Estimation of Genetic Parameters in Bread Wheat (*Triticum Aestivum* L.) Genotypes Evaluated Under High Temperature Yield Trial in Ethiopia

Abstract

The study was carried out to estimate genetic parameters of 49 bread wheat genotypes and standard check evaluated at Kulumsa and Melkasa using alpha lattice design with two replications. The analysis of variance result showed highly significant differences among the genotypes for all traits (P< 0.001), implying the presence of considerable genetic variability for these traits. 60% of genotypes have mean grain yield above the overall mean and 30% above the check. High and moderate heritability estimates were found for most of traits showing that the variation observed was mainly under genetic control. The highest PCV and GCV values were observed for grain yield at both locations indicating better opportunity for improvement in these traits via selection. The genotypic correlations between grain yield with thousand kernel weight and hectoliter weight were highly significant showing their important contribution to grain yield. Therefore, theidentified genotypes with better performance could be utilized inadvanced bread wheat yield trialtargeted for high temperature condition in the country.

Keywords: Coefficient of variation, Correlation, Genetic parameters and Heritability

1. Introduction

In Ethiopia, bread wheat (*Triticum aestivum L.*) is one of the most important cereal crops in terms of production and consumption.Wheat is also a strategic commodity that generates farm income and improves food security. It is an important staple food in the diets of many Ethiopians, providing an estimated 12% of the daily per capita caloric intake for populationthe country (FAO, 2020).It is predominantly grown by small-scale farmers under rain-fed condition and in the altitude range of 1500 to 3000 *m.a.s.l* (Bekele *et al*., 2000). However,In spite of presence of wide agro-ecologies suitable for wheat production; elasticity of wheat to be grown from extreme lowlands to highlands; increased demand for wheat due to population growth, urbanization, expansion of agro-industries; wheat production is left behind by 25 to 30% to its demand in Ethiopia(Hondson *et a*l., 2020).

Bread wheat is the most widely adapted compared to other cultivated species and this situation favored the crop to be one of the most cultivated food crops worldwide (Rajaram, 2005). Grain yield is one of the traits of importance and breeders often seek to identify genotypes with high and stable yield across environments (Forgone, 2009).In Ethiopia, about 4.6 million farmers engaged in wheat production on their small-scale lands. Despite the potential of the country, the productivity is lower than the world average 3.3 t/ha. This is mainly because of the productivity constraints such as biotic and abiotic stresses out of which Wheat rust the major factors for low productivity of wheat in the country. The yield of bread wheat should be increased in parallel with the increasing population (Karaman, 2019).To improve grain yield in wheat, selection of genotypes should not only be based on grain yield alone, and the other grain yield components should also be considered. It is therefore, very important to know the relationship between grain yield and its component, and among the component themselves. The relationship among different traits in wheat can be determined using genotypic and phenotypic correlation analysis. It is an effective tool for the enhancement of crop improvement for traits of interestJohnson*et al*.(1956).The correlation coefficient among traits shows a complex chain of interacting relationships and the direction of the relationship.Hence, correlation coefficient studies and heritability provide detailed information to identify important characters to be considered in improvement genotypes with traits of interest through selection.

Developing high yielding, stable and rust diseases resistance genotypes are important in wheat variety development strategy and evaluation across locations.Thus, the national wheat research program at Kulumsa Agricultural Research Center Ethiopia works in developing and releasing bread wheat variety with wheat rust resistance, high grain yield, and satisfactory wheat qualityTherefore, breeding for grain yield, disease resistance and wide adaptability has become priority of the national wheat improvement program in the country(Alemu *et al.,* 2019; Gadisa *et al*., 2022).Hence, Ethiopian Wheat Research Program introduces thousands of bread wheat germplasm annually from International Research Institutes and evaluates germplasm under quarantine blocks and in series of yield trials over locations and years. Knowledge of the genetic variability present in existingcrop species for the character under improvement is ofparamount importance for the success of any plant breeding program.Thus, the estimation of genetic parameters such as heritability and genetic advance can provide essential knowledge that can be decisive in predicting the transfer of traits from parental plants to offspring. Moreover, heritability and genetic advance are important selection parameters that help plant breeders in determining the characters for which selection would be performed (Johnson *et al,*1956). Phenotypic and genotypic coefficients of variation are also other important genetic parameters. The magnitude of difference between PCV and GCV values indicates the level of environmentalinfluences on genotypic performance.Therefore, the present study was carried out to evaluate the genotypes for their performance, analyze and estimatethe geneticparameters for yield and other related traits present in wheat genotypes under study.

