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Genetic Variability in Bread Wheat (Triticum aestivum L.) Germplasm for Yield and Yield Component Traits

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Abstract
The overall objective was to study the extent of genetic variation and association among grain yield and yield related traits. Sixty eight germplasm of bread wheat were tested in an augmented design. The Germplasm showed significant variation for treatment adjusted, for most test entries and test versus control studied and relatively wide range of the mean values for most of the characters indicated the existence of variations among the tested germplasm. The phenotypic coefficients of variation values were higher than genotypic coefficients of variation values. High PCV and GCV were recorded for productive tiller, spike length, kernel per spike, 1000 grain weight, biomass yield, harvest index and grain yield. High heritability values were observed for all the characters studied. Among the characters heading date, grain filling, spikelet spike^{-1}, spike length, kernel per spike, 1000 grain weight, harvest index and grain yield had high values of genetic advance as percent of mean (GAM). The D^2 analysis showed the 68 germplasm clustered into six clusters. This shows the germplasm to become moderately divergent. Principal components (PC1 to PC3) considered eigenvalue greater than one (significant), accounted nearly 63.2% of the total variation.. Based on these result we cannot reach to the final decision. But it can be used as a bench mark for further study. Therefore; it needs additional study over several years and multi locations.
Keywords: Germplasm, PCV, GCV, Heritability, Genetic advance, principal component, diversity.

1 .INTRODUCTION

Bread wheat (*Triticuma estivum* L), a self-pollinating annual plant in the true grass family *Gramineae (Poaceae*), is the largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi*et al*., 2011). It is one of the most important export and strategic cereal crop in the world and in Ethiopia in terms of production and utilization (Ranjana and Kumar, 2013). Ethiopia is the first largest wheat producer in Sub Saharan Africa followed by South Africa and fourth in Africa with harvested area of 1.51 million hectares with production of 3.78 million tons and an average yield of 2.5 tons ha-1, which was about 45% below the world average during 2012/13 growing season (CSA, 2012; Degewione and Alamerew, 2013).

Narrow genetic background has rendered improved varieties less tolerant to biotic and a biotic stresses (Maqboo*et al*., 2010). Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes (Aremu, 2012).Therefore, precise information on the nature and degree of genetic variability and divergence present in wheat would help to select parents for evolving superior varieties.

For a successful breeding program, the presence of genetic variability plays a vital role. It is true that the more diverse plants, the greater chance of exploiting to generate productive recombinants and broad variability in segregating generations during genetic improvement (Mohammadi and Prasanna, 2003).Rauf*et al.* (2012) stated that precise knowledge about germplasm variability and genetic relationship among breeding materials is a pre requisite for crop improvement programs as it helps in the development of superior recombinants.

Research efforts made in the country lead to the development of more than 87 bread wheat varieties from 1974 to 2011; thirty varieties 1974 to 1997 (Degewione and Alamerew, 2013) and from 1998 to 2011 fifty seven varieties were released and some of them are in production in different agro ecological zones of the country. Significant genetic variability was reported in Ethiopian bread wheat (Tarekegne*et al*., 1994; Degewione*et al*., 2013). However, previous studies have revealed that, little information is generated about genetic variability of yield and yield component traits in these exotic bread wheat germplasm in Ethiopia.The present study *was to* study the extent of genetic variation among these germplasmusing yield and yield related traits.

2. MATERIALS AND METHODS

Description of the study area

The germplasm were tested at Kulumissa Agricultural Research Center in cropping season of 2013 to 2014. It has an altitude of 2200 m.a.s.l. with annual average rainfall of 850mm.The annual average temperature of the study area is 16.65oC with maximum and minimum temperature of 22.8^{oC}and 10.5^{oC}respectively. With the soil type classified as clay loam soil with a pH of 6.

Experimental Materials
The experimental material is consisted of 68 germplasm of bread wheat (*Triticumaestivum*) including four standard checks (*Danda'a, Huluka, Shorima and Kakaba*).

