



Genetic Divergence Study in Agro-Morphological Traits among Bread Wheat (*Triticum aestivum* L.) Genotypes at Raya Valley of Southern Tigray, Ethiopia

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ABSTRACT

Assessment of genetic divergence in crop species is one of the major activities of plant breeding which helps to analysis to quantify the genetic distance among the selected germplasm and reflects the relative contribution of specific traits towards the total divergence. Therefore, this field experiment was conducted to assess the genetic divergence in bread wheat genotypes, to determine the extent of genetic variation and for selection of suitable diverse parents for yield and yield related traits among wheat genotypes based on quantitative traits using multivariate analysis which could be further utilized in breeding. The field evaluation of 32 genotypes and 4 released varieties were conducted in 6 x 6 Triple Lattice Design at Mehoni Agricultural Research Station in 2017 cropping season. Results of analysis of variance revealed the presence of significant differences among genotypes for 12 quantitative traits. The first four principal component axes (PCA) with Eigen values >1 accounted for 70.5% variation of genotypes. Euclidean distance was used to estimate the genetic distances of all possible pairs of 36 bread wheat genotypes and its ranged from 1.15 to 9.20 with the mean, standard deviation and coefficient of variation of 4.47, 1.28 and 28.71%, respectively. Higher genetic distances were estimated among the new entries than among the four check varieties and check varieties with new entries. The genotypes were grouped into eight distinct clusters of which Cluster VI, VIII and III consisted of 11 (30.5%), 8 (22.2%) and 6 (16.7%) genotypes, respectively. Cluster VII were with two released varieties (Fentalle and Gambo) but Cluster IV, II and V with 3, 4 and 2 genotypes, respectively, while Cluster I was solitary. Generally, the results of this study showed the presence of variation among genotypes for agro-morphology traits with wide range of genetic distances that could allow selection and/or hybridization of genotypes after the results of this study are confirmed across locations and over years.

Keywords: Genotypes; Clustering and Genetic distance

1. INTRODUCTION

Bread wheat (*Triticumaestivum* L.) is a hexaploid species with ($2n=6x=42$) having AABBDD with A, B and D genomes (Sleper and Poehlman, 2006). World wheat production in 2017 was 743.2 million tons with average yield of 3.3 t ha^{-1} and it accounts for nearly 30% of global cereal production (FAO, 2017). Ethiopia is the second largest wheat producer in sub-Saharan Africa after South Africa. Wheat is cultivated on 1.7 million hectares of land and has a production of 4.5 million tons with low productivity of 2.7 t ha^{-1} (CSA, 2017) in the country as compared to the world average yield of 3.3 t ha^{-1} (FAO, 2017). In Ethiopia, wheat is grown at altitudes ranging from 1500 to 3000 meters above sea level (Abu, 2012). Wheat is produced in Tigray regions largely as compared to other crops of the area. The total wheat area and production in Tigray region are 107.7 thousand ha and 212.8 thousand tons with the average yield of 1.9 t ha^{-1} . Wheat stands second both in area and production among all crops followed by barely (*Hordeum vulgare* L.) and tef (*Eragrostis tef*). In the southern zone (Tigray Region), the area coverage and productivity of wheat is 49.2 thousand ha and 1,01.9 thousand tons with the average yield of 2.1 t ha^{-1} respectively which is lower than from national (CSA, 2017).

Principal component analysis simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components. The first principal component accounts for maximum variability in the data with respect to succeeding components (Leilah and Al-Khateeb, 2005). The Eigen values are often used to determine how many factors to retain. The sum of the Eigen values is usually equal to the number of variables (Sharma, 1998). In the case of this study, the traits, which contributed more to PC1, were days to maturity, days to heading, harvest index and number of spikelet per spike, whereas for second PC, grain yield, plant height, number of kernels per spike and spike length, for the third PC, biomass yield and number of fertile tillers per plant and for the fourth PC, grain filing period and 1000-kernel weight According to Chahal *et al.* (2002) characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero.

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. The extent of diversity present between germplasm determines the extent of improvement gained through selection and hybridization. The more divergent the two germplasm are the more will be the probability of improving through selection and hybridization (Dergicho *et al.*, 2015). The study of genetic divergence can assist in the choice of genotypes to be used in breeding programs for the development of new populations as it estimates the extent of diversity existed among selected genotypes (Mondal, 2003). Genetic distances are measures of the average genetic divergences between cultivars or populations and genetic similarity is the converse of genetic distance and it refers to the extent of genetic similarities among cultivars (Smith, 1984). In any breeding program, therefore, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981). Mihratu *et al.* (2014) also suggested that crossing of genotypes not genetically diverse or with little genetic diversity might not give higher heterotic value in F₁ and narrow range of variability in the segregating F₂ population.

In the Southern Zone of Tigray Regional State, at mid and highland areas, some genetic divergence studies in wheat genotypes have been made to develop varieties (Adhiena *et al.*, 2016). Raya Valley is the part of Southern Zone of Tigray Regional State; however, neither genetic divergence studies in wheat genotypes nor introduction of improved wheat varieties were attempted. Raya Valley are one of the areas where improved varieties are not widely distributed so far, most probably due to several constraints including the remoteness and inaccessibilities of the growing areas that limited to test the adaptability and yields of the varieties in such areas. Particularly, the potential of the area to wheat crop is not exploited due to lack of improved varieties. There is no detail information indicating the adaptability and production status of the improved bread wheat varieties in the area. This is due to the insufficient rain fall to support the growth and yield production of wheat in the area and the largest part of the valley is at low altitude (≤ 1600 m.a.s.l.) experiencing warm to hot weather conditions. But, the dependence on rainfall alone in the area has in recent years been gradually replaced by supplemental irrigation and irrigated crop production. The number of farmers and investors using irrigation and supplemental irrigation is increasing. However, the absence of recommended varieties for the area remains as one of the major wheat production constraints in the area. Therefore, it is necessary to undertake research to develop wheat varieties using genetic divergence studies. Thus, the present research was undertaken with the

objective of identifying genetically divergent bread wheat genotypes with desirable traits for hybridization particularly for yield

2. MATERIALS AND METHODS

2.1. Description of the Experimental Area

The study was carried out at the research station of Mehoni Agricultural Research Center (MhARC) under supplemental irrigation in the 2017 main cropping season. Mehoni is located in Raya Valley in the northern parts of Ethiopia about 668 km from county's capital city of Addis Ababa and about 120 km South of Mekelle, the capital city of Tigray regional state, Northern Ethiopia. Geographically, the experimental site is located at 12°41'50" N latitude and 39°42'08" E longitude with an altitude of 1578 m.a.s.l. The site receives mean annual rainfall of 750 mm with an average minimum and maximum temperature of 22°C and 32°C, respectively. The soil type and textural class of the experimental area is verty soil and clay loam respectively with pH of 7.9-8.1 (Hailelassieet *al.*, 2015).

