

## Full Length Research Paper

# Genetic variability and traits association in bread wheat (*triticum aestivum* L.) genotypes

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### ABSTRACT

Bread wheat is one of the most important small cereal crops produced in different regions of Ethiopia. The aim of this study was to estimate the extent of genetic variability and traits association in bread wheat genotypes. Twenty six bread wheat genotypes obtained from ICARDA-CIMMYT through Kulumasa Agricultural Research Center were tested at Gode and Kelafo research sites from 2010 to 2012 under irrigation in randomized complete block design (RCBD) with three replications. Ten agronomic traits were included in the study. Variances component methods were used to estimate components of variation, heritability and genetic advance. The bread wheat genotypes differed significantly for all characters studied, indicating existence of sufficient genetic variability within different genotypes. High phenotypic coefficient of variation and genotypic coefficient of variation were recorded grain filling period, number of tillers plant<sup>-1</sup> and grain yield plot<sup>-1</sup>. High genetic coefficient of variation along with high heritability and genetic advance were recorded in grain yield plot<sup>-1</sup> and days to heading. Positive and Highly significant association were obtained between grain yield plot<sup>-1</sup>, number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup> at both phenotypic and genotypic levels. Path coefficient analysis displayed maximum positive direct effect on grain yield plot<sup>-1</sup> mostly by days to heading, grain filling period, number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup>, was major contributors of towards grain yield plot<sup>-1</sup>. The two traits which showed significant contribution towards grain yield plot<sup>-1</sup> were number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup> and these traits should be given emphasis for future bread wheat yield improvement program.

**Keywords:** Bread wheat, variability, heritability, association studies, path analysis

## INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most important small cereal crops widely produced in Ethiopia. It grows on 1.5 million ha with a total production of 3.78 million tons and ranks fourth both in area and production among cereal crops in different regions of Ethiopia (CSA, 2012). Wheat is exclusively produced under rain fed conditions, meher and belg (long and short rainy seasons), respectively. Smallholders are major producers and suppliers of bread wheat, accounting for more than 89% of the market supply (USAID, 2010). Wheat is one of a major cereal of choice in the country, due to its higher productivity, broader adaptation and input responsive high yielding improved varieties. This significantly increased the national wheat area from almost 0 to 60% of the area (Tarekenge et al., 1995). As for as the variability and association among characters in bread wheat genotypes is concerned nothing has been

done in Somali region of Ethiopia. Therefore, the objective of this study was to determine the extent of variability of yield and associated traits and the extent of correlation among traits at both phenotypic and genotypic levels and thereby compare the direct and indirect influence of the traits on grain yield.

## MATERIALS AND METHODS

### Experimental sites

The study was conducted at Gode Pastoral and Agro-pastoral Research Center and Kelafo Research Sub-center in the Eastern part of Ethiopia from 2010 to 2012 using irrigation. Gode (lat. 5°57'.025N, long. 43°33'.033'E) and Kelafo (lat. 5°35'08.9"N, long. 4°11'36.2'E) research stations have altitude of 300 and 246m above sea level, respectively. The two locations

are characterized as arid to semi-arid agro-ecology, where crop cultivation is undertaken along Webi-Shabelle river bank. The mean annual rainfall of the areas is 300-340 to 150-220 mm. The mean maximum and minimum annual temperature of area is 30-35 °C and 22.2-32 °C, respectively, (Gebre-Mariam, 2005). The soil is clay and clay loam in textural type with alkaline PH (Badel, 2012).

### Experimental materials and design

The experiments were conducted in randomized complete block design with three replications at two locations, Gode and Kelafo research stations. Twenty six bread wheat genotypes, imported from ICARDA-CIMMYT through Kulumasa Agricultural Research Center were used in the study (Table 1). Total plot size of 2m x 3m consisted of 14 rows per plot and net plot size of 2m x 2.8m with 12 harvestable rows were used. Distance of 20cm and 10cm were used between rows and plants, respectively. Seed rate of 150 kg/ha was used and sown by hand drilling at 20 cm row spacing. DAP (18-46-0) was applied basally during planting at the rate of 100kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>. Total Nitrogen was applied at rate of 100kg ha<sup>-1</sup> N as UREA (46.5%) in two splits: first split (2/3) and the second split, (1/3) of the total dose at mid-tillering and flowering stages, respectively. All experimental plots at both locations were subjected to uniform recommended package of agronomic and plant protection practices to obtain a healthy plants.

### Data collected

Data on phenological basis was recorded on days to heading, days to maturity and grain filling period. Days to heading were counted from the date of sowing till 50% of the heads emerged while days to maturity were recorded from the date of sowing till 75% of the plant were matured. A plant was assumed to be physiologically matured when 75 percent of the glumes of the primary spike turned yellow. Morphological data on plant height (cm), spike length (cm), number of tillers/plant, number of spikelets/spike, number of grains/spike and 1000-grain weight were recorded on five randomly selected plants in each variety per replication. Grain yield per plot recorded and were converted into quintal/ha.

### Statistical analysis

Mean data collected for the two locations of three years were subject to analysis of variance using PROC GLM procedure of SAS version 9.2, (SAS Institute Inc., 2008) for randomized complete block and combined analysis from all locations were performed for each variant, following the procedure of Steel et al. (1997). The treatment effects were compared using LSD test at 1% and 5% probability level and the pooled analysis of experiment, locations were considered random effect with genotypes as fixed (SAS Institute Inc., 2008). The variability present in the genotypes was estimated by phenotypic and genotypic variances and coefficient

of variations using the procedure suggested by Burton and De Vane (1953) as follows:

$$\delta^2 p = \delta^2 g + \delta^2 e \quad \text{and}$$

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

Where,  $\delta^2 g$  =Genotypic variance,  $\delta^2 P$  = Phenotypic variance,  $\delta^2 e$  = Environmental (error) variance or Error mean square,  $MSg$  = Mean square due genotypes,  $MSe$  =Mean square of error (environmental variance),  $r$  = Number of replications, Phenotypic coefficient of variation (PCV):

$$PCV = \frac{\sqrt{\delta^2 p}}{\bar{x}} \times 100$$

Genotypic coefficient of variation (GCV):

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{x}} \times 100 \quad \text{where, } \bar{x} = \text{Population}$$

mean of the character being evaluated.