2. Material and Method

Forty nine bread wheat genotypes introduced byNational Wheat Research breeding program from CIMMYTwith check variety (Dursa), were used in this study. The experiment was performed in an alpha lattice design with two replications and a plot size of $3m^2$ areas(1.2m width by 2.5m length) having 10 rows and 5 columnsover two locations, Kulumsa and Melkassa, during 2021 main cropping season. All management practices were applied as per the recommendationfor each location.

2.1. Analysis of Variance and Estimation of Genetic Parameters

The analysis of variance (ANOVA) for an alpha lattice design was performed for each trait using SAS software version 4.0.1. The genotypic and phenotypic components of variance were computed according to formulae given by Choudhary*et. al*.(1968)for the observed characteristics.

Genotypic variance ($\sigma^2 g$)=(MSg-MSe)/r, Environmental variance ($\sigma^2 e$) =MSe/r

Phenotypic variance ($\sigma^2 p$)=$\sigma^2 g+\sigma 2e$, Where: MSg = mean square due to genotypes,MSe= environmental variance (error mean square), error variance = $\sigma^2 e$, r = number of replication.

The genotypic and phenotypic coefficients of variation were computed according to Burton*et.al*(1953) and expressed as a percentage using R-software version 4.0.1.

PCV= ($\sqrt{\sigma^2 p}$ /grand mean) *100and GCV= ($\sqrt{\sigma^2 g}$ / grand mean) *100, Where, $\sigma^2 p$ = phenotypic variance, $\sigma^2 g$= genotypic variance,PCV=Phenotypic Coefficient of Variation;GCV= Genotypic Coefficient of Variation. PCV and GCV values were categorized as: 0–10%:low,10–20%: moderate, and >20: high as indicated by Sivasubramanian and Menon(1973).

2.2.2.Broad Sense heritability($h^2 bs$): Broad sense heritability was estimated as the ratio of genotypic variance to phenotypic variance and expressed in percentage (Hanson *et al*., 1956).

H^2= $\sigma^2 g$ / $\sigma^2 p$ *100, Where:$\sigma^2 g$= genotypic variance, $\sigma^2 g$= genotypic variance,

2.2.3. Genetic Advance: The extent of genetic advance to be expected for each character was computedusing the formula was computed using the formula given by Johnson *et al*. (1956) and Allard (1960).

G.A = ix h^2 x δp where, G.A= Genetic advance,i= selection differential (at 5% selection intensity, k=2.06), h^2 = Heritability in a broad sense, δp = Phenotypic standard deviation

2.2.4. Genetic Advance as Percent of Mean (GAM): GAM was categorized as low, moderate, and high as follows by *Johnson et al*. (1956): 0–10%: low, 10–20%: moderate, and 20 and above: high.

GAM=(GA/grand mean) x 100, where GA is the genetic advance

2.2.5.Genotypic and phenotypic correlations: The formula used to compute genotypic and phenotypic correlation is;

Phenotypic correlation coefficient=$COVp_{xy}/\sqrt{(\sigma^2 px)(\sigma^2 py)}$,Genotypic correlation coefficient(rg_{xy})= $COVg_{xy}/\sqrt{(\sigma^2 gx)(\sigma^2 gy)}$, Environmental correlation coefficient (re_{xy}) = $COVe_{xy}/\sqrt{(\sigma 2e_x)(\sigma 2e_y)}$, Where: rp_{xy} = Phenotypic correlation coefficient between traits x and y ,rg_{xy} = Genotypic correlation coefficient between traits x and y, $pcov_{xy}$=Phenotypic covariance between traits x and y, $gcov_{xy}$ = Genotypic covariance between traits x and y , $ecov_{xy}$= Environmental covariance between character x and y.

Table 1.Agro-ecological description of the study Sites

Location	Geographic position		Altitude (m)	Temperature (°C)		Rainfall (mm)
	Latitude	Longitude		Min.	Max.	
Kulumsa	08°01'10"N	39°09'11"E	2200	10.5	22.8	820
Melkasa	08°.24'N	39°.12'E	1550	13.6	28.6	763

3. RESULT AND DISCUSSION

3.1. ANALYSIS OF VARIANCE

The results of the combined analysis of variance across the two locations are presented in Table 2. Accordingly, the analysis of variance showed highly significant differences among the genotypes for all traits implying the presence of considerable amount of genetic variability for all the studied characters. Significant differences among the genotypes for different traits were also reported by Singh *et al.* (2019) and Kumar *et al*. (2021) inBread wheat.Hence, selection could be effective for different quantitative characters including creating variability for base population in crossing program. The existence of variability among the genotypes in all parameters is very useful in plant breeding which is a tool for the selection of elite genotypes. Similar findings were also reported by Dabi *et al*. (2019).

