48.50	107.50
SL	3.6	13	5.9	2.090**	14.0337*	1.89**	1.40
NSPS	11.8	27	18.2	4.41	5.22	4.13	4.47
NGPS	10.8	73	38.6	116.40	337.60	128.2 *	97.40
GYD	0.14	4.65	13.4	95.5***	1389.4***	75.5***	18.90
TKW	16	40	19.7	24.3	15.40	24.40	20.80

*= significant at *P<0.05*,**= significant at *P<0.01*, and ***= Significant at *P<0.001,* DTH = Days to heading; DTF = Days to flowering; DTM = Days to maturity; CC = Chlorophyll content; NET = Numbers of Effective tiller per plant; PH = Plant height (cm); SPL= Spike length (cm); NSPS = Number of spikelet per spike; NGPS = number of grains per spike; GYD = Grain yield; and TKW = 1000 kernel weight. GEN = Genotype; ENV = Environment.

The present study was undertaken to assess the phenological, physiological, and agronomic traits of Ethiopian durum wheat cultivars, breeding materials, and landraces for further insight into their phenotypic variation and heritability. Additionally, the study aimed to examine the correlation between different traits and the grouping pattern of the germplasm and to identify high-yielding germplasm that could be used in durum wheat breeding programs.

MATERIALS AND METHODS

Genetic materials

In this study, 169 durum wheat accessions comprising 30 released varieties (cultivars), 75 breeding lines from the Debrezeit Agricultural Research Center (DARC), and 64 gene bank accessions were used (Supplementary Table 1).

The cultivars and breeding materials in the test materials were obtained from the DARC, which is part of the Ethiopian Institute of Agricultural Research (EIAR). The gene bank accessions are landraces originally collected from major durum wheat-producing regions of Ethiopia and were obtained from the Ethiopian Biodiversity Institute (EBI). Hereafter, Cultivars, breeding lines, and landraces will be used as “Genotypes” for simplicity.

Description of the study area

The field experiment was carried out during the 2021/2022 main crop-growing season at the Debrezeit and Akaki field experimental locations, part of DARC. The Debrezeit location is located at an altitude of 1900 m above sea level (m.a.s.l) and has a geographical position of 08°44'N latitude and 38°58'E longitude. The location is characterized by vertisol soil type, an average annual temperature of 18°C, and rainfall of 851 mm. The Akaki site is located at an altitude of 2203 m.a.s.l and has a geographical position of 08°53'N latitude and 38°49'E longitude. The site is characterized by heavy clay and vertisol soil types, an average annual temperature of 17°C, and rainfall of 1025 mm.

Experimental design

The experiment was laid out in a simple lattice design (2 replications) as described by Cochran and Cox (1957), with 13 blocks per replication and 13 plots per block. The plot size was 1.2 m × 1 m (1.2 m^2). Planting on each plot was done in 6 rows with a between-row spacing of 20 cm and within-row spacing of 10 cm. The fertilizer rate was 100 $kgha^{-1}$ urea and 100 $kgha^{-1}$ DAP. Urea was divided into 2 parts, with the first half applied at planting and the second half applied at early tillering. DAP was applied once at planting.

Phenotypic traits recorded

The genotypes were evaluated for the following phenological, physiological, and agronomic traits: Days to 50% heading (DTH), Days to 50% flowering (DTF), Days to maturity (DTM), Chlorophyll content (CC, in mgm^{-2}), Numbers of the effective tiller(NET), plant height (PH; in cm), Spike length (SPL; in cm), Number of spikelets per spike (NSPS), Number of grains per spike (NGS), GYD (in tha-1), and 1000 kernel weight (TKW; in g). These phenotypic data were collected following the International Board for Plant Genetic Resources (IBPGR)'s revised wheat descriptors (Cross et al., 1992).

DTH and DTF refer to the number of days it takes from planting to booting and flowering of 50% of the plants on a plot, respectively. DTM refers to the number of days it takes from planting to the physiological maturity of plants on a plot. GYD was estimated in t/ha at a moisture content of 12.5% based on the whole harvest of each plot. TKW of each harvest was measured based on randomly selected seeds. For the remaining traits (CC, NET, PH, SPL, NSPS, and NGS), data were collected from 5 randomly selected and tagged individual plants per plot, and average values were recorded.

Data analysis

Analysis of variances (ANOVA) and genotype-by-environment interaction (GEI) was performed using the R program version 4.10

(Team 2013). Prior to conducting the statistical analyses, the Shapiro test was used to determine whether the collected data had a normal distribution using the Shapiro test function of the R Stats package. The GEI was calculated by treating testing sites as random effects and genotypes as fixed effects. The combined analysis of variance was conducted to determine the variation resulting from genotypes, environments, and GEI. The variance components of scored traits were estimated employing the linear mixed model (LMM) fitted by the Restricted/Estimated Maximum Likelihood approach (REML) Corbeil and Searle (1976) in the R package "lme4" (Bates et al., 2015). The correlation between quantitative phenotypic traits was computed using the correlation function of the Performance analytics package in R (Peterson et al., 2019). The Principal Component Analysis (PCA) was also carried out using the fviz_pca_var (), and corr () function ggcorrplot2 (), corr () and FactoMineR () package in R.

