

Full Length Research

Genetic Variability for Malting Quality, Yield and Yield Related Traits of Ethiopian Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes

¹Gobezayohu Haftu Mengesha, ²Dr. Firew Mekbib Hailemariam, ³Dr. Taye Tadesse Mindaye and ⁴Dr. Berhane Lakew

¹Cereals Breeding, Ethiopian Institute of Agricultural Research Mekhoni Agricultural research Centre, Maichew, Tigray Ethiopia, P.O.Box = 47, Mekhoni, Ethiopia. Email = gobazicc@gmail.com, Telle = +251346641394/42066/44797

²Plant Sciences, Haramaya University, Harar Ethiopia, P.O. Box = 138, Dre Dawa Ethiopia.

Email = firew.mekbib@gmail.com, +251346641394/42066/44797

³Plant breeding, Melkassa agricultural research centre, Melkassa Ethiopia, P.O. Box = 436, Melkassa Ethiopia.

Email = tayabo@gmail.com, +251915081067

⁴Plant breeder, Holeta agricultural research centre, Holeta Ethiopia, P.O.Box = 31, Holeta Ethiopia.

Email = berhanekaz@yahoo.com, Telle = +251911002198

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Sorghum is drought tolerant C₄ tropical crop with wide diversity grown for food, feed and beverages. There is a growing demand for food and malt type sorghum varieties due to the low supply of malt barley, climate resilient and gluten free nature of the crop. Therefore, this study was initiated to characterize the malting quality, genetic variability and heritability of sorghum genotypes. The experiment was conducted at Fachagama in Mehoni ARC, Northern Ethiopia in 2016/17 in α - lattice design. Data were collected on agronomic traits and 300g pure seeds of each plot were malted (18hr steeping, 72hr in 28 °c germinated and 24hr in 50 °c dried) for malt quality analysis. The genotypes Baji, Tseada Achire, Abare-1, Yeju, Dabar, Degalit yellow-1 and Degalit Yellow produced better malt quality; considering the most important malt quality parameters of DP, FHWE, CP, ET and MWL. High heritability ranging 85.00-98.99 was observed for all the traits, except for PH (77.83) and CP (61.42) which was moderate. Thus wide genetic variability, medium to high GCV, moderate to high heritability and high GAM (20.89-128.43) of DF, DM, PH, NPT, GY, TKW, KW, KT, MWL and DP indicating these traits were controlled by additive genetic factors and are important for sorghum yield and malt quality improvement. Significant differences among the genotypes for all traits found and those genotypes with sufficient DP and wort extracts could be used for brewing commercial beers and soft drinks.

Key words: Diastatic power, Genetic advance as percent of mean, genotypic coefficient of variation, Heritability, Phenotypic coefficient of variation, Sorghum malt

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INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is classified under the grass family of Poaceae, genus Sorghum Moench (Poehlman and Sleper, 1995). It is originated in

Africa, more precisely in Ethiopia, between 5000 and 7000 years ago Vavilov, (1951) and/or diversity Harlan, (1992). The crop has spread to other parts of Africa,

India, and Southeast Asia, Australia and the United States (Mesfin and Tileye, 2013).

Sorghum is drought tolerant C_4 tropical crop with wide diversity. It is the fifth most important cereal crop in the world with grain production grown in arid and semi-arid parts of the world (FAO, 2016). It contributes to the protein and energy requirements for millions of people mainly living in Sub Saharan Africa and Asia Orr *et al.*, 2016). Sorghum is one of the major staple food crops on which the lives of millions of Ethiopians depend. The majority of grain production goes for the preparation of diverse food recipes, like porridge, "injera", "Kitta", "Nifro", infant food and syrup (Asfaw, 2007). A small fraction of the grain it is being malted for local beverages, such as "Arake", "Tella" and "Borde" (Abegaz *et al.*, 2002).

Malting is the controlled germination of cereals in moist air, under controlled conditions for mobilizing the endogenous hydrolytic enzymes, especially α -amylase and β -amylase enzymes of the grain. The malting process modifies the grain structure, so that it will be readily solubilized during the brewing process to produce fermentable wort (Taylor and Belton, 2002).

Regardless of the availability of several other cereal types, barley is the grain of choice for malting in modern brewing (Taylor and Dewar, 2000). In tropical Africa, however, barley cultivation has not seen any success and industries are relying on imports of this grain. This is still problem to the brewing industries and also to the economies of mostly tropical African countries. Researchers showed next to barley sorghum malt found the most appropriate alternative for brewing Taylor *et al.*, (2006); Ogbonna, (2011); Agu and Palmer, (2013).

Sorghum has been used for brewing beer in Africa for ages, mainly for producing opaque beer in many parts of Sub-Saharan Africa. Brewing clear lager beer from sorghum was put on industrial platform by Nigeria in the 1980s after government banned importation of malt barley. The brewing qualities of sorghum are further advanced due to gluten-free nature of sorghum protein to substitute the gluten rich cereals in the diet of people suffering from celiac disease Delserone, (2007); Anheuser-Busch, (2010) and evaluation on the malting and brewing qualities of the sorghum varieties have resulted in successful use of sorghum malt in the brewing of beers in Nigeria and other countries, including Cuba, Israel, Mexico the South Africa and USA Ijasa, *et al.*, (2011).

In any crop improvement program, the first thing that the breeder looks into is the existence of

genetic variability for the characters of interest (Acquaah 2012). Hence, estimation and Selection of genotypes meeting specific local food and industrial requirements of the existing variability in the available germplasm is essential to breeders for food security.

For the first time sorghum is used as a beer ingredient

in the form of adjunct in Ethiopia by Meta Beer company (subsidiary of Diageo) in 2016 (2SCALE, 2017). Eventhough, Ethiopia is the centre of origin with diverse genetic resources of sorghum; several improved food sorghum varieties are adapted to semi arid tropical regions; only two malt sorghum varieties (Red Swazi and Macia) have been released and little efforts have been made to promote the varieties to be used by the brewery industries and the landraces were not characterized, for their malting potential to be used as malt and considerable scope remains to use in the brewing industries Asfaw, (2007); Asfaw *et al.*, (2011). This is mainly due to sorghum industrial processing is largely missed (EIAR, 2014), high demand of sorghum grain for food, and lack of access for potential malt sorghum varieties. It has been speculated that the demand for malting type sorghum will be increased for the reason that sorghum is climate resilient crop and the area for barley production is not growing with malt demand. Hence, it is high time to explore the genetic variability in order to address the growing malting sorghum demand with higher malting quality and yield. Hence, selecting genotypes meeting the specific malt quality clear malt drink, malted extruded instant flour, to save foreign currency used to import malt barley and improve livelihood of sorghum farmers. Therefore, the study was undertaken with the following objectives) to determine the malting quality of sorghum genotypes and ii) to assess genetic variability, heritability, and genetic advance for malting quality, yield and related traits.

MATERIALS AND METHODS

Description of the Experimental Area

The experiment was carried out at Mehoni Agricultural Research center (MhARC) Fchagama test station site in Raya Azebo Woreda using supplementary irrigation in 2016/2017 cropping season. Fachagama is located 668 Km from the capital Addis Ababa and about 120 Km south of Mekelle, capital city of Tigray regional state. Geographically the experimental site is located at 12.70° N latitude and 39.70°E longitude with an altitude of 1578 m.a.s.l. The site receives a mean annual rainfall of 539 mm with an average minimum and maximum temperature of 12.81 and 23.24°C, respectively. The soil textural class of the experimental site was clay with pH of 6.89 (Gebremeskel *et al.*, 2017).

Treatments and experimental design

The study genotypes (Table 1) including the two checks (Redswazi and Macia) were kindly availed by the national

Table 1. List of fifty six Sorghum genotypes including two checks used in the study

G.N	Genotype	Seed color	Seed Source	G.N.	Genotype	Seed color	Seed Source
1	Abamelko	Brown	JARC	29	Degalit Yellow	Yellow	SARC
2	AL-70	White	MARC	30	Demhay	Chalky	TARI
3	Baji	Red	MARC	31	Dima	Red	MARC
4	Birimash	Red	MARC	32	Jamiyu	Red	MARC
5	Osmel	Red	MhARC	33	Jeru	Yellow	MARC
6	Chiro	Red	MARC	34	Jigurti	Red	MARC
7	Dagim	Red	MARC	35	Kodem	Yellow	MARC
8	E36-1	White	MARC	36	Lalo	Brown	TARI
9	Emahoy	Brown	PARC	37	Masugi Red	Red	MARC
10	Merawi	Chalky	MhARC	38	Masugi Yellow	yellow	MARC
11	AbaAre-1	White	MARC	39	Tetron White	Chalky	MARC
12	America-1	Red	MARC	40	Tewzale	Red	TARI
13	Baduqane	Yellow	MARC	41	Tseada Achire	White	TARI
14	Berjokecoll#1	Red	MARC	42	Tseada chimure	White	MARC
15	DagalitYellow-1	Yellow	MARC	43	Wediarse	Chalky	TARI
16	Gorade-2	White	MARC	44	Wegere	Yellow	MARC
17	Hodem-1-3	Yellow	MARC	45	Wetetbegunchie	Red	MARC
18	JimmaLocal-2	Brown	MARC	46	Wode aker	Chalky	MARC
19	Marye#2	Yellow	MARC	47	Yeju	White	SARC
20	Meminay-4	White	MARC	48	ZeriAdis	Yellow	TARI
21	Welenchity Col # 3	Redish	MARC	49	Goronjo	White	MARC
22	Wollo Col#050	Red	MARC	50	Gedo	White	SARC
23	Gano	Yellow	MhARC	51	Melkam	White	MARC
24	Bobe red	Red	MARC	52	Misikir	White	SARC
25	Bobe white	White	MARC	53	Dekeba	White	MARC
26	Dabar	White	MARC	54	Seredo	Buff	MARC
27	Dagnaw	Yellow	TARI	55	Macia (check)	White	MARC
28	Degalit	Yellow	JARC	56	Redswazi (check)	Buff	MARC