Heritability ( $h^2$ ) in the broad sense was computed using the formula suggested by Singh and Chaudhary (1985):

$$h^2 = \frac{\delta^2 g}{\delta^2 p} \times 100$$

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,  $\delta_p$  =phenotypic standard deviation on mean basis, and K =selection differential (K=2.06 at 5% selection intensity). Genetic advance mean (GAM) was computed to compare the extent of predicted genetic advance of different traits under selection using the formula:

$$GAM = \frac{GA}{\bar{X}} * 100$$

The correlation coefficients between all possible pairs of characters from the genotypic means by procedure of Steel and Torrie (1960) and the direct and indirect effects of the independent characters on grain yield per plot were estimated by the simultaneous solution of the formula suggested by Dewey and Lu (1959) using statistical package for genetical Researchers (GenRes) Version 7.01(Genres, 1994). In the path coefficient analysis, grain yield plot<sup>-1</sup> was taken as the result (dependent) variable while the rest of the characters were considered as casual (independent) variables.

## RESULTS AND DISCUSSION

Combined analysis of variance results for different studied traits is shown in Table 2. The location effect was

Table 1. Bread wheat genotypes used in the study

Entry	Pedigree	Selection history	Origin
511	PBW343*2/KUKUNA/ /PBW343*2/ KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-20WGY-0B	BV2008\C4THEBWYT\12
512	CNDO/R143//ENTE/MEXI_2/3/	CMSS04Y00421S-099Y-099ZTM-099Y-099M-4WGY-0B	BV2008\C4THEBWYT\17
529	WHEAR/SOKOLL	CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B	BV2008\C4THEBWYT\52
525	PFAU/SERI.1B//AMAD*2/3/PBW343*2/KUKUNA	CGSS04B00021T-099Y-099ZTM-099Y-099M-22WGY-0B	BV2008\C4THEBWYT\45
522	SW89.5277/BORL95//SKAUZ/3/PRL/*PASTOR/4/	CMSS04M01483S-0TOPY-099ZTM-099Y-099M-1WGY-0B	BV2008\C4THEBWYT\41
519	PRL/2*PASTOR//PBW343*2/KUKUNA	CMSS04Y00086S-0Y-099ZTM-099Y-099M-4WGY-0B	BV2008\C4THEBWYT\29
523	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/	CGSS04B00018T-099Y-099ZTM-099Y-099M-10WGY-0B	BV2008\C4THEBWYT\43
527	WAXWING*2//PBW343*2/KUKUNA	CGSS04BB00027T-099Y-099ZTM-099Y-099M-3WGY-0B	BV2008\C4THEBWYT\48
530	WHEAR//2*PRL/2*PASTOR	CGSS03B00090T-099Y-099M-099Y-099M-6WGY-0B-1B	BV2008\C4THEBWYT\56
504	SERI/RAYON*2//PFAU/WEAVER	CGSS04Y00001T-099M-099Y-099ZTM-099Y-099M-2WGY-0B	BV2008\C4THEBWYT\1
516	WBLL1*2/KIRITATI	CGSS01B00063T-099Y-099M-099M-099Y-099M-3WGY-0B	BV2008\C4THEBWYT\25
521	KAUZ//ALTAR84/AOS/3/PASTOR/4/MILAN/CUPE//	CMSS04M01386S-0TOPY-099ZTM-099Y-099M-2WGY-0B	BV2008\C4THEBWYT\39
506	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/5/CNO79//	CGSS04Y00058T-099M099Y-099M-099Y-099M-11WGY-0B	BV2008\C4THEBWYT\7
508	WHEAR//INQALAB91*2/TUKRU	CGSS04Y00076S-099Y-099M-099Y-099M-5WGY-B	BV2008\C4THEBWYT\9
505	SAAR/2*WAXWING	CGSS04Y00040T-099M-099Y-099M-099Y-099M-4WGY-0B	BV2008\C4THEBWYT\5
514	KIRITATI//SERI/RAYON	CGSS02Y00152S-099M-099Y-099M-11WGY-0B	BV2008\C4THEBWYT\23
526	PRL/2*PASTOR//PBW343*2/KUKUNA/3/	CGSS04B00025T-099Y-099ZTM-099Y-099M-3WGY-0B	BV2008\C4THEBWYT\46
510	PBW343*2/KUKUNA// PBW343*2/KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-18WGY-0B	BV2008\C4THEBWYT\11
528	HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/	CGSS04B00033T-099Y-099ZTM-099Y-099M-11WGY-0B	BV2008\C4THEBWYT\49
507	PBW343*2/KUKUNA/3/PASTOR//CHIL/PRL/4/	CGSS04Y00060T-099M-099T-099M-099Y-099M-11WGY-0B	BV2008\C4THEBWYT\8
517	WBLL1*2/KIRITATI	CGSS01B00063T-099T-099M-099M-099Y-099M-18WGY-0B	BV2008\C4THEBWYT\26
520	PBW343*2/HUITES/4/YAR/AE.SQUARROSA(783)//	CMSS04M00348S-0Y-099ZTM-099Y-099M-10WGY-0B	BV2008\C4THEBWYT\37
524	PFAU/SERI.1B//AMAD*2/3/ PBW343*2/KUKUNA	CGSS04B00021T-099Y-099ZTM-099Y-099M-15WGY-0B	BV2008\C4THEBWYT\44
518	WBLL1*2/KIRITATI	CGSS01B00063T-099Y-099M-099M-099Y-099M-31WGY-0B	BV2008\C4THEBWYT\27
513	MINO/898.97	CMSS04Y00921S-099Y-099ZTM-099Y-099M-2GWY-0B	BV2008\C4THEBWYT\22
509	PBW343*2/KUKUNA// PBW343*2/KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-10WGY-0B	BV2008\C4THEBWYT\10

