

Genetic Variability for Yield and Yield Related Traits in Advanced Bread Wheat (*Triticum aestivum* L.) Lines in Eastern Ethiopia

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Abstract: Developing high yielding bread wheat genotypes with superior agronomic trait requires understanding the extent of genetic variability in existing germplasm. The current study was designed to generate information on genetic variability and inheritance of yield and its component traits using 36 advanced bread wheat lines. Field experiment was conducted in 2018 cropping season at Haramaya and Hirna in eastern Ethiopia using triple lattice design. Fifteen quantitative traits were measured and subjected to analysis of variance and genetic analyses. Analysis of variance revealed that there was highly significant difference among genotypes for all quantitative traits at both locations. The lowest and the highest phenotypic (PCV) and genotypic (GCV) values were obtained for hectoliter weight and number of fertile tillers per plant, respectively at both locations. Heritability in broad sense and genetic advance as percent of mean ranged from 39.1% (number of kernels per spike) to 90.1% (days to heading), and from 2.4% (hectoliter weight) to 48.5% (number of fertile tillers), respectively at Haramaya. At Hirna, these parameters ranged from 29.3% (hectoliter weight) to 91.9% (grain yield), and from 1.5% (hectoliter weight) to 27.6% (total tillers per plant), respectively. high heritability coupled with high genetic advance as percent of mean was observed for total number of tillers per plant, number of fertile tillers per plant, grain yield per hectare, and above ground biomass per hectare at Haramaya. and for spike length, total number of tiller per plant, number of fertile tiller per plant, grain yield per hectare, and above ground biomass per hectare at Hirna. This indicates that improvement of these traits through selection is easier than other traits measured.

Keywords: Variability, Genetic Advance, Heritability

1. Introduction

Bread wheat, *Triticum aestivum* L. ($2n=6x=42$) is a self-pollinating annual plant that belongs to the botanical tribe Triticeae in the family Gramineae (Poaceae). It is one of the most important cereal crops in the world and in Ethiopia in terms of production and utilization [23]. Wheat ranks fourth after Tef [*Eragrostis tef* (Zucc.) Trotter], Maize (*Zea mays* L.) and Sorghum [*Sorghum bicolor* L.] Moench in crop area coverage and is one of the major staple and strategic food security crops in Ethiopia. It is cultivated on 1,637,647 ha with average productivity close to 2.11 t/ha [11]. Domestic wheat

production in Ethiopia covers only 75% of the demand and the remaining 25% wheat is imported commercially and through food aid [12].

The development of an effective plant breeding program to improve the characteristics of crops relies on the existence of genetic variability. The knowledge of nature and magnitude of variation existing in available breeding materials have great importance for successful selection of varieties for yield [16, 18]. Reduction in the genetic variability makes the crops increasingly vulnerable to

diseases and adverse climatic changes [3]. Therefore, precise information on the nature and degree of genetic variability present in wheat would help to select parents for evolving superior varieties.

The history of wheat breeding in Ethiopia dates back to the early 1960's and as the result of the efforts made hitherto, a number of improved varieties have been developed and released to farmers. However, most of the varieties become out of production within a few years after release. Due to this, new varieties have to be identified and released in a continuous manner by utilizing the existing germplasm in the breeding programs. This entails precise understanding of the extent of genetic variation in existing bread wheat germplasms. In view of this, the current study was designed to generate such information on advanced Ethiopian bread wheat advanced lines.

2. Materials and Methods

2.1. Experimental Design and Trial Management

The experiment was conducted on thirty six advanced bread wheat lines during 2018 main cropping season at Haramaya and Hirna sub-research center of Haramaya. The experiment was laid out in 6x6 triple lattice design with the plot of five rows and 2 m length with 0.2 m row spacing *i.e.* 1m x 2 m = 2m² and spacing between plots and blocks was 0.5 m and 1m, respectively. Thirty six advanced bread wheat lines obtained from Kulumsa Agricultural Research Center were used for the study (Table 1) and planting was done by drilling at seeding rate of 150kg/ha (30 g/plot). Fertilizer was applied at a rate of 150/150kg/ha in the forms of Urea and DAP for N and P₂O₅ respectively, at both locations. For data collection, the middle three rows (1.2m² area) were used.

Table 1. List of advanced bread wheat lines with their pedigree used for experiment at Haramaya and Hirna.