Key: TARI = Tigray Agricultural Research Institute, MARC = Melkassa Agricultural Research center, MhARC = Mehoni Agricultural Research center, SARC = Sirinka Agricultural Research center, JARC = Jimma Agricultural Research center and PARC = Pawe Agricultural Research center and G.N=Genotype number

Sorghum Research Program of Melkasa Agricultural Research Center (MARC). The genotypes are selected based on their dominancy in production and historical usage for local beverage preparation and for some are recently released food varieties to evaluate whether they can to use for both food and malting. The treatments (genotypes) were grown in (7, 8) α - lattice in two replications, 2m path width between replications and 0.5 m path between plots found within incomplete blocks but no path for plots between (across) incomplete blocks. The gross size of experimental plot was 1.5 m x 3 m (4.5 m²) accommodating two rows with spacing of 75 cm between rows and 20 cm between plants. The two outer most rows at both ends of first and the last blocks were treated as borders leaving two middle rows of each of the genotypes for sampling. The experimental field was prepared by using farm tractor plough according to semi conventional farming practice. It was sown July 11/2016

at a spacing of 75 x 20 cm. The full dose of DAP (46% P₂O₅: 18% N) at the rate of (100 kg/ha) were drilled at planting. Nitrogen fertilizer in the form of urea (46% N at a rate of 100 kg/ha were applied half at sowing by mixing with DAP 5 cm apart from the seed and the remaining half top-dressed at knee height. The seeds were sown by hand in the rows as uniformly as possible and covered with soil manually and thinning of seedlings was done two weeks after emergence.

Data Collection and Measurements

Agronomic Traits

Agronomic data's were collected from two rows in each plot on the following parameter: Days to flowering (DF), days to maturity (DM), plant height (PH cm), number of

productive tillers per plant (NPT), thousand kernel weight (TKW g) and grain yield (GY kg): The moisture level for TKW and GY adjusted to 12.5% according to Biru (1979).

$$\text{Adjusted seed weight} = \text{Initial seed weight} \left(\frac{100 - \text{OMC}}{100 - \text{DMC}} \right)$$

Where: OMC = Original moisture content and DMC = Desired moisture content

Sorghum grain quality parameters

Hectoliter weight (HLW Kg/hL): Calculated using the instrument which uses hectoliter weight, electronic balance and moisture tester together according to the American Association of Cereal Chemists (AACC) (2000) method 55-10 and the obtained values were adjusted to moisture content of 12.5% by the following equation

$$\begin{aligned} & \text{HLW (12.5\% M basis)} \\ & = \text{HLW} \frac{100 - \% \text{ moisture measured in the grain}}{100 - 12.5} \end{aligned}$$

Where, HLW= Hectoliter weight

Kernel size (KS): The kernel width (KW), kernel length (KL) and kernel thickness (KT) of ten kernels of each variety of each plot were measured and average value were taken using digital caliper (+0.01 mm) according to modified method of (Schuler *et al.*, 1994).

Germination energy (GE %): This was done in Haramaya university food science laboratory. It was done by placing 100 representative grains on damp filter paper with 4ml water in closed petridshs and allowed to germinate at temperature of 25 °C and 100% relative humidity and counting germinated seeds after 24, 48 and 72 hours. Germinated seeds were counted and expressed in percentage (Taylor, 2008).

Endosperm texture (ET): The relative proportion of vitreous (corneous) to floury were determined by cutting 5 kernels in halves longitudinally and evaluated using rating scale of 1 (corneous), 2 (intermediate to corneous), 3 (intermediate), 4 (intermediate to flowery) and 5 (floury) as described by Rooney and Millner (1982).

Grain crude protein content (CP %): The total protein content was measured by using Near Infrared reflectance spectrometry (NIRS), Model EU Perten Machine- IM9500 at Melkassa Agricultural research center food science laboratory. Finally, the results were taken from the display screen after 1 to 3 minutes.

Sorghum malt preparation and Sorghum malt quality traits

The malting process was done in Haramaya university

food science laboratory.

Steeping: Sorghum grain samples of 300 g of each plot were cleaned by hand picking to remove any defectives and washed three times to remove dirty, dusty and other foreign matters. The samples of the cleaned grains were placed in 300 x 300 mm nylon bags and steeped for 6h in steeping vessels (1 Kg) containing 0.1% NaOH solution (Taylor, 2008). At the end of 6 hr, the vessel were drained off and then refilled with fresh tap water at 25 °c and the water was drained of every 3 hrs after 1hr of air rest for total of 18 hrs (Dewar *et al.*, 1997a).

Germination: The steeped samples of each genotype were allowed to germinate in a germination vessel at optimal temperature (28 °c) for 72 h germination time and keeping the relative humidity high (95%). Distilled water (20 ml) was sprayed using hand sprayer twice daily to avoid the decrease of relative humidity. The grain was turned to avoid meshing roots and shoots. The germinated samples of the test genotypes were transferred to temperature controlled drying oven for kilning (Dewar *et al.*, 1997b).

Drying or Kilning: The germinated samples were dried in a temperature controlled drying oven at 50°C for 24 hrs according to Dewar *et al.* (1997a).

Malting weight loss (MWL %): The total malting weight loss was determined by weighing the grains before and after malting by using the following equation (Dewar *et al.*, 1997b).

$$\begin{aligned} & \text{Malting weight loss} \\ & = \frac{\text{Initial dry weight of grains} - \text{dry weight of malt}}{\text{Initial dry weight of grains}} \times 100 \end{aligned}$$

Malt moisture content (MMC %): The Moisture Content of the malt was estimated by gravimetric method of the European brewing convention (EBC) EBC (1997.). Malt flour of 5g was dried in an air forced dry oven for 3 hrs at 103°C. The mass loss on dry mass was determined as % moisture by using the equation

$$\% \text{MC (Moisture content)} = \frac{(W_2 - W_3)}{(W_2 - W_1)} * 100$$

Where: MC = Moisture content of the malt, W₁ = Weight of container, W₂ = Weight of container and the sample before drying and W₃ = Weight of the container and the sample after 3hr drying

Diastatic power of malt (DP) (°WK): The diastatic power of the malt was determined using EBC Method 4.12, (1997) in Asela malt factory.

Fine grind hot water extract (FHWE %): It was done in

Asela malt factory using the method of American Society of Brewing Chemists (ASBC 2008).

Data Analyses

Analysis of Variance

Data on phenological parameters, growth parameters, yield, yield components, grain quality parameters and malt quality parameters were subjected to analysis of variance (ANOVA) using SAS Computer Statistical Package version 9.0 (SAS Institute, 2004) by the model:

$$Y_{ijk} = \mu + R_j + B_{ij} + T_k + e_{ijk}$$

Where; μ = overall mean, R_j = replication effect (fixed) of the j th genotype, B_{ij} = random effect of block j within replication i , T_k = effect of treatment k (random or fixed), and e_{ijk} = the environmental effect of the ijk th observation.

Duncan's Multiple Range Test (DMRT) was used for mean separation at 5% probability level. Analysis of variance for NPT was done after the data had transferred using square root.

Genotypic and Phenotypic Variances

The phenotypic and genotypic variance estimated as suggested by Burton and De Vane (1953).

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

$$\sigma^2_g = \frac{Mg - Me}{r}$$

Where, σ^2_p = phenotypic variance, σ^2_g = Genotypic variance, σ^2_e = Environmental (error) variance (Error mean square), Mg = mean sum square of genotypes, Me = mean sum square of error and r = Number of replications.

Genotypic and phenotypic coefficient of variation (GCV and PCV)

The GCV and PCV were estimated according the methods of Burton and De Vane (1953).

$$\text{Phenotypic coefficient of variation, PCV} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} * 100$$

$$\text{Genotypic coefficient of variation, GCV} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} * 100,$$

Where \bar{x} = population mean

Broad Sense Heritability and genetic advance

Broad sense heritability was computed based on the formula developed by Allard (1960) as:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p} * 100$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e,$$

Where σ^2_e = Environmental (error) variance

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960) as: $GA = (K) (\delta P) (h^2)$

Where, GA = Expected genetic advance, δP = the phenotypic standard deviation, h^2 = the heritability, K = Selection differential (K=2.06 at 5% selection intensity).

GA (as % of the mean) = $\frac{GA}{\bar{x}} * 100$, Where, \bar{x} = population mean.

The GAM categorized as low, moderate and high as suggested by Johnson *et al.* (1955a) as follows. 0 - 10% = Low, 10 - 20 = Moderate and > 20 = High.

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of Variance (ANOVA) showed that the mean squares due to genotypes were highly significant ($P < 0.01$) for all of the traits recorded. (Table 2), indicating the existence of adequate variations among the tested genotypes. A significant difference for the agronomic traits of Ethiopian sorghum was found (Haile *et al.*, 2016; Mihret *et al.*, 2015). Highly significant variation for MWL, MMC, DP and FGHWE while, significant variation for HLW, KL, KT, GE and crude protein content for six varieties was reported (Aychew *et al.*, (2012). Similarly observed highly significant variation ($P < 0.01$), grain size, DP, malting MWL, GE and wort extract (Adetunji *et al.*, 2013).

Agronomic traits

The mean in days to flowering was 96.69 and ranged from 70.5 to 122.5 days (Table 3). The mean for days to maturity was 149.55 and ranged from 112.5 to 177 days. A partially agreed result for days to flowering and maturity was also reported for Ethiopian sorghum landraces Amsalu and Endashaw (2012) Haile *et al.* (2016).

