International Journal of Sustainable Agricultural Research
2020 Vol. 7, No. 2, pp. 56-65.
ISSN(e): 2312-6477
ISSN(p): 2313-0393
DOI: 10.18488/journal.70.2020.72.56.65

VARIABILITY, HERITABILITY AND GENETIC ADVANCE ANALYSIS IN BREAD WHEAT (*Triticum Aestivum L.*) GENOTYPES IN NORTHWESTERN ETHIOPIA

Misganaw Ferede[1+]
Fisseha Worede[2]

[1]*Plant Breeder, Adet Agricultural Research Center, Bahir Dar, Ethiopia.*
Email: misganaw1129@gmail.com Tel: +251918082129
[2]*Plant Breede, Bahir Dar University, Bahir Dar, Ethiopia.*
Email: fisseha.kirkos@gmail.com Tel: +251961269503

(+ Corresponding author)

Article History
Received: 7 October 2019
Revised: 14 November 2019
Accepted: 17 December 2019
Published: 27 January 2020

Keywords
Bread wheat
Breeding investigation
Genetic advance
Genetic coefficient of variation
Grain yield
Heritability
Phenotypic coefficient of variation
Variability
Wheat rust.

ABSTRACT

Studies on degree of genetic advance as well as rate of genetic progress in grain yield and yield associated traits in bread wheat genotypes over years are limited. Therefore, this study was initiated to explore genetic advance and rate of genetic progress over years in bread wheat breeding program. Twelve bread wheat genotypes released in between 1995-2012 were used as experimental treatments. The experimental treatments were laid out on randomized complete block design with three replications across locations over years. The study was conducted at Adet, Debretabor, Finoteselam, Injibara and Simada in 2014 and 2015 cropping seasons. The traits grain yield, biological yield, spike length, number of seeds per spike and thousand seed weight showed medium genetic and phenotypic variation, higher heritability and medium genetic advance to the mean of the population whereas days to physiological maturity, plant height, and test weight showed negligible in both genotypic and phenotypic variation, higher heritability and negligible genetic advance to the mean of the population. In the genetic advance analysis over years, only thousand seed weight showed positive significant increment while grain yield, biological yield, days to physiological maturity, plant height and test weight showed positive non-significant increment. Meanwhile spike length and number of seeds per spike showed negative non-significant decrement over 18 years. Therefore, breeders should be considered the yield related traits to bring the desired genetic enhancement as well as to develop demanded genotypes in the future bread wheat breeding investigations.

Contribution/Originality: This study is one of very few studies which have investigated the magnitude of genetic advance of grain yield and yield related traits in bread wheat released varieties in Ethiopia. This study documents is vital to plant breeders to consider the non-significant steady increment of grain yield in bread wheat released varieties over 18 years.

1. INTRODUCTION

Wheat is a staple food all over the World. In the World among 125 countries, Ethiopian wheat area coverage and productivity is ranked 25th (1.7 million hectare) and 63th (2812 kg/ha), respectively. Its productivity is by far lower compare to wheat producing countries such as Ireland (10174kg/ha), New Zealand (9863kg/ha) and Netherlands (9093kg/ha) (FAOSTAT, 2017). In Ethiopia, bread wheat variety development research program has been started since 1970s, and 89 bread wheat genotypes have been released in between 1970-2017 through landrace collection, introduction and intraspecific hybridization (MoANR (Ministry of Agriculture and Natural Resource), 2016). However, due to evolving of new races of wheat rusts primary stem and yellow rusts only few bread wheat genotypes are used as genetic material to wheat production in Ethiopia (Oliver, 2014). As a result the yielding potential of the genotypes declined due to breakdown of race-specific resistance over years (Kolmer, 2013). The productivity of bread wheat is affected by factors such as genotypes, environments, management practices and their interactions (Gashaw *et al.*, 2013; Haile *et al.*, 2013; Fentaw *et al.*, 2015; Misganaw, 2017) as well as pests in particular wheat rusts. However, it is difficult to estimate simultaneously the interaction effects of these factors over years.

Knowledge on nature and magnitude of variation in genotypes is of great importance to develop genotypes for high yield and other desirable traits (Chekole *et al.*, 2016). The magnitude of genetic variability, heritability and genetic advances in selection of desirable traits are pertinent and compulsory issues for the plant breeder to consider the traits during crossing in breeding program (Bello *et al.*, 2012). Monitoring of genetic advance in crop improvement programs is necessary to measure the efficiency of the program. Periodic measurement of genetic advance also allows the efficiency of new technologies incorporated into a program to be quantified (Benhilda *et al.*, 2017).