When there was termination of rainfall during the execution of the experiment, the crop was affected by moisture stress. During this time supplementary irrigation was provided using ground water resource to compensate the amount of water needed by the crop and also to provide the essential moisture for normal growth. This practice helps in alleviating the adverse effects of unfavorable rain patterns and improves crop yields. Therefore, amount of irrigation water to supplement to each experimental plot was directed using drip irrigation which was installed in the experimental site, and the amount of water was measured using soil squeezed method to test soil moisture manually by hand.

2.2. Experimental Plant Materials

A total of 36 bread wheat genotypes were used including four standard checks (Table.1) obtained from the National Wheat Research Program specifically from Werer (WARC) and Kulumsa (KARC) Agricultural Research Centers. The genotypes were selected based on adaptation to drought tolerance and classified under lowland types. In this experiment, four released for drought tolerance of bread wheat varieties were included as standard checks.

Table 1. List and pedigree of the thirty-six bread wheat genotypes including four released varieties

G*	Genotype (Pedigree)	Origin
G1	HUBARA-3*2/SHUHA-4	CIMMYT/ICARDA
G2	Atila-7	CIMMYT/ICARDA
G3	ETBW5535	EIAR/KARC
G4	ETBW5957	EIAR/KARC
G5	ATILA/AWSEQ-4	CIMMYT/ICARDA
G6	FENTALLE (CHECK)	CIMMYT/ICARDA
G7	ADEL-2	CIMMYT/ICARDA
G8	DAJAJ-1//VEE'S'/SAKER'S'	CIMMYT/ICARDA
G9	PASTOR-2/HUBARA-5	CIMMYT/ICARDA
G10	HIDDAB/ATTILA-7	CIMMYT/ICARDA
G11	PASTOR-2/HUBARA-3	CIMMYT/ICARDA
G12	HUBARA-5/ANGI-1	CIMMYT/ICARDA
G13	GAMBO (CHECK)	CIMMYT/ICARDA
G14	ANGI-2/HUBARA-3	CIMMYT/ICARDA
G15	ETBW 5898 (SETII C1)	EIAR/KARC
G16	QAFZAH-2/FERRIUG-2 (SET II C1)	CIMMYT/ICARDA
G17	TAGANA	CIMMYT/ICARDA
G18	JNRB.5/PIFED	CIMMYT/ICARDA
G19	KINGBIRD (CHECK)	EIAR/KARC
G20	OGOLCHO (CHECK)	EIAR/KARC
G21	ETBW5955 SET II C2)	EIAR/KARC
G22	REYNA-28	CIMMYT/ICARDA
G23	ETBW5963(SET II C3)	EIAR/KARC
G24	PRINIA-1//NESMA*2/14-/3/DUCULA	CIMMYT/ICARDA
G25	FRANCOLIN #1/BAJ #1	CMSS09B00490S-099M-099Y-2WGY-0B
G26	KAUZ'S'/FLORKWA1//GOUMRIA-3	CIMMYT/ICARDA
G27	BJY/COC//PRL/BOW/3/BLOYKA-1	CIMMYT/ICARDA
G28	KUBSA	CIMMYT/ICARDA
G29	PBW343*2/KUKUNA//KIRITATI	CIMMYT/ICARDA
G30	HUBARA-2/QAFZAH-21//DOVIN-2	CIMMYT/ICARDA
G31	INQALAB 91*2/TUKURU//WHEAR	CIMMYT/ICARDA
G32	ATILA*2//CHIL/BUC*2/3KUKUNA	CIMMYT/ICARDA
G33	SERI 82/SHUHA'S'//PASTOR-2 (SET I)	CIMMYT/ICARDA
G34	FLORKWA2/6/SAKER'S'/5/RBS /ANZA/3/KVZ/HYS/YMH/TOB /4/BOW	CIMMYT/ICARDA
G35	KATILA17/DEEK2/8VEE'S'/7/CEBECO148/3/RON/CHA//NOR67/5/HK/38M	CIMMYT/ICARDA
G36	ATTILA 50Y//ATTILA/BCN/3/STAR*3/ MUSK-3	CIMMYT/ICARDA

Source: G*=short list name of genotypes to represent the name of genotypes from 1-36. i.e. genotype code number like G1 (HUBARA-3*2/SHUHA-4), G2(Atila-7), etc.

2.3. Experimental Design and Layout

The field experiment was laid out in 6x6 triple-lattice design. The width of 1.2 m and length of 2.5 m and a total 3 m² area was allocated for each plot in each incomplete block of replication. Each plot had six rows at the spacing of 20 cm between rows, 0.5 m path between plots, 1 m spacing between sub-blocks (incomplete block) and 1.5 m distance between replications with total area of 19.5 m x 41.6 m. The net plot size of experimental plot was 1 m x 2.5 m (2.5 m²) since the plants in the two outer most rows were treated as border plants and excluded.

2.4. Land Preparation, Sowing and Management

The experimental field was prepared by using farm tractor plough. It was ploughed two times, the first at the beginning of May the second at the middle of June and the third manually using labor worker during planting in early July 2017.

The full dose of blended fertilizer recommended for the study area are NPSzn (19% N, 38%P: 7% S and 2.5% Zn) at the rate of 100 kg ha⁻¹ was applied as band application at planting time under supplemental irrigation. Nitrogen fertilizer in the form of Urea (46% N) at a rate of 150 kg ha⁻¹ was applied in two split doses; with half applied two weeks after sowing and remaining half after early booting stage. The seeds (125 kg ha⁻¹ rate) were sown by hand drilling in the rows as uniformly as possible. All other necessary field management practices were carried out as per the recommendations.

