Global Journal of Science Frontier Research: D
Agriculture and Veterinary
Volume 16 Issue 7 Version 1.0 Year 2016
Type : Double Blind Peer Reviewed International Research Journal
Publisher: Global Journals Inc. (USA)
Online ISSN: 2249-4626 & Print ISSN: 0975-5896

Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Bread Wheat (*Triticum Aestivum L.*) Genotypes

By Birhanu Mecha, Sentayehu Alamerew, Alemayehu Assefa, Ermias Assefa & Dargicho Dutamo

Wachemo University

Abstract- Sixty four wheat genotypes were tested in 8x8 simple lattice design at Ginchi, West Shewa in 2012/13 cropping season. The overall objective was to study the extent of genetic variability, heritability and genetic advance. Analysis of variance revealed that there was a significant difference among the sixty four genotypes for all the characters studied. The phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for all the traits studied. Medium phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were recorded for plant height, number of kernels per spike, thousand kernels weight, grain yield per plot, biomass yield per plot and harvest index. Medium phenotypic coefficients of variation (PCV) and low genotypic coefficients of variation (GCV) values were displayed for days to heading.

Keywords: PCV, GCV, heritability, genetic advance.

GJSFR-D Classification : FOR Code: 079999

Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Bread Wheat (*Triticum Aestivum L.*) Genotypes

Birhanu Mecha[α], Sentayehu Alamerew[σ], Alemayehu Assefa[ρ], Ermias Assefa[ω] & Dargicho Dutamo[¥]

Abstract- Sixty four wheat genotypes were tested in 8x8 simple lattice design at Ginchi, West Shewa in 2012/13 cropping season. The overall objective was to study the extent of genetic variability, heritability and genetic advance. Analysis of variance revealed that there was a significant difference among the sixty four genotypes for all the characters studied. The phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for all the traits studied. Medium phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were recorded for plant height, number of kernels per spike, thousand kernels weight, grain yield per plot, biomass yield per plot and harvest index. Medium phenotypic coefficients of variation (PCV) and low genotypic coefficients of variation (GCV) values were displayed for days to heading. Low phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values were recorded for days to maturity, spike length, number of spikelets per spike and hectoliter weight (test weight), which suggests the limitation of selection for these traits. High heritability values were observed in all the characters studied. The expected genetic advance as a percent of mean ranged from 7.4 to 25.93 9. Characters with a high genetic advance as a percent of mean allow the improvement of this character through selection.

Keywords: PCV, GCV, heritability, genetic advance.

I. INTRODUCTION

Bread wheat (*Triticum aestivum* L. em Thell. 2n=6x=42), a self-pollinating annual plant in the true grass family *Gramineae* (*Poaceae*), is largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi *et al*., 2012). It is one of the most important export and strategic cereal crop in the world and in Ethiopia in terms of production and utilization (Ranjana and Kumar, 2013). It has been described as the 'King of cereals' because of the largest hectare it occupies, high productivity and the observable position it holds in the international food grain trade (Shashikala, 2006). The Food and Agriculture Organization of the United Nations (FAO) gracefully project the worldwide acclaim sticking with wheat as human food and the International Maize and Wheat Improvement Center (CMMYT) have chosen a wheat spike symbol in their logo with the description "Let there be bread." It is a major source of energy, protein and dietary fiber in human nutrition (Rizwana *et al*., 2010).

In Ethiopia, wheat is grown at an altitude ranging from 1500 to 3000 meters above sea level, between 6-16^0 N latitude and 35-42^0 E longitude. The most suitable agro- ecological zones, however, fall between 1900 and 2700 masl (Tefera, 2012). The major wheat producing areas in Ethiopia are located in Oromiya (Arsi, Bale, Shewa, Ilubabor, and Western Hareghe), in SNNPR (Hadiya, Sidamo, Silite, Guraghe, Kambata), Tigray, Amhara (Northern Gondar and Gojam zones) (Zerihun *et al.,* 2012). Wheat is the third most important small cereal crops in Ethiopia in terms of cultivated land, food value and number of smallholders engaged in production after Tef *(Eragrostis tef* L.*)* and Maize (*Zea mays* L.).

For a successful breeding program, the presence of genetic variability plays a vital role. It is true that the more diverse plants, the greater chance of exploiting high heterotic crosses or to generate productive recombinants and broad variability in segregating generations during genetic improvement (Mohammadi and Prasanna, 2003; Verma *et al.,* 2013). Rauf *et al.* (2012) stated that precise knowledge about germplasm diversity and genetic relationship among breeding materials is a pre-requisite for crop improvement programs as it helps in the development of superior recombinants. Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, pest and disease resistance (Ferdous *et al*., 2011).