As Mekuria *et al.* (2018) reported, estimation of genetic progress in variety development help breeders to make a decision on the increment of productivity as well as to consider the breeding strategies in the future. Hereby the study was initiated with the objectives to analyze the performance, genetic variability, heritability, extent of genetic advance and genetic improvement of grain yield and agronomic traits in bread wheat released genotypes over 18 years.

2. MATERIALS AND METHODS

2.1. Description of the Study Areas

The study was conducted in bread wheat producing moisture deficit to acidic prone highland areas in Northwestern Ethiopia. The experiment was done at Adet Agricultural Experimental sites namely Adet, Debretabor, Finoteselam, Injibara and Simadain 2014 and 2015 cropping seasons. The agro-ecological data of the experimental sites are listed in Table 1.

Table-1. Geographical locations and climate data of the experimental sites.

			Geographical		Climate data for two cropping seasons			
					2014		**2015**	
Testing sites	**Code**	**Altitude (masl)**	**Latitude**	**Longitude**	**RF (mm)**	**Average temp(^{0}C)**	**RF (mm)**	**Average temp (^{0}C)**
Adet	E1	2240	11^{0}16'N	37^{0}29'E	658.6	17.53	948.9	19.4
Simada	E2	2460	11^{0}03N	37^{0}30'E	736.1	13.27	770.6	15.07
Debretabor	E3	2591	11^{0}51'N	38^{0}01'E	1102.7	15.48	958.1	15.94
FinoteSelam	E4	1917	1042N	3716E	NA	18.76	NA	NA
Injibara	E5	2560	1057N	3656E	1562	NA	NA	NA

Source: Adet Agricultural Research Center and Ethiopia Meteorological Agency, Bahirdar Branch.

RF (mm) = total amount of rain fall in the cropping season; Average tem (^{0}C) = average temperature in the cropping season and NA=Not Available.

2.2. Experimental Materials and Procedures

The experimental bread wheat genotypes were selected purposively which are used as genetic materials for production. The treatment consisted of twelve bread wheat genotypes which are released in between 1995-2012. The agro ecological zones and productivity of the experimental genotypes data are given in Table 2. The experimental land was ploughed three times and labeled manually at time of planting. The treatments were laid out as randomized complete block design with three replications per treatment at each site. Planting was done in the first and the second week of July with seeding rate of 150 kg/ha on the plot area of 1.2 x 2.5 m with a net plot area of 0.8 x 2.5 m. Urea and DAP fertilizers as a source of nitrogen and phosphorous were applied at the rate of 74 kg N/ha and 46 kg P_2O_5/ha for Adet, whereas 120 kg N/ha and 46 kg P_2O_5/ha for Simada, Debretabor, Finoteselam and Injibara. The total amount of DAP and 1/3 of urea were applied at planting and the remaining 2/3rd of urea was applied at tillering after the first weeding. Weeding was done manually two times at tillering stage and booting stage (50-60 days before heading) depending on the weed infestation of the trial sites.

Table-2. Description of bread wheat genotypes evaluated at five locations during 2014 and 2015 cropping seasons in Northwestern Ethiopia.

Genotypes	Code	Breeder center	Year of release	Grain yield (t/ha) at time of release at time		Recommended Agro-ecology Zone	
				On station	On farm	Alt(masl)	RF(mm)
Hidase(ETBW 5795)	V1	KARC	2012	4.4-7	3.5-6	2200-2600	>500
Huluka(Flag 5)	V3	KARC	2012	4.4-7	3.8-6	2200-2600	500-800
Ogolcho(ETBW 5520)	V2	KARC	2012	2.8-4	2.2-3.5	1600-2100	400-500
Shorima(ETBW 5483)	V11	KARC	2011	2.9-7	2.3-4.4	2100-2700	700-1100
Gambo(QUIAU#2)	V4	KARC	2011	3.5-5.7	4.5	750	NA
Tsehay(HAR 3837)	V9	DBARC	2011	3.8	2.8-3.5	2600-3100	>900
Danda'a(DANPHE#1)	V5	KARC	2010	3.5-5.5	2.5-5	2000-2600	>600
Bolo(HAR 3816)	V8	DBARC	2009	2.8-3.5	2.3-3.3	2580-3100	>904
Menze(HAR 3008)	V10	DBARC	2007	1.9-3.3	1.5-2.7	2800-3100	>904
Gassay(HAR 3730)	V6	ADARC	2007	4.4-5	3.5-4.7	1890-2800	>700
Tay (ET-12 D4/ HAR-604(1)	V7	ADARC	2005	2.5-6.1	3.4-5.8	1900-2800	>700
Kubsa(HAR 1685)	V12	KARC	1995	5.8-6.3	4-4.5	1850-2800	500-800

[a] **Source:** MoA, Crop Variety Register (1995-2012).