2.5. Data Collection

Data were collected both on plot and plant bases. The four central rows were used for data collection on plot basis, whereas 10 randomly selected plants from the four central rows of each plot were used for data collection on plant basis. Mean data of the 10 sample plants were used for data analyses.

Data were collected both on plot and plant bases. The four central rows were used for data collection on plot basis, whereas 10 randomly selected plants from the four central rows of each plot were used for data collection on plant basis. Mean data of the 10 sample plants were used for data analyses. Data collected on plot basis were days to heading (days), days to 90%

physiological maturity (days), grain filling period, thousand kernel weight (g), grain yield plot⁻¹(g plot⁻¹), grain yieldha⁻¹(t ha⁻¹), biomass yields (t ha⁻¹) and Harvest index (%) while data collected on plant basis for the following characters were recorded on 10 randomly selected plants from each experimental plot. The averages of the ten plants in each experimental plot were used for data analysis. Those data were plant height (cm), number of fertile tillers per plant (in number), kernels per spike (in number), spikelet per spike (in number) and spike length (cm).

2.6. Data Analyses

2.6.1. Analysis of variance

The data were subjected to analysis of variance (ANOVA) using SAS statistical software version (9.2) (SAS, 2008) as per the expectations shown on Table 2. The comparison of mean performance of genotypes was done following the significance of mean squares using Duncan’s Multiple Range Test (DMRT).

Table 2. Analysis of variance in triple lattice design and expected mean square

Source of variation	DF	Sum of squares (SS)	Mean square $MS = \frac{SS}{df}$	Computed F	Expected mean squares
Replication	r – 1	SSR	MSR	$\frac{MSR}{MSE}$	$\sigma^2 + k\sigma b^2 + v\sigma r^2$
Treatment (unadj.)	k ² – 1	SST (unadj.)	MST (unadj.)	$\frac{MST(unadj)}{MSE}$	$\sigma^2 (\frac{k}{k+1}) m \sigma t^2$
Blocks within replication (adj.)	r(k-1)	SSB (adj.)	MSB (adj.)	$\frac{MSB(adj)}{MSE}$	$\sigma^2 + \sigma t^2 + k\sigma t^2$
Intra block error	(k-1)(rk-k-1)	SSE	MSE		a ²
RCB Error	(t-1) (r-1)	SSe	Mse		$\sigma^2 e$
Total	rk ² – 1	SST			

r = Number of replications. k² = Number of treatments, k= Number of plots in a block, SS = Sum square, MS = Mean square, σ^2 = Variance, t = Number of genotypes, MSE = Mean squares for error and $\sigma^2 e$ = Error variance, SSR= sum square of replication, SST= sum square of treatment, RCB=randomized complete block, MSR= mean square of replication, SSB= sum square of block, MST= Mean square of treatment.

Relative efficiency = $\frac{\text{mean square error in RCBD design}}{\text{mean square error in triple lattice design}} \times 100$ (Gomez and Gomez (1984)).

Genetic diversity was estimated from quantitative traits of genotypes using Euclidean distance (Unweighted Pair-group methods with Arithmetic Means (UPGMA)) computed by Statistical Software.

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3. RESULTS AND DISCUSSION

3.1. Analysis of Variance

The analysis of variance showed highly significant differences ($P < 0.01$) among wheat genotypes for all studied traits (Table 3). Such considerable range of variations would provide a good opportunity for yield improvement. The results also justify carrying out further genetic analysis considering all (12) agro-morphology traits. The relative efficiency of triple lattice design was greater than one for more than half quantitative traits but it was greater than 0.95 for all quantitative traits indicating the advantage of triple lattice design over RCBD in increasing the experimental precision (Table 3). Masood *et al.* (2008) and Idrees and Khan, (2009) reported that alpha lattice designs were on the average more efficient in reducing the experimental error and hence provide the efficient estimation of treatment contrasts. Hence, the present analyses were done using triple-lattice design. Coefficients of variation in percent were also used to compare the precision of the experimentation, i.e., means with lower CV% for most of the characters revealed the reliability of the data collected from the experiment (Gomez and Gomez, 1984).

Adhiena *et al.* (2016) conducted genetic divergence study in 26 bread wheat genotypes considering twelve traits in Southern Zone of Tigray Regional State, at mid and highland areas. They reported the presence of significant differences among genotypes for all traits except for plant height and number of spikelets per plant. According to Dawit *et al.* (2012), days to maturity, number of tillers per plant, biological yield and harvest index were not significantly different in durum wheat genotypes. This disparity may be due to the differences in the genotypes and test environments used in different studies.

Table 3. Mean squares from analysis of variance for twelve traits of thirty-six bread wheat genotypes evaluated at Mehoni in 2017

Traits	Replications (d.f =2)	Block Within replication (Adj.) (df=15)	Treatments (d.f=35)		Intra block Error (d.f=55)	RCBD Error	Rel. to effic. (%)	CV (%)
			(Unadj)	(Adj)				
Plant height (cm)	1293.51**	20.43**	94.92	91.22**	17.49	18.12	100.51	4.88
Days to heading (days)	7.06**	4.82**	142.80	122.83**	4.04	4.21	100.64	2.80
Grain filling period (days)	2.26ns	5.71**	28.04	27.50**	6.12	6.08	98.39	8.59
Days to maturity (days)	1.69ns	9.04**	157.00	132.74**	8.13	8.32	100.24	2.84
No. of fertile tillers/plant (no.)	0.11ns	0.07ns	0.50	0.38**	0.09	0.08	95.67	13.53
Spike length (cm)	0.14ns	0.24ns	2.70	2.17**	0.25	0.25	98.89	5.28
No. of spikelets/spike (no.)	0.22ns	0.98ns	7.31	6.48**	1.21	1.16	95.92	5.98
No. of kernels/ spike(no.)	15.53**	17.32**	65.39	56.24**	12.22	13.31	102.49	7.54
1000-kernel weight (g)	3.77ns	12.70**	58.66	53.33**	12.99	12.93	99.51	10.07
Grain yield (t ha ⁻¹)	0.14ns	0.09ns	1.13	0.96**	0.12	0.12	94.46	8.38
Biomass yield (t ha ⁻¹)	0.04ns	0.08ns	0.25	0.25**	0.10	0.09	95.31	10.26
Harvest index (%)	2.09ns	7.83**	82.19	74.19**	6.91	7.11	100.33	7.60

Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively. DF= degree freedom
Rel.effic. = relative efficiency, RCBD= randomized completely randomized design, CV= coefficient of variations and adj. and uadj. =
adjusted or unadjusted treatment

3.2. Principal Component Analysis

Principal component analysis showed that the gross variability observed among the 36 test genotypes can be explained with four principal components with eigen values greater than unity (Table 4). The first four components together accounted for about 70.56% of the total variation among the genotypes with respect to all the 12 traits evaluated and showed the presence of considerable genetic diversity among the genotypes for most of the traits under consideration. Individually, PC1, PC2, PC3 and PC4 in that order accounted for about 33% 18%, 10% and 9% of the gross variation among the 36 bread wheat genotypes evaluated for 12 traits.

The traits, which contributed more to PC1, were days to maturity, days to heading, harvest index and number of spikelet per spike, whereas for second PC, grain yield, plant height, number of kernels per spike and spike length, for the third PC, biomass yield and number of fertile tillers per plant and for the fourth PC, grain filling period and 1000-kernel weight. The first two principal components PC1 and PC2 with values of 33% and 18% respectively, contributed more than half to the total variation. Therefore, the present study confirmed that the bread wheat genotypes showed significant variations for the characters studied and it suggested many opportunities for genetic improvement through selection. Similar works have been done by Khodadadi *et al.* (2011), Dawit *et al.* (2012) and Ashraf *et al.* (2012) and Awale and Sentayehu (2013) for grouping of genotypes by principal component analysis. Singh *et al.* (2014) also reported that the character contributing the maximum to divergence should be given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization.

Table 4. Eigenvectors and eigenvalues of the first four principal components of 36 bread wheat genotypes evaluated for twelve traits

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
Plant height (cm)	0.193	0.405	-0.044	0.001
Days to heading (days)	0.422	0.019	-0.128	-0.200
Grain filling period (days)	0.095	-0.320	-0.006	0.603
Days to maturity (days)	0.440	-0.135	-0.123	0.104
No. of fertile tillers/plant (no.)	-0.297	0.181	-0.332	0.115
Spike length (cm)	0.257	0.331	0.256	-0.114
No. of spikelets/spike (no.)	0.352	0.121	0.151	0.110
No. of kernels/ spike (no.)	0.152	0.386	0.223	0.206
Thousand-kernel weight (g)	-0.171	-0.051	-0.184	0.480
Grain yield (t ha ⁻¹)	-0.187	0.514	-0.074	0.226
Biomass yield (t ha ⁻¹)	0.256	0.252	-0.472	0.285
Harvest index (%)	-0.378	0.271	0.265	0.003
Eigenvalue	4.32	2.37	1.28	1.20
Variance explained (%)	33.24	18.23	9.86	9.23
Cumulative variance explained (%)	33.24	51.47	61.33	70.56
Difference	1.95	1.09	0.08	0.34

3.3. Genetic Divergence Analysis

3.3.1. Genetic distances among wheat genotypes

The genetic distance of all possible pairs of 36 bread wheat genotypes ranged from 1.15 to 9.20 with the mean, standard deviation and coefficient of variation of 4.47, 1.28 and 28.71%, respectively (Table 5). The mean genetic distance, standard deviation and coefficient of variation among four released varieties were 5.20, 1.67 and 32.06%, respectively (Table 5). G19 (KINGBIRD) was distant and G6 (FENTALLE) the closest to check varieties with mean genetic distances of 4.71 and 6.61, respectively. This indicated that the check varieties had lower genetic distances among them than among considerable number of new entries. Arega *et al.* (2007) conducted research on title to estimate the genetic divergence among indigenous durum wheat (*Triticum durum* Desf.) genotypes of diverse origin and clustered them into homogenous groups and suggested an opportunity for improvement of grain yield through hybridization of genotypes from different clusters and subsequent selection from segregating generations for hybridization programmes.

The mean genetic distance of each bread wheat genotype to other 35 genotypes was calculated to generate information on the most distant and closest genotypes (Table 5). Depending on the mean Euclidean distance, G11 (6.22) followed by G8 (6.15) and the check variety, G19 (KINGBIRD) (5.87) was the most distant to other genotypes while the two check varieties, G6 (FENTALLE) and G13 (GAMBO) had mean genetic distances lower than the overall mean genetic distance of genotypes indicating that the varieties were not distant (were close) to the other genotypes. A total of 11 (34.38%) of the new entries had mean genetic distances greater than the overall mean genetic distance of genotypes. The result suggested the presence of considerable number of distant bread wheat genotypes to others that could be used in crossing program to combine the desirable traits of the genotypes. Initiation sound hybridization program needs the availability of genetically divergent genotypes for quantitative characters that contribute towards yield (Singh, 1983); and therefore, in any breeding program, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981).



Table 5. Range and mean Euclidean distance of thirty-six bread wheat genotypes estimated from twelve quantitative traits as evaluated at Mehoni in 2017