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PVC), broad-sense heritability (h^2b), and genetic advance (GA) were computed according to commonly used equations. The overall mean values of each trait were used to estimate the *GCV* and PVC, as described by Johnson et al. (1955).

$$GCV(\%) = \frac{\sqrt{\sigma 2\,g}}{x} \times 100 \quad (1)$$

$$PCV(\%) = \frac{\sqrt{\sigma 2\,p}}{x} \times 100 \quad (2)$$

where σ^2_g and σ^2_p are genotypic and phenotypic variance, respectively, and x is the overall mean value for each trait. The GCV and PCV values were considered high, moderate, and low when the values were above 20%, 10–20%, and below 10%, respectively, according to Burton and DeVane (1953). Broad-sense heritability (h^2b) was calculated using the formula described in Allard (1960):

$$\text{Broad sense heritability } (h^2b) = \frac{\sigma^2 g}{\sigma^2 p} \times 100 \quad (3)$$

where σ^2_g and σ^2_p are genotypic and phenotypic variance, respectively. The broad sense heritability values of below 25, 25 to 50%, and above 50% were considered low, moderate, and high, according to Johnson et al. (1955). The expected genetic advance and genetic advance as a percent of the overall mean values of each trait were estimated as described in Johnson et al. (1955).

$$GA = h^2b \times k \times \sqrt{\sigma 2\,p} \quad (4)$$

$$GAM = \frac{GA}{x} \times 100 \quad (5)$$

where GA is expected genetic advance, GAM is genetic advance as a percent of the overall phenotypic mean, σ^2_p is phenotypic variance; x is the overall phenotypic mean of a trait, and k is a constant value of 2.06 for a selection intensity of 5%. The GAM is considered low, moderate, and high when its values are below 10, 10 to 20%, and above 20%, respectively, as described in Falconer (1996).

RESULTS

Descriptive statistics and analysis of variance

The days to booting (DTB), flowering (DTF), and maturity (DTM) of the 169 accessions across the 2 locations ranged from 50 to 79, 55 to 84, and 97 to 129, respectively, with the mean values of 62.6, 67.8, and 111.4 days. A large variation in CC was observed, which ranged from 19.9 to 63.1 mgm^{-2} with a mean value of 46.8 mgm^{-2} (Table 1). The genotypes also showed large variations in NET and PH, which ranged from 3 to 11 and 50 to 110 cm, respectively. The mean SPL and NSPS across accessions and locations were 5.9 and 18.2 cm, respectively. The GPS, GYD, and TKW ranged from 10.8 to 73, 0.14 to 4.65 tha^{-1}, and 16 to 40 g, respectively, with mean values of 38.6, 1.34 tha^{-1}, and 19.7 g (Table 1).

The analysis of variance (ANOVA) revealed that variance due to genotypes was significant for DTM (*P< 0.01*), CC (*P<0.001*), PH (*P<0.001*), SL (*P<0.01*), and GYD (*P<0.001*), whereas environmental variance (EV) was significant for DTB (*P<0.001*), DTF (*P<0.01*), DTM (*P<0.001*), SL (*P<0.05*), and GYD (*P<0.001*). Significant GEI was recorded for DTM (*P<0.001*), SL (*P<0.01*), NGPS (*P<0.05*), and GYD (*P<0.001*) (Table 1). Environmental variance was the highest contributor to phenotypic variance in seven of the 11 traits, including DTB, NSPS, NGPS, and TKW. Genotypic variance (GV) contributed the most to CC and PH variation among the three components of phenotypic variance. In the case of GYD, all three variance components had significant contributions with the highest contribution coming from GEI (Table 2).

Coefficients of variation

Both the GCV and PCV were estimated for the traits (Table 2). All traits had low GCV except PH (GVC = 10.7) and GYD (GCV = 11.2), which could be considered moderate, as per Burton and DeVane (1953) GCV classification. PH, NGPS, and GYD had moderate PCV with 13.5, 14.6, and 17.4 values, respectively. The PCV for the other eight traits was low (<10%).

Broad-sense heritability and genetic advance

The broad-sense heritability (h^2b) of the traits ranged from 30% for NGPS to 63 for PH (Table 2). As per the grouping of broad-sense heritability by Johnson et al. (1955), PH (63%) and CC (56%) had high heritability, while all the other traits had moderate heritability in the present study: NGPS (30%), DTB (32%), NSPS (33%), DTF (34%), SPL (35%), TKW (35%), NET (36%), DTM (40%), GYD (42%), and CC (56%).

The genetic advance (GA) of the traits ranged from 0.82 for SL to 15.6 for PH (Table 2). GYD and TKW had GA values of 5.5 and 2.9, respectively. Their corresponding GAM (genetic advance as a percent of the overall phenotypic mean) values were 41% and 14.8% in that order. Hence, the GAM for GYD and TKW can be regarded as high and moderate, respectively, as described in Falconer (1996). Other traits with moderate

Table 2. Mean values, estimates of variance components, coefficients of variation, heritability, and genetic advance for 11 phenotypic traits estimated based on field trial data for 169 durum wheat genotypes.

Trait	Mean	GCV (%)	PCV (%)	h^2b (%)	GA	GAM (%)
DTH	62.62	3.25	5.71	32	3.01	4.81
DTF	67.76	3.08	5.25	34	3.06	4.52
DTM	111.41	1.16	1.83	40	1.58	1.42
CC	46.84	7.00	9.33	56	7.40	15.79
NET	6.12	2.74	4.58	36	0.84	13.68
PH	79.04	10.74	13.54	63	15.59	19.73
SL	5.86	2.78	4.70	35	0.82	13.97
NSPS	18.15	2.46	4.29	33	1.24	6.85
NGPS	38.57	8.03	14.58	30	5.66	14.66
GYD	1.34	11.24	17.38	42	5.47	40.97
TKW	19.73	5.42	9.21	35	2.92	14.81

DTB = Days to heading; DTF = Days to flowering; DTM = Days to maturity; CC = Chlorophyll content; NET = Number of effective tillers per plant; PH = Plant height (cm); SPL= Spike length (cm); NSPS = Number of spikelet per spike; NGPS = Number of grains per spike; GYD = Grain yield; and TKW = 1000 kernel weight.

