



Genetic variability of yield and yield related traits in bread wheat (*Triticum aestivum*. L) Genotypes under high temperature condition

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ABSTRACT

Information on the extent and pattern of genetic variability of bread wheat genotypes under high temperature stress condition is limited. The present study was conducted with the objective of assessing the presence of genetic variability in 36 bread wheat genotypes under high temperature stress condition for yield and yield related traits. The genotypes were evaluated using Triple Lattice Design with three replications at Werer agricultural research center, Afar region in 2017. The data generated from the experiment were subjected to analysis of variance and genetic analyses. The analysis of variances of bread wheat genotypes evaluated for 11 traits revealed highly significant difference between the genotypes for most traits except days to emergence. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were high for grain yield/ha, biomass yield/ha and harvest index. Also, moderate values for both GCV and PCV were obtained for traits. The magnitude of PCV values higher than GCV which indicates the degree of influence of environment over genotypic effect. The value of heritability in broad sense ranged from 66.72% for Number of kernel per spike to 97.79 for days to heading while genetic advance as percent of mean was ranged from 16.07(number of spikelet per spike) to 41.20 yield kg/ha. High heritability accompanied with high genetic advance as percent of the mean was recorded for days to heading, plant height, spike length, biomass, thousand kernel weights and harvest index which revealed traits was simply inherited. Hence, from the current results it has been observed adequate existence of variability for most of the traits in the studied genotypes and these genotypes could be exploited in future bread wheat breeding for high temperature stress condition.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereal crop world-wide that grown in many areas and major staple crops with about 751.4 million tons' annual production (USDA, 2017). In Sub-Saharan Africa (SSA), wheat is grown by millions of resource poor smallholder farmers predominantly under rain-fed conditions. The consumption of wheat also is increasing by approximately 650,000,000 tons per year in SSA (Mason *et al.*, 2012). Similarly, wheat is the most important crop in Ethiopia and ranked 4th in area (13.38%) and grain production (15.17%) of total grain crops next to Tef, Maize and Sorghum which has resulted to increase in a production mainly by smallholder farmers using rain-fed based production system and used mainly for food (CSA, 2018). Both bread wheat (*Triticum aestivum* L. *em. Thell*) and durum wheat (*Triticum turgidum* L. subsp. *duru m.*) are the two most important wheat species which are mainly grown in the country (Amsal, 2001). The consumption of wheat in our country is increasing with increasing food variety. There are seven bread wheat varieties have been officially released for irrigated lowland areas of Ethiopia (Desta *et al.*, 2017 and Mihratu *et al.*, 2019) which is in a good progress. The released bread wheat varieties at Middle and Lower-Awash areas are only for off season growing from October to February. However, for the main growing season that runs from May to September which is characterized by high temperature, there are no heat adaptable varieties. The generation of adaptable varieties largely depends on the availability of desirable genetic variability for important traits (Pratap *et al.*, 2012). Success in crop breeding program depends on the magnitude of genetic variability present in a material and the extent to which the desirable characters are heritable (Kahrizi *et al.*, 2010).

Estimation of the magnitude of variation with in genotype for important plant attributes will enable breeders to exploit genetic variability more efficiently. This is due to the serious role of genetic variability in determining the amount of progress to be made by selection. However, the existence of variation alone in the population is not sufficient to improve desirable traits and also high heritability is needed to have better opportunity to select directly for the traits of interest which delivers information about the extent to which a specific trait can be transmitted to the successive generation and estimates of genetic advances are important initial steps in any breeding programs they provide information about effective selection. High

genetic advance coupled with high heritability estimates offer a most suitable condition for selection (Larik and Joshi, 2004). Therefore, selection is an important part by which genotypes with high productivity in a given environment could be developed and it will be effective when there is a significant amount of variability among the breeding materials (Sumanth *et al.*, 2017). The available variability can be measured using genotypic and phenotypic coefficient variation which used to partition genetic and environmental variance (Oniya *et al.*, 2017; Pratap *et al.*, 2012,). Therefore, the current study was carried out with the objective of assessing the genetic variability, genetic advance and heritability between yield and yield related traits of bread wheat genotypes under high temperature stress environment.