Experimental Design and Trial Management
The experiment was carried out in an Augmented Block Design (ABD) comprising of four blocks, where each block contains 16 test entries and 4 checks (randomly allocated) with the total of 20 germplasm in each blocks. The germplasm were grown under rain fed conditions. Each germplasm was sown in two rows of 1.25 meter long and 20 cm apart, with seed rate of 7.5g, 150 kg/h. Weeds were controlled manually. Planting was done by hand drilling on July 05, 2013.Recommended fertilizer rate of 100/100 kg/ha N/P2O5 in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing.

Statistical Analysis
The data were subjected to analysis of variance according to Weber*et al* (1988),using the SPAD software developed by IASRI New Delhi, India (Federer, 1956), cluster analysis and principal component analysis were done by SAS Version 9.2

Analysis of variance (ANOVA)
The analysis of variance (ANOVA) was carried out to dissect total variability of the entries into sources attributable to genotype and error using the SPAD software developed by IASRI, New Delhi, India (Federer,1956) .The statistical model for the augmented design was the same as that of the randomized complete block design.
yij= μ+ gi+ cj+ βj+ εij Federer (1956) Where:
yij is the observation of treatment i in jth block μ is the general mean, g is the effect of test treatment,
cj is the effect of control treatments in jth block, βj is the block effects, (ε) is the error.

Estimation of variance components
The phenotypic, genotypic and environmental variances were calculated according to the formula investigated the possibilities to obtain such estimates by Weber *et al* (1988) as follows: Phenotypic variance (σ^2p) = $\sigma^2g+\sigma^2e$, where, σ^2g is genotypic variance and σ^2e is environmental variance, whereas genotypic variance (σ^2g) = MST - σ^2e, where, MST mean square treatment and σe is environmental variance.

Phenotypic coefficient of variation $(\sigma 2g) = \frac{\sqrt{\sigma^2 g}}{\bar{x}} x100$ (Singh and Chaudhury, 1985)

Genotypic coefficient of variation $(\sigma 2g) = \frac{\sqrt{\sigma^2 p}}{\bar{x}} x100$ (Singh and Chaudhury, 1985)

Where: σ2p =Phenotypic variation
σ2g= Genotypic variation and
x̄= Grand mean of the character studied

GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20% and above) values as indicated by Burton and de vane (1953).

Broad-Sense Heritability (H^2B)
Broad sense heritability for all characters was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage according to the methods suggested by Falconer and Mackay (1996).

$$(h^2 b) = \frac{\sigma 2g}{\sigma 2p} X100$$

Where, H^2B =heritability in broad sense Robinson *et al.* (1949) classified heritability values as High (>60%), Moderate (30-60%) andLow (0-30%).

Genetic Advance Under Selection (GA)
The expected genetic advance expressed under selection in broad sense, assuming selection intensity of 5% of the superior progeny was estimated in accordance with the methodology described by Allard (1960) as:

$GA = Kh^2b.\sigma 2p$ (Allard, (1960) Where, h2b= Heritability in broad sense σp = Phenotypic standard deviation

GA= Expected genetic advance k = the standardized selection differential at 5% selection intensity (K = 2.063).

Genetic Advance as Percent Of Mean

Genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under selection, using the following formula:

$$GAM = \frac{GA}{\overline{X}} * 100$$

Where, GAM=Genetic advance as percent of mean GA=Genetic advance under selection and $\bar{x}$=Grand Mean of the population Genetic advance as percent mean was categorized as low, moderate and high as given by Falconer and Mackay (1996).

0-10%: Low, 10-20%: Moderate, 20% and above: High.

Cluster Analysis

Clustering analysis is a multivariate statistical analysis technique involving partitioning a set of objects into groups so that objects within a group are more similar and objects in different groups are more dissimilar Mahalanobis (1936).The bread wheat germplasm for quantitative characters were clustered using the proc cluster of SAS software with average linkage method of clustering strategy version 9.2 (SAS Institute, 2008), which grouped and sorted the germplasm into clusters to form Dendrogam. Cubic clustering criterion (CCC), pseudo F (PSF), and pseudo t2 (PST2) statistics were used in determining the number of clusters in the data.

