
Analysis of Genetic Variability Among Bread Wheat (*Triticum aestivum* L.) Genotypes for Growth, Yield and Yield Components in Bore District, Oromia Regional State

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To cite this article:

Obsa Chimdesa, Wassu Mohammed, Firdissa Eticha. Analysis of Genetic Variability Among Bread Wheat (*Triticum aestivum* L.) Genotypes for Growth, Yield and Yield Components in Bore District, Oromia Regional State. *Agriculture, Forestry and Fisheries*.

Vol. 6, No. 6, 2017, pp. 188-199. doi: 10.11648/j.aff.20170606.12

Received: April 19, 2017; **Accepted:** August 30, 2017; **Published:** October 17, 2017

Abstract: In Ethiopia, a number of improved bread wheat (*Triticum aestivum* L.) varieties have been released by different research centres. All of these varieties were, however, not evaluated in Bore District for growth, yield and yield components which are necessary for identification of adaptable varieties for this major wheat growing District. Field experiments was conducted in 2013/14 cropping season by utilizing 21 released varieties and 4 promising lines using Randomized Complete Block Design where genotypes were replicated three times and 14 characters were recorded. Results of the analysis of variance revealed that genotypes were differed significantly for all characters studied. Genotypic coefficient of variation (GCV) ranged from 4.59 (days to maturity) to 13.76% (grain yield per hectare), while phenotypic coefficient of variation (PCV) ranged between 5.03 (days to maturity) to 20.85% (grain yield per hectare). Heritability in broad sense and genetic advance as percent of mean (GAM) ranged from 33.33% (Tillers per plant) to 84.67% (Peduncle length) and 8.66% (Days to maturity) to 18.74% (grain yield per hectare), respectively. Grain yield per hectare was positively correlated with biological yield per plot and harvest index, but was negatively correlated with peduncle length both at genotypic and phenotypic level. The computed path coefficient for yield showed that days to maturity, number of productive tillers, and biological yield per plot, harvest index, and spike length had positive direct effect, while days to heading and grain filling period, had high negative direct effect at both genotypic and phenotypic levels. Generally, it has been observed the presence of variability among the genotypes studied and 18.74% grain yield gain is possible by exerting 5% selection intensity which can be exploited to improve yield in the District.

Keywords: Bread Wheat, Genetic Variability, GCV, PCV, Heritability, Path Coefficient, Yield Component

1. Introduction

Globally, attainment of food security and protection of the environment are two of the greatest challenges facing human kind today. Particularly, the population growth phenomenon in developing countries, diversity of foods, and their high consumption in the advanced countries have led to an increase in the global demand for food to an unprecedented level in the history [1]. The role of more productive, profitable agricultural production in fostering food security, generating

local employment, raising local incomes, and thus alleviating poverty particularly in developing world, where it serve as an economic source is incomparable to other economic sectors [2]. Cereals account for approximately two-thirds of all human energy intake and are grown on roughly half of the world's crop land [3]. It was reported that, eight cereal crops viz., wheat, rice, maize, barley, oat, rye sorghum and millets collectively accounts 99% of the world cereal production [4]. This also true for Ethiopia where the five major cereal crops; tef, maize, wheat, sorghum and barley have the largest share of cultivated land (92.72%) and production (95.8%) [5].

In 2011/2012 cropping season, out of the total grain crop area, 79.34% (9.59 million hectares) was under cereals, of which, wheat accounted for 15% (1.44 million hectares) of the grain crop area. In terms of production, cereals contributed 86.06% which is about 188.10 million quintals of the grain production. Among cereals, wheat accounts 15.5% (29.16 million quintal) grain [5]. The productivity of the crop remains low (1.8 ton ha⁻¹) in the country compared to the world average yield (3.19 ton/ha) [4]. The low yield per hectare was attributed by many factors, such as the increased costs of farm inputs, Biotic (Diseases, insect pests, and weeds) [6], changes in farming practices, and availability of quality seed for varieties that are high yielding.

Many wheat varieties have been released by national and regional research institutes that are adaptable to a wide range of environments for commercial production. However, those varieties are not widely distributed to all parts of the country. This is because of several constraints including the remoteness and inaccessibilities of the growing areas that limit the testing of adaptability and yields of these varieties.

Bore district in Guji Zone of Oromia region is one of the areas where improved varieties are not widely distributed. The potential of the area to wheat crop is not exploited due to lack of improved varieties, poor management practices, biotic factors (weeds, diseases and insect pests etc.) and a biotic factors (frost), rain fall variability (intensity as well as duration). As a result, there is no information on the adaptability and production of the improved bread wheat varieties in the area as most of the farmers are still using diseases susceptible cultivars [7]. It is therefore paramount to evaluate the varieties released by different research centers in Guji Zone to identify those that are high yielding and more adaptable for improved productivity and production. This should be done by analyzing the genetic variability which provides information that can be utilized to improve wheat yield through breeding. So, the study was conducted to address the following objectives:

- a) To estimate the extent of both genotypic and phenotypic variability in bread wheat genotypes
- b) To estimate the heritability and genetic advance under selection
- c) To study the degree of mutual association among yield and yield components

2. Materials and Methods

2.1. Descriptions of the Study Area

This study was carried out at Bore Agricultural Research Centre during 2013/14 cropping season. The research site was located some 7km from Bore district which is geographically located between 6°24'37" N latitude and 38°34'76" E longitudes. The research site represents highlands of Guji Zone with an altitude of 2736 m.a.s.l. receiving high rainfall and characterized by bimodal rainfall distribution which the first rainy season is from April up to October and the second season starts from late November and ends to the beginning of

March. The soil type of the site is mostly black cotton soils.

2.2. Plant Materials and Experimental Design

Twenty-five (25) bread wheat genotypes (Table 1) obtained from different Research Centers within the country. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications.

Each experimental plot was 5m long and 1.2m wide, with 6 rows 20cm apart, giving a gross plot area of 6m². Spacing for adjacent blocks 1.5 m and 1 m between plots were used. Sowing was done by hand drilling and covered lightly with soil. The seed and fertilizer rate were 150kg/ha seed; 41N and 46 P₂O₅ kg/ ha, respectively. All other agronomic practices were applied as recommended for wheat production [8].

Table 1. List and description of bread wheat genotypes.

No	Genotypes	Breeding Center*	Year of release	Adaptation area (altitude m.a.s.l)
	Shorima	KARC	2011	2100-2700
	Hoggana	KARC	2011	2200-2800
	Danda'a	KARC	2010	2000-2600
	Kulkulu	HU	2009	1790-2500
	Tosa	SRARC	2004	2400-300
	ETBW6217	KARC	NA	NA
	Digalu	KARC	2005	2300-2800
	ET-13A2	KARC	1981	2200-2900
	ETBW6250	KARC	NA	NA
	Pavon-76	KARC	1982	750-2500
	K6295-4A	KARC	1980	1900-2400
	Sofumar	SARC	1999/00	2300-2800
	ETBW6230	KARC	NA	NA
	Madda walabu	SARC	1999/00	1900-2800
	Hawi	KARC	1999/00	1800-2200
	Alidoro	HARC	2007	2200-2900
	Gasay	ADARC	2007	1890-2800
	Tay	ADARC	2007	1900-2800
	Huluka	KARC	2011	2200-2600
	ETBW6272	KARC	NA	NA
	Tuse	KARC	1997	2000-2500
	Bolo	DBARC	2009	2580-3100
	Senkegna	ADARC	2005	1900-2800
	Menze	DBARC	2007	2800-3100
	Dinkinesh	SRARC	2007	2400-3000

*KARC-Kulumsa Agricultural Research Center, SRARC-Sirinka Agricultural Research Center, DBARC-Debre-Birhan Agricultural Research Center, SARC-Sinana Agricultural Research Center, ADARC-Adet Agricultural Research Center and HARC-Holeta Agricultural Research Center. NA=Unavailable information for genotypes under variety trial (under variety release trial)

2.3. Data Collection

2.3.1. Data Recorded on Plot Basis

Data were collected for eight characters on plot basis (Days to heading, Days to maturity, grain filling period, Number of productive tillers/M², Biological yield, Harvest index, Thousand kernel weight and Grain yield). Four central rows of each plot in each replication were used for collecting data for those traits that has been recorded on plot basis.

