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## Research Article

# Estimation of Heritability and Genetic Advance of Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes at Ofla District, Northern Ethiopia

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## Abstract

A field experiment was conducted at Ofla District, Northern Ethiopia in 2014, with the objective of estimating nature and magnitude of variations existing in bread wheat genotypes. Twenty six genotypes were laid out in randomized complete block design with 3 replications. Twelve quantitative traits were subjected to analysis of variance and genetic analyses. There were significant differences ( $p < 0.05$ ) among genotypes for 10 quantitative traits including grain yield. Heritability in broad sense ranged from 4.57% for number of tillers per plant to 96.86% for thousand kernel weight. The range for genetic advance as percent of mean was 3.04% (number of tillers per plant) to 19.74% (biomass yield). High heritability estimates and moderate genetic advance as percent of mean was computed for days to heading, days to maturity and thousand kernel weight. Besides, genotypic coefficient of variance and phenotypic coefficient of variance had low magnitude of differences for these traits. Hence, the traits are highly heritable, selection based on these traits would improve the characters. The top 3 genotypes that performed better than the standard checks for grain yield and early maturity were ETBW7888, ETBW7892 and ETBW7887 with grain yield of 6.4, 5.6 and 5.5 t ha<sup>-1</sup>, respectively. Grain yields of the standard checks were 3.9, 4.7 and 3 t ha<sup>-1</sup> for Danda, Hidase and Digalu respectively. Besides, those genotypes were earlier to mature (110-112 days) than the standard checks (119-129 days). Therefore, direct selection of these genotypes can be rewarding. As the result is based on single location in a year, confirming across locations and over years is important.

**Key words:** Bread wheat, heritability, genetic advancement, variations, ETBW7888, ETBW7892, ETBW7887

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**Competing Interest:** The authors have declared that no competing interest exists.

**Data Availability:** All relevant data are within the paper and its supporting information files.

## INTRODUCTION

Ethiopia, with its range of altitudes, soils and climatic conditions provide ecological settings suitable for the cultivation of diverse species of wheat (Harlan, 1971). Previously durum wheat and bread wheat accounted for about 70 and 30% of the total area of wheat production in Ethiopia, respectively. However, now a days the area under bread wheat has surpassed the durum wheat (Taffesse *et al.*, 2011).

In Ethiopia, wheat stands fourth both in area coverage and total production among cereal crops next to maize, sorghum and tef. Total area production during, 2013 growing season was 1627647.16 ha with national average productivity of 2.10 t ha<sup>-1</sup> (CSA., 2013). In Southern zone of Tigray Regional State, where the trial was conducted, wheat stands first both in area and production among all crops followed by barley, sorghum and tef. In this zone, the area coverage and productivity of this crop was 49241.73 ha and 1.93 t ha<sup>-1</sup>, respectively, which is below even from national average productivity (2.1 t ha<sup>-1</sup>) (CSA., 2013). The low productivity of the crop is due to many factors including biotic (disease, insects and weeds), abiotic (drought, low soil fertility etc.) and not using appropriate technologies (improved variety and fertilizer). Therefore, developing improved varieties is one of the measures to alleviate these constraints. In this regard, studying genetic variability for the characters of interest is the primary precondition when the breeders look for the development of varieties (Scossiroli *et al.*, 1963). Tesfaye *et al.* (2014), Degewione *et al.* (2013) and Demelash *et al.* (2013) had studied heritability and genetic advance in bread wheat genotypes in different parts of Ethiopia, but not in Southern Tigray region of Ethiopia. Therefore, the present study was implemented to estimate heritability and genetic advance of bread wheat genotypes in Southern Tigray region of Ethiopia.

## MATERIALS AND METHODS

Field experiment was conducted at Ofla District, Korem Station of Alamata Agricultural Research Center (39°33'E longitude and 12°31'N latitude) in Southern part of Tigray Region, Northern Ethiopia. The site receives an annual rainfall in the range of 450-1200 mm during main cropping season and 180-250 mm during Belg (winter season).

Twenty three bread wheat genotypes which were developed for optimum area through different crossing procedures and three released and well adapted varieties were included in the experiment (Table 1).

Randomized complete block design with three replications were used. Each genotype was planted in a plot

consisting of six rows of 2.5 m long with spacing of 20 cm between rows with a seed rate of 150 kg ha<sup>-1</sup>. Nitrogen and phosphorus fertilizers were applied at the rate of 46 and 64 kg ha<sup>-1</sup>, respectively.

