

Genetic Variability, Correlation and Path Analysis of Yield and Yield Related Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes for Moisture Stress Areas of Borana

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Abstract: Thirty-six bread wheat genotypes were evaluated in 6*6 simple lattice design at Yabello on station. The experiment was objected to estimate the genotypic and phenotypic variance, heritability, genetic advance and coefficient of variation analysis of yield and yield contributing traits and to identify the trait and breeding procedure for bread wheat yield and yield contributing traits improvement. The result revealed difference among genotypes for all measured traits except harvest index. The estimates of genetic phenotypic variance were greater than genetic variance for all traits. The highest genetic variability was recorded for days to maturity 46.09 while the lowest was recorded for harvest index (0.0002). Among all traits, higher GCV and PCV values (>20%) were observed for grain yield and spike length while the lowest GCV and PCV values (<10%) were recorded for days to maturity, thousand seed weight, plant height and harvest index. The result revealed, all traits showed, in the range of high heritability above 60%. The knowledge on heritability of traits is helpful to decide the selection procedure to be followed to improve the trait in a situation. Generally, direct selection may be effective based on days to maturity, grain yield, and total biomass yield to develop a high yielding bread wheat variety with better quality. For the traits like plant height, thousand seed weight and harvest index Heterosis breeding is suitable to develop a variety. Therefore, it was suggested that breeders should consider the yield related traits to get the desired genetic constitute for future breeding strategy.

Keywords: Bread Wheat, Genetic Advance, GCV, Heritability and PCV

1. Introduction

Bread Wheat (*Triticum aestivum* L. $2n=6x=42$) belongs to the family of *Poaceae*, tribe *Triticeae* of the family *Gramineae* originated in South West Asia area known as Fertile Crescent [1] (Mergoum *et al.*, 2009). Wheat is the second only to rice which provides 21% of the total food calories and 20% of the protein for more than 4.5 billion people in 94 developing countries. Wheat is the ‘king of cereals’ due to its acreage, productivity and the prominent position in international food grain trade [2] (Rehman, 2013). Ethiopia is the largest wheat producer from sub-sahara Africa. The total production of wheat in 2019/20 cropping season was 4.93 million tons [3] (FAO, 2020)

Genetic variability is the measure of the tendency of individual genotypes in a population to vary from one another

for certain traits of interest, which is the base of crop improvement [4] (Debele, et al., 2014). The presence of genetic variability in a population can be divided into heritable and non-heritable variation. The efficiency of selection is dependent upon the variability present in the materials you are going to evaluate and the extent to which it is heritable to its successive offsprings which sets the limit of progress that can be achieved through selection [5]. Heritability knowledge provide reliable tool to the breeder to predict a successful cross with high heritability transmission to the progeny and thus are useful in the incorporation of characters into the offspring and early selection in generation’s improvement [6]. Genetic advances measure the expected genetic progress that would result from the best performing genotypes for the trait being evaluated [7]. Character exhibiting high heritability may not necessarily give high genetic advance. [8] showed high

heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. However, heritability and genetic advance should be considered simultaneously because it is not always true that high heritability will always be associated with high genetic advances [8, 9]. Genotypic and phenotypic coefficients of variation are used to quantify the variability among different genotypes [9]. The differences between genotypic and phenotypic coefficient of variation indicate the environmental influence. Low difference between PCV and GCV indicates the effect of environment is low on selected traits. But if PCV is high and GCV is low then it may imply that environmental effects on the selected traits [10]. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability (h^2_B) and genetic advance as percent of mean (GA) of the traits studied. Different studies conducted by various researchers have shown that high heritability alone is not enough for selection; it must be accompanied with substantial amount of genetic advance [11, 12]. However, if a trait is controlled by non-additive gene heritability becomes high but low genetic advance, while if the trait ruled by additive gene, both heritability and genetic advance would be high [13, 14]. Knowledge of genetic variability, heritability, genetic advance and genetic advance as percent of mean are important tools in crop improvement for plant breeders in predicting the behavior of successive generation and making desirable selections. Therefore, the following investigation is objected

to estimate the heritability, genetic advance and coefficient of variation analysis of yield and yield contributing traits.

