

Full Length Research Paper

Assessment of Yield and Yield Related Traits in Durum Wheat (*Triticum Turgidum*) Genotypes in Northern Ethiopia

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Received 3 April, 2018; Accepted 24 April, 2018

The main objective of this study was to evaluate 21 durum wheat genotypes for grain yield and agronomic traits under rain fed condition in three districts of Axum Agricultural Research Center, namely Hatsebo, Tahtay-Maichew and Ahferom during 2014 cropping season. Completely randomized block design with three replications was conducted for each location. The result of analysis of variance indicated that there was a significant difference among the genotypes for all the traits except harvest index. Thus, considerable variation was recorded among durum wheat genotypes. However, the effect of location on grain yield was non-significant. Among the genotypes, the highest grain yield was obtained from genotype 34thIDONMD/134/off2011 (2.39 t ha⁻¹) across all environments. High value of genotypic coefficient of variation (GCV) was calculated for panicle length, biomass yield, grain yield and harvest index both at Hatsebo and Tahtay-Maichew. However, at Ahferom, medium GCV was observed for these traits, which might be due to terminal moisture stress during the cropping season. High genotypic coefficient of variation, heritability and genetic advance as percent of mean were found in panicle length, biomass yield, grain yield and harvest index at Hatsebo and Tahtay-Maichew. This indicated that these characters could be useful basis of selection. The association of grain yield was positive and significant with harvest index (0.67), days to maturity (0.25), days to heading (0.22) and biomass yield (0.2), however the association between biomass yield and harvest index was negative (-0.54).

Key words: Durum wheat, genetic variation, heritability, quantitative traits.

INTRODUCTION

Durum wheat is the oldest traditional crop in Ethiopia covering significant proportion of arable land devoted to national wheat production. It is among the most diversified crop species in Ethiopia accounting for about 12% (more than 7000 accessions) of the national gene

bank holdings. Negassa et al. (2012) indicated that durum wheat covers about 20% of the total area under wheat production, and estimated to contribute between 18 to 20% to the national wheat production with average productivity of 1.8 t ha⁻¹ (Teklu and Hammer, 2008).

Farmer varieties, which are often referred as 'landraces' in the literatures, are characterized a

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Table 1. Altitude, rainfall, temperature, latitude, longitude and soil type of study locations.

Location	Altitude (m.a.s.l)	Total annual rainfall (mm)	Temperature (°C)		latitude	longitude	Soil type
			Min	Max			
Hatsebo	2118	782.8	10	29	14° 06' 40.2''	038° 45' 45.8''	Verti soil
Tahtay maichew	2090	656.6	12.6	25.51	14° 06' 76.2''	038° 39' 14.5''	Clay loam
Ahferom	2014	618.0	11.3	27.1	14° 06' 40.2'' N	039° 04' 15.6'' E	loamy

National Meteorological Agency (Mekelle Branch).

significant genetic variability, even though their genetic constitution is mostly unknown, attributed to a number of factors including the natural and artificial selections (Mengistu and Pè, 2016). Environmental conditions and seeds exchanges among farmers resulted as key factors in the landrace variability (Pagnotta et al., 2005) and the pattern of variability is different among some of the Ethiopian regions (Mondini et al., 2010). As reports suggested, Ethiopian durum wheat have valuable genetic basis for abiotic and biotic stresses adaptations like resistance to *Erysiphe graminis* f. Sp. *Triticum*, *Puccinia* spp. and *Septoria anodorum* (Negassa, 1986), stem rust (Ug99 or TTKS race) (Klindworth et al., 2007) and drought tolerance (Mengistu et al., 2015). Despite such merits endowed in the farmer's cultivars, their cultivation was progressively minimized with the advent of improved and genetically uniform modern varieties. The farmers cultivars were seldom, if any utilized in modern wheat breeding efforts to improve production and productivity. For example, only less than 2% of the improved varieties cultivated in Ethiopia were composed of gene from Ethiopian landraces (CIMMYT, 2014). The remaining 98% of the improved durum wheat varieties are introductions of exotic materials from international breeding blocks. Identification of better genotypes with desirable traits and their subsequent use in plant breeding program and establishment of suitable selection criterion can be helpful for successful varietal improvement program. Analysis of variability among the traits and association of a particular character in relation to other traits contributing to yield of a crop would be great importance in planning a successful breeding program (Mary and Gopalan, 2006). Development of high yielding varieties requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only genetic one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be in conjunction with estimates of genetic advance, the change in mean value between generations (Shukla et al., 2006). One of the main objectives of any breeding program is to produce high yielding genotypes for release as cultivars to farmers. Introduction of new populations can be made from one region to the other easily and may be used for further manipulation to develop breeding genotypes

