Estimation of Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.)

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Abstract: *Wheat (Triticum aestivum L.) is high yielder and wider adaptability of the staple food for a large part of the world population including Ethiopia. Although the productivity of wheat has increased in the last few years in Ethiopia, it is still very low as compared to other wheat producing countries mainly due to biotic and abiotic factors. Therefore, in this study conducted on genetic variability in grain yield and yield related characters of 49 bread wheat genotypes. An experiment was undertaken at two locations viz; Holetta and Kulumsa Agricultural research center in Ethiopia in 2016/17 cropping season. The materials were evaluated in the simple lattice design with two replications. Data on yield and yield component were collected and analyzed using SAS version 9.3 software. Results revealed that very high estimates of heritability across locations were obtained in the case of days to heading (95.66%), plant height (90.74%) and grain filling period (85.21%). High heritability coupled with moderate genetic advance as a percent of means were noted for days to heading, Plant height, grain filling period and spike length. So, it concluded that this trait may be considered as the selection criteria for the improvement of grain yield. However, further study needs to be conducted the future bread wheat breeding effort should be focus on varietal development.*

Keywords: *Bread wheat, Broad sense heritability, Genetic advance, Grain yield*

1. INTRODUCTION

World wheat production is based almost completely on two modern species: hexaploid bread wheat *(Triticum aestivum L, 2n = 6X = 42, AABBDD)* and tetraploid wheat *(T. turgidum subsp. durum, 2n = 4X =28, AABB* (Sears, 1966). Wheat can grow in the Ethiopian highlands, which are located between 6° and 16° N, latitude and 35° and 42°E, longitude at altitude ranging from 1500 - 3000 m.a.s.l. However, the most appropriate altitude zones of wheat fall between 1900 - 2700 m.a.s.l (Bekele *et al.*, 2000). Dissimilar rice and maize, which prefer to tropical environment, wheat is extensively grown in temperate regions occupying 17% of all crop acreage worldwide. Currently it is also attractive most important cereals grown on a large scale (Fasil *et al.*, 2000), because of its significance as cash crop, high level of production per unit area, its major role in providing the nutritional requirements of the society.

Wheat is one of the major staple and strategic food security crops in Ethiopia (Letta, 2013; Bezabeh *et al.,* 2015) cultivated by half a million house holders on about 1.7 million ha. In spite of its incredible contributions to food and nutritional security of the country, the national average wheat productivity is 2.37 t/ ha far below the global average of 3.27 t/ha (FAOSTAT, 2018).

A gap in the yield was attributed mainly due to shortage of improved varieties for different agro ecological zones of the country. In addition, poor agronomic practices, drought, poor soil fertility, diseases and insect pests, etc. are the major constraints of wheat production in Ethiopia (Fikire *et al.,* 2015). Hence, it is necessary to generate information on phenotypic and genotypic variances as well as heritability and genetic advance among bread wheat varieties as one of the approaches to alleviate these limitations.

The success of a breeding program depends largely upon the amount of genetic variability present in the population and the extent to which the desired traits are heritable (Majumder *et al.,* 2008).

Heritability is an indicator for transfer of traits of interest from parents to its progeny and is widely used in breeding programs (Falconer, 1981).

The genetic advance (GA) is another important parameter to selection (Shukla *et al.,* 2004) Phenotypic and genotypic coefficients of variations, heritability and genetic advance have been widely used in wheat to assess the magnitude of variance in breeding material, to determine appropriate selection procedures and to predict the breeding advance in improvement of important traits (Zecevic, 2001; Shukla *et al.,* 2004, Clarke *et al.,* 2010).

High genetic advancement together with high heritability estimates offers the most suitable condition for selection (Johnson *et al.,* 1955). The presence of variability, heritability and genetic advance in different yield related characters of bread wheat has been reported by different authors (Obsa *et al*., 2017; Dabi *et al.,* 2019; Zerga *et al.,* 2016; Awale *et al*., 2013 and Gezahegn *et al.*, 2015). More importantly changes in genetic variability such as grain yield and related traits of bread wheat were studied not incorporated the recent one including candidates. Therefore, the objective of the present study was accomplished with to estimate genotypic and phenotypic variability in bread wheat genotypes and estimate the heritability and genetic advance under selection.