Table 2. Analysis of variance using RCBD for the 10 traits across the locations

Source	Loc	Replication	Genotype	Locx Genotype	Error	C.V. (%)
Days to heading	2353.05**	4.32	160.36**	52.77**	9.26	6.42
Grain filling period	2155.59**	45.47	90.34**	114.45**	20.70	15.61
Days to maturity	1381.15**	18.04	111.87**	75.33**	15.13	4.91
Plant height	614.20**	32.96	83.45**	77.27**	12.45	6.62
Number of tillers plant <sup>-1</sup>	9.32**	1.71	3.52**	1.62**	0.64	17.35
Spike length	123.32**	1.15	1.63*	2.75**	1.01	12.31
Number of spikelets spike <sup>-1</sup>	1017.76**	4.15	6.54**	2.13*	1.77	14.91
Number of grains spike <sup>-1</sup>	476209.19**	439.711	554.65**	646.73**	104.32	16.64
1000 grain weight	8451.24**	2.67	41.09**	38.18**	10.20	10.63
Grain yield plot <sup>-1</sup>	377.21**	134.70	191.55**	74.27**	15.93	16.29

\*and \*\* indicate significant at the 0.05 and 0.01 probability levels, respectively, and loc: location

Table 3. Estimate of ranges, mean, phenotypic (PV) and Genotypic (GV) component of variances, broad sense heritability, and genetic advance as percent of mean for 10 characters of bread wheat lines at Gode and Kelafo research stations.

Trait	Range	Mean ± S. E.	PV	GV	PCV (%)	GCV (%)	h <sup>2</sup> (%)	GA	GA (%)
DH	32.00-71.00	47.40 ± 7.38	84.81	75.55	19.43	18.34	89.08	16.90	35.65
GFS	11.00-66.00	29.15 ± 8.35	55.52	34.82	25.56	20.24	62.72	9.63	33.02
MD	59.00-105.00	79.17 ± 7.11	63.50	48.37	10.07	8.78	76.17	12.50	15.79
PHT	35.00-68.00	53.30 ± 6.30	47.95	35.50	12.99	11.18	74.04	10.56	19.81
NT	1.00-8.00	4.62 ± 1.10	2.08	1.44	31.22	25.97	69.23	2.06	44.52
SL	1.00-13.00	8.15 ± 1.63	1.32	0.31	14.10	6.83	23.48	0.56	6.82
NSPS	2.20-17.00	8.92 ± 3.47	4.16	2.39	22.85	17.31	57.40	2.41	27.02
NSS	131.67 -259.00	61.36 ± 69.76	329.49	225.17	9.71	8.03	68.34	25.55	13.67
TGW	10.60-54.00	30.05 ± 10.04	25.65	15.45	16.85	13.08	60.23	6.28	20.91
YLD	12.07-48.21	24.50 ± 6.95	103.74	87.81	41.57	38.25	84.64	17.76	72.49

S.E =standard error, PV=phenotypic variance, GV=genotypic variance, h<sup>2</sup>(%)= broad sense heritability, GCV (%)= genotypic coefficient of variation, PCV (%)= phenotypic coefficient of variation, GA= genetic advance, (%) GAM= genetic advance as percent of mean

significant for all traits, indicating the different climatic conditions in two locations. The location × genotype interaction effect was significant for all traits indicating different performance of bread wheat advanced lines across the two locations. Furthermore, Mean square of genotypes for all characters studied were significant (P<0.05 and P<0.01) differences among the bread wheat advanced lines, indicating the existence of sufficient genetic variability within different genotypes to be exploited in the breeding programs that was also reflected in the broad ranges observed for each traits (Table 2).

#### Mean performance of genotypes

Based on three years data, all traits studied showed a wide range of variation in days to heading (32.00 to 71.00 days), grain filling period (11.00 to 66.00 days), days to maturity (59.00 to 105.00 days), plant height (35.00 to 68.00 cm), number of tillers plant<sup>-1</sup> (1.00 to 8.00), spike length (1.00 to 13.00 cm), number of

spikelets spike<sup>-1</sup> (2.20 to 17.00), number of grains spike<sup>-1</sup> (131.67 to 259.00), 1000-grain weight (10.60 to 54.00) and grain yield plot<sup>-1</sup>(12.07-48.21qt/ha) (Appendix 1a and 1b ) indicating good opportunity for grain yield improvement.

#### Phenotypic and genotypic variations

The progress of a breeding program is conditioned by the degree and the nature of the genotypic and non-genotypic variation in the different characters. Since most of the economic traits (yield) are complex in heritability and are significantly influenced by various environmental conditions, the study of inheritance and genetic advance is very valuable in order to estimate the scope for improvement by selection. Heritability degree indicates the reliability with which the genotype will be recognized by its phenotype expression (Chandrababu and Sharma, 1999). The estimates of variability parameters for morphological and growth traits and yield are shown in Table 3. Phenotypic variances ranging

Table 4. Phenotypic correlation coefficient ( $r_p$ ) (upper diagonal) and genotypic correlation coefficient ( $r_g$ ) of 10 characters of 26 bread wheat advance lines tested at Gode and Kelafo research centers of Somali region (2010-2012)