Among the tested genotypes, the most early flowering were Yeju (74) followed by Dagnaw (75.5) and Seredo (77), Tseadachumure (77.5) and Wedi Aker (77.5). However, Lalo (122.5) days followed by Chiro (120.5) days had the most late flowering period. The check

Table 2. Mean square values from analysis of variance, coefficient of variation (CV) and coefficient of determination (R^2) for 17 traits

Traits	Source of variation				C V (%)	R^2
	Error df=41	Gen df=55	Rep df=1	Rep/Block df=14		
DF	3.45	372.72**	42.57 *	16.29	2.12	99.36
DM	12.98	585.50**	86.75 **	59.54*	2.41	99.48
PH	935.71	7506.65**	6967.79**	1889.06*	11.77	92.22
NPT	0.004(0.0007)	0.374(0.0981)**	0.009(0.0017) ^{NS}	0.002(0.0004) ^{NS}	19.66(3.09)	99.31(99.49)
GY	178714.6	2571289.5**	506874.1**	339422.9*	9.01	98.05
TKW	3.85	65.50**	18.00*	4.37	6.39	96.26
HLW	0.54	8.50**	0.76 ^{NS}	0.73 ^{NS}	1.01	95.94
KL	0.01	0.24**	0.09 *	0.01 ^{NS}	2.11	97.38
KW	0.02	0.30**	0.05 ^{NS}	0.03 ^{NS}	3.75	95.45
KT	0.01	0.20**	0.19**	0.01 ^{NS}	2.78	97.93
GE	5.44	88.26**	14.29 ^{NS}	5.12 ^{NS}	2.49	96.27
CP	0.37	1.59**	2.12*	0.66 ^{NS}	5.46	87.27
MWL	0.86	12.48**	0.03 ^{NS}	0.73 ^{NS}	5.05	95.51
FHWE	4.17	60.72**	13.30 ^{NS}	4.52	3.05	95.86
MMC	0.07	0.78**	0.01 ^{NS}	0.04 ^{NS}	3.15	94.67
DP	4.64	994.17**	5.29 ^{NS}	5.55 ^{NS}	6.04	99.68

df = degrees of freedom, * = highly significant at $P \leq 0.01$, ** = significant at $P \leq 0.05$ and NS = non significant, respectively, CV (%) = coefficient of variation, R^2 = coefficient of determination.

N.B. The values for number of productive tillers (NPT) in the parenthesis are the transformed values.

variety Redswazi matured in 112.5 days and none of the tested genotypes matured earlier than the check; as the other standard check variety Macia matured in 126.5 days. In comparison to Macia five genotypes matured earlier (Yeju, Dagnaw, Wediakir, Gedo and Wediarase) with the range between 120.5 to 126 days. The top three late maturing were Lalo (177), Bobe Read (176) days and Zeri Adis (176) days followed by Chiro (175.5), Gorade -2 (175) and AL-70 (174.5) days. This result indicated that those late maturing genotypes could not be suitable for the targeted environment. Among 56 genotypes 12 genotypes showed 112.5-129.5 days to maturity which can be used for development of early and medium maturing varieties for moisture stress areas.

Minimum and maximum plant heights of 132 cm and 426cm were recorded for Gedo and Lalo, respectively, with mean of 259.99cm (Table 3). The genotypes Gedo (132 cm) and Wedi aker (140 cm) showed shortest plant height than the second check Macia (144.13cm) and above the check Redswazi (112.3cm) which was the shortest. Previous studies showed the existence of large genetic variability in plant height in Ethiopian sorghum

landraces (Amsalu and Endashaw, 2012; Haile *et al.*, 2016). The sufficient variability in plant height among the genotypes suggested that the huge potential to make an improvement through selection and crossing for this trait.

Twenty one genotypes produce productive tillers while thirty five of the 56 genotypes do not produce productive tillers (Table 3). Number of productive tillers per plant for tested genotypes ranged from 0.2 for Welenchity Col#3 to 1.45 for Meminay-4 and with mean of 0.31. Alam *et al.* (2014) and Yalemtesfa (2014), found fertile tiller numbers with mean 2.25, 1.86 and 1.28 for inbred lines and released varieties respectively. However, those tillering genotypes are not preferred, due to their inefficient water use efficiency in water-limiting environments of tillering type sorghums (Hammer *et al.*, 2006).

Thousand kernel weight showed a mean of 36.34g with a range of 23-53g (Table 3). The maximum and minimum values of TKW were obtained from Lalo and Hodem-1-3, respectively (Table 5). The genotypes Hodem-1-3 (53), abaAre-1(52) and Marye#2 (51) were the top three with high TKW followed by Dgalit yellow-1 (44.5). Twenty-five genotypes were identified with TKW above the grand

Table 3. Mean separation of 17 traits of 56 sorghum genotypes tested at Raya Azebo, Fachagama site during 2016/17

G.N	Genoytpes	DF	DM	PH	NPT	GY	TKW	HLW	KL	KW
1	Abamelko	94.5 ^{o-r}	149 ^{m-p}	304.13 ^{c-g}	0.8(1.12) ^{fg}	6316.5 ^{bc}	37.5 ^{e-n}	74.05 ^{c-k}	4.33 ^{r-u}	3.42 ^{v-y}
2	AL-70	116 ^{cd}	174.5 ^{ab}	320.88 ^{b-e}	0(0.70) ⁿ	4562 ^{i-m}	35.75 ^{h-p}	71.6 ^{l-w}	4.68 ⁱ⁻ⁿ	3.93 ^{j-q}
3	Baji	96 ^{o-q}	152 ^{l-n}	207.4 ⁱ⁻ⁿ	0(0.70) ⁿ	3522 ^{q-t}	33.55 ^{l-q}	70.95 ^{r-w}	4.44 ^{o-s}	3.57 ^{q-w}
4	Birimash	96.5 ^{op}	146.5 ^{o-q}	204 ^{j-o}	0.35(0.91) ^l	4175 ^{j-q}	29.25 ^{q-u}	71.7 ^{l-v}	4.6 ^{k-p}	3.8 ^{l-t}
5	Osmel	87 ^{tu}	141 ^{rt}	313.5 ^{b-f}	1.15(1.28) ^c	7062.6 ^a	43.05 ^{b-d}	74.6 ^{b-h}	5.19 ^{b-d}	3.96 ^{i-o}
6	Chiro	120.5 ^{ab}	175.5 ^{ab}	289.63 ^{c-h}	0(0.70) ⁿ	4500.5 ^{i-m}	36 ^{h-p}	71.5 ^{p-w}	4.75 ^{h-m}	4.23 ^{e-j}
7	Dagim	95 ^{o-q}	147 ^{op}	210.88 ⁱ⁻ⁿ	0.7(1.09) ^{h-i}	3032.5 ^t	29.5 ^{q-u}	68.3 ^{xy}	4.23 ^{s-v}	3.18 ^{xy}
8	E36-1	82.5 ^{vw}	127.5 ^{uv}	166.88 ^{m-p}	0(0.70) ⁿ	3725 ^{n-s}	32.5 ^{o-s}	75.55 ^{a-c}	4.75 ^{h-m}	3.91 ^{j-r}
9	Emahoy	89 ^{s-u}	142 ^{q-t}	206.63 ⁱ⁻ⁿ	0(0.70) ⁿ	4776.5 ^{h-j}	35 ^{j-p}	70.7 ^{t-w}	4.46 ^{n-s}	4.03 ^{g-n}
10	Merawi	86 ^{uv}	147 ^{op}	273 ^{c-j}	0.75(1.12) ^{gh}	4157 ^{j-q}	36.9 ^{g-o}	72.75 ^{i-r}	4.62 ^{i-o}	4.05 ^{g-n}
11	Aba Are-1	105.5 ^{j-l}	163 ^{h-j}	295.38 ^{c-g}	0(0.70) ⁿ	5567 ^{d-g}	52 ^a	73.95 ^{c-k}	4.83 ^{f-k}	4.65 ^{a-d}
12	America-1	90.5 ^{r-t}	147.5 ^{n-p}	260.25 ^{d-k}	0(0.70) ⁿ	6820 ^{ab}	41.88 ^{b-f}	76 ^{ab}	5.28 ^{b-c}	4.61 ^{a-d}
13	Baduqane	113 ^{d-g}	165 ^{f-1}	310.63 ^{c-f}	0(0.70) ⁿ	4376 ⁱ⁻ⁿ	35.55 ^{h-p}	70.2 ^{u-w}	4.63 ^{i-o}	4.06 ^{g-n}
14	Berjokecoll#1	111.5 ^{e-h}	173.5 ^{a-c}	298.5 ^{c-g}	0(0.70) ⁿ	3866 ^{m-r}	32.9 ^{m-r}	70 ^{vw}	4.98 ^{d-h}	4.32 ^{d-i}
15	DagalitYellow-1	106 ^{i-l}	161.5 ^{ij}	288.5 ^{c-h}	0(0.70) ⁿ	5970 ^{c-e}	44.5 ^b	72.95 ^{h-q}	4.39 ^{p-t}	4.21 ^{e-k}
16	Gorade-2	114.5 ^{c-e}	175 ^{ab}	301 ^{c-g}	0(0.70) ⁿ	5565 ^{d-g}	41.5 ^{b-g}	70.95 ^{s-w}	5.39 ^{ab}	3.69 ^{n-w}
17	Hodem-1-3	95 ^{o-q}	147 ^{op}	305.38 ^{c-g}	1.1(1.26) ^{cd}	6906.1 ^{ab}	53 ^a	75.3 ^{a-e}	5.3 ^{b-c}	4.53 ^{b-e}
18	JimmaLocal-2	106 ^{i-k}	158.5 ^{ji}	297 ^{c-g}	0.9(1.18) ^{ef}	5542 ^{d-g}	35.15 ^{j-p}	74.75 ^{a-g}	4.37 ^{q-t}	3.45 ^{t-x}
19	Marye#2	108 ^{h-j}	164.5 ^{g-i}	322.5 ^{b-e}	0(0.70) ⁿ	6871 ^{ab}	51 ^a	75.6 ^{a-c}	4.81 ^{f-k}	4.43 ^{c-f}
20	Meminay-4 Welenchity	92.5 ^{p-s}	140 st	261.88 ^{c-k}	1.45(1.39) ^a	5733.5 ^{c-f}	37 ^{g-o}	75.2 ^{a-e}	4.86 ^{f-j}	4.06 ^{g-m}
21	Col#3	92 ^{q-s}	147 ^{op}	247.5 ^{e-k}	0.2(0.84) ^m	4585.5 ^{i-l}	33 ^{l-r}	72.65 ^{i-s}	4.64 ^{i-o}	3.76 ^{l-v}
22	WolloCol#050	87.5 ^{tu}	144 ^{p-s}	291.13 ^{c-h}	0(0.70) ⁿ	6174.5 ^{cd}	39 ^{d-k}	73.6 ^{d-k}	5.04 ^{d-f}	3.75 ^{m-v}
23	Gano	102 ^{l-n}	156.5 ^{kl}	321.75 ^{b-e}	0(0.70) ⁿ	5607.5 ^{d-g}	36.75 ^{g-o}	74.3 ^{b-i}	4.75 ^{h-m}	4.82 ^{ab}
24	Bobere red	117.5 ^{bc}	176 ^a	281 ^{c-i}	0(0.70) ⁿ	4562.5 ^{i-m}	40 ^{b-i}	72.4 ^{k-t}	4.88 ^{e-i}	4.38 ^{c-g}
25	Bobere white	92.5 ^{p-s}	145.5 ^{o-r}	249 ^{d-k}	0(0.70) ⁿ	4016 ^{k-r}	31.75 ^{p-t++}	73.55 ^{e-l}	4.83 ^{f-k}	4.12 ^{f-l}
26	Dabar	89.5 ^{s-u}	145.5 ^{o-r}	193.25 ^{k-o}	0(0.70) ⁿ	4300 ^{j-o}	31.5 ^{p-t}	71.4 ^{q-w}	3.9 ^{wx}	3.44 ^{u-x}
27	Dagnaw	75.5 ^y	122 ^{wx}	305.13 ^{c-g}	0.6(1.04) ^{ij}	3985.5 ^{k-r}	37.1 ^{g-o}	73.4 ^{f-m}	5.03 ^{d-f}	3.9 ^{j-r}
28	Degalit	110 ^{f-i}	164.5 ^{g-i}	277.5 ^{c-j}	0(0.70) ⁿ	5615 ^{d-g}	41.5 ^{b-g}	72.95 ^{h-q}	4.75 ^{h-m}	4.95 ^a
29	Degalit Yellow	115 ^{c-e}	168.5 ^{c-f}	319 ^{b-e}	0(0.70) ⁿ	5345 ^{e-h}	36.75 ^{g-o}	71.5 ^{p-w}	4.86 ^{f-j}	4.68 ^{a-c}
30	DemHay	96.5 ^{op}	147.5 ^{n-p}	281.63 ^{c-i}	0(0.70) ⁿ	3853.5 ^{m-r}	32.75 ^{n-r}	70.7 ^{t-w}	4.55 ^{m-r}	3.58 ^{p-w}
31	Dima	118 ^{bc}	173.5 ^{a-c}	298 ^{c-g}	0.75(1.12) ^{gh}	4558.5 ^{i-m}	39.25 ^{c-j}	70.85 ^{t-w}	4.83 ^{f-k}	4.22 ^{e-j}
32	Jamiyu	98.5 ^{no}	152.5 ^{lm}	209.38 ⁱ⁻ⁿ	1.1(1.25) ^{cd}	5305 ^{f-h}	34.3 ^{k-p}	72.5 ^{j-t}	4.81 ^{f-k}	4.48 ^{b-e}
33	Jeru	114 ^{c-f}	169.5 ^{c-f}	384.25 ^{ab}	0(0.70) ⁿ	6318.5 ^{bc}	43.25 ^{b-d}	73.55 ^{e-l}	5.1 ^{b-e}	4.37 ^{c-g}
34	Jigurti	88.5 ^{s-t}	141.5 ^{rt}	324 ^{b-d}	1.15(1.29) ^c	7164.2 ^a	35.95 ^{h-p}	75.4 ^{a-c}	5.52 ^a	4 ^{h-n}
35	Kodem	89.5 ^{s-u}	139 ^t	242.75 ^{f-l}	0.9(1.21) ^{5e}	6108.5 ^{cd}	43.75 ^{bc}	76.5 ^a	5.17 ^{b-d}	4.7 ^{a-c}
36	Lalo	122.5 ^a	177 ^a	426 ^a	0.65(1.06) ^{hi}	2359.5 ^u	23 ^v	67.25 ^y	3.87 ^x	3.09 ^y