Genotype	Minimum	Maximum	Mean	SD	CV (%)
G1	1.80	6.41	3.64	1.16	31.89
G2	2.09	6.37	3.79	1.25	32.99
G3	1.89	7.25	4.05	1.49	36.91
G4	1.87	9.05	4.99	1.60	32.12
G5	1.45	6.84	3.87	1.44	37.09
G6	2.37	6.62	3.96	1.21	30.60
G7	3.06	9.20	5.53	1.35	24.41
G8	3.53	9.20	6.15	1.52	24.75
G9	2.64	6.60	4.20	1.12	26.63
G10	2.43	9.00	5.47	1.66	30.40
G11	3.57	8.10	6.22	1.14	18.35
G12	1.18	6.37	3.45	1.16	33.60
G13	2.05	7.62	4.54	1.45	31.94
G14	1.15	6.39	3.60	1.22	33.89
G15	1.73	7.60	4.09	1.40	34.14
G16	2.71	8.52	4.91	1.45	29.45
G17	2.44	7.44	4.47	1.27	28.46
G18	2.44	7.35	4.50	1.35	30.09
G19	3.14	7.76	5.87	1.28	21.82
G20	2.18	8.39	4.96	1.56	31.53
G21	2.24	6.90	4.38	1.14	26.13
G22	2.10	7.02	4.84	1.10	22.70
G23	2.18	7.20	4.06	1.26	30.88
G24	2.10	7.38	4.65	1.29	27.67
G25	1.47	6.48	3.95	1.42	35.95
G26	1.60	6.48	3.89	1.19	30.53
G27	1.15	6.61	3.77	1.18	31.24
G28	1.45	7.10	4.10	1.58	38.59
G29	2.61	7.39	4.96	1.28	25.84
G30	4.32	6.86	5.41	0.73	13.53
G31	2.24	6.13	4.06	0.99	24.34
G32	2.55	8.07	5.11	1.41	27.52
G33	1.60	7.10	4.03	1.35	33.57
G34	2.06	6.29	3.78	1.06	27.99
G35	1.18	6.01	3.48	1.00	28.77
G36	2.04	6.25	4.26	1.15	26.97
Overall	1.15	9.20	4.47	1.28	28.71

3.3.2. Clustering of Genotypes

The Euclidean distance matrix of 630 pair of wheat genotypes estimated from 12 quantitative traits was used to construct dendrograms based on the Unweighted Pair-group methods with Arithmetic Means (UPGMA). Accordingly, the 36 wheat genotypes were grouped into eight distinct clusters (Figure 1 and Table 6). Cluster VI was the largest, and consisted of eleven genotypes (30.56%) of the total genotypes. Cluster VIII consisted of eight (22.22%) and cluster III consisted of six (16.67%) in which cluster III genotypes included two released varieties (Ogolcho and Kingbird). Cluster VII included two released varieties (Fentalle and Gambo), Cluster IV and II with four and six genotypes, respectively, while Cluster I and V consisted only by one genotype. This indicates that the crossing between superior genetic divergences of above diverse clusters might provide desirable recombinants for developing high yielding bread wheat genotypes. This is because cluster analysis grouped genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters (Jaynes *et al.*, 2003).

Several authors reported the presence of divergence among the bread wheat genotypes indicating grouping in different numbers of distinct clusters. Dergicho *et al.* (2015) classified 68 bread wheat germplasm in to six groups; Ahmad *et al.* (2014), classified 19 genotypes into 3 clusters on the basis of average linkage and Salman *et al.* (2014) classified 65 bread wheat genotypes into 6 clusters. Awale and Sentayehu (2013) grouped 26 bread wheat genotypes into six clusters. Likewise, Shashikala (2006) grouped 169 wheat genotypes in to 11 clusters. Ajmal *et al.* (2013) classified 50 genotypes of wheat into 5 clusters while Desheva and Cholakov (2014), categorized winter wheat genotypes into three clusters.