Location effect revealed highly significant differences for all measured traits at ($p \leq 0.001$) except Hectoliter Weightwhich showed significant difference (Table 2). The very high significant genotype by the location interaction ($P<0.001$) was also found for all traits except for thousand Kernel Weight which had significant difference among the genotypes. However, non-significant interaction was found for replication within the location for all traits except grain yield, Hectoliter weight and stem rust which exhibited highly significant differences. Thus, the existence of highly significant difference at ($P<0.001$) for GXE interaction implies that the genotypes didn't perform consistently over locations with regard to these traits. On the other hand, if varieties don't perform consistently for those traits over locations, it is better to perform extensive varietal evaluation by selecting appropriate testing sites and modifying the breeding strategy. Hence, 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 bread wheat by Dabi *et al*.(2019.).

Table 2.Combined analysis of variance for grain yield and related traits of bread wheat genotypes evaluated under high temperature yield trial over locations at Kulumsa and Melkassa in 2021.

Source of variation							Mean	CV
Trait	Loc (Df=1)	Rep(Loc) (Df=2)	Block(Loc*Rep) (Df=16)	Genotype (Df=49)	Genotype(G*Loc) (Df=49)	Error (Df=82)		
DTH	15277.52**	1.48^{NS}	2.90^{NS}	53.21**	5.42**	3.03	60.76	2.86
DTM	55444.50**	2.72NS	3.38*	5.49**	9.86**	1.93	107.91	1.29
GFP	12513.62**	8.20NS	6.66^{NS}	51.26**	13.27**	6.33	47.15	5.34
PHT	6050.00**	8.32NS	35.80*	53.87**	43.73**	22.86	83.70	5.71
TKW	950.48**	7.12NS	34.40*	50.48**	26.67*	18.32	29.46	14.53
SrR	24753.13**	423.87**	125.38^{NS}	459.87**	192.50**	81.94	17.60	51.45
HLW	15.92*	13.09**	11.20^{NS}	21.40**	11.72**	2.69	63.88	2.57
GY	1114225.92**	208705.41**	154505.19**	204177.77**	194499.16**	30406.4	1171.89	14.88

DTH=Days to Heading; DTM=Days to Maturity; PHT=Plant Height; TKW=Thousand Kernel Weight, SrR= stem rust reaction, HLW: Hectoliter Weight, GY= Grain Yield, CV (%)= Coefficient of Variation, Df=degree of freedom

The analysis of variance showed very highly significant differences among the genotypes for all the studied traits across location and at Kulumsa, implying that all traits exhibited genetic variability.On the other hand, at Melkassa, very highly significant differences among the tested genotypes for days to heading, days to maturity and hectoliter weight was obtained whereas none- significant differences among the genotypes for plant height and thousand Kernel Weight, butonly significant differences between the genotypes for grain yield was recorded (Table 3).

Table 3. Analysis of variance of the 6 traits of 50 bread wheat genotypes tested at Kulumsa and Melkassa in 2021

Sources of variation	DTH		DTM		PHT		TKW		HLW		YLD	
	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK
Replication (df=1)	1.96	1.00	4.00	1.44	0.64	16.00	10.24	4.00	0.70	25.48***	7939.0	409472.0**
Genotype Variance (df= 49)	30.43***	28.49***	10.79***	5.07**	70.84***	31.65ns	48.33***	31.41ns	25.6***	10.58***	360417.0***	80456.0*
Residuals (df=49)	2.49	3.24	1.39	2.44	18.33	26.71	11.46	27.84	3.72	2.00	16683.0	42455.00
Max. Mean	81	58	130	103	105	85	40	50	72.5	69.18	2098	1745
Min. mean	63	44	120	89	70	60	12	20	69.5	55.82	78	280
Grand mean	69.5	52	124.56	91.26	89.20	78.20	27.28	31.64	71.00	63.58	1246.53	1097.25

DTH=Days to Heading; DTM=Days to Maturity; PHT=Plant Height; TKW=Thousand Kernel Weight, HLW: Hectoliter Weight, GY=Grain Yield, Ku = Kulumsa, MK = Melkassa