Table 3. continuation

37	Masugi Red	115 ^{c-e}	173 ^{a-d}	314 ^{b-e}	0(0.70) ⁿ	4315 ^{j-o}	40.15 ^{b-h}	72.5 ^{i-t}	4.38 ^{q-t}	3.99 ^{h-o}
38	Masugi Yellow	103 ^{k-m}	156 ^{kl}	256.88 ^{d-k}	0(0.70) ⁿ	5019.5 ^{g-i}	41.5 ^{b-g}	74.35 ^{b-i}	4.99 ^{d-g}	3.79 ^{l-u}
39	Tetron White	95 ^{o-q}	150 ^{m-o}	232.75 ^{g-m}	0(0.70) ⁿ	4237.5 ^{j-o}	33.65 ^{l-q}	76.5 ^a	4.09 ^{vw}	3.39 ^{w-y}
40	Tewzale	88.5 ^{s-u}	145 ^{o-r}	239.4 ^{f-m}	1(1.22) ^{de}	4626 ^{i-k}	35.25 ^{i-p}	74.25 ^{b-j}	4.59 ^{k-q}	3.85 ^{k-s}
41	Tseada Achire	92 ^{q-s}	139 ^t	277.38 ^{c-j}	0(0.70) ⁿ	3850 ^{m-r}	37.75 ^{e-l}	72.35 ^{l-t}	4.79 ^{g-l}	3.89 ^{i-r}
42	Tseada chimure	77.5 ^{xy}	129.5 ^u	250.5 ^{d-k}	0(0.70) ⁿ	4370.5 ⁱ⁻ⁿ	34.3 ^{k-p}	75.35 ^{a-d}	4.67 ^{i-o}	3.91 ^{j-r}
43	Wediarase	81 ^{wx}	126 ^{u-w}	275 ^{c-j}	0(0.70) ⁿ	3752.5 ^{n-s}	28.8 ^{r-u}	71.65 ^{l-v}	4.56 ^{l-q}	3.81 ^{l-t}
44	Wegere	114.5 ^{c-e}	171 ^{b-e}	291 ^{c-h}	0(0.70) ⁿ	5693 ^{c-f}	42.13 ^{b-e}	73.2 ^{g-p}	4.63 ^{j-o}	3.83 ^{l-s}
45	Wetetbegunchie	101 ^{mn}	158.5 ^{ik}	336.38 ^{bc}	0.5(1.00) ^{jk}	5236.5 ^{f-h}	35.25 ^{i-p}	69.85 ^{wx}	4.85 ^{f-j}	3.87 ^{j-r}
46	Wode aker	77.5 ^{xy}	123 ^{v-x}	140 ^{n-p}	1.3(1.34) ^b	3687.5 ^{o-s}	25.8 ^{uv}	70.05 ^{u-w}	4.25 ^{s-v}	3.77 ^{l-v}
47	Yeju	74 ^{yz}	120.5 ^x	169.25 ^{l-p}	0(0.70) ⁿ	3987.5 ^{k-r}	37.6 ^{e-m}	75.9 ^{ab}	4.66 ^{i-o}	4.11 ^{g-m}
48	ZeriAdis	116 ^{cd}	176 ^a	270.3 ^{c-j}	0(0.70) ⁿ	4151 ^{k-q}	37.25 ^{f-o}	71 ^{r-w}	4.3 ^{s-v}	3.95 ^{j-p}
49	Goronjo	109.5 ^{g-i}	167 ^{e-h}	242.38 ^{f-l}	0.4(0.94) ^{kl}	2350 ^u	27.95 ^{s-u}	68.35 ^{xy}	4.25 ^{s-v}	3.63 ^{o-w}
50	Gedo	80 ^{wx}	126 ^{u-w}	132.63 ^{o-p}	0.8(1.14) ^{fg}	2975 ^t	27.85 ^{tu}	71.8 ^{l-u}	4.26 ^{s-v}	3.88 ^{j-r}
51	Melkam	81 ^{wx}	126.5 ^{u-w}	167.75 ^{m-p}	0(0.70) ⁿ	4202 ^{j-p}	35.5 ^{h-p}	73.35 ^{f-n}	4.795 ^{g-k}	4.32 ^{d-h}
52	Misikir	82.5 ^{vw}	127 ^{uv}	233.38 ^{g-m}	0(0.70) ⁿ	3920 ^{k-r}	32.85 ^{m-r}	74.75 ^{a-g}	4.63 ^{j-o}	3.93 ^{j-q}
53	Dekeba	82 ^{vw}	127 ^{uv}	218.75 ^{h-m}	0(0.70) ⁿ	4050 ^{k-r}	36 ^{h-p}	74.95 ^{a-g}	4.17 ^{t-v}	3.92 ^{j-q}
54	Seredo	77 ^{xy}	126.5 ^{u-w}	166.25 ^{m-p}	0(0.70) ⁿ	3550 ^{p-t}	29.5 ^{q-u}	71.55 ^{o-w}	4.25 ^{s-v}	3.51 ^{s-x}
55	Macia	82.5 ^{vw}	126.5 ^{u-w}	144.13 ^{n-p}	0(0.70) ⁿ	3206 st	35.05 ^{j-p}	75.1 ^{a-e}	4.32 ^{s-v}	3.55 ^{r-w}
56	Redswazi	70.5 ^{yz}	112.5 ^y	112.3 ^{o-p}	1(1.23) ^{de}	3414 ^{r-t}	27.75 ^{tu}	73.3 ^{g-o}	4.1 ^{u-w}	3.35 ^{w-y}

N.B. The values for number of productive tillers (NPT) in the parenthesis are the transformed values.