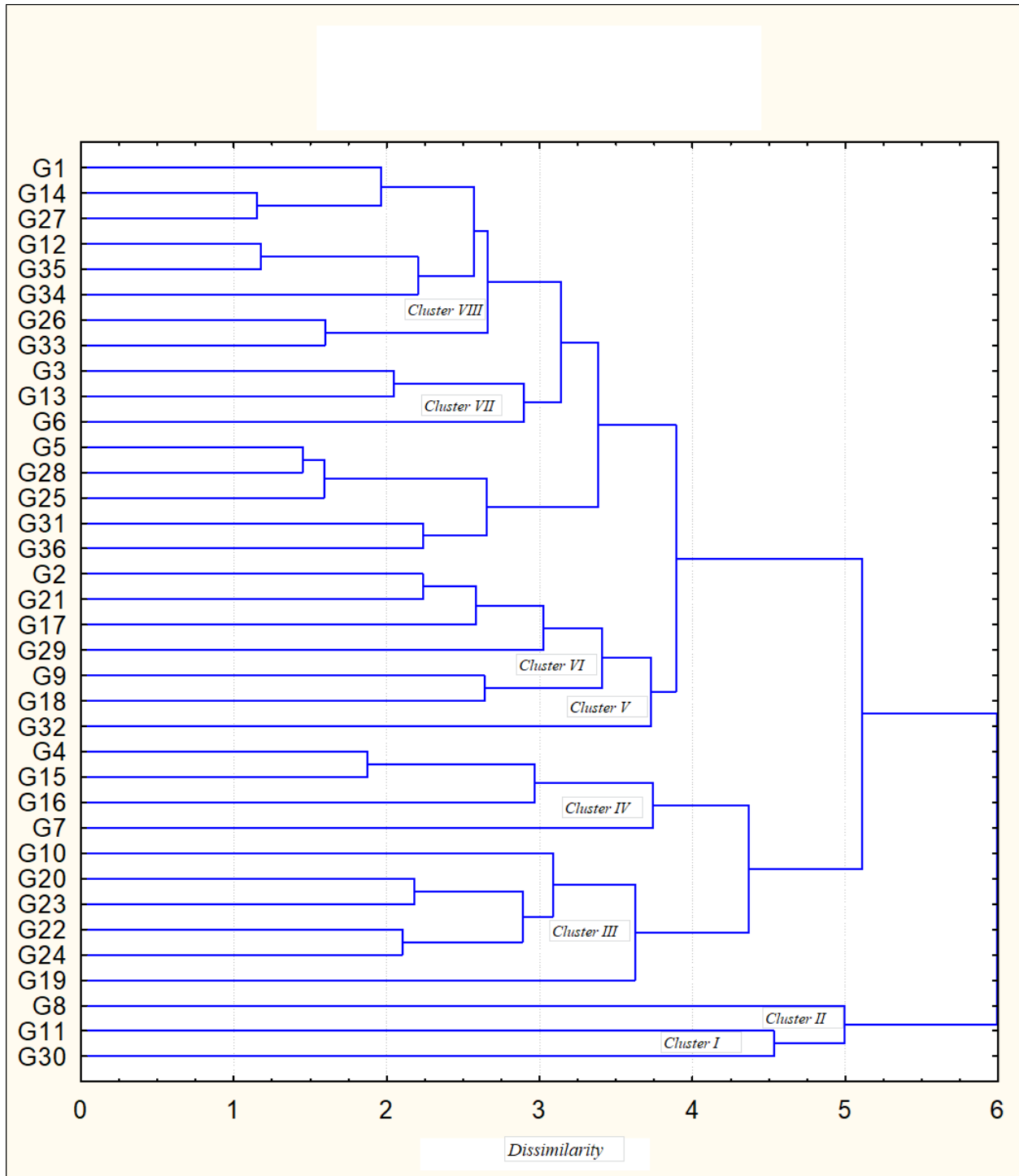


Figure 1. Dendrogram depicting dissimilarity of 36 bread wheat genotypes (G1- G36 genotypes code as description given in Table 1) by Unweighted Pair group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 12 phenological/ growth traits, grain yield and yield components.

Table 6. Distribution of twelve wheat genotypes in to eight different clusters based on twelve quantitative traits evaluated at Mehoni in 2017

Cluster	Number of Genotypes	Genotype (G*)
Cluster I	1 (2.78%)	G30
Cluster II	2 (5.56%)	G8, G11
Cluster III	6 (16.67%)	G10, G19(King bird), G20(Ogolcho), G22, G23, G24
Cluster IV	4 (11.11%)	G4, G7, G15, G16
Cluster V	1 (2.78%)	G32,
Cluster VI	11 (30.56%)	G2, G5, G9, G17, G18, G21, G25, G28, G29, G31, G36
Cluster VII	3 (8.33%)	G3, G6(Fentalle), G13(Gambo)
Cluster VIII	8 (22.22%)	G1, G12, G14, G26, G27, G33, G34, G35

G* Genotypes are numbered as shown on Table 1.

3.3.3. Cluster Mean Analysis

The mean values of eight clusters for 12 quantitative characters are presented in (Table 7). Cluster I and II had mean values greater than overall mean values of genotypes for days to heading, grain filling period, days to maturity, number of spikelets per spike and number of kernels per spike. In addition, Cluster I and II for thousand kernels weight and biomass yield respectively, had mean values greater than overall mean values, but for the remaining traits both clusters had mean values lower than overall mean values of genotypes. Cluster III and IV had mean values greater than overall mean values of genotypes for number of fertile tillers per plant, thousand kernel weight and harvest index. However, Cluster III and IV distinguished each other by having mean values of grain filling period and grain yield greater than overall mean values respectively. These clusters had mean values lower than overall mean values of genotypes for the remaining traits. Adhiena (2015) evaluated 26 bread wheat genotypes at Korem in Southern part of Tigray Regional State which is a few kilometers distance from the current study site but at higher elevation (2490m.a.s.l.). He reported that six genotypes were grouped together in Cluster III that had higher mean grain yield and early maturing habit and suggested that selection for early maturity could be done more effectively from this cluster which could be used for environments with shorter duration of rainfall distribution. The grouping of bread wheat

genotypes in one or two clusters that had desirable traits to be used for crossing and/or selection programs has been reported by other authors.

Cluster VII and VIII had mean values greater than overall mean values of genotypes for number of fertile tillers per plant, number of spikelets per spike, number of kernels per spike, grain yield, biomass yield and harvest index. In addition, Cluster VII had mean values greater than overall mean values of genotypes for plant height and spike length while Cluster VIII had mean values greater than overall mean values for thousand kernel weight. However, these clusters had mean values lower than overall mean values of genotypes for the remaining traits. These two clusters consisted of 11 (30.5%) genotypes with higher grain yield and mean values greater than overall mean values of genotypes for most desirable traits suggesting that selection of genotypes and/or further evaluation of members of these clusters is possible to develop varieties for the study area.

The two clusters (I and II) consisted of three genotypes with low mean grain yield but the members of these clusters were late maturing when compared to the average crop maturity of the genotypes. Cluster III consisted of six genotypes having late grain filling period but with higher mean values for number of fertile tillers per plant, thousand kernel weight and harvest index. Similarly, Cluster V and VI consisted of twelve genotypes characterized as late maturing, tall plants, higher mean values for most spike characters and biological yield, but these clusters had lower mean values for number of fertile tillers per plant, grain yield, thousand kernel weight and harvest index. The genotypes included in these clusters might not be considered for selection and/or further evaluation to develop varieties in the study area due to the undesirable traits of low yield and late maturity since the study area is known by short duration of rainfall period. However, crossing among the members of these clusters and Cluster IV, VII and VIII which consisted of early maturing but high yielding genotypes, might be possible to obtain high yielding and late maturing genotypes from segregating progenies that might be appropriate for areas with long duration of rainfall period.

Cluster IV consisted of four genotypes with the highest mean grain yield among the clusters with early maturing which suggested the advantage of further evaluation of the genotypes in this cluster along with the members of Cluster VII and VIII to develop/identify high yielding variety (ies) for the study area. However, it is also possible to suggest crossing among the genotypes in

Cluster IV and VII to obtain progenies that combine early maturing, highest yield, higher mean values for spike characters, tall plants and high biological yield. But, for obtaining progenies with short plant height and short spike length but with high mean values for other desirable traits (early maturing, high yield, spike characters etc.), it is suggested crossing among genotypes in Cluster IV and VIII. Mean value analysis for clusters revealed the higher chance of obtaining bread wheat genotypes that combine high yield and early maturity (Cluster IV, VII and VIII) that fit the study area having shorter duration of rainfall distribution. It is also possible to use the genotypes as source of genes for early maturity, high yield and for many yield related traits in crossing programs. Salman *et al.* (2014) identified one cluster among six to be used as source of early maturing materials while Desheva and Cholakov (2014) reported genotypes suitable for hybridization programs aimed at developing high yielding wheat varieties.