2. MATERIALS AND METHODS

Table1. *Description of the experimental sites in terms of geographical position*

Description	Location	
	Holetta	**Kulumsa**
Latitude	09°04' N	08°01' N
Longitude	38°29' E	39°09' E
Altitude(m.a.s.l.)	2400	2200
Mean annual rainfall(mm)	1102	832
Mean annual temperature(°c)	14.23	16.68
Soil type	Nitosols	Luvisols

Source: Tamene. *et al*. (2015).

Planting Materials

The experiment was conducted to examine the genetic variability, heritability and genetic advance percent of mean for thirteen yield contributing traits in bread wheat. The experiment was evaluated on station of Holetta and Kulumsa Agricultural Research Center 2016-17 cropping season. The experimental materials consist of Fourty nine genotypes of bread wheat namely., Lakech, Enkoy, Dereselegn, K6290-Bulk, K6295-4A, Et-13 A2, Pavone-76, Batu, Dashen, Mitike, Kubsa, Galama, Tusi, Katar, Wetera, Hawi, Meda - Welabu, Sofumer, Sirbo, Doddota, KBG01, Bobicho, Digelu, Tay, Mararo, Alidoro, Millinium, Gassay, Danda'a, Kakaba, Hoggena, Shorima, Huluka, Ogolcho, Jefferson, Hidasse, Honqolo, Biqa, Mandoye, Sanate, Kingbird, Liben, Buluk, Dembel, Lemu, Wane,,ETBW8506, ETBW 8491and ETBW 9027. Those materials were grown in simple lattice incomplete block design; the arrangements

Of (7*7) with two replications. The plot size was six rows of 2.5m length with 0.2m row spacing (1.2m*2.5m = 3m^2). The spacing was between plots (0.4m), block (0.5m) and replications (1.5m).The rate of seed was 150 kg ha^{-1}(45g/plot) with recommended fertilizer rate of 60:69 N$_2$:P$_2$O$_5$ per hectare. All other crop management practices were applied uniformly to all plots as required.

Data on agro morphological traits of wheat varieties were collected on plot and plant basis on the following characters viz., Days to (heading and maturity), Grain Filling Period, Thousand Kernel Weight, Hectoliter Weight, Grain Yield, Biomass Yield, Harvest Index, Plant Height, Spike Length, Number of Kernels per Spike, and Number of spikelets per spike. The analysis of variances heritability in broad sense (H2Bs) is suggested by Hanson (1956) and genetic advance (GA) was estimated by Johnson (1956).

Statistical Analysis

The data were subjected to analysis of variance (ANOVA), according to general linear model using SAS 9.3 (SAS Institute, 2012) and Microsoft Excel (2010). Data of mean values of all experimental units were subjected to analysis of variance (ANOVA) based on (Table 2).For pooled analysis of

variance over location was conducted to measure the total variation among the varieties using the following model:

$P_{ijkz} = \mu + g_i + b_k(j)(z) + r_j(z) + l_z + (gl) + e_{ijkz}$

Where, Pijkz = phenotypic value of ith genotype under j^{th} replication at z^{th} location and k^{th} incomplete block within replication j and location z; μ =grand mean; gi = the effect of ith genotype; bk(j)(z)= the effect of incomplete block k within replication j and location z; rj(z)=the effect of replication j within location z; lz= the effect of location z; (gl)is = the interaction effects between genotype and location; and eijkz = the residual or effect of random error.

Table1. *Analysis of variance model combined over location*

Source of variation	Degree freedom	Mean square (MS)	Expected mean square (EMS)
Location (L)	L-1	MSL	$\sigma^2e + r\sigma^2gi + g\sigma^2L$
Replication(r)	r-1	MSR	$\sigma^2 e + g \sigma^2r$
Blocks within replication(b)	r(b-1)	MSB	$\sigma^2e + r\sigma^2gi + r\sigma^2 g$
Genotypes (g)	g-1	MSG	$\sigma e 2 + r\sigma^2gi + rL\sigma^2g$
g x L interaction (i)	(g-1)(L-1)	MSGL	$\sigma^2 e + r\sigma^2gi$
Error (e)	Lg(r-1)-(rb-1)	MSE	$\sigma^2 e$

Where, b represent blocks; δ^2g= genotypic variance, σ^2e = environmental variance, σ^2L =location variance, σ^2r = replication variance, and σ^2gi = genotype x location interaction variance, L = number of locations, g =number of genotypes and r = number of replications.