SN	Genotype	Pedigree
1	ETBW7610	KACHU/KIRITATI
2	ETBW7598	ROLF07*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC
3	ETBW7638	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
4	ETBW7399	FRNCLN/ROLF07
5	ETBW7436	ROLF07*2/4/BOW/NKT//CBRD/3/CBRD
6	ETBW8489	VORB/6/CPI8/GEDIZ/3/GOO//ALB/CRA/4/AE.SQUARROSA (208)/5/2*WESTONIA/7/ CPI8/GEDIZ/3/GOO//ALB/CRA/4/AE.SQUARROSA (208)/5/2*WESTONIA
7	ETBW8492	KRICHAUFF/2*PASTOR//CHONTE
8	ETBW7650	FRANCOLIN #1/AKURI #1
9	ETBW7652	WBLL1*2/KURUKU/4/PFAU/SERI.1B//AMAD/3/WAXWING
10	ETBW7713	ATTILA/3*BCN//BAV92/3/PASTOR/4/TACUPETO F2001*2 /BRAMBLING/5/ PAURAQ
11	ETBW7718	MUNAL/3/KIRITATI//PRL/2*PASTOR/4/MUNAL
12	ETBW7790	VEE7/KAUZ//NAAMA-6
13	ETBW8048	QAFZAH-35/AMIR-2
14	ETBW9015	SUP152//ND643/2*WBLL1/3/ND643/2*WBLL1
15	ETBW9018	SWSR22T.B.//TACUPETO F2001*2/ BRAMBLING/3/2*TACUPETO F2001*2/ BRAMBLING
16	ETBW9041	T.DICOCCON CI9309/AE.SQUARROSA (409)//MUTUS/3/2*MUTUS
17	ETBW9051	CROC-1/AE.SQUARROSA (224) //OPATA/3/QAFZAH-21/4/SOMAMA-3
18	ETBW7808	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
19	ETBW8484	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING
20	ETBW8486	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
21	ETBW7511	BECARD/AKURI
22	ETBW7582	SAUAL/YANAC//SAUAL
23	ETBW8491	WORRAKATTA/2*PASTOR//DANPHE #1
24	ETBW7670	WBLL1*2/KUKUNA/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
25	ETBW7956	QAFZAH-19/ICARDA-SRRL-7
26	ETBW7968	KUBSA/ETBW4698
27	ETBW9019	MUTUS//KIRITATI/2*TRCH/3/WHEAR/KRONSTAD F2004
28	ETBW9026	AGUILAL/FLAG-3
29	ETBW9027	ND/VG1944//KAL//BB/3/YACO'S'/4/VEE#5'S
30	ETBW9029	ND643/2*WBLL1/4/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92/5/BECARD
31	ETBW9040	T.DICOCCON CI9309/AE.SQUARROSA (409)// MUTUS/3/2*MUTUS
32	ETBW9042	HUW234+LR34/PRINIA//PFAU/WEAVER/3/CMH83.30
33	ETBW7698	FRNCLN/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
34	ETBW6832	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311
35	ETBW6850	FRNCLN/ROLF07
36	ETBW6875	WAXWING/KIRITATI*2//YANAC

2.2. Description of Data Collected

All yield and yield related data were recorded from the middle three central rows in each plot. The following agronomic traits were included: Days to heading, Days to maturity, Grain filling

period, Grain yield yield at 12.5% moisture, 1000-kernel weight, Above ground biomass, Harvest index, Hectoliter weight, Plant height, Spike Length, Number of spikelets per spike, Number of kernels per spike, Number of tillers per plant, Number of fertile tillers per plant, Grain yield per plant.

2.3. Statistical Analysis

The relative efficiency of triple lattice design relative to RCBD was tested and was found almost similar with RCBD for most of the characters and coefficient of variation (CV) value for both designs were nearly similar. Therefore, for the flexibility of lattice design [6] the data were subjected to analysis of variance (ANOVA) based on randomized complete block following the standard procedure given by Gomez and Gomez [13] using SAS Software (Version 9.0).

Analysis of variance of randomized complete block design for each test location was computed using the following mathematical model: for each test location was computed using the following mathematical model:

$$Y_{ij} = \mu + r_j + g_i + \epsilon_{ij}$$

Where: Y_{ij} = the observed value of the trait Y for the i th genotype in j th replication

μ = the general mean of trait Y

r_j = the effect of j th replication

g_i = the effect of i th genotypes and

ϵ_{ij} = the experimental error associated with the trait y for the i th genotype in j th replication.

Test of mean separation was employed depending on the significance of the analysis of variance using Duncan's Multiple Range Test.