Table 3. continued...

G.N	Genotypes	KT	GE	CP	MWL	FHWE	MMC	DP
1	Abamelko	2.6 ^{q-u}	74.5 ^l	9.88 ^{o-r}	15.39 ^{p-u}	74.39 ^{a-d}	7.1 ^{pq}	36.81 ^{h-j}
2	AL-70	2.93 ^{h-l}	93 ^{c-f}	12.11 ^{a-i}	15.68 ^{o-u}	71.2 ^{b-j}	8.75 ^{c-g}	51.84 ^e
3	Baji	2.7 ^{m-s}	99 ^{ab}	9.66 ^{q-r}	15.4 ^{p-u}	76.83 ^a	9.45 ^{ab}	49.48 ^e
4	Birimash	2.69 ^{n-t}	94 ^{a-f}	10.90 ^{g-r}	14.81 ^{q-u}	72.55 ^{a-g}	8.25 ^{g-l}	51.42 ^e
5	Osmel	3.04 ^{f-i}	96.5 ^{a-e}	11.27 ^{c-n}	17.1 ^{i-p}	60.6 ^{r-u}	8.75 ^{c-g}	98.07 ^a
6	Chiro	2.86 ^{i-o}	86 ^{h-i}	11.44 ^{b-m}	20.49 ^{a-g}	61.4 ^{q-t}	7.05 ^q	25.76 ^{lm}
7	Dagim	2.54 ^{s-v}	78.5 ^{i-l}	11.58 ^{a-j}	18.46 ^{g-l}	71.75 ^{b-i}	9.5 ^{ab}	41.57 ^{gh}
8	E36-1	2.64 ^{p-u}	88.5 ^{f-h}	12.20 ^{a-h}	17.13 ^{i-p}	66.5 ^{r-p}	8.95 ^{b-f}	15.19 ^{op}
9	Emahoy	2.87 ^{i-o}	98.5 ^{a-c}	9.56 ^r	13.48 ^u	66.35 ^{i-p}	8.1 ^{h-m}	15.16 ^{op}

Table 3. *continued...*

10	Merawi	2.97 ^{g-j}	97.5 ^{a-d}	12.49 ^{a-d}	16.71 ^{k-r}	63.25 ^{n-t}	8 ⁱ⁻ⁿ	18.59 ^{no}
11	Aba Are-1	3.41 ^{a-c}	97.5 ^{a-d}	12.21 ^{a-h}	19.92 ^{b-h}	74.05 ^{a-c}	7.8 ^{j-o}	58.89 ^d
12	America-1	3.18 ^{d-f}	98 ^{a-d}	11.30 ^{c-n}	20.52 ^{a-g}	69.1 ^{d-m}	8.3 ^{g-l}	29.84 ^{kl}
13	Baduqane	2.79 ^{j-p}	99 ^{ab}	12.54 ^{a-d}	16.99 ^{i-q}	65.95 ^{k-q}	7 ^q	14.71 ^{op}
14	Berjokecoll#1	3.28 ^{c-e}	91.5 ^{e-g}	10.49 ^{k-r}	18.76 ^{e-k}	67.6 ^{g-o}	9.1 ^{b-d}	33.57 ^{i-k}
15	DagalitYellow-1	3.07 ^{f-h}	91.5 ^{e-g}	11.11 ^{e-q}	19.03 ^{c-i}	74.89 ^{a-b}	8 ⁱ⁻ⁿ	52.6 ^e
16	Gorade-2	2.52 ^{s-w}	99 ^{ab}	10.53 ^{k-r}	18.74 ^{f-k}	72.6 ^{a-f}	9.05 ^{b-d}	22.64 ^{mn}
17	Hodem-1-3	2.9 ^{h-m}	99.5 ^a	11.61 ^{a-l}	21.7 ^{ab}	72.3 ^{a-h}	7.7 ^{l-p}	67.13 ^c
18	JimmaLocal-2	2.85 ^{i-o}	87 ^{g-i}	9.73 ^{o-r}	19.89 ^{b-h}	75.25 ^{ab}	8.8 ^{c-g}	40.6 ^{gh}
19	Marye#2	3.19 ^{d-f}	98 ^{a-d}	12.08 ^{a-j}	20.58 ^{a-g}	71.6 ^{b-i}	8.2 ^{g-m}	48.98 ^{ef}
20	Meminay-4	3.07 ^{f-h}	96.5 ^{a-e}	11.23 ^{d-p}	22.66 ^a	73.4 ^{a-e}	7.85 ^{j-o}	37.58 ^{hi}
21	Welenchity Col#3	2.79 ^{j-p}	99 ^{ab}	12.88 ^{ab}	15.51 ^{p-u}	65.9 ^{k-q}	8.4 ^{e-j}	22.4 ^{mn}
22	WolloCol#050	2.55 ^{s-v}	97 ^{a-e}	12.18 ^{a-h}	19.09 ^{c-i}	58.9 ^{tu}	7.7 ^{l-p}	44.47 ^{fg}
23	Gano	3.08 ^{f-h}	95.5 ^{a-e}	10.95 ^{g-r}	21.61 ^{ab}	72.2 ^{a-i}	8.2 ^{g-m}	50.29 ^e
24	Bobere red	3.17 ^{d-f}	82 ^{i-k}	10.75 ^{h-r}	18.53 ^{g-l}	62.75 ^{o-t}	8.8 ^{c-g}	13.38 ^p
25	Bobere white	2.86 ^{i-o}	98.5 ^{a-c}	11.44 ^{b-m}	16.94 ^{i-q}	68.5 ^{e-m}	9.25 ^{bc}	29.82 ^{kl}
26	Dabar	2.68 ^{o-t}	99 ^{ab}	10.69 ^{h-r}	14.77 ^{q-u}	73.9 ^{a-d}	8.1 ^{h-m}	43.42 ^{fg}
27	Dagnaw	2.75 ^{l-r}	99.5 ^a	12.96 ^a	21.16 ^{a-c}	64.3 ^{m-s}	8.1 ^{h-m}	44.66 ^{fg}
28	Degalit	3.58 ^a	98.5 ^{a-c}	10.72 ^{h-r}	19.95 ^{b-h}	72.3 ^{a-h}	7.7 ^{l-p}	70.4 ^c
29	Degalit Yellow	3.28 ^{c-e}	93 ^{c-f}	12.20 ^{a-h}	20.98 ^{a-e}	73.8 ^{a-d}	8.1 ^{h-m}	60.75 ^d
30	DemHay	2.77 ^{k-q}	99.5 ^a	12.29 ^{a-g}	18.86 ^{d-k}	60.25 ^{r-u}	9.1 ^{b-d}	44.98 ^{fg}
31	Dima	3.35 ^{b-d}	83.5 ^{h-j}	10.46 ^{k-r}	13.89 ^{tu}	67.3 ^{i-o}	7.05 ^q	11.36 ^p
32	Jamiyu	3.2 ^{d-f}	99.5 ^a	11.49 ^{a-j}	16.41 ^{l-s}	69.8 ^{b-l}	8.5 ^{d-i}	26.17 ^m
33	Jeru	3.4 ^{bc}	98.5 ^{a-c}	9.96 ^{m-r}	20.93 ^{a-f}	70.3 ^{b-k}	8.2 ^{g-m}	43.77 ^{fg}
34	Jigurti	2.95 ^{g-k}	91.5 ^{e-g}	11.88 ^{a-k}	15.15 ^{p-u}	60 ^{s-u}	8.3 ^{g-l}	18.83 ^{no}
35	Kodem	3.12 ^{e-g}	93.5 ^{b-f}	10.41 ^{k-r}	16.7 ^{k-r}	70.4 ^{b-k}	7.9 ⁱ⁻ⁿ	42.11 ^{gh}
36	Lalo	2.39 ^{v-x}	68.5 ^m	10.59 ^{i-r}	17.86 ^{h-o}	67.4 ^{h-o}	9.15 ^{bc}	34.03 ^{i-k}
37	Masugi Red	2.75 ^{l-r}	82 ^{i-k}	9.71 ^{p-r}	16.81 ^{j-r}	67.6 ^{g-o}	9.2 ^{bc}	32.7 ^k
38	Masugi Yellow	3.51 ^{ab}	92.5 ^{d-f}	10.56 ^{j-r}	21.03 ^{a-d}	65.1 ^{l-r}	7.75 ^{k-o}	40.84 ^{gh}
39	Tetron White	2.32 ^x	99.5 ^a	9.86 ^{o-r}	18.56 ^{g-l}	56.05 ^{uv}	8.4 ^{e-j}	29.87 ^{kl}

Table 3. *Continued...*

G.N	Genotypes	KT	GE	CP	MWL	FHWE	MMC	DP
40	Tewzale	2.53 ^{s-w}	94.5 ^{a-e}	10.25 ^{l-r}	21.75 ^{ab}	69.9 ^{b-l}	8 ⁱ⁻ⁿ	66.93 ^c
41	Tseada Achire	2.89 ^{i-m}	95.5 ^{a-e}	9.95 ^{m-r}	21.75 ^{ab}	74.89 ^{a-b}	7.25 ^{o-q}	70.06 ^c
42	Tseada chimure	2.03 ^x	98 ^{a-d}	11.89 ^{a-k}	21.21 ^{a-c}	63.2 ^{n-t}	8 ⁱ⁻ⁿ	15.15 ^{op}
43	Wediarase	2.5 ^{t-w}	97.5 ^{a-d}	11.04 ^{e-r}	14.39 ^{r-u}	60.9 ^t	7.6 ^{m-q}	18.5 ^{no}
44	Wegere	2.88 ⁱ⁻ⁿ	98.5 ^{a-c}	12.33 ^{a-g}	14.25 st	68.5 ^{e-m}	8.35 ^{f-k}	44.58 ^{fg}
45	Wetetbegunchie	2.47 ^{u-x}	95 ^{a-e}	12.18 ^{a-h}	22.4 ^a	60.85 ^{r-t}	7.4 ^{n-q}	96.03 ^a
46	Wode aker	2.85 ^{j-o}	99.5 ^a	11.56 ^{a-j}	19 ^{c-j}	53.45 ^v	8.7 ^{c-h}	15.24 ^{op}
47	Yeju	2.65 ^{p-u}	98.5 ^{a-c}	11.05 ^{e-r}	22.5 ^a	73.7 ^{a-d}	8.1 ^{h-m}	85.6 ^b

Table 3. Continued...

