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Cluster and Principal Component Analysis among Bread Wheat (*Triticum Aestivum L*) Genotypes in Mid Rift Valley of Oromia, Ethiopia

Urgaya Balcha[1*], **Firew Mekbib**[2] **and Dagnachew Lule**[3]

[1]*Department of Agricultural Sciences, Adami Tulu Agricultural Research Center, Adami Tullu, Ethiopia*

[2]*Department of Plant Science, College of Agriculture and Environmental Science, Haramaya University, Dire Dawa, Ethiopia*

[3]*Department of Agricultural Sciences, Oromia Agricultural Research Institute, Finfine, Ethiopia*

Abstract

Cluster and principal component analysis techniques are suitable in identification plant traits separately and it helps breeders to genetic improvement of traits in bread wheat genotypes. This research was conducted at Adami Tulu, mid rift valley of Oromia, Ethiopia, with the objectives of studying the extent of clustering of bread wheat genotypes and identifying the important traits in distinguishing the genotypes. A total of 36 breads wheat genotypes were evaluated in 6 × 6 simple lattice design during 2017-2018 cropping season. Analysis of variance showed the existence of highly significant (P ≤ 0.01) variation among genotypes for most of the studied traits. Cluster analysis revealed that the 36 breads wheat genotypes were grouped into 4 clusters. The Principal Component Analysis (PCA) showed that the first 7 principal components with Eigen values greater than one combined explained about 82.82% of the total variation. The study showed the presence of possibility of improving yield and other desirable characters through selection. However, this study was conducted for one growing season and therefore further testing in different locations for more than one cropping season is necessary.

Keywords: Cluster analysis; Multivariate analysis; Principal component analysis

Introduction

Bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum durum desf*) are the world's two principal commercial types of wheat. Bread wheat is a self-pollinating annual plant in the true grass family Gramineae (Poaceae) which is the largest cereal crop extensively grown as staple food sources in the world [1]. It is one of the most important and strategic cereal crop in the world and in Ethiopia in terms of production and utilization [2]. In Ethiopia, wheat is grown at an altitude ranging from 1500 to 3000 meters above sea level, between 6-16°N latitude and 35-42°E longitude. The most suitable agro ecological zones, however, fall between 1900 and 2700 m.a.s.l. [3]

Ethiopia is the second largest wheat producing country in Africa following South Africa. Wheat accounts for about one-fourth of the nation's total cereal production. In Ethiopia, from the total cereal crops produced, about 18.24% of production is from wheat [4]. The production loss due to both biotic and abiotic factors coupled with the increasing population has made it difficult to attain food security in the country. Improving the adaptability of crop varieties to a changing environment supported by appropriate crop management strategies is the working principle worldwide in ensuring crop productivity [5]. However, crop improvement for water stress is a much complicated task as drought damage is manifested in various forms at various crop growing stages making breeding for drought resistance uneasy task [6-8].Cluster analysis is very important to broaden the genetic basis through crossing of genotypes in the different cluster. Principal component analysis is suitable multivariate technique in identification and determination of independent principal components that are effective on plant traits separately. Principal component analysis also helps breeders to genetic improvement of traits such as yield [9]. Agronomic, morphological and phenological traits are very important for grouping wheat genetic resources, and also are essential and useful for plant breeders seeking to improve existing germplasm by introducing novel genetic variation for certain traits into the breeding populations [10].

The study on cluster analysis portrays the presence of wider genetic variability among genotypes and the possibility to broaden the genetic basis through crossing of genotypes in the different cluster. Multivariate analysis techniques are suitable in identification of plant traits separately and it helps breeders to genetic improvement of traits in bread wheat genotypes has been given little attention in moisture stress environments, particularly in the mid rift valley of Oromia. Therefore, the present study was initiated with the objectives of studying the extent of clustering of bread wheat genotypes and to identify the important traits in distinguishing the genotypes.

***Corresponding author:** Urgaya Balcha, Department of Agricultural Sciences, Adami Tulu Agricultural Research Center, Adami Tullu, Ethiopia, Tel: +251922039011; E-mail: urgayab@gmail.com

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Materials and Methods

Description of the study area

The experiment was conducted at Adami Tulu Agricultural Research Center (ATARC) during 2017 cropping season. ATARC is located in Adami Tulu Jido Kombolcha District, East Shoa Zone of Oromia, and it is located in the mid Rift Valley of Ethiopia about 167 km south of Addis Ababa. It lies at a latitude of 7°9'N and longitude of 38°7'E. It has an altitude of 1650 m.a.s.l and it receives a bimodal unevenly distributed average annual rainfall of 760.9 mm per annum. The long-term mean minimum and the mean maximum temperatures are 12.6 and 27°C, respectively. The pH of the soil is 7.88. Having sandy loamy and andosol soil type with sand, clay and silt in proportion of 34,48 and 18% respectively [11].