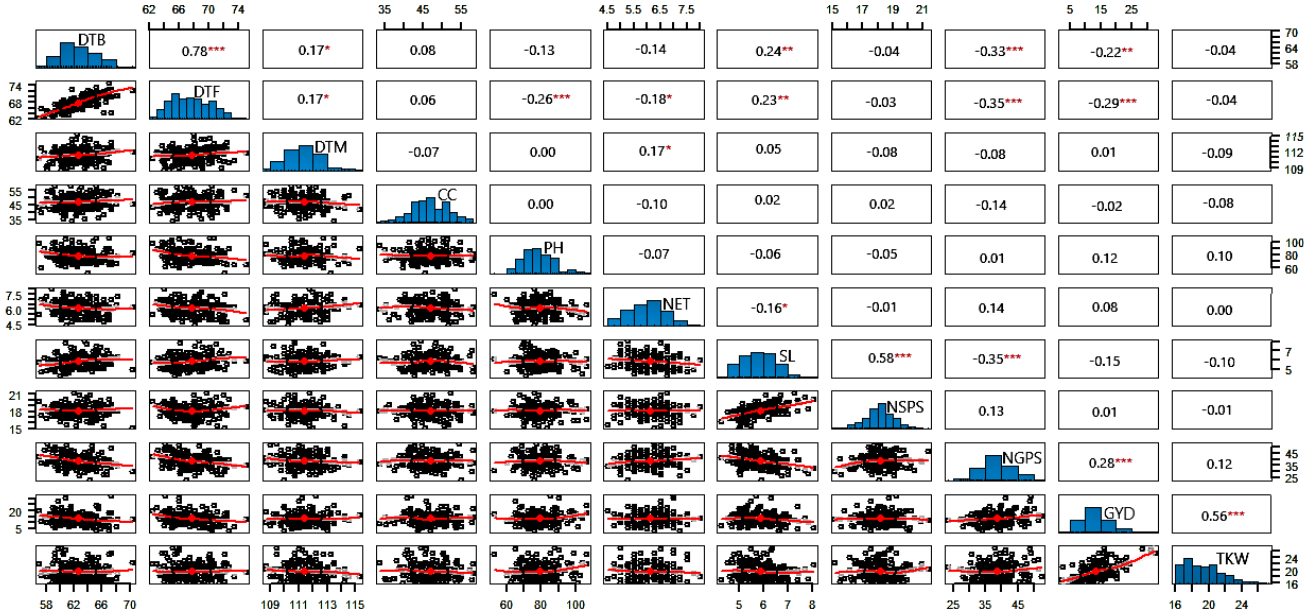


Figure 1. Pearson's correlation coefficients (r) between 11 quantitative traits targeted in the present study. *, **, and *** show significant correlations (positive or negative) between pairs of traits at $P < 0.05$, $P < 0.01$, and $P < 0.001$, respectively. DTH = Days to heading; DTF = Days to flowering; DTM = Days to maturity; CC = Chlorophyll content; NET = Number of effective tillers per plant; PH = Plant height (cm); SPL= Spike length (cm); NSPS = Number of spikelet per spike; NGPS = number of grains per spike; GYD = Grain yield; and TKW = 1000 kernel weight.

GAM were PH (19.7), CC (15.8), NGPS (14.7), SPL (14.0), and NET (13.7).

Correlation between traits

Figure 1 presents Pearson's correlation coefficient (*r*) between the 11 quantitative traits included in the present study. Highly significant positive correlation (*P<0.001*) was obtained between DTB and DTF (r = 0.78), SL and NSPS (r = 0.58), NGPS and GYD (r = 0.28), and GYD and TKW (r = 0.56) (Figure 1). Other significant positive correlations were obtained between DTF and DTB (r = 0.24; *P<0.01*), DTF and SL (r = 0.23; *P<0.01*), DTM and DTF (r = 0.17, *P < 0.05*), DTM and DTB (r = 0.17; *P<0.05*), and DTM and NET (r = 0.17; *P<0.05*).DTF had

