Genetic Variability Studies in Bread Wheat (Triticum Aestivum L.) Genotypes at Kulumsa Agricultural Research Center, South East Ethiopia

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Abstract

Sixty four bread wheat genotypes were tested in a simple lattice design at Kulumsa Agricultural Research Center during 2014/15 main cropping seasonto estimate the extent of genetic variability. The genotypes showed significant variation for all the traitsstudied except for biomass yield ha^{-1} and relatively wide range of the mean values for most of the characters indicated the existence of variations among the tested genotypes.Moderate PCV and GCV were recorded for 1000 kernel weight, grain yield, harvest index, number of grains spike^{-1} and number of productive tiller. High heritability values were observed for days to heading, days to maturity, grain filling period, 1000 kernel weight, number of spikelet spike^{-1}, spike length and plant height. Moderate PCV and GCV were recorded for 1000 kernel weight, grain yield, harvest index, number of grains spike^{-1} and number of productive tiller. Among the characters 1000 kernel weight showed high values of genetic gain whereas days to maturity, grain yield, harvest index, productive tillers and number of grains plant^{-1} had moderate values of genetic advance as percent of mean (GAM). The D^2 analysis showed that the 64 genotypes were clustered into nine clusters. Maximum inter cluster distance was observed between cluster I and IX (D^2=5112.1), followed by that between clusters III and IX (D^2=4694.4) and VIII and IX (D^2=3871.9) which had shown they were genetically more divergent from each other than any other clusters. Crosses between genotypes selected from cluster I with cluster IX, cluster III with cluster IX and cluster VIII with cluster IX are expected to produce relatively better genetic recombination and segregation in their progenies.Principal components (PC1 to PC6) having Eigenvalue greater than one (significant), accounted 77.20% of the total variation. The first two principal components PC1 and PC2 with values of 22.3% and 17.4% respectively, contributed more to the total variation. According to their mean performance, genotypes Alidoro (5955.0 ± 480.83261a), Dure (5627.5 ± 604.57630ab) and Sanate (5322.5±781.35299abc) were the best yielders. The present result is only an indication and we cannot reach a definite conclusion. Therefore, it is advisable to continue with this study over several years and locations.

Keywords: Genetic variability, Heritability, PCV, GCV, Genetic advance

1. INTRODUCTION

Wheat, 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 exclusively produced under rain fed conditions, meher and belg (long and short rainy seasons), respectively. Smallholders are major producers and suppliers of bread wheat, accounting for more than 89% of the market supply. Wheat is one of a major cereal of choice in the country, due to its higher productivity, broader adaptation and input responsive high yielding improved varieties. This significantly increased the national wheat area from almost 0 to 60% of the area (Tarekegne *et al*., 1994). The genetic origin of wheat is of interest; since it is a classic example of how closely related species may be combined in nature into a polyploid series. The species of *Triticum* (*T*.) and their close relatives can be divided into diploid, tetraploid and hexaploid groups, with chromosome numbers of 2n = 14, 28 and 42,respectively, in which the basic chromosome number of wheat is x = 7. *Triticum durum* originated thousands of years ago from a hybridisation between the wild diploid *T. monococcum*L. (A genome donor) and the donor of the B genome which, according to morphological, geographical and cytological evidence, has been recognized as *T. speltoides*(Tausch) Gren. or a closely related species.

Wheat is grown at an altitude ranging from 1500 to 3000 meters above sea level, between 6-16^0 N latitude and 35-42^0 E longitude in our country. The most suitable agro- ecological zones, however, fall between 1900 and 2700m.a.s.l (Abu Terefe, 2012). The major wheat producing areas in Ethiopia are located in Oromiya (Arsi, Bale, Shewa, Ilubabor, and Western Harerghe), in SNNPR (Hadiya, Sidamo, Silte, Guraghe, Kambata), Tigray, Amhara (Northern Gondar and Gojam zones). Within Ethiopia, the Oromia and Amhara regions produce 59% and 27% of the country's wheat, respectively, with an additional nine percent coming from the Southern Nations, Nationalities, and Peoples Region. Narrow genetic background has rendered improved varieties less tolerant to biotic and a biotic stresses (Maqbool *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 amd Prasanna, 2003). 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 (Rauf, 2012).

Due to the use of traditional production systems, use of low level of production inputs, the influence of biotic and abiotic factors, environmental fluctuations, shortage of improved varieties and more importantly genetic factors the productivity of wheat per hectare in Ethiopia is low as compared to that of most of the countries of the world like Germany (7.9 tons/ha), France (7.6 tons/ha), Egypt (6.4 tons/ha). A wide gap in the yield is attributed to shortage of improved varieties for different agro ecological zone of the country, poor agronomic practices, drought, poor soil fertility, diseases and insect pests, etc. are the major constraints of wheat production in Ethiopia.