2.3.2. Data Recorded on Plant Basis

Ten plants were selected randomly from the four central

rows of the plots before heading and tagged for recording the characters (Plant height, Number of tillers/plant, peduncle length, spike length, Number of spikelet's/spike and Kernels/spike).

2.4. Data Analysis

2.4.1. Analysis of Variance

The recorded data were subjected to analysis of variance (ANOVA) as suggested by [9] using SAS Software (Version 9.0). Mean separation was carried out using Least Significant Difference (LSD) at 5 percent levels of significance. The structure of ANOVA for RCBD is shown in Table 2.

Table 2. The structure of ANOVA table for RCBD.

Source of variation	DF	SS	MS	EMSS
Replication	r-1	SSr	Msr	$\sigma_r^2 + \sigma_e^2$
Genotype	g-1	SSg	Msg	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	SSe	Mse	σ_e^2
Total	rg-1	SST		

Where r and g represents number of replication and genotype respectively. DF=degree of freedom, SSr=sum of square due to replication, SSg=sum of square due to genotype, SSe=sum of square due to error, SST=sum square of total, Msr= mean square due to replication, Msg=mean square due to genotype, Mse=mean square due to error, EMSS=Expected mean square.

2.4.2. Phenotypic and Genotypic Variability

The variability present in the genotypes was estimated by simple measure, namely range, mean, standard error, phenotypic and genotypic variance and coefficient of variation. The phenotypic and genotypic variance and coefficient of variation were estimated according to the methods suggested by [10] as follows:

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

Where; $\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental (error) variance (Error mean square)

Mg=mean square of genotypes

Me=mean square of error,

r= Number of replication

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

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

Where x= population mean

2.4.3. Estimate of Heritability

Heritability specifies the proportion of the total variability that is due to genetic cause. Information on heritability provides the relative practicability of selection for a particular character. Different characters have different levels of heritability that can contribute for yield improvement in breeding programs. Heritability estimates classified as low

(<30%), moderate (30 -60%) and high (>60%) [11].

Heritability (H^2) for all characters was computed using the formula adopted by [12] as:

$$H^2 = \left[\frac{\sigma^2 g}{\sigma^2 p} \right] \times 100$$

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

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

$\sigma^2 p$ = phenotypic variance

$\sigma^2 e$ = error variance

2.4.4. Estimation of Expected Genetic Advance

Although high heritability estimates have been found to be effective in the selection of superior genotypes on the basis of phenotypic performance, [11] suggested that heritability estimates along with genetic advance will be more useful in predicting the effect for selecting the best individual. Genetic advance as part of the mean (GA) for each characters was computed using the formula adopted from [11] and [12]

$$GA = (k) (\sigma p) (H^2), \text{ and}$$

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

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

σp = phenotypic standard deviation

H^2 = heritability (Broad sense)

X= Grand mean

2.4.5. Estimation of Phenotypic and Genotypic Correlations

Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by [13].

$$r_{pxy} = \frac{COV_{pxy}}{\sqrt{\sigma^2 px \cdot \sigma^2 py}}$$

Where: r_{pxy} = phenotypic correlation coefficient between character x and y

COV_{pxy} = phenotypic covariance between character x and y

$\sigma^2 px$ = phenotypic variance for character x

$\sigma^2 py$ = phenotypic variance for character y

$$r_{gxy} = \frac{COV_{gxy}}{\sqrt{\sigma^2 gx \cdot \sigma^2 gy}}$$

Where; r_{gxy} = genotypic correlation coefficient between character x and y

COV_{gxy} = genotypic covariance between character x and y

$\sigma^2 gx$ = genotypic variance for character x

$\sigma^2 gy$ = genotypic variance for character y

The coefficient of correlation at phenotypic level was tested for their significance by comparing the values of correlation coefficient with tabulated r-value at g-2 degree of freedom,

where 'g' is number of genotypes. However, the coefficient of correlations at genotypic level was tested for significance using the formula described by [14]:

$$t = \frac{(rg_{xy})}{SE_{rg_{xy}}}$$

The calculated 't' value was compared with the tabulated 't' value at g-2 degree of freedom at 5% level of significance. Where, g= number of genotypes, rg_{xy}=genotypic correlation coefficient and SE_{rg_{xy}}=standard error of genotypic correlation coefficient between character x and y which was calculated as:

$$SE_{rg_{xy}} = \sqrt{\frac{(1 - r^2)^2}{2 H^2_x \cdot H^2_y}}$$

Where: SE_{rg_{xy}}=standard error of genotypic correlation coefficient between character x and y

H²_x =Heritability value of character x

H²_y =heritability value of character y

2.4.6. Path Coefficient Analysis

The direct and indirect effect of yield related traits on grain yield per plot has been analyzed through path coefficient analysis. This analysis was computed as suggested by [15] using the following formula:

$$r_{ij} = P_{ij} + \sum r_{ik} p_{kj}$$

Where: r_{ij}= mutual association between the independent (i) and dependent character (j) as measured by the correlation coefficient. P_{ij}= component of direct effects of independent character (i) and dependent character (j) as measured by the path coefficient and, $\sum r_{ik} p_{kj}$ = Summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent character (k). The residual effect was estimated by the formula:

$$\sqrt{1 - R^2}$$

Where: R²= $\sum p_{ij} * r_{ij}$

p_{ij}=component of direct effects of the independent character (i) and dependent character (j) as it has been measured by the path coefficient; r_{ij}=mutual association between the independent character (i) and dependent character (j) as it was measured by the correlation coefficient.

3. Result and Discussion

The results of analysis of variance for 14 characters are presented in Table 3. The results revealed that the mean squares due to genotypes were significant (P<0.05/0.01) for all characters. This indicates that the presence of appreciable differences among genotypes for all the characters studied and justifies carrying out further genetic analysis. Similar results were reported by [16]; [17]; [18]; [19] and [20] were reported

the presence of highly significant differences among the studied wheat genotypes for days to maturity, days to 50% flowering, days to heading, plant height, spike length, spikes per plant, grains/ spike, 1000 grain weight, harvest index, grain yield per plant. However, the present study results were in contrast to [21] findings who obtained non-significant differences for days to maturity, spike length, fertile tillers, spikelet per spike, grain per spike and grain yield per plot. Non-significant difference of bread wheat genotypes for grains per spike and grain yield was reported by [22] indicating that the studied genotypes were close to each other in terms of these traits.

Mean performance variations among genotypes

Phenological Characters

Range and mean values for the 14 characters are shown in Tables 4. The variation with respect to days to heading and days to maturity ranged from 69.33 days to 93 days, and 147.63 days to 172 days respectively, showing a wide range of variation among the genotypes for maturity. However, the results obtained were in contrast to the findings of [18] and [19] who reported the range of 16.40 days to 71 days and 59 days to 177 days for days to heading and days to maturity, respectively. The observed wide range of these characters may be due to the differences of environments where wheat genotypes were tested and may be due to the variability of materials used in this experiment (variety and lines).

Among the genotypes, ET-13A2, Alidoro and Menze were late for days to maturing followed by Huluka, ETBW6230 and K6295-4A which spend 172, 172, 171, 169, 162 and 161 days to mature respectively. Hoggana and Sofumar followed by Pavon-76 were early maturing genotypes both for days to maturity and days to heading. Late heading was recorded for ET-13A2 (93 days), Huluka (93 days) and ETBW6230 (90.33 days). In this experiment, early and late maturing coincided with early and late days of heading. The results are in line with the findings of [23]; [24] and [25], but in disagreement with the findings of [21] who reported that the two characters did not coincide with each other for most of the studied materials.

Growth Characters

A highly significant variability was seen among the genotypes for plant height, which ranged from 80.28 to 112.59 cm with the mean of 93.34 cm and coefficient of variation 4.14% (table 4). Comparative coefficient of variability (4.56%) was obtained by [21], but maximum coefficient of variability 27.64% and (10.68%) was reported by [23] and [24] respectively. Minimum plant height was observed in genotypes ETBW6217 (80.28cm) and Tosa (84.73), while, ET-13A2 (112.59cm), Alidoro (100.43) and Senkegna (100.38cm) exhibited maximum plant height, which can lead the genotypes to water-logging in areas with continuous rain fall such as the area where the present study was conducted.