Trait	DH	GFS	MD	PHT	NT	SL	NSPK	NSS	TCW	YLD
DH		-0.548**	0.590*	-0.055	-0.104	0.011	0.011	-0.123	-0.040	-0.166
GFS	-0.613**		0.343	0.022	-0.109	-0.084	-0.084	-0.173	0.203	-0.060
MD	0.767**	0.033		-0.035	-0.223	-0.087	-0.087	-0.320	0.150	-0.257
PHT	0.032	-0.151	-0.065		0.263	0.011	0.011	0.104	-0.051	0.107
NT	-0.106	-0.345	-0.405*	0.257		0.270	0.270	0.478*	-0.130	0.516**
SL	0.064	-0.030	0.027	-0.388*	-0.103			0.227	-0.206	0.107
NSPK	0.575**	-0.235	0.561**	0.892**	-1.090**	-1.379**		-0.119	0.353	0.021
NSS	-0.172	-0.332	-0.455**	0.133	0.868**	0.034	0.056		-0.311	0.416*
TSW	-0.169	0.806**	0.474*	-0.242	-0.609**	-1.662**	-1.673**	-0.517		-0.168
YLD	-0.202	-0.115	-0.365	0.159	0.839**	0.096	-0.296	0.664**	-0.612**	

\*, \*\* Indicate significance at 0.05 and 0.01 probability levels, DH=days to main heading, GFS=grain filling period, MD=days to maturity, PHT=plant height, NT=number of tillers plant, SL=spike length, NSPK=number of spikelets per spike, NSS=number of grains per spike, TGW=1000-grain weight, and YLD=yield per plot, respectively.

Table 5. Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at genotypic level in 26 bread wheat lines over three years

Trait	$g_r$	DH	GFS	MD	PHT	NT	SL	NSPK	NSS	TCW
DH	-0.202	<b>15.872</b>	-6.486	-9.466	-0.001	-0.062	-0.016	0.068	-0.127	0.017
GFS	-0.115	-9.736	<b>10.572</b>	-0.411	0.007	-0.202	0.008	-0.028	-0.245	-0.080
MD	-0.365	12.177	0.352	<b>-2.338</b>	0.003	-0.237	-0.007	0.067	-0.335	-0.047
PHT	0.159	0.513	-1.593	0.806	<b>-0.044</b>	0.151	0.098	0.106	0.098	0.024
NT	0.839**	-1.684	-3.649	5.002	-0.011	<b>0.585</b>	0.026	-0.130	0.640	0.060
SL	0.096	1.009	-0.315	-0.327	0.017	-0.061	<b>-0.254</b>	-0.164	0.025	0.164
NSPK	-0.296	9.119	-2.489	-6.924	-0.040	-0.638	0.350	<b>0.119</b>	0.041	0.165
NSS	0.664**	-2.725	-3.509	5.610	-0.006	0.508	-0.009	0.007	<b>0.737</b>	0.051
TSW	-0.612**	-2.687	8.520	-5.842	0.011	-0.356	0.422	-0.199	-0.381	<b>-0.099</b>

Residual = 0.236 and \*, \*\* Indicate significance at 0.05 and 0.01 probability levels, DH=days to main heading, GFS=grain filling period, MD=days to maturity, PHT=plant height, NT=number of tillers plant, SL=spike length, NSPK=number of spikelets per spike, NSS=number of grains per spike, TGW=1000-grain weight and YLD=yield per plot, respectively

between 1.32 and 329.49 and genotypic variances ranging between 0.32 and 225.17 for the characters studied (Table 3). Relatively higher phenotypic variance values of 329.49 for number of grains spike<sup>-1</sup> and 103.74 for grain yield plot<sup>-1</sup> were recorded in the study. Likewise, the genotypic variances for these traits were also high, indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these traits. Result of present study concurs with that of Motzo et al. (2001), reported that high genotypic variation for heading date and grain weight in triticale. The GCV ranged from 6.83 for spike length to 38.25 for grain yield, whereas, PCV ranged from 9.71 for number of grains spike<sup>-1</sup> to 41.57 for grain yield plot<sup>-1</sup> (Table 3). Deshmukh et al. (1986) classified PCV and GCV values as high (>20%), medium (10-20%) and low (<10%). Accordingly, high PCV and GCV were observed in traits grain fill period, number of tillers plant<sup>-1</sup>, and grain yield plot<sup>-1</sup>.

Other workers have reported high PCV and GCV for grain yield, biomass, harvest index, 1000-grain weight and plant height in wheat (Tarekenge et al., 1994; Sharma et al., 1995; Bekele et al., 1996; Desalegn et al., 1996).

The high PCV and GCV indicated that selection may be effective based on these traits and their phenotypic expression would be good indication of the genotypic potential (Singh et al., 1994). On the other hand, number of grains spike<sup>-1</sup> showed low GCV and PCV, indicating less scope of selection as they are under the influence of environment. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied, indicating the influence of growing environments (Table 3). In most of cases, the two values differ slightly indicating less influence of environmental factors. Wide difference between PCV and GCV values were observed in spike length and number of spikelets spike<sup>-1</sup> may indicate the high contribution of the

environmental variance to the phenotypic variance. Therefore, it would be appropriate to consider the above traits depending on the objective of bread wheat advanced lines improvement program.

#### Estimates of heritability ( $h^2$ ) in broad sense

In this study the heritability estimate ranged from 23.48% for spike length to 89.08% for days to heading (Table 3). The heritability was larger for most of traits due smaller phenotypic variances. According to Pramoda and Gangaprasad, 2007 heritability estimates can be low (<40%), medium (40-59%), moderately high (60-79%), and very high ( $\geq 80\%$ ). Accordingly heritability estimates were very high for days to heading (89.08%) and grain yield plot<sup>-1</sup> (84.64%), indicating the possibility of success in selection. Similar results were reported by Kaul and Kumar (1982); Mehertre et al.(1996) and Sarma et al.(1996). Grain filling period (62.72%), days to maturity (76.17%), plant height (74.04%), number of tillers plant<sup>-1</sup> (69.23%), number of grains spike<sup>-1</sup>(68.34%), and 1000-grain weight (60.23%) showed moderately high heritable, indicating these characters, therefore, may respond effectively to selection pressure. These findings agreed with that of Vange and Ojo (1997). Moderate heritability estimates were recorded for number spikelets spike<sup>-1</sup>(57.40%). Result may indicate possibility due to influence of the environment on the polygenic nature of this trait. On the other hand, low heritability estimates were also recorded for spike length (23.48%), indicating the limited scope of improvement of this trait through selection.