**Data collection:** Data were collected both from plot basis and from plant basis. The four central rows were used for data collected on plot basis such as days to heading, days to physiological maturity, grain yield and biomass yield. Grain filling period was obtained by subtracting days to heading from days to physiological maturity. Harvest index was calculated from the ratio of grain yield and biomass yield. Ten randomly selected plants from the four central rows of each plot were used for data collection and the averages of the ten plants in each experimental plot were used for statistical analysis for the traits such as plant height, fertile tillers per plant, number of kernels per spike, number of spikelets per spike and spike length.

**Data analysis:** Data was subjected to analysis of variance using the procedures outlined by Gomez and Gomez (1984) and SAS Computer Statistical Package 9.2. Analysis of covariance was done for each pair of characters to obtain the sum of cross products to be used in covariance calculation. The randomized complete block design analysis of variance was also used to derive variance components as structured by Cochran and Cox (1957).

The phenotypic and genotypic variances of each trait were estimated from the RCBD analysis of variance and the expected mean squares under the assumption of random effects model computed from linear combinations of the mean squares and the phenotypic and genotypic coefficient of variations were also computed as per the methods suggested by Burton and Devane (1953). The genotypic and phenotypic coefficients of variability were undertaken according to the formulae of Singh and Chaudhary (1977).

Broad sense heritability values were estimated based on the formula of Falconer and Mackay (1996) and the genetic advance as percent of population mean was also estimated following the procedure of Johnson *et al.* (1955b).

## RESULTS AND DISCUSSION

**Analysis of variance:** The analysis of variance results for the twelve studied traits showed significant ( $p < 0.01$ ) differences among genotypes for days to heading, days to maturity, grain filling period, number of tillers per plant, spike length, number of kernels per spike, thousand kernel weight, biomass and harvest index and significant ( $p < 0.05$ ) differences were observed for grain yield. However, genotypes exhibited

Table 1: List and pedigree of the 26 bread wheat genotypes included in the experiment

Genotypes	Pedigree
ETBW7870	FRINCLIN/ROLFO7
ETBW7884	SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92/5/VORB
ETBW7862	PRL/2*PASTOR
ETBW7888	VORB/4/D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/5/D67.2/PARANA66.270/AE.SQUARROSA(320)/3/CUNNINGHAM
ETBW7881	D67.2/PARANA66.270//AESQUARROSA(320)/3/CUNNINGHAM/4/VORB
ETBW7879	PVN/5/2*REH/HARE//2*BCN/3/CROC-1/AE.SQUARROSA(213)//PGO/4/HUITES
ETBW7868	ROLFO7*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC
ETBW7866	ROLFO7*2/5/REH/HARE//2*BCN/3/CROC-1/AESQUARROSA(213)//PGO/4/HUITES
ETBW7889	VORB/6CPI8/GEDIZ/3/GOO//ALB/CRA/4/AE.SQUARROSA(208)/5/2*WESTONIA/7CPI8/GEDIZ/3/GOO//ALB/CRA/4/AE.SQUARROSA(208)/5/2*WESTONIA
ETBW7864	WBLL1*2/4/BABAX/LR42//BABAX/BABAX/LR42//BABAX
ETBW7891	VORB*2/3/PFAU/WEAVER//KIRITATI
ETBW7867	ATTILA*2/PBW65*2/4/BOW/NKT//CBRD/3/CBRD
Hidase	YANAC/3/PRL/SARA/TSIVEE#5/4
ETBW7875	BECARD/AKURI
ETBW7869	MUNAL#1/FRANCOLIN#1
ETBW7874	ALTAR84/AE.SQUARROSA(221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/MILAN/S87230//BAV92
ETBW7892	VORB*2/3/PFAU/WEAVER//KIRITATI
ETBW7887	VORB/R/D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/5/D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM
ETBW7877	UB2338*2/VIVITISI/3/FRET2/TUKURU//FRET2/4/MISR1
ETBW7880	D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/4/VORB
Dandaa	KIRITATI//2*BBW65/2*SERIJV
ETBW7890	KRICHAUFF/2*BASTOR/3/PFAU/WEAVER//KIRITATI/4/PFAU/WEAVER//KIRITATI
ETBW7873	BECARhd/KACHU
ETBW7882	VORB/3/T.DICOCCONP194625/AE.SQUARROSA(372)//3*PASTOR
Digalu	SHA7/KAUZ; CM95113-9Y-OM-OE-1Y-1Y-ON-OFC-4FUS
ETBW7876	UB2338*2/VIVITISI/3/FRET2/TUKURU//FRET2/4/MISR1