Genetic divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal, 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Hailegiorgis *et al*., 2011).

Author α: Wachemo University, College of Agricultural Sciences, Hosanna, Ethiopia
Author σ: Jimma University, College of Agriculture and Veterinary Medicine, Ethiopia.
Author ρ: Ethiopian Institute of Agricultural Research (EIAR); Addis Ababa, Ethiopia.
Author ω: Southern Agricultural Research Institute, Ethiopia, Jimma University, College of Agriculture and Veterinary Medicine, Ethiopia.
e-mail: ethioerm99@gmil.com
Author ¥: Mizan-Tepi University, college of Agriculture and natural resources, Mizan Teferi, Ethiopia.

To make an effective selection for grain yield, understanding the genetic variability, heritability and genetic advance as percent of mean as well as the association of grain yield with yield contributing characters is important. In addition, to evolve superior genotype for further hybridization and selection it is important to get precise information on the nature and degree of genetic diversity present in wheat collections from principal areas of cultivation. Existence of genetic diversity is very essential to meet the present and future crop breeding challenges. It is a prerequisite for the development of improved cultivars with wider adaptability and broad genetic base (Hailu, 2011). Currently, large numbers of bread wheat accessions were introduced from CIMMYT through bread wheat improvement program of Ethiopian Agricultural Research Institute (EIAR). So far, little or no information is generated about genetic variability, divergence and character associations between yield and yield contributing characters in these exotic bread wheat genotypes in Ethiopia. Hence, the present study was undertaken with the objectives of to estimate the extent of variability, heritability and genetic advance.

II. MATERIALS AND METHODS

a) Description of the study area

The experiment was conducted at Ginchi, West Shewa in 2012/13 cropping season. Ginchi Agricultural Research Sub Center is located at an altitude of 2240 meters above sea level, 84 kilometers (kms) to the West of Addis Ababa, and at a Latitude and Longitude of 09°03'N and 38°15'E, respectively. It is the center where the cereal crops like Teff, barley and wheat are grown. The maximum and minimum temperatures of the area are 24.72°C and 8.76°C, respectively, whereas the mean annual rainfall is 1080.4mm. The major soil types are black (Vertisol) and clay loam with pH of 6.4, which is heavy clay with 0.91-1.32% organic matter (HARC, Soil Analysis and Plant Physiology Team, 2012).

b) Experimental Materials

A total of sixty four bread wheat (*Triticum aestivum L.*) genotypes that include three standard checks and sixty one exotic bread wheat accessions introduced from CIMMYT were included in this study. The accessions were obtained kindly from HARC. The three released cultivars Digelu, Alidoro and Meraro were used as a standard checks. They were selected based on their agronomic performances and suitability to the growing conditions (Table 1).

The details of the genotypes used in the experiment are given in Table 2.

Table 1 : List of genotypes used in the study

Entry	Pedigree	Seed source	Entry	Pedigree	Seed source
1	CIMMYTOB/2	CIMMYT	33	CIMMYTOB/65	CIMMYT
2	CIMMYTOB/7	CIMMYT	34	CIMMYTOB/66	CIMMYT
3	CIMMYTOB/14	CIMMYT	35	CIMMYTOB/67	CIMMYT
4	CIMMYTOB/22	CIMMYT	36	CIMMYTOB/68	CIMMYT
5	CIMMYTOB/23	CIMMYT	37	CIMMYTOB/70	CIMMYT
6	CIMMYTOB/24	CIMMYT	38	CIMMYTOB/71	CIMMYT
7	CIMMYTOB/25	CIMMYT	39	CIMMYTOB/75	CIMMYT
8	CIMMYTOB/27	CIMMYT	40	CIMMYTOB/76	CIMMYT
9	CIMMYTOB/29	CIMMYT	41	CIMMYTOB/77	CIMMYT
10	CIMMYTOB/32	CIMMYT	42	CIMMYTOB/78	CIMMYT
11	CIMMYTOB/33	CIMMYT	43	CIMMYTOB/79	CIMMYT
12	CIMMYTOB/35	CIMMYT	44	CIMMYTOB/80	CIMMYT
13	CIMMYTOB/39	CIMMYT	45	CIMMYTADT/1	CIMMYT
14	CIMMYTOB/40	CIMMYT	46	CIMMYTADT/2	CIMMYT
15	CIMMYTOB/41	CIMMYT	47	CIMMYTADT/3	CIMMYT
16	CIMMYTOB/44	CIMMYT	48	CIMMYTADT/4	CIMMYT
17	CIMMYTOB/45	CIMMYT	49	CIMMYTADT/5	CIMMYT
18	CIMMYTOB/48	CIMMYT	50	CIMMYTADT/6	CIMMYT
19	CIMMYTOB/49	CIMMYT	51	CIMMYTADT/7	CIMMYT
20	CIMMYTOB/50	CIMMYT	52	CIMMYTADT/8	CIMMYT
21	CIMMYTOB/51	CIMMYT	53	CIMMYTADT/9	CIMMYT
22	CIMMYTOB/52	CIMMYT	54	CIMMYTADT/11	CIMMYT
23	CIMMYTOB/53	CIMMYT	55	CIMMYTADT/13	CIMMYT
24	CIMMYTOB/54	CIMMYT	56	CIMMYTADT/15	CIMMYT
25	CIMMYTOB/57	CIMMYT	57	CIMMYTADT/16	CIMMYT
26	CIMMYTOB/58	CIMMYT	58	CIMMYTADT/17	CIMMYT
27	CIMMYTOB/59	CIMMYT	59	CIMMYTADT/19	CIMMYT
28	CIMMYTOB/60	CIMMYT	60	CIMMYTADT/20	CIMMYT
29	CIMMYTOB/61	CIMMYT	61	CIMMYTADT/21	CIMMYT
30	CIMMYTOB/62	CIMMYT	62	ALIDORO	HARC
31	CIMMYTOB/63	CIMMYT	63	MERARO	KARC
32	CIMMYTOB/64	CIMMYT	64	DIGELU	KARC