2.3.1. Phenotypic and Genotypic Variability

The phenotypic and genotypic variances and the coefficient of variations were estimated according to the methods suggested by [5] as follows:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

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

Where; σ_p^2 = phenotypic variance

σ_g^2 = genotypic variance

σ_e^2 = environmental variance = (Error mean square)

M_g = mean square of genotypes

M_e = mean square of error,

r = number of replications

Phenotypic coefficient of variation, $PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$

Genotypic coefficient of variation, $GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$

Where \bar{x} = population mean

2.3.2. Estimate of Heritability and Expected Genetic Advance

Heritability (H^2) in broad sense was computed for all parameters recorded using the formula adopted by [2, 10]

$$H^2 = [\sigma_g^2 / \sigma_p^2] \times 100$$

Where: σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

Genetic advance (GA) for each character was computed using the formula adopted from [2, 14].

$$GA = (k) (\sigma_p) (H^2)$$

$$GA \text{ (as \% of the mean)} = \frac{GA}{\bar{x}} \times 100$$

Where, k = selection differential ($k=2.06$ at 5% selection intensity)

σ_p = phenotypic standard deviation

H^2 = heritability (Broad sense)

\bar{x} = Grand mean

3. Results and Discussion

3.1. Analysis of Variance

The mean squares of 15 characters of advanced bread wheat lines measured in this study are presented in Tables 2 and 3 with the corresponding coefficients of variation (CV) values from analysis of variance (ANOVA) for Haramaya and Hirna, respectively. At both Hirna and Haramaya, highly significant differences ($P < 0.01$) were observed for all studied characters, indicating the presence of variability for the characters among the tested lines. This would provide ample scope for selecting superior and desired genotypes for further improvement of the characters. Different researchers also reported significant genetic variation for grain yield and yield related traits [1, 4, 7, 15, 19, 22, 24, 25].

Table 2. Mean squares and CV values for 15 traits of 36 bread wheat advanced lines tested at Haramaya, 2016.

Traits	Msr (2)	MSG (35)	Mse (70)	CV%
DTH	5.53*	44.44**	1.57	2.1
DTM	16.26 ^{ns}	101.08**	12.24	3.1
GFP	10.45 ^{ns}	37.5**	7.53	5.1
PH	40.68 ^{ns}	118.37**	16.37	4.7
NS	7.59**	2.89**	0.97	6.3
SL	9.15**	2.96**	0.33	6.3
NT	9.03**	10.29**	0.81	11.7
NFT	9.06**	10.33**	0.76	12.8
GYP	0.05 ^{ns}	0.24**	0.05	10.6
NK	1.01 ^{ns}	87.53**	29.89	10.8
GY	120827 ^{ns}	1664544**	69569.6	5
TKW	7.20 ^{ns}	37.94**	6.09	5.7
BY	636584 ^{ns}	5684761**	495045	6.1
HI	0.0001 ^{ns}	0.003**	0.0002	3.1
HLW	12.08**	5.5**	1	1.2

Numbers in the parenthesis indicate degrees of freedom, **=highly significant ($P < 0.01$), *=significant ($p < 0.5$), ns=non significant, CV =coefficient of variation, Msr =mean square due to replication, Msg =mean square due to genotypes, Mse=mean square due to error, DTH=days to heading, DTM=days to maturity, GFP= grain filling period, PH=plant height, NS=number of spikelets per spike, SL=spike length, NT=total number of tillers, NFT=number of fertile tillers, GYP=grain yield per plant, NG=number of grains per plant, GY=grain yield, TKW=thousand kernel weight, BY=above ground biomass, HI=harvest index, HLW=hectoliter weight.

Table 3. Mean squares and CV values for 15 traits of 36 bread wheat advanced lines tested at Hirna, 2016.

Traits	MSr (2)	MSG (35)	Mse (70)	CV%
DTH	5.45 ^{ns}	24.38**	5.42	3.8
DTM	50.58 ^{ns}	83.66**	33.16	5
GFP	26.26 ^{ns}	51.83**	16.88	7.5
PH	6.87 ^{ns}	97.58**	6.86	3.7
NS	4.32 ^{ns}	8.01**	1.39	7
SL	2.47**	3.8**	0.3	6.1