2. MATERIALS AND METHODS
2.1. Description of the study area
The field experiment was conducted at Kulumsa Agricultural Research Center (KARC). KARC is located in Oromiya Regional State Arsi Zone, 160 km South East ofAddis Ababa and 8 kms to the North of Asella town. It is located in latitude of $8^0 1'7''$Nand longitude of $39^0 9'35''$E. Its altitude and annual rainfall are 2,200 m.a.s.l and 832 mm respectively. The annual average temperature of the study area is 17^0C with maximum and minimum temperature of 22.8°C and 10.5°C respectively. The soil type classified as clay loam soil with a pH of 6.

2.2. Experimental Material
A total of sixty four released & elite bread wheat genotypes (52 released and 12 Pipe lines) were grown at Kulumsa in 2014 cropping season.

2.3. Field Experimental Design, Trail management and Season
The experiment was carried out in 8 x 8 Simple Lattice Design. The genotypes were grown under uniform rain fed conditions. The plot/block dimension was six rows of 2.50m length with 0.20m row spacing. Planting was done by hand drilling on July 08, 2014 with the seed rate of 150 kg/ha (45 g/plot).

2.4. Statistical Analysis
The mean values of the genotypes were subjected to analysis of variance based on simple lattice design using SAS procedure. Cluster analysis and principal component analysis were done by using SAS Version 9.2 (SAS, 2008) and Minitab 16.

Environmental variance (σ^2e) = MS_E

Genotypic variance (σ^2g) = $\dfrac{MSG - MSE}{r}$

Phenotypic coefficient of variation (PCV) = $\dfrac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$

Genotypic coefficient of variation (GCV) = $\dfrac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$

Heritability (H²b) = $\dfrac{\sqrt{\sigma^2 g}}{\sqrt{\sigma^2 p}} \times 100$

GA = K.H²b.σ^2p

GAM = $\dfrac{GA}{\bar{x}} \times 100$

The generalized genetic distance between clusters was calculated using the generalized Mahalanobis' D^2 statistics equation: $D^2_{ij} = (x_i - x_j)s^{-1}(x_i - x_j)$

3. RESULTS AND DISCUSSION
Mean squares of the 13 characters from analysis of variance (ANOVA) are presented in Table 1. Highly significant differences among genotypes (P<0.01) were observed for nine characters (days to 50% heading, days to 75% maturity, grain filling period, 1000 kernel weight, plant height, spike length, number of productive tillers per plant, number of spikelet's per spike and number of grains per plant). Significant differences at (p<0.05) were observed for three characters namely; grain yield per plot, harvest index and hectoliter weight whereas biomass yield showed non-significant difference among the bread wheat genotypes under study.

3.1. Estimates of variance components
3.1.1. Range and Mean Values

Estimates of phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 2.The mean values for days to 50% heading ranged from 56.5 (ETBW-8532) to 80 (ET13-A2), days to 75% maturity ranged from 112.5 (Dure) to 130 (Mitikie). Thousand kernel weight was ranged from 21.39 (Sirbo) to 37.84 (Dinknesh) and grain yield per plot showed a wide variation which ranged from 2115 (Menze) to 5955 (Alidoro). Biomass yield ranged from 13,750 (Simba) to 18,945 (Sanate) with a mean value of 16,008.9 kg ha^{-1}and harvest index ranged from 12.71 (Millennium) to 35.28 (Alidoro) with a mean value of 25.59. Hectoliter weight varied from 64.58 (ETBW-8532) to 74.31 (K6295-4A), plant height ranged from 71.9 (KBG-01) to 105.6 (K6290-Bulk) and spike length ranged from 7.25 (Digelu) to 10.5 (Sulla). Similarly, the mean values for number of productive tillers per plant, number of spikeletes per spike and number of grains per plant were ranged from 3.25 (ETBE-5879) to 5.38 (ETBW-8540), 16.6 (Hidasse) to 22.0 (Sirbo) and 25.5 (ETBE-5879) to 49.7 (ETBW-8530) respectively. Thus, high variability for thirteen traits in sixty four bread wheat genotypes implied that there was reasonably sufficient variability which provides ample scope for selecting superior and desired genotypes by plant breeders for further improvement. Generally, the range of variation was wide for all the characters studied. Radhu *et al*., (1995) observed high range of variation for yield, thousand-kernel weight, plant height and days to flowering. Maqbool *et al.,* (2010) reported wide range of variation for plant height, grain filling period, number of spikelet's per spike, biological yield per plot, grain yield and thousand-kernel weight. Moreover, Sajjad *et al.,* (2011) reported large variation for grain yield, thousand kernels weight and number of kernels per spike. Based on their mean performance in kilograms per hectare, genotypes Alidoro (5955.0 ± 480.83261a), Dure (5627.5 ± 604.57630ab), Sanate (5322.5±781.35299abc), Dinknesh (5320.0 ± 84.85281abc) and ETBE-6095 (5227.5 ± 222.73864abcd) were found to be top yielders (Appendix 1). These high yielding genotypes could be utilized in further breeding.