Table 2: Mean squares for twelve traits of 26 bread wheat genotypes

Traits	Rep (2)	Gen (25)	Error (50)	CV (%)
DH	7.54**	38.27**	1.45	2.10
DM	26.32 <sup>ns</sup>	135.02**	8.61	2.57
GFP	5.86**	52.45**	7.05	4.65
NT	0.32 <sup>ns</sup>	0.55**	0.48	31.68
PH (cm)	34.44 <sup>ns</sup>	53.68 <sup>ns</sup>	47.83	7.97
SL (cm)	0.20 <sup>ns</sup>	1.08**	0.28	7.22
Splt	6.61**	3.82 <sup>ns</sup>	0.95	7.17
NKS	17.80 <sup>ns</sup>	54.68**	17.98	10.60
TSW (g)	57.64 <sup>ns</sup>	223.94**	67.70	10.25
BY (t ha <sup>-1</sup> )	1.99 <sup>ns</sup>	17.47**	7.72	27.06
GY (t ha <sup>-1</sup> )	0.97 <sup>ns</sup>	2.23*	1.08	24.44
HI (%)	14.0 <sup>ns</sup>	36.27**	9.67	7.38

\*\*\*Significant difference at  $p < 0.05$ ,  $p < 0.01$  respectively, ns: Non-significant. Numbers in parenthesis refers to degrees of freedom. Rep: Replication, Gen: Genotype, CV: Coefficient of variation, DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NT: Number of tillers per plant, PH: Plant height, SL: Spike length, Splt: Number of spikelets per spike, NKS: Number of kernels per spike, TKW: Thousand kernel weight, BY: Biomass yield, GY: Grain yield and HI: Harvest index

non-significance differences for plant height and number of spikelets per spike (Table 2). This suggested the presence of considerable variations among genotypes for many of the traits studied. This also indicated the presence of ample scope of selection for different quantitative characters for the improvement of the crop.

**Mean performance of bread wheat genotypes:** The mean performances of the genotypes (Table 3) showed variation

for days to heading which ranged from 49.3-63 days with a mean of 56.9 days and days to maturity ranged from 102.7-129.7 days with a mean value of 114 days. The genotypes had mean value of 57.1 days for grain filling period and the range was from 47.7-66.7 days. The result showed that the presence of wide range of variations among the genotypes for maturity. Tesfaye *et al.* (2014) also reported wide range of variation among bread wheat genotypes for days to heading and days to maturity.

Among the genotypes, ETBW7868 was early to heading which took 49 days while Digalu was late heading and took 63 days. The ETBW7876 had short period for maturity as well as for grain filling while Digalu had long period both for maturity and grain filling. As compared to the early maturing check variety (Hidase), 69.2% of the genotypes were early maturing. This suggested that the presence of higher chance of selecting early genotypes which can escape the terminal moisture stress which is one of the wheat production problems in the study area.

Number of fertile tillers per plant ranged from 1.53 for ETBW7890 to 3.27 for Hidase (the standard check). Hence, the standard variety should be considered when selection is made in favor of number of fertile tillers per plant. The mean value of spike length recorded was 7.3 cm with maximum of 8.9 cm and minimum of 5.9 cm for ETBW7864 and Digalu, respectively. Maximum and minimum biomass yields were

harvested from ETBW7882 (16.17 t ha<sup>-1</sup>) and Digalu (6.46 t ha<sup>-1</sup>), respectively. Regarding to biomass yield 27% of the genotypes exceeded the highest biomass yielder standard check, Dandaa (11.28 t ha<sup>-1</sup>), respectively. Accordingly, there is plenty of variability among the genotypes for selection designed for improvement of this trait. This finding is in agreement with Mollasadeghi *et al.* (2012) which stated the existence of variability for biomass yield among bread wheat genotypes.

The range for number of kernels per spike was from 34.3 for ETBW7875 to 47.6 for ETBW7874. Five genotypes: ETBW7874 (47.6), ETBW7887 (46.9), ETBW7879 (49.9), ETBW7866 (46.7) and ETBW7865 (44.7) had higher number of kernels per spike than the standard check with high number of kernels per spike, Dandaa (44.6). Therefore, those genotypes can be considered when increment of this trait is required. The mean value of thousand kernel weight was 57.16; ETBW7874, ETBW7879, ETBW7887, ETBW7866 and ETBW7865 showed superiority for thousand kernel weight than the standard check with high thousand kernel weight, Dandaa (89.20). Consequently, progress of this trait can be more effective when those genotypes are used.