Traits	MSr (2)	MSg (35)	Mse (70)	CV%
NT	0.19 ^{ns}	4.24**	0.47	9.5
NFT	0.78 ^{ns}	3.59**	0.55	11.4
GYP	0.19 ^{ns}	0.34**	0.08	13.3
NK	58.48 ^{ns}	128.72**	26.45	9.9
GY	156537**	704477.7**	19989.8	3.4
TKW	10.87 ^{ns}	39.82**	9.39	9.4
BY	848274*	3634755**	219238	5
HI	0.0001 ^{ns}	0.004**	0.0004	4.7
HLW	11.9*	7.6**	3.3	2.2

Numbers in the parenthesis indicate degrees of freedom, **=highly significant ($P < 0.01$), *=significant ($p < 0.5$), ns=non significant, CV =coefficient of variation, Msr =mean square due to replication, Msg =mean square due to genotypes, Mse=mean square due to error, DTH=days to heading, DTM=days to maturity, GFP= grain filling period, PH=plant height, NS=number of spikelets per spike, SL=spike length, NT=total number of tillers, NFT=number of fertile tillers, GYP=grain yield per plant, NG=number of grains per plant, GY=grain yield, TKW=thousand kernel weight, BY=above ground biomass, HI=harvest index, HLW=hectoliter weight.

3.2. Mean Performances of Genotypes for Different Characters

The range and mean values for 15 characters of 36 bread wheat advanced lines evaluated at Haramaya and Hirna are presented in Table 4 and Table 5, respectively for the two locations. The range of all studied traits shows great variations that indicate presence of sufficient genetic variability among genotypes for these traits which provide wide scope for selection.

Highly significant variation was observed for grain yield kg ha⁻¹, which ranged from 3731-6234 kg ha⁻¹ with a mean of 5230.6kg ha⁻¹ at Haramaya and from 3319.3-4937.5 kg ha⁻¹ with a mean of 4180.6 kg ha⁻¹ at Hirna. At Haramaya, the highest grain yield 6234 kg ha⁻¹ was recorded for ETBW7713 followed by ETBW7610 6145.9 kg ha⁻¹ and ETBW9041 6126.3 kg ha⁻¹, while the lowest yield of 3731 kg ha⁻¹ was obtained from ETBW7968 followed by ETBW7670 3750.4kg ha⁻¹ and ETBW9019 3779.8 kg ha⁻¹. At Hirna, the highest grain yield 4937.5 kg ha⁻¹ was recorded for ETBW6850 followed by

ETBW9051 4859.9 kg ha⁻¹ and ETBW8491 4839kg ha⁻¹, while the lowest yield 3319.3 kg ha⁻¹ was obtained from ETBW9042 followed by ETBW7598 3432.7 kg ha⁻¹ and ETBW7399 3444.4kg ha⁻¹. Similarly other study by [8] who reported highly significant variation for grain yield in bread wheat agreed with the present result. Cumulatively, based on the observation of yield performance of genotypes that gave high yield, it is an apparent that, these genotypes might be useful for future breeding program. In addition, the observation of yield performance differences of genotypes at both locations indicated the need for developing varieties for each location.

3.3. Phenotypic and Genotypic Variations

Estimated phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of the characters measured in this study are presented in Tables 4 and 5 respectively for Haramaya and Hirna. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied at both locations, though the magnitude of the differences were small for most of the traits, indicating that the environmental effect on the expression of most characters was small. Different author also reported slit difference between PCV and GCV for different treats of bread wheat [24-26].

High PCV and GCV were observed for number of fertile tillers and total number of tillers per plant at Haramaya. This finding is consistent with the finding of [9] who reported high PCV and GCV for total number of tillers per plant. Medium PCV and GCV values were recorded for spike length, grain yield per plant, number of kernels per spike, grain yield per hectare and above ground biomass at Haramaya. At Hirna, medium PCV and GCV values were recorded for number of fertile tillers, total number of tillers, spike length, grain yield per plant, number of kernels per spike, grin yield per hectare, and above ground biomass. The high and medium PCV and GCV indicate that selection may be effective based on these traits.

Table 4. Estimates of mean, range, standard error; variance components, heritability, genetic advance and genetic advance aspercent of mean of 15 bread wheat characters studied at Haramaya, 2016.