3.1.2. Phenotypic and genotypic coefficients of variation

Estimates of phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 3.The phenotypic coefficients of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 2.90% (days to maturity) to 17.26% (grain yield ha^{-1}) and 2.16% (hectoliter weight plot^{-1}) to 11.31% (thousand kernel weight plot^{-1}) respectively.

Table 1: Analysis of variance (Mean squares) for the 13 characters of 64 bread wheat genotypes grown at Kulumsa (2014/15)

Characters	Replication (D.F.=1)	Genotype (D.F.=63)	Intra Block Error (D.F.=49)	C.V (%)	Efficiency Relative to RCBD
Days to 50% heading	0.781250	64.347803**	11.542621	5.201	1.136%
Days to 75% maturity	6.125000	25.014016**	9.323817	2.501	1.938%
Grain filling period (days)	10.125000	40.577139**	16.033475	7.107	1.863%
1000 kernel weight per plot(g)	1.746113	29.226132**	7.515515	9.449	1.428%
Grain yield per plot (kg/ha)	3841645.51	985027.36*	574163.7	18.65	0.436%
Biomass yield per plot (kg/ha)	56465236.1	2793695.4	2283935.0	9.440	1.797%
Harvest index per plot (%)	672.436128	36.956978*	20.197455	17.5	0.8679%
Hectoliter weight per plot (kg/hL)	2.5792883	11.3431088*	6.922708	3.822	0.772%
Plant height (cm)	6.480000	80.732619**	24.676632	5.608	1.476%
Spike length (cm)	25.0278125	0.91613831**	0.3329242	6.675	2.373%
Number of productive tillers/plant	0.04205000	0.47278197**	0.22463951	11.291	1.503%
Number of spikelet's/ spike	0.0312500	2.4277316**	0.6529676	4.168	1.150%
Number of grains/plant	22.194453	49.23018**	21.446217	12.055	1.884%

D.F.=degrees of freedom, *=significant at 5% probability level and **=highly significant at 1% probability level, C.V= Coefficient of Variation, RCBD=Randomized Complete Block Design**.**

Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. The maximum phenotypic variance value of 1,396,847.7 kg ha^{-1} and 492,513.68 kg ha^{-1} was noted for the traits biomass yield and grain yield respectively. Similarly, the genotypic variances for these characters were also high indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters.

Moderate phenotypic and genotypic coefficients of variation were observed for 1000 kernel weight, grain yield and harvest index. This indicated that selection may be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential.

Number of productive tillers per plant and number of grains per plant were found to be moderate for PCV while low for GCV. The rest of the characters grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment. The result obtained in the present study was in agreement with the of findings of Shashikala, (2006) for 1000 kernels weight and grain yield per plot, Kalim Ullah *et al*., (2011) for yield/plant and 1000 grains weight in bread wheat. Ali *et al*., (2012) reported moderate PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Degewione and Alamerew, (2013) reported moderate PCV and GCV for 1000 grain weight, plant height and days to heading in twenty six bread wheat genotypes.

3.1.3. Heritability, Genetic advance and Genetic Advance as percent of mean

Moderate heritability values were observed in harvest index, grain yield and hectoliter weight whereas low heritability value was observed for biomass yield. High heritability values were observed for the rest traits indicating that the variation observed were mainly under genetic control and were less influenced by the environment and the possibility of progress from selection. The obtained results were in accordance with results of Ashraf *et al.,* (2012) and Farshadfar and Mohammadi, (2012). Rahim *et al*. (2010) noticed higher heritability value for plant height, days to 50% flowering, number of productive tillers per meter length, grain yield per plot, and number of grains per spike. Adewale.*et al*. (2010) also reported high heritability values for plant height, tillers per meter and spike length.