MATERIALS AND METHODS

The experiment was conducted at Werer Agricultural Research Center (WARC) during main cropping season in 2017. WARC is located at middle Awash of Afar National Regional state at a distance of 278 km from Addis Ababa to the east direction near to the main road from Addis to Djibouti at altitude of 740 m above sea level. The center is located at 9° 16' 8" N latitude and 40° 9' 41" E longitudes. The area has a mean maximum and minimum annual temperature of 34°C and 19°C and monthly temperature of 38.06°C and 21.06°C during main season, respectively. The precipitation in study area is characterized by unpredictable and uneven distribution with annual average rainfall about 571 mm which is not sufficient for crop production. The main irrigation water source is from Awash River. The soil in the testing field of Werer is predominantly Fluvisols (Wendmagegn and Abere, 2012) while vertisol are the second dominant soil that occupies about 30% of the total area. The experiment was carried out in Triple Lattice Design consisted of 36 entries sown in three replications on 9 m² plot size which accommodated five ridge at 0.6m spacing with two rows each with net harvestable plot area 7.2 m². The planting date was June 24, 2017. Seeds were sown on rows with manual drilling at a rate of 100 kg ha⁻¹ basis. Fertilizer was applied at a rate of 50 kg ha⁻¹ P₂O₅ in DAP form once at sowing time and 100kg of N (Urea) ha⁻¹ applied in split; half at seedling stage and the remaining 50% at booting stages. The irrigation water was applied at every 10days interval using furrow method and agronomic activities were applied uniformly for each treatment.

Table 1. The evaluated bread wheat genotypes are listed below.

Trt	Cross/Pedigree	Origin
1	MILAN/KAUZ//PRINIA/3/BAV92/5/TRAP#1/BOW	CIMMYT/ICARDA
2	RL6043/4*NAC//PASTOR/3/BAV92/4/ATTILA/BAV92	CIMMYT/ICARDA
3	ESDA/KKTS	CIMMYT/ICARDA
4	ATTILA*2/PBW65//TAM200/TUI	CIMMYT/ICARDA
5	ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE	CIMMYT/ICARDA
6	THB/KEA//PF85487/3/DUCULA/4/WBLL1*2/TUKURU	CIMMYT/ICARDA
7	ATTILA*2//CHIL/BUC*2/3/KUKUNA	CIMMYT/ICARDA
8	ATTILA*2/PBW65//KACHU	CIMMYT/ICARDA
9	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI	CIMMYT/ICARDA
10	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR	CIMMYT/ICARDA
11	ROLF07/4/BOW/NKT//CBRD/3/CBRD/5/FRET2	CIMMYT/ICARDA
12	MUNAL#1/FRANCOLIN#1	CIMMYT/ICARDA
13	WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX	CIMMYT/ICARDA
14	BECARD/AKURI	CIMMYT/ICARDA
15	BAJ#1/AKURI	CIMMYT/ICARDA
16	ATTILA*2PBW65//MUU#1/3/FRANCOLIN#1	CIMMYT/ICARDA
17	WAXWING*2/HEILO	CIMMYT/ICARDA
18	BOHAINE	CIMMYT/ICARDA
19	SERI.IBKAUZ/HEVO/3/AMAD/4/ESD/SHWA/BCN	CIMMYT/ICARDA
20	FERROUG-2/FOW-2	CIMMYT/ICARDA
21	SOKOLL//PBW343*2/KUKUNA/3/ATTILA/PASTOR	CIMMYT/ICARDA
22	QUATU3//MILAN/AMSEL	CIMMYT/ICARDA
23	ATTILA*2/PBW65*2/4/CROC1/AE.SQUARROSA(205)	CIMMYT/ICARDA
24	ATTILA*2/PB W65*2/W485/HD29	CIMMYT/ICARDA
25	SAUAL/3/ACHTAR*3//KANZ/KS85.8.4/4/SAU	CIMMYT/ICARDA
26	ALTAR84/AE.SQUARROSA (221)//3*BORL95	CIMMYT/ICARDA
27	TACHUPETOF2001/6/OASIS/5*BORL95/5/CNDO/R143	CIMMYT/ICARDA
28	KAUZ/RAYON/3/N5732/HER//CASKOR	CIMMYT/ICARDA
29	KSAYONGENARO81//TEVEE.II./4/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/KAUZ	CIMMYT/ICARDA
30	IMAM	CIMMYT/ICARDA
31	SHUHA-8/DUCULA	CIMMYT/ICARDA
32	TUKURU//BAV92/RAYON/3/FRNCLN	CIMMYT/ICARDA
33	TACUPETOF2001*2/BRAMBLING/WBLL1*2/BRANBLING	CIMMYT/ICARDA
34	WAXWING/4/BL1496/MILAN/3/CROC- 1/AE.SQUA9205)//kauz/5/frncln	CIMMYT/ICARDA
35	WAXWING/2*ROLF07	CIMMYT/ICARDA
36	SAMAR-13/PASTOR-1	CIMMYT/ICARDA