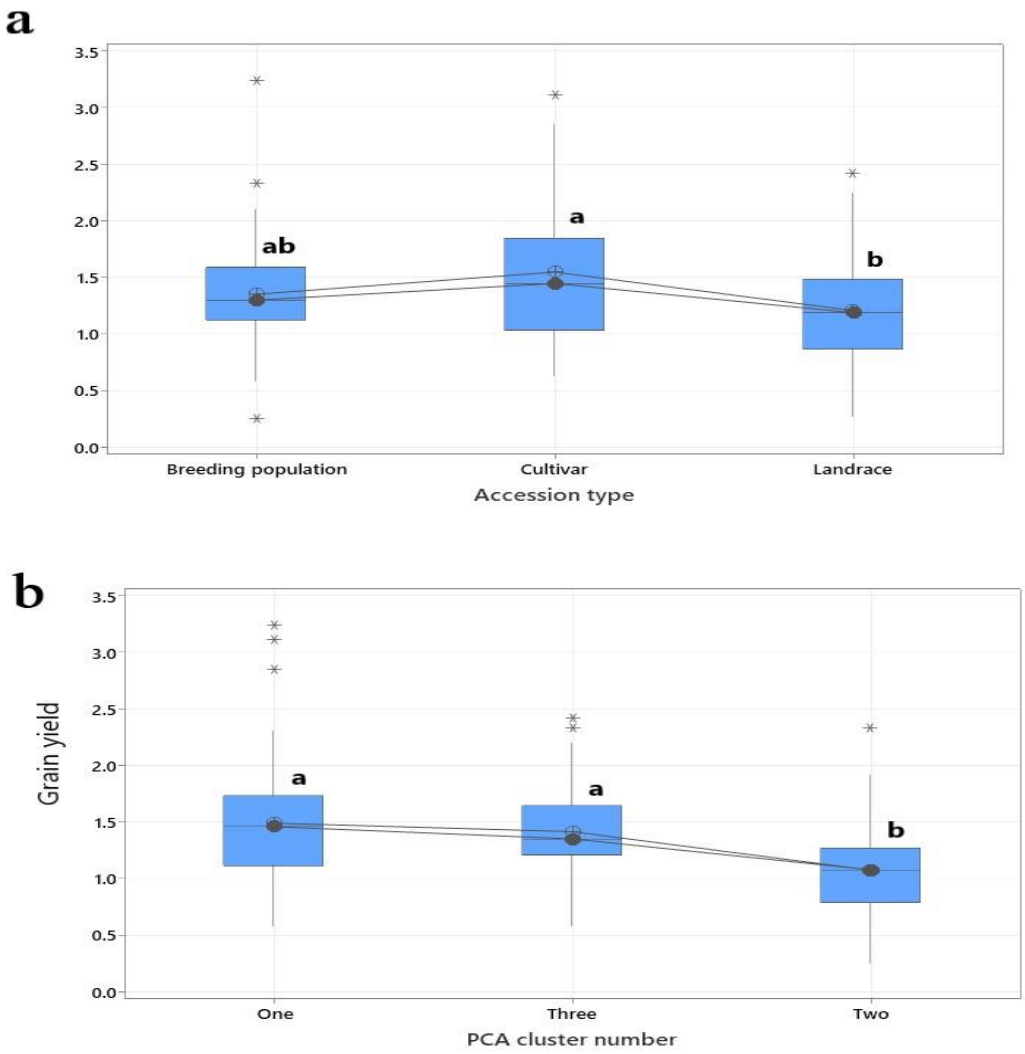


Figure 2. Box plots depicting the distribution of GYD of breeding populations, cultivars, and landraces used in this study (A) and between genotypes belonging to different clusters identified through principal component analysis (PCA) (B). Plots that do not share letters are significantly different, as revealed by Tuke's pairwise comparison conducted following Analysis of variance (ANOVA) for the 3 groups in both A and B (*P< 0.05*).

(r = -0.26), NGPS (r = -0.35), and GYD (r = -0.29). The other highly significant negative correlations were between NGPS and SL (r = -0.35) and NGPS and DTB (r = -0.33). Significant negative correlations (*P < 0.05*) were also obtained for DTB versus GYD (r = -0.22; *P < 0.01*), NET versus DTF (r = -0.18; *P < 0.05*), and NET versus SL (r = -016; *P < 0.05*). The results revealed that GYD had significant positive correlations with NGPS and TKW and significant negative correlations with DTB and DTF (Figure 1). It is noteworthy that CC was not significantly correlated with any of the other traits studied.

Mean GYD, 1000kernel weight and CC

This study showed that the mean GYD of cultivars (1.6 t/ha) was significantly higher than that of landraces (1.26 t/ha). However, the mean grain yield (1.4 t/ha) breeding populations were not significantly different from both cultivars and landraces (Figure 2B). The mean GYD, 1000kernel weight, and CC of the top ten and bottom ten genotypes ranked based on their grain yields are presented in Table 3. The mean grain yields of the top ten genotypes ranged from 2.2 (for genotype Tob-66) to 3.256 t/ha (for genotype DW193592), averaging 2.5 t/ha (Table 3). In contrast, the mean GYD of the bottom ten genotypes ranged from 0.25 (for genotype DW193505) to 0.63 t/ha (for genotype 31176-1), averaging 0.52 tha^{-1}. The top ten genotypes had a mean TKW of 23.4 g, while the bottom ten had a mean TKW of 18.0 g. Furthermore, the top and bottom ten genotypes had a mean CC of 46.8 and 46.4 mgm^{-2}, respectively. ANOVA revealed that the

Table 3. Overall mean GYD, TKW, and CC of the top ten and bottom ten genotypes ranked based on their mean GYD.

Material name	Gen. code	Source/Collection location	Category	CC_mean	GYD_Mean	TKW_Mean
DW193592*	141	CIMMYT	Breeding line	42.1	3.25	25.5
Gerardo*	89	EIAR	Cultivar	40.9	3.12	26.5
Denbi*	76	EIAR	Cultivar	46.0	2.85	27.0
33517*	7	Oromiya	Landrace	46.3	2.43	22.0
DW193593*	109	CIMMYT	Breeding line	49.85	2.33	20.0
Leliso*	82	EIAR	Cultivar	51.2	2.33	24.0
Mukiye*	67	EIAR	Cultivar	53.7	2.31	22.5
31146*	63	Oromiya	Landrace	53.8	2.26	22.0
Ejersa*	90	EIAR	Cultivar	41.7	2.22	23.0
Tob-66*	93	EIAR	Cultivar	41.8	2.20	21.0
31176-1**	22	Amhara	Landrace	45.9	0.63	17.5
DW193493**	133	CIMMYT	Breeding line	48.1	0.63	16.0
DW193569**	101	CIMMYT	Breeding line	46.1	0.63	17.5
31170**	20	Amhara	Landrace	44.9	0.59	17.0
31132**	1	Oromiya	Landrace	44.4	0.58	21.8
DW193556**	148	CIMMYT	Breeding population	53.5	0.58	18.0
31220-1**	55	INA	Landrace	47.0	0.54	17.5
33681-2**	24	Amhara	Landrace	43.8	0.49	17.0
31250-1**	57	INA	Landrace	47.0	0.27	21.0
DW193505**	124	CIMMYT	Breeding line	43.6	0.25	17.0
Top ten_Mean	-	-	-	46.8^{a}	2.53^{a}	23.4^{a}
Bottom ten_Mean	-	-	-	46.4^{a}	0.52^{b}	18.0^{b}

*= Top ten; ** = bottom ten; INA = Information not available. Gen = Genotypes. Values in the bottom 2 rows with different superscripts within a column are significantly different.

differences between the 2 groups in GYD and TKW were highly significant ($P < 001$). However, there was no significant difference between the 2 groups in CC. Among the top 10 accessions, 6, 2, and 2 were cultivars, breeding materials, and landraces, respectively. On the other hand, six of the bottom ten genotypes were landraces, whereas the remaining four were breeding populations (Table 3).