#### Estimates of expected genetic advance (GA)

The expected genetic advance expressed as a percentage of the mean by selecting the top 5% (high grain yielder) of the bread wheat advanced lines, varied between 6.82% for spike length and 72.49% for grain yield plot<sup>-1</sup> (Table 3), indicating that selecting the top 5% of the base population could result in an advance of 6.82 to 72.49 percent over the respective population mean. Genetic advance as percentage of mean was maximum for percentage of grain yield plot<sup>-1</sup> followed by number of tillers plant<sup>-1</sup>, days to heading, grain filling period. Similarly, genetic advance was maximum for number of grains spike<sup>-1</sup>, grain yield plot<sup>-1</sup>, and days to heading. Burton (1952) suggested that genetic coefficient of variation together with heritability estimate give the best picture of the amount genetic advance to be expected from selection. Similarly, Johnson et al. (1955) and Johnson and Hernandez (1980) reported that high genotypic coefficients of variation along with high heritability and high genetic advance provide better information than each parameter alone. High genetic coefficient of variation, heritability and genetic advance were found in grain yield plot<sup>-1</sup> and days to heading. Result indicated these characters could be useful basis of selection. Jalata et al. (2006) obtained similar results in Ethiopian barely.

#### Association of characters

Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are given in Table 4. The results showed that, in general, the genotypic correlation coefficients ( $r_g$ ) were higher than the phenotypic correlation coefficients ( $r_p$ ) which indicated that association among these characters was under genetic control and indicating the preponderance of genetic variance in expression of characters. It might be due to depressing effect of environment on character association as reported earlier for wheat crop (Ahmad et al., 1978; Paroda and Joshi, 1970). Days to heading showed positive and significant association with days to maturity at both phenotypic and genotypic levels ( $r_p=0.590^*$ ,  $r_g=0.767^{**}$ ). However, it displayed negative and highly significant association with grain tilling period at both phenotypic and genotypic levels ( $r_p=-0.548^{**}$ ,  $r_g=-0.613^{**}$ ), indicating the difficulty in simultaneous improvement of these traits. Grain filling period showed positive and highly significant association with 1000-grain weight at genotypic level ( $r_g=0.806^{**}$ ). Days to maturity showed negative and significant association with number of tillers plant<sup>-1</sup> and grain spike<sup>-1</sup> at genotypic level ( $r_g=-0.405^*$  and  $r_g=-0.455^{**}$  in that order). However, it showed positive and highly significant association with number of spikelets spike<sup>-1</sup> at genotypic level ( $r_g=0.561^{**}$ ), indicating simultaneous improvement of these traits. Plant height had negative and significant association with spike length at genotypic level ( $r_g=-0.388^*$ ) similar results have been found by Saleem et al.(2006). Plant height displayed positive and highly significant association with number of spikelets spike<sup>-1</sup> at genotypic level ( $r_g=0.892^{**}$ ). Iqbal et al. (2007) found similar results in their studies. Spike length showed negative and highly significant association with number of spikelets spike<sup>-1</sup> and 1000-grain weight at genotypic level ( $r_g=-1.379^{**}$ ,  $r_g=-1.662^{**}$  in that order). Number of spikelets spike<sup>-1</sup> showed negative and highly significant association with 1000-grain weight at genotypic level ( $r_g=-1.673^{**}$ ), similar with the result of Shahid et al. (2002) and Kashif and Khaliq (2004). On the contrary, Khokhar et al. (2010) reported that number of spikelets spike<sup>-1</sup> showed positive and significant association with 1000-grain weight.

The correlation between number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup> and grain yield plot<sup>-1</sup> was positive and significant association at both phenotypic and genotypic levels ( $r_p=0.416^*$ , and  $r_g=0.664^{**}$  in that order), suggesting that an increase in number of tillers plant<sup>-1</sup> could result from increase in all these traits. Number of tillers plant<sup>-1</sup> was positively and significantly associated with number of grain spike<sup>-1</sup> at both phenotypic and genotypic levels ( $r_g=0.868^{**}$ ). This findings indicated that number of tillers plant<sup>-1</sup> and grain spike<sup>-1</sup> should be given prime importance regarding its contribution to grain yield plot<sup>-1</sup>. These results suggest that selections should be based on number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup> for developing new wheat varieties and it may be effective

traits to select higher yielding genotypes. These results are similar with Inamullah et al. (2006). However, number of tillers plant<sup>-1</sup> had negative and highly significant association with number of spikelets spike<sup>-1</sup> and 1000-grain weight at genotypic level ( $r_g = -1.090^{**}$  and  $r_g = -0.609^{**}$  in that order). 1000-grain weight showed negative and highly significant association with grain yield plot<sup>-1</sup> at genotypic level ( $r_g = -0.612^{**}$ ) indicating the practical difficulty of simultaneous improvement of these characters due to lack of closely linked genes that cause co-variation in the traits (Falconer, 1989). These results are in agreement with the result of Sarkar et al. (2002) and Khaliq et al. (2004). The study of association of characters suggests that number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup> were the most important characters with positive association with grain yield plot<sup>-1</sup>. In general, an intensive selection for these characters will automatically improve grain yield in bread wheat advanced lines. Since the two traits are correlated, selection in one of the traits will implicitly result in the improvement of the others. Therefore, these traits could be used in breeding program to improve varieties for higher yield.