[b]ADARC = Adet Agricultural Research Center; Alt= Altitude; DBARC = Debrebirhan Agricultural Research Center; KARC = Kulumsa Agricultural Research Center; RF=Rainfall; SC =Standard Check and NA=Not available.

2.3. Data Collection and Statistical Analysis

The phonological data such as days to 95% physiological maturity as well as agronomic traits such as grain yield, biological yield, plant height, and spike length, number of seeds per spike, thousand seed weight and test weight were collected in the study.

The data were analyzed using GenStat (18thedn), SAS version9.0 and Micrsoft Excell 2007 software for the analysis of variances as well as genetic variability, heritability, genetic advance, linear regression analysis over years.

The variance components of genotypes over environments were calculated following the equations suggested by Bello *et al.* (2012) and Mathew (2015).

Genetic variance ($\delta^2 g$) = $\frac{MSg - MSge}{rl}$

Variety by environment interaction variance ($\delta^2 ge$) = $\frac{MSge - MSe}{r}$

Phenotypic variance ($\delta^2 p$) due to genetic effects = $\delta^2 g + \frac{\delta^2 ge}{e} + \frac{\delta^2 e}{rl}$

Where $\delta^2 g$ = genetic variance, MSg = mean square of genotypes, MSge = mean square of genotype by environment interaction, $\delta^2 ge$= genotype by environment interaction variance, MSe= mean square oferror, $\delta^2 e$ =error variance, $\delta^2 p$ =Phenotypic variance, e= number of environments and r = number of replications

The coefficient of variation of genotypes and phenotypes were calculated as the following equations suggested by Burton and Devane (1953).

Genetic coefficient of variation (GCV %) = $\left[\frac{\sqrt{\delta^2 g}}{\bar{x}}\right] * 100$

Where $\sqrt{\delta^2 g}$ = the square root of genetic variance and $\bar{x}$ = grand mean.

Phenotypic coefficient of variation (PCV %) = $\left[\frac{\sqrt{\delta^2 p}}{\bar{x}}\right] * 100$

Where $\sqrt{\delta^2 p}$ = the square root of phenotypic variance and $\bar{x}$ = grand mean, PCV and GCV values were classified as low (0-10%), moderate (10-20%) and high (>20) values as indicated by Sivasubranian and Menon (1973).

Broad sense heritability (H^2) of genotypes across environments was calculated as follows suggested by Falconer and Mackay (1996) and Bello *et al.* (2012).

$$H^2 = \frac{\delta^2 g}{\delta^2 p} = \frac{\delta^2 g}{\delta^2 g + \frac{\delta^2 ge}{e} + \frac{\delta^2 e}{re}}$$

Where heritability was classified as suggested by Robinson *et al.* (1949) into low (0-30%), moderate (30.1-60%) and high (>60%).

Genetic advance (GA) between genotypes over environments was calculated as follows according to Bello *et al.* (2012).

$$GA = \sqrt{\delta^2 p} * H^2$$

Genetic advance as a percent of means (GAM) in genotypes was done by the following formula according to Bello *et al.* (2012).

GAM= $GA/\bar{x} * 100$

Where the GA as percent of mean categorized as suggested by Johnson *et al.* (1955) as follows:

0 - 10% = Low, 10 – 20% = Moderate and > 20% = High.

Linear regression analysis on dependent variable Y and independent variable X is represented by the equation: $Y = \beta x + \alpha$

Where Y= the value of the dependent variable, X= the value of independent variable, α= the intercept of the line, β= the regression coefficient (slope of the line), or the changes in y per unit change in X (Yan and Su, 2009). The relative annual genetic advance per year was determined as a ratio of genetic advance to the corresponding mean value of oldest variety.