(Jamal et al., 2009). Adaptability and yield stability of the outstanding genotypes will be tested in the national uniform yield trials and in farmer's fields, and the best ones will be proposed for release, after being evaluated for their grain yield and quality. The present study was conducted to evaluate the performance of twenty-one promising durum wheat genotypes in order to assess the presence of variability for desired traits and a significant amount of variation for different parameters.

MATERIALS AND METHODS

The experiment was conducted at three locations named Hatsebo, Tahtay-Maichew and Ahferom under rain fed condition during 2014 main cropping season. These locations represent the varying agro-ecologies of the major wheat growing areas of central Tigray. Climatic condition, soil type, altitude and longitudes of the experimental sites are presented in Table 1. It was conducted using RCBD design with three replications at three locations. A total of 21 durum wheat genotypes including two checks (Mukiye and Mangudo), and one local check (Shehan) were planted in a plot that consisted of four rows with 2.5 m long and 20 cm apart. The middle four rows were used for data collection. Planting was done by hand drilling using a seed rate of 150 kg/ha for each variety. Nitrogen and phosphorous fertilizers were applied at the rate of 100 kg/ha Urea (in split) and 100 kg/ha Di-ammonium phosphate (DAP) at planting. All other management practices were uniformly applied to all plots.

Data collected

Both the phenological and agronomic data were collected from plot and plant basis. The four central rows were used for data collection based on plots, such as days to 50% heading, days to physiological maturity, grain yield, bio-mass yield and harvest index. Ten randomly selected plants from the four central rows of each plot were used for data collection on plant basis and the averages of the ten plants in each experimental plot were used for statistical analysis for traits such as plant height and spike length.

Statistical analysis

Data were subjected to analysis of variance (ANOVA) using the linear model SAS version 9.1.3 (SAS Institute Inc, 2004) after testing the ANOVA assumptions. The phenotypic and genotypic coefficients of variation were estimated according to the methods suggested by Burton and De Vane (1953). However, cluster analysis was carried out using the Squared Euclidean distance-Ward's clustering method and conducted using the statistical package for social sciences (SPSS Inc., 2009) software. Mean separations were estimated using Duncan's Multiple Range (DMRT) test at 5% probability levels.

Estimation of variance components and association among components

The phenotypic and genotypic variances were estimated according to the methods suggested by Burton and De Vane (1953).

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

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

Where, $\delta^2 p$ = phenotypic variance

$\sigma^2 g$ = Genotypic variance

$\delta^2 e$ = Error variance

(Error mean square)

Mg = mean sum square of genotypes

Me = mean sum square of error

r = Number of replications.

The phenotypic and genotypic coefficient of variation was estimated according to the methods suggested by Burton and De Vane (1953).

Phenotypic coefficient of variation

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} * 100$$

Where, $\sigma^2 p$ = phenotypic variance and
 \bar{X} = mean of the characters evaluated

Genotypic coefficient of variation

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} * 100$$

Where, $\sigma^2 g$ = genotypic variance

\bar{X} = mean of the characters evaluated.

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

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} * 100$$

Where, $\delta^2 p$ = phenotypic variance, $\delta^2 g$ = Genotypic variance,

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

$\delta^2 e$ = Environmental (error) variance.

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960) as:

$$GA = K * \sigma_p * H^2$$

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

$$GA \text{ (as \% of the mean) (GAM)} = \frac{GA}{\bar{X}} * 100$$

Where, \bar{x} = population mean

Estimation of genotypic correlation coefficients was done based on

the procedure of Dabholkar (1992).

$$r_g = \frac{g \text{ COV } x, y}{\sqrt{\sigma^2_g x \cdot \sigma^2_g y}}$$

Where, r_g is genotypic correlation coefficients.