The expected genetic advance expressed as a percentage of the mean ranged from 2.78% for both hectoliter weight and biomass yield to 20.13% for 1000 kernel weight plot[-1] (Table 2), indicating that selecting the top 5% of the base population could result in an advance of 2.78 to 20.13 percent over the respective population mean. GAM was moderate for 1000 kernel weight plot[-1] (20.13%) followed by harvest index (15.68%), grain yield plot[-1](14.85%), days to 50% heading (14.70%) and number of grains per plant(14.65%). Similarly, genetic advance was high for grain yield ha^{-1} (603.05 kilograms), followed by biomass yield ha^{-1} (444.64 kilograms) and it was moderate for days to 50% heading (10.6 days). Degewione.*et al*. (2013) obtained similar results in twenty six bread wheat genotypes. High heritability and moderate genetic advance as percent of mean were found in days to heading, 1000 kernel weight, plant height and spike length; indicating that these characters could be useful basis for selection. Moderate heritability coupled with high genetic advance was observed for grain yield (41.71%, 603.05%) whereas high heritability couple with moderate genetic advance as percent of mean was observed for days to 50% heading (82.06%, 14.70%), 1000 kernel weight (74.28%, 20.13%), plant height (69.43%, 10.27%) and spike length (63.66%, 10.34%) respectively.

Table 2: Estimate of ranges, mean, standard error, phenotypic (σ^2p) and genotypic (σ^2g) component of variances, broad sense heritability and genetic advance as percent of mean for 13 characters of bread wheat genotypes tested at Kulumsa (2014)

Character	Mean ± SE	Range		σ^2p	σ^2g	PCV (%)	GCV (%)	H^2_{bs} (%)	GA (k =2.063)	GAM (k=2.063)
		Min.	Max.							
DH	65.33 ± 6.18	56.50	80.0	32.17	26.40	8.68	7.87	82.06	10.60	14.70
DM	122.09 ± 4.28	112.50	130.0	12.50	7.84	2.90	2.29	62.73	4.58	3.75
GFP	56.34 ± 4.76	47.50	66.5	20.29	12.27	7.99	6.21	60.49	5.62	9.97
TKW	29.09 ± 4.00	21.39	37.84	14.61	10.85	13.13	11.31	74.28	5.86	20.13
GY	4062.22 ± 501.10	2115.00	5955.00	492,513.68	205,431.80	17.26	11.16	41.71	603.05	14.85
BY	16,008.9±1159.1	13750.00	18945.00	1,396,847.70	254,880.20	7.38	3.15	18.25	444.64	2.78
HI	25.59 ± 4.60	12.71	35.28	18.48	8.38	16.76	11.29	45.35	4.01	15.68
HLW	68.84 ± 2.56	64.58	74.31	5.67	2.21	3.46	2.16	38.97	1.91	2.78
PH	88.59 ± 6.94	71.90	105.60	40.36	28.03	7.17	5.91	69.43	9.10	10.27
SL	8.64 ± 0.71	7.25	10.50	0.46	0.29	7.87	6.25	63.66	0.89	10.34
NPT	4.20 ± 0.54	3.25	5.38	0.24	0.12	11.67	8.33	52.49	0.53	12.63
NSP	19.39 ± 1.16	16.60	22.00	1.21	0.89	5.67	4.85	73.10	1.66	8.56
NGP	39.42 ± 4.98	25.50	49.70	24.61	13.34	12.58	9.46	56.44	5.78	14.65

SE = Standard error, σ2p =Phenotypic variation, σ2g =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H2bs= Broad sense heritability, GA=genetic advance, and GAM=Genetic advance as percent of mean

The results are in accordance with reports of earlier work done by Munir *et al.,* (2007) reported that high heritability with moderate genetic advance for plant height and spike length. Kalim ullah *et al*. (2012) reported similar findings for plant height, biomass yield per plot and1000 grain weight, which supports the present result.

3.2. Genetic Divergence study
3.2.1. Clustering of genotypes

The D[2] values based on the pooled mean of genotypes resulted in classifying the 64 bread wheat genotypes in to nine clusters (eight groups and one solitary) (Table 3). Distribution of the genotypes showed that two genotypes in cluster I (3.13%), twelve genotypes in cluster II (18.75%), fifteen genotypes in III (23.44%), four genotypes in cluster IV (6.25%) whereas another twelve genotypes in cluster V (18.75%), ten genotypes in cluster VI

(15.62%), six genotypes in cluster VII (9.37%), two genotypes in cluster VIII and one genotype in cluster IX (3.13%).