Principal Component Analysis

The principal component analysis was carried out using Statistical Analysis System Version 9.2 (SAS Institute, 2008). Moreover, the analysis is characterized by the fact that it includes the total variance of variables, explains maximum of variance within a data set, and is a function of primary variables (Katarzyna*et al*. 2013).

3. RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

Mean squares of the 12 characters from analysis of variance (ANOVA) are presented in Table 1. Significant differences were observed among treatments for all characters studied. Among tests, significant differences were observed for all characters except number of spikelet per spike.Among test versus control all the character showed significant difference for 68 bread wheat germplasm. This indicating the presence of variability, which can be exploited through selection for further breeding programs. Similarly, works of Kalimulla*het al*. (2012) reported that grains per spike number of tillers per plant, 1000 grain weight, spike density, and grain yield per plant showed significant differences between forty one bread wheat genotypes were studied. Shashikala (2006) reported significant differences among 169 genotypes for 11 morphological traits such as days to 50% heading, days to 75% maturity, plant height, spike length, number of tillers per, number of spikelet per spike, 1000 grain weight and grain yield per plot.

Phenotypic and genotypic coefficient of variation

The PCV ranged from 10.6 for maturity date to 65.1 for thousand grain weight whereas (Table 2). GCV ranged from 10.5 for maturity date to 65.00 for thousand grain weights. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied indicating that the influence of growing environments. In most of cases, the two values differ slightly indicating less influence of environmental factors. Burton and devane**(**1953) classified PCV and GCV values as high (>20%), medium (10-20%) and low (<10%). Accordingly, high PCV and GCV were observed in traits number of tillers plant^{-1}, spike length, kernel per spike, thousand-grain weight, biomass yield per plot, harvest index, and grain yield per plot.The high PCV and GCV indicate that selection may be effective based on these traits. In support of such study several workers reported high PCV and GCV for grain yield, biomass, harvest index, 1000 grain weight and plant height in wheat. We recorded medium PCV and GCV values, for the rests of the characters. The high and medium PCV and GCV indicate that selection may be effective based on these traits. In support of this study Tarekeng *et al*. (1994) reported high PCV and GCV for grain yield, biomass, harvest index, 1000 grain weight and plant height in wheat. In addition, findings of Ali *et al* (2012) reported medium PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Degewione *et al*. (2013) reported medium PCV and GCV for 1000-grain weight, plant height, and days to heading in twenty-six bread wheat genotypes.

Table 1: Analysis of Variance (Mean Squares) for the 12 Characters of 68 Bread Wheat Germplasm.

Character	Block (adj) (df=3)	Error (df=)	Trt (adj) (df=67)	Among-controls (df=3)	Among-test (df=63)	Test v Control (df=1)	CV (%)
Days to 50% heading(DH)	10.22	4.84	110.78**	17.72	49.99**	4219.5**	3.42
Days to 75% maturity(DM)	1.16	4.22	152.48**	676.5	93.76**	2273.7**	1.77
Grain filling period(GF)	7.89	4.61	63.66**	13.56	62.83**	266.45**	4.68
Plant height(cm)	5.59	5.52	418.21**	221.8	204.76**	14456.8**	1.99
No. of productive tillers	0.24	0.32	2.12**	0.10	1.44*	50.96**	12.27
Spike length(cm)	3.50	0.34	7.65**	0.07	4.39**	235.93**	5.57
Number of spikelet's spike^{-1}	2.08	0.88	6.95**	1.10	3.00^{ns}	273.8**	4.80
Number of kernels spike^{-1}	8.40	6.09	322.14**	58.25	73.25**	1679.6**	6.22
Thousand kernels weight(g)	2.16	0.51	91.84**	21.19	14.48**	5051.1**	4.89
Grain yield plot^{-1}(kg/h)	1488.91	28643.8	3117652.8**	31044.9	1570742.6**	109832814.6**	6.16
Biomass yield plot^{1}(kg/h)	141272.9	94100.6	23697859.7**	1613822.9	9676011.6**	973326400.3**	1.64
Harvest index (%)	0.16	0.55	82.71**	1.8	79.16**	549.04**	4.99

DF =Degrees of freedom, *=significant at 5% probability level and **=highly significant at 1% probabilitylevelCV= Coefficient of Variation