Cluster analysis

Based on the squared distances values, clustering of genotypes was done using Ward's method as described by Singh (2001). Cluster analysis was conducted using the statistical package for social sciences (SPSS Inc., 2009).

RESULTS AND DISCUSSION

The analysis of variance revealed that there was a significant variation ($p < 0.05$) among the genotypes for most of the traits studied (Table 2). However, the interaction effect (genotype by location) was non-significant for grain yield (Table 3). This tells us that varieties responded constantly to the different locations suggesting the best genotype here identified can be recommended for all the three locations. The mean performances of the genotypes over three locations for the characters are presented in Table 2. Genotypes showed variation for days to heading ranging from 59 to 64.08 days with a mean of 61.19 days, and days to maturity ranging from 99 to 104.33 days with a mean of 100.81 days. Dejene et al. (2016), Yonas et al. (2016), and Rathwa et al. (2018) also reported variation among durum wheat genotypes for days to heading and days to maturity.

In this study, almost all the genotypes have matured early, hence these genotypes could be classified as early to the study area, suggested the chance of selecting early genotypes which can reduce the risk to face with the terminal moisture stress which is one of the wheat production problems in the study area. However, earliness alone is not guarantee as other characters like grain yield matters for adaptation of genotypes by farmers. The good thing is that some of the identified early maturing genotypes (that is, Mangudo and CD11-Y10 BIR SEL/67/off2011) were found to give average to high grain yield which makes them desirable as they contain both earliness and high grain yield which are mostly contradicting traits. Hence, after testing these genotypes in more locations and different seasons they can be the best varieties for the testing regions and other similar agro-ecologies. Panicle length ranged from 4.19 cm for CD11-Y10 BIR SEL/67/off2011 to 6.2 cm for 34thIDONMD/134/off2011 with mean value of 4.5 cm. The computed harvest index for genotypes ranged from 35% for Mukiyeye to 48% for CD11-Y10 BEK SEL/82/off2011. The effect of locations on the performance of the genotypes was non-significant with respect to grain yield (Table 3). It can be inferred that the

Table 2. Mean performances of durum wheat genotypes over three locations for yield and other agronomic characters.

Treatments	GY (t ha ⁻¹)	DH	DM	GFP	PH (cm)	PL (cm)	BM (t ha ⁻¹)	HI
CD11-Y10 BIR SEL/18/off2011	1.92	62.08	100.08	38.00	68.42	4.75	5.17	0.38
34thIDONMD/21/off2011	2.26	63.58	104.33	40.75	69.98	4.92	5.08	0.45
CD11-Y10 BIR SEL/12/off2011	2.10	61.17	98.92	37.75	64.35	4.87	4.83	0.44
CD11-Y10 BEK SEL/82/off2011	2.05	60.42	101.58	41.17	68.12	5.08	4.42	0.48
34thIDONMD/66/off2011	2.15	62.75	101.08	38.33	70.95	4.42	5.00	0.44
34thIDONMD/109/off2011	1.98	61.08	99.00	37.92	67.52	4.72	5.58	0.36
CD11-Y10 BEK SEL/117/off2011	1.85	59.83	99.75	39.92	83.35	4.80	5.08	0.38
34thIDONMD/134/off2011	2.39	64.08	103.42	39.33	69.98	6.32	5.42	0.45
CD11-Y10 BIR SEL/172/off2011	1.91	61.42	101.25	39.83	68.22	4.88	5.75	0.35
CD11-Y10 BIR SEL/64/off2011	1.91	59.08	99.08	40.00	66.05	4.20	4.67	0.41
CD11-Y10 BIR SEL/67/off2011	2.20	59.92	99.50	39.58	65.97	4.19	5.42	0.42
CD11-Y10 BIR SEL/11/off2011	1.82	59.08	97.67	38.58	70.27	4.95	5.00	0.37
CD11-Y10 BIR SEL/68/off2011	2.06	60.67	101.50	40.83	72.18	4.70	5.00	0.43
34thIDONMD/60/off2011	2.10	63.75	102.83	39.08	65.98	4.68	5.25	0.39
CD11-Y10 BIR SEL/70/off2011	1.92	60.25	100.50	40.25	70.25	4.63	4.83	0.41
EGYPT-KUL/26/off2011	1.79	60.75	101.42	40.67	63.58	4.82	5.08	0.38
CD11-Y10 BIR SEL/114/off2011	2.06	60.75	102.67	41.92	71.50	4.98	4.58	0.45
CD11-Y10 BIR SEL/181/off2011	2.07	61.18	99.67	38.50	68.55	4.83	5.00	0.41
Mangudo	2.38	60.08	100.25	40.17	68.62	4.63	5.67	0.43
Mukiye	1.61	61.08	102.75	41.67	67.18	4.70	4.75	0.35
Local/ shehan/	2.04	62.08	99.67	37.58	66.63	4.53	5.25	0.39
LSD(0.05)	0.13	1.70	1.18	0.99	1.44	0.30	0.25	1.02
MEAN	2.03	61.19	100.81	39.61	68.91	4.50	5.08	0.41
R2	0.43	0.78	0.60	0.74	0.62	0.72	0.50	0.43

DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height, PL= panicle length, BM= biomass yield, GY= grain yield, HI= harvest index.

Table 3. Sum of squares and its percentage (out of total) contribution of the combined analysis of grain yield of 21 durum wheat varieties tested over 3 locations.

Source	DF	SS	MS	F value
Location	2	2.85	1.42	7.90*
Rep(loc)	9	3.19	0.35	1.96*
Treatment	20	8.75	0.44	2.42*
Loc*trt	40	9.75	0.24	1.35 ^{ns}
Error	180	32.49	0.18	
Total	251	57.03		
CV(%)=	20.96			

**, * Significant at $p < 0.01$ and $p < 0.05$, respectively; ns= non-significant, Where: loc*trt= location by treatment interaction.

overall performance of the genotypes was better at Hatsebo followed by Tahtay-Maichew and then Ahferom (Table 4). The lack of significance in the genotype by location interaction for grain yield indicating a stability of the genotypes over location which is a very determinant factor for crop adaptation. The non-significant effect of location on genotypes for grain yield may indicate that genotypes selected for better performance for the trait at one location may display a similar relative performance at

another location.

Phenotypic and genotypic coefficient of variation, H^2 (heritability in broad sense) and GAM (genetic advance as percent of mean)

The estimated GCV, PCV, heritability in broad sense and expected genetic advance are presented in Tables 5, 6

Table 4. Mean grain yield (t ha) and rank of 21 varieties at 3 locations in central Tigray, Ethiopia, 2014.

Genotypes	Hatsebo		Tahtay maichew		Ahferom	
	Yield (t ha ⁻¹)	Rank (R)	Yield (t ha ⁻¹)	Rank (R)	Yield (t ha ⁻¹)	Rank (R)
CD11-Y10 BIR SEL/18/off2011	2.225	10	1.700	21	1.820	15
34thIDONMD/21/off2011	2.67	2	1.850	13	2.260	5
CD11-Y10 BIR SEL/12/off2011	2.1251	12	1.750	19	2.47	2
CD11-Y10 BEK SEL/82/off2011	2.251	8	1.800	17	2.098	6
34thIDONMD/66/off2011	2.75	1	2.100	7	2.064	7
34thIDONMD/109/off2011	1.900	17	2.125	5	1.945	9
CD11-Y10 BEK SEL/117/off2011	1.875	20	1.80	15	1.867	13
34thIDONMD/134/off2011	2.175	11	2.425	1	2.58	1
CD11-Y10 BIR SEL/172/off2011	2.250	9	1.975	11	1.522	19
CD11-Y10 BIR SEL/64/off2011	1.725	21	1.950	12	2.030	8
CD11-Y10 BIR SEL/67/off2011	2.35	6	2.300	3	1.938	10
CD11-Y10 BIR SEL/11/off2011	2.100	14	1.750	20	1.628	18
CD11-Y10 BIR SEL/68/off2011	2.1250	13	2.125	6	1.924	11
34thIDONMD/60/off2011	2.57	3	1.800	16	1.912	12
CD11-Y10 BIR SEL/70/off2011	1.8750	19	2.225	4	1.672	17
EGYPT-KUL/26/off2011	1.8751	18	2.075	8	1.414	20
CD11-Y10 BIR SEL/114/off2011	2.27	7	2.050	10	1.836	14
CD11-Y10 BIR SEL/181/off2011	2.050	15	1.825	14	2.263	3
Mangudo	2.55	4	2.350	2	2.260	4
Mukiye	1.950	16	1.750	18	1.122	21
Local/ shehan/	2.40	5	2.050	9	1.702	16

Table 5. Genotypic and phenotypic coefficient of variation, broad sense heritability, genetic advance and genetic advance as percent of mean for 8 characters of 21 durum wheat varieties at Hatsebo.