3.2. Mean performances

The average performance of fifty genotypes along with Grand mean and CV are presented in Table 4.Comparing the mean values obtained from different genotypes for grain yield, it was registered that the mean value ranged from 482.95to 1530.2kg/ha.Out of 50 genotypes, four genotypes such as EBW2113062, EBW2113039, EBW2113037 and EBW2113056 were the top yielding genotypes with the grain yield of 1530.2,1527.83, 1517.58 and 1504.60kg/ha across the locations, respectively(Table 4). This suggested that these genotypes proved to be outstanding bread wheat genotypes which can be released as variety after testing their stability in diverse environmental situation. Furthermore, thirty of the fifty genotypes gave grain yield above grand mean(1171.890Kg/ha),whereas fourteen genotypes had grain yield above the check, Dursa, (1295.05kg/ha). In another word, about 60% of genotypes were having mean grain yield above the overall mean and 30% of them provided grain yield above the checkvariety. Generally, the range of variation was wide for all the characters studied. Gezahegn *et al.* (2015) reported similar results on bread wheat study. Therefore, high variability for six traits of fifty bread wheat genotypes evaluated under this study implied that there was reasonably sufficient variability which provides good chancesof selecting superior and desired genotypes for further improvement. With regards to overall mean performance of the genotypes for all traits, EBW2113062 gave not only the highest yield but also showed better performance for most of the traits among the evaluated genotypes as wells as it surpassed the check variety (Dursa) for yield and most of other associated traits. Regarding other traits, early heading was recorded in genotype EBW213049(53.7days) followed by EBW213029(54.9days),EBW213066(55days) and EBW213067(55.7days).

Early maturing was registered for EBW213053(104.8days) genotype followed by EBW213033 (105.2days) and EBW213058(105.8days) genotypes whereas the check variety,DURSA, (110.3 days) was found to be late in maturity.Maximum plant height was observed in genotypeEBW213046 (92cm) followed by EBW213062 (89.1cm).Furthermore, thousand Kernel Weight was highest forEBW213039(37.9gm) followed by EBW213059(36.3g) and EBW213053(36.1gm)genotypes. The check variety, DURSA(68.58) was observed to have highest value of hectoliter weight followed by EBW213030 (67.8) and BW213062(67.62)genotypes.

On the other hand, most of the genotypes showed susceptible(31 genotypes) to moderately susceptible(13 genotypes) for stem rustmean reaction, moreover, six genotypes such as EBW213051, EBW213054, EBW213062, EBW213026, EBW213031 and EBW213042 were withmoderately resistance(MR) and moderately susceptible(MRMS) for stem rust at Melkasa. Whereas, at Kulumsa, most of the genotypes exhibited resistance (30 genotypes with zero score) to moderately resistance(10 genotypes with MS) to stem rust severity. Hence, all resistant genotypes for stem rust disease couple with high grain yield could be advanced to the next stage of breeding program. Furthermore, the check (Dursa) variety had record of susceptibility at both locations with 30 and 50 score of stem rust severity at Kulumsa and Melkassa, respectively, which indicates the need for evaluation of superior genotypes from other sources, like the current study,for stem rust resistance there by release the top performing genotype as variety.

Table 4. Mean performance of different characters among fifty bread wheat genotypes evaluated across locations

Genotypes	DTH	DTM	GFP	PHT	TKW	SrS	HLW	GYD
DURSA	58.20	110.28	52.08	87.13	30.25	44.10	68.58	1295.05
EBW212109	66.15	109.83	43.68	82.93	28.75	17.90	61.21	905.28
EBW213021	60.05	106.90	46.85	86.03	28.40	33.33	64.23	1291.10
EBW213022	57.80	109.08	51.28	82.45	26.95	19.73	63.49	983.58
EBW213023	63.20	108.30	45.10	82.08	28.15	18.88	59.27	796.63
EBW213024	61.45	108.28	46.83	78.88	26.75	11.85	61.54	839.80
EBW213025	58.05	107.40	49.35	78.03	27.40	12.33	65.85	1257.85
EBW213026	62.80	109.33	46.53	82.45	27.45	7.48	61.38	1074.83
EBW213027	59.20	109.55	50.35	86.33	28.15	18.88	64.58	1222.38
EBW213028	60.65	109.40	48.75	79.03	29.70	22.95	64.92	1136.73
EBW213029	54.90	106.90	52.00	72.53	30.20	25.45	65.08	1257.48
EBW213030	57.18	106.80	49.63	83.25	32.15	12.90	67.80	1392.35

