



Genetic Analysis in Bread Wheat (*Triticum Aestivum* L.) Genotypes Tested Under Early Stage of High Temperature Yield Trial in Ethiopia

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Abstract

This study was carried out to evaluate 49 Bread wheat genotypes introduced from CIMMYT with a check (Hidasse) at Kulumsa and Melkasa Agricultural Research Centers during 2022 cropping season. Hence, the objective of the study was to analysis quantitative genetic parameters of Bread Wheat genotypes evaluated under high temperature Yield Trial in 2022 main cropping season. The experiment was performed in an alpha lattice design with 2 replications having plot size of 3m². The overall results from analysis of variance showed highly significant differences among the genotypes for all traits ($P < 0.001$) at both locations. The correlation analysis revealed a higher genotypic correlation than the corresponding phenotypic correlation for most of the traits. Hectoliter Weight (HLW) and thousand-grain weight were significantly correlated with grain yield indicating their important contribution to grain yield. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all characters. Generally, Moderate to high heritability associated with high genetic gain was observed for days heading, thousand-grain weight and grain yield indicating that the variation observed was mainly under genetic control and less affected by environment, referring the influence of additive gene action and improvement of these traits can be made through direct phenotypic selection. 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 further bread wheat yield enhancement under targeted area of high temperature condition in the country.

Keywords: Correlation, heritability, genetic gain, genotypic and phenotypic coefficient of variations.

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 population the 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 al.*, 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 rusts 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 interest (Johnson *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 quality. Therefore, 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 existing crop species for the character under improvement is of paramount 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 environmental influences on genotypic performance. Hence, this study was carried out to evaluate the genotypes for their performance and analyze quantitative genetic parameters for yield and other related traits present in wheat genotypes under study.

2. Material and Method

Forty nine bread wheat genotypes introduced by National Wheat Research breeding program from CIMMYT with check variety (Hidasse), were used in this study. The experiment was performed in an alpha lattice design with two replications and a plot size of 3m² areas (1.2m width by 2.5m length) having 10 rows and 5 columns over two locations, Kulumsa and Melkassa, during 2022 main cropping season. All management practices were applied as per the recommendation for 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 and R-Software version 4.0.1. The genotypic and phenotypic components of variance were computed according to Formulae given by Chaudhary *et al.* (1968) for the observed characteristics.

Genotypic variance (σ^2_g) = (MSg-MSe)/r, Environmental variance (σ^2_e) = MSe/r

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$, where: MSg = mean square due to genotypes, MSe= environmental variance (error mean square), error variance = σ^2_e , r = number of replications.

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) * 100 and GCV = ($\sqrt{\sigma^2_g}$ / grand mean) * 100, Where, σ^2_p = phenotypic variance, σ^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: σ^2_g = genotypic variance, σ^2_p = phenotypic variance,

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

G.A = $i \times h^2 \times \delta p$ 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.

$GAM = (GA/\text{grand mean}) \times 100$, where GA is the genetic advance

2.2.5. Genotypic and phenotypic correlations: The formula used to compute genotypic and phenotypic correlation is; henotypic correlation coefficient = $COV_{pxy}/\sqrt{(\sigma^2_{px})(\sigma^2_{py})}$, Genotypic correlation coefficient (rg_{xy}) = $COV_{gxy}/\sqrt{(\sigma^2_{gx})(\sigma^2_{gy})}$, Environmental correlation coefficient (re_{xy}) = $COV_{exy}/\sqrt{(\sigma^2_{ex})(\sigma^2_{ey})}$, Where: r_{pxy} = 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) in Bread 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 Weight which showed significant difference (Table 2). The very high significant genotype by the location interaction ($P < 0.001$) was also found for all traits which had significant difference among the genotypes. However, non-significant interaction was found for replication within the location for all traits except grain yield, and Hectoliter weight 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 at both locations with regard to these traits. 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 agronomic traits of bread wheat genotypes across locations