Estimates of Heritability (H^2) In Broad Sense

In this study, the heritability estimate ranged from 84.9% for number of tillers per plant to 99.6% for biomass yield per plot (Table 2). Robinson *et al.* (1949) classified heritability values as high (>60%), moderate (30-60%) and values less than 10% low. Accordingly, high heritability was observed for all twelve characters of 68 bread wheat germplasm. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. This may be attributed due to uniform environmental conditions during the conduct of the experiment. Indicating that the possibility of success in selection. The obtained results were in agreement with results of Ashraf *et al*. (2012) noticed higher heritability values for plant height, days to 50 per cent flowering, number of productive tillers per plant, grain yield per plot, and number of grains per spike. Further, Salem *et al* (2008), Ali *et al*. (2008) recorded high heritability estimates for grain yield, number of kernels per main spike, plant height and thousand kernel weights and number of tillers per plant.

Estimates of Expected Genetic Advance (GAM %)

Genetic advance expressed as a percentage of the mean ranged from 13.7% for maturity date to112.8% for number of productive tillers per plant. Falconer and Mackay (1996) classified genetic advance as percent of mean as low (0-10%), medium (10 - 20%) and high (20% and above). Accordingly, genetic advance as percentage of mean was maximum for all characters studied except for maturity date,plant height and biomass yield which had medium values.The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Accordingly, Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.,* 1955). high heritability associated with high genetic advance were observed for days to heading, grain filling period, fertile productive tillers, spikelet per spike, spike length, kernel per spike, thousand grain weight, grain yield per plot, biomass yield per plot and harvest index respectively .These are simply inherited traits indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Kalimullah*et al*. (2012) reported similar findings for plant height, biomass yield per plot and 1000 grain weight, which supports the present studies.

Table2: Estimate of Ranges, Mean, Phenotypic (PV) and Genotypic (GV) Coefficient of Variation, Broad Sense Heritability and Genetic Advance as Percent of Mean for 12 Characters of 68 Bread Wheat Germplasm Tested At KARC (2013)

Character	Mean	Range		σ^2p	σ^2g	PCV (%)	GCV (%)	H^2_{BS} (%)	GA(k =2.063	GAM(k= 2.063)
		Min	Max							
HD	64.21	47.75	87.18	110.7	105.9	16.3	16.0	95.6	14.5	22.6
MD	115.58	99.5	136.75	152.4	148.2	10.6	10.5	97.2	15.8	13.7
GF	45.92	29.81	70.56	63.6	59.04	17.3	16.7	92.7	12.5	27.4
PH	117.96	82.09	155.43	418.2	412.6	17.3	17.2	98.6	20.4	17.3
FTPP	4.66	1.73	6.98	2.12	1.8	31.2	28.7	84.9	5.2	112.8
SP	19.62	13.33	23.8	6.9	6.06	13.4	12.5	87.2	7.1	36.3
Sl	10.60	5.89	14.59	7.65	7.31	26.00	25.5	95.5	7.4	70.4
KPS	39.68	18.26	74.35	322.14	316.04	45.2	44.7	98.1	19.1	48.2
TGW(g)	14.70	3.69	32.26	91.8	91.3	65.1	65.00	99.4	14.00	95.4
BIM(kg/h)	18618.25	8004.37	26107.5	23697860	23603759	26.14	26.09	99.6	31.6	16.9
HI	14.65	6.65	24.25	82.71	82.17	62.06	61.8	99.4	13.6	93.2
GY(kg/h)	2744.4	533.37	6335.87	3117653	3089009	64.3	64.04	99.08	19.02	69.3

σ^2p =Phenotypic variation, σ^2g =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, $H^2_{BS=}$ Broad sense heritability, GA=genetic advance, GAM=Genetic advance as percent of mean.

Genetic Divergence

Genetic divergence analysis quantifies the genetic distance among the selected germplasm and reflects the relative contribution of specific traits towards the total divergence. Divergence analysis is a technique used to categorize germplasm that are as similar as possible into one group and others into a different. D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups. The extent of diversity present between germplasms determines the extent of improvement gained through selection and hybridization. The more divergent the two germplasms are the more will be the probability of improving through selection and hybridization.