3.2.2. Cluster mean analysis

Cluster I exhibited the lowest values of 1000 kernel weight (22.83g/plot) and plant height (76.80cm) and it exhibited the highest values for number of grains (42.60 grains plant^{-1}) and number of productive tillers (4.58 tillers plant^{-1}) while intermediate for the rest traits. Cluster V was characterized by the highest values of hectoliter weight (70.41kg/hL) and harvest index (29.49%) having intermediate values for the rest characters. The lowest biomass yield per plot (14,433.8kg/ha) was recorded in cluster III being intermediate for the rest traits. Cluster IV was characterized by highest value of days to 50% heading (67.25days) and lowest values for grain filling period (54.63days) and number of spikelet's (18.75spikelets spike^{-1}). Clusters II and VI revealed intermediate characteristics for all the traits under the study. Genotypes in cluster VII showed the highest spike length (9.04cm) being intermediate for the other traits. On the other hand genotypes in cluster VIII were characterized by the longest plant height (100.28cm) and greatest number of spikelet's (21.20 spikelet's spike^{-1}). Furthermore, early heading time (59.50days), delayed maturity time (118.0days), lowest grain yield (2,383.75kg/ha), lowest harvest index per plot (14.49%), lowest hectoliter weight per plot (66.66kg/hL), shortest spike length (7.50cm) and lowest number of productive tillers (3.61 tillers/plant) were recorded in cluster VIII. Genotyped in cluster IX were characterized by late maturity (125.50dyas), longest grain filling period (62.50days), highest 1000 kernel weight (34.06g/plot), highest grain yield (5,322.5kg/ha) and highest biomass yield (18,945kg/ha). From the result of cluster mean analysis, we can conclude that genotypes that had high yielding potential, late maturity, delayed grain filling period and highest 1000 kernel weight are in cluster IX. The crosses between genotypes selected from cluster I (shortest plant height) with cluster IX (highest grain yield) and cluster III (lowest biomass yield) with cluster IX (highest grain yield) are expected to produce better genetic recombination and segregation in their progenies. Therefore, selecting superior genotypes of this cluster will be important to improve grain yield.

Table 3: Distribution of 64 bread wheat genotypes tested at Kulumsa (2014) in to nine clusters based on D^2 analysis

Cluster No	Amount of Genotypes		Name of the genotypes
	in No	in %	
I	2	3.13	Laketch&Sirbo
II	12	18.75	Dereselign, Abolla, Tusie, Bobicho, Kakaba, Shorima, Hidasse, Huluka, King Bird, ETBW-8520, ETBW-8537 &ETBW-8540
III	15	23.44	Enkoy, K6290-Bulk, Dashen, Kubsa, Katar, Hawi, Mada-Wolabu, Simba, Sofumar, KBG-01, QulQulu, Mekelle-02, Ogolcho, ETBW-8523 & ETBW-8538
IV	4	6.25	K6295-4A, ET13-A2, Sulla &Hoggana
V	12	18.75	Pavon-76, Dodota, Dure, Alidoro, Dinknesh, Millennium, Jefferson, ETBE-5879, ETBE-6095, ETBW-8525, ETBW-8526 & ETBW-8530
VI	10	15.62	Mitikie, Galama, Meraro, Tay, Bollo, Galil, Mekelle-01, Mekelle-03, ETBW-8532 & ETBW-8536
VII	6	9.37	Tossa, Gassay, Danda'a, ETBW-8528, Gambo& Mekelle-04
VIII	2	3.13	Digelu&Menze
IX	1	1.56	Sanate

3.2.3. Average intra and inter cluster distance (D2)

Maximum average intra cluster D^2 was shown by cluster V (D2=539.5) followed by cluster III (D^2=519.0) and cluster IV (D^2=499.7) as shown in Table 4. The lowest intra cluster distance D^2 was recorded in cluster I (D^2=209.2) followed by cluster VII (D^2=249.6), indicating the existence of less genetic variability or diversity within this clusters. This signifies that, crossing of genotypes from these two clusters might not give higher hetrotic value in F$_1$ and narrow range of variability in the segregating F$_2$ population. Maximum inter cluster distance was observed between cluster I and IX (D^2=5112.1), followed by that between clusters III and IX (D^2=4694.4) and VIII and IX (D^2=3871.9) which had shown they were genetically more divergent from each other than any other clusters. Since maximum genetic recombination and variation in the subsequent generation is expected from crosses that involve parents from the clusters characterized by maximum distances, crosses between genotypes selected from cluster I with cluster IX, cluster III with cluster IX and cluster VIII with cluster IX are expected to produce relatively better genetic recombination and segregation in their progenies. However, the selection of parents should be also considering the special advantages of each cluster and each genotype within a cluster depending on the specific objective of hybridization program.