2. Materials and Methods

The experiment was done at Yabello site in 2018 main cropping season. Yabello is Borana Zone capital town and is situated 563km from Addis Ababa to south direction. Yabello is situated at 04°52'49" and 038°08' 55" latitude and longitude, respectively, at an altitude of 1636masl. The soil of study area is characterized by well-drained sandy loam (46% sand, 36% silt and 18% clay), with a pH of 7.03. It has 0.026% total nitrogen, 15.36 ppm Phosphorus and 20.4 meq of/100 gm soil CEC.

2.1. Experimental Materials and Design

Thirty-six bread wheat genotypes were used for the current investigation. Fentale 2, variety was used as a standard check. The genotypes were obtained from Werer Agricultural research center. The experiment was conducted by triple square lattice 6*6 with three replications. Each experimental unit consisted of six rows. Data were collected from the central four rows of 2.5m length with 20cm spacing between rows and 2m height. A seed rate of 125kg/ha⁻¹ was used. Recommended cultural practices for maize production were applied during the growing season.

Table 1. The lists of materials used for the current experiment.

Code	Pedigree
YB-2018-1	Atila-7
YB-2018-2	ANGI-2/HUBARA-3
YB-2018-3	FLORKWA2/6/SAKER'S/5/RBS/ANZA/3/KVZ/HYS/YMH/TOB/4/BOW
YB-2018-4	KAUZ'S/FLORKWA-1//GOURMIA-3
YB-2018-5	Fentale/Moontij-3
YB-2018-6	HIDDAB/ATTILA-7
YB-2018-7	PRINIA-1//NESMA*2/14-2/3/DUCULA
YB-2018-8	HUBARA-5/ANGI-1
YB-2018-9	HUBARA-3*2/SHUHA-4
Fentale 2	fentale 2
YB-2018-10	ADEL-2
YB-2018-11	KAUZ'S/FLORKWA1//GOURMIA-3
YB-2018-12	ATTILA/AWSEQ-4
YB-2018-13	ETBW5535
YB-2018-14	PASTOR-2/HUBARA-5
YB-2018-15	KAUZ'S/FLORKWA-1//GOURMIA-33
YB-2018-16	PASTOR-2/HUBARA-55
YB-2018-17	DAJAJ-1//VEE'S/SAKER'S
YB-2018-18	ETBW5957
YB-2018-19	BJY/COC//PRL/BOW/3/BLOYKA-1
YB-2018-20	NAVJ07/SHORTENED SR26 TRASLOCATION/3/ATTILA/BAV92
YB-2018-21	TUKURU/BAV92/RAYON/6/PG8201KAUZ/4/SHA7 (2)
YB-2018-22	TUKURU/BAV92/RAYON/6/PG8201KAUZ/4/SHA7 (3)
YB-2018-23	KRICHAUFF/2*PASTOR//SHUHA-8/DUCULA
YB-2018-24	BAVIS*2/4/PASTOR//HXL7573/2*BAU/3/SOKOLL
YB-2018-25	NELOKI*2/PRL
YB-2018-26	TUKURU/BAV92/RAYON/6/PG8201/KAUZ/4/SHA7 (7)
YB-2018-27	FRANCOLIN#1
YB-2018-28	KS82W418/SPN/3/CHEN/AE.SQ//2*OPATA/4/FRET2/5/2*SOKOLL
YB-2018-29	ATILA 50Y//ATTILA/BCN/3/STAR*3/MUSK-3
YB-2018-30	HUBARA-1//ACHTAR/INRA 1764
YB-2018-31	KATILA-11/ETBW4919//SIRAJ-1