Principal component analysis (PCA)

Principal component analysis (PCA) was conducted to identify the variables that contributed the most to overall phenotypic variation. Here, genotypes were given sequential numerical codes from 1 to 169 with the corresponding genotypes names provided in (Supplementary Table 1). The first and second principal components (PC1 and PC2) accounted for 23.4 and 13.9 of the total phenotypic variance, and therefore, the 2 PCs together accounted for 37.3% of the total phenotypic variance (Figure 3). The major contributing variables to PC1 were DTF, DTH, SL, NGPS, and GYD. The first 3 variables (traits) were negatively correlated with PC1, while the last 2 were positively correlated with PC1. The major contributing variables to PC2 were NSPS and NL both negatively correlated with PC2 (Figure 3A).

The principal component analysis clustered the 169 genotypes into 3 subgroups. Interestingly, most of the top ten high-yielding accessions (Table 3) were grouped in cluster I (Figure 3C), whereas most of the bottom 10 low-yielding genotypes were clustered in cluster II. Hence, GYDs play a significant role in the clustering of durum wheat genetic resources into distinct clusters. The analysis revealed the presence of distinct genetic resources that may result in high GYDs.

DISCUSSION

Crop improvement in target traits like GYD through breeding requires genetic variation within the breeding material and heritability of the traits (Chawade et al., 2018). Heritability of traits is a measure of phenotypic variance due to genetic influences and is used in plant breeding to predict outcomes. In general, traits with high heritability are less affected by environmental factors and can, therefore, be targeted for crop improvement through phenotype-based selection (Johnson et al., 1955; Eid, 2009). Similarly, understanding the extent and distribution of genetic variation in available germplasms is crucial, as it could help breeders develop effective breeding

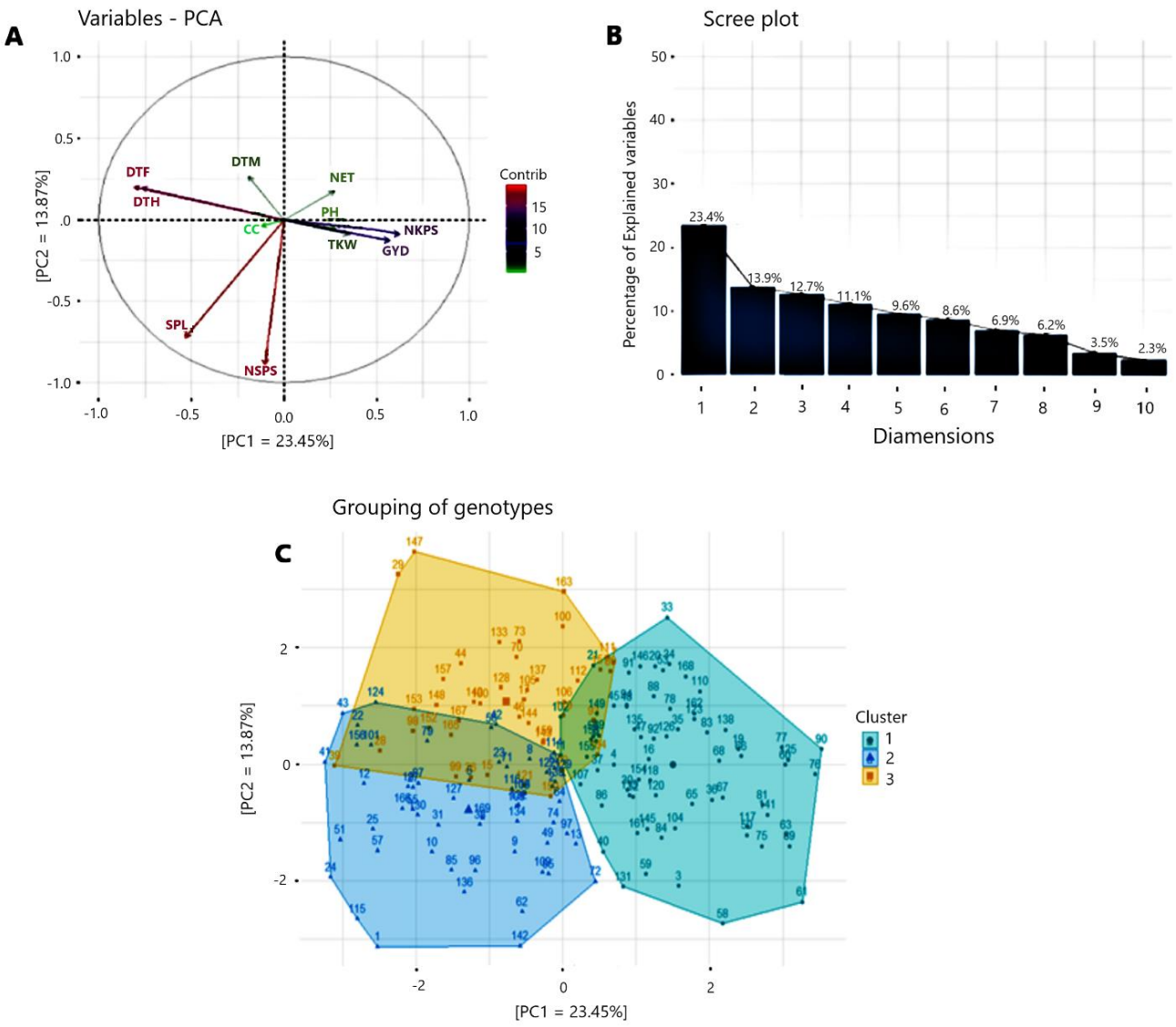


Figure 3. A PCA loading plot illustrating the correlation between traits and their contribution to the variability in the first 2 PCs, with the % and colors indicating the contribution of each trait to the principal components (A), spree plot showing the % of the total phenotypic variance explained by the first 10 PCs (B), and the clustering of genotypes based on similarities in their phenotypic traits (C). DTB = Days to booting; DTF = Days to flowering; DTM = Days to maturity; CC = Chlorophyll content; NET = Number of effective tillers; PH = Plant height (cm); SPL= Spike length (cm); NSPS = Number of spikelets per spike; NGPS = number of grains per spike; GYD = Grain yield; and TKW = 1000kernel weight.

strategies for the crops they breed. Previous studies have demonstrated that Ethiopian durum wheat landraces have the potential to contribute desirable alleles to durum wheat breeding programs. In the present study, 169 durum wheat genotypes comprising 64 landraces of Ethiopian origin, 30 cultivars, and 75 breeding lines were analyzed for 11 phenotypic traits, including GYD.