CIMMYT=International Maize and Wheat Improvement Center, ICARDA=International Center for Agricultural Research in the Dry Land Areas.

Observations were recorded for Days to emergence, Days to heading, Days to maturity, Plant height, Spike length, 1000 grain weight, Number of spikelet /spike, Number of seed/spike, Grain yield, Biomass yield and Harvest index. The recorded data were subjected to analysis of variance (ANOVA) as suggested by Gomez and Gomez (1984) using SAS Software (Version 9.0). Different genetic parameters including genotypic variance (σ^2_g), phenotypic variance (σ^2_p), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated by using the formula adopted from Burton and De vane (1953) and Johnson *et al.*, (1955a and 1955b).

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

$$\text{Genotypic variance } \sigma^2_g = \frac{\text{MSG} - \text{MSe}}{r}$$

$$\text{Phenotypic Coefficient of Variation PCV} = (\sqrt{\sigma^2_p} / \text{grand mean}) * 100$$

$$\text{Genotypic Coefficient of Variation GCV} = (\sqrt{\sigma^2_g} / \text{grand mean}) * 100$$

$$H^2 = \sigma^2_g / \sigma^2_p * 100$$

Where:

σ^2_p = phenotypic variance

σ^2_e = Environmental (error) variance

σ^2_g = genotypic variance

MSg = mean square due to genotypes.

MSe= environmental variance (error mean square)

r = number of replication

H^2 = heritability

Genetic advance (GA) for each character was computed using the formula adopted from Johnson *et al.* (1955a) and Allard (1960).

$$GA = K. \sigma_p. H^2 \text{ and GA (as \% of the mean)} \\ = \frac{[(GA)]}{\bar{X}} * 100$$

Where: σ_p = Phenotypic standard deviation

k= selection differential (at 5% selection intensity, k=2.06)

X=Grand mean

RESULTS AND DISCUSSIONS

Analysis of Variance

Analysis of variances of 36 bread wheat genotypes evaluated for 11 traits revealed that highly significant ($P \leq 0.01$) difference among genotypes for all traits except for days to emergence (Table 2). The significant difference among genotypes for the traits indicated the presence of a considerable amount of variability among genotypes which is an essential to the study of plant breeders for enhancement of these traits through breeding. The mean square due to replication showed highly significant difference for biomass yield and significant difference for days to emergence, spike length and grain yield which indicate the heterogeneity present in the field.

Table 2. The Analysis of Variance (ANOVA) for different sources of variations and the corresponding CV in percentage for eleven traits.