ETBW7888, ETBW7892, ETBW7887, ETBW7882 and ETBW7862 also produced higher grain yield (6.35, 5.63, 5.50, 5.06 and 4.99 t ha<sup>-1</sup>, respectively) than the standard checks and at the same time these genotypes are early maturing as compared to the standard checks. Hence, these genotypes can be considered for grain yield improvement in the study area, where the distribution of rainfall is for short period of time.

### **Estimates of variability components**

**Phenotypic and genotypic variations:** According to Deshmukh *et al.* (1986), Phenotypic Coefficient of variance (PCV) and Genotypic Coefficient of Variation (GCV) can be categorized as low (<10%), moderate (10-20%) and high (>20%). Accordingly, high PCV values were recorded for biomass yield, number of tillers per plant and grain yield, while traits with moderate PVC value were spike length, number of grains per spike and harvest index. Considering GVC, biomass yield and grain yield were categorized as moderate. The rest other characters had low GCV values.

The PCV was relatively greater than GCV for all the twelve traits, however, the magnitude of the difference was low for days to heading, days to maturity, grain filling period, spike length, thousand kernel weight and harvest index. This suggested that the marked influence of environmental factors for the phenotype expression of genotypes was low and the higher chance of improvement of these traits through

selection based on the phenotype performance. Similar results were reported by Kumar *et al.* (2014) for biomass yield and grain yield that both GCV and PCV were moderate to high and they were nearly same in magnitude.

The difference between PCV and GCV was relatively high for number of tillers per plant, number of kernels per spike, biomass yield and grain yield (Table 4). This implies greater influence of environmental factors for the phenotypic expression of these characters that make difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the characters. This result was in close agreement with the findings of Demelash *et al.* (2013) who reported relatively high environmental variance than genotypic variance for number of tillers per plant, number of kernels per spike, biomass yield and grain yield.

**Estimates of heritability in broad sense:** According to Singh (2001), heritability of a trait is considered as very high or high when the value is 80% or more and moderate when it ranged from 40-80% and when it is less than 40%, it is low. Accordingly, high heritability was computed for days to heading, days to maturity and thousand kernel weight (Table 4). This result suggested selection could be fairly easy and improvement is possible using selection breeding for these traits improvement. In agreement with this result. Mollasadeghi *et al.* (2012) also reported high estimates of heritability for days to heading (84%) and thousand kernel weight (89%).

Moderate heritability was computed for grain filling period, spike length, number of spikelets per plant, seeds per spike and harvest index which suggested that selection should be delayed to more advance generations for these traits. Low heritability was estimated for number of tillers per plant, biomass yield and grain yield. This implies that selection may be considerably difficult or virtually impractical due to the masking effect of the environment for these traits. In harmony to this investigation, Mollasadeghi *et al.* (2012) also reported low heritability estimates for grain yield (12.27%) and number of tillers per plant (29.78%). Demelash *et al.* (2013) also reported low heritability estimates for biomass yield and moderate heritability for grain filling period, spike length, number of kernels per spike and harvest index. In opposite to the current study, Salman *et al.* (2014) reported high heritability estimates for grain yield, number of kernels per spike, spike length and number of tillers per plant. The parity of heritability values reported by different authors is due to heritability of a character was computed for different

Table 3: Mean values of 12 traits of 26 bread wheat genotypes tested at Korem in 2014