Variation in phenotypic traits

The DTM of durum wheat genotypes used in the present study across 2 environments varied from 97 to 129, respectively, with a mean of 111.4 days. As revealed by ANOVA, DTM displayed highly significant variation for all three components of phenotypic variance (GV, EV, and GEIV; $P < 0.01$). In their study involving 420 durum wheat genotypes (mostly Ethiopian landraces), Mulugeta et al., (2023) found that DTM varied from 127-153 days across 5 environments with a mean of 136 days. Although the 2 studies used germplasm mainly originated from the Ethiopian durum wheat gene pool, on average, the genotypes included in this study reached physiological maturity faster than those reported in Mulugeta et al.

(2023). Besides the genetic differences between some genotypes used in the 2 studies that contribute to variation in maturity, environmental variation of the study sites, such as altitudes could be the main contributors to the differences, as environmental variance is the major contributor to variation in DTM (P<0.001).

The study sites used in the present study ranged in altitude from 1900 to 2203 m.a.s.l, while those used by Mulugeta et al. (2023) ranged from 2203 to 2400 m.a.s.l. Although genotypes interact differently with the environment as demonstrated by highly significant variances in GEI, plants mature more slowly at higher altitudes than at lower altitudes in general, which is demonstrated in the present study as well as in that of Mulugeta et al. (2023). This is due to a relatively cooler temperature at higher altitudes than at lower altitudes.

Developing improved cultivars for different agroecologies requires knowledge of variation in DTM. In this study, the DTM of the genotypes ranged from 97 to 107 days at Debrezeit location (1900 m.a.s.l) while it ranged from 114 to 129 days at Akaki location (2203 m.a.s.l). Wheat production (both bread wheat and durum wheat) has significantly increased in Ethiopia recently, as the government is actively working towards food self-sufficiency. Wheat cultivation has expanded both to lower and higher altitudes, thereby increasing its attitudinal range. The results of the present study showed that early maturing accessions that fit well into lowland areas exist in the durum wheat genetic resources available in Ethiopia. This suggests that such genotypes could serve as the basis for developing early-maturing cultivars suitable for cultivation in areas where moisture deficits and short rainy seasons affect the production of this crop. These genotypes may also be suitable in similar environments worldwide where durum wheat is grown. DTM showed moderate broad-sense heritability (h^2b) in this study, in line with the report of Dagnaw et al. (2022). However, Wolde et al. (2016) reported high broad-sense heritability for this trait.

The CC of the durum wheat genotypes used in the current study varied about threefold and showed a highly significant genotypic variance. However, CC was not significantly correlated with GYD or any other traits targeted in this study. This is in contrast to previous studies, which reported a significant positive correlation between these 2 traits in durum wheat (Yıldırım et al., 2010; Talebi, 2011). Further research will shed light on the factors contributing to correlation inconsistencies between these traits.

Similar to previous studies (Mulugeta et al., 2022; Dagnaw et al., 2022), the present study found several-fold variation among genotypes in GYD, with highly significant variances due to genotype, environment and GEI. GYD demonstrated moderate broad-sense heritability (h2b = 42%) and genetic coefficient of variation (GCV = 11.2%), with high genetic advance as a percentage of the overall phenotypic mean (GAM = 41%). This consistency is noted with previous studies (Abinasa et al., 2011; Mulugeta et al., 2023; Dagnaw et al., 2022).

In plant breeding, considering estimates of genetic advance and heritability jointly can effectively estimate genetic progress achieved through selecting desirable individuals (Johnson et al., 1955; Ghuttai et al., 2015).

Hence, GYD is suitable for selecting desirable genotypes in breeding programs. It is desirable in plant breeding for traits to have a significant positive correlation, as this allows their simultaneous improvement directly or directly through breeding. GYD correlated significantly positively with NGPS and TKW, in agreement with previous reports (Mulugeta et al., 2023; Dagnaw et al., 2022), and negatively with DTB and DTF.

Given that TKW and NGPS are yield component traits, their positive correlations with GYD are expected. Although GYD was negatively correlated with DTB and DTF, it was not associated with DTM in this study. This suggests that there is no strong trade-off between early maturity and high GYD, and hence, developing early maturing cultivars with high GYD through breeding is possible. The fact that DTF was negatively correlated with the NET may indirectly suggest a positive contribution of NET to GYD, which was reported in previous studies (Sharadhi et al., 2023).

In this study, PH ranged between 50 and 110 cm across the 2 sites, which is within the range reported by Zewdu et al. (2021) for Ethiopian durum wheat. The range of SPL obtained in this study (3.6 to 13 cm) was, however, slightly narrower than the range reported by Zewdu et al. (2021) (4.8 to 19.3 cm). These differences could be attributed to both the environmental conditions in which the field experiments were conducted as well as the genetic differences between the germplasm used in each study. Interestingly, the NSPS and NGPS showed significant positive and negative correlations with spike length (SPL). It appears that durum wheat plants with longer spikes have fewer seeds per spike, a finding also reported by Sharadhi et al., (2023), despite having more spikelets. Thus, the results of this study indicate that SPL cannot be considered a reliable indicator of GYD.