3.2.4. Principal component analysis

The principal component analysis (Table 5) showed that six principal components PC1, PC2, PC3, PC4 PC5 and PC6 exhibited more than one Eigen value (2.8944, 2.2624, 1.4732, 1.2257, 1.1383 and 1.0392 respectively) and accounted for 77.20% of the total variation so these six were given due importance for further explanation. The PC1 had 22.3%, PC2 showed 17.4%, PC3 exhibited 11.3% PC4 showed 9.4% PC5 exhibited 8.8% and PC6 had 8.0% variability among the genotypes for the characters under study. The first two principal components PC1 and PC2 with values of 22.3% and 17.4% respectively, contributed more to the total variation.
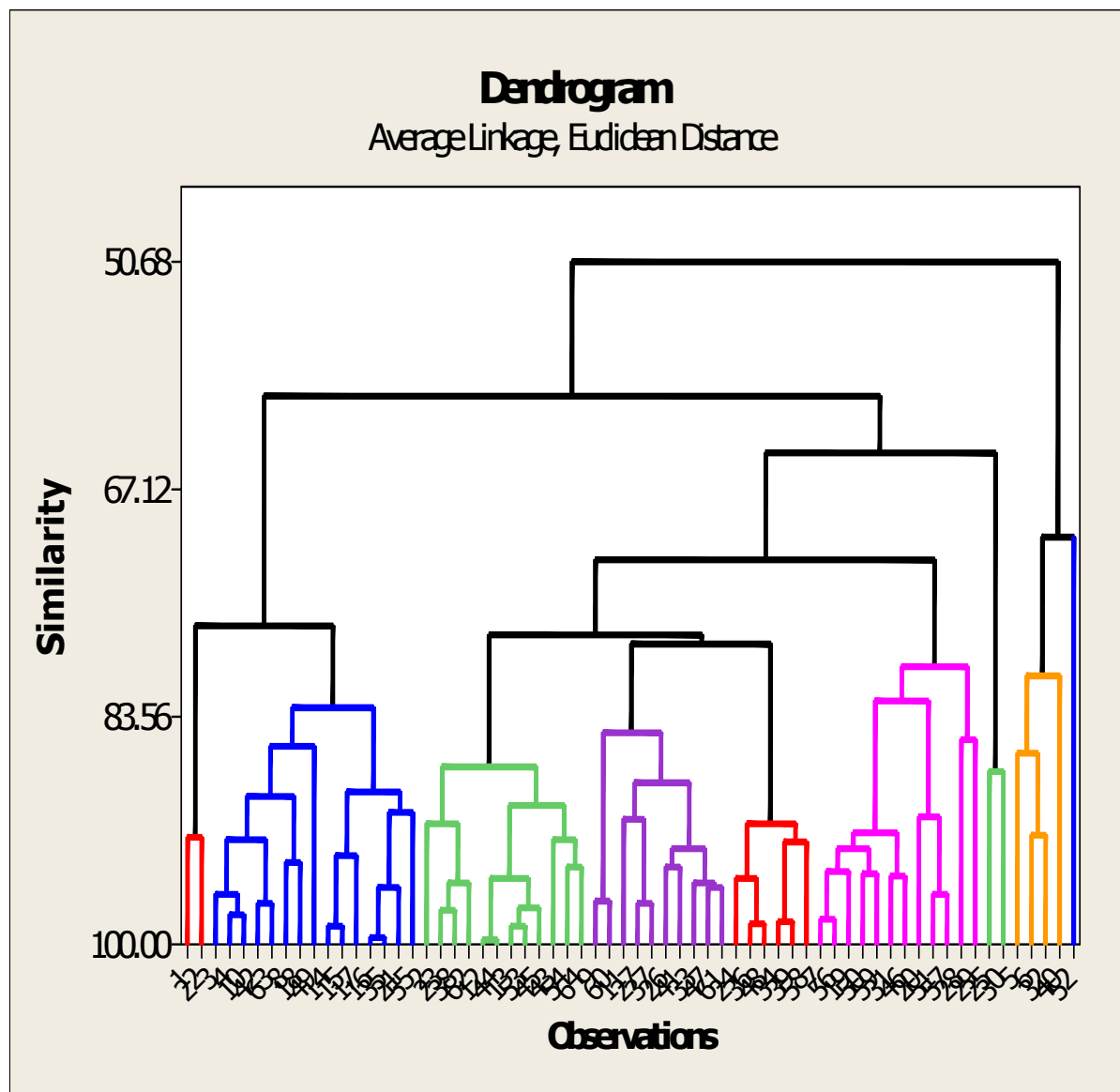
Appendix 2: Dendogram of bread wheat genotypes for 13 characters with average linkage clustering strategy

According to Chahal and Gosal, (2002) characters with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different clusters was because of a cumulative effect of a number of characters rather than the contribution of specific few characters. Characters having relatively higher value in the principal component (PC1), like grain yield per plot, harvest index per plot, thousand kernel weight per plot and hectoliter weight per plot had more contribution to the total variation and they were the ones that most differentiated the clusters. Variation in second principal component (PC2) was chiefly due to days to 50% heading, followed by days to 75% maturity, grain filling period, number of productive tillers and number of grains per plant. Traits such as plant height, biomass yield per plot and spike length were the major contributors of variation in the third principal component (PC3). Variation in the fourth principal component (PC4) was mainly due to number of spikelets per spike, grain filling period, number of productive tillers per plant, days to 75% maturity and number of grains per plant. Characters having relatively

higher value in the principal component PC5 like plant height, biomass yield per plot, grain filling period, number of spikelet's spike^{-1} and grain yield plot^{-1} had more contribution to the total variation.