#### Path coefficient analysis

Results in Table 5 showed path coefficient analysis of all traits on grain yield plot<sup>-1</sup>. High magnitude and maximum positive direct effects on grain yield was exerted by days to heading (15.872) followed by grain filling period (10.572), number of grains spike<sup>-1</sup> (0.737), tillers plant<sup>-1</sup> (0.585) and spikelets spike<sup>-1</sup> (0.119), indicating the true relationship between these traits as good contributors to grain yield. As a result, these traits could be considered as important traits for selection in a breeding program for higher grain yield of the bread wheat advanced lines. This is in agreement with findings of Dhonde et al. (2000) and Khan and Dar (2010). On the other hand, the maximum negative direct effect was exhibited by days to maturity (-12.338), followed by spike length (-0.254) and plant height and 1000-grain weight but negligible (-0.044 and -0.099). The indirect effect of days to heading through grain filling period (-6.486), days to maturity (-9.466), plant height (-0.001), number of tillers plant<sup>-1</sup> (-0.062), spike length (-0.016), and number grains spike<sup>-1</sup> (-0.127) counter balanced the direct effect of days to heading on grain yield (15.872) and reduced the correlation coefficient to (-0.202). Furthermore, the indirect effect of grain filling period through days to heading (-9.736), days to maturity (-0.411), number of tillers plant<sup>-1</sup> (-0.202), number spikelets spike<sup>-1</sup> (-0.028), number grains spike<sup>-1</sup> (-0.245), and 1000-grain weight (-0.080) counter balanced the direct effect of grain filling period on grain yield (10.572) and reduced the correlation coefficient to (-0.115). This result is in agreement with findings of Yilddirim et al. (1996) and Narwal et al. (1999). The indirect effect of number of tillers plant<sup>-1</sup> through days to heading (-1.684), grain

filling period (-3.649), plant height (-0.011), and number spikelets spike<sup>-1</sup> (-0.130) counter balanced the direct effect of number of tillers plant<sup>-1</sup> on grain yield (0.585) and reduced the correlation coefficient to (+0.839). Similarly, the indirect effect of number grains spike<sup>-1</sup> through days to heading (-2.725), grain filling period (-3.509), plant height (-0.006), and spike length (-0.009) counter balanced the direct effect of number grains spike<sup>-1</sup> on grain yield (0.737) and reduced the correlation coefficient to (+0.664). Similar result to those obtained by Ali et al. (2008) and Mollasadeghi and Shahryari (2011).

Thousand-grain weight exhibited negative direct effect with negligible correlation. Selection of for this trait will not be improving grain yield of bread wheat advanced lines. Therefore, the direct selection of this character is ineffective. The indirect effect of this trait via grain filling period and spike length were positive whereas it was negative via days to heading and maturity, number of grains spike<sup>-1</sup> and tillers plant<sup>-1</sup> (Table 5). This was not in line with the work of Aycicek and Yilddirim (2006), and Soghi et al. (2006) whom reported positive but small direct effects of 1000-grain weight on grain yield of bread wheat lines. Residual effects (0.236) indicated that nine characters included in the study explained high percentage of variation in grain yield plot<sup>-1</sup>, indicating that in addition to the previous characters, there are also other factors to justify grain yield plot<sup>-1</sup> changes.

#### CONCLUSION

Highly significant differences were observed among bread wheat advanced lines evaluated for all the 10 studied characters. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in all characters. Positive and highly significant association were obtained between grain yield plot<sup>-1</sup>, number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup> at both phenotypic and genotypic levels. However, 1000-grain weight contributing negatively towards grain yield plot<sup>-1</sup> at both phenotypic and genotypic levels. Path coefficient analysis displayed that maximum positive direct effect on grain yield plot<sup>-1</sup> were mostly by days to heading, followed by grain filling period, number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup>, were major contributors of towards grain yield plot<sup>-1</sup>. The two traits which showed significant contribution towards the final grain yield plot<sup>-1</sup> are number of tillers plant<sup>-1</sup> and grains spike<sup>-1</sup>, indicating these two characters should be given emphasis for future bread wheat yield improvement programs.

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Appendix 1a. Mean performance of genotypes across locations