For combined analysis of variance over location, the homogeneity of error variance was tested using F – max test method of Hartley (1950), which is based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller mean square of error variance given by the following formula: F - Max = $\frac{Largest\ MSE}{Smallest\ MSE}$

If the calculated value of F-max was less than three, it means that the ratio of the highest error mean square is not three fold larger than the smallest error mean square, and this indicates that the variance was considered homogenous thereby making it to possible to proceed with the combine analysis of variance (Gomez and Gomez, 1984). Then pooled analysis of variance over locations was done using SAS Statistical package (SAS Institute, 2012). Mean separation was carried out using Least Significant Difference (LSD) at 5 % of significance.

Estimation of Genetic Parameters

The genotypic, phenotypic and environmental variance component and coefficient of phenotypic (PCV %) and genotypic coefficient of variation (GCV %) were estimated based on the method suggested by Burton and devane (1953).

Genotypic variance = $\frac{Msg-Msgl}{rl}$

Environmental variance (δ^2e) = error mean square

Phenotypic variance ($\sigma^2p = \delta^2g + \delta^2e + \delta^2gl$) combined over location

$\sigma^2{}_p = \delta^2{}_g + \frac{\sigma2gL}{L} + \frac{\sigma2e}{rL}$, where $\sigma^2gl = \frac{MSgl-MSe}{r}$

Where σ^2gl = variance of genotype by location interaction

MSe = error mean square; MSgl = genotype by location interaction mean square

MSg = genotype mean square; r = replication; l = location

Phenotypic coefficient of variation (PCV %), PCV = $\frac{\sqrt{\delta^2P}}{\bar{x}}$ x 100

Genotypic coefficient of variation (GCV %), GCA = $\frac{\sqrt{\delta^2g}}{\bar{x}}$ x100

Broad-Sense Heritability (H²B)

Broad sense heritability on plot and plant basis was computed for all traits based on the formula given by Falconer and Mackay (1996).

Heritability (H²B) $= \dfrac{\sigma 2g}{\sigma 2p}$ x100, h2 $= \dfrac{\sigma 2g}{\delta 2g + \frac{\sigma 2gL}{L} + \frac{\sigma 2\epsilon}{rL}}$ x 100, for combined locations

Where: H = Heritability in Broad sense; $\delta^2 p$ = Phenotypic variance; $\delta^2 g$ = Genotypic variance

Genetic advance under selection (GA)

The expected genetic advance for each trait at selection intensity of 5 % was computed using methodology given by Allard (1960).

GA = K.h²b.σp;

Where: GA= Expected genetic advance; k = the standardized selection differential at 5% selection intensity (K = 2.063); σp = Phenotypic standard deviation; H = Heritability in broad sense

Genetic advance as percent of mean

Genetic advance as percent of mean was calculated to compare the amount of predicted advance of different traits under selection, using the following formula:

GAM $= \dfrac{GA}{\bar{x}}$ x100;

Where: GAM = Genetic advance as percent of mean; GA = Genetic advance under selection; $\bar{x}$ = Grand Mean of the population

3. RESULTS AND DISCUSSION

Analysis of Variance

Prior to performing analysis of variance, tests were made to confirm the homogeneity of error variances. The two locations showed homogeneity of error variances. Consequently, the data were pooled across locations and analyzed. The results of the combined analysis of variance across the two locations are presented on (Table 2).

The combined analysis of variance over two locations presented (Table 2) mean squares of genotypes were significant (P ≤ 0.01) for all characters including days to heading, days to maturity, plant height, grain filling period, thousand kernel weight. Hector liter weight, spike length, number of spike let per spike .number of grain per spike, biomass yield, harvest index and grain yield except number of tiller. The significant of those traits indicated that the existence of enormous amount of genetic variability for growth and yield attributes. Hence, selection could be effective to different quantitative characters including crossing program as well as creating variability. Similar findings were also reported by Navi *et al*. (2014); Dabi *et al*. (2019).

The location* genotypes interaction for thirteen characters of Fourty nine genotypes presented (Table 2) highly significant for all the characters except biomass yield, number of tillers, spike length and number of spikelet per spike. This implies that the not performed consistently over locations with regard to this traits. On the other hand reveal variety selected for those traits at one location may not exhibit a similar relative performance at another location. If varieties not perform consistently for those traits over locations, breeders may be able to extensive varietal evaluation by appropriate testing sites and by modifying the breeding programs. To effectively assess varietal performance for significant traits, it's essential to consider wide location interaction and identify trait performance in relations to location effect. Similar findings were also reported on bead wheat by Dabi *et al*. (2019) for most of the traits studied.