3. RESULTS AND DISCUSSION

3.1. Traits performance in Bread Wheat Genotypes over Environments

The analysis of variance in bread wheat genotypes, environments and interactions showed significant difference ($P<0.01$) for all measured traits as depicted in Table 3.

Table-3. Performance of grain yield and agronomic traits in 12 bread wheat genotypes across environments in 2014 and 2015 cropping seasons.

Year of release	Genotypes	Code	Traits								
			GY (qt/ha)	BY (qt/ha)	HI(%)	DPM	PH (cm)	SL (cm)	NSPS	TSW (g)	TW (g/hl)
1995	Kubsa	V12	33.22	94.7	33.45	113.9	77.52	7.96	44.43	25.94	71.64
2005	Tay	V7	38.4	108.4	34.75	123.8	95.02	9.098	54.94	29.78	74.63
2007	Gasay	V6	35.36	105.9	33.74	122.9	86.19	8.582	48.12	30.9	76.25
2007	Menze	V10	28.73	89.5	32.24	130.2	93.24	6.561	54.78	26.74	73.7
2009	Bolo	V8	30.02	95	31.85	130.8	94.48	6.64	55.01	27.33	74.16
2010	Danda'a	V5	35.19	110.4	33.05	127.7	94.61	8.103	49.35	33.48	72.14
2011	Gambo	V4	48.92	125.7	39.41	119.2	89.69	8.077	48.86	33.71	77.37
2011	Tsehay	V9	39.3	100.9	38.98	115.4	86.79	8.309	50.39	32.9	76.17
2011	Shorima	V11	42.25	110.4	38.15	118.3	86.45	8.82	43.72	30.85	76.7
2012	Hidase	V1	34.55	94.3	37.94	113.6	80.3	7.724	45.11	32.7	71.94
2012	Ogolcho	V2	46.34	117.8	39.4	119.4	89.92	8.109	47.68	33.63	77.05
2012	Huluka	V3	37.39	100.5	37.68	123.6	80.33	7.942	44.68	28.84	74.53
Mean			37.47	104.5	35.89	121.57	87.88	7.99	48.92	30.57	74.69
CV			9.9	9.6	7.3	3.05	4.5	5.7	9	7.1	2.4
LSD (5%)			5.98	16.07	4.2	1.6	6.43	0.73	7.06	3.48	2.93
Genotypes			**	**	**	**	**	**	**	**	**
Environments			**	**	**	**	**	**	**	**	**
Var*Env			**	**	**	**	**	**	**	**	**

Note: GY=Grain yield, BY= Biological yield, HI=Harvest index, DPM= Days to 95% physiological maturity, PH=Plant height, SL=Spike length, NSPS= Number of seeds per spike, TSW= Thousand seed weight, TW= Test weight, Rep=Replications, Env=Environments, Var by Env= Genotypes by environments, CV= Coefficient of variance and LSD=Least significant difference.

3.2. Variability, Heritability and Genetic Advance in Bread Wheat Genotypes

The genetic variability in tested 12 bread wheat genotypes for the measured traits showed only grain yield had higher phenotypic variation while biological yield, spike length, number of seeds per spike and thousand seed weight showed moderate genotypic and phenotypic variation to the arithmetic mean values as per each trait in the tested bread wheat genotypes. The remaining traits namely days to physiological maturity, plant height and test weight showed negligible in both genotypic and phenotypic variation to the arithmetic mean values as per each trait in the tested bread wheat genotypes. The coefficients of variations in between genotypic and phenotypic variance were narrow differences in all measured traits in bread wheat genotypes Table 4. As Abebe *et al.* (2017) in rice, Gezahegn *et al.* (2015) in bread wheat reported the narrow differences between genotypic and phenotypic coefficient of variation in which indicates the limited effect of environment in expression on the traits.

In the study all the measured traits showed higher broad sense heritability in the tested bread wheat genotypes Table 4. As Abebe *et al.* (2017); Benhilda *et al.* (2017); Chekole *et al.* (2016); Gezahegn *et al.* (2015); Mathew (2015); Moslem *et al.* (2014) and Bello *et al.* (2012) reported, the higher in broad sense heritability mean that the traits performance variations are mainly under genetic control and less influenced by environments.

Table-4. Mean squares, genetic and phenotypic variability, heritability and genetic advance in 12 bread wheat genotypes across environments over years (2014 &2015).