Character	δ^2g	δ^2p	δ^2e	GCV (%)	PCV (%)	H ² (%)	GA	GAM
Days to heading	19.57	23.33	3.76	7.08	7.73	83.89	8.36	13.38
Days to maturity	31.97	39.65	7.68	5.46	6.08	80.63	10.47	10.11
Grain filling periode	11.33	18.44	7.11	8.19	10.45	61.45	5.44	13.24
Plant height	19.91	29.45	9.54	6.44	7.83	67.61	7.57	10.93
Panicle length	1.35	2.17	0.82	23.86	30.25	62.21	1.89	38.82
Biomass yield	1.45	1.96	0.51	24.80	28.84	73.94	2.13	43.99
Grain yield	0.42	0.47	0.05	29.98	31.70	89.44	1.27	58.50
Harvest index	0.01	0.01	0.002	22.22	24.34	83.33	0.19	41.85

δ^2g = Genotypic variance, δ^2e = Environmental variance, δ^2p = Phenotypic variance, H² (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

and 7. Higher magnitude of differences of genotypic and phenotypic variances was observed for some of the traits studied. The higher genotypic variance was computed for days to maturity while the lowest was for harvest index at all locations. Generally, the phenotypic variance was higher than the corresponding genotypic variance for days to heading, days to maturity, grain filling period and plant height, this indicated greater influence of environmental factors for the phenotypic expression of the traits. This result was in close agreement with the

findings of Tesfaye et al. (2016). According to Sivasubramanian and Madhavamenon (1973), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) can be categorized as high (>20%), moderate (10-20%) and low (<10%). As per this category, high values of genotypic coefficient of variation was calculated for panicle length, biomass yield, grain yield and harvest index both at Hatsebo and Tahtay-Maichew. Medium GCV was recorded for panicle length (14.98%), grain yield (14.15%) and harvest index (13.36%) at

Table 6. Genotypic and phenotypic coefficient of variation, broad sense heritability, genetic advance and genetic advance as percent of mean for 8 characters of 21 durum wheat varieties at Tahtay-Maichew.

Character	δ^2g	δ^2p	δ^2e	GCV (%)	PCV (%)	H ² (%)	GA	GAM
Days to heading	19.15	25.11	5.96	6.90	7.90	76.26	7.88	12.43
Days to maturity	22.28	53.36	31.08	4.82	7.46	41.75	6.29	6.43
Grain filling period	5.20	24.11	18.91	6.61	14.23	21.58	2.19	6.33
Plant height	19.91	29.45	9.54	6.44	7.83	67.61	7.57	10.93
Panicle length	1.59	1.67	0.08	25.97	26.62	95.22	2.54	52.29
Biomass yield	1.36	2.19	0.83	23.77	30.18	62.04	1.89	38.63
Grain yield	0.62	0.75	0.13	39.66	43.64	82.59	1.47	74.36
Harvest index	0.04	0.05	0.01	46.70	52.69	78.57	0.35	85.41

δ^2g = Genotypic variance, δ^2e = Environmental variance, δ^2p = Phenotypic variance, H² (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

Table 7. Genotypic and phenotypic coefficient of variation, broad sense heritability, genetic advance and genetic advance as percent of mean for 8 characters of 21 durum wheat varieties at Ahferom.

Character	GCV (%)	PCV (%)	H ² (%)	GA	GAM
Days to heading	3.64	5.02	52.56	3.33	5.44
Days to maturity	3.02	3.78	63.64	4.87	4.97
Grain filling periode	3.96	9.15	18.72	1.40	3.53
Plant height	9.47	11.71	65.44	10.89	15.81
Panicle length	14.98	16.90	78.63	1.31	27.41
Biomass yield	8.75	18.54	22.25	0.43	8.51
Grain yield	14.15	21.04	45.21	0.40	19.63
Harvest index	13.36	20.41	42.86	0.07	18.04