Clustering of germplasm

The D^2 values based on the pooled mean of germplasm resulted in classifying the 68 bread wheat germplasm in to six groups (Table 5).It was indicated that the tested bread wheat germplasm were moderately divergent. The germplasm were clustered in such a way that 46 germplasm (67.6%) were grouped into cluster I, 9 germplasm (13.23%) in to cluster II, 6 germplasm (8.82%) into cluster III, 2 germplasm (2.94%) into clusters IV, 1 germplasm (1.47%) in to cluster V and 4 germplasm (5.88%) in to cluster VI respectively. This indicates that the crossing between superior germplasm of above diverse cluster pair's might provide desirable recombinants for developing high yielding bread wheat varieties. Similarly, Degewione and Alamerew (2013) grouped 26 bread wheat genotypes into six clusters; Shashikala (2006) grouped 169 wheat genotypes in to 11 clusters.

Table 3: Distribution of 68 Bread Wheat Germplasm in to Six Clusters Based on D^2Analysis

Cluster number	No. of germplasm	Percentage	Accession Number
I	46	67.6%	1,2,3,4,5,7,9,10,11,14,15,16,17,20,22,23,24,25,26,27,28,30,32,35,36, 37,38,39 40,43,44,47,48,50,51,52,53,54,55,57,59,60,61,62,63,64
II	9	13.23%	6,19,21,29,31,33,34,46,58
III	6	8.82%	8,12,13,41,42,56
IV	2	2.94%	18,45
V	1	1.47%	49
VI	4	5.88%	65,66,67,68

Average intra and inter cluster distance (D^2)

The average intra and inter cluster distance D2 values are presented in Table 4. Maximum average intra cluster D^2 (differences among the germplasm within the same cluster) was shown by cluster I (31.14) followed by cluster III (27.51**)** and IV (24.03)**.**The lowest intra cluster distance D^2 was recorded in cluster V (0.00), which shows the absence of genetic variability within this cluster. The inter cluster distance was range from 44.83 to 179.72. Cluster IV and VI showed maximum inter cluster distance of 179.72 followed by that between clusters IV and V (162.18) which had shown they were genetically more divergent from each other than any other clusters. The lowest inter cluster distance was noticed between clusters I and III (44.83) followed by that between clusters II and IV (51.41). The F-test for the six clusters indicated that there were statistically accepted differences between all clusters (Table 4).This result agreed with findings of Ali *et al*. (2008). According to Rahim*et al.* (2010) who showed that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Therefore, more emphasis should be given on cluster IV and VI for selecting germplasm as parents for crossing with the germplasm of cluster, which may produce new recombinants with desired traits.

Table 4: Average Intra (Bold) and Inter Cluster (Off Diagonal) D^2Values Among Six Clusters in 68 Bread Wheat Germplasm.

	I	**II**	**III**	**IV**	**V**	**VI**
I	***31.14***	63.12**	44.83**	105.13**	72.83**	101.68**
II		***22.10***	58.57**	51.41**	128.82**	154.26**
III			***27.51***	80.79**	84.63**	105.67**
IV				***24.03***	162.18**	179.72**
V					***0.00***	62.02**
VI						**14.23**

X^2= 19.67at 5% probability level and x^2=24.72 at 1% probability level

Principal component analysis (PCA) based on phenotypic traits

Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). The data matrix of 12*68 was prepared for principal component analysis. It was obvious from the analysis that three PCs out of twelve were selected having >1 Eigen value and contributed 63.2% variation among 68 bread wheat germplasm for all parameters (Table 5). It was noted that principal component first contributed 33.7%, Principal component second 16.7% and Principal Component third 12.8% of the total genetic variability for all the germplasm. In principal component 1 (PC1) variation was chiefly attributed due to number of kernel per spike, grain yield, thousand kernel weight and spike length. In principal component 2 (PC2) the variation was due to days to heading, days to maturity, plant height and spike length. Whereas in principal component 3 variations was chiefly originated from plant height, number of effective tillers per plant, grain yield, biomass yield per plot and harvest index. Similar results were reported bySajjad*et al* (2011), Ashraf *et al.* (2012), Degewione and Alamerew (2013).