Genotypes	DH	DM	GFP	NT	PH	SL	NSt	NKS	TSW	BY	GY	HI
Dandaa	61.3	121.3	60.0	2.07	93.7	7.3	14.93	44.6	89.20	11.28	3.85	0.34
Digelu	63.0	129.7	66.7	2.07	89.9	5.9	14.40	43.0	86.00	6.46	2.96	0.45
ETBW7862	55.7	115.3	59.7	2.27	88.3	7.5	13.00	35.0	70.00	11.65	4.99	0.43
ETBW7863	55.3	115.7	60.3	2.00	85.1	7.1	13.33	37.1	74.13	8.48	3.87	0.46
ETBW7864	61.3	121.7	60.3	2.40	83.1	8.9	13.80	42.0	84.00	7.68	3.30	0.43
ETBW7865	57.0	113.0	56.0	1.87	85.2	7.9	14.67	44.7	89.33	12.05	4.67	0.39
ETBW7866	54.7	110.3	55.7	2.40	89.8	7.3	15.47	46.7	93.33	10.42	4.50	0.44
ETBW7867	57.3	111.0	53.7	2.27	85.3	7.9	13.00	39.7	79.33	9.87	4.44	0.45
ETBW7868	49.3	104.7	55.3	2.67	87.5	7.3	12.47	34.7	69.47	9.95	4.27	0.44
ETBW7869	59.3	111.7	52.3	1.67	86.0	7.0	13.00	35.8	71.60	9.27	3.66	0.39
ETBW7870	52.7	103.7	51.0	2.53	85.7	6.8	12.53	36.5	73.07	8.97	3.72	0.41
ETBW7873	61.3	122.3	61.0	2.40	90.2	8.5	16.47	40.6	81.13	11.05	4.42	0.41
ETBW7874	56.3	110.7	54.3	1.73	85.8	7.4	13.20	47.6	95.20	8.73	3.80	0.44
ETBW7875	62.3	117.7	55.3	2.07	78.6	7.1	14.07	34.3	68.53	7.65	3.17	0.42
ETBW7876	55.0	102.7	47.7	1.87	82.7	6.9	12.33	34.8	69.60	8.23	3.25	0.40
ETBW7877	56.0	108.0	52.0	1.80	87.9	7.9	12.53	40.7	60.78	7.58	2.99	0.40
ETBW7879	50.7	106.7	56.0	2.00	79.5	7.0	14.27	46.9	93.87	9.33	4.48	0.48
ETBW7880	55.3	113.7	58.3	1.93	87.4	7.3	12.33	39.1	78.13	11.40	4.83	0.43
ETBW7881	56.7	113.7	57.0	2.27	86.1	6.7	12.87	35.9	71.87	8.90	4.02	0.45
ETBW7882	60.7	123.3	62.7	3.13	90.3	7.0	14.07	40.1	80.27	16.17	5.06	0.32
ETBW7884	59.3	121.0	61.7	2.27	96.1	7.2	15.00	39.9	79.73	11.28	4.74	0.42
ETBW7887	55.7	110.0	54.3	1.93	83.9	7.6	13.60	46.9	93.87	12.48	5.50	0.44
ETBW7888	56.0	111.0	55.0	1.93	91.9	7.4	14.73	42.6	85.20	15.95	6.35	0.40
ETBW7890	62.3	120.7	58.3	1.53	79.3	6.9	12.93	37.8	75.60	7.70	3.34	0.43
ETBW7892	54.3	112.7	58.3	2.87	90.6	6.9	11.87	36.7	73.47	13.63	5.63	0.41
Hidase	57.0	118.7	61.7	3.27	86.4	6.7	13.00	36.9	73.73	10.28	4.72	0.46
Mean value	56.91	113.99	57.06	2.19	86.51	7.27	13.63	40.28	79.79	10.21	4.26	0.42

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NT: Number of fertile tillers per plant, PH: Plant height, SL: Spike length, NSt: Number of spikelet per spike, NKS: Number of kernels per spike, BY: Biomass yield t ha<sup>-1</sup>, GY: Grain yield t ha<sup>-1</sup>, HI: Harvest index

Table 4: Mean and range, phenotypic and genotypic variances and coefficient of variations; heritability in broad sense and genetic advance for 10 traits of 26 bread wheat genotypes studied at Korem in 2014

Traits	Ranges	Mean ± SE	σ <sup>2</sup> g	σ <sup>2</sup> p	PCV (%)	GCV (%)	H <sup>2</sup> b (%)	GA	GAM (%)
DH	49.33-63	57.15 ± 0.69	12.27	13.72	6.48	6.13	89.43	6.83	11.96
DM	102.7-129.7	114.26 ± 1.69	42.14	50.75	6.23	5.68	83.03	12.20	10.68
GFP	47.67-66.67	57.10 ± 1.53	15.13	22.18	8.25	6.81	68.23	6.63	11.61
NT	1.53-3.27	2.20 ± 0.40	0.02	0.50	32.23	6.82	4.57	0.07	3.04
SL	5.87-8.87	7.29 ± 0.30	0.27	0.55	10.15	7.09	48.81	0.75	10.22
NKS	34.27-47.6	40.02 ± 2.45	12.23	30.21	13.74	8.75	40.49	4.59	11.48
TKW	68.53-95.20	57.16 ± 4.70	12.34	12.74	6.24	6.15	96.86	7.13	12.48
BY	6.46-16.17	10.25 ± 1.61	3.25	10.97	32.29	17.56	29.63	2.02	19.74
GY	2.96-6.35	4.25 ± 0.60	0.38	1.46	28.47	14.56	26.18	0.65	15.38
HI	32-48	42.12 ± 1.80	8.87	18.53	10.22	7.07	47.87	4.25	10.09