Table2. *Combined analysis of variance over locations for grain yield and yield related character of bread wheat varieties grown in the yield potential trials at Kulumsa and Holetta.*

Trait	Mean squares (MS)		

	MSL (1)	MSG (48)	MSLG (48)	Group (Loc.) (1)	Block (Group) (12)	MSE (85)	Mean	CV (%)	R2	LSD (5%)
DH	75.94**	133.06**	5.77**	0.33ns	2.52ns	1.34	66.58	1.74	0.99	1.62
DM	32015.43**	57.33**	12.08**	4.90ns	10.19*	5.19	133.62	1.70	0.99	3.2
PH	1929.72**	246.86**	22.85**	36.86ns	18.14ns	12.46	99.19	3.56	0.95	4.96
GFP	28972.90**	70.78**	10.47**	2.69ns	5.39ns	5.39	67.04	3.47	0.99	3.27
TKW	305.001**	46.79**	21.002**	10.28ns	10.53*	5.12	36.06	6.27	0.91	3.18
HLW	2486.52**	12.70**	5.54**	5.92*	1.29ns	1.08	76.18	1.36	0.97	1.46
BMY	7427703.9**	2202267.8**	1060555.4ns	2215130.4ns	1893042.9**	763314.7	7543.3	11.58	0.78	1228.5
HI	1800.002**	186.53**	99.43**	281.11*	65.16ns	47.86	45.66	15.15	0.83	9.73
NT	128.98**	128.98ns	1.96ns	1.47ns	4.31*	2.001	5.49	25.74	0.70	1.99
SL	6.76**	1.89**	0.42ns	0.02ns	0.36ns	0.47	8.11	8.46	0.76	0.97
NSS	218.62**	6.02**	2.09ns	8.58*	1.80ns	1.62	19.41	6.56	0.84	1.79
NGS	5476.00**	56.82**	39.99**	39.51ns	14.25ns	14.99	51.81	7.47	0.89	5.44
GlY	14571953.80**	950202.14**	891217.93**	298039.56ns	146700.06ns	164031.2	3534.33	11.46	0.90	569.51

*, ** Significant at $p \leq 0.05$, and $p \leq 0.01$ probability level respectively and ns = non-significant, ( ) parenthesis indicate degrees of freedom. MSL= Mean Squares of locations, MSG= Mean squares of genotypes, MSLG = Mean square of genotype x location interaction, MSE = Mean squares of error, CV = Coefficient of variation. *Abbreviations: DH=Days to heading,* DM=*Days to maturity* , PH = Plant Height , GFP = Grain Filling Period , TKW = Thousand Kernels Weight , HLW= Hectoliter weight , BMY = Biomass Yield , HI = Harvest Index , NT= Number of Tiller/plant , SL= Spike Length , NSS = Number of spikelet per spike, NGS = Number of Kernels per Spike , GlY= Grain yield (Kg/ha).

Range and Mean value

The mean values for days to 50% heading ranged from 53 (Dereselegn) to 80 days (Dashen), days to 75% maturity ranged from 126 (Dereselegn) to 143 days (Buluk). Thousand kernel weight was ranged from 26 (Lakech) to 45 g/plot (Hidasse) and grain yield per hectare showed a wide variation which ranged from 2245 (Lakech) to 4592 kg/ha (Dashen). Biomass yield ranged from 5641 (KBG-01) to 9588 kg/ha (Mandoye) with a mean value of 7543.3 kg ha^{-1} and harvest index ranged from 25 (ET-13 A2) to 61 % (KBG-01) with a mean value of 45.66. Hectoliter weight varied from 72 (Lakech) to 80 kg/hl (Digelu), plant height ranged from 80 (Mandoye) to 119 cm (K6295-4A), grain filling period varied from 58 (Galama) to 78 days (Meda-Welabu) and spike length ranged from 7 (Digelu) to 10 cm (Alidoro). Similarly, the mean values for number of spikelets per spike and number of grains per plant were ranged from 17 (Mandoye) to 23 number (Alidoro) and 44 (Enkoy) to 64 number (ETBW 9027) respectively are presented (Table 2). Therefore, high variability for thirteen traits of Fourty nine bread wheat genotypes implied that there was reasonably sufficient variability which provides ample scope for selecting superior and desired genotypes by plant breeders for further improvement. Generally, the range of variation was wide for all the characters studied. Gezahegn *et al.* (2015) reported similar results on bread wheat study.

Estimates of Variance Components

Genotypic and phenotypic variance, genotypic and phenotypic coefficient of variability, broad sense heritability and genetic advance expressed as percentage of mean for thirteen characters are presented in Table 3.