δ^2g = Genotypic variance, δ^2e = Environmental variance, δ^2p = Phenotypic variance, H² (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

Ahferom. This indicated the marked influence of environmental factors for the expression of these traits was less, hence traits can respond to selection. This is because estimation of genotypic coefficient of variation provides measure for comparing variability in the various traits and better improvement through selection (Guendouz et al., 2014). The phenotypic coefficient of variation was high for panicle length, biomass yield, grain yield and harvest index but medium for grain filling period both at Hatsebo and Tahtay-Maichew. However, at Ahferom Medium PCV was calculated for plant height, panicle length, biomass yield, grain yield and harvest. For some of the traits at both locations the difference in magnitude between GCV and PCV was high; this suggested large influence of environmental factors in masking the expression of these traits in durum wheat genotypes along with the practicality difficult for their improvement.

The heritability values ranged from 61.45 to 89.44% at Hatsebo, from 21.58 to 95.22% at Laelay-Maichew and from 18.72 to 78.63% at Ahferom. High heritability (>80%) was computed for grain yield (89.4%), days to

heading (83.8%), harvest index (83.3%) and days to maturity (80.6%) at Hatsebo; for panicle length (95.22%) and grain yield (82.59%) at Tahtay-Maichew. According to Singh (2001), heritability of a trait is considered as very high or high when the value is 80% or more. The traits which exhibited high heritability suggested selection could be fairly easy and improvement is possible using selection breeding. In agreement to this study results, Jalal and Ahmad (2012), Adhiena (2015) and Tesfaye et al. (2016) also reported high estimates of heritability for days to heading, days to maturity and grain yield. Moderate heritability (>40 and <80) was computed for plant height, panicle length and biomass yield both at Hatsebo and Tahtay-Maichew and, for days to heading, days to maturity, plant height, panicle length, grain yield and harvest index at Ahferom. This suggested that selection should be delayed to more advanced generations for these traits (Singh, 2001). Large heritability values showed relative ease with which selection can be made based on phenotype but their practicality in plant breeding is further enhanced if accompanied by high genetic advance estimates

Table 8. Genotypic correlation coefficient of 21 durum wheat varieties over 3 locations.

Variable	DM	GFP	PH	PL	BM	GY	HI
DH	0.32**	-0.41**	0.004	0.26**	-0.06	0.22*	0.19*
DM	1	0.73**	0.01	0.11	0.15*	0.25**	0.11
GFP		1	0.01	-0.08	0.19*	0.08	-0.03
PH			1	0.19*	0.18*	-0.07	-0.17*
PL				1	-0.03	0.03	0.06
BM					1	0.2*	-0.54**
GY						1	0.67**

DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height, PL= panicle length, BM= biomass yield, GY= grain yield, HI= harvest index.

(Johnson et al., 1955). The estimated genetic advance as percent of mean for the traits studied at Hatsebo, Tahtay-Maichew and Ahferom are presented in Tables 5, 6 and 7, respectively.

Genetic advance as percent of mean showed a wide range of variations across locations. It ranged from 10.11 to 58.5% at Hatsebo, from 6.3 to 85.4% at Tahtay-Maichew and from 3.5 to 27.4% at Ahferom. Johnson et al. (1955) reported that high genotypic coefficient of variation along with high heritability and genetic advance as percent of mean provide better information than each parameter alone. High genotypic coefficient of variation, heritability and genetic advance as percent of mean were found in panicle length, biomass yield, grain yield and harvest index at Hatsebo and Tahtay-Maichew. Similarly, Jalal and Ahmad (2012) reported high heritability accompanied with high genetic advance as percent of mean in case of kernel weight of main spike, grain yield per plant, number of kernel per main spike, biological yield per plant, number of spikelet per main spike and plant height. Rathwa et al. (2018) also reported high heritability coupled with high genetic advance expressed as percentage of mean for days to 50% flowering, grain filling period, number of productive tillers per plant, number of grains per main spike, grain weight per main spike, grain yield per plant, biological yield per plant and harvest index. This indicated that these characters could be useful basis of selection. However, at Ahferom the values for GCV, H^2 and GAM are low comparing with the other locations, this might be due to low rain fall pattern during 2014 cropping season.

