Genetic Variability, Diversity and Correlation Studies in Bread Wheat (T*riticum aestivum* L.) Genotypes At Holeta

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Abstract

One hundred bread wheat genotypes were grown at Holetta Agricultural Research center main station during main cropping season 2021-2022. Those genotypes were evaluated for variability parameters and correlation for grain yield per hector, grain filling period, and total number of tillers per plant, 1000-kernel weight, and kernel per spike. All traits shown significant genotypic differences. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield, thousand kernel weight and kernel per spike. This indicates that selection will be effective based on these traits and their phenotypic expression would be a good indicator of the genotypic potential of the studied wheat materials. All the studied characters recorded its heritability. These traits also indicate high expected genetic advance except grain filling period. Grain yield per plant showed highly significant positive correlation with thousand kernel weight, spikelet per spike, kernel per spike, and significant negative correlation with total number of tiller per plant. Based on quantitative data, bread wheat genotypes were grouped by cluster analysis on the basis of Euclidean distances of similarity to their distinct groups.

Key words: Genetic variability, bread wheat germplasm, correlation, Heritability

NTRODUCTION

Wheat is the staple food for a large part of the world population including Ethiopia. Grain yield is highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, the selection of individual from population directly for yield as such could be misleading. The leading wheat producing countries in the world are China, India, Russia Federation, the United States, and France; and the global average wheat productiveness is 3.54 t ha^{-1} with a total production of about 778.6 million tons (FAO, 2021/2022).

South Africa and Ethiopia are the largest wheat producers in sub-Saharan Africa (USDA, 2019). Ethiopia's annual production is about 5.8 million tons with mean productivity of 3 tons per hectare (tha^{-1}) (CSA, 2021), which is relatively lower than the attainable yield of the crop, reaching up to 5 tha^{-1} (Zegeye *et al.,* 2020).The productivity of wheat in Ethiopia has increased in the last few years, but its average yield (2.28 t ha^{-1}) remains extremely low compared to other wheat-producing countries. On the other hand, about 85 improved varieties were released in Ethiopia which can provide up to 5.5 and 6.5 t ha^{-1} on farmers' and research fields, respectively (MoANR, 2018). Thus demonstrated that wheat productivity can be improved through the use of improved varieties and production packages.

Rajendra *et al.* (2015) reported the presence of a wide range of variability for grain yield, plant height, days to heading, number of grains/ spike, number of spikelet/spike, and yield/plant in the population of bread wheat. The presence of variability, heritability, and genetic advance in different yield-related characters of bread wheat has been done by Desalegn and Chauhan (2016), Kifle *et al*. (2016), and Rahman *et al*. (2016). However, no variability study has been done on the genotypes used in this study. To develop new varieties, the first step is to evaluate the genetic variability of available genotypes for the desired traits (Rahman *et al.,* 2016). In this investigation, the study of different genotypes were made with an attempt to generate information on inheritance, relationship of yield and its components and their implication in selection of best genotypes of wheat for cultivars and germplasm improvement.

MATERIALS AND METHODS

The wheat germplasm consisted of 100 genotypes were collected from CIMYTT Department as presented in Table 1. The experiment was done at Holetta Agricultural Research Center Main station. Each plot consisted of two rows, each 2.5 m long by 1.2m with 20cm spacing between rows. All the cultural practices were performed as usual. At maturity five guarded plants from each plot were selected at random for recording data on grain filling period, grain yield,

thousands kernel weight, spikelet per spike, total number of tillers per plant and kernel per spike. The mean data were subjected to analysis of variance for the measured trait was estimated using the list significant difference (LSD) using SAS (SAS Institute Inc., 2014).

The phenotypic and genotypic variations were estimated according to the method suggested by Burton and Devane (1953). The coefficient of variations at phenotypic, genotypic and environmental level were estimated using the formula adopted by Johnson *et al.* (1955). Heritability (H_b^2): in a broad sense of all characters was computed using the formula given by Falconer (1989). Using the STATISTICA software, cluster analysis according to Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix.

RESULTS AND DISCUSSION

Genetic variability: Mean squares of grain yield per hector, total number of tillers per plant, 1000-kernel weight, spikelet per spike and kernel per spike showed highly significant differences between genotypes (Table 1).

Genotypic and phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and expected genetic advance expressed as percentage of mean or six characters are presented in Table 3. The estimates of GCV were high for grain yield (35.951), thousand kernel weight (20.851) and kernel per spike (20.969).

The other traits observed moderate to low GCV estimates. Tesfaye *et al.* (2014) reported that thousand seed weight had high heritability while grain yield, hectoliter, day to heading, and plant height had medium heritability, but in the present study those traits had high heritability. High heritability estimates and expected genetic advance were recorded for most traits studied except grain filling period which was moderate. Such considerable range of variations provides a good opportunity for yield improvement. The PCV values of all the characters were higher than its GCV values which indicated that the influence of environment on the expression of all the characters.

High heritability accompanied with high expected genetic advance in case of grain yield, thousand kernel weight, total number of tiller per plant and kernel per spike. The combination of heritability and genetic advance is a better indication of the selection of traits (Anshuman *et al.*, 2013).