The magnitude of genetic variability for peduncle length ranged from 35.2 to 50.1 cm with the mean value of 41.43 cm and coefficient variability of 3.5%. Maximum peduncle length was scored in genotype ET-13A2 (50.1 cm) while minimum was registered by Tuse (35.1 cm). The results of this

study indicates that, genotypes with longer peduncle length are more sensitive to water-logging than those with balanced peduncle length. This is because, the genotypes may not adequately with stand adverse weather conditions such as high rain, strong wind and hail. The problem may arise due to poor thickness of stem wall, quantity and intensity of mechanical tissue, quantity of vascular bundle, content of cellulose and lignin in stem cell wall, the amount of carbohydrate stored in stem, quantity of silicon and potassium and mapping quantitative trait loci for the lodging resistance [26].

Yield and Yield Components

Highly significant mean square was observed among genotypes for grain yield $t\ ha^{-1}$ (table 3). Variability of the genotypes was ranged from 3.75-7.83 with the mean value of 6.32 $t\ ha^{-1}$ and coefficient of variation 15.68%. The highest grain yield (7.83 $t\ ha^{-1}$) was recorded for Huluka followed by Kulkulu (7.75 $t\ ha^{-1}$). While low yield of 3.75 $t\ ha^{-1}$ was obtained from Tosa followed by Pavon-6 (4.41 $t\ ha^{-1}$). Highly significant mean square for grain yield was also reported by [27], [17], [16] and [19]. The study result also revealed that, highly significant Mean square of genotypes for number of productive tillers per meter. Maximum number of productive tillers per meter was recorded for Kulkulu (100), while minimum number was scored by Danda'a (64). Similar highly significant genetic variability was reported by [19]. However, the results of the present study do not agreed with the results obtained by [28] and [21] who reported non-significant mean squares for the character.

The tested Genotypes showed highly significant mean square for biological yield per plot (table 3). The variability was observed with the range of 6660 to 10805g with the mean value of 8964.73g and coefficient of variation 13.73%. Maximum biological yield per plot was recorded in Huluka (10805 g) and Digalu (10787g), while the minimum value was recorded for Tosa (6660g) and ETBW6217 (7018g). Highly significant mean squares for biological yield with high coefficient of variation which supplement the present result was also reported [21].

Harvest index exhibited significant mean square among

genotypes having the range of 0.34% to 0.46% with a mean value of 0.42% and coefficient of variation 9.13% with the highest value computed for Kulkulu and Tay (0.46%) and the lowest for Tosa (0.34%) followed by Hawi (0.36%) and Pavon-76 (0.37%). highly significant difference among bread wheat varieties having comparative harvest indices that ranged from 0.31% to 0.45% also reported by [25]. But non-significant mean square for this character was reported on bread wheat by [29]. The results of the present study show that the harvest index for most of the studied characters was >0.40 indicating that genotypes had high yields compared to the biological yield as harvest index (HI) is the proportion of grain yield to biological yield.

Analysis of variance revealed highly significant differences among genotypes for 1000 seed weight. The values for 1000 seed weight ranged from 25 to 46.67 g with a mean of 39.67g and coefficient of variability 10.58%. Accordingly, Danda'a, and Hoggana exhibited maximum 1000 seed weight of 46.67 and 46.67g, respectively, followed by genotype Alidoro (45g), while Tosa and Pavon-76 had minimum 1000 seed weight of 25g and 30g, respectively.

The present study result also revealed significant variability for the character tillers per plant, which ranged from 3.0 to 4.67 with mean of 3.77 and coefficient of variation of 18.8%.

The highest number of tillers per plant was recorded in the genotype shorima (4.67) while the lowest shown by ET-13A2. Highly significant difference among genotypes was also observed for Kernels per spike which ranged from 8.0 to 11.33, and mean 9.33 and coefficient of variation 4.97. The highest value was recorded for ET-13A2 (11.33) followed by Sofumar, Senkegna, MaddaW alabu, Tay and Alidoro having each a value of 10 kernels per spike. However, ETBW6217 exhibited the lowest number of kernels per spike. Spikelet per spike revealed highly significant difference among genotypes with a range of 15.33 to 20.67 with mean of 17.81 and coefficient of variation 5.15%. Among the tested genotypes ETBW6230 and Alidoro had shown maximum number of spikelet per spike (20.67 and 19.67) respectively where the lowest revealed by Hoggana (15) followed by K6295-4A (16) and Hawi (16).

Table 3. Mean squares from analysis of variance for the 14 characters of 25 bread wheat genotypes grown at Bore (2013/14).

Traits	Rep (Df=2)	Genotype (Df=24)	Error (Df=48)	CV (%)
Days to heading (days)	17.61*	66.41**	4.39	2.52
Days to mature (days)	43.21*	165.49**	10.29	2.05
Grain filling period (days)	6.33 ^{ns}	83.33**	5.96	3.33
Number of productive tillers/m (No)	176.85 ^{ns}	241.29**	90.69	11.96
Grain yield per hectare (tone)	0.86 ^{ns}	3.25**	0.98	15.68
Biological yield (kg/plot)	764410.57 ^{ns}	3927181**	1515824	13.73
Harvest index (%)	0.003 ^{ns}	0.0026*	0.001	9.13
Thousand seed weight (kg)	2.33 ^{ns}	69.44**	17.61	10.58
Tillers per plant (No)	0.17 ^{ns}	0.75**	0.3	14.42
Plant height (cm)	24.99 ^{ns}	119.42**	14.96	4.14
Kernel per spike (No)	0.49 ^{ns}	1.31**	0.22	4.97
Spikelet per spike (No)	0.49 ^{ns}	4.42**	0.84	5.15
Peduncle length (cm)	4.13 ^{ns}	37.25**	2.12	3.5
Spike length (cm)	0.16 ^{ns}	2.43**	0.29	6.71

*, ** & ns, significant at $P<0.05$, $P<0.01$ and non-significant, respectively

Estimates of Phenotypic and Genotypic Coefficient of Variation

Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances and phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in table 4. The phenotypic variance was greater than its corresponding genotypic variance (low magnitude of difference) for the phenological characters (days to heading, days to maturity and grain filling period), growth characters (plant height, peduncle length and spike length) and yield components (thousand seed weight, tillers per plant, number of kernels/spike and grain yield per hectare). This indicates the significant contribution of genotype, environment and their interaction in the phenotypic expression of these characters [30]. But, high magnitude of difference between phenotypic and genotypic variance was observed for the characters; number of productive tillers per meter, biological yield per plot, harvest index, 1000 seed weight. Results of the present study were in close agreement with those of [16] who reported relatively high phenotypic variance for days to maturity, plant height, spike length, 100 seed weight, and spikes per plant and grain yield but high difference for grains per spike and harvest index.

As indicated by the study result, environmental variation had large effect on the improvement of number of productive tillers per meter, grain yield per hectare, biological yield per plot, 1000 seed weight and tillers per plant which implies selection on phenotypic bases of these characters may not be effective for genetic improvement unless the environmental conditions under which the genotypes will be grown are optimized.

Phenotypic coefficient of variability ranged from 5.03% (days to maturity) to 20.85% (grain yield per hectare) (table 4). As per [31], moderate (10-20%) PCV and GCV was computed for grain yield per hectare, biological yield per plot, 1000 seed weight, tillers per plant and spike length, while low (<10%) for days to heading days to maturity, grain filling period, harvest index, plant height, kernels per spike, spikelet per spike and peduncle length. Highest PCV (>20%) was recorded for grain yield per hectare (20.85%). This reflect the marked influence of environmental factors for the expression of these characters. In other cases, low phenotypic coefficient of variability was observed for number of days to maturity (5.03%) and days to heading (6.01%). Similarly, [32] and [33] also reported moderate PCV and GCV for grain yield, 1000 seed weight and tillers per plant but low for days to heading, days to maturity, grain filling period and plant height. However, the results of this study does not agree with those of [19] who reported high PCV and GCV for grain filling period and number of tillers moderate for days to heading and plant height.