Code	Pedigree
YB-2018-32	PBW343*2/KUKUNA//KIRITATI
YB-2018-33	INQALAB 91*2/BUC*2/KUKUNA
YB-2018-34	KATILA17/DEEK2/8VEE'S/7/CEBECO148/3/RON/CHA//NOR67/5/HK/38M
YB-2018-35	JNRB, 5/PIFED

2.2. Collected Data

Plant height and spike length were collected in plant base while the others (days to heading, days to maturity, grain yield and total biomass) were collected in plot base. Harvest index (HI) was calculated by using the following formula:

$$HI (\%) = \frac{\text{Grain yield}}{\text{Biological yield}} \times 100$$

2.3. Data Analysis

The collected data were subjected to SAS computer software to test significance of variation among genotypes. Least significant difference (LSD) test at 1% and 5% significance level were used for mean comparisons.

Estimation of variance

Genotypic variance: It is the inherent variation which remains unaltered by the environment. It is the variation due to genotypes. It is denoted by VG and is calculated using the formula:

$$VG = \frac{Mst - MSe}{r}$$

Where Mst = mean sum of squares of treatments

Mse= mean sum of squares of error

r= number of replications

Environmental variance: it is the non-heritable variation which is due to the environment which varies depending upon the environments. It is denoted as

VE and calculated as

$$VE = Mse$$

Phenotypic variance: it is the total variation which is observable and is the sum total of genotypic and environmental variances. It is represented by VP and calculated as

$$VP = VG + VE$$

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated following the method [15].

$$PCV = \frac{\sqrt{\text{phenotypic variance}}}{\text{mean value of the trait}} \times 100$$

$$GCV = \frac{\sqrt{\text{genotypic variance}}}{\text{mean value of the trait}} \times 100$$

Environmental coefficient of variation (ECV): It is the ratio of environmental standard deviation to the mean expressed as percentage and is calculated using the formula

$$ECV = \frac{\sqrt{\text{Environment variance}}}{\text{mean value of the trait}} \times 100$$

GCV and PCV are classified as Low (< 10%), Moderate (10 – 20%) and High (> 20%) according to the research [16].

Variance components were estimated [17]. Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), broad sense heritability (h^2), genetic advance (GA) and genetic advance in percentage of mean (GA%) estimated as suggested [18].

Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance according to [19].

$$\text{Heritability } (h^2B) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability could be classified as low (<30%), medium (30-60%) and high (above 60%) according to [8] Johnson *et al.* (1955).

Estimation of genetic advance: Genetic Advance (GA) and percentage of the mean (GAM) assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated [8] as:

$$GA = \frac{K \times \sqrt{\sigma^2 p} \times \sigma^2 g}{\sigma^2 p}$$

Where

GA= Expected genetic advance

K=Standardized selection differential at 5% selection intensity (K = 2.063)

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

The genetic advance as percentage of mean (GAM) was computed as:

$$GAM(\%) = \frac{GA}{\bar{X}} \times 100$$

Where

GAM=Genetic advance as percentage of mean

GA=Expected genetic

X=grand mean of character

GA as percent of mean categorized as suggested [8] Johnson *et al.* (1955) 0–10% = Low, 10–20% = Moderate and >20% = High

3. Results

The analysis of variance, showed significant difference among genotypes for all measured traits except harvest index which was presented in Table 2. Estimation of phenotypic variance was greater than genotypic variance for all traits under study. The highest genetic variability was recorded for days to maturity 46.09 followed by days to heading (21.80) while the lowest genetic variability was recorded for harvest index (0.0002) followed by grain yield (0.50) (Table 3). Based

on genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) results, PCV values, were greater than GCV values for all traits but the differences were small for all traits except spike length. Among all traits, higher GCV and PCV values (>20%) were observed for grain yield and spike length and the moderate GCV and PCV values (10%-20%) were recorded for days to heading and total biomass yield which suggest possible to manipulate these traits through breeding while the lowest GCV and PCV values (<10%) were recorded for days to maturity, thousand seed weight, plant height and harvest index suggesting the difficulty of manipulating these traits through breeding.