c) *Experimental Design and Trial Management*

The experiment was carried out in 8x8 Simple Lattice Design at random. The genotypes were grown under uniform rain fed conditions. The plot size was six rows of 2.5 m length with 0.2 m row spacing i.e. 1.2 m x 2.5 m = $3m^2$ (standard plot size for variety trial). Planting was done by hand drilling on July 06, 2012. Seed rate was 150 kg/ha (45g/plot). Recommended fertilizer rate of 100/100 kg/ha N/P_2O_5 in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing. For data collection, the middle four rows were used ($2m^2$ area). The central four rows were harvested for grain yield and biomass yield from each plot leaving boarder rows to avoid boarder effects. All other agronomic practices were undertaken uniformly to the entire plot as recommended for wheat production in the area during the growing season to raise a healthy crop.

d) *Description of Data Collected*

The data on the following attributes was collected on the basis of the central four rows in each plot per replication.

Days to 50% heading (DH): The numbers of days from sowing to 50% of plants have started heading.

Days to 75% maturity (DM): The numbers of days from date of sowing to a stage at which 75% of the plants have reached physiological maturity or 75% of the spikes on the plots turned golden yellow color.

Grain filling period: The grain filling period in days was computed by subtracting the number of days to heading from the number of days to maturity.

Thousand Kernels weight (TKW): The weight (g) of 1000 kernels from randomly sampled seeds per plot measured by using sensitive balance. It was the weight (gm) of 1000 kernel estimated by counting 1000 seeds randomly drawn from the grain yield of each plot.

Grain yield per plot (GYP): The grain yield per plot was measured in grams using sensitive balance after moisture of the seed is adjusted to 12.5%. Total dry weight of grains harvested from the middle four rows out of six rows was taken as grain yield per plot and expressed as grams per plot.

Biomass yield per plot (BMYP): It was recorded by weighing the total above ground yield harvested from the four central rows of each experimental plot at the time of harvest.

Harvest index (%): It was estimated by dividing grain yield per plot to biological yield per plot. It is ratio of grain yield to the above ground biomass yield.

Hectoliter weight (HLW): It is grain weight of one hectoliter volume random sample of wheat grain for each experimental plot expressed by (kg/ha).

Plant height (cm): The average height (cm) of ten randomly taken plants at the maturity time from the middle four rows of each plot of the replication was measured from the ground level to the top of the spike excluding the awn.

Number of productive tillers per plant: The numbers of tillers per plant bearing productive heads were counted at the time of harvest and average was recorded for the ten randomly taken plants from the middle four rows.

Spike length (cm): The average spike length of ten randomly taken plants from the base of the main spike to the top of the last spikelet excluding awns was recorded in centimeter from four central rows of each plot.

Number of spikelets per spike: Total numbers of spikelets on main spike of all ten plants from four central rows were counted at the time of maturity and average was recorded.

Number of kernels per spike (NKPS): Total number of grains in the main spike were counted at the time of harvest from ten randomly taken plants and expressed as average and recorded from four central rows of each plot.

e) *Statistical Analysis*

i. *Analysis of variance (ANOVA)*

The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2, (SAS Institute, 2008) after testing the ANOVA assumptions.