Table 7. Mean values of characters for eight clusters based on twelve quantitative traits evaluated at Mehoni in 2017

Trait	Cluster								Overall Mean
	I	II	III	IV	V	VI	VII	VIII	
PH (cm)	62.13	81.18	78.38	84.98	89.07	88.52	95.51	85.01	85.7
HD (days)	75	80.89	60.05	66.75	78.33	77.24	71.66	71.04	71.7
GFP (days)	31.33	33.16	31.78	24.92	33.00	28.61	26.47	28.29	28.93
MD (days)	106.33	114.17	91.83	91.67	111.33	105.88	98.11	99.21	100.5
FTPP (no.)	1.97	1.48	2.38	2.67	1.43	1.96	2.25	2.38	2.18
SL (cm)	9.08	8.97	8.39	9.01	11.38	9.90	10.02	9.40	9.46
SPS (no.)	19.7	19.86	16.84	15.94	19.1	19.03	19.02	19.05	18.38
KPS (no.)	48.2	49.25	42.18	40.24	43.93	48.66	50.50	47.09	46.1
TKW (g)	40.4	35.38	38.17	40.73	31.4	33.18	33.20	36.21	35.79
GY (t ha ⁻¹)	3.33	2.92	4.07	4.81	4.11	3.9	4.53	4.63	4.18
BY (t ha ⁻¹)	2.97	3.27	2.65	3.02	3.4	3.14	3.15	3.1	3.05
HI (%)	28.08	22.62	38.69	39.70	30.24	31.38	35.98	37.4	34.61

PH=Plant height (cm), DH=Days to heading, GFP=Grain filling period (days), DM=Days to maturity, FTTP=No. of fertile tillers/plant, SL=Spike length (cm), SPS=No. of spikelets/spike, KPS=No. of kernels/ spike, TKW=Thousand-kernel weight (g), GY=Grain yield (t/ha), BY=Biomass yield (t/ha), HI=Harvest index (%) no.=number.

4. SUMMARY AND CONCLUSIONS

Thirty-six bread wheat genotypes were grown in 2017 at Mehoni Agricultural Research Station in Southern Tigray using 6x6 Triple-Lattice Design to determine genetically divergent bread wheat genotypes with desirable traits for hybridization particularly for yield. To generate such information, data were collected on 12 traits of which some were taken on plot basis while the others were assessed on single plant basis. The four central rows were used for data collection on plot basis.

The analysis of variance revealed highly significant differences among the genotypes for all characters. Principal component analysis showed that the first four principal components having eigen values greater than one accounted for 70.56% of the total variation of the 36 genotypes evaluate for 12 traits. The genetic distances among 36 bread wheat genotypes estimated using Euclidean distance ranged from 1.15 to 9.20 with the mean, standard deviation and coefficient of variation of 4.47, 1.28 and 28.71%, respectively. A total of 11 (34.38%) out of 32 new entries had mean genetic distances greater than the overall mean genetic distance of genotypes. Higher genetic distances were estimated among the new entries than among the four check varieties and check varieties with new entries. The genotypes were grouped into eight distinct clusters of which Cluster VI , VIII and III consisted of 11 (30.56%), 8 (22.22%) and 6 (16.67%) genotypes, respectively. Cluster VII and III were consists of two released varieties (Fentalle and Gambo) and (Ogolcho and Kingbird), Cluster IV, II and V with 3, 4 and 2 genotypes, respectively, while Cluster I was solitary. Cluster IV was distinguished by having the highest mean values for thousand kernel weight (41 g), fertile tillers per plant (3), grain yield (4.8 t ha⁻¹) and harvest index (40) and Cluster V characterized as consisting of genotypes with the highest mean values for spike length and biomass yield. The result suggested the presence of considerable number of distant bread wheat genotypes that could be used in crossing program to combine the desirable traits of the genotypes. However, since this is a one-year result, it is necessary to repeat the field experiment and evaluate the genotypes over several locations and years in order to make conclusive and comprehensive conclusions and recommendations.

5. REFERENCES

- Abu T (2012) Grain and feed annual report. Grain report number: ET1201, Addis Ababa, Ethiopia. *Res. in Pl Bio.*, 3(1): 33-36.
- Acevedo E, Silva P, Silva H (2002) Wheat in the world. Bread wheat production and improvement. *FAO Plant Production and Protection Series No. 30*.
- Adhiena M, Wassu M, Tadesse D (2016) Estimation of Heritability and Genetic Advance of Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes at Ofla District, Northern Ethiopia. *Int Journ Plant Breeding and Genetics*. 10:31-37.
- Ahmad HM, Awan SI, Aziz O, Muhammad AA (2014) Multivariate analysis of some metric traits in bread wheat (*Triticum aestivum* L.). *Eur Jour Bio and Biosci*, 1 (4): 22-26.
- Ajmal SU Minhas, NM, Hamdani A, Shakir A, Zubair M, Ahmad Z (2013) Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*) germplasm. *Paki Jour Bot*, 45(5):1643-1648.
- Ali SL (2013) Genetic Variability and Heritability Estimates in F2 wheat Genotypes. *Int Jou Agri Crop Sci*, 5(9): 983-986.
- AregaGashaw, Mohammed H, Singh H (2007) Genetic divergence in selected durum wheat genotypes of Ethiopian plasm. *Afri Crop Sci Journ*, 15(2).
- Ashraf A, Abd El- Mohsen, Samir R, Abo Hegazy, Taha MH (2012) Genotypic and phenotypic interrelationships among yield and yield components in Egyptian bread wheat genotypes, Cairo University, Giza, Egypt.
- Awale D, Sentayehu A (2013) Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Genotypes. *Paki Jour Bio Sci*, DOI: 10, 3923/pjbs.
- Chahal GS, Gosal SS (2002) Principles and Procedures of Plant Breeding, Biotechnology and Conventional Approaches. Narosa Publishing House, New Delhi.
- Cholastova T, Knotova D (2012) Using morphological and Microsatellites (SSR) markers to assess the genetic diversity in Alfalfa (*Medicago Sativa* L.) *Int Jour Bio*, 6(9):78-787.
- CSA (Central Statistical Agency) (2017) Report on Area and Production of Major Crops (Private Peasant Holdings, Meher Season) Agricultural Sample Survey 2016/2017. *Central Statistics Agency*, Addis Ababa, Ethiopia.
- Dawit T, Tadesse D, Yigzaw D, Getnet Sh (2012) Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum* Desf). *Wudpecker Res Jour*, 1(4):107 -112.