| Sources of variation | DTH | DTM | PHT | TKW | HLW | GYLD |
|-----------------------------------|-----------|-----------|----------|----------|--------|------------|
| Genotype Variance (Df=49) | 11.88** | 10.00** | 1.31** | 5.66** | 2.03** | 1210.00** |
| Loc Variance (Df=1) | 1725.25** | 4525.32** | 523.47** | 458.25** | 11.25* | 13212.65** |
| Gen x Loc Variance(G*Loc) (Df=49) | 1.43** | 3.01** | 13.19** | 4.39** | 5.40** | 1.04** |
| Residual Variance (Df=82) | 2.84 | 1.91 | 22.24 | 18.90 | 2.60 | 0.32 |
| Grand Mean | 60.76 | 107.91 | 83.70 | 29.46 | 63.87 | 3.91 |
| CV | 2.77 | 1.28 | 5.63 | 14.76 | 2.53 | 14.50 |
| Genotype significance | 0.00 | 1.00 | 0.72 | 0.05 | 0.11 | 1.00 |
| Gen x Env significance | 0.00 | 0.00 | 0.00 | 0.14 | 0.00 | 0.00 |

DTH = Days to Heading; DTM = Days to Maturity; PHT = Plant Height; TKW = Thousand Kernel Weight, 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, but only 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 2022.

| Sources of variation | DTH | | DTM | | PHT | | TKW | | HLW | | YLD | |
|----------------------------|---------|--------|--------|--------|---------|-------------|----------|-------------|---------|--------|-------------|------------|
| | KU | MK | KU | MK | KU | MK | KU | MK | KU | MK | KU | MK |
| Replication (df=1) | 0.49 | 4.00 | 0.20 | 1.00 | 88.36 | 324.00 | 4.84 | 1.96 | 74.82 | 0.15** | 77340.0 | 481914.0** |
| Genotype Variance (df= 49) | 17.39** | 2.45** | 16.5** | 5.79** | 45.09** | 69.51 ns | 45.02*** | 16.43 ns | 31.47** | 14.8** | 344489.0*** | 127089.0* |
| Residuals(df =49) | 0.69 | 0.76 | 2.01 | 1.84 | 13.58 | 54.10 | 6.06 | 7.18 | 13.07 | 3.75 | 32156.0 | 54846.0 |
| Max. Mean | 73.00 | 56.00 | - | 103.00 | 120.00 | 90.00 | 44.00 | 36.00 | 72.44 | 68.60 | 2816.00 | 1687.00 |
| Min. mean | 58.00 | 51.00 | - | 93.00 | 90.00 | 55.00 | 22.00 | 20.00 | 31.76 | 54.18 | 616.00 | 174.00 |
| Grand mean | 65.55 | 52.52 | | 95.82 | 102.00 | 71.30 | 32.00 | 26.54 | 65.83 | 62.15 | 1776.73 | 846.58 |

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 488.30(Hidasse) to 1834.1kg/ha (EBW22205). Out of 50 genotypes, four genotypes such as EBW22205, EBW222208, and EBW222079 were the top yielding genotypes with the grain yield of 1834.15, 1783.02 and 1707.81kg/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. Generally, the range of variation was wide for all the characters studied. Gezahegn *et al.* (2015) reported similar results on bread wheat study. With regards to overall mean performance of the genotypes for all traits, EBW22205 gave not only the highest yield but also showed better performance for most of the traits among the evaluated genotypes as well as it surpassed the check variety (Hidasse) for yield and most of other associated traits. Regarding other traits, early heading was recorded in genotype EBW222096 (54.5days) and Early maturing was registered for Hiddase(55.07) genotype whereas the genotype, EBW22209,(68 days) was found to be late in maturity. Maximum plant height was observed in genotype EBW222080(37.00cm) and lowest was for EBW222098(23.50cm). Furthermore, thousand Kernel Weight was highest for EBW222090(97.6gm) and the lowest TKW was recorded for EBW222055(78.00gm) genotypes. Therefore, high variability for six traits of fifty bread wheat genotypes evaluated under this study implied that there was reasonably sufficient genetic variation among the genotypes which provides good chances of selecting superior and desired genotypes for further improvement.