The Mathematical Model for Simple Lattice Design is:

$$Y_{ijr} = \mu + A_r + G_{ij} + B_{ir} + B_{jr} + e_{ijr},$$

where Y_{ijr} = the value observed for the plot in the r^{th} replication containing the genotype G_{ij}, μ = grand mean, G_{ij} = genotype effect in the i^{th} row & j^{th} column, A_r = replication effect, B_{ir} = i^{th} block effect, B_{jr} = j^{th} block effect, e_{ijr}, = the plot residual effect*

ii. *Analysis of genetic parameters*

a. *Estimation of phenotypic and genotypic coefficient of variation*

The phenotypic and genotypic variances and coefficients of variation were estimated according to the method suggested by (Singh and Chaudhary, 1999) as follows:

Environmental variance ($\sigma^2 e$)

$$\sigma^2 e = MSe$$

Genotypic variance (σ^2 g)

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

Where, r = number replication, MSg = mean square due to accessions and MSe = mean square of error (Environmental variance).

Phenotypic variance (σ^2p)

$$\sigma^2\mathbf{P} = \sigma^2\mathbf{g} + \sigma^2 e$$

Where, σ^2g = genotypic variance and $\sigma^2 e$ = mean square of error (Environmental variance).

Phenotypic coefficient of variation (PCV)

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

Where, σ^2P = phenotypic variance and $\bar{X}$ = mean of the character being evaluated.

Genotypic coefficient of variation (GCV)

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

Where, σ^2g = genotypic variance and $\bar{X}$ = mean of the character.

iii. *Heritability (in the broad sense)*

Heritability in the broad sense for quantitative characters was computed using the formula suggested by (Allard, 1999) as:

$$\mathbf{H} = \frac{\sigma^2\mathbf{g}}{\sigma^2\mathbf{P}} \times 100$$

Where, H= heritability in the broad sense, σ^2g = genotypic variance and σ^2P = phenotypic variance.

iv. *Genetic advance expected (GA)*

The genetic advance expected under selection assuming selection intensity of the superior 5% of the plants was estimated in accordance with the methods illustrated by (Allard, 1999):

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

Where, GA = expected genetic advance, H = heritability in the broad sense, K = the selection differential and σ_p = is phenotypic standard deviation on mean basis.

The Genetic advance as % of mean (GAM) was computed as:

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

Where, GAM = genetic advance as percent of mean, GA = genetic advance under selection and $\bar{x}$ = mean of the population in which selection was employed.

III. Results and Discussion

a) *Analysis of variance (ANOVA)*

Mean squares of the 13 characters from analysis of variance (ANOVA) are presented in (Table 2). Highly significant differences among genotypes (P<0.01) were observed for seven characters (days to heading, number of productive tillers per plant, spike length, number of spikelets per spike, 1000 kernel weight, grain yield plot^{-1} and hectoliter weight or test weight), significant at (p<0.05) for the rest six characters; namely, days to 75% maturity, grain filling period, plant height, number of kernels spike^{-1}, biomass yield and harvest index. This result indicating that there is variability among the genotypes studied and would respond positively to selection.

Several researchers reported significant differences among wheat genotypes studied. Shashikala (2006) reported significant differences among 169 genotypes for 11 morphological traits such as days to 50% heading, days to 75% maturity, plant height, spike length, peduncle length, number of tillers per m^2, number of spikelets per spike, 1000 grain weight, protein content and grain yield per plot. Similarly, works of Kumar *et al*. (2009) and Monpara (2011) showed that significant differences among 30 genotypes of bread wheat for 8 quantitative characters and among 21 genotypes of bread wheat for 11 quantitative characters respectively. Kalimullah *et al*. (2012) reported that grains per spike, number of tillers per plant, 1000 grain weight, spike density and grain yield per plant showed highly significant differences between forty one bread wheat genotypes were studied. Thus, it indicated that there was sufficient variability in the material used for their study, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

b) *Range and mean values*

Range and mean values for the 13 characters is presented in Table 3.. The mean grain yield ranged from 500 to 1182 gram per plot. 43.75% of the genotypes gave above the grand mean. Phenological characters, days to 50% heading and days to maturity ranged from 53 (CIMMYTADT/3) to 82 CIMMYTOB/27) and 111 (CIMMYTOB/50, CIMMYTADT/2 CIMMYTADT/3) to 131(CIMMYTOB/27), respectively. Grain filling period is an important trait in wheat that ultimately affects the overall grain yield by increasing grain weight. It ranged from 43 (CIMMYTOB/39) to 72(CIMMYTADT/17) with a mean value of 56.27 days, which is slightly higher than our commercial varieties Alidoro, Meraro and Digelu 51, 52 and 55 days respectively. A significant number of lines (90.625%) took 50-72 days to fill the grains.