48	ZeriAdis	2.8 ^{j-p}	84 ^{h-i}	10.55 ^{k-r}	18.37 ^{g-l}	62.8 ^{o-t}	9.3 ^{bc}	60.57 ^d
49	Goronjo	3.08 ^{f-h}	94 ^{a-f}	12.27 ^{a-g}	16.02 ^{m-t}	69.4 ^{c-l}	8 ⁱ⁻ⁿ	29.74 ^{kl}
50	Gedo	2.71 ^{m-s}	77 ^{kl}	12.77 ^{a-c}	14.59 ^{r-u}	61.9 ^{p-t}	8.4 ^{e-j}	18.50 ^{no}
51	Melkam	2.59 ^{q-u}	98.5 ^{a-c}	11.25 ^{d-o}	15.87 ^{n-t}	60.5 ^{r-u}	9 ^{b-e}	30.06 ^{kl}
52	Misikir	2.58 ^{q-u}	98.5 ^{a-c}	12.64 ^{a-d}	17.93 ^{h-n}	65.9 ^{k-q}	8.8 ^{c-g}	25.88 ^{lm}
53	Dekeba	2.56 ^{r-v}	93.5 ^{b-f}	11.37 ^{b-n}	21.65 ^{ab}	67.9 ^{f-n}	8.5 ^{d-i}	22.19 ^{mn}
54	Seredo	2.6 ^{q-u}	96.5 ^{a-e}	10.94 ^{g-r}	18.23 ^{h-m}	53.2 ^v	10 ^a	38 ^{hi}
55	Macia	2.35 ^{wx}	98 ^{a-d}	10.97 ^{f-r}	21.35 ^{ab}	59.25 ^{tu}	8.5 ^{d-i}	60.07 ^d
56	Redswazi	2.3 ^x	97 ^{a-e}	12.15 ^{a-h}	17 ^{i-q}	54.5 ^v	8.7 ^{c-h}	26.09 ^{lm}

mean (36.34) excluding the checks. The high grain weight might be related to larger seed size of the genotypes due to the supplementary irrigation and correlation between thousand kernel weights and the grain hardness Adetunji (2012), which results in good milling quality attributes. Amsalu and Endashaw, (2012); Hile *et al.*, (2016) have reported the existence of large genetic variability in TKW of Ethiopian sorghum varieties and landrace.

For grain yield, which is the primary interest in most breeding programs the genotypes showed wide range of variability i.e. 2350-7164.2 kg ha⁻¹ with a mean 4705.34 kg ha⁻¹ (Table 3). Overall, the highest grain yield per hectare was obtained from Jigurti (7164.2 kg ha⁻¹) and Osmel (7062.6 kg ha⁻¹) followed by Hodem-1-3 (6906.1 kg ha⁻¹), Marye #2 (6871 kg ha⁻¹) and America-1 (6820) (Table 3). The genotypes Goronjo (2350 kg ha⁻¹), Lalo (2359 kg ha⁻¹), Gedo (2975 kg ha⁻¹) and Dagim (3032 kg ha⁻¹) showed grain yield below the checks (Redswazi (3414 kg ha⁻¹) and Macia (3206 kg ha⁻¹) and were the last four low yielding. The checks were among the low yielding genotypes. This is agreed with the results of Tesfaye *et al.*, (2011); Haile *et al.* (2016) for grain yield in Ethiopian sorghum accessions.

Sorghum grain quality parameters

The hectoliter weight (HLW) ranged from 67.25 for Lalo to 76.5 for Tetron white (Table 3). Ten genotypes showed HLW above the check Macia (75.1 Kg/hL) and twenty five showed above Redswazi (73.3 Kg/hL). Chiremba *et al.* (2011) and Adetunji *et al.* (2013) reported HLW ranged 74.0-77.1 Kg/hL and 69.3- 78.5 kg/hL respectively.

The value ranged for kernel length 3.87 to 5.52 mm, kernel width 3.09 to 4.95 mm and kernel thickness 2.02 to 3.58 mm, and with mean value of 4.66 mm, 3.98 mm

and 2.84 mm, respectively (Table 3). The maximum kernel length, width and thickness were found in Jigurti (5.52mm), Degalit (4.95 mm), and Degalit (3.58mm), respectively, whereas the minimum kernel length, width and thickness were found in Lalo (3.87mm), Lalo (3.09mm) and Tseada chimure (2.02mm). Significant difference in kernel length, width and thickness ranging 4.04-4.4, 3.23-3.97 and 2.36-2.67 mm were reported by Aychew *et al.* (2012). Abuajah *et al.* (2016) Reported major, minor and interior diameter with 3.88-4.92, 3.85-4.89 and 2.42-2.92 mm respectively. According to Cuevas *et al.* (2017) seed size 2.8-5.2 mm was found from the USDA-NPGS Ethiopian sorghum germplasms collection. The kernel size and shape affects malting properties and water uptake of the grain especially the germination energy and capacity. Large kernel size contributes to having high milling yield because of higher level of starchy endosperm (Lee *et al.*, 2002) and also one key consideration among grains is size: bigger grains or kernels are often preferred because they contain proportionately with less husk and therefore higher starch content than smaller ones. So, those genotypes with larger grain size are preferred.

The germination energy was highly significantly different among the genotypes and ranged from 68.5 to 99.5% (Table 3). The minimum germination energy for sorghum is recommended to be greater than 90% (Dewar *et al.*, 1995; Taylor and Taylor, 2008). In this study, except for Lalo, Abamelko, Gedo, Dagim, Bobe read, Musgi red, Zeri Adis, Dima, Chiro, Jimma local and E36-1 the rest of the genotypes gave more than 90% germination energy indicating the grains were viable enough to be malted and enzyme modification of the endosperm substrates. Similar results of grains of sorghum varieties with high enough germination energy were reported by Kassahun *et al.* (2011) and Okrah (2008).

There was a significant difference among the genotypes in protein content and varied from 9.31-12.96 % with a mean of 10.89 % (Table 3). The highest protein content was found in Dagnaw (12.96%) followed by Welenchity Col#3 (12.88 %) and Gedo (12.77%) while Emahoy (9.56) had the lowest protein content. Thirty four genotypes revealed protein content above the check Macia (10.96%), and thirteen genotypes revealed above the second check Redswazi (12.15%). Differences in protein content can be attributed to the genetic and influence of cultivation environmental factors (growing conditions in terms of moisture and temperature determine the relative proportions of starch to protein deposited in the sorghum kernel). Similar results were reported by Kassahun *et al.* (2011), Chiremba *et al.* (2011) and Adetunji *et al.* (2013). Protein content ranged from 1 to 16.9% of Ethiopian core site collection of sorghum germplasm were reported by Cuevas *et al.* (2017).

The protein value of sorghum grain, 8-11% (Palmer, 1989) and 10 ±1% (Mackintosh *et al.*, 2004) is an acceptable level for proteolysis during malting. Based on the result obtained in this study, the 23 genotypes with protein content ranging from 9-11% meets the malting specification.

Sorghum malt quality traits

The highest FHWE were observed in Baji (76.8%) followed by Jimma Local-2 (75.25%), Degalit yellow-1 (74.89%), Tseada Achirie (74.89%), AbaAre-1 (74.05%) and Dabar (73.9) (Table 3). Twenty genotypes showed above 70% extract which can be considered for improvement of sorghum malt quality development program as extract which is the single most important parameter. In comparison to the other check variety Macia, which had 59.25 %, the genotypes WolloCol#050 (58.9), Tetron White (56.05%), Seredo (53.2%), and Wede Aker (53.45%) had lower values. Higher malt extract content of South African varieties PAN 3860 63.8% to 81% and Orbit 63.8-84.5% were reported (Adetunji, (2012) and Adetunji *et al.*, (2013)). Malt extract is the estimate of fermentable sugars and dextrins that can be obtained when the malt is mashed, is the most important single parameter that determines malt suitability in beer brewing, because it is directly related to the level of starch hydrolyzed by the amylases, as well as to starch content and availability, which in turn are influenced by protein content and composition of the grain (Taylor and Duodu, 2009). Accordingly, genotypes that gave very near to and above 74% of FHWE were Baji (76.8%), JimmaLocal-2 (75.25%), Degalit yellow-1 (74.89%), Tseada Achirie (74.89%), AbaAre-1 (74.05%), Dabar (73.9), Degalit Yellow (73.8%) and Yeju (73.7%).