		Mean squares					**Variance Components**		**Coefficient of variation (%)**				
Traits	**Grand mean**	**Rep (2)**	**Genotypes (11)**	**Env (7)**	**Var x Env(77)**	**R (190)**	**δ^2g**	**δ^2p**	**GCV (%)**	**PCV (%)**	**H^2**	**GA**	**GAM (%)**
GY	37.47	187.4	883.7**	4300.8**	191.8**	13.8	46.1	58.9	18.1	20.5	0.78	6.0	16
BY	104.5	720.2	2744.7**	41205**	711.7**	99.62	135.5	183.0	11.1	12.9	0.74	10.0	10
HI	35.89	6.66	210.0**	582.61**	52.77**	6.81	10.5	14.0	9.0	10.4	0.75	2.8	8
DPM	121.57	16.07	850.2**	5423.18**	28.74**	3.59	54.8	56.7	6.1	6.2	0.97	7.3	6
PH	87.88	53.03	881.0**	2134.69**	64.64**	15.96	54.4	58.7	8.4	8.7	0.93	7.1	8
SL	7.99	0.38	13.84**	9.46**	0.56**	0.25	0.9	0.9	11.8	12.0	0.96	0.9	12
NSPS	48.92	3.63	419.0**	1345.26**	56.81**	19.2	24.1	27.9	10.0	10.8	0.86	4.6	9
TSW	30.57	6.59	191.9**	203.54**	34.09**	4.68	10.5	12.8	10.6	11.7	0.82	2.9	10
TW	74.69	4.44	100.6**	184.77**	30.68*	12.8	4.7	6.7	2.9	3.5	0.70	1.8	2

Note: GY=Grain yield, BY= Biological yield, HI=Harvest index, DPM= Days to 95% physiological maturity, PH=Plant height, SL=Spike length, NSPS= Number of seeds per spike, TSW= Thousand seed weight, TW= Test weight, Rep=Replications, Env=Environments, Varx Env= Genotypes by environments interaction, R=Residual, δ^2g= Genetic variance, δ^2p=Phenotypic variance, GCV= Genetic coefficient of variation, PCV= Phenotypic coefficient of variation, H^2 =Broad sense heritability, GA=Genetic advance, GAM=Genetic advance as percent of mean and**= Significant at $P \leq 0.01$.

Among the measured traits, grain yield, biological yield, spike length, number of seeds per spike and thousand seed weight showed moderate genetic advance whereas the remaining traits showed negligible (lower) genetic advance to the mean values in the bread wheat genotypes Table 4. Grain yield only showed medium genotypic variation and higher phenotypic variation, higher heritability and medium genetic advance to the mean of the population in bread wheat genotypes. The traits namely biological yield, spike length, number of seeds per spike and thousand seed weight showed medium variation in both genotypic and phenotypic variation, higher heritability and medium genetic advance to the mean of the population. The observations are in conformation with the findings of Bello *et al.* (2012) the traits showed higher GCV and PCV as well as higher heritability with higher genetic advance were under the control of additive gene effects. While Chekole *et al.* (2016) higher heritability with lower genetic advance indicates that the traits expression by additive gene effect is lower than environmental effects. Hereby grain yield genetic advance in released bread wheat genotypes was medium over 18 years.

3.3. Genetic Advance Progress of Grain Yield and Associated Traits in Bread Wheat Genotypes

The linear regression analysis of the measured traits in bread wheat genotypes showed that only thousand seed weight had positive significant increment over 18 years while grain yield, biological yield, days to physiological maturity, plant height and test weight showed positive non significant increment over 18 years. On the other hand, spike length and number of seeds per spike showed negative non significant decrement over 18 years in bread wheat genotypes Table 5.

Table-5. Linear regression of grain yield and yield related traits in bread wheat genotypes over 18 years.

Traits	Mean of traits	R^2	β	α	Sig. F level	$Y = \beta x + \alpha$
GY	37.47	0.15	0.50^{ns}	-970.25	0.19	y= 0.50x-970.25
BY	104.5	0.12	0.77^{ns}	-1448.8	0.26	y= 0.77x-14488
HI	35.89	0.30	0.90^{ns}	1976	0.06	Y= 0.90x+1976
DPM	121.57	0.01	0.09^{ns}	1997	0.71	Y= 0.09x+1997
PH	87.88	0.05	0.05^{ns}	1992	0.46	Y= 0.05x+1992
SL	7.99	0.0006	-0.049^{ns}	2008	0.98	Y= -0.049x+2008
NSPS	48.92	0.008	-0.033^{ns}	2010	0.92	Y= -0.033x+2010
TSW	30.57	0.43	1.13**	1973	0.01	Y= 1.13x+1973
TW	74.53	0.2	1.08^{ns}	1927	0.13	Y= 1.08x+1927

Note: R^2=Coefficient of determination, β= Coefficient of regression/slope of the line, α=Intercept, GY=Grain yield, BY= Biological yield, HI=Harvest index, DPM= Days to 95% physiological maturity, PH=Plant height, SL=Spike length, NSPS= Number of seeds per spike, TSW= Thousand seed weight and TW= Test weight.