Table 5: Eigen Values and Eigenvectors of the First 3 Principal Components (PCs) For 12 Characters Of 68 Bread Wheat Germplasm.

Trait	PC1	PC2	PC3
Eigen value	4.38	2.17	1.66
Difference	2.20	0.50	0.69
Proportion	0.337	0.167	0.128
Cumulative	0.337	0.504	0.632
Eigenvectors			
Days to 50% heading (DH)	-0.265	-0.453	-0.068
Days to 75% maturity (DM)	0.176	-0.544	0.037
Grain filling period (GFP)	0.191	-0.263	-0.171
Plant height(cm)	-0.218	-0.444	-0.314
Number of effective tillers per plant	0.210	0.022	0.326
Spike length (cm)	0.307	-0.340	0.060
Number of spikelet's per spike	0.247	-0.289	0.240
Number of kernels per spike	0.424	0.101	0.025
Thousand kernels weight(g)	0.375	-0.008	-0.051
Grain yield (kg/h)	0.403	0.091	-0.326
Biomass yield (kg/h)	0.224	-0.038	0.474
Harvest index (%)	0.287	0.112	-0.604

Where, DH= Days to heading, DM= Days to maturity, GFP= Grain filling period, PH= Plant height (cm), NPTPP= No. of productive tiller plant^{-1}and, SL= Spike length (cm), NSPS = No. of spikelet's spike^{-1}, NKPS= No. of kernels spike^{-1}, TKW=1000 kernel weight (g), GY= Grain yield kg ha^{-1}, BMY= Biomass yield kg ha^{-1}, HI = Harvest index.

4. Summary and Conclusion

The present study comprises sixty eight bread wheat germplasm that were evaluated at Kulumsa Agricultural research center with the objective of assessing the genetic variability of yield and yield related traits for quantitative traits and diversity for qualitative traits. Analysis of variance revealed that highly significant differences were obtained among the treatments for all the twelve selected quantitative characters, which indicated adequate variability among the germplasm considered in this study.

The estimates of ranges of mean values revealed that bread wheat germplasm possess good amount of genetic variability. Productive tillers per plant, spike length, kernel per spike, thousand grain weights, biomass yield per plot, harvest index, and grain yield per plot showed high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values. While heading date, maturity date, grain filling period, and plant height showed medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The high to medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values of characters suggest that the possibility of improving the desired traits through selection**.**

The values of heritability for all the quantitative characters were high. The expected genetic advance as a percentage of the mean was ranged from 13.7% for maturity date (MD) to 112.8% 5% for productive tiller per plant (PTP). Characters with high genetic advance as a percent of mean allow the improvement of the characters through selection. The cluster analysis based on D^2analysis on pooled mean of germplasm classified the sixty eight germplasm in to six clusters, which makes them moderately divergent. There was a statistically approved difference between all the clusters.

It was obvious from the analysis that three PCs out of twelve were selected having >1 Eigen values and contributed 63.2% variation among sixty eight bread wheat germplasm for all parameters. It was noted that principal component first contributed 33.7%, principal component second 16.7%, and principal component third 12.8% of the total genetic variability for all the germplasm.Productive tillers per plant, spikelet per spike, spike length, kernel per spike thousand grain weight and harvest index showed high heritability with high genetic advance of percent mean, these traits may be included as components of indirect selection.

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5. REFERENCES

Allard, R.W., 1960. Principles of Plant Breeding. John Wiley and Sons, Inc., New York.

Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z (2008) Genetic variability, association and diversity studies in wheat (*Triticumaestivum* L.) germplasm. Pak J Bot 40: 2087- 2097.