As germination time increases the extract content

increases; in this study the germination time (72h) might not be enough for those larger grain sizes and their extract content might increase from what is found. Extract yield results by refractometry were probably higher than by the specific gravity method due to differences in analytical principle involved. In this study the extract content is measured by specific gravity method and could be the reason for the relatively low extract content. Malt extract is affected by several factors these are, environment (growing condition, temperature, fertilizer and nitrogen), genetic biochemical components that influence (protein, starch, grain size, non starch polysaccharides and enzymatic production) and malting process (Collins *et al.*, 2003). Low extract yield for some of the sorghum genotypes could also primarily due to interaction between condensed tannins and the amylase enzymes during mashing. Condensed tannins also complex irreversibly with the sorghum grain kafirin proteins (Emmambux and Taylor, 2002) and this may have also contributed to poor starch hydrolysis in the type three tannin sorghum types.

The malt moisture content (MMC) shown in (Table 2) reveals highly significant ($p < 0.01$) difference among the genotypes with highest being Seredo (10.0%) and lowest Chiro (7.0%) (Table 3). Thirty five genotypes revealed MMC below the check Redswazi (8.7%) and thirty four genotypes below the check Macia (8.5%). According to Daiber and Taylor (1995) moisture content of sorghum malt dried at 50 °C for 24 h were around 10%. However, Aychew *et al.* (2012) found MMC dried at same time and temperature for six varieties ranging from 7-7.3%.

High diastatic power was observed by Osmel (98.07) and Wetetbegunchie (96.03) followed by Yeju (85.6). The low DP was observed by the genotypes Dima (11.36 °WK) and Bobe Red (13.38) (Table 3). In comparison to the check Macia with DP of (60.07°WK) the genotypes Osmel (98.07), Wetetbegunchie (96.03), Yeju (85.6), Degalit (70.4), Tseada Achirie (70.06), Hodem-1-3 (67.13), Tewzale (66.93), Dgalit Yellow (60.75) and Zeri Adis (60.57) showed greater diastatic power. Sorghum varieties having sorghum diastatic unit (SDU) values ranging from 53-71 were reported by Adetunji (2012). Elgorashi *et al.* (2016) Found sorghum DP ranging from 28 - 79.84 SDU; which is supported by the current study. The GH- malting and high-tannin are known for their high DP. It is not known why tannin sorghums produce malt with high DP. However, it could be due the higher level of water uptake than that of non-tannin cultivars. Thus, as a result of adequate hydration, enzyme activities would be maximized during malting of high tannin genotypes as mentioned by Agu and Palmer (1998).

Diastatic power (DP) is the primary and most limiting sorghum malt quality parameter, which determines sorghum suitability in malting and brewing (Taylor, 2003). The minimum DP specification for sorghum malt by

sorghum brewing is between 28-30 SDU/g (Raschke *et al.*, 1995). Thus, the genotypes having above 28 SDU/g meets the minimum brewing requirement. The malt DP value could be enhanced based on each genotype germination time requirement which is influenced by seed size and water absorption characteristics. The DP values of the 56 sorghum genotypes obtained in °WK were converted to Sorghum Diastatic Unit (SDU) (Table 4) using the regression equation (Etokakpan, 2004).

$$Y=0.5595x+15.677$$

Where, Y is SDU and x is the European brewing convention unit of measuring DP in Winds Kolbach (°WK).

The maximum MWL was obtained by Yeju (22.66%) and the minimum from Emahoy (13.47%). Aychew *et al.*, (2012) found MWL ranging from 15.65 (Teshale) to 26.34% (Meko) at 96h germination time. Eighteen genotypes showed malting weight loss below the check Redswazi (17%) while, eight genotypes showed above the check Macia (21.35%) (Table 3). Most of the genotypes that showed high malting weight loss are those having high DP. Genotypes with the higher total malting weight loss could be due to the high diastatic power and the 28 °c temperature, as malting loss is mostly affected by temperature. Malting weight loss is the key aspects of malting as it depends on malting condition and variety of sorghum used. Malting loss ranged from 13.77%-37.74 for ten Nigerian varieties germinated in four days (Nnamchi *et al.*, 2014) . Therefore, minimizing malting weight loss is essential for using sorghum at commercial level.

Endosperm Texture

The endosperm texture of the genotypes is shown in (Table 5). Six genotypes i.e. Aba Are- 1, Marye ≠ 2, Musgi yellow, Tseada Chimure, Dekeba and Yeju were found corneous. However, eighteen genotypes i.e. Bobe Red, Abamelko, Dagim, America - 1, Berjoke Col≠ 1, Jimma Local-2, Meminay-4, Welenchity Colldolgon-3, Bobe white, Dem Hay, Dima, Jamiyu, Lali, Tewzale, Wetet Begunchie, Goronjo and Seredo are found to be with floury endosperm texture. Six genotypes i.e. E36-1, Dabar, Dagnaw, Musgi Red, Jeru and Macia were intermediate to corneous, whereas, AL - 70, Osmel, Baduquane, Gano, Jigurti, Kodem, Wede Aker, Zeri Adis, Gedo and Redswazi were intermediate to floury. Appendix Table 5, sixteen genotypes i.e. Baji, Chiro, Emahoy, Merawi, Degalit yellow-1, Gorade-2, Hodem-1-3, Wollo Col≠050, Bobe Red, Dgalit, Degalit Yellow, Tetron White, Tseada Achire, Wediarse, Wegere, Melkam and Misikir showed intermediate texture. In corneous endosperm, the structure gives a translucent

appearance which appears as dark shades while that of floury has an opaque or chalky appearance which appears as brighter white shades. Sorghum genotypes having different endosperm texture (Corneous to floury) range were reported by Kassahun *et al.* (2011) and Adetunji (2012). Similar result was reported by Haile *et al.* (2016) for north eastern Ethiopian sorghum landraces. According to Adeole *et al.* (2002) in general, those sorghums genotypes with intermediate endosperm texture were suitable than those floury endosperm texture. Generally, genotypes possessing intermediate to corneous endosperm are preferred for both malt quality and since serving as defense mechanism against mould and possible insect attack in non-tannin sorghum types.

Estimation of Variance Components

The genotypic coefficient of variation (GCV) ranged from 2.39 % for HLW to 136.93 (25.30) % for NPT, while phenotypic coefficient of variation (PCV) ranged from 2.74 % for HLW to 138.34 (25.49) % for NPT (Table 6). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (<10%), moderate (10-20%) and high (>20%) (Deshmukh *et al.*, 1986). High GCV was recorded for PH (22.05 %), NPT [136.93 (25.30) %], GY (23.24 %) and DP (49.44%). High PCV were recorded for PH (24.99 %), NPT [138.34 (25.49) %], GY (24.92%) and DP (49.44 %). These high values of PCV and GCV revealed that the varieties have a broad base genetic background, so that they can respond positively to selection. This was in line with the results reported by Kassahun *et al.* (2011) for grain yield, plant height and effective tillers by Abraha *et al.* (2015); and PCV (>20%) values for □□ and □□—amylase enzymes by Alhassan and Adedayo (2010).

PCV and GCV values computed were moderate for days to flowering, days to maturity, thousand kernel weight, malting weight loss, kernel width and kernel thickness. This was in line with the results reported by Kassahun *et al.* (2011) for days to flowering and Badigannavar *et al.* (2015) for thousand kernel weight. Moderate GCV values of these traits suggest the possibility of improving these traits through selection. The phenotypic coefficient of variation was relatively greater than genotypic coefficient of variation for all these traits studied. The magnitude of the difference between PCV and GCV in the present study was low for all of the traits (Table 6). This indicated that the environmental effects on genetic expression of these traits were low and selection based on the phenotype or genotypes would result in genetic improvement. The present study was in agreement with the results for days to flowering, days to maturity, hectoliter weight and grain yield (Muhammad *et al.*, 2015) and (Chavan *et al.* 2010). Low PCV and GCV values were computed for fine grind hot water extract,

Table 4. Diastatic power values in Windis Kolbach (°WK) and in Sorghum diastatic units (SDU)

G.N	Genotypes	DP WK	DP		G. N	Genotypes	DP WK	DP	
			SDU	SDU				SDU	SDU
1	Abamelko	36.81	36.27	29	Degalit Yellow	60.75	49.66		
2	AL-70	51.84	44.68	30	DemHay	44.98	40.84		
3	Baji	49.48	43.36	31	Dima	11.36	22.03		
4	Birimash	51.42	44.45	32	Jamiyu	26.17	30.32		
5	Osmel	98.07	70.55	33	Jeru	43.77	40.17		
6	Chiro	25.76	30.09	34	Jigurti	18.83	26.21		
7	Dagim	41.57	38.93	35	Kodem	42.11	39.24		
8	E36-1	15.19	24.18	36	Lalo	34.03	34.72		
9	Emahoy	15.16	24.16	37	Masugi Red	32.70	33.97		
10	Merawi	18.59	26.08	38	Masugi Yellow	40.84	38.53		
11	AbaAre-1	58.89	48.62	39	Tetron White	29.87	32.39		
12	America-1	29.84	32.37	40	Tewzale	66.93	53.12		
13	Baduqane	14.71	23.91	41	Tseada Achire	70.06	54.87		
14	Berjokecoll#1	33.57	34.46	42	Tseada chimure	15.15	24.15		
15	DagalitYellow-1	52.60	45.11	43	Wediarse	18.50	26.03		
16	Gorade-2	22.64	28.34	44	Wegere	44.58	40.62		
17	Hodem-1-3	67.13	53.24	45	Wetetbegunchie	96.03	69.40		
18	JimmaLocal-2	40.60	38.4	46	Wode aker	15.24	24.20		
19	Marye#2	48.98	43.08	47	Yeju	85.60	63.57		
20	Meminay-4	37.58	36.70	48	ZeriAdis	60.57	49.56		
21	Welenchity Col#3	22.40	28.21	49	Goronjo	29.74	32.32		
22	WolloCol#050	44.47	40.56	50	Gedo	18.51	26.03		
23	Gano	50.29	43.82	51	Melkam	30.06	32.50		
24	Bobere red	13.38	23.16	52	Misikir	25.88	30.16		
25	Bobere white	29.82	32.36	53	Dekeba	22.18	28.09		
26	Dabar	43.42	39.97	54	Seredo	38.00	36.94		
27	Dagnaw	44.66	40.66	55	Macia	60.07	49.28		
28	Degalit	70.40	55.07	56	Redswazi	26.09	30.27		