Entry	Pedigree	Selection history	DH	GFS	MD	PHT	NT
511	PBW343*2/KUKUNA/ PBW343*2/ KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-20WGY-0B	45.08ljk	28.92fgdjeich	76.67khjgi	55.33bedc	4.39gf
512	CNDO/R143//ENTE/MEXI_2/3/	CMSS04Y00421S-099Y-099ZTM-099Y-099M-4WGY-0B	45.25ljk	27.83fgjih	76.00khji	49.42lk	4.72gfde
529	WHEAR/SOKOLL	CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B	42.33nm	29.25fgdjeich	73.92k	56.62bac	5.818ba
525	PFAU/SERI.1B//AMAD*2/3/PBW343*2/KUKUNA	CGSS04B00021T-099Y-099ZTM-099Y-099M-22WGY-0B	44.58lkm	28.00fgjih	75.42kji	54.45fedc	5.27bdac
522	SW89.5277/BORL95//SKAUZ/3/PRL/*PASTOR/4/	CMSS04M01483S-0TOPY-099ZTM-099Y-099M-1WGY-0B	48.50gfehi	26.25jkih	78.00fhegi	50.42lkji	4.62gfde
519	PRL/2*PASTOR//PBW343*2/KUKUNA	CMSS04Y00086S-0Y-099ZTM-099Y-099M-4WGY-0B	46.25jki	29.42fgdeich	78.17fhegi	54.45fedc	4.81fdec
523	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/	CGSS04B00018T-099Y-099ZTM-099Y-099M-10WGY-0B	47.17gjhi	28.50fgdjeih	78.83fhegd	55.53bdc	4.63gfde
527	WAXWING*2//PBW343*2/KUKUNA	CGSS04BB00027T-099Y-099ZTM-099Y-099M-3WGY-0B	53.83a	25.75jk	82.08cb	54.32fedc	5.44bac
530	WHEAR//2*PRL/2*PASTOR	CGSS03B00090T-099Y-099M-099Y-099M-6WGY-0B-1B	48.75gfeh	28.58fgdjeih	80.00fcedb	52.50gfejhi	4.21gfhi
504	SERI/RAYON*2//PFAU/WEAVER	CGSS04Y00001T-099M-099Y-099ZTM-099Y-099M-2WGY-0	51.00bcd	28.08fgjeih	81.58cbd	51.12glkji	4.19ghi
516	WBLL1*2/KIRITATI	CGSS01B00063T-099Y-099M-099M-099Y-099M-3WGY-0B	54.67a	23.17k	80.58cedb	55.44bdc	4.59gfe
521	KAUZ//ALTAR84/AOS/3/PASTOR/4/MILAN/CUPE	CMSS04M01386S-0TOPY-099ZTM-099Y-099M-2WGY-0B	45.58ljk	28.00fgjih	75.92khji	55.02edc	4.34gf
506	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/5/CNO79//	CGSS04Y00058T-099M099Y-099M-099Y-099M-11WGY-0B	49.83fecd	28.00fgjih	80.08fcedb	52.88gfedhi	4.32gf
508	WHEAR//INQALAB91*2/TUKRU	CGSS04Y00076S-099Y-099M-099Y-099M-5WGY-B	49.58gfec	28.08fgjeih	80.25fcedb	53.68gfed	4.80gfdec
505	SAAR/2*WAXWING	CGSS04Y00040T-099M-099Y-099M-099Y-099M-4WGY-0B	52.83ba	25.83jki	81.67cbd	53.27gfedh	4.70gfde
514	KIRITATI//SERI/RAYON	CGSS02Y00152S-099M-099Y-099M-11WGY-0B	47.08jhi	32.50bac	82.17cb	51.91gfkji	5.81a
526	PRL/2*PASTOR//PBW343*2/KUKUNA/3/	CGSS04B00025T-099Y-099ZTM-099Y-099M-3WGY-0B	45.42ljk	31.67bdec	79.58fcedg	49.87lkj	4.43gf
510	PBW343*2/KUKUNA// PBW343*2/KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-18WGY-0B	44.17lkm	30.25fgdec	76.33khji	53.83gfedc	4.17gfhi
528	HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/	CGSS04B00033T-099Y-099ZTM-099Y-099M-11WGY-0B	41.33n	32.08bdac	75.83khji	53.32gfedh	5.17bdec
507	PBW343*2/KUKUNA/3/PASTOR//CHIL/PRL/4/	CGSS04Y00060T-099M-099T-099M-099Y-099M-11WGY-0B	42.42nm	29.75fgdech	74.67kj	49.20lk	4.30gfh
517	WBLL1*2/KIRITATI	CGSS01B00063T-099T-099M-099M-099Y-099M-18WGY-0B	50.75becd	26.67gjkij	79.83fcedb	48.483l	4.39gf
520	PBW343*2/HUITES/4/YAR/AE.SQUARROSA(783)//	CMSS04M00348S-0Y-099ZTM-099Y-099M-10WGY-0B	47.42gfjhi	31.75bdc	81.58cbd	53.85gfedc	4.75gfde
524	PFAU/SERI.1B//AMAD*2/3/ PBW343*2/KUKUNA	CGSS04B00021T-099Y-099ZTM-099Y-099M-15WGY-0B	43.17lnm	31.25fbdec	77.42fhjgi	58.93a	4.65gfde
518	WBLL1*2/KIRITATI	CGSS01B00063T-099Y-099M-099M-099Y-099M-31WGY-0B	51.25bc	28.58fgdjeih	82.83b	57.89ba	4.48gf
513	MINO/898.97	CMSS04Y00921S-099Y-099ZTM-099Y-099M-2GWY-0B	49.83fecd	34.33ba	86.50a	53.33gfedh	3.67hi
509	PBW343*2/KUKUNA// PBW343*2/KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-10WGY-0B	44.33lkm	35.50a	82.58cb	50.78lkjhi	3.59i
	<b>Mean</b>		<b>47.40</b>	<b>29.15</b>	<b>79.17</b>	<b>53.30</b>	<b>4.62</b>
	<b>CV (%)</b>		<b>5.85</b>	<b>14.46</b>	<b>4.48</b>	<b>5.86</b>	<b>15.83</b>
	<b>LSD(0.05)</b>		<b>1.82</b>	<b>2.72</b>	<b>2.33</b>	<b>2.05</b>	<b>0.48</b>

DH=days to main heading, GFS=grain filling stage, MD=days to maturity, PHT=plant height, NT=number of tillers plant, SL=spike length, NSPS=number of spikelets per spike, NSS=number of grains per spike, TGW=thousand grain weight, and YLD=grain yield per plot, respectively.