Table1. Mean squares of 15 traits of bread wheat genotypes tested at Holeta Agricultural Research center main station**.**

Traits	Mean Square				Mean		CV (%)	R-
	Geno (DF=99)	Rep (DF=1)	BL(Rep) (DF=18)	Error (DF=81)		LSD (at 5%)		Square
GFP	54.79**	6.13ns	84.55*	2.43	73.20	3.20	2.10	0.97
GYPHa	2399578.3**	14.8ns	4446.6	3901.0	3192.958	124.27	2.00	0.99
TKW	85.95**	1.38ns	2.98**	1.08	31.40	2.05	3.30	0.99
SPS	3.68**	4.50**	0.78ns	0.54	18.10	1.41	3.90	0.90
TNTPP	3.88**	0.06ns	0.23ns	0.18	7.40	0.85	5.70	0.96
KPS	206.69**	0.39ns	0.68ns	1.37	48.30	2.47	2.60	0.99

Note, ns, **,* indicates non-significant, highly significant at 1% and significant at 5% probability levels, Rep =Replication, CV = Coefficient of variations and DF= degree of freedom, BL =Block, GFP = grain filling period, GYPHa = grain yield per hectare, HI = harvest index, TKW= thousand kernel weight, SPS = spikelets per spike, TNTPP= total number of tillers per plant,KPS=kernelsperspike.

Table 2. Estimates of heritability in broad sense, genetic advance and coefficients of variations in 100 genotypes**.**

Traits	Mean± SD	$\sigma^2 g$	$\sigma^2 p$	GCV(%)	PCV (%)	$H^{2(\%)}$	GA	GAM (%)
GFP	73.225±5.358	25.766	26.980	6.932	7.094	95.5	10.219	13.955
GYPHa	3192.958±1146.995	1197838.65	1199789.15	35.951	35.978	99.8	225290.82	70.527
TKW	31.382±6.593	42.816	43.354	20.851	20.981	98.8	13.395	42.686
SPS	18.080±1.459	1.579	1.847	6.950	7.517	85.5	2.393	13.236
TNTPP	7.444±1.422	1.844	1.935	18.242	18.687	95.3	2.730	36.680
KPS	48.318±10.174	102.658	103.343	20.969	21.039	99.3	20.803	43.054

Note, $\sigma^2 g$= genotypic variance, $\sigma^2 p$=phenotypic variance, $\sigma^2 e$= error variance=error mean square, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, Hb^2 =Heritability in broad sense, GA= genetic advance, GAM=genetic advance as percent of mean, GYPHa= grain yield per hectare, TKW= thousand kernel weight, SPS= spikelets per spike, , TNTPP= total number of tillers per plant,KPS=kernelsperspike,SD=standarddeviat*ion.*

Correlation coefficient analysis: The phenotypic and genotypic correlations for morphological traits were presented in table 4. The results indicated that at the phenotypic level there was a positive and highly significant correlation of grain yield with thousand kernel weight (r=0.786), kernels per spike (r=0.716),spikelets per spike (r=0.325. Wasif *et al*. (2015) reported significant positive phenotypic correlations of above-ground biomass, kernels per spike and plant height with grain yield. The same auther reported a non-significant correlation of thousand kernel weight and harvest index with grain yield which contradicted our finding.

At the genotypic level, grain yield showed a highly positive significant correlation with harvest index (0.827), thousand kernel weight (0.793), spikelets per spike (0.350), kernels per spike (0.719), and a highly negative significant correlation with and total number of tillers per plant (-0.087). Balcha, (2002) observed that grain yield was positively correlated with grain filling period, spike length, and harvest index, but negatively correlated with days to heading and maturity, plant height, and thousand kernel weights.

Table 3. Genotypic (above diagonal and phenotypic (below diagonal) correlations among different quantitative characters in wheat.

Traits	GFP	GYPHa	TKW	SPS	TNTPP	KPS
GFP		0.179**	0.256**	-0.048**	0.046*	0.062**
GYPHa	0.174*		0.793**	0.350**	-0.087**	0.719**
TKW	0.251**	0.786**		0.181**	-0.102**	0.556**
SPS	-0.043ns	0.325**	0.163*		-0.094ns	0.527**
TNTPP	0.048ns	-0.085ns	-0.099ns	-0.095ns		-0.077**
KPS	0.058ns	0.716**	0.551**	0.491**	-0.076ns	

Note, GFP = grain filling period, GYPHa = grain yield per hectare, TKW= thousand kernel weight, SPS = spikelets per spike, TNTPP = total number of tillers per plant.

Cluster analysis: cluster analysis according to Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix.

Table 4.Cluster of tested genotypes tested in 2021 main season

Cluster No.	No. of Genotypes	Proportion	Ave.distance from Centroid	Max.distance from centroid
Cluster1	45	40.75%	3.01	5.2
cluster2	33	25.95%	2.95	5.01
Cluster3	15	10.4%	3.12	5.69
Cluster4	2	9.70%	1.69	1.69
Cluster5	4	6.90%	2.21	3.33
Cluster6	1	6.30%	0	0

Conclusion

One hundred bread wheat genotypes were grown at Holetta Agricultural Research center main station during main cropping season 2021-2022. Those genotypes were evaluated for variability parameters and correlation for grain yield per hector, grain filling period, and total number of tillers per plant, 1000-kernel weight, and kernel per spike. All the traits shown significant genotypic differences indicating that considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield, thousand kernel weight and kernel per spike. This indicates that selection will be effective based on these traits and their phenotypic expression would be a good indicator of the genotypic potential of the studied wheat materials.

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