Table 2 : Analysis of variance (Mean squares) for the 13 characters of 64 bread wheat genotypes grown at Ginchi (2012/13)

Characters	Replication (df=1)	Genotype (df=63)	Intra Block Error (df=49)	CV (%)	Efficiency Relative to RCBD
Days to 50% heading (days)	8.51	86.99**	9.22	10.62	107.38
Days to 75% maturity (days)	2.53	37.75*	5.42	4.04	100.49
Grain filling period (days)	13.78	47.30*	5.58	10.16	100.72
Plant height (cm)	29.5488	248.40*	22.48	11.94	101.24
Number of productive tillers per plant	0.0183	0.68**	0.1563	10.58	105.37
Spike length (cm)	0.71252	1.0870**	0.1043	8.84	109.36
Number of spikelets per spike	3.30	2.5444**	0.2479	6.87	102.31
Number of kernels per spike	25.9200	50.4459*	8.8261	16.20	111.15
1000 kernels weight (g)	0.131328	43.2103**	3.722	12.628	103.52
Biomass yield per plot (g)	22578	160197*	9604	19.50	115.26
Harvest index (%)	18.9036	37.2436*	6.1859	18.09	103.12
Hectoliter weight (kg/hL)	6.7070	18.4252**	3.4176	13.75	116.27
Grain yield per plot(g)	1287.78	22864**	4066	2.07	120.90

df=Degrees of freedom

**=significant at 5% probability level and **=highly significant at 1% probability level*

CV= Coefficient of Variation, RCBD=Randomized Complete Block Design

The mean plant height was 97.51cm with a range of 79.5 cm (CIMMYTOB/32) to 129 cm (CIMMYTOB/35). Number of productive tillers plant^{-1} showed a wide variation, which ranged from 4.8 (CIMMYTADT/13) to 8.63 (CIMMYTOB/33) and mean value for this trait was 6.19. A range of 6.85 cm (CIMMYTOB/40) to 11.2 cm (the standard check, ALIDORO) with the mean value of 8.73 cm was observed for spike length. Number of spikelets spike^{-1} ranged from 14.8 (CIMMYTADT/3) to 21 (one of the standard check, ALIDORO) with the mean value of 17.38. Number of kernels per spike ranged from 23 (CIMMYTOB/80) to 52 (CIMMYTADT/17) with a mean of 38.38.

The average 1000-kernel weight was 38.46g and it ranged from 28.3 g (CIMMYTOB/7) to 49g (CIMMYTOB/70). Genotypes CIMMYTOB/22 and CIMMYTOB/25 were yielding as low as 500 g/plot to as high as 1182 g/plot respectively, with over all mean of 742 grams plot^{-1}. The range for biological yield varied between 1100 grams plot^{-1} for genotype CIMMYTOB/54 to 3500 grams plot^{-1} for CIMMYTOB/25 among the 64 genotypes studied with over all mean of 2056 grams plot^{-1}. A wide range was observed for this character with the minimum value being 25% and the highest 58% in respect of genotype CIMMYTADT/6 and CIMMYTOB/54, respectively. The mean harvest index was noted to be 36%.

The average hectoliter weight was 80.06 kg/hL and it ranged from 76.10 kg/hL (CIMMYTOB/7) to 83.1 kg/ha (DIGELU, one of the three standard checks). Generally, the range of variation was wide for all the characters studied. Similarly, Radhu *et al*. (1995) observed high range of variation for yield, 1000-kernel weight, plant height and days to flowering, Maqbool *et al*. (2010) reported wide range of variation for plant height, grain filling period, number of spikeletes per spike, biological yield per plot, grain yield and 1000-kernel weight. Moreover, Sajjad et al (2011) reported large variation for grain yield, 1000 kernels weight and number of kernels per spike. From the result it was obtained that those characters with the higher range of values were also had higher mean values and vice versa. Such considerable range of variations provided a good opportunity for yield improvement. Thus, high variability for thirteen traits in 64 bread wheat genotypes used for this study implied that there was reasonably sufficient variability, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

c) Variability components and coefficients of variation

Estimates of phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic (PCV) and genotypic coefficients of variation (GCV are given in Table 3. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 3.8% (days to maturity) to

Table 3 : Table 3 Estimate of ranges, mean, phenotypic (σ^2p) and genotypic (σ^2g) component of variances, broad sense heritability and genetic advance as percent of mean for 13 characters of bread wheat genotypes tested at Ginchi (2012/13)