Association of characters

The analysis of variance indicated the presence of variability among the genotypes tested for 8 traits that allow breeders to make improvement through selection. The analysis of the relationship among the characters and their association with grain yield is essential to establish selection criteria (Singh et al., 1990). Environment also plays an important role in the correlation. In some cases, environment affects both the

traits in the same direction or some time in different directions. The genetic and environment causes of correlation combine together and give phenotypic correlation. Genotypic correlation coefficient estimates between each pair of characters are presented in Table 8.

The association of grain yield was positive and highly significant with harvest index (0.67). Grain yield have also positive and significant correlation with days to maturity (0.25), days to heading (0.21) and biomass yield (0.22). Therefore any improvement of these characters would result in a substantial increment on grain yield. These results are sustained with those of Dawit et al. (2012) and Alemu et al. (2016) that stated positive and significant correlation of grain yield with harvest index, days to maturity and biomass yield. Besides, grain yield have positive and non-significant correlation with grain filling period and panicle length. This suggested that improvement of these traits would not affect the increment of grain yield. Biomass yield have positive and significant correlation with days to maturity, grain filling period and plant height; however, it has negative and highly-significant correlation with harvest index. This suggested that selection of genotypes for high biomass yield might lower harvest index. In line with this finding, Adhiena (2015) indicated negative and significant correlation of biomass yield with harvest index in bread wheat genotypes.

Clustering of genotypes

The D^2 values calculated based on Euclidean dissimilarity distance using Ward's method from the pooled mean of genotypes for the eight traits resulted in classifying the 21 durum wheat genotypes into four distant clusters (Figure 1). This indicated that the presence of genetic divergence among the tested genotypes. Cluster I was the largest cluster consisted of twelve genotypes (57.1%), cluster II contained only one genotype. The third and the fourth clusters contained five and four genotypes respectively. Different authors also reported the presence of diversity among the durum wheat genotypes classifying into