Table 5. Endosperm texture (ET) of the 56 Sorghum genotypes

G. N	Genotype	E T	Entry No	Genotype	ET	G. N	Genotype	ET	G.N	Genotype	E T
2	AL - 70	4	16	Gorade-2	3	30	Dem Hay	5	44	Wegere Wetet	3
3	Baji	3	17	Hodem-1-3	3	31	Dima	5	45	Begunchie	5
4	Birimash	5	18	Jimma Local-2	5	32	Jamiyu	5	46	Wede Aker	4
5	Osmel	4	19	Marye ≠ 2	1	33	Jeru	2	47	Yeju	1

Table 5. continuation

6	Chiro	3	20	Meminay-4 Welenchity	5	34	Jigurti	4	48	Zeri Adis	4
7	Dagim	5	21	Col#3	5	35	Kodem	4	49	Goronjo	5
8	E36-1	2	22	Wollo Col#050	3	36	Lalo	5	50	Gedo	4
9	Emahoy	3	23	Gano	4	37	Musgi Red Musgi	2	51	Melkam	3
10	Merawi	3	24	Bobbe Red	2	38	yelow Tetron	1	52	Misikir	3
11	Aba Are- 1	1	25	Bobbe white	5	39	White	3	53	Dekeba	1
12	America - 1	5	26	Dabar	2	40	Tewzale Tseada	5	54	Seredo	5
13	Baduqane Berjoke	4	27	Dagnaw	2	41	Achire Tseada	3	55	Macia	2
14	Col# 1	5	28	Degalit	3	42	Chimure	1	56	Redswazi	4

Subjectively scored on a scale of 1-5, where: 1= corneous, 2 = intermediate to corneous 3 = intermediate, 4 = intermediate to flourey and 5 = flourey

germination energy, protein, and malt moisture content and hectoliter weight. This suggests these traits were more influenced by the environment for their phenotypic expression and relatively smaller variability. This was in line with the studies reported for protein content by Kassahun *et al.* (2011). Low, moderate and higher PCV and GCV values were reported for protein, germination energy and malting loss by Alhassan and Adedayo (2010).

Broad sense heritability

According to Singh (2001), very high estimate of heritability values were detected for DF, DM, NPT, GY, TKW, KL, KW, KT, GE, MWL, FGHE, MMC, DP and HLW ranging from 85.00% to 98.99 (98.52) % (Table 6). This result is in agreement with Ali *et al.* (2012) who reported very high broad sense heritability estimates for days to flowering, grain yield and thousand kernel weights. The traits which exhibited high heritability suggested the effect of selection could be fairly easy and improvement is possible using breeding. On the contrary, medium heritability estimates were noted for plant height (77.83%) and protein content (Raschke *et al.*, 1995; Yalemtesfa, 2014). Similar results were previously reported in sorghum by Abraha *et al.* (2015) for plant height (78.1 %) and Motlhaodi (2016) for protein (78%). Wright (1921) also stated that genetic coefficient of variation along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. So, the traits which had moderate and high GCV in magnitude i.e. DF, DM, PH, NPT, GY, TKW, KW, KT, MWL and DP showed medium to high heritability and can be selected based on their

phenotype.

Generally, except PH and Pro, the rest studied traits showed high to very high H^2 estimates indicating the possibility of improving these traits through selection. According to Poehlmon and Sleper (1995), if a trait has high heritability accompanied with high genetic advance, it indicates that the influence of the environment on the trait is less and selection becomes easy.

Expected genetic advance as percent of mean

Genetic advance as percent of mean ranged from 4.92% for HLW to 282.08 (51.73) % for NPT (Table 6). According to Johnson *et al.* (1955a), GAM was classified as low (<10%), moderate (10-20%) and high (>20%); the traits DF, DM, PH, NPT, GY, TKW, KW, KT, MWL and DP revealed high genetic advance as percent of mean. High value of expected genetic advance expressed as percent of mean for genetic advance under selection refers to improvement in selected genotypes as compared to the base population with a single cycle of selection at a given selection intensity (Singh, 2001). Therefore, the results suggested that selecting the top 5% of the genotypes could result in genetic advance values of 4.92% to 282.08 (51.73) %. However, KL, GE, Pro, FHWE and MMC showed relatively low GCV, high H^2 and relatively moderate GAM. Protein content revealed low GCV, medium H^2 and moderate GAM.

According to Johnson *et al.* (1955b) heritability along with genetic advances are usually more useful than heritability alone in predicting the resultant effect of selecting the best individuals and stated that high heritability along with high genetic advance as percentage of mean implies the role of additive genes for

Table 6. Estimates of phenotypic and genotypic variances and coefficient of variations, heritability in broad sense, genetic advance and genetic advance as per cent of mean

Traits	GV σ^2_g	PV σ^2_p	GCV (%)	PCV (%)	H ² (%)	GA	GAM (%)
DF	182.08	185.61	13.95	14.09	98.1	27.53	28.47
DM	286.25	299.25	11.31	11.56	95.66	34.09	22.79
PH	3285.47	4221.18	22.05	24.99	77.83	104.17	40.07
NPT	0.18(0.048)	0.19(0.049)	136.93 (25.30)	138.34 (25.49)	98.99 (98.52)	0.89 (45.13)	282.08 (51.73)
GY	1196287	1375002	23.24	24.92	87	2101.6	44.66
TKW	27.55	31.01	14.89	15.8	94.26	10.81	30.68
HLW	3.02	3.96	2.39	2.74	87.27	3.58	4.92
KL	0.16	0.17	8.5	8.76	94.11	0.83	17.51
KW	0.17	0.2	10.14	10.94	85	0.84	20.89
KT	0.1	0.11	10.9	11.25	90.91	0.64	22.45
GE	41.41	46.85	6.87	7.3	88.38	13.26	14.15
CP	0.54	0.9	6.77	8.69	61.42	1.52	13.94
MWL	5.81	6.67	13.16	14.09	87.11	4.97	27.1
FHWE	28.27	32.44	7.95	8.52	87.15	10.95	16.38
MMC	0.36	0.42	7.16	7.83	85.71	1.23	14.76
DP	382.75	387.16	49.16	49.44	98.75	40.07	99

N.B. The values for NPT in the parenthesis are the transformed values

the expression of the traits and thus it could be very effective in improvement upon selection. As indicated by Burton and De Vane (1953), the GCV together with H² estimate gives the best picture of expected advances from selection. Therefore, high H² with high GCV provides the required expected genetic advance through selection.

Selection for the traits DF, DM, PH, NPT, GY, TKW, KW, KT, MWL, DP is likely to be effective as medium to medium to high heritability values were associated with high genetic advance in the improvement of the performance of the genotypes through these traits. Similar results of high genetic advance estimates was found for grain yield and thousand kernel weights by Ranjith *et al.* (2017), plant height and number of tillers by Kumari *et al.* (2016), days to flowering and days to maturity by Nyadanu and Dikera (2014).

SUMMARY AND CONCLUSIONS

Analysis of variance indicated highly significant differences ($P < 0.01$) among the genotypes for all the traits studied. The highest grain yield were obtained from Jigurti (7164.2 kg ha⁻¹) and Osmel (7062.6 kg ha⁻¹) followed by Hodem-1-3 (6906.1 kg ha⁻¹), Marye #2 (6871

kg ha⁻¹) and America-1 (6820 kg ha⁻¹) while the lowest from Goronjo (2350 kg ha⁻¹), Lalo (2359 kg ha⁻¹) with mean of 4705.34 kg ha⁻¹. The highest FHWE was observed in Baji (76.83%) followed by Jimma Local-2 (75.25%), Degalit yellow-1 (74.89%), and Tseada Achirie (74.89%) also meets the FHWE recommendation whereas, the lowest was observed by Seredo (53.2%) followed by Wede Aker (53.45%). Nine genotypes, Osmel, Wetetbegunchie, Yeju, Degalit, Tseada Achrie, Hodem-1-3, Tewzale, Dgalit Yellow and Zeri Adis showed diastatic power greater than the checks Macia (60.07 °WK) and Redswazi (30.27 °WK) and also meets DP recommendation.

Considering the most important parameters DP, FHWE, CP, MWL and ET; the genotypes, Baji, Tseada Achire, Abare-1, Yeju, Dabar, Degalit yellow-1 and Degalit Yellow were producing better malt quality and those genotypes with sufficient DP and wort extracts could be used for brewing commercial beers and soft drinks.

For all of the traits studied, higher phenotypic over genotypic coefficient of variation were observed with range of GCV 2.39% for HLW to 136.93 (25.30) % for NPT, PCV 2.74 % for HLW to 138.34 (25.49) % for NPT, H² 61.42% for protein content to 98.99 (98.52) % for NPT and GAM 4.92% for HLW to 282.08 (51.75) % for NPT.

High H^2 estimates coupled with relatively high GAM were computed for DF, DM, NPT, GY, TKW, KW, KT, MWL and DP, whereas, PH showed higher GCV, medium broad sense H^2 and high GAM suggesting the variability of these traits is controlled by additive genetic factors and less environmental influence in the phenotypic expression.

All in all, the present study revealed the existence of significant genetic variability among the tested genotypes for different traits.

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