- Dergicho D, Sentayehu A, Firdisa E, Gezahegn F 2015a Genetic Variability in Bread Wheat (*Triticumaestivum L.*) Germplasm for Yield and Yield Component Traits. *Jour Bio, Agri and Healthcare* 5(13).
- Desheva, G, Cholakov T (2014) Variability, heritability and genetic progress for some yield components in common winter wheat genotypes (*Triticum aestivumL.*). *Genetics and Plant Physiology*, Conference “Plant Physiology and Genetics-Achievements and Challenges”, Sofia, Bulgaria, 4(3-4): 191-200.
- FAO (2017) Food and Agricultural Organization. CROP PROSPECTS and FOOD SITUATION. Quarterly Global Report. March 2018.
- GAIN (Global Agricultural Information Network) (2014) Report: ET1401, Addiss Ababa
- Gezahegn F, Sentayehu A, Zerihun T (2015) Genetic Variability Studies in Bread Wheat (*Triticumaestivum L.*) Genotypes at Kulumsa Agricultural Research Center, South East Ethiopia. *Jour Bio, Agri Healthcare*.5(7)2224-3208.
- Gomez KA, Gomez A A (1984) Statistical Procedures for Agricultural Research, 2nd.
- Hailesslassie G, Haile A, Wakuma B, Kedir J 2015 Performance evaluation of hot pepper (*Capsicum annum L.*) varieties for productivity under irrigation at Raya Valley, Northern, Ethiopia. *Basic Res Jour Agri Sci. Rev.* 4(7):211-216.
- Idrees N, Khan MI (2009) Design improvement using uniformity trials experimental data. *Pak. J. Agri. Sci*, 46(4), pp.315-320. Jaynes, DB, Kaspar, TC, Colvin, TS, James, DE. 2003. Cluster analysis of spatiotemporal corn yield patterns in an Iowa field. *Agro Jour* 95:574–586.
- Jaynes DB, Kaspar TC, Colvin TS, James DE (2003) Cluster analysis of spatiotemporal corn yield pattern in an Iowa field. *Agro Jour*, 95:574-586.
- Kamali JM (2008) Review on wheat status in the past, present and future. *Key papers for 10th conference on sciences of breeding in Iran: 23-45.*
- Khabiri E, Imani AA, Shahbazi H (2012) Studying the grain yield and yield components in advanced rain fed wheat genotypes. Scholars Research Library. *Annals of Biological Research*, 3 (12):5647-5650.
- Khan N, Naqvi FN (2011) Heritability of Morphological Traits in Bread Wheat Advanced Lines Under Irrigated and Non-Irrigated Conditions. *Asian Jour Agri Sci* 3(3): 215-222.
- Khodadadi M, Fotokian MH, Miransari M (2011) Genetic diversity of wheat (*Triticum aestivum L.*) genotypes based on cluster and principal component analyses for breeding strategies. *Afri Jour Crops Sci*, 5(1):17-24.

- Leilah AA, Al-Khateeb SA (2005) Statistical analysis of wheat yield under drought conditions. *Journal of Arid environments*, 61(3):483-496.
- Mahalanobis PC (1936) The generalized distance in statistics. *Proceeding of Indian National Institute of Science* 2: 49-55.
- Masood MA, Faroo K, Mujahid Y, Anwar ZM (2008) Improvement in precision of agricultural field experiments through design and analysis. *Paki Jour Life and Social Sci*, 6(2): 89-91.
- Mihratu A, Firew M, Firdissa E (2014) Evaluation of Bread Wheat (*Triticum aestivum* L) Genotypes for Heat tolerance Middle Awash, Ethiopia. MSc Thesis, Postgraduate Program Directorate Haramaya University, Haramaya, Ethiopia.
- Mollasadeghi V, Shahryari R (2011) Important morphological markers for improvement of yield in bread wheat. *Advances in Environmental Biology*, 5(3): 538-542.
- Mondal MAA (2003) Improvement of Potato (*Solanum tuberosum* L.) through hybridization and in-vitro culture technique. Ph.D. Thesis. Rajshahi University, Rajshahi, Bangladesh.
- Pradip K Akotkar DK De, AK Pal (2010) Genetic variability and diversity in Okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic Jour Plant Breeding*, 1(4): 393-398
- Salman S (2014) Genetic Variability Studies in Bread Wheat (*Triticum aestivum* L.) Accessions. *Paki Jour Agri Res*: 27.
- SAS (2008) Statistical Analysis System. Version 9.2, SAS Institute Inc., Cary, NC., USA.
- Sharma JR (1998) Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited Publishers, New Delhi: 432.
- Shashikala SK (2006) Analysis of genetic diversity in wheat. M.Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.
- Shewry PR (2009) Wheat. *Jour Experi Bot*, 60, 1537-1553.
- Shujaat A, Azhar HS, Rehmani G, Habib A, Hasnian N, Sikandar KS (2014). Morpho agronomic characterization of okra [*Abelmoschus esculentus* (L.) Moench]. *World Appl Sci Jour*, 31(3):336-340.
- Singh SP, Singh AK, Sharma M, Salgotra SK (2014) Genetic divergence study in improved bread wheat varieties (*Triticum aestivum*). *Afri Jour Agri Res*, 9(4):507-512.
- Sleper DA, Poehlman JM (2006) *Breeding Field Crops*. 5th edition. Black well Publishing, Professional, Ames, Iowa.
- Smith JL (1984) Genetic variability with U.S. hybrid maize: multivariate analysis of isozyme data. *Crop science*, 24:1041-1046.

Tsegaye B, Berg T (2007) Utilization of durum wheat landraces in East Shewa, central Ethiopia: Are home uses an incentive for on-farm conservation? *Agriculture and Human Values*.24, 219- 230.

Welsh JR (1981) *Fundamentals of plant genetics and breeding*, John Willey and Sons, Inc. New York. P 290.

Yadawad Arati RR, Hanchinal HL, Nadaf SA, Desai Suma Biradar, RudraNaik V (2015) Genetic variability for yield parameters and rust resistance in f₂ population of wheat (*Triticum aestivum* L.) Karnataka, India. *The Bioscan*. 10(2): 707-710.

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