*, ** and ns, significant at 5%, 1% probability level and non-significant, respectively.

Traits	Mean Squares				CV%
	Replication d.f=2	Block(group) d.f=15	Genotype d.f=35	Error d.f=55	
DE	2.23*	0.60	0.62ns	0.64	12.07
DH	2.12	2.85	108.46**	2.94	3.16
DM	8.08	5.82	117.93**	7.23	3.09
PH	75.58	29.85	124.20**	27.35	8.50
SL	1.638*	0.83*	2.77**	0.41	8.06
NSSP	2.36	0.49	4.10**	0.86	6.21
NKSP	26.96	22.56	59.12**	18.94	12.15
BY	11287194.60**	1493156.10	4950469.40**	1024604.50	14.62
TKW	6.38	4.13	26.40**	4.08	7.30
GY	736350.08*	122589.13	482329.00**	105636.47	16.76
HI	5.11	9.22	77.84**	12.43	12.32

Where: d.f= degree of freedom, CV= coefficient of variation, DE=days to emergence, DH=days to heading, DM= days to maturity, PH= plant height, SL= spike length, NSSP= number of spikelet per spike, NKSP=number of kernels per spike, BY=biomass yield kg/ha, TKW= thousands kernel weight, GY=grain yield kg/ha, HI= harvest index.

Genotypic and Phenotypic Coefficient of Variation

Values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated and presented in table 3. According to Sivasubramanian and Madhavamenon (1973), GCV and PCV can be categorized as high (>20%), moderate (10-20%) and low (<10%). Based on this category, PCV values were high for grain yield, biomass and harvest index. Similar findings also reported by Kumer *et al.* (2013) and Bilgin *et al.* (2011) that show high PCV for grain yield and harvest index. Moderate values for both GCV and PCV were obtained for days to heading (12.08, 12.48), spike length (11.67, 14.24), number of kernel per spike (10.13, 16.01), biomass/ha (18.25, 23.47), thousand kernel weight

(10.32, 12.65), yield/ha (18.88, 25.39) and harvest index (17.04, 20.83) indicated these traits was under control of additive genes and modified selection would be effective for improvement of these traits. The finding of this study is in agreement with results reported by Kumar *et al.* (2013) and Ali *et al.* (2008) for plant height and Mohammed *et al.* (2011) for plant height and kernels per spike that moderate values for both genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded.

Low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated for days to maturity (7.89, 8.45) and number of spikelets per spike (7.39, 9.47) 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) and Mohammad *et al.* (2011) for days to maturity and current results was at par with findings of Ashfaq *et al.*, (2014) and Haq *et al.*, (2016). Generally, the observation of higher PCV values than GCV values might suggest greater role of environment than genotype effect on the expression of the traits. Hence, the magnitude of difference between PCV and GCV values indicates the degree of influence of environment over genotypic effect.

Heritability and Genetic Advance

Although the genotypic coefficient of variation showed the extent of genetic variability present in the genotypes for various traits, it does not provide full scope to assess the variation that is heritable. The genotypic coefficient of variation along with heritability estimates provide reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Burton, 1952). The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955a).

Heritability in broad sense ranged from 66.72% for Number of kernel per spike to 97.79 for days to heading while genetic advance as percent of mean was ranged from 16.07(number of spikelets per spike)