Character	Mean	Range		σ^2p	σ^2g	PCV (%)	GCV (%)	H^2_{BS} (%)	GA (k =2.063)	GAM (k=2.063)
		Min.	Max.							
DH	65.55	53	82	48.1	38.90	10.6	9.50	81.00	11.60	17.70
DM	122.2	111	131	21.58	16.20	3.8	3.30	75.10	9.06	7.40
GFP	56.27	43	72	26.44	20.90	9.14	8.10	79.05	8.40	14.90
PH	97.51	79.5	129	135.6	112.96	11.94	10.90	83.30	20.01	20.52
NTPP	6.19	4.8	8.63	0.43	0.264	10.64	8.30	61.40	0.83	13.4
SL	8.73	6.85	11.2	0.596	0.497	8.84	8.10	83.34	1.33	15.20
NSPS	17.38	14.8	21	1.40	1.20	6.81	6.30	85.72	2.64	15.20
NKPS	38.38	23	52	29.6	18.31	14.18	11.15	62.00	6.95	18.13
TKW	38.46	28.3	49	23.5	19.75	12.60	11.56	84.04	8.40	21.90
GY	742	500	1182	13465	9399	15.64	13.07	69.80	167.00	22.52
BMY	2056	1100	3500	84900	75297	14.17	13.35	88.70	533.00	25.93
HI	36	25	58	21.71	15.53	12.95	10.95	71.53	6.88	19.11
HLW	80.06	76.1	83.1	10.92	7.51	4.3	3.43	68.77	4.69	5.86

σ^2p =Phenotypic variation, σ^2g =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, $H^2_{BS=}$ Broad sense heritability, GA=genetic advance, and GAM=Genetic advance as percent of mean

15.64% (grain yield plot^{-1}) and 3.3% (days to maturity) to 13.35% (biomass yield plot^{-1}), respectively. Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. The maximum phenotypic variance value of 84900 grams plot^{-1} was noted for the trait biomass yield and 13465 grams plot^{-1} for grain yield. Similarly, the genotypic variances for these characters 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 characters.

Deshmukh *et al.* (1986) classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. Based on this delineation, characters which showed moderate phenotypic and genotypic coefficients of variation were plant height, number of kernels per spike, thousand kernels weight, grain yield, biomass yield and harvest index. This indicated that selection may be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Days to 50% heading and number of productive tillers per plant were found to be medium for PCV while low for GCV. The rest of the characters grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment. The result obtained was in accordance with the of findings Shashikala (2006) reported for 1000 kernels weight and grain yield per plot, Kalim *et al.* (2011) and Wani *et al.* (2011) for yield/plant, 1000 grains weight, number of kernels per spike in bread wheat. Monpara (2011) obtained moderate PCV with low GCV for grain filling period in 21 bread wheat genotypes. Ali *et al* (2012) reported moderate PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Degewione *et al*. (2013) reported moderate PCV and GCV for 1000 grain weight, plant height and days to heading in twenty six bread wheat genotypes.

d) Heritability and genetic advance

Although the genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for various traits, it does not provide full scope to assess the variation that is heritable. The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection (Burton, 1952). Heritability (H^2_{BS}), genetic advance (GA) and genetic advance as percent of mean (GAM) estimates for characters under study are indicated in Table 3. Robinson *et al.* (1949) classified heritability values as high (>60%), moderate (30-60%) and values less than 30% low. Accordingly, the results of the present study indicated that high heritability values were observed in all the characters studied. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. Rahim *et al*. (2010) noticed higher heritability value for plant height, days to 50 per cent flowering, number of productive tillers per meter length, grain yield per plot, and number of grains per spike. Further, Salem *et al* (2008), Ali *et al*. (2008) and Khan *et al* (2010) recorded high heritability estimates for grain yield, number of kernels per main spike, plant height and thousand kernel weights and number of tillers per plant.

The expected genetic advance expressed as a percentage of the mean by selecting the top 5% (high grain yielder) of the bread wheat advanced genotypes, ranged from 5.86% for hectoliter weight to 25.93% for biomass yield plot^{-1}(Table 3), indicating that selecting the top 5% of the base population could result in an advance of 5.86 to 25.93 percent over the respective population mean. Falconer and Mackay (1996) classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). Genetic advance as percentage of mean was maximum for biomass yield plot^{-1} (25.93%) followed by grain yield plot^{-1}(22.52%), thousand kernels weight (21.90%) and plant height. Similarly, genetic advance was maximum for biomass yield plot^{-1} (533grams), followed by grain yield plot^{-1} (167grams) and plant height (20.01cm). Degewione *et al*. (2013) obtained similar results in twenty six bread wheat genotypes. Johnson and Hernandez (1980) reported that high heritability and high genetic advance as percentage of mean provide better information than each parameter alone. High heritability and genetic advance as percent of mean were found in biomass yield, plant height, thousand kernels weight and grain yield plot^{-1}; indicated that these characters could be useful basis of selection.