Table 4. Mean performance of different characters among fifty bread wheat genotypes evaluated across locations in 2022.

| Genotype | DTH | DTM | PHT | TKW | HLW | GYLD |
|-----------|-------|-------|-------|-------|--------|---------|
| EBW222050 | 59.25 | 62.93 | 28.50 | 88.00 | 106.50 | 1290.46 |
| EBW222051 | 56.50 | 64.97 | 29.50 | 82.25 | 108.25 | 1306.39 |
| EBW222052 | 57.75 | 62.60 | 25.50 | 86.25 | 106.25 | 922.47 |
| EBW222053 | 58.00 | 63.22 | 27.00 | 84.00 | 107.00 | 1200.55 |
| EBW222054 | 58.75 | 56.61 | 26.50 | 86.25 | 107.00 | 1299.46 |
| EBW222055 | 56.25 | 66.89 | 28.50 | 78.00 | 107.00 | 1250.89 |
| EBW222056 | 58.25 | 65.25 | 28.00 | 81.25 | 108.58 | 1142.72 |
| EBW222057 | 62.25 | 64.18 | 35.50 | 88.00 | 108.00 | 1297.86 |
| EBW222058 | 59.25 | 59.45 | 28.00 | 85.25 | 104.25 | 992.86 |
| EBW222059 | 59.75 | 67.77 | 30.00 | 84.50 | 107.42 | 1834.15 |
| EBW222060 | 58.25 | 64.74 | 24.00 | 88.25 | 105.25 | 929.23 |
| EBW222061 | 60.00 | 62.90 | 28.50 | 88.00 | 108.00 | 1183.32 |
| EBW222062 | 59.00 | 65.77 | 27.50 | 80.75 | 107.25 | 1219.28 |
| EBW222063 | 58.00 | 64.72 | 32.50 | 89.25 | 109.25 | 1568.82 |
| EBW222064 | 58.50 | 64.10 | 31.00 | 92.00 | 106.75 | 1168.53 |
| EBW222065 | 58.25 | 64.37 | 30.50 | 88.75 | 107.50 | 1207.98 |
| EBW222066 | 57.25 | 65.00 | 33.50 | 95.00 | 108.50 | 1252.38 |
| EBW222067 | 59.75 | 62.89 | 31.50 | 91.25 | 108.00 | 1638.65 |
| EBW222068 | 61.75 | 59.37 | 25.00 | 87.50 | 107.50 | 1351.38 |
| EBW222069 | 62.75 | 64.27 | 33.00 | 87.00 | 111.75 | 1617.07 |
| EBW222070 | 58.25 | 66.48 | 31.00 | 93.50 | 106.00 | 1638.42 |
| EBW222071 | 58.75 | 64.98 | 32.00 | 91.25 | 109.00 | 1421.68 |
| EBW222072 | 59.50 | 64.89 | 29.00 | 91.25 | 108.25 | 1486.86 |
| EBW222073 | 58.25 | 65.16 | 32.00 | 82.50 | 107.50 | 1469.77 |
| EBW222074 | 61.50 | 64.11 | 33.00 | 80.50 | 108.00 | 1537.68 |
| EBW222075 | 61.00 | 61.67 | 26.50 | 80.25 | 107.50 | 1352.86 |
| EBW222076 | 63.00 | 60.95 | 26.50 | 88.75 | 108.50 | 1152.77 |
| EBW222077 | 59.75 | 62.95 | 27.50 | 91.25 | 107.25 | 1404.07 |
| EBW222078 | 60.25 | 65.43 | 28.50 | 90.00 | 108.75 | 1522.92 |
| EBW222079 | 60.50 | 62.95 | 36.00 | 91.75 | 109.00 | 1707.81 |
| EBW222080 | 57.00 | 67.96 | 37.00 | 84.50 | 107.50 | 1474.89 |
| EBW222081 | 60.00 | 65.57 | 32.50 | 83.25 | 108.50 | 1366.72 |
| EBW222082 | 59.25 | 64.48 | 32.00 | 88.25 | 108.00 | 1316.62 |
| EBW222083 | 59.75 | 63.90 | 32.50 | 84.00 | 109.25 | 1524.27 |
| EBW222084 | 58.00 | 65.01 | 26.00 | 83.75 | 104.75 | 1034.64 |
| EBW222085 | 61.50 | 64.32 | 29.00 | 92.50 | 107.75 | 1142.97 |
| EBW222086 | 60.75 | 62.12 | 29.00 | 90.75 | 108.42 | 709.62 |
| EBW222087 | 57.00 | 64.77 | 30.50 | 79.50 | 104.00 | 1363.56 |