The annual rate of genetic advance of grain yield in bread wheat genotypes was 5 kg/ha/year in between 1995-2012, although non-significant as depicted in Figure 1 and Table 5. This might be due to breakdown of rust resistance of the bread wheat genotypes as well as inconsistency in performance of genotypes across the test environments. However, significant increase in grain yield of relatively recently released genotypes over older variety was reported by Mekuria *et al.* (2018) in durum wheat genotypes, Tibebu (2011) in check pea genotypes, Demissew (2010) in soybean genotypes and Wondimu (2010) in food and malt barley genotypes. In biological yield, there was non-significant annual rate of genetic advance (77 kg/ha/year) in bread wheat genotypes over 18 years. Similar works reported by Wondimu (2010) in food barley genotypes. Genetic advance of days to physiological maturity was non-significant positive trends over years in tested bread wheat genotypes. This study was in line with the reports of Mekuria *et al.* (2018) in durum wheat and Teklu and Tefera (2005) in tef. Genetic advance of plant height was non-significant positive trends in bread wheat genotypes, whereas plant height was decreased significantly in durum wheat genotypes as reported by Mekuria *et al.* (2018) Annual genetic advance of spike length was non-significant decrease in bread wheat genotypes over 18 years, while spike length was decreased significantly in durum wheat genotypes and linseed lines as reported by Mekuria *et al.* (2018) and Wondimu (2010) respectively. Genetic advance of number of seed per spike was non-significant negative trends in bread wheat genotypes over years. On the other hand, genetic advance of number of seed per spike was significant positive trends in durum wheat genotypes and in bread wheat genotypes as reported by Mekuria *et al.* (2018) and Amsal *et al.* (1995) respectively. Genetic advance of thousand seed weight was significant positive trends in the tested bread wheat verities over years. Similar works were reported by Mekuria *et al.* (2018); Tibebu (2011) and Tamene (2008) in durum wheat, cheakpea and fababean genotypes, respectively, over years. Genetic advance of test weight was non-significant positive trends in bread wheat genotypes over 18 years. Similar results were reported by Mekuria *et al.* (2018) in durum wheat over 49 years.

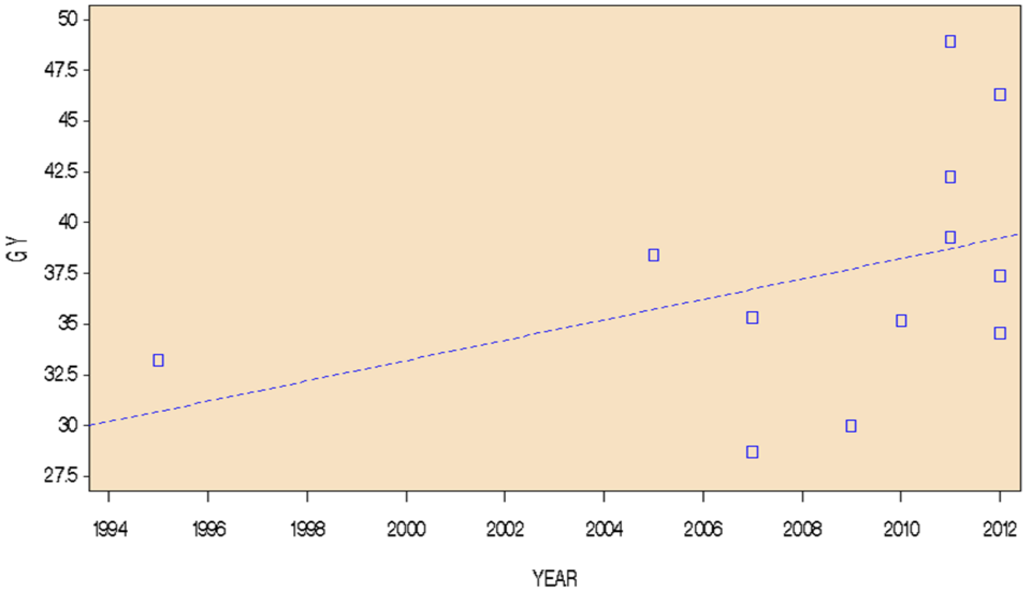

Figure 1. Grain yield regression(Y= 0.50x-970.25) in bread wheat genotypes over years using SAS version 9.