Table 4: Average intra cluster (bold) and inter cluster (off diagonal) D^2 values among nine clusters in bread wheat genotypes tested at Kulumsa (2014/15)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**209.2**	2126.2**	1153.1 **	3817.9 **	3198.5**	2372.1**	1257.6**	2024.7**	**5112.1**
II		**376.6**	1550.5**	2206.2 **	**1097.1**	1152.5 **	1124.5**	2072.4 **	3145.4**
III			**519.0**	3673.8 **	2619.7**	2341.6 **	1395.1**	2579.1 **	4694.4**
IV				**499.7**	1561.9**	1445.9**	2563.9**	2330.8**	1569.1**
V					**539.5**	1409.9**	2063.6**	2617.8**	2096.4**
VI						**422.1**	1120.4**	1214.9**	2831.7**
VII							**249.6**	1220.6 **	3870.6**
VIII								**341.8**	3871.9**
IX									**0.000**

*=significant at P<0.05 for χ^2=**22.36** and **=significant at P<0.01 for χ^2= **27.69**, respectively

Table 5: Eigen values and Eigenvectors of the first six principal components (PCs) for 13 characters of 64 bread wheat genotypes tested at Kulumsa (2014)

Characters	PC1	PC2	PC3	PC4	PC5	PC6
Days to 50% heading (days)	0.111	-0.625	0.093	-0.110	-0.109	-0.008
Days to 75% maturity (days)	0.056	-0.485	0.163	0.335	0.084	0.419
Grain filling period (days)	-0.097	0.353	0.032	0.529	0.302	0.401
1000 kernel weight per plot(g)	0.465	0.155	0.050	-0.010	0.021	-0.146
Grain yield per plot (kgha^{-1})	0.518	0.073	0.024	0.119	-0.218	0.192
Biomass yield per plot (kgha^{-1})	0.034	0.108	0.551	0.045	-0.548	-0.061
Harvest index per plot (%)	0.510	0.008	-0.207	0.081	0.041	0.234
Hectoliter weight per plot (kghL^{-1})	0.416	0.203	0.025	-0.012	0.070	-0.313
Plant height (cm)	0.057	-0.068	0.656	0.133	0.165	-0.018
Spike length (cm)	-0.064	0.011	-0.339	0.150	-0.653	0.269
No of productive tillers plant^{-1}	0.105	-0.272	-0.211	0.445	0.146	-0.401
No of spikelet's per spike	-0.191	0.156	0.040	0.531	-0.234	-0.355
No of grains per plant	0.033	-0.253	-0.150	0.228	-0.070	-0.299
Eigenvalue	2.8944	2.2624	1.4732	1.2257	1.1383	1.0392
Proportion	22.3	17.4	11.3	9.4	8.8	8.0
Cumulative	22.3	39.7	51.0	60.4	69.2	**77.20**