| | | | | | | |
|-----------|-------|-------|-------|-------|--------|---------|
| EBW222088 | 59.00 | 67.55 | 35.50 | 93.25 | 108.25 | 1783.02 |
| EBW222089 | 56.00 | 68.67 | 33.50 | 88.75 | 107.25 | 1660.57 |
| EBW222090 | 60.25 | 64.87 | 31.50 | 97.50 | 109.00 | 1413.36 |
| EBW222091 | 57.75 | 66.89 | 29.00 | 85.25 | 105.50 | 1337.69 |
| EBW222092 | 61.00 | 65.85 | 31.50 | 90.00 | 110.75 | 1388.19 |
| EBW222093 | 59.25 | 64.27 | 28.00 | 89.50 | 107.75 | 1300.82 |
| EBW222094 | 59.50 | 64.00 | 26.00 | 81.00 | 106.50 | 1170.92 |
| EBW222095 | 55.50 | 68.74 | 31.00 | 85.50 | 108.25 | 1304.61 |
| EBW222096 | 54.50 | 62.15 | 29.50 | 85.75 | 103.50 | 1135.77 |
| EBW222097 | 57.50 | 63.51 | 30.00 | 87.25 | 104.25 | 1288.02 |
| EBW222098 | 59.50 | 58.32 | 23.50 | 84.50 | 105.25 | 1008.92 |
| Hidase | 58.50 | 55.07 | 24.50 | 86.25 | 104.00 | 488.30 |
| Mean | 59.04 | 63.99 | 29.76 | 87.07 | 107.36 | 1311.66 |

DTH = Days to Heading; DTM = Days to Maturity; PHT = Plant Height; TKW = Thousand Kernel Weight, HLW = Hectoliter Weight, GYD = Grain Yield

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 phenotype variances, genotypic (GCV) and phenotypic coefficient of variation (PCV) for various characters studied are presented in Table 5. Based the result, the phenotypic 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 influenced by the environment. However, differences between them were small for most of the traits implying that low effect of environment on the expression of characters at both locations.

At Kulumsa, high PCV and GCV values were observed for grain yield (PCV=24.42) and (GCV=22.24) and thousand Kernel Weight (PCV=13.38) and (GCV=15.32) 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 GCV were recorded for Plant height and Hectoliter weight, this is in agreement with findings of Ashfaq *et al.* (2014). 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=35.63) and (GCV=22.45) and thousand kernel weight (PCV=12.95) and days to heading (GCV= 8.10) indicating better opportunity for improvement in these traits through selection at location. However, moderate PCV and GCV were obtained for Plant height and Hectoliter weight. The lowest estimates of PCV (2.41 and 2.04) and GCV (1.75 and 1.47) were recorded for days to heading and days to maturity, respectively 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 characters with high phenotypic coefficient of variation indicated more influence of environmental factors. Similar results on variability for different characters were reported by Prasad *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 days to heading (92%) and grain yield (83%) while moderately high heritability values were obtained for hectoliter weight (60%). Moderate value of broad sense heritability was showed for Plant height, days to maturity and thousand kernel weight traits at Kulumsa. 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). On the other hand, at Melkassa, high for while moderately high broad sense heritability estimates were showed for days to heading (78%) and thousand kernel weight (76%). Low broad sense heritability was recorded for plant height (12%) at Melkassa. Low estimates of broad sense heritability have been also reported by previous researchers for number of kernels 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%). At Kulumsa, Genetic advance as percent of the means (GAM) in this study ranged from 2.18% to 41.72% for days to maturity and grain yield, respectively (Table 5). However, moderate to high heritability associated with a high genetic gain was observed for TKW (24.07%) and GYD (41.72%) indicating the involvement of additive gene action. 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).