EBW213031	59.18	107.53	48.35	84.30	32.25	8.13	65.00	1353.53
EBW213032	56.78	106.08	49.30	81.38	31.45	16.25	65.44	1439.55
EBW213033	64.13	105.15	41.03	87.70	32.20	5.73	62.02	1197.45
EBW213034	65.53	108.33	42.80	87.63	30.45	3.75	63.84	1305.55
EBW213035	62.38	106.65	44.28	81.20	28.20	9.48	60.74	964.70
EBW213036	58.18	108.78	50.60	86.80	23.75	13.13	63.30	1216.53
EBW213037	57.78	108.90	51.13	85.20	34.90	11.10	66.80	1517.58
EBW213038	57.68	106.80	49.13	85.25	31.15	14.15	63.32	1163.85
EBW213039	59.03	108.40	49.38	81.70	37.90	22.35	67.06	1527.83
EBW213040	68.85	109.68	40.83	84.13	31.30	3.23	65.72	1083.63
EBW213041	58.25	108.18	49.93	83.38	34.00	2.35	64.08	1278.75
EBW213042	61.15	107.08	45.93	81.68	28.75	2.90	59.06	1042.03
EBW213043	61.50	107.10	45.60	88.80	28.55	6.25	63.97	1177.98
EBW213044	64.65	107.80	43.15	74.23	20.35	20.63	56.7	482.95
EBW213045	61.00	107.85	46.85	76.55	24.05	11.25	62.9	724.23
EBW213046	64.65	108.30	43.65	91.98	28.85	16.88	66.10	1352.45
EBW213047	65.60	108.93	43.33	82.88	25.80	25.73	59.44	989.38
EBW213048	59.50	109.68	50.18	77.88	22.00	29.85	58.33	657.25
EBW213049	53.70	108.70	55.00	83.75	32.30	21.25	66.50	1185.08
EBW213050	57.60	108.18	50.58	87.88	26.00	24.40	63.89	1175.13
EBW213051	59.85	108.15	48.30	84.68	28.10	8.13	62.85	1361.55
EBW213052	62.70	107.53	44.83	85.08	21.25	24.85	63.70	1015.10
EBW213053	59.05	104.78	45.73	87.58	36.05	38.23	65.29	1433.98
EBW213054	68.85	109.18	40.33	84.88	32.00	5.40	66.85	1425.63
EBW213055	59.85	108.90	49.05	79.18	27.10	39.38	63.85	1193.30
EBW213056	57.95	106.78	48.83	82.08	33.25	39.85	64.60	1504.60
EBW213057	67.45	108.45	41.00	80.50	24.80	7.75	61.78	1110.58
EBW213058	59.30	105.78	46.48	87.33	33.55	13.23	65.10	1231.98
EBW213059	60.43	107.55	47.13	86.50	36.30	9.40	64.80	1353.78
EBW213060	65.58	107.23	41.65	85.18	30.55	28.68	61.35	1204.38
EBW213061	59.23	106.45	47.23	84.30	25.75	34.08	62.32	997.68
EBW213062	61.98	108.45	46.48	89.05	33.75	4.08	67.62	1530.18
EBW213063	64.43	107.80	43.38	85.75	30.30	14.65	66.15	1321.03
EBW213064	66.83	107.55	40.73	87.75	29.00	16.03	63.72	997.15
EBW213065	61.08	106.98	45.90	86.93	30.05	11.18	64.42	1212.88

EBW213066	54.98	106.43	51.45	85.35	30.85	21.05	64.14	1138.10
EBW213067	55.73	108.68	52.95	83.10	31.35	23.30	63.51	1166.85
EBW213068	56.08	108.80	52.73	84.50	30.50	26.03	63.27	1107.40
Mean	60.76	107.91	47.15	83.70	29.46	17.60	63.88	1171.890
CV	2.86	1.29	5.34	5.71	14.53	51.45	2.57	14.88

DTH=Days to Heading; DTM=Days to Maturity; PHT=Plant Height; TKW=Thousand Kernel Weight, SrR= stem rust reaction,HLW=Hectoliter Weight GYD= Grain Yield, LSD= Least Sign. Difference, CV (%) = Coefficient of Variation

3.3. Estimation of genetic parameters

3.3.1. Genotypic and Phenotypic Coefficient of Variation(PCV and GCV)

The estimates of mean, range, genotype and phenotypevariances, genotypic (GCV) and phenotypic coefficient of variation (PCV) for various characters studied are presented in Table 5. Based the result, thephenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all characters at both locations.The difference between PCV and GCV was large in thousand kernel weight followed by plant height and grain yield indicating that these traits are influencedby the environment. However, differences between them were small for most of the traits implying that low effect of environment on the expression of charactersat both locations.

At Kulumsa, high PCV and GCV values were observed for grain yield (PCV=33.26) and (GCV=34.83) and thousand Kernel Weight (PCV=15.74) and (GCV=20.04)showing better opportunity for improvement in these traits through selection. Similar findings also reported by Kumer *et al*. (2013) that show high PCV for grain yield.However, moderate PCV and GCV was observed for Plant height (PCV=5.74) and (GCV=7.49) and days to heading (PCV=5.38) and (GCV=5.84). Kumar *et al.* (2013) also found similar results for plant height.The lowest estimates of PCV (1.74) and GCV(1.98) were recorded for days to maturity,this is in agreement withfindings of Ashfaq *et al*.(2014).The magnitude of PCV ranged from 1.98 for days to maturity to 33.26 for grain yield while GCV ranged from 1.74 to 34.83 for days to maturity and grain yield, respectively, at Kulumsa. The characters with high phenotypic coefficient of variation indicated more influence of environmental factors.These results were supported by the findings of Bhushan *et al*. (2013) for days to maturity and current results was at par with findings of Ashfaq *et al*.,(2014).