4. CONCLUSIONS

The assessments on genetic variability, heritability and genetic advance as well as genetic improvement over years in released genotypes which exploits the information on the effectiveness of breeding works and the directions in the future breeding strategies in genetic enhancement so far. In this study, grain yield, biological yield, spike length, number of seeds per spike and thousand seed weight showed medium genetic and phenotypic variation, higher heritability and medium genetic advance to the mean of the population whereas the remaining traits namely days to physiological maturity, plant height, and test weight showed negligible in both genotypic and phenotypic variation, higher heritability and negligible genetic advance to the mean of the population in bread wheat genotypes. In the genetic advance analysis over years, only thousand seed weight showed positive significant increment over 18 years; while grain yield, biological yield, days to physiological maturity, plant height and test weight showed positive non significant increment over 18 years. Meanwhile, spike length and number of seeds per spike showed negative non significant decrement over 18 years in bread wheat genotypes. Therefore, breeders should consider the yield related traits to bring the desired genetic enhancement as well as to develop demanded genotypes in the future bread wheat breeding investigation.

Funding: The research study is funded by Adet Agricultural Research Center, Amhara Agricultural Research Institute and College of Agriculture and Environmental Science, Bahirdar Universty.
Competing Interests: The authors declare that they have no competing interests.
Acknowledgement: The authors greatly would like thank you, all of you who are participated this piece of research work from the beginning to the end.

REFERENCES

Abebe, T., S. Alamerew and L. Tulu, 2017. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (Oryza sativa L.) genotypes at Fogera and Pawe, Ethiopia. Advances in Crop Science and Technology, 5(2): 1-8.Available at: https://doi.org/10.4172/2329-8863.1000272.

Amsal, T., D.G. Turner and G. Getinet, 1995. Improvement in yield of bread wheat cultivars released in Ethiopia from 1949 to 1987. African Crop Science Journal, 3(1): 41-49.

Bello, O., S. Ige, M. Azeez, M. Afolabi, S. Abdulmaliq and J. Mahamood, 2012. Heritability and genetic advance for grain yield and its component characters in maize (Zea mays L.). International Journal of Plant Research, 2(5): 138-145.Available at: https://doi.org/10.5923/j.plant.20120205.01.

Benhilda, M., N.A. Gary, M. Olsen, M. Cosmos, L. Maryke, C. Jose and B. Marianne, 2017. Gains in maize genetic improvement in Eastern and Southern Africa: I. CIMMYT hybrid breeding pipeline. Crop Science, 57(1): 168-179.Available at: https://doi.org/10.2135/cropsci2016.05.0343.

Burton, G.W. and d.E. Devane, 1953. Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material 1. Agronomy Journal, 45(10): 478-481.Available at: https://doi.org/10.2134/agronj1953.00021962004500100005x.

Chekole, N., W. Mohammed and T. Damte, 2016. Genetic variation, correlation and path coefficient analysis in Tef [Eragrostis Tef (Zucc.) Trotter] genotypes for yield, yield related traits at Maysiye, Northern Ethiopia. American Journal of Research Communication, 4(11): 73-102.

Demissew, T., 2010. Genetic advance in grain yield and associated traits of early and medium maturing genotypes of soybean [Glycine max (L.) Merrill]. MSc. Thesis Presented to the School of Graduate Studies of Haramaya University.

Falconer, D.S. and T.F.C. Mackay, 1996. Introduction to quantitative genetics. 4th Edn., England: Benjamin Cummings. pp: 464.

FAOSTAT, 2017. Wheat area harvested and productivity. Available from http://www.fao.org/faostat/en/#data/QC.

Fentaw, A., M. Firew and D. Yigzaw, 2015. GGE biplot analysis of multi environment yield traits of durum wheat (Triticum turgidum L.) genotypes in Northwestern Ethiopia. America Journal of Experimental Agriculture, 8(2): 120-129.Available at: https://doi.org/10.9734/ajea/2015/9994.