Genotypic coefficient of variability ranged from 4.59% (days to maturity) to 13.76% (grain yield per hectare). Grain yield/hectare followed by 1000 seed weight, spike length, tillers per plant and biological yield per plot exhibited

moderate genotypic coefficient of variability (13.76%, 10.48%, 10.44%, 10.22% and 10%) respectively. However, the low genotypic coefficient of variability was observed for days to maturity (4.59%) followed by days to heading (5.46%), Harvest index (5.54%), number of spikelet per spike (6.13%), plant height (6.32%), kernel per spike (6.46%), grain filling period (6.93%), peduncle length (8.22%) and number of productive tillers (8.9%) (Table 4).

Estimates of heritability

Heritability estimate for characters under study are shown in table 4. There was high heritability in peduncle length (84.67%) followed by days to maturity (83.41%), days to heading (82.48%), grain filling period (81.23), spike length (71.1%), plant height (69.95%) and kernels/spike (62.29%). These results clearly demonstrate that environment had low influence on the expression of the characters suggesting direct selection using these characters as major contributors of yield components. Spikelet per spike (58.69%), 1000 seed weight (49.52%), grain yield per hectare (43.57%), number of productive tillers/meter (35.63%), harvest index (35.33%), biological yield/plot (34.65%) and number of tillers/plant (33.33%) shows moderate level of heritability which may be due to influence of the environment on the polygenic nature of these trait. Low heritability was not found among the studied characters this indicates the possibility of including all the characters in order to select desirable genotypes. High level of heritability for days to heading, days to maturity, grain filling period, plant height, and grain yield/ plot and moderate heritability estimates for number spikelet's/spike and tillers per plant was also reported by [25].

Estimates of genetic advance

Genetic advance (as percent of mean) was classified as low (<10%), moderate (10-20%) and high (>20%) [31]. Based on this classification, it appears that none of the characters had highest genetic advance as percent of mean. But, most of the characters revealed moderate genetic advance as percentage of mean except spikelet per spike (9.69%), days to maturity (8.66%) and harvest index (6.80) that shows low genetic advance as percent of mean. High genetic advance as percent of mean for days to heading (35.65%), grain filling period (33.02%), number of tillers (44.52), 1000 seed weight (20.91%), grain yield (72.49%) and number of spikelet per spike (27.02%) where as moderate genetic advance as percent of mean for days to maturity (15.79%), plant height (19.81%) and number of grains per spike (13.67%) reported by [25].

High heritability accompanied with moderate genetic advance was observed in case of days to heading, grain filling period, plant height, kernels per spike, peduncle length and spike length. This indicates that most likely the heritability of these traits is due to additive gene effects and selection may be effective in early generations for these characters [17]. But moderate heritability with low genetic advance as percent of mean was obtained for harvest index and spikelet per spikelet (table 4).

Table 4. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as percent of mean for the 14 characters of bread wheat genotypes studied at Bore (2013/14)

	Range	Mean	SE	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	H (%)	GA	GA (%)
DH	69.33-93.00	83.31	1.185	25.06	20.67	4.39	6.01	5.46	82.48	8.52	10.23
DTM	143.67-172	156.57	1.815	62.02	51.73	10.29	5.03	4.59	83.41	13.55	8.66
GFP	67.67-87.67	73.27	1.381	31.75	25.79	5.96	7.69	6.93	81.23	9.44	12.89
NPT	64-100.33	79.61	5.387	140.89	50.20	90.69	14.91	8.90	35.63	8.72	10.96
Gy/ha	3.75-7.83	6.32	0.560	1.74	0.76	0.98	20.85	13.76	43.57	1.18	18.74
BY g/P	6660-10805	8964.73	696.465	2319609.77	803785.77	1515824.00	16.99	10.00	34.65	1088.76	12.14
HI	0.34-0.46	0.42	0.018	0.002	0.001	0.001	9.32	5.54	35.33	0.03	6.80
TSW	25.00-46.67	39.67	2.374	34.89	17.28	17.61	14.89	10.48	49.52	6.03	15.21
TPP	3.0-4.67	3.79	0.310	0.45	0.15	0.30	17.70	10.22	33.33	0.46	12.17
PHT	80.28-112.59	93.34	2.188	49.78	34.82	14.96	7.56	6.32	69.95	10.18	10.91
KPS	8.0-11.33	9.33	0.265	0.58	0.36	0.22	8.19	6.46	62.29	0.98	10.52
SkPs	15.33-20.67	17.81	0.518	2.03	1.19	0.84	8.01	6.13	58.69	1.73	9.69
PL (cm)	35.2-50.1	41.63	0.824	13.83	11.71	2.12	8.93	8.22	84.67	6.50	15.60
SL (cm)	6.15-9.88	8.09	0.305	1.00	0.71	0.29	12.38	10.44	71.10	1.47	18.16

Where: SE=Standard error of mean, σ^2_p =Phenotypic variance, σ^2_g =Genotypic variance, σ^2_e = environmental variance, PCV = phenotypic coefficient of variance, GCV = Genotypic coefficient of variation, H=Broad sense heritability, GA= genetic advance, GA (%) = Genetic advance as percent of mean, DH=Days to heading, DTM = Days to maturity, GFP= Grain filling period, NPT=Number of productive tillers, Gy/ha=Grain yield per hectare, BYg/P=Biological yield per plot, HI=Harvest index, TSW=Thousand seed weight, TPP=Tillers per plant, PHT=plant height, KPS=Kernels per spike, SkPs Number of spikelet per spike, PL=Peduncle length, SL= Spike length

Genotypic and Phenotypic Correlation Coefficients

Genotypic correlation coefficients of grain yield to other traits

Table 5 shows grain yield per hectare with varying trends of correlation with its components at genotypic level. Positive, but insignificant association of the character was observed with kernels/spike (0.108) and spikelet/spike (0.324). This result conforms to the findings of [34] but contrasts the findings of [35] who reported positive and negative non-significant correlation of grain yield with biological yield and harvest index, respectively. The results of this study demonstrate that genotypes with higher 1000 seed weight would produce more grain yield than those with lower 1000 seed weight. Similar results indicating positive and significant association of 1000 seed weight with grain yield was reported by [36] and [37].

The correlation of grain yield per hectare with plant height was positive and non-significant (0.192) while negative and non-significant was observed with, tillers per plant (-0.054), spike length (-0.072) and peduncle length (-0.131). Similar result, positive non-significant correlation of plant height with grain yield was also reported by [22].

In general, positive and significant association of grain yield with its component at genotypic level appears to reflect the presence of interaction among the characters in which a gene conditioning an increase in one character will also influence another character.

Genotypic correlation coefficients of among other traits

Phenological characters

Days to heading had positive and highly significant association with days to maturity (0.709**), where it exhibited positive and significant association with spikelet per spike (0.463**). But positive and non-significant correlation of this character was observed with grain filling period (0.106), biological yield per plot (0.338), harvest index (0.065), plant height (0.388), kernels per spike (0.321), peduncle length (0.118) and spike length (0.019) whereas the character was revealed negative non-significant association with number of productive tillers (-0.15), 1000 seed weight (-0.122) and tillers

per plant (-0.387). The result show that early heading genotypes have a probability to mature early with significant spikelet per spike setting that contribute for formation of better spike length, kernels per spike and harvest index. Similar results have been reported by [19] and [35] who found a highly significant association of days to heading with days to maturity and spikelet per spike, positive non-significant association of the character with plant height, spike length, biological yield and kernels per spike.

Results in table 5 show that days to maturity had positive and highly significant association with grain filling period (0.777**), while positive and significant association with plant height (0.517*), kernel per spike (0.454*) and spikelet/spike (0.558*). This indicates that genotypes that reach grain filling period early will have better chance to mature early having significant plant height, spikelet per spike and kernels per spike. Days to maturity had positive and non-significant correlation coefficient with harvest index (0.117), peduncle length (0.285), grain yield/hectare (0.278), biological yield (0.286) and 1000 seed weight (0.095) whereas it exhibited negative and non-significant correlation with number of productive tillers (-0.355), tillers/plant (-0.257) and spike length (-0.083). Negative non-significant correlation of days to maturity with tillers per plant and spike length was also reported by [35] whereas the result was contradicted with the finding of [16].