In the present investigation, depending on heritability estimates, heritability ranged from 62.50% (for harvest index) to 92.44% (total biomass) which was in the range of high heritability. The highest heritability was recorded for total biomass (92.44%) followed by grain yield (90.39%) (table 3).

From the investigation, the result of genetic advance showed that, the highest genetic advance was recorded for maturity date (13.30) followed by days to heading (8.65), while the lowest genetic advance was recorded for harvest index (0.03) followed by grain yield (1.39). Genetic advance as percentage of a mean is the amount of increase in performance that is achieved annually through artificial selection as percentage of grand mean of the traits under study. If the value of GA% is from 0-10% is low, if the value lay between 10 to 20% GA% is moderate, if the value lay above 20% GA% is high. Based on this description, the highest GA% were recorded for spike length (38.92%), grain yield (38.39%) and total biomass (31.79%). The medium GA% were obtained for days to heading (18.60%) and days to maturity (15.45%). The lowest GA% were recorded for plant height (2.41%), thousand seed weight (8.59%) and harvest index (8.05%). (Table 3)

Table 2. Mean square (ANOVA) table of Bread wheat genetic variability analysis.

Source of variation	Df	DH (day)	DM (day)	PH (cm)	SL (cm)	TSW (gm)	GY (ton. ha)	BM (tone/ha)	HI
Group	2	10.04ns	3.12ns	1.17ns	0.25ns	2.57ns	0.10ns	0.08ns	0.0002
Block (group)	15	7.13ns	6.16ns	3.34ns	1.00**	3.16ns	0.04ns	0.17ns	0.0001
Genotypes	35	52.28***	119.16***	91.81**	2.80***	30.34***	1.39***	4.92**	0.0008
Error	55	4.73	4.71	3.60	0.15	3.16	0.06	0.12	0.0002
CV		4.69	2.52	2.35	4.91	1.81	6.83	4.38	4.71
R ² %		90.90	95.18	94.85	93.44	3.75	94.42	96.38	70.79
LSD (1%)		4.70	4.69	4.10	0.84	83.35	0.52	0.75	0.03
LSD (5%)		3.54	3.54	3.09	0.63	2.29	0.39	0.56	0.02
Variance of D		3.15	3.14	2.40	0.10	1.34	0.04	0.08	0.0001

Df=degree of freedom, DH=days of heading, DM=days to maturity, PH=plant height, SL=spike length, TSW=thousand seed weight, GY=grain yield, BM=biomass, HI=harvest index, CV=coefficient of variance, LSD=least significant difference, Variance of difference

Table 3. Grand means, genotypic and phenotypic coefficient of variability, heritability and genetic advance of the 8 agronomic traits of the sixteen durum wheat genotypes tested.

Trait	VG	VP	VE	Gm	GCV	PCV	ECV	PCV-GCV	h ² (%) (broad sense)	GA	GA%
DH	21.80	27.04	5.25	46.49	10.04	11.19	4.93	1.14	80.60	8.65	18.60
DM	46.09	51.12	5.03	86.07	7.89	8.31	2.60	0.42	90.17	13.30	15.45
PH	1.01	1.16	0.15	80.59	1.25	1.33	0.47	0.09	87.42	1.94	2.41
SL	3.55	5.65	2.10	7.92	23.80	30.02	18.30	6.22	62.84	3.08	38.92
TSW	3.55	5.65	2.10	35.87	5.25	6.62	4.04	1.37	62.84	3.08	8.59
GY	0.50	0.55	0.05	3.62	19.57	20.59	6.38	1.01	90.39	1.39	38.39
BM	1.60	1.73	0.13	7.89	16.02	16.67	4.58	0.64	92.44	2.51	31.79
HI	0.0002	0.0004	0.0001	0.3125	4.94	6.25	3.82	1.31	62.50	0.03	8.05

VG=genotypic variance, VP=phenotypic variance, VE=environmental variance, GCV=genotypic coefficient variance, PCV=phenotypic variance, GA=genetic advance, GA%=percentage of genetic advance, Gm=grand mean.