Mean GYD, 1000 kernel weight, and CC

The higher mean GYD of cultivars than that of landraces obtained in this study and previous studies (Mengistu et al., 2018; Ayed et al., 2021; Chegdali et al., 2022) is clear evidence of the role of plant breeding in improving crop yields and achieving sustainable food security. However, it should be noted that 2 of the top ten genotypes in terms of GYDs were landraces (accessions 33517 and 31146).

This indicates the existence of high-yielding landraces in the Ethiopian durum wheat gene pool, in agreement with previous research (Mengistu et al., 2018; Mulugeta et al., 2022), which could be used in the durum wheat breeding program for further improvements. It is

particularly possible since GYD had moderate broad-sense heritability and high expected genetic advance. The higher mean TKW of the top ten genotypes compared to the bottom ten genotypes ranked based on GYDs is in line with the positive correlation between the 2 traits obtained through correlation analysis.

Clustering pattern of accessions

A principal component analysis of the 169 genotypes identified three clusters (Figure 3C). When selecting genotypes for breeding and conservation, more emphasis should be placed on traits with higher contributions to grouping the genotypes into clusters. In this regard, GYD, NGPS, DTF, DTH, SL, and NSPS were major contributors to the obtained clustering pattern. On average, genotypes in Clusters 1 and 3 had significantly higher GYDs than those in Cluster 2 (Figure 2B). Accordingly, most of the high-yielding genotypes (Table 3) were clustered in Cluster 1, whereas most of the low-yielding genotypes were clustered in Cluster 2. Additionally, GYD was a major contributing factor to the clustering pattern along PC1 (Figure 3A). This shows that GYD plays a significant role in the clustering of durum wheat genetic resources into distinct groups. Additionally, in line with previous studies (Mulugeta et al., 2022; Alemu et al., 2020), the results suggest the presence of distinct durum wheat genetic resources that may result in higher GYDs.

Conclusions

Genetically, diverse breeding materials and heritable target traits are necessary for crop improvement. Hence, to succeed in traditional and genomic-driven plant breeding, it is necessary to understand the extent and distribution of genetic variation in the gene pool, the components contributing to phenotypic variation, and the heritability of the traits targeted for improvement. In this regard, all three components of phenotypic variance were significant for (DTM), which showed moderate broad-sense heritability (h^2b). GYD showed several-fold variation among genotypes where genotype, environment, and GEI variances were highly significant. Similarly, the (CC) of the genotypes varied threefold, although it was not correlated with GYD. On the other hand, GYD demonstrated high GAM, moderate GCV, and moderate h^2b, making it an appropriate trait for selecting genotypes for breeding.

A significant positive correlation between desirable traits allows their simultaneous improvement through breeding. DTM was not correlated with GYD in this study, suggesting that there is no strong trade-off between early maturity and high GYD, making it possible to breed early-maturing cultivars with high GYDs. The NSPS and (NGPS correlated positively and negatively with SL, suggesting that plants with longer spikes has fewer seeds per spike despite having more spikelets. Therefore, SL cannot be considered a reliable indicator of GYD. Grain yield was higher for cultivars than landraces, supporting plant breeding's role in improving crop yields and sustainability. In addition, early-maturing landraces suitable for cultivation in lowland areas with moisture deficits and short rainy seasons exist in the crop's gene pool and, hence, are suitable for developing early-maturing cultivars. Moreover, this study revealed that the Ethiopian durum wheat gene pool contains high-yielding landraces that could be used locally and globally to improve GYDs.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Table S1. Description of durum wheat genotypes used in the experiment

S/N	Accession	Region of origin/Source	Geographic position	Altitude	Category	Germplasm provider
1	31132	Oromiya	07°00'00"N, 39°24'00"E	2583	Landrace	EBI
2	33840	Oromiya	07°00'00"N, 39°42'00"E	2583	Landrace	EBI
3	31215-1	Oromiya	07°15'00"N, 39°07'00"E	2740	Landrace	EBI
4	31215-2	Oromiya	07°15'00"N, 39°07'00"E	2740	Landrace	EBI
5	31209	Oromiya	07°55'00"N, 39°36'00"E	2520	Landrace	EBI
6	33555-2	Oromiya	08°38'00"N, 38°56'00"E	1870	Landrace	EBI
7	33517	Oromiya	08°47'00"N, 38°54'00"E	INA	Landrace	EBI
8	33239	Oromiya	08°51'00"N, 39°15'00"E	INA	Landrace	EBI
9	33244	Oromiya	08°51'00"N, 39°04'00"E	2300	Landrace	EBI
10	33511	Oromiya	08°51'00"N, 39°15'00"E	INA	Landrace	EBI
11	33496-1	Oromiya	08°52'00"N, 38°47'00"E	INA	Landrace	EBI
12	33761	Oromiya	08°58'00"N, 38°59'00"E	2500	Landrace	EBI
13	31637	Oromiya	08°58'00"N, 38°59'00"E	2500	Landrace	EBI
14	31609	Oromiya	09°01'00"N, 38°20'00"E	INA	Landrace	EBI
15	31979	Oromiya	09°01'00"N, 38°56'00"E	2510	Landrace	EBI
16	33523	Oromiya	09°01'00"N, 39°03'00"E	2400	Landrace	EBI
17	31141	Oromiya	09°03'00"N, 39°05'00"E	2510	Landrace	EBI
18	31292	Oromiya	09°11'00"N, 39°10'00"E	2580	Landrace	EBI
19	31137	Oromiya	09°35'00"N, 42°07'00"E	INA	Landrace	EBI
20	31170	Amhara	09°45'00"N, 39°40'00"E	2920	Landrace	EBI
21	31218	Oromiya	09°46'00"N, 38°45'00"E	2800	Landrace	EBI
22	31176-1	Amhara	09°49'00"N, 39°42'00"E	3020	Landrace	EBI
23	31176-2	Amhara	09°49'00"N, 39°42'00"E	3020	Landrace	EBI
24	33681-2	Amhara	10°27'00"N, 38°43'00"E	2520	Landrace	EBI
25	33499	Amhara	11°20'00"N, 38°32'00"E	2800	Landrace	EBI
26	31230-1	Amhara	12°25'00"N, 37°20'00"E	1750	Landrace	EBI
27	31151	Tigray	12°43'00"N, 39°32'00"E	2713	Landrace	EBI
28	33778	Amhara	13°04'00"N, 37°48'00"E	2670	Landrace	EBI
29	31374	Tigray	13°30'00"N, 39°37'00"E	INA	Landrace	EBI
30	31368-3	Tigray	13°30'00"N, 39°37'00"E	INA	Landrace	EBI
31	31372-1	Tigray	13°30'00"N, 39°37'00"E	INA	Landrace	EBI
32	31372-2	Tigray	13°30'00"N, 39°37'00"E	INA	Landrace	EBI
33	31255	Tigray	13°30'00"N, 39°27'00"E	INA	Landrace	EBI
34	31356	Tigray	14°7'00"N, 38°43'00"E	2000	Landrace	EBI
35	31358-2	Tigray	14°14'00"N, 39°30'00"E	2430	Landrace	EBI
36	31334-2	Amhara	INA	2033	Landrace	EBI
37	31158	INA	INA	INA	Landrace	EBI
38	31237	INA	INA	INA	Landrace	EBI
39	31239	INA	INA	2350	Landrace	EBI
40	31246	INA	INA	INA	Landrace	EBI
41	31248	INA	INA	INA	Landrace	EBI
42	31266	INA	INA	INA	Landrace	EBI
43	31269	INA	INA	INA	Landrace	EBI
44	31297	INA	INA	2300	Landrace	EBI
45	31299	INA	INA	1470	Landrace	EBI
46	31326	INA	INA	INA	Landrace	EBI
47	31354	INA	INA	2550	Landrace	EBI
48	31361	INA	INA	INA	Landrace	EBI
49	31696	INA	INA	INA	Landrace	EBI