Grain filling period had positive and significant association with number of spikelet per spike (0.373*) and plant height (0.383*) where as positive and non-significant correlation with kernel per spike (0.353), biological yield per plot (0.101), harvest index (0.107), 1000 seed weight (0.243) and peduncle length (0.297) but exhibited negative and non-significant correlation with number of productive tillers (-0.366), tillers per plant (-0.016) and spike length (-0.134).

Growth characters

Plant height had positive and highly significant correlation with kernel per spike (0.977**) while positive and significant correlation with days to maturity (0.454*) and peduncle length

(0.617^{*}). It had positive and non-significant correlation with spikelet per spike (0.347) and spike length (0.120). But, the association of the character with the rest characters was negative and non-significant. However, [16] reported negative non-significant correlation of plant height with kernel per spike and spike length. Spike length had positive and non-significant correlation with days to heading, number of productive tillers, 1000 seed weight, plant height, kernel per spike and spikelet/spike but it had negative correlation with the rest of characters. Also found positive and non-significant correlation of spike length with tillers per plant, 1000 seed weight and spikelet per spike was also founded by [37]. Peduncle length had positive and significant correlation with plant height and kernels per spike indicating that the genotypes with longer peduncle length may also be longer in plant height with more number of kernels per spike (table 5).

Yield related characters

Spikelet/spike showed positive and significant correlation with days to maturity (0.558^{*}) and grain filling period (0.373^{*}) while shows non-significant correlation with the other characters which contradicts the findings of [19]. Number of kernel/spike correlated positively and highly significantly with plant height (0.977^{**}), positive and significant correlation with days to maturity (0.454^{*}) and peduncle length (0.617^{*}) but it had positive and non-significant correlation with days to heading (0.321), grain filling period (0.353), biological yield (0.187), 1000 seed weight (0.190), spike length (0.114) and spikelet per spike (0.249).

However, [17] reported strong positive correlation with number of productive tillers per plant, number of spikelet's per spike, spike length and number of grains per spike and strong negative association of the character with plant height.

Biological yield shows positive and non-significant correlation with harvest index (0.074), tillers per plant (0.209), plant height (0.276), kernels per spike (0.187), spikelet per spike (0.194) and peduncle length (0.05). Harvest index had displayed positive and non-significant correlation with days to heading (0.065), days to maturity (0.117), grain filling period (0.107), 1000 seed weight (0.464) and spikelet per spike (0.285) whereas negative and significant with number of productive tiller (-0.449^{*}) which was in close agreement with the finding reported by [23]. The character number of productive tillers had negative and significant correlation with harvest index (-0.449^{*}) and 1000 seed weight (-0.397^{*}). In other cases, this character exhibited positive and non-significant correlation with tillers per plant (0.358), spike length (0.107) and biological yield (0.049). Positive and significant association of the character with 1000 seed weight was reported by [17] whereas negative and non-significant association of number of fertile tillers with spike length and seed number per spike was reported by [28].

Phenotypic correlation coefficients of grain yield to other traits

Phenotypic correlation between yield and its components are presented in table 5. It is clear from these results that grain yield per hectare was positively and highly significantly correlated with biological yield (0.567^{**}), harvest index (0.752^{**}) and 1000 seed weight (0.552^{**}) whereas positively and significantly

correlated with spikelet/spike (0.296^{*}). Positive and non-significant association of grain yield was observed with tillers per plant (0.042) and kernels per spike (0.110).

The correlation of this character with days to heading, days to maturity, grain filling period was positive and non-significant (0.184, 0.184 and 0.094) respectively. This indicate that, increment in day of heading, day of maturity and grain filling period will not bring significant yield increment there by, selecting genotypes with early character is more effective than those with late heading, mature and grain filling that will leads to better yield improvement.

Grain yield was positively and significantly correlated with spike length (0.047^{*}) at phenotypic level that indicates, genotypes with long spike length will produce high grain yield than those with short spike length. Positive and significant association of the character was also observed with plant height (0.211^{*}).

Other authors were reported positive and non-significant correlation of grain yield with plant height, spike length, kernel per spike and 1000 seed weight [16] where as negative and non-significant correlation of grain yield with other characters was reported by [35].

Phenotypic correlation coefficients of among other traits

Other than grain yield, other characters also exhibited varying trends of association among themselves at phenotypic level as shown in table 5. Among phenological characters, days to heading was observed to be associated positively and highly significantly with days to maturity (0.707^{**}) where as positively and significantly correlated with biological yield per plot (0.271^{*}), plant height (0.339^{*}), kernels per spike (0.283^{*}) and spikelet per spike (0.365^{*}) that indicates genotypes with early heading could have a chance to mature early, high biological yield, high number of spikelet's and kernels per spike. Negative and significant association of days to heading was observed with number of productive tillers per meter (-0.121^{*}) and tillers per plant (-0.303^{*}). However the character was revealed positive and non-significant association with grain filling period (0.101), harvest index (0.005), peduncle length (0.142) and spike length (0.03). Highly significant association of days to maturity with days to flowering, plant height, and spike length, positive and significant with biomass but positively and non-significantly correlated with tillers per plant, peduncle length and grains per spike was reported by [38].

The number of productive tillers had negative and significant association with days to heading (-0.121^{*}), days to maturity (-0.261^{*}), grain filling period (-0.259^{*}) and 1000 seed weight (-0.258^{*}). Number of spikelet's per spike exhibited positive and significant correlation with days to heading (0.365^{*}), grain filling period (0.3^{*}), plant height (0.292^{*}) and peduncle length (0.267^{*}). Biological yield had positive and highly significant association with grain yield (0.567^{**}) but positive and significant correlation with days to heading (0.271^{*}), days to maturity (0.237^{*}), plant height (0.33^{*}) and 1000 seed weight (0.311^{*}) which was displayed positive and negative association with the other characters. Like that of spike length, tillers per plant was negatively and significantly correlated only with days to heading (-0.303^{*}) where as it had

displayed positive and negative association with the rest characters. Harvest index had positive and significant correlation with 1000 seed weight (0.433^{*}).

Kernels per spike had positive and highly significant

correlation with plant height (0.926^{**}) and peduncle length (0.583^{**}) whereas positively and significantly correlated with days to heading (0.283^{*}), grain filling period (0.301^{*}) and days to maturity (0.394^{*}) (Table 5).

Table 5. Genotypic (above diagonal) and phenotypic correlation coefficients for the 14 characters studied at Bore.

	DTH	DTM	GFP	NPT	Gy/ha	BY	HI	TSW	TPP	PH	KPS	SPPS	PL	SL
DTH		0.709**	0.106	-0.150	0.290	0.338	0.065	-0.122	-0.387	0.388	0.321	0.463	0.118	0.019
DTM	0.707**		0.777**	-0.355	0.278	0.286	0.117	0.095	-0.257	0.517*	0.454*	0.558*	0.285	-0.083
GFP	0.101	0.775**		-0.366	0.133	0.101	0.107	0.243	-0.016	0.383	0.353	0.373*	0.297	-0.134
NPT	-0.121*	-0.261*	-0.259*		-0.238	0.049	-0.449*	-0.397*	0.358	-0.191	-0.189	-0.318	-0.124	0.107
Gy/ha	0.184	0.184	0.094	-0.019		0.741**	0.719**	0.622*	-0.054	0.192	0.108	0.324	-0.131	-0.072
BY	0.271*	0.237*	0.091	0.180	0.567**		0.074	0.478*	0.209	0.276	0.187	0.194	0.050	0.000
HI	0.005	0.042	0.055	-0.200	0.752**	-0.103		0.464	-0.279	-0.026	-0.064	0.285	-0.274	-0.134
TSW	-0.142	-0.022	0.190	-0.258*	0.552**	0.311*	0.433*		-0.147	0.261	0.190	0.151	-0.104	0.032
TPP	-0.303*	-0.215	-0.032	0.318	0.042	0.216	-0.128	-0.141		-0.195	-0.183	-0.114	0.036	-0.149
PH	0.339*	0.461**	0.346*	0.028	0.211*	0.330*	-0.024	0.240*	-0.098		0.977**	0.347	0.617*	0.120
KPS	0.283*	0.394*	0.301*	-0.026	0.110	0.223	-0.054	0.163	-0.152	0.926**		0.249	0.644*	0.114
SPPS	0.365*	0.446*	0.300*	-0.056	0.296*	0.216	0.199	0.050	0.058	0.292*	0.185		-0.014	0.106
PL	0.142	0.282*	0.270*	-0.055	-0.080	0.083	-0.190	-0.046	0.052	0.583**	0.584**	-0.025		-0.089
SL	0.030	-0.065	-0.119	0.226	0.047*	0.110	-0.047	-0.042	0.039	0.131	0.091	0.267*	-0.059	