Variable	Mean	Range		SE	σ^2_{ph}	σ^2_g	PCV	GCV	H ²	GA	GAM
		Min	Max								
DH	61.0	54.0	69.0	0.7	15.9	14.3	6.6	6.2	90.1	7.4	12.2
DTM	114.0	106.0	129.0	2.0	41.9	29.6	5.7	4.8	70.8	9.4	8.3
GFP	54.0	49.0	64.0	1.7	17.5	10.0	7.8	5.9	57.1	4.9	9.2
PH	85.8	65.1	97.1	2.3	50.4	34.0	8.3	6.8	67.5	9.9	11.5
NS	15.6	13.7	17.8	0.6	1.6	0.6	8.1	5.1	39.7	1.0	6.6
SL	9.0	6.7	11.4	0.3	1.2	0.9	12.2	10.4	72.8	1.7	18.3
NT	7.7	4.8	14.5	0.5	4.0	3.2	26.0	23.2	79.6	3.3	42.7
NFT	6.8	3.9	13.8	0.5	4.0	3.2	29.1	26.2	80.7	3.3	48.5
GYP	2.2	1.5	2.9	0.1	0.1	0.1	15.5	11.4	53.5	0.4	17.2
NK	50.7	37.7	62.9	3.2	49.1	19.2	13.8	8.7	39.1	5.7	11.2
GY	5230.6	3731.0	6234.0	152.3	601227.8	531658.1	14.8	13.9	88.4	1414.5	27.0
TKW	43.3	36.6	49.4	1.4	16.7	10.6	9.4	7.5	63.5	5.4	12.4
BY	11506.5	8099.0	13519.4	406.2	2224950.0	1729905.0	13.0	11.4	77.8	2392.5	20.8
HI	0.5	0.4	0.5	0.01	0.001	0.001	7.9	7.2	84.1	0.1	13.6
HLW	81.8	78.0	83.7	0.6	2.5	1.5	1.9	1.5	61.0	2.0	2.4

SE=standard error, σ^2_{ph} =phenotypic variance, σ^2_g =genotypic variance PCV=phenotypic coefficient of variation, GCV=genotypic coefficient of variation, H²=heritability in broad sense GA=genetic advance, GAM=genetic advance as percent of mean, DTH=days to heading, DTM=days to maturity, GFP= grain filling period, PH=plant height, NS=number of spikelets per spike, SL=spike length, NT=total number of tiller, NFT=number of fertile tiller, GYP=grain yield per plant, NG=number of grain per plant, GY=grain yield, TKW=thousand kernel weight, BY=above ground biomass, HI=harvest index, HLW=hectoliter weight.

Table 5. Estimates of mean, range, standard error, variance components, heritability, genetic advance and genetic advance as percent of mean of 15 bread wheat characters studied at Hirna, 2016.

Variable	Mean	Range		SE	σ^2_{ph}	σ^2_g	PCV	GCV	H^2	GA	GAM
		Min	Max								
DH	62.0	58.0	69.0	1.34	11.7	6.3	5.5	4.1	53.9	3.8	6.2
DTM	116.0	107.0	129.0	3.32	50	16.8	6.1	3.5	33.7	4.9	4.2
GFP	55.0	46.0	64.0	2.37	28.5	11.7	9.8	6.3	40.8	4.5	8.2
PH	71.4	59.0	82.5	1.51	37.1	30.2	8.5	7.7	81.5	10.2	14.3
NS	16.9	13.3	20.1	0.68	3.6	2.2	11.2	8.8	61.3	2.4	14.2
SL	9.1	6.2	11.6	0.32	1.5	1.2	13.4	11.9	79.5	2.0	21.9
NT	7.2	5.4	10.1	0.40	1.7	1.3	18.2	15.5	72.7	2.0	27.2
NFT	6.5	4.4	9.7	0.43	1.6	1.0	19.3	15.5	64.9	1.7	25.8
GYP	2.1	1.4	2.9	0.16	0.2	0.1	19.1	13.8	51.6	0.4	20.4
NK	51.9	37.9	65.9	2.97	60.5	34.1	15	11.3	56.3	9.0	17.4
GY	4180.6	3319.3	4937.5	81.63	248152.4	228162.6	11.9	11.4	91.9	944.9	22.6
TKW	40.9	34.9	49.3	1.77	19.5	10.1	10.8	7.8	51.9	4.7	11.6
BY	9406.9	7306.1	10834.2	270.3	1357743	1138506	12.4	11.3	83.9	2015.8	21.4
HI	0.5	0.4	0.5	0.01	0.001	0.001	8.6	7.2	70.5	0.1	12.5
HLW	81	77.6	83.5	1.05	4.7	1.4	2.7	1.5	29.9	1.3	1.7

SE=standard error, σ^2_{ph} =phenotypic variance, σ^2_g =genotypic variance PCV=phenotypic coefficient of variation, GCV=genotypic coefficient of variation, H^2 =heritability in broad sense GA=genetic advance, GAM=genetic advance as percent of mean, DTH=days to heading, DTM=days to maturity, GFP= grain filling period, PH=plant height, NS=number of spikelets per spike, SL=spike length, NT=total number of tiller, NFT=number of fertile tiller, GYP=grain yield per plant, NG=number of grain per plant, GY=grain yield, TKW=thousand kernel weight, BY=above ground biomass, HI=harvest index, HLW=hectoliter weight.