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 grains 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 Melkassa, Highest value of expected genetic advance expressed as percent of mean was observed for grain yield (29.14%) and TKW (10.44%). High heritability with moderately high GMA (%) was observed for these 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 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 estimates for PHT (12%) indicated that selection for this character 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.

Table 5. Estimation of Genetic parameters for different traits in Bread Wheat Genotypes Evaluated at Kulumsa and Melkasa during 2022 G.C.

| Statistics | DTH | | DTM | | PHT | | TKW | | HLW | | GLD | |
|-------------------------|------|------|------|------|-------|-------|-------|--------|-------|------|---------|---------|
| | KU | MK | KU | MK | KU | MK | KU | MK | KU | MK | KU | MK |
| Genotype Variance | 8.35 | 0.85 | 7.22 | 1.98 | 15.75 | 7.70 | 19.48 | 4.62.4 | 9.20 | 5.52 | 1561.23 | 3612.57 |
| Phenotypic Variance | 9.04 | 1.65 | 9.23 | 3.81 | 29.34 | 61.81 | 25.54 | 11.80 | 22.27 | 9.28 | 1883.31 | 9096.48 |
| Envt(Residual) variance | 0.69 | 0.76 | 2.01 | 1.41 | 13.58 | 54.10 | 6.06 | 7.18 | 13.07 | 3.75 | 3215.08 | 5484.90 |

| | | | | | | | | | | | | |
|--------------|-------|-------|------|-------|--------|-------|-------|-------|-------|-------|---------|---------|
| GCV | 4.41 | 1.75 | | 1.47 | 3.86 | 3.89 | 13.38 | 8.10 | 4.61 | 3.78 | 22.24 | 22.45 |
| PCV | 4.59 | 2.41 | | 2.04 | 5.27 | 11.03 | 15.32 | 12.95 | 7.17 | 4.90 | 24.42 | 35.63 |
| ECV | 1.27 | 1.60 | | 1.41 | 3.59 | 10.32 | 7.47 | 10.10 | 5.49 | 3.12 | 10.09 | 27.66 |
| GA | 5.72 | 1.38 | 4.89 | 2.09 | 5.99 | 2.02 | 7.94 | 2.77 | 4.02 | 3.74 | 74.32 | 24.71 |
| GAM (%) | 8.73 | 2.62 | | 2.18 | 5.83 | 2.83 | 24.07 | 10.44 | 6.10 | 6.01 | 41.72 | 29.14 |
| Heritability | 0.92 | 0.53 | 0.78 | 0.52 | 0.54 | 0.12 | 0.76 | 0.39 | 0.41 | 0.60 | 0.83 | 0.40 |
| Max. mean | 73.0 | 56.00 | | 3.00 | 120.00 | 90.00 | 44.00 | 36.00 | 72.44 | 68.60 | 2816.00 | 1687.00 |
| Min. mean | 58.0 | 51.00 | | 93.00 | 90.00 | 55.00 | 22.00 | 20.00 | 31.76 | 54.18 | 616.00 | 174.00 |
| Grand Mean | 65.55 | 52.52 | | 95.82 | 102.84 | 71.30 | 32.98 | 26.54 | 65.83 | 62.15 | 1776.73 | 846.58 |