4. Discussion

The presence of significant variation among genotypes for the traits implies the presence of substantial variation among genotypes, which is central to the study of both quantitative and qualitative traits and provides an opportunity for plant breeders to improve these characters through breeding. The amount of genotypic and phenotypic variability in a species is critical in breeding better varieties and beginning a breeding program. The variability in a population is assessed using genotypic and phenotypic coefficients of variation. Table 2 shows the estimated genotypic and phenotypic coefficients of variability (GCV and PCV), broad sense heritability (h²B),

and genetic advance as a percent of mean (GA) of the traits studied. High estimates of genotypic variance and phenotypic variance recorded for days to maturity, days to heading, spike length and thousand seed weight implies presence of sufficient inherent genetic variance over which selection can be effective. Similar results were reported [20-25]. For traits PCV values greater than GCV values for all traits but the differences were small for all traits except spike length. This indicated influence of environmental effect was small for the expression of the character, but for spike length, the environment plays a substantial role in the expression of the trait hence, selection based on this trait is not advisable. The finding of different scholar's states similar result [23, 26].

The estimates of heritability act as analytical instrument in

expressing the consistency of phenotypic value. The result of the finding revealed, all traits showed, in the range of high heritability above 60%. High heritability comforts in effective selection for a given trait. The higher in broad sense heritability exhibited the additive genetic variation was the major component of genetic variation in the inheritance of these traits and the traits performance variations are mainly under genetic control less influenced by environments. The plant breeder therefore, may make his selection safely on the basis of phenotypic expression of these traits in the individual plant by adopting simple selection methods and the traits can be easily improved. In the study, all studied traits showed higher broad sense heritability in the tested bread wheat genotypes as indicated in table 3. Naik, V. R. et al. [27] found similar result in their study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. In the same line, the authors [28-31] reported high heritability value for different bread wheat traits.

The genetic advance is the expected genetic progress for particular trait under selection cycle and measures the extent of its stability under selection pressure [27]. Genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value [8]. High heritability accompanied by high genetic advance was observed for days to maturity suggesting predominance of additive gene action in the expression of this trait hence, pedigree method of selection will be a rewarding to improve the traits. Other traits like plant height, grain yield and biomass yield recorded high heritability with low genetic advance may be attributed to non-additive or epistasis, indicating that the characters were influenced by the environment thus, improvement through selection may not be advisable. Accordingly, improvement these characters could be through hybridization and heterosis [32, 33]. In contrary, Naik, V. R. et al. [27] found high genetic advance for grain yield while low for days to heading. High heritability coupled with high genetic advance as percent of mean is observed for the traits like total biomass, grain yield and spike length indicating that these traits are under the strong influence of additive gene action and hence direct selection based on these traits would be effective. High heritability but low GA% values is observed for the traits like plant height and thousand seed weight this may be attributed to non-additive or epistasis gene action, indicating that the characters were highly influenced by the environment thus, improvement through selection may not be advisable. Accordingly, improvement in these characters could be through hybridization and heterosis [32, 33]. Similar findings have been reported [34, 35]. However, high heritability for test weight and relatively lower estimates for genetic advance.

5. Conclusion

From the present study, the analysis of variance showed significant difference among genotypes for all measured traits except harvest index. Genetic variance was greater than

phenotypic variance for all traits. From the present study, it is evident that genotypes studied may provide good source of material for further breeding program. Therefore, information on the genetic parameters such as genetic variation, phenotypic variance and environmental variance, coefficient of variation, heritability and genetic advance can help the breeder to evolve suitable cultivars within a short time. The knowledge on heritability of traits is helpful to decide the selection procedure to be followed to improve the trait in a situation. Generally, direct selection may be effective based on days to maturity, grain yield, and total biomass yield to develop a high yielding bread wheat variety with better quality. For the traits like plant height, thousand seed weight and harvest index Heterosis breeding is suitable to develop a variety.

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