Appendix 1b. Mean performance of genotypes across seasons

Entry	Pedigree	Selection history	SL	NSPK	NSS	TGW	Yield (Qt/ha)
511	PBW343*2/KUKUNA/ /PBW343*2/ KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-20WGY-0B	8.14ebdacf	8.45gfdehi	190.33gfdec	27.94h	24.69feg
512	CNDO/R143//ENTE/MEXI_2/3/	CMSS04Y00421S-099Y-099ZTM-099Y-099M-4WGY-0B	7.82edf	8.28gfefhi	199.33bdec	31.91bdc	26.16ed
529	WHEAR/SOKOLL	CMSS04Y00201S-099Y-099ZTM-099Y-099M-11WGY-0B	8.15ebdacf	9.06fdec	233.33a	29.36gefhdh	36.84a
525	PFAU/SERI.1B//AMAD*2/3/PBW343*2/KUKUNA	CGSS04B00021T-099Y-099ZTM-099Y-099M-22WGY-0B	8.36ebdacf	9.76bac	229.00ba	28.25gh	28.45cbd
522	SW89.5277/BORL95//SKAUZ/3/PRL/*PASTOR/4/	CMSS04M01483S-0TOPY-099ZTM-099Y-099M-1WGY-0B	8.29ebdacf	8.14gfhi	160.67gkijh	28.76gfgh	22.10jfhig
519	PRL/2*PASTOR//PBW343*2/KUKUNA	CMSS04Y00086S-0Y-099ZTM-099Y-099M-4WGY-0B	8.94a	9.00fdec	164.00gfjih	30.13gefhdh	21.79jhig
523	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/	CGSS04B00018T-099Y-099ZTM-099Y-099M-10WGY-0B	8.15ebdacf	9.07fdec	160.67gkijh	30.80gefddc	22.45fhig
527	WAXWING*2//PBW343*2/KUKUNA	CGSS04BB00027T-099Y-099ZTM-099Y-099M-3WGY-0B	8.08ebdcf	9.22bdec	207.67bdac	28.89gfgh	30.88cb
530	WHEAR//2*PRL/2*PASTOR	CGSS03B00090T-099Y-099M-099Y-099M-6WGY-0B-1B	7.71ef	9.23bdec	163.67gfjih	29.68gefhdh	22.55fhig
504	SERI/RAYON*2//PFAU/WEAVER	CGSS04Y00001T-099M-099Y-099ZTM-099Y-099M-2WGY-0	8.80ba	10.21ba	174.00gfjeih	27.97h	22.40fhig
516	WBLL1*2/KIRITATI	CGSS01B00063T-099Y-099M-099M-099Y-099M-3WGY-0B	8.35ebdacf	9.82bac	131.67k	29.66gefhdh	26.15ed
521	KAUZ//ALTAR84/AOS/3/PASTOR/4/MILAN/CUPE	CMSS04M01386S-0TOPY-099ZTM-099Y-099M-2WGY-0B	7.97edcf	10.36a	188.67gfdec	29.01gefgh	27.93cd
506	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/5/CNO79//	CGSS04Y00058T-099M099Y-099M-099Y-099M-11WGY-0B	7.85edf	9.79bac	191.67fdec	34.40ba	19.17j
508	WHEAR//INQALAB91*2/TUKRU	CGSS04Y00076S-099Y-099M-099Y-099M-5WGY-B	7.60f	8.33gfefhi	181.33gfdeih	32.76bac	19.57ji
505	SAAR/2*WAXWING	CGSS04Y00040T-099M-099Y-099M-099Y-099M-4WGY-0B	8.43ebdac	8.68gfdeh	184.67gfdech	29.37gefhdh	22.69fhig
514	KIRITATI//SERI/RAYON	CGSS02Y00152S-099M-099Y-099M-11WGY-0B	8.59bdac	7.90ghi	229.33ba	28.89gfgh	31.62b
526	PRL/2*PASTOR//PBW343*2/KUKUNA/3/	CGSS04B00025T-099Y-099ZTM-099Y-099M-3WGY-0B	8.19ebdacf	7.58i	189.33gfdec	34.77a	23.44fheg
510	PBW343*2/KUKUNA// PBW343*2/KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-18WGY-0B	8.69bac	8.78gfdec	194.67dec	28.47gh	23.37fheg
528	HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/	CGSS04B00033T-099Y-099ZTM-099Y-099M-11WGY-0B	7.83edf	7.65hi	195.33dec	31.48edc	26.34ed
507	PBW343*2/KUKUNA/3/PASTOR//CHIL/PRL/4/	CGSS04Y00060T-099M-099T-099M-099Y-099M-11WGY-0B	8.42ebdac	8.55gfdehi	150.67jk	27.74h	22.89fhg
517	WBLL1*2/KIRITATI	CGSS01B00063T-099T-099M-099M-099Y-099M-18WGY-0B	7.74ef	8.63gfdehi	152.33jki	29.43gefhdh	25.26fed
520	PBW343*2/HUITES/4/YAR/AE.SQUARROSA(783)//	CMSS04M00348S-0Y-099ZTM-099Y-099M-10WGY-0B	8.42ebdac	9.14fdec	183.33gfdech	29.55gefhdh	20.85jhi
524	PFAU/SERI.1B//AMAD*2/3/ PBW343*2/KUKUNA	CGSS04B00021T-099Y-099ZTM-099Y-099M-15WGY-0B	7.58f	9.47bdac	181.67gfdeih	31.23efdc	22.01jhig
518	WBLL1*2/KIRITATI	CGSS01B00063T-099Y-099M-099M-099Y-099M-31WGY-0B	7.82edf	9.43bdac	186.33gfdech	31.09efdc	22.70fhig
513	MINO/898.97	CMSS04Y00921S-099Y-099ZTM-099Y-099M-2GWY-0B	7.97edcf	9.14fdec	157.33jkijh	30.61gefddc	22.25jfhig
509	PBW343*2/KUKUNA// PBW343*2/KUKUNA	CGSS04Y00099S-099Y-099M-099Y-099M-10WGY-0B	7.91edcf	8.29gfefhi	213.33bac	29.05gefgh	22.46fhig
<b>Mean</b>			<b>8.15</b>	<b>8.92</b>	<b>15885</b>	<b>30.05</b>	<b>24.50</b>
<b>CV (%)</b>			<b>11.14</b>	<b>13.96</b>	<b>9.32</b>	<b>9.65</b>	<b>15.15</b>
<b>LSD(0.05)</b>			<b>0.60</b>	<b>0.82</b>	<b>9.71</b>	<b>9.10</b>	<b>2.44</b>

DH: days to main heading, GFS=grain filling stage, MD=days to maturity, PHT=plant height, NT=number of tillers plant, SL=spike length, NSPK= number of spikelets per spike, NSS=number of grains per spike, TGW=thousand grain weight, and YLD=grain yield per plot, respectively.