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NT: Number of fertile tillers per plant, PH: Plant height(cm), SL: Spike length(cm), NKS: Number of kernels per spike, TKW: Thousand kernel weight(g), BY: Biomass yield, GY: Grain yield t ha<sup>-1</sup>, HI: Harvest index, σ<sup>2</sup>g: Genotypic variance, σ<sup>2</sup>p: Phenotypic variance PCV: Phenotypic coefficient of variance, GCV: Genotypic coefficient of variance, H<sup>2</sup>b: Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as percent of mean

genotypes and refers to a particular population under particular environmental conditions (Dabholkar, 1992).

**Estimates of expected genetic advance:** Genetic advance as percent mean ranged from 3.04% for number of fertile tillers per plant to 19.74% for biomass yield. This result showed that selecting the top 5% of the genotypes could result in an improvement range of 3.04% for number of fertile tillers per plant to 19.74% for biomass yield. Deshmukh *et al.* (1986)

classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%). Based on this classification, none of the characters had high genetic advance as percent of mean in the current study.

Moderate genetic advance as percent of mean was computed for days to heading, days to maturity, grain filling period, spike length, number of kernels per spike, thousand kernel weight, biomass yield, grain yield and harvest index. Low genetic advance as percent of mean was computed for

number of fertile tillers per plant (3.04%). This refers to improvement of this character in genotypic value for the new population compared with the base population with one cycle of selection is not rewarding. Kumar *et al.* (2013) also recorded nearly similar genetic advance for thousand kernel weight and days to maturity. Degewione *et al.* (2013) also reported nearly similar figures for number of kernels per spike (13.67%), spike length (6%) and days to maturity (15.79%).

It was suggested that the importance of considering both the genetic advance and heritability of traits rather than considering separately in determining how much can progress be made through selection (Johnson *et al.*, 1955a). In this study, high heritability accompanied with moderate genetic advance was observed in case of days to heading, days to maturity and thousand kernel weight. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the characters. Most likely the heritability of these traits is due to additive gene effects and selection may be effective in early generations for these traits (Ali *et al.*, 2007). Likewise, Salman *et al.* (2014) reported high and moderate heritability and genetic advance for days to heading, days to maturity and thousand kernel weight.

Moderate estimates for both heritability and genetic advance as percent of mean was recorded for grain filling period, spike length, seeds per spike and harvest index. Low values for both heritability and genetic advance as percent of the mean was computed for number of tillers per plant. This suggested that the low heritability of traits due to the influence of environment limit the scope of improvement using selection. The low heritability of traits may be due to the presence of non-additive type of gene action (Ali *et al.*, 2007).

## CONCLUSION

Results of analysis of variance showed statistically significant difference among the twenty six tested genotypes for ten of the twelve traits considered. Suggesting the genotypes were phenotypically divergent. Therefore, there is higher chance of selecting genotypes for different quantitative traits. The genotypic variance took relatively greater proportion of the total variances for days to heading, days to maturity, grain filling period, spike length, number of fertile tillers per plant, number of kernels per spike, thousand kernel weight, biomass yield, grain yield and harvest index. Hence, genetic components of these traits are important and selection based on these traits is effective.

Days to heading, days to maturity and thousand kernel weight showed high or very high heritability estimates.

suggested that a good progress can be made if these traits are considered as selection criteria. Medium heritability estimates were computed for grain filling period, spike length, seeds per spike and harvest index. This indicated that selection should be delayed to more advance generations for those traits.

The top three genotypes that performed better than the released check varieties for grain yield and early maturity were ETBW7888, ETBW7892 and ETBW7887 with grain yield of 6.4, 5.6 and 5.5 t ha<sup>-1</sup>, respectively. Grain yields of the standard checks were 3.9 t ha<sup>-1</sup> for Dandaa for 4.7 t ha<sup>-1</sup> for Hidase and 3 t ha<sup>-1</sup> for Digalu. Besides, those genotypes were early maturing which ranged from 110-112 days. However, a range for days to maturity for the standard checks was from 119-129 days. That implies the existence of genotypes with a grain yield advantage of 17%-36% over the highest yielder standard check (Hidase) in the area. Therefore, direct selection of those genotypes can be rewarding.

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