Dendrogram

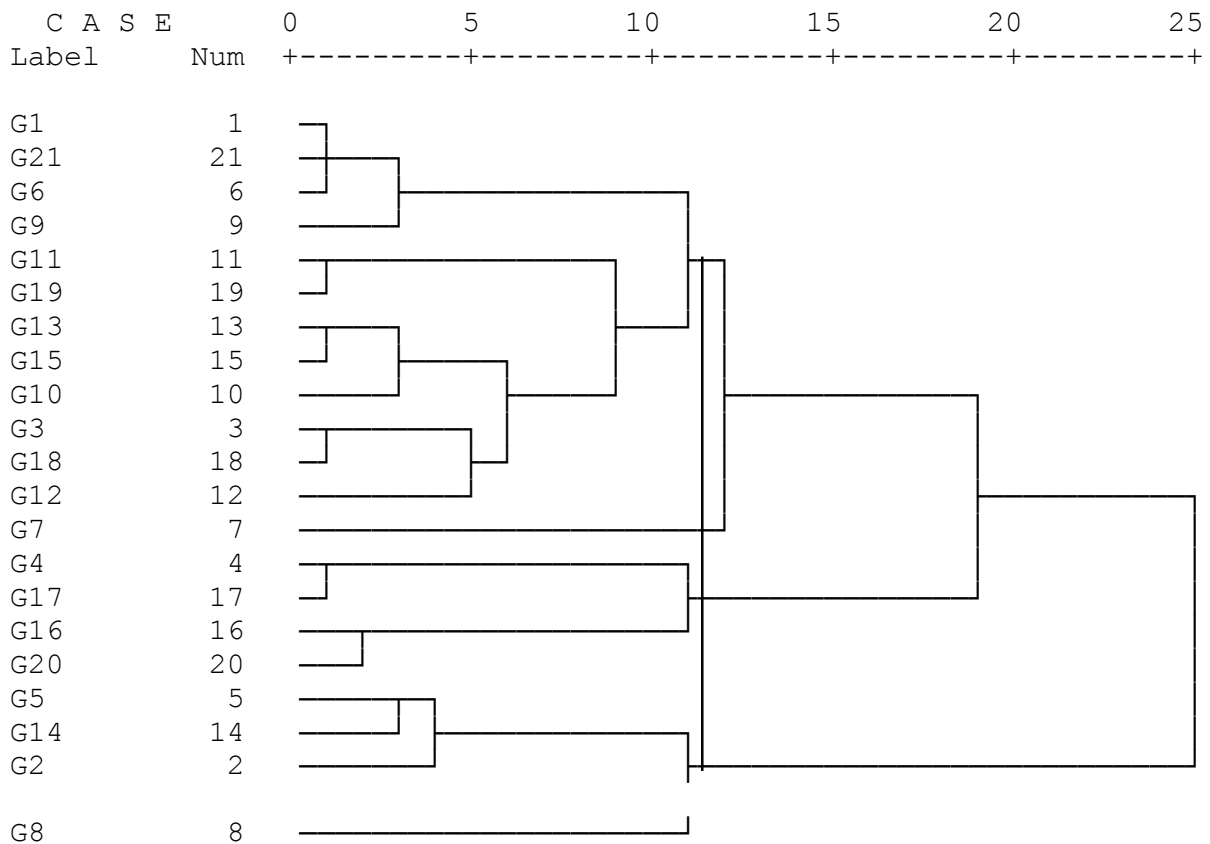


Figure 1. Dendrogram depicting the clustering of 21 genotypes using means of 3 locations, Where, **G1**= CD11-Y10 BIR SEL/18/off2011, **G2**= 34thIDONMD/21/off2011, **G3**= CD11-Y10 BIR SEL/12/off2011, **G4**= CD11-Y10 BEK SEL/82/off2011, **G5**=34thIDONMD/66/off2011, **G6**= 34thIDONMD/109/off2011, **G7**=CD11-Y10 BEK SEL/117/off2011, **G8**=34thIDONMD/134/off2011, **G9**= CD11-Y10 BIR SEL/172/off2011, **G10**= CD11-Y10 BIR SEL/64/off2011, **G11**= CD11-Y10 BIR SEL/67/off2011, **G12**= CD11-Y10 BIR SEL/11/off2011, **G13**= CD11-Y10 BIR SEL/68/off2011, **G14**= 34thIDONMD/60/off2011, **G15**= CD11-Y10 BIR SEL/70/off2011, **G16**= EGYPT-KUL/26/off2011, **G17**= CD11-Y10 BIR SEL/114/off2011, **G18**= CD11-Y10 BIR SEL/181/off2011, **G19**= Mangudo, **G20**= Mukiyie, **G21**= Local/ shehan.

different number of distinct clusters. Geleta and Grausgruber (2013) study on morphological and quality traits variation in tetraploid (*Triticum turgidum* L.) and hexaploid (*Triticum aestivum* L.) wheat accessions from Ethiopia and classified 53 bread wheat accessions into four clusters. Similarly, Dargicho et al. (2015) grouped 68 bread wheat germplasm into six clusters using Mahalanobis D^2 statistics based on the pooled mean of germplasm. Thus, the presence of such kind of variability among the germplasm is crucial to develop desirable recombinants for developing high yielding durum wheat varieties through crossing between superior germplasm.

Conclusion

Knowledge on the extent and pattern of genetic variability

in a population, interrelationship among different agronomic characters and information on the naturally occurring diversity are essential to design breeding program in crop improvement. To generate such information, 21 durum wheat genotypes were tested using randomized complete block design under rain-fed condition at Hatsebo, Tahtay-Maichew and Ahferom testing sites of Axum Agricultural Research Center in 2014. Results of analysis of variance showed statistically significant difference among the tested durum wheat genotypes suggesting the genotypes was phenotypically divergent. However, the effect of locations on the performance of the genotypes was non-significant with respect to grain yield. This indicates that genotypes selected for better performance for the trait at one location may display a similar relative performance at another location; thus there may be no need for spatial

replication as evaluation at a single location may be sufficient for the purpose. High values of genotypic coefficient of variation were calculated for panicle length, biomass yield, grain yield and harvest index both at Hatsebo and Tahtay-Maichew. This indicated that the marked influence of environmental factors for the expression of these traits was less; hence traits can respond to selection. Genetic correlation coefficient analysis indicated that important agronomic traits (days to maturity, biomass yield and harvest index) were positively and significantly correlated with grain yield. This suggests a common genetic/physiological basis among these traits. Hence, simultaneous improvement of these traits would be possible. Generally, the national durum wheat program should plan and implement good breeding strategy to improve the genetic gain via releasing early and high yielder durum wheat varieties.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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