Estimates of genotypic and phenotypic coefficients of variation

According to Deshmukh (1986), the result of Phenotypic and genotypic coefficient of variation exhibited that harvest index showed wide range and moderate PCV and GCV whereas, grain yield showed moderate PCV. Similar findings were reported by earlier researchers for harvest index (Dabi *et al*., 2019, Bayisa *et al.,* 2020; Mecha *et al*., 2016; Muhder *et al.,* 2020). Similar findings were reported by earlier researchers for grain yield (Destaw *et al.,* 2020).

The remaining traits recorded low GCV and PCV estimate are presented (Table 3). Through this studied, revealed low GCV and PCV reported by earlier researchers for days to heading (Bayisa *et al.,* 2020; Meles *et al*., 2017; Ullah *et al.,* 2011), days to maturity (Bayisa *et al.,* 2020; Meles *et al*., 2017; Mecha *et al.,*2016; Ullah *et al.,* 2011), plant height (Meles *et al.,* 2017; Bayisa *et al.,* 2020; Ullah *et al.,* 2011; Bharat *et al.,*2013),spike length (Meles *et al.,* 2017; Mecha *et al.,*2016; Bayisa *et al.,* 2020; Ullah *et al.,* 2011) and hectoliter weight (Bayisa *et al.,* 2020;Meles *et al*., 2017; Mecha *et al.,*2016).

In general, the studied traits, for days to heading and maturity, gain filling period, plant height and hectoliter weight revealed that phenotypic coefficient of variation slightly higher than genotypic coefficient of variations, those traits indicated that less influenced by environment. While, for grain yield, harvest index, number of grain spike^{-1}, biomass yield, thousand kernel weight, number of spikelet spike^{-1} and spike length were showed that higher phenotypic coefficient of variation than genotypic coefficient of variations.

Estimation of broad sense heritability and genetic advance

According to Singh (2001) that heritability values greater than 80% were very high, values from 60 – 79% were moderately high, values from 40-59% were medium and values less than 40% were low. Accordingly, very high broad sense heritability estimates were revealed for days to heading (95.66%), plant height (90.74%) and grain filling period (85.21%), while high heritability values were obtained for days to maturity (78.93%), spike length (77.78%), and number of spikelet per spike (65.28%). Moderate values of broad sene heritability were showed for traits namely; thousand kernel weights (55.11%), hectoliter weight (56.38%), harvest index (46.69%) and biomass grain yield (51.84%). Low values of broad sense heritability were revealed; number of grain per spike (29.62%) and grain yield (6.21%).

Very high estimates of broad sense heritability have been also reported by previous researchers for days to heading, plant height (Negasa *et al.,* 2016; Kefale and Menzir, 2019; Bayisa *et al*., 2020); for grain filling period (Bayisa *et al.,* 2020). Low estimates of broad sense heritability have been also reported by previous researchers for number of kernel per spike, grain yield (Adhiena *et al*., 2016).

Heritability values are helpful in predicting the expected progress to be achieved through selection process. Traits with high broad sense heritability estimates might respond effective to selection since it expected that, environment expression on phenotypic expression is low. Thus indicates higher relative magnitude of genotypic variance for the total variations among the studied genotypes with respective high heritability traits. Therefore, based on their phenotypic expression selection on high and very high broad sense heritability may be respond effective because it is expected that traits with high heritability estimate have a close correlation between phenotypic and genotypic appearance.

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotype. Hence, knowledge on heritability coupled with genetic advance is more useful. Genetic advance (GA) under selection referred to the improvement of characters in genotypic value for the new population compared with the base population for one cycle of selection at given selection intensity (Singh, 2001). Furthermore, Hamdi *et al*. (2003) stated that Genetic advance (GA) is importance to predicting the expected genetic gain from one cycle of selection. Estimates of GA values for all characters studied are displayed in (Table 3).

Genetic advance as percent of the means (GAM) in this study ranged from 1.77 to 17.10 % for grain yield kg/ha and days to heading respectively (Table 3). According to Johnson *et al*. (1955) that the value of genetic advance as percent of the mean is categorized as low (< 10%), moderate (10 –20%) and high (>20%). The estimates of genetic advance as percentage of the mean were moderate for days to heading (17.10%), plant height (14.83%), and grain filling period (11.03%), thousand kernel weight (10.78%), biomass grain yield (10.52%), spike length (13.60%) and harvest index (14.41%). However, the

estimates of genetic advance as percentage was low for days to maturity (4.61%), hectoliter weight (2.72%), number of spikelet per spike (8.51%), number of grain per spike (4.45%) and grain yield (1.77). Similar results have been reported for spike length by (Ghallab *et al.,* 2016).