3.4. Estimates of Heritability in Broad Sense

Heritability estimates in broad sense (H^2) for characters studied is presented in table 4 at Haramaya and table 5 at Hirna. Moderate to high heritability estimates was obtained for most of the traits considered at both locations except hectoliter weight at Hirna. This result indicates that environmental influences were low relative to genotypic effects for the expression of these characters. This suggests that direct selection using these characters as major yield components would enable developing progeny with improved yield Performance. Different researchers had also reported high heritability for different traits consistent with the present findings [15, 16, 20, 21, 25-27].

3.5. Estimates of Genetic Advance

In this study, genetic advance as a percent of mean ranged from 2.4% for hectoliter weight to 48.5% for number of fertile tillers per plant (table 4) at Haramaya and from 1.7% for hectoliter weight to 27.2% for total number of tiller per plant (table 5) at Hirna. Therefore, the result suggested that selecting the top 5% of the genotypes could result in an advance of 2.4% to 48.5% at Haramaya and 1.7% to 27.2% at Hirna over the respective population mean for these studied traits.

High genetic advance as percent of mean was recorded for number of fertile tillers per plant, total number of tillers per plant, grain yield per hectare and above ground biomass per hectare at both locations. In addition, high genetic advance as percent of mean was recorded for spike length and grain yield per plant at Hirna. High genetic advance as percent of mean values were also presented by [4, 17] for biomass, grain yield, spike length and total number of tillers per plant which agrees with the present finding.

Johnson, H. W. *et al.* suggested the importance of considering both the genetic advance and heritability of traits simultaneously rather than considering them separately in determining how much progress can be made through selection [14]. In this study, high heritability accompanied with high genetic advance as percent of mean was observed for total number of tillers per plant, number of fertile tillers per plant, grain yield per hectare, and above ground biomass per hectare at Haramaya (Table 4), and for spike length, total number of tiller per plant, number of fertile tiller per plant, grain yield per hectare, and above ground biomass per hectare at Hirna (Table 5). This indicates that these traits are highly heritable and selection of high performing genotypes is possible for 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 characters.

4. Conclusion

The progress of crop improvement program depends on the choice of genetic material, the extent of variability present in the germplasm, and the knowledge of associations of quantitative characters with grain yield and among themselves. The present study was conducted at two locations Haramaya and Hirna) in eastern Ethiopia using 36 advanced bread wheat lines. The objectives of the study were to assess the genetic variability present in the advanced bread wheat lines and to assess associations among important yield related traits.

Fifteen quantitative traits were measured and subjected to statistical analyses. The analysis of variance for each location showed highly significant difference ($P<0.01$) for all characters at both locations, indicating the presence of appreciable level of variability. The ranges of mean values for most of the characters were large showing the existence of variations among the tested bread wheat advanced lines. The

genotypic variance took relatively greater proportion of the total variances for all characters studied at both locations, implying that expression of the characters were mostly due to genetic factor than environmental effect. Hence, selection based on these traits may be effective for improvement.

Estimates of broad sense heritability were high for most of studied traits which suggests that sufficient progress can be made if these traits are considered as selection criteria. high heritability coupled with high genetic advance as percent of mean was observed for total number of tillers per plant, number of fertile tillers per plant, grain yield per hectare, and above ground biomass per hectare at Haramaya and for spike length, total number of tiller per plant, number of fertile tiller per plant, grain yield per hectare, and above ground biomass per hectare at Hirna. This indicates that improvement of these traits through selection is easier than other traits measured.

5. Recommendation

This study revealed that there was significance genetic variability among the studied genotypes for different traits. Hence, selection for these traits may be relatively safe and great emphasis should be given for these traits to improve the next bread wheat breeding program and to increase the farmer's productivity. However, since this is a one-year result, it is necessary to repeat the field experiment and evaluate the genotypes over several locations and years. In addition to these it is recommended if the study is under taken using molecular marker for further identification selection.

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