At Melksaa, high PCV and GCV values were registered for grain yield ((PCV=22.59) and (GCV=12.56)and thousand kernel weight(PCV=17.20) and days to heading(GCV= 6.83) indicating better opportunity for improvement in these traits through selection at location. However, moderate PCV and GCV were obtained for days to heading, (7.66) and (6.823), Plant height (6.91) and (2.01) and Hectoliter weight (3.94) and (3.28), respectively. The lowest estimates of PCV(2.12) and GCV(1.26) were recorded for days to maturity which revealed that these traits are highly influenced by environmental factors and difficult for manipulating through direct selection. These results were supported by the findings of Bhushan *et al*. (2013) for days to maturity. The magnitude of PCV ranged from 2.12 for days to maturity to 22.59for grain yield while GCV ranged from 1.256 to 12.56 for days to maturity and grain yield, respectively, at Melkassa. The characters with high phenotypic coefficient of variation indicated more influence of environmental factors. Similar results on variability for different characters were reported byPrasad et al. (2022) and Hassani *et al.* (2022)

3.3.2. Estimation of Broad Sense Heritability and Genetic Advance

Estimates of heritability, genetic advance and genetic advance as percent of mean values for all characters studied are displayed in Table 5. According to Singh (2001) that heritability values greater than 80% were very high, 60-79% moderately high, 40-59% medium and values less than 40% were low. Accordingly, very high broad sense heritability estimates were revealed for grain yield (91%) and days to heading (85%) while moderately high heritability values were obtained for days to maturity (77%), hectoliter weight (75%),and thousand kernel weight (62%). Moderate value of broad sense heritability was showed for Plant height (59%)at Kulumsa. On the other hand, at Melkassa, high broad sense heritability estimates were showedfor days to heading(79.55%) while moderately high for HLW(68.21%). Very high estimates of broad sense heritability have been also reported by previous researchers for days to heading (Negasa *et al.,* 2016 and Bayisa *et al*., 2020). Low broad sense heritability was recorded for all traits except DTH and HLW which revealed high(79.55%) and moderately high (68.21%), respectively at Melkassa. 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 is expected that, environment expression on phenotypic expression is low. This 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 respond effective because it is expected that traits with high heritability estimate have a close correlation between phenotypic and genotypic appearance (Singh, 2001).

Heritability alone could not provide any indication of the amount of genetic progress which would be resulted from selection of individual genotype. Thus, knowledge on heritability coupled with genetic advance is very crucial for further improvement in the traits under study. Furthermore, Hamdi *et al*. (2003) stated that Genetic advance (GA) is important for predicting the expected genetic gain from one cycle of selection. 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). 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%). Genetic advance as percent of the means (GAM) in this study ranged from 1.20% to 14.39% for plant height and grain yield, respectively (Table 5). The estimates of GAM were moderate for grain yield (14.39%) and days to heading (12.54%). Hence, selection for improvement of these characters may be satisfying. Similar agreement also reported for days to heading, grain filling period and spike length (Obsa *et al*., 2017). However, moderate to high heritability associated with a high genetic gain was observed for TKW and GYD indicating the involvement of additive gene action.

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. This is in line with Khalil *et al.* (2010) findings for number of grain per spike.High and moderate heritability estimates were found for most of the studied traits indicating that the variation observed was mainly under genetic control and was less affected by environment, referring the influence of additive gene action for these traits. 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 sense heritability along with high genetic advance as percentage of mean (Raia *et al.,* 2016).