P<0.05*, P<0.01**

Where, DH= Days to heading, DTM = Days to maturity, GFP= Grain filling period, NPT=Number of productive tillers, Gy/ha=Grain yield per hectare, BYg/P=Biological yield per plot, HI=Harvest index, TSW=Thousand seed weight, TPP=Tillers per plant, PHT=plant height, KPS=Kernels per spike, SkPs=Number of spikelet per spike, PL=Peduncle length, SL= Spike length

Path Coefficient Analysis

Direct and indirect effects of various characters on grain yield at genotypic level

The results of path coefficient analysis at genotypic level (table 6) revealed that harvest index exerted the highest positive direct effect (0.7096) on grain yield followed by biological yield per plot (0.7060) and days to maturity (0.519). Similar results also reported by [39] and [40]. Whereas the lowest positive direct effect was shown by number of productive tillers per meter. In other cases, the highest negative direct effect was displayed by kernel per spike followed by days to heading and days to maturity.

Path coefficient results in table 6 also show that direct effect of spikelet's per spike on grain yield was negative (-0.0443) which was similarly reported by [37]. However, [19] reported positive direct effect of the character on grain yield. The indirect effects via days to maturity (0.2895),

biological yield (0.137), harvest index (0.202), plant height (0.161), tillers per plant (0.0025), peduncle length (0.0001) and spike length (0.0017) were found positive (table 6). The indirect effects of spikelet's per spike via days to heading (-0.173), grain filling period (-0.138), number of productive tillers (-0.0025), 1000-grain weight (-0.0136) and kernels per spike (-0.098) was negative. From the results obtained, it appears that kernels per spike had negative direct contribution on grain yield (-0.3945). The Indirect effect of this character via days to maturity, biological yield per plot, tillers per plant, plant height, and spike length were positive. However, negative indirect effects were recorded via days to heading, grain filling period, number of productive tillers per meter, harvest index, 1000 seed weight, and spikelet per spike and peduncle length. Number of productive tiller per meter had positive direct effect on grain yield (0.0079) (Table 6).

Table 6. Genotypic path coefficients of direct (main diagonal) and indirect effects of the 13 characters studied at Bore.

	DTH	DTM	GFP	NPT	BY	HI	TSW	TPP	PH	KPS	SPPS	PL	SL	Rg
DTH	-0.3745	0.3678	-0.0392	-0.0012	0.2388	0.0460	0.0110	0.0086	0.1798	-0.1265	-0.0205	-0.0005	0.0003	0.290
DTM	-0.2653	0.5190	-0.2877	-0.0028	0.2017	0.0828	-0.0085	0.0057	0.2396	-0.1789	-0.0247	-0.0011	-0.0013	0.279
GFP	-0.0396	0.4031	-0.3704	-0.0029	0.0710	0.0756	-0.0218	0.0004	0.1771	-0.1392	-0.0165	-0.0012	-0.0021	0.133
NPT	0.0563	-0.1843	0.1357	0.0079	0.0348	-0.3187	0.0356	-0.0080	-0.0883	0.0744	0.0141	0.0005	0.0017	-0.238
BY	-0.1267	0.1482	-0.0372	0.0004	0.7060	0.0522	-0.0430	-0.0046	0.1279	-0.0739	-0.0086	-0.0002	0.0000	0.741**
HI	-0.0243	0.0606	-0.0395	-0.0036	0.0519	0.7096	-0.0416	0.0062	-0.0120	0.0252	-0.0126	0.0011	-0.0021	0.719**
TSW	0.0457	0.0493	-0.0899	-0.0031	0.3377	0.3291	-0.0898	0.0033	0.1209	-0.0748	-0.0067	0.0004	0.0005	0.622**
TPP	0.1450	-0.1333	0.0060	0.0028	0.1475	-0.1978	0.0132	-0.0222	-0.0902	0.0722	0.0051	-0.0001	-0.0024	-0.054
PH	-0.1454	0.2686	-0.1417	-0.0015	0.1951	-0.0184	-0.0234	0.0043	0.4629	-0.3854	-0.0154	-0.0025	0.0019	0.199
KPS	-0.1201	0.2354	-0.1307	-0.0015	0.1322	-0.0453	-0.0170	0.0041	0.4522	-0.3945	-0.0110	-0.0026	0.0018	0.103
SPPS	-0.1733	0.2895	-0.1381	-0.0025	0.1369	0.2022	-0.0136	0.0025	0.1608	-0.0981	-0.0443	0.0001	0.0017	0.324
PL	-0.0440	0.1479	-0.1099	-0.0010	0.0353	-0.1946	0.0093	-0.0008	0.2857	-0.2541	0.0006	-0.0040	-0.0014	-0.131
SL	-0.0071	-0.0429	0.0495	0.0008	0.0000	-0.0954	-0.0029	0.0033	0.0557	-0.0450	-0.0047	0.0004	0.0160	-0.072

Residual effect=0.0205 where, DH= Days to heading, DTM = Days to maturity, GFP= Grain filling period, NPT=Number of productive tillers, BY=Biological yield, HI=Harvest index, TSW=Thousand seed weight, TPP=Tillers per plant, PHT=plant height, KPS=Kernels per spike, SkPs=Number of spikelet per spike, PL=Peduncle length, SL= Spike length, rg=Genotypic correlation.

Direct and indirect effects various characters on grain yield at phenotypic level

Phenotypic path coefficient analysis revealed that harvest index (0.7964) and biological yield (0.599) exerted high and favorable direct effects on grain yield. This justify that the presence of true relationship between these characters and grain yield, there by direct selection through these characters would result reasonable effect on grain yield. But, the highest negative direct effect on grain yield at phenotypic level was displayed by grain filling period (-0.4114) followed by days to heading (0.310). The highest positive indirect effect at this level was exerted by grain filling period and days to heading via days to maturity.

In other cases, the highest negative indirect effect on grain yield at phenotypic level was recorded by days to maturity via days to heading (-0.2192) followed by number of productive tillers through days to maturity. From the result, spikelet per spike had moderate positive significant correlation with grain yield ($r_p=0.296^*$) with its positive and negative indirect effects through other characters which counter balance each other and result in this moderate association with grain yield (Table 7).

Among the phenological characters, days to heading and grain filling period had exerted negative direct effect on grain yield (-0.31) and (-0.4114) respectively. The indirect effect of days to heading on grain yield via days to maturity, biological yield per plot, harvest index, peduncle length and spike length was positive but exerted negative indirect effect via other characters. Grain filling period had positive indirect effect on grain yield via days to maturity, biological yield per plot, harvest index, 1000 seed weight and peduncle length. Their indirect effects via days to maturity was highly positive (0.3989 and 0.4368) followed by biological yield (0.1622 and 0.0545) whereas low to negligible via other characters. However, the characters had negative indirect effect through the rest of characters (table 7). Positive direct effect of days to maturity on grain yield was observed again at phenotypic level (0.564).

Residual effects (0.1078) indicated that 14 characters included in the study explained 89.22% of the variability in grain yield. This further elaborates that the choice of yield attributing characters in the study was quite better, even if other characters are also needed to justify grain yield per hectare.