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 and other 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 and 7) 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 grain yield and hectoliter weight 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 between TKW and HLW. Similarly, highly significant phenotypic correlation was found for grain yield with hectoliter weight followed by thousand kernel weight and plant height ($P < 0.0001$). 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 and phenotypic correlations were registered for grain yield with plant height, while negatively non-significant genotypic correlation was observed for grain yield with days to heading and days to maturity. 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 reveal that there is interaction among the characters in which a gene favoring increment in one character will also influence another character (Table 6 and 7).

Days to heading (DTH) exhibited positive and non-significant association with days to maturity and PHT whereas negative and non-significant correlation of this character was observed with TKW and HLW at genotypic level. Whereas, at phenotypic level, positive and highly significant correction was found between days to heading with DTM and PHT. 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 and HLW while, it exhibited negative and non-significant correlation with plant height, TKW and GYD 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, whereas, negatively significant correlation was obtained with TKW. Plant height revealed positive and non-significant correlation with TKW and HLW. Similar result was reported by Ashebr *et al.*, (2020). While at phenotypic level, PHT had highly significant association with GYD and had positively significant correlation with HLW. On other hand, TKW revealed positive and highly significant association with HLW and GYD, while HLW had positively higher association with grain yield 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. Estimate of Correlation coefficient at phenotypic (above diagonal) and genotypic (below diagonal) level among six traits of introduced BW genotypes at Kulumsa in 2022

| Traits | DTH | DTM | PHT | TKW | HLW | GYLD |
|--------|----------|---------|---------|----------|----------|----------|
| DTH | 1 | 0.556ns | 0.102ns | -0.175ns | -0.063ns | -0.163ns |
| DTM | 0.631** | 1 | 0.173ns | 0.070ns | 0.103ns | 0.089ns |
| PHT | 0.122** | 0.251** | 1 | 0.378ns | 0.177ns | 0.509* |
| TKW | -0.162** | 0.105** | 0.557ns | 1 | 0.788ns | 0.864** |
| HLW | -0.005ns | 0.139** | 0.082* | 0.585** | 1 | 0.851** |
| GYLD | 0.131ns | 0.112ns | 0.620** | 0.963** | 0.561* | 1 |

Signif. 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘

Table 7. Estimate of Correlation coefficient at phenotypic (above diagonal) and genotypic (below diagonal) level among six traits of introduced BW genotypes at Melkassa in 2022

| Traits | DTH | DTM | PHT | TKW | HLW | GYLD |
|--------|----------|----------|----------|----------|----------|----------|
| DTH | 1 | -0.419ns | 0.234ns | -0.219ns | -0.303ns | -0.046ns |
| DTM | -0.511** | 1 | -0.449ns | -0.236ns | -0.232ns | -0.482ns |
| PHT | 0.325** | -0.527** | 1 | 0.257ns | 0.330 | 0.573* |
| TKW | -0.736** | -0.629** | 1.000 | 1 | 0.425ns | 0.498** |
| HLW | -0.421ns | -0.099** | 0.518 | 0.919 | 1 | 0.679** |
| GYLD | -0.174ns | -0.330ns | 0.719** | 1.000** | 0.716* | 1 |

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘

DTH=Date to heading; DTM=Date to maturity; GFP= Grain filling period, PHT=Plant height; TKW= Thousand kernel weight, HLW=Hectoliter weight; GYLD= Grain yield

4. Conclusion

Based on this study, genetic variability of bread wheat genotypes under high temperature areas revealed highly significant differences between the genotypes were 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. Selection and hybridization of genotypes with high genotypic coefficient of variation, heritability and genetic advance can be recommended for future bread wheat yield enhancement. 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. 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 further bread wheat yield enhancement under targeted area of high temperature condition in the country.

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