Gashaw, A., W. Bayu, K. Teshome and L. Admassu, 2013. Varietal differences and effect of nitrogen fertilization on durum wheat (triticum turgidum var. Durum) grain yield and pasta making quality traits. International Journal of Agronomy and Plant Production, 4(10): 2460-2468.

Gezahegn, F., S. Alamerew and Z. Tadesse, 2015. Genetic variability studies in bread wheat (Triticum aestivum L.) genotypes at Kulumsa Agricultural Research Center, South East Ethiopia. Journal of Biology, Agriculture and Healthcare, 5(7): 89-98.

Haile, D., D. Nigussie and F. Girma, 2013. Seeding rate and genotypes on agronomic performance and grain protein content of durum wheet (Triticum turgidium. L.Var.Durum) in Southeastern Ethiopia. African Journal of Food, Agriculture, Nutrition and Development, 3(3): 7693-7710.

Johnson, H.W., H. Robinson and R. Comstock, 1955. Estimates of genetic and environmental variability in soybeans 1. Agronomy Journal, 47(7): 314-318.Available at: https://doi.org/10.2134/agronj1955.00021962004700070009x.

Kolmer, J., 2013. Leaf rust of wheat: Pathogen biology, variation and host resistance. Forests, 4(1): 70-84.Available at: https://doi.org/10.3390/f4010070.

Mathew, I., 2015. Combining ability, genetic advances and path coefficient analyses of maize hybrids developed from maize streak virus and downy mildew resistant recombinant inbred lines. M.Sc. Thesis Presented to the School of Graduate Studies of University of KwaZulu-Natal, South Africa. pp: 172.

Mekuria, T., M. Hussein and L. Tesfaye, 2018. Genetic improvement in grain yield and yield related traits of durum wheat (Triticum turgidum var.durum L.) in Ethiopia. International Journal of Advances in Scientific Research and Engineering, 4(8): 150-162.Available at: http://doi.org/10.31695/IJASRE.2018.32838.

Misganaw, F., 2017. Stability analysis in bread wheat (Triticum eastivum L.) genotypes in Northwestern Ethiopia. East Africa Journal of Science, 20(2): 56-65.

MoANR (Ministry of Agriculture and Natural Resource), 2016. Plant variety release, protection and seed quality control directorate. Addis Abeba, Ethiopia: Crop Variety Register, 19: 1-450.

Moslem, B., M.R. Raij, A.R. Seloki and K. Shirkool, 2014. Assessment of broad sense heritability and genetic advance in safflower. International Journal of Biosciences, 4(8): 131-135.

Oliver, R.P., 2014. A reassessment of the risk of rust fungi developing resistance to fungicides. Pest Management Science, 70(11): 1641-1645.Available at: https://doi.org/10.1002/ps.3767.

Robinson, H.F., R.E. Comstock and P.H. Harvey, 1949. Estimates of heritability and the degree of dominance in corn. Agronomy Journal, 41(8): 353-359.Available at: 10.2134/agronj1949.00021962004100080005x.

Sivasubranian, S. and M. Menon, 1973. Heterosis and inbreeding depression in rice. Madras Agricultural Journal, 60(29): 1139-1144.

Tamene, T., 2008. Genetic advance and morpho-agronomic basis of genetic improvement in grain yield potential achieved by faba bean breeding in Ethiopia. A M.Sc. Thesis Presented to the School of Graduate Studies of Hawasa University.

Teklu, Y. and H. Tefera, 2005. Genetic improvement in grain yield potential and associated agronomic traits of tef (Eragrostis tef). Euphytica, 141(3): 247-254.Available at: https://doi.org/10.1007/s10681-005-7094-7.

Tibebu, B., 2011. Genetic advance in grain yield and associated traits of Chickpea (Cicer arietinum L.) in Ethiopia. A M.Sc. Thesis Presented to the School of Graduate Studies of Haramaya University, Ethiopia. pp: 121.

Wondimu, F., 2010. Assessment of genetic improvement in grain yield potential, malting quality and associated traits of barley (Hordeum vulgare L.) in Ethiopia. A M.Sc. Thesis Presented to the School of Graduate Studies of Haramaya University.

Yan, X. and X.G. Su, 2009. Linear regression analysis: Theory and computing. USA: World Scientific Publishing Co.Pte. Ltd. pp: 1–2.