Table S1. Contd.

50	33235	INA	INA	INA	Landrace	EBI
51	33283	INA	INA	INA	Landrace	EBI
52	33286	INA	INA	INA	Landrace	EBI
53	33296	INA	INA	2250	Landrace	EBI
54	31220-2	INA	INA	INA	Landrace	EBI
55	31220-1	INA	INA	INA	Landrace	EBI
56	31230-2	INA	INA	INA	Landrace	EBI
57	31250-1	INA	INA	INA	Landrace	EBI
58	31252-2	INA	INA	2340	Landrace	EBI
59	31260-1	INA	INA	INA	Landrace	EBI
60	31260-2	INA	INA	INA	Landrace	EBI
61	31334-1	INA	INA	INA	Landrace	EBI
62	33581-2	INA	INA	INA	Landrace	EBI
63	31146	Oromiya	INA	INA	Landrace	EBI
64	33230	Oromiya	INA	INA	Landrace	EBI
65	Yerer	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
66	Oda	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
67	Mukiye	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
68	Bakalcha	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
69	Utuba	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
70	Mangudo	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
71	Bichena	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
72	Obsa	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
73	Malefia	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
74	Alem Tena	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
75	Gin chi	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
76	Denbi	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
77	ude	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
78	Boohai	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
79	Foka	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
80	Robe	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
81	Selam	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
82	Leliso	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
83	Tesfaye	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
84	Hitosa	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
85	Werer	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
86	Tate	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
87	Asassa	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
88	Dire	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
89	Gerardo	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
90	Ejersa	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
91	Bullalla	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
92	Ld-357	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
93	Tob-66	EIAR	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
94	Cocorit/71	CIMMYT	08°53'39"N, 38°49'13"E	2400	Cultivar	EIAR
95	DW193633	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
96	DW193571	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
97	DW193477	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
98	DW193540	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
99	DW193600	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
100	DW/F3DZ #18/8	NA	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
101	DW193569	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR

102	DW193623	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR

Table S1. Contd.

103	DW193497	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
104	CDSS09B00408D-5Y-014B-4Y-5B-9Y-3B-06Y-0B	NA	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
105	DW193513	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
106	DW193534	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
107	DW193471	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
108	DW193470	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
109	DW193593	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
110	DW/F3DZ#59/24	NA	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
111	DW193552	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
112	DW193616	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
113	DW193546	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
114	DW193472	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
115	DW193547	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
116	DW193562	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
117	DW193566	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
118	DW193605	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
119	DW193635	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
120	DW193605	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
121	DW193631	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
122	DW193627	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
123	DW193484	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
124	DW193505	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
125	DW193581	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
126	DW193575	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
127	DW193468	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
128	DW193583	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
129	DW/F3DZ #20/12	NA	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
130	DW193641	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
131	DW193636	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
132	DW193608	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
133	DW193493	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
134	DW193555	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
135	DW193495	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
136	DW193490	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
137	DW193518	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
138	DW193577	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
139	DW193637	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
140	DW193588	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
141	DW193592	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
142	DW193626	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
143	DW193590	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
144	DW193479	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
145	DW193632	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
146	DW193584	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
147	DW193499	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
148	DW193556	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
149	DW193599	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
150	DW193567	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
151	DW193504	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
152	DW2018	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR

153	DW193613	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR

Table S1. Contd.

154	DW193512	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
155	DW193614	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
156	DW193558	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
157	DW/F3DZ #42/22	NA	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
158	DW193519	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
159	DW193537	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
160	DW193630	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
161	DW193640	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
162	DW193549	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
163	DW193551	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
164	DW193528	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR
165	DW193579	CIMMYT	08°53'39"N, 38°49'13"E	2400	Breeding population	EIAR

INA = Information not available