to 41.20(yield kg/ha) (Table 4). Pramoda and Gangaprasad (2007) generally classified heritability estimates as low (<40%), medium (40-59%), moderately high (60-79%) and very high (80-100%). Hence, high heritability were obtained for biomass yield (82.13%), number of spikelet's per spike (82.37%), thousand kernel weight (85.66%), harvest index (85.86%), spike length (85.99%), days to maturity (95.34%) and days to heading (97.79%). Moderately high heritability was recorded for number of kernel per spike (66.72), yield/ha (78.77) and plant height (79.44). This results in agreement with the finding of Awale *et al.* (2013) who reported heritability estimates were very high for days to heading (89.08%) and moderately high heritable for plant height (74.04%). Similarly Kalimullah *et al.* (2012) also showed high heritability estimates for thousand seed weight (98.11%). Selection based on phenotypic performance would be effective for trait that show high heritability, as indicated by Tabbal and Fraihat, (2012); Kaddem *et al.*, (2014) and Navil *et al.*, (2014). Moderate genetic advance as percent of mean was obtained for number of spikelet per spike (16.07%) and days to maturity (16.60%). Therefore, simple selection would be not effective for improvement and modified selection would be playing an important role in enhancement of these traits. Taken together high heritability accompanied with high genetic advance as percent of the mean was recorded for days to heading, plant height, spike length, biomass yield, thousand kernel weight and harvest index which imply that phenotypic selection to improve these traits.

Table 3. Estimation of variability components (genotypic and phenotypic variances and coefficient of variations) for traits studied in bread wheat genotypes.

Traits	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)
DH	42.96	45.87	2.91	12.08	12.48
DM	47.26	54.19	6.93	7.89	8.45
PH	35.90	63.79	27.88	9.73	12.97
SL	0.87	1.29	0.42	11.67	14.24
NSSP	1.22	2.00	0.78	7.39	9.47
NKSP	13.17	32.88	19.71	10.13	16.01
BY	1596637.68	2638815.50	1042177.82	18.25	23.47
TKW	8.14	12.23	4.09	10.32	12.65
YLD	134089.78	242532.32	108442.54	18.88	25.39
HI	23.77	35.50	11.74	17.04	20.83

σ^2_g , σ^2_p and σ^2_e = genotypic, phenotypic and environmental variances, respectively. GCV (%) and PCV (%) = genotypic and phenotypic coefficient of variations, respectively. DH=days to heading, DM= days to maturity, PH= plant height, SL= spike length, NSSP= number of spikelet's per spike, NKSP=No of kernel per spike, BMS=biomass yield kg/ha, TKW= thousands kernel weight, YLD=yield kg/ha, HI= harvest index.

Table 4. Estimation of heritability and genetic advance for ten traits studied in bread wheat genotypes.

Traits	GA	GAM (%)	H ² (%)
DH	13.64	25.15	97.79
DM	14.46	16.60	95.34
PH	13.07	21.23	79.44
SL	2.01	25.23	85.99
NSSP	2.40	16.07	82.37
NKSP	7.88	22.01	66.72
BY	2748.37	39.70	82.13
TKW	6.17	22.32	85.66
YLD	799.09	41.20	78.77
HI	10.54	36.84	85.86

GA and GAM (5%) = genetic advance at 5% selection intensity and genetic advance as percent of mean respectively. H² = heritability in broad sense in percent. DH=days to heading, DM= days to maturity, PH= plant height, SL= spike length, NSSP= number of spikelet's per spike, NKSP=No of kernel per spike, BMS=biomass yield kg/ha, TKW= thousands kernel weight, YLD=yield kg/ha, HI= harvest index.

CONCLUSION

Based on this study genetic variability of bread wheat genotypes under high temperature stress condition evaluated for their traits revealed highly significant difference between the genotypes for most traits and significant difference among genotypes were observed. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were observed for grain yield, biomass yield and harvest index. Moderate values for both GCV and PCV were obtained for traits indicated that traits were under control of additive genes and modified selection would be effective for improvement of the traits. Generally, the magnitude of difference between PCV and GCV values indicates the degree of influence of environment over genotypic effect. Heritability in broad sense accompanied with high genetic advance as percent of the mean was recorded for traits imply that phenotypic selection can be used to improve the traits. Overall from the study results it has been observed adequate existence of variability for most of the traits studied among genotypes. These genotypes could be exploited in wheat improvement and promising for development of heat stress tolerant varieties in future bread wheat breeding for high temperature stress condition.

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