Table 7. Phenotypic path coefficients of direct (main diagonal) and indirect effects of the 14 characters studied at Bore.

	DTH	DTM	GFP	NPT	BY	HI	TSW	TPP	PH	KPS	SPPS	PL	SL	Rp
DTH	-0.3100	0.3989	-0.0414	-0.0063	0.1622	0.0042	-0.0130	-0.0061	-0.0035	-0.0043	-0.0025	0.0056	0.0004	0.184
DTM	-0.2192	0.5640	-0.3187	-0.0136	0.1418	0.0338	0.0040	-0.0044	-0.0048	-0.0060	-0.0030	0.0111	-0.0009	0.184
GFP	-0.0312	0.4368	-0.4114	-0.0135	0.0545	0.0437	0.0173	-0.0006	-0.0036	-0.0046	-0.0020	0.0106	-0.0016	0.094
NPT	0.0376	-0.1474	0.1066	0.0520	0.1076	-0.1595	-0.0235	0.0064	-0.0003	0.0004	0.0004	-0.0022	0.0031	-0.019
BY	-0.0839	0.1335	-0.0374	0.0093	0.5990	-0.0823	0.0284	0.0044	-0.0034	-0.0034	-0.0015	0.0033	0.0015	0.567**
HI	-0.0016	0.0239	-0.0226	-0.0104	-0.0619	0.7964	0.0394	-0.0026	0.0002	0.0008	-0.0013	-0.0074	-0.0006	0.752**
TSW	0.0440	-0.0121	-0.0781	-0.0134	0.1865	0.3447	0.0911	-0.0029	-0.0025	-0.0025	-0.0003	-0.0018	-0.0006	0.552**
TPP	0.0938	-0.1213	0.0131	0.0165	0.1291	-0.1020	-0.0128	0.0203	0.0010	0.0023	-0.0004	0.0020	0.0005	0.042
PH	-0.1050	0.2601	-0.1423	0.0014	0.1974	-0.0193	0.0219	-0.0020	-0.0103	-0.0141	-0.0020	0.0229	0.0018	0.211
KPS	-0.0878	0.2222	-0.1239	-0.0013	0.1337	-0.0432	0.0148	-0.0031	-0.0095	-0.0152	-0.0012	0.0229	0.0012	0.110
SPPS	-0.1133	0.2513	-0.1235	-0.0029	0.1297	0.1585	0.0045	0.0012	-0.0030	-0.0028	-0.0068	-0.0010	0.0036	0.296*
PL	-0.0441	0.1591	-0.1109	-0.0029	0.0496	-0.1510	-0.0042	0.0010	-0.0060	-0.0089	0.0002	0.0393	-0.0008	-0.080
SL	-0.0093	-0.0367	0.0488	0.0117	0.0659	-0.0371	-0.0039	0.0008	-0.0013	-0.0014	-0.0018	-0.0023	0.0136	0.047

Residual effect=0.1078 Where, DH= Days to heading, DTM = Days to maturity, GFP= Grain filling period, NPT=Number of productive tillers, BY=Biological yield, HI=Harvest index, TSW=Thousand seed weight, TPP=Tillers per plant, PHT=plant height, KPS=Kernels per spike, SkPs=Number of spikelet per spike, PL=Peduncle length, SL= Spike length, r_p =Phenotypic correlation

4. Summary and Conclusion

This study sought to estimate the extent of genotypic and phenotypic variability, heritability and genetic advance under selection and to determine the degree of mutual correlations among growth, yield and yield components in 25 bread wheat genotypes at Bore Agricultural Research Centre, during 2013/14 cropping season. The data recorded for 14 characters were subjected to analysis of variance and the results showed the presence of significant differences ($P<0.01/0.05$) among the tested genotypes for all traits indicating the presence of appreciable variability among the tested 25 bread wheat genotypes.

The ranges of mean values for most of the characters were large showing the existence of variations among the tested genotypes. Hoggana, Sofumar and Pavon-76 were found to

be early heading and maturing genotypes, while ET-13A2, Alidoro and Menze were late genotypes for both characters. These genotypes can be used whenever early and late maturing is becoming the objective of the breeding program. Huluka, Kulkulu, Digalu, Danda'a and Alidoro were the promising high yielding genotypes which can be considered for future cultivation to increase production and productivity of the crop in the District.

Results of the estimates of variance component showed that, phenotypic variance was relatively greater than its corresponding genotypic variance for the phenological characters (days to heading, days to maturity and grain filling period), growth characters (plant height, peduncle length and spike length) and yield components (thousand seed weight and number of kernels/spike). This shows the pronounced contribution of environmental factors than genotype in the phenotypic expression of these characters.

High genotypic variance as compared to environmental variance was observed for days to heading, days to maturity, grain filling period, biological yield per plot, plant height, kernels per spike spikelet per spike, peduncle length and spike length indicating that phenotypic variation among the genotypes was due mainly to variation between genotypes as they differ in several parameters.

From this study, it was observed that, PCV values were higher than that of GCV for the characters number of productive tillers per meter, grain yield per hectare, harvest index, tillers per plant, 1000 seed weight, yield and spikelet per spike studied. This reflect the marked influence of environmental factors for the expression of these characters and there by selection based on these characters may not significantly effective for genetic improvement.

High heritability estimates were observed for peduncle length followed by days to maturity, days to heading and grain filling period. This result indicates that, it is reliable to improve yield through direct selection using these traits as major contributors of yield components.

High heritability accompanied with moderate genetic advance was observed in case of days to maturity, days to heading, grain filling period and peduncle length. This indicates that most likely the heritability of these characters is due to additive gene effects.

Correlation analysis among the characters studied revealed that positive and significant association of yield and its component were more explained at phenotypic than genotypic level. This implies that the correlations of these traits are reasonably expressed as a result of environmental factors rather than their genetic characteristics. Among the characters, days to maturity, grain filling period, biological yield per plot and harvest index were positively and highly significantly correlated with grain yield both at genotypic and phenotypic level. The significant positive correlations between grain yield and its components at genotypic and phenotypic level indicated that these characters contributed positively towards yield, and should be considered when selecting for high grain yield.

Path coefficient analysis revealed that harvest index exerted the highest positive direct effect on grain yield followed by biological yield per plot at both genotypic and phenotypic levels.

This justifies that the presence of true relationship between these characters and grain yield, there by direct selection through these characters would result reasonable effect on grain yield. In other cases, the highest negative direct effect on grain yield at genotypic level was exerted by kernels per spike followed by days to heading and grain filling period. At phenotypic level, grain filling period was exerted highest positive indirect effect on grain yield via days to maturity that counter balance its negative direct effect.

In general, the present study showed the presence of considerable variability among the tested wheat genotypes and the possibility of improving yield and other desirable traits through selection. The study also revealed the importance of considering other traits in the process of

selection genotypes for yield.

Acknowledgements

The authors greatly indebted to thank Oromia Agricultural Research Institute (IQOO) for the financial support for this study. In addition, Bore agricultural Research Center administration and staff are also highly appreciated for facilitating the finance allocated for this research and for their cooperation during the execution of the work.