Genetic advance as percentage of mean was maximum for biomass yield plot^{-1} (25.93%) followed by grain yield plot^{-1}(22.52%) and thousand kernels weight (21.90%). Similarly, genetic advance was maximum for biomass yield plot^{-1} (533grams), followed by grain yield plot^{-1} (167grams) and plant height (20.01cm). Accordingly, days to heading, grain filling period, number of productive tillers per plant, spike length, number of spikelets per spike, number of kernels per spike and harvest index showed moderate genetic advance as percent of mean; whereas days to maturity and hectoliter weight showed low genetic advance as percent of mean.

Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al*., 1955). The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1999).

High heritability associated with high genetic advance were observed for plant height (83.3%, 20.52%), 1000 grain weight (84.04%, 21.9%), grain yield per plot (69.8%, 22.52%) and biomass yield per plot (88.7%, 25.93%), respectively. These are simply inherited traits indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. The results are in accordance with reports of earlier work done by Munir *et al* (2007) reported high heritability with high genetic advance for plant height and number of spikelets per spike and Kalimullah *et al*. (2012) was reported similar findings for plant height, biomass yield per plot and1000 grain weight, which supports the present results.

In general, traits such as plant height, thousand kernels weight, grain yield per plot and biomass yield per plot had high heritability and high genetic advance as percent of the mean. Selection based on these characters will result in the improvement of the performance of the genotypes for the traits.

IV. CONCLUSION

This study generally indicated that there was genetic variability among the genotypes. Thus, there is enormous opportunity in the improvement bread wheat genotypes. Therefore, the information generated from this study needs to be used by breeders who are interested in different traits. However, the present result is only an indication and we cannot reach a definite conclusion. Therefore, since the experiment was carried out at one location in one season, it is advisable to continue with this study over several years and locations.

V. ACKNOWLEMENTS

The authors would like to thank Jimma University College of Agriculture and Veterinary Medicine (JUCAVM) and Holeta Agricultural Research Center (HARC) for their financial support.

REFERENCES RÉFÉRENCES REFERENCIAS

1. Abu Tefera, 2012. Grain and feed annual report. Grain report number: ET1201, Addis Ababa, Ethiopia.
2. Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z (2008) Genetic variability, association and diversity studies in wheat (Triticum aestivum L.) germplasm. Pak J Bot 40: 2087- 2097.
3. Ali, I. H. and Shakor, E. F. 2012. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. Mesoptamia J. of Agri., 40 (4): 27 - 39.
4. Allard, R.W. (1999). Principles of Plant Breeding (second edition). John Wiley and Sons. Inc., New York, USA.
5. B.A. Monpara, 2011. Grain filling period as a measure of yield improvement in bread wheat, Crop Improv. (2011) 38(1): 1-5.
6. Daniel Hailegiorgis, Mebrahtom Mesfin and Tsige Genet, 2011. Genetic Divergence Analysis on some Bread Wheat Genotypes Grown in Ethiopia, 2Bahir Dar University, Amhara, Ethiopia.