Residue: 0.228

Appendix 1: Genotypes that had greater mean yield than the Grand Mean

Entry	Name of genotype	Code	Yield mean ± Std. Dev.	Rank
From the Released Varieties				
2	Dereselign	-	$4145.0 \pm 502.04^{c-n}$	25
3	Enkoy	-	$4432.5 \pm 45.96^{b-l}$	16
4	K6290-Bulk	-	$4355.0 \pm 721.24^{b-m}$	19
5	K629-4A	-	$4472.5 \pm 300.52^{b-l}$	15
7	Pavon-76	-	$4875.0 \pm 339.41^{a-f}$	6
10	Kubsa	HAR 1685	$4240.0 \pm 120.21^{b-n}$	21
12	Abolla	HAR 1522	$4730.0 \pm 1265.72^{a-g}$	12
13	Tusie	HAR 1407	$4102.5 \pm 470.22^{c-n}$	11
15	Hawi	HAR 2501	$4595.0 \pm 650.53^{a-j}$	26
19	Dodota	HAR 2508	$4635.0 \pm 806.10^{a-i}$	8
20	Dure	HAR 1008	5627.5 ± 604.57^{ab}	2
23	Bobicho	HAR 2419	$4162.5 \pm 293.45^{c-n}$	22
28	Alidoro	HK-14-R251	5955.0 ± 480.83^{a}	1
29	Dinknesh	HAR 3919	5320.0 ± 84.85^{abc}	4
31	Millennium	ETBW 4921	$4392.5 \pm 187.38^{b-m}$	18
32	Sulla	HAR710/RBC	$4300.0 \pm 1166.72^{b-m}$	20
38	Kakaba	Picaflor#1	$4145.0 \pm 834.39^{c-n}$	24
42	Mekelle-02	HI-1418	$4147.5 \pm 1191.47^{c-n}$	23
43	Shorima	ETBW 5483	$4687.5 \pm 95.46^{a-h}$	9
44	Hidasse	ETBW 5795	$4590.0 \pm 49.49^{a-j}$	13
45	Huluka	ETBW 5496	$4740.0 \pm 1216.22^{a-g}$	7
46	Jefferson	NA	$4662.5 \pm 915.70^{a-i}$	10
49	Ogolcho	ETBW 5520	$4570.0 \pm 0.00^{a-k}$	14
50	ETBE-5879	-	$4410.0 \pm 763.67^{b-m}$	17
51	ETBE-6095	-	$5227.5 \pm 222.74^{a-d}$	5
52	Sanate	-	5322.5 ± 781.35^{abc}	3
From the Pipelines				
Entry	Name of genotype	Code	Yield mean ± Std. Dev.	Rank
53	King Bird	-	$4567.5 \pm 484.37^{a-k}$	3
54	ETBW-8520	-	$4380.0 \pm 1103.08^{b-m}$	5
56	ETBW-8525	-	$4780.0 \pm 134.35^{a-g}$	2
57	ETBW-8526	-	$5037.5 \pm 830.85^{a-e}$	1
59	ETBW-8530	-	$4520.0 \pm 70.71^{b-l}$	4
63	ETBW-8538	-	$4220.0 \pm 360.6^{b-n}$	6
64	ETBW-8540	-	$4205.0 \pm 35.36^{c-n}$	7
Grand Mean			**4062.23**	

In the sixth principal component, variation was chiefly due to days to 75% maturity followed by grain filling period, number of productive tillers, number of spikelet's spike^{-1} and hectoliter weight plot^{-1}.

The present study confirmed that the bread wheat genotypes showed significant variations for the characters studied and it suggested that many opportunities for genetic improvement through selection and conservation of the genotypes for future utilization. Similar works have done by Hailegiorgis *et al.* (2011), Sajjad *et al* (2011), Tsegaye *et al.* (2012), Ashraf *et al.* (2012) and Degewione and Alamerew (2013) for grouping of genotypes by principal component analysis.

4. CONCLUSION

Genetic variability is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, pest and disease resistance. It is a prerequisite for the development of improved cultivars with wider adaptability and broad genetic base. The PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits.Genetic advance was high for grain yield ha^{-1} (603.05 kilograms), followed by biomass yield ha^{-1} (444.64 kilograms) and it was moderate for days to 50% heading (10.6days).Genetic advance as percentage of mean was moderate for 1000 kernel weight plot^{-1} (20.13%) followed by harvest index (15.68%), grain yield plot^{-1} (14.85%), days to 50% heading (14.70%) and number of grains per plant(14.65%).High heritability coupled with moderate genetic advance as percent of mean were found in days to heading, 1000 kernel weight, plant height and spike length;

indicating that these characters could be useful basis for selection. Moderate heritability coupled with high genetic advance was observed for grain yield (41.71%, 603.05%) whereas high heritability coupled with moderate genetic advance as percent of mean was observed for days to 50% heading (82.06%, 14.70%), 1000 kernel weight (74.28%, 20.13%), plant height (69.43%, 10.27%) and spike length (63.66%, 10.34%) respectively. These are simply inherited traits indicate that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Maximum average intra cluster D^2 was shown by cluster V (D2=539.5) followed by cluster III (D^2=519.0) and cluster IV (D^2=499.7). The lowest intra cluster distance D^2 was recorded in cluster I (D^2=209.2) followed by cluster VII (D^2=249.6), indicating the existence of less genetic variability or diversity within this clusters. This signifies that, crossing of genotypes from these clusters will not give higher hetrotic value in F_1 and narrow range of variability in the segregating F_2.Maximum inter cluster distance was observed between cluster I and IX (D^2=5112.1), followed by that between clusters III and IX (D^2=4694.4) and VIII and IX (D^2=3871.9) which had shown they were genetically more divergent from each other than any other clusters. Since maximum genetic recombination and variation in the subsequent generation is expected from crosses that involve parents from the clusters characterized by maximum distances, crosses between genotypes selected from cluster I with cluster IX, cluster III with cluster IX and cluster VIII with cluster IX are expected to produce relatively better genetic recombination and segregation in their progenies. From the six principal components, the first two principal components, PC1 and PC2 with values of 22.3% and 17.4% respectively, contributed more to the total variation.

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