References

- [1] Khabiri E., Imani A. A., and Shahbazi H. 2012. Studying the grain yield and yield components in advanced rain fed wheat genotypes. *Scholars Research Library. Annals of Biological Research*, 3 (12): 5647-5650.
- [2] Reeves, T. G., S. Rajaram, M. van Ginkel, R. Trethowan, H. J. Braun and K. Cassaday, 1999. *New Wheat's for a Secure, Sustainable Future*. Mexico, D. F. CIMMYT.
- [3] USAID (United States Agency for International Development), 2013. Feed the future food security innovation center. Accessed on March, 2014. Web site: <http://www.feedthefuture.gov/research>.
- [4] FAO (Food and Agriculture Organization of the United Nations), 2011. FAOSTAT: World Crop production data. Accessed on 16 December, 2014. Available at: (<http://www.faostat.fao.org/site>)
- [5] CSA (Central Statistical Agency), 2012. Crop production forecast sample survey, 2012/13. Report on Area and Crop Production forecast for Major Crops (for private Peasant Holdings 'Meher' season). Addis Ababa, Ethiopia.
- [6] Alemayehu Hailu Wolderufael, Getaneh Woldeab Wolderufael, Woubit Dawit Bedane, Endale Hailu Abera. Evaluation of Bread Wheat Varieties to Dominant Races of Stem Rust (*Puccinia Graminis f. sp. Tritici*) Pathogen. *Science Innovation*. Vol. 3, No. 6, 2015, pp. 121-126. doi: 10.11648/j.si.20150306.20
- [7] Tolessa Taye, Chemada Fininsa, Getaneh Woldeab. Importance of Wheat Stem Rust (*Puccinia Graminis F. Sp. Tritici*) in Guji Zone, Southern Ethiopia. *Plant*. Vol. 2, No. 1, 2013, pp. 1-5. doi: 10.11648/j.plant.20140201.11
- [8] Ministry of Agriculture, 2011. Animal and plant Health Regulatory Directorate. *Crop variety Register Issue No. 14*. Addis Ababa, Ethiopia.
- [9] Gomez, K. A. and A. A. Gomez. 1984. *Statistical Procedures for Agricultural Research, 2nd edit*. John Wiley and Sons, New York.
- [10] Burton, G. W. and E. H. Devane, 1953. Estimating heritability in Tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* 45: 487-488.
- [11] Johnson, H. W., Robinson, H. F., and Comstock, R. E., 1955. Genotypic and phenotypic correlations and their implication in selection. *Agronomy Journal* 47: 477-483.
- [12] Allard, R. W., 1960. *Principles of Plant Breeding*. John Wiley and Sons. Inc. New York.

- [13] Miller, P. A., J. C. Williams, H. F., Robinson and R. E., Comstock, 1958. Estimates genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agronomic Journal*, 50: 126-131.
- [14] Robertson, G. E. 1959. The sampling variance of the genetic correlation coefficient. *Biometrics* 15: 469-485.
- [15] Dewey, D. R., and K. H. Lu., 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51: 515-518.
- [16] Majumder DAN, Shamsuddin AKM, Kabir MA, Hassan L, 2008. Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. *J. Bangladesh Agric. Univ.* 6 (2): 227-234.
- [17] Ali, Y., Barbar, M. A., Javed A., Philippe M., and Zahid L., 2008. Genetic variability, Association and diversity Studies in Wheat (*Triticum aestivum* L.) Germplasm. *Pak. J. Bot.*, 40(5): 2087-2097.
- [18] Ullah K., Khan S. J., Irfaq M., Muhammad T., and Muhammad S., 2011. Genotypic and phenotypic variability, heritability and genetic diversity for yield components in bread wheat (*Triticum aestivum* L.) germplasm. *African Journal of Agricultural Research* Vol. 6(23): 5204-5207.
- [19] Degewione A., Dejene T., and Sharif M., 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. *International Research Journal of Agricultural Sciences* Vol. 1(2): 19-29.
- [20] Wani B., Yasin A., Ali M., Pandith A., and Mir R., 2013. Seedling vigour in wheat (*Triticum aestivum* L.) as a source of genetic variation and study of its correlation with yield and yield components. *African Journal of Agricultural Research* 8 (4): 370-372.
- [21] Khan S. A., 2013. Genetic Variability and Heritability Estimates in F2 wheat Genotypes. *International Journal of Agriculture and Crop Sciences* 5 (9): 983-986.
- [22] Salih Hadi Farhood Al-salim, Reem Al-edelbi, Hassin kassar, Hayder Najm Abed. Evaluation of the Variations of Some Traits among Entries Genotypes of Bread Wheat (*Triticum aestivum* L.) and Their Relationship with Grain Yield. *International Journal of Applied Agricultural Sciences*. Vol. 1, No. 3, 2015, pp. 79-83. doi: 10.11648/j.ijaas.20150103.16
- [23] Kotal B. D., Das A., and Choudhury B. K., 2010. Genetic variability and association of characters in wheat (*Triticum aestivum* L.). *Asian journal of crop science* 2(3): 155-160.
- [24] Verma PN., B N Singh, and R K Yadav, 2013. Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (*T. Aestivum* L.). *International Journal of Agricultural Sciences: Vol. 3 (2):*. 395-399.
- [25] Demelash A. L., Desalegn T., and Alemayehu G., 2013. Genetic variation of bread wheat (*Triticum aestivum* L.) genotypes based on number of phenological and morphological traits at Marwold Kebele, Womberma Woreda and West Gojam. *Wudpecker Journal of Agricultural Research* 2(6): 160-166.
- [26] Tripathi, S. C., K. D. Sayre, J. N. Kaul and R. S. Narang. 2003. Growth and morphology of spring wheat culms and their association with lodging: effects of genotypes, N levels and ethephon. *Field Crops Res.* 84(3): 271-290.
- [27] Cheema N. M, Mian, M. A, Rabbani M. I. G and Mahmood A., 2006. Studies on Variability and Some Genetic Parameters in Spring Wheat. *Pak. J. Agri. Sci.* 43(1-2): 32-35.
- [28] Mollasadeghi V., Elyasi S., and Mirzamasoumzadeh B., 2012. Genetic variation of 12 bread wheat genotypes based on number of phenological and morphological traits. *Annals of Biological Research*, 3 (10): 4734-4740.
- [29] Khan M. A. U, Malik T., Abbas S. J, Abbas Z., Khan A., Malik M., Asghar S., 2011. Study of genetic variability and correlation among various traits of F5 wheat (*Triticum aestivum* L.) populations. *International Research Journal of Agricultural Science and Soil Science* Vol. 1(8): 344-348.
- [30] Bruce Walsh, 2002. Quantitative Genetics, Genomics and the Future of Plant Breeding. Quantitative Genetics, Genomics and Plant Breeding. Edited by Manjit S. Kang. *Louisiana USA*.
- [31] Sivasubramanian, V. and Madhavamenon, P., 1973. Path analysis for yield and yield components of rice. *Madras Agric. J.* 60: 1217-1221.
- [32] Kumar S, Singh D, Dhivedi VK, 2010. Analysis of yield components and their association in wheat for architecturing the desirable plant type. *Indian J. Agric. Res.* 44(4): 267-273.
- [33] Baranwal D. K., Mishra V. K., Vishwakarma M. K., Yadav P. S. and Arun B., 2012. Studies on Genetic Variability, Correlation and Path Analysis for yield and yield contributing traits in Wheat (*T. Aestivum* L. Em Thell.). *Plant Archives* 12 (1): 99-104.
- [34] Ali S., Shah A. S. A, Hassnain A. Shah Z., and Munir I., 2007. Genotypic variation for yield and morphological traits in wheat. *Sarhad J. Agric.* Vol. 23, No. 4.
- [35] Kumar B., Singh C. M., and Jaiswal K. K., 2013. Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). *An international quarterly journal of life science*. The Bioscan 8(1): 143-147.
- [36] Kalimullah S. J. K., Irfaq M., and Rahman H. U., 2012. Genetic Variability, Correlation and Diversity Studies in Bread Wheat (*Triticum aestivum* L.) Germplasm. *The Journal of Animal & Plant Sciences*, 22(2): Pp.: 330-333.
- [37] Iftikhar R., Khaliq I., Ijaz M., and Rashid M. A. R., 2012. Association Analysis of Grain Yield and its Components in Spring Wheat (*Triticum aestivum* L.). *American-Eurasian J. Agric. & Environ. Sci.*, 12 (3): 389-392.
- [38] Gelalcha S. and R. R. Hanchinal, 2013. Correlation and path analysis in yield and yield components in spring bread wheat (*Triticum aestivum* L.) genotypes under irrigated condition in Southern India. *African Journal of Agricultural Research* 8(24): 3186-3192.
- [39] Ali, IH and Shakor, EF, 2012. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. *Mesopotamia J. Agric.* 40(4): 27-39.
- [40] Peymaninia Y, Valizadeh M, Shahryari R, Ahmadizadeh M, Habibpour M (2012). Relationship among morpho-physiological traits in bread wheat against drought stress at presence of a Leonardite derived humic fertilizer under greenhouse condition. *Int. Res. J. Appl. Basic Sci.* 3(4): 822-830.