7. Degewione A.and Alamerew S., 2013. Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Genotypes. Pakistan Journal of Biological Sciences, 16: 1330-1335.
8. Deshmukh, S. N., M. S. Basu, and P. S. Reddy. (1986). Genetic variability, character association and path coefficients and quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences 56: 816-821.
9. Faris Hailu, 2011. Genetic Diversity and Grain Protein Composition of Tetraploid Wheat (*Triticum durum* Desf.) Germplasm from Ethiopia. Doctoral (Agri.) Thesis University of Agricultural Sciences. Alnarp, Sweden.
10. Johnson, H. W., H. E. Robinson and R. E. Comstock. (1955). Estimates of genetic and environmental variability in soybean. Agron. J., 47: 314-318.
11. Kalim Ullah, K., S.J. Khan, S. Muhammad, M. Irfaq and T. Muhammad, 2011. Genotypic and
12. Kalimullah, S. J. Khan, M. Irfaq and H. U. Rahman, 2012. Genetic variability, correlation, and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. The Journal of Animal & Plant Sciences, 22(2), Page: 330-333, ISSN: 1018-7081, Page: 330-333 ISSN: 1018-7081, Khan, Pakistan.
13. Khan, A. A., A. Iqbal, F. S. Awan and I. A. Khan (2010a). Genetic diversity in wheat germplasm collections from Balochistan province of Pakistan. Pakistan J. Bot., 42(1): 89-96.
14. Kumar, B., G.M. Lal, Ruchi and A. Upadhyay, 2009. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (Triticum aestivum L.). Asian J. Agric. Sci., 1: 4–6.
15. M. Ferdous, U. K. Nath and A. Islam, 2011. Genetic divergence and genetic gain in bread wheat through selection practices. J. Bangladesh Agril. Univ. 9(1): 1–4.
16. Mondal, S.K. and Khajuria, M.R. 2001. Correlation and path analysis in bread wheat (*Triticum aestivum* L.) under rainfed condition. Environment and Ecology, 18 (2): 405 - 408.
17. Munir M, M. A. Chaudhary and T. A. Malik. (2007). Correlation studies among yield and its components in bread wheat under drought conditions. Intl J. Agri. and Bio. 15 (2): 287–290.
18. P N Verma1, B N Singh, 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), pp. 395-399. University of Agriculture and Technology, Faizabad, India.
19. phenotypic variability, heritability and genetic diversity for yield components in bread wheat (*Triticum aestivum* L.) germplasm. African J. Agric. Res., 6(23): 5204-5207.
20. Radhu, A. S., S. K. Solanki, and I. Singh, 1995. Genetic diversity in some Indian and exotic wheat varieties. Crop Improvement, 22(2): 214-217.
21. Ranjana and Suresh Kumar, 2013. Study of genetic variability and heritability over extended dates of sowing in bread wheat (*Triticum aestivum* L.). Research in Plant Biology, 3(1): 33-36.
22. Rauf, S., Tariq, S.A., Hassan, S.W. (2012). Estimation of pedigree based diversity in Pakistani wheat (*Triticum aestvium* L.) germplasm. Communications in Biometry and Crop Science 7 (1), 14–22
23. Rizwana Maqbool, Muhammad Sajjad, Ihsan Khaliq, 2010. Morphological diversity and traits association in bread wheat (Triticum aestivum L.). American-Eurasian J. Agric. Environ. Sci.,8(2): 216-224.
24. S. A. Mohammadi and B. M. Prasanna, "Analysis of genetic diversity in crop plants—salient statistical tools and considerations," Crop Science, vol. 43, no. 4, pp. 1235–1248, 2003.
25. Sajjad, M., S.H. Khan and A.S. Khan, 2011. Exploitation of germplasm for grain yield improvement in spring wheat (*Triticum aestivum*). Int. J. Agric. Biol., 13: 695-700.
26. Salem K. F. M., A. M. El-Zanaty and R. M. Esmail. (2008). Assessing wheat (*Triticum aestivum* L.) genetic diversity using morphological characters and microsatallite Markers. World J.Agri. Sci. 4 (5): 538-544.
27. SAS, 2008. Statistical Analysis System. Version 9.2, SAS Institute Inc., Cary, NC., USA.
28. Shashikala, S.K. 2006. Analysis of genetic diversity in wheat. M.Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.
29. Shashikala, S.K. 2006. Analysis of genetic diversity in wheat. M.Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.
30. Singh, P., & Narayanan, S.S. (1999). Biometrical techniques in plant breeding. Kalyani, Publishers New Delhi.
31. Singh, R.K. and B.D. Chaudhary, 1999. Biometrical Methods in Quantitative Genetics Analysis. Kalyani Publishers, New Delhi, India, Pages: 318.
32. Vahid Mollasadeghi, Mostafa Valizadeh, Reza Shahryari and Ali Akbar Imani, 2012. Selection of superior wheat genotypes against end-season drought of Ardabil in the presence of humic fertilizer by utilization of multivariate statistics. African Journal of Biotechnology Vol. 11(69), pp. 13396-13402.
33. Zecevic V, Kenezevic D, Micanovic D (2010). Genetic correlations and path-coefficient analysis of yield and quality components in wheat (*Triticum aestivum* L.). Genetika 36(1):13-21.
34. Zecevic V., J. Boskovic, M. Wani, B.A., M. Ram, A. Yasin and E. Singh, 2011. Physiological traits in integration with yield and yield components in wheat

(*Triticum aestivum* L.) study of their genetic variability and correlation. Asian J. Agric. Res., 5: 194-200.

35. Zerihun T., Firdissa E.,Fekadu F., Kebede T., Mathewos A., MohamedA., Mizan T., Muluken B.,Yosef G., Alemayehu A., and Birhanu B, 2012. Exploiting yield potential of Ethiopian commercial bread wheat (Triticum aestivum L.) varieties outside their original recommended domains. Wheat for food security in Africa Conference Oct8-12, Addis Ababa, Ethiopia.

This page is intentionally left blank