At Melkasa, the heritability estimates ranged from 6% to 79%for for TKW and DTH, respectively.Thus, in this study, at Melkassa, a high heritability estimate was recorded for days to heading (79%) and HLW(68%) showing that the characters were least influenced by environmental factors. Fellahi *et al.* (2013) and Hayadar *et al*. (2020) also estimated high heritability for important morphological traits.The obtained results are in agreement with results reported by Tesfaye *et al*. (2016).It has been suggested that heritability estimates together with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone in selecting best individuals because heritability does not provide indication of amount of genetic progress that would result from selecting the best individuals (Johnson *et al*., 1955).Highest value of expected genetic advance expressed as percent of mean was observed for grain yield/plant (14.39) and DTH (12.55). High heritability with moderately high GMA(%) was observed for DTH and HLW suggested that these characters can be considered as favorable for improvement through selection.Similar results were obtained by Salman *et al. (*2014) and Degewione *et al*. (2013). While high heritability with low genetic advance was observed for days to maturity. Low heritability with low genetic advance values was found in TKW and PHT indicating slow progress through selection for these characters. Similar findings were also reported by Kumar *et al.*(2013) and Bhanu *et al*. (2018). At Melkassa, low heritability estimate for PHT(8%) and TKW(6%) indicated that selection for these characters would not be effective due to the predominant effects of non-additive genes. In agreement with the current study,Desalegn and Chauhan (2016) also reported low heritability for tillers per plant and harvest index.

Statistics	DTH		DTM		PHT		TKW		HLW		GLD	
	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK	KU	MK
Genotype Variance	13.97	12.62	4.70	1.31	26.25	2.47	18.43	1.79	10.92	4.29	171867.15	19000.58
Phenotypic Variance	16.46	15.86	6.09	3.75	44.59	29.18	29.90	29.62	14.63	6.29	188550.16	61455.72
Envt(Residual) variance	2.49	3.24	1.39	2.44	18.33	26.71	11.46	27.83	3.72	1.99	16683.01	42455.13
GCV	5.38	6.82	1.74	1.25	5.74	2.00	15.74	4.22	4.50	3.25	33.26	12.56
PCV	5.84	7.65	1.98	2.12	7.49	6.90	20.04	17.20	3.50	3.94	34.83	22.59
ECV	2.27	3.46	0.95	1.71	4.80	6.60	12.41	16.67	2.50	2.22	33.26	18.77
GA	7.09	6.52	3.92	1.39	8.10	0.94	6.94	0.67	5.88	3.52	815.35	157.88
GAM(%)	10.21	12.54	3.15	1.53	9.08	1.20	25.46	2.13	2.00	5.54	65.41	14.38
Heritability	0.85	0.79	0.77	0.34	0.59	0.08	0.62	0.06	0.75	0.68	0.91	0.31
Max. mean	81.00	58.00	130.0	103.0	105.0	85	40.00	50	72.50	69.18	2098.0	1745
Min.mean	63.00	44.00	120.0	89.0	70.00	60	12.00	20	69.50	55.82	78.00	280
Grand Mean	69.50	52.02	124.5	91.2	89.20	78.2	27.28	31.64	71.00	63.58	1246.53	1097.25
Replicates	2	2	2	2	2	2	2	2	2	2	2	2
Genotype significance	***	**	***	Ns	**	Ns	***	**	***	Ns	***	**

Table 5. Estimation of Genetic parameters for different traits in Bread Wheat Genotypes Evaluated at Kulumsa and Melkasa during 2021G.C.

KU=Kulumsa; MK=Melkasa; DTH=Date to heading; DTM=Date to maturity; PHT=Plant height; TKW= Thousand kernel weight; HLW=Hectoliter weight; GYD= Grain yield, GCV= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, ECV= environmental coefficient of variation, GA= Genetic advance, GAM(%)=Genetic advance as percent of mean

3.3.3. Genotypic and Phenotypic Correlation for Grain yield andother traits

Overall results from correlations showed a higher phenotypic correlation than the corresponding genotypic correlation for most of the traits.Genotypic correlation coefficients of grain yield to other traits (Table 6) shows that grain yield exhibited varying trends of correlation with its components at genotypic level. As observed from result of this study, genotypic correlation between grain yield and thousand kernel weight (rg= 0.77***), grain yield and hectoliter weight (rg= 0.69***) are positive and highly significant at (P<0.001)

(Table 6) indicating their important contribution to grain yield.The work of Surma *et al*. (2012) showed positive and significant correlation of grain yield with thousand kernel weight, hectoliter weight and starch content..There was also positive and significant correlation (0.57) between TKW and HLW. Similarly, highly significant phenotypic correlation was found for grain yield with hectoliter weight (rp=0.68**) followed by thousand kernel weight (rp=0.49)and plant height (rp= 0.49)(P=<.0001).In contrast to the current study result, Singh (2014) reported the presence of negative correlation between grain yield and plant height. The high correlation between grain yield and hectoliter weight at both genotypic and phenotypic levels was also obtained by Ashebr *et al.,*(2020).This demonstrates that genotypes with higher TKW and HLW would produce more grain yield than those with lower TKW and HLW.