The traits having high values of heritability coupled with moderate genetic advance as percent of the mean namely; days to heading, plant height, grain filling period, and spike length suggest that selection for improvement of these characters may be satisfying. It also indicates greater role of non-additive gene action in their inheritance.

Similar agreement with also reported by previous researchers for plant height Dargicho *et al.* (2015), for days to heading, grain filling period and spike length (Obsa *et al.*, 2017). Low heritability with low genetic advance as percent of the mean revealed for number of grain per spike and grain yield. The expression of economically importance characters through additive gene action make selection for crop improvement might be rewarding and can be confirmed by recording high value of broad sene heritability along with high genetic advance as percentage of mean (Raia *et al.,* 2016).

Low heritability together with low genetic advance as percent of the mean for number of grain per spike and grain yield the major effect of non-additive gene action on their expression, so the genetic potential of such traits would be exploited through heterosis breeding followed by recurrent selection. The presence of higher environmental factors along with non-additive gene action might be the possible causes for the lower values of heritability and genetic advance as percentage of the mean. In line with Khalil *et al.* (2010) findings for number of grain per spike.

Table3. *Estimation of ranges, mean, standard error (SE), variance, and coefficient of variation, heritability, genetic advance and genetic advance as % of mean for different quantitative traits in bread wheat varieties.*

Traits	$\bar{x}$ ±SE	Range		δ^2g	δ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GA (%)
		Min.	Max.							
DH	66.58 ±0.82	52.50	79.50	31.82	33.27	8.47	8.66	95.66	11.38	17.10
DM	133.62 ±1.61	126.25	143.00	11.31	14.33	2.52	2.83	78.93	6.16	4.61
PH	99.19 ±2.50	79.50	119.25	56.00	61.72	7.54	7.92	90.74	14.71	14.83
GFP	67.04 ±1.64	57.75	78.25	15.08	17.70	5.79	6.27	85.21	7.39	11.03
TKW	36.06 ±1.60	26.02	44.80	6.45	11.70	7.04	9.48	55.11	3.89	10.78
HLW	76.18 ±0.73	72.31	80.26	1.79	3.18	1.76	2.34	56.38	2.07	2.72
BMY	7543.3 ±617.78	5641.2	9588.3	285428.10	550566.95	7.08	9.84	51.84	793.58	10.52
HI	45.66 ±4.89	24.86	60.94	21.78	46.63	10.22	14.96	46.69	6.58	14.41
SL	8.11 ±0.48	6.70	10.30	0.37	0.47	7.47	8.48	77.78	1.10	13.60
NSS	19.41 ±0.90	17.00	23.00	0.98	1.51	5.11	6.32	65.28	1.65	8.51
NGS	51.81 ±2.74	43.75	64.25	4.21	14.21	3.96	7.27	29.62	2.30	4.45
GlY	3534.33 ±286.38	2245.10	4591.60	14746.05	237550.54	3.44	13.79	6.21	62.42	1.77

Where: δ^2p =Phenotypic variance, δ^2g =Genotypic variance,δ^2g l= variance of genotype by location interaction, PCV = phenotypic coefficient of variance, GCV = Genotypic coefficient of variation, H^2=Broad sense heritability, GA= genetic advance, GA (%) = Genetic advance as percent of mean. Abbreviations: DH=Days to heading, DM=Days to maturity, PH=Plant height, GFP=Grain Filling Period, TKW=Thousand Kernels Weight, HLW=Hectoliter weight, BMY=Biomass Yield, HI=Harvest

Index, SL=Spike Length, NSS=Number of spikelet per spike, NGS=Number of Kernels per Spike, GlY= Grain yield (Kg/ha).

4. SUMMARY AND CONCULUSSION

Genetic variability among the tested varieties from different traits helpful for direct and indirect selection. Attention should be given for traits which has moderate to high variability and genetic advance in order to bring an effective response of grain yield improvement. The variability among the genotypes, heritability and associations in the tested traits of the genotypes confirmed possibility to increase wheat productivity in target area. Hence, selection and hybridization on those genotypes based on the trait with high GCV, heritability, and genetic advance on grain yield can be recommended for further yield improvement of bread wheat at particular location.

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