Ashraf A. Abd El- Mohsen, Samir R. Abo Hegazy and Moemen H. Taha, 2012.Genotypic and phenotypic interrelationships among yield and yield components in Egyptian bread wheat genotypes, Cairo University, Giza, Egypt.
Burton GW and EH DeVane (1953). Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. Agron. J., 45:478-481.
Chowdhry, M.A., Ali, M., Subhani, G.M and Khaliq, I. (2000). Path coefficient analysis for water use efficiency, evapo-transpiration efficiency, transpiration efficiency and some yield related traits in wheat. *Pakistan Journal of Biological Sciences* 3: 313-317.
Degewione and S.Alamerew, 2013.Genetic Diversity in Bread Wheat (*Triticumaestivum* L.)Genotypes. Pakistan Journal of Biological Sciences, 16: 1330-1335.
Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to Quantitative Genetics. 4th Ed. Longman, Essex, England.
Federer W. T. (1956). Augmented (or hoonuiaku) designs. Hawaii. Plant. Rec.55, 191–208.
Johnson, H.W., H.E.Robinson and R. E.Comstock.(1955). Estimates of genetic and environmental variability in soybean.Agron. J., 47: 314-318.
Kalimullah, S. J. Khan, M. Irfaq and H. U. Rahman, 2012.Genetic variability, correlation, and diversity studies in bread wheat (*Triticumaestivum*L.) germplasm. The Journal of Animal and Plant Sciences, 22(2), Page: 330-333, ISSN: 1018-7081, Page: 330-333 ISSN: 1018-7081, Khan, Pakistan.
KatarzynaBryc, Jack W.Silverstein 2013.Separation of the largest Eigen values in Eigen analysis of genotype data from district sub populations.
Mahalanobis, P.C., 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci., 2: 49-55.
Maqbool, R., M. Sajjad, I. Khaliq, Aziz-ur-Rehman, A.S. Khan and S.H. Khan, 2010. Morphological diversity and traits association in bread wheat (*Triticumaestivum* L.). Am. Eurasian J. Agric. Environ. Sci., 8: 216-224.
Mohammadi SA, Prasanna BM (2003) Analysis of genetic diversity in crop plants: salient tools and considerations. Crop Sci 43: 1235-1248.
Mollasadeghi, V., Shahryari, R. 2011.Important morphological markers for improvement of yield in bread wheat. Advances Environ. Biol., 5 (3): 538 – 542.
O. Aremu (2012). Exploring Statistical Tools in Measuring Genetic Diversity for Crop Improvement, Genetic Diversity in Plants, Prof. MahmutCaliskan (Ed.), ISBN: 978-953-51-0185-7.
Ranjana and Suresh Kumar, 2013.Study of genetic variability and heritability over extended dates of sowing in bread wheat (*Triticumaestivum*L.).Research in Plant Biology, 3(1): 33-36.
Rauf, S., Tariq, S.A., Hassan, S.W. (2012). Estimation of pedigree based diversity in Pakistani wheat (*Triticumaestvium* L.) germplasm. Communications in Biometry and Crop Science 7 (1), 14–22.
Sajjad, M., S.H. Khan and A.S. Khan, 2011. Exploitation of germplasm for grain yield improvement in spring wheat (*Triticumaestivum*). Int. J. Agric. Biol., 13: 695-700.
Salem K. F. M., A. M. El-Zanaty and R. M. Esmail. (2008). Assessing wheat (*Triticumaestivum*L.) genetic diversity using morphological characters and microsatellite Markers. World J. Agri. Sci. 4 (5): 538-544.
SAS, 2008. Statistical Analysis System.Version 9.2, SAS Institute Inc., Cary, NC., USA.
Sharma, P.K., Gupta, P.K. and Balayn, H.S., 1998, Genetic diversity in a large collection of wheats (*Triticum*spp.).*Indian Journal of Genetics and Plant Breeding*, 58(3): 271-278.
Shashikala, S.K. 2006.Analysis of genetic diversity in wheat. M.Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.
Singh P, Narayanan SS (1993) Biometrical techniques in plant breeding. 1st ed. Kalayani Publishers, New Delhi, Indi.
Singh RK, Chaudhary BD (1985). Biometrical methods in quantitative genetic analysis.Kalyani Publ., New Delhi. India.
Tarekegne A, Tanner DG, Gebeyehua G (1994). Effect of genetic improvement of morpho-physiological character related to grain yield of bread wheat in Ethiopia. African Crop Sci. J. 2(3): 247-255.

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