Positively significant genotypic (0.44) and phenotypic(0.49) correlations were registered for grain yield with plant height,while negatively non-significant genotypic correlation was observed for grain yield with days to heading (-0.22), days to maturity(-0.15) and Stem rust reaction (-0.05).Other hand, positively non-significant correlation of plant height with grain yield was reported by Khalil*et al.* (2010). In general, positive and significant association of grain yield with its components at genotypic level appears to revealthat there is interaction among the characters in which a gene favoring increment in one character will also influence another character (Table 6).

Days to heading (DTH) exhibited positive and non-significant association with days to maturity (0.22) and PHT (0.15) whereas negative and non-significant correlation of this character was observed with grain filling period (-0.95), TKW(-0.27) andHLW(-0.24) at genotypic level.Whereas, at phenotypic level,positive and highlysignificant correction was found between days to heading with DTM (0.91), GFP(0.62) and PHT(0.67). Similar to this finding, Kumar,*et al.*(2020)reported a highly significant association of days to heading with days to maturity and spikelet per spike at phenotypic level and positive and non-significant association of the character with plant height at genotypic level.Days to maturity had positive and non-significant correlation coefficient with grain filling period (0.11) and HLW (0.07),while, it exhibited negative and non-significant correlation with plant height (-0.03), TKW(-0.17), Srs(-0.05)and GYD(-0.15) at genotypic level. Similar findings were also reported by Ashebr *et al.* (2020).At phenotypic level, DTM had positive and highly significant correlation with PHT(0.66 and GFP(0.89)whereas, negatively significant correlation was obtained with TKW(-0.37) and SrS(-0.59) score.Plant height revealed positive and non-significant correlation with TKW (0. 0.29) and HLW (0.29) while negative and non- significant correlation with SrS (-0.05).Similar result was reported byAshebr *et al.,*(2020).While at phenotypic level,PHT had highly significant association with GYD(0.49)and had positively significant correlation with HLW(0.23). On other hand, TKW revealed positive and highly significant association with HLW(0.48) and GYD(0.49) while HLW had positively higher association with grain yield(0.68) at phenotypic level.Generally, most of studied traits revealed positive and significant at both genotypic and phenotypic correlation coefficient with each other which indicated that selection for the correlated characters could give better result to enhance grain yield.

Table 6. Genotypic (above diagonal) and phenotypic correlation coefficients for the charactersof Bread wheat Genotypesstudiedacross locations in 2021

	Correlation Coefficients / Pr > |r|							
Variable	DTH	DTM	GFP	PHT	TKW	HLW	SrS	GYLD
DT	1	0.22ns	-0.95**	0.15ns	-0.27ns	-0.24ns	-0.29ns	-0.22ns
DTM	0.91**	1	0.11ns	-0.03ns	-0.17ns	0.07ns	-0.05ns	-0.15ns
GFP	0.62**	0.89**	1	-0.16ns	0.22ns	0.27ns	0.28ns	0.18ns
PHT	0.67**	0.66**	0.52**	1	0.30ns	0.29ns	-0.05ns	0.44*
TKW	-0.40**	-0.37**	-0.26**	-0.10ns	1	0.57**	-0.05ns	0.77**
HLW	0.02ns	0.09ns	0.15ns	0.23*	0.48**	1	-0.03ns	0.69**
SrS	-0.63**	-0.59**	-0.43**	-0.39**	0.16ns	-0.15ns	1.00	-0.05ns
GYD	0.17ns	0.20ns	0.19ns	0.49**	0.49**	0.68**	0.19*	1

DTH=Date to heading; DTM=Date to maturity; GFP= Grain filling period, PHT=Plant height; TKW= Thousand kernel weight, HLW=Hectoliter weight; SrS= stem rust scores, GYD= Grain yield

4. CONCLUSION

Based on this study, genetic variability of bread wheat genotypes under high temperature areas revealed highly significant differences between the genotypeswere observed for most traits. The magnitude of PCV values higher than GCV which indicates the degree of influence of environment over genotypic effect. High heritability accompanied with high genetic advance as percent of the mean was recorded for days to heading, plant height, thousand kernel weights and grain yield which revealed traits was simply inherited. Hence,from the present study it is concluded that sufficient genetic variability was present in the experimental materials for most of the traits and these genotypes could be exploited in future bread wheat breeding for high temperature environments.In conclusion, to generate a new technology, a variety with improved grain yield and related traits, a breeder needs to apply selection for yield components from early stage of nurseries to sets for advanced yield trials in the breeding program.The traits with moderate to high variability and genetic advance should be given attention to produce an effective response to yield enhancement. Selection and hybridization of genotypes with high genotypic coefficient of variation, heritability and genetic advance can be recommended for further bread wheat yield enhancement under targeted area of high temperature condition in the country.

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