Experimental materials, design and management

In this experiment 11 released bread wheat varieties and 25 advanced breeding lines, a total of 36 genotypes obtained from Kulumsa Agricultural Research Center (KARC) were used for the experiment (Table 1). The experiment was arranged in 6 × 6 simple lattice designs at random. The genotypes were grown under uniform rain fed conditions. The experimental plots consisted of 6 rows of 2.5 m length, 1.2 m width and 0.2 m row space (3 m^2). The central 4 rows were harvested to estimate grain yield. The spacing between adjacent replications, blocks and plots were 1 m, 0.5 m and 0.5 m, respectively. Sowing was done on July 13th, 2018 by hand drilling and covered lightly with soil. Seeding rate of 150 kg/ha and fertilizer rate of 41 and 46 kg/ha of N and P2O5, respectively or 89 kg/ha of urea and 100 kg/ha of DAP, were applied where nitrogen fertilizer was applied in split (1/2 at planting, 1/4 at tillering and 1/4 at flowering) [12]. Weeding and other management practices were done as per the recommendation for wheat.

S.N	Genotypes tested		Cross	Selection history	Origin	Year of release
1	Variety	K6290-Bulk	(AF.MAYOxGEM)Xromany	k6290-bulk	Kenya	1977
2	Variety	Ogolcho (ETBW5520)	WORRAKATA/2*PASTOR	2STEMRRSN#10	CIMMYT	2012
3	Variety	BIKA	PASTOR//MXL7573/2*BAU/3/SOKOLL/WBLL1	-	CIMMYT	2014
4	Variety	WANE (6130)	SOKOLL/EXCALIBUR	-	CIMMYT	2016
5	Variety	Hawii (2501)	CHIL/PRL	CM92803-91Y-0H-05Y-5M-0RES05Y	CIMMYT	1999
6	Variety	Pvon-76	VCM//CNO*S*/7C/3/KAL/BB	CM8399-D-4M-3Y-1M-1Y-1M-0Y	CIMMYT	1982
7	Variety	Derselign	CI8154/2*FR	CI8154/2*FR	Mexico	1974
8	Variety	Kakaba (Picaflor #1)	KRITATI//SERI/RAYON	CGSS02Y00152-099M-099Y-099M-46Y-0B	CIMMYT	2010
9	Variety	Gambo (Quaiu # 2)	BBAX/LR42//BABAX*/3/VIVITSI	CGSS01B00046T-099Y-099M-099M-099Y-099M--29Y-0B	CIMMYT	2011
10	Variety	KINGBIRD	TAM-200/TUI/6/PAVON-F-76//CARIANCA-422/ANAHUAC-F-75/5/BOBWHITE/CROW//BUCKBUCK/PAVON-F-76/3/YECORA-F-70/4/TRAP-1.	-	CIMMYT	2015
11	Variety	GALIL	not available	not available	Israel	2010
12	Advanced line (A1)		KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07	CMSS09Y00249S-099Y-099M-099Y-1M-0WGY	CIMMYT	-
13	Advanced line (A2)		KACHU*2//WHEAR/SOKOLL	CMSS09Y00818T-099TOPM-099Y-099ZTM-099NJ-099NJ-10WGY-0B	CIMMYT	-
14	Advanced line (A3)		PAURAQUE #1/3/PBW343*2/KUKUNA//	CMSS09Y00835T-099TOPM-099Y-099M-099Y-3WGY-0B	CIMMYT	-

		PBW343*2/ KUKUNA/4/BAJ #1			
15	Advanced line (A4)	WBLL1*2/ BRAMBLING//SAAR/ 2*WAXWING/4/ PBW343*2/ KUKUNA// KRONSTAD F2004/3/ PBW343*2/KUKUNA	CMSS09Y00843T-099TOPM-099Y-099M-099Y-12WGY-0B	CIMMYT	-
16	Advanced line (A5)	MELON//FILIN/ MILAN/3/FILIN/4/ PRINIA/PASTOR// HUITES/3/MILAN/ OTUS//ATTILA/ 3*BCN/5/MELON// FILIN/MILAN/3/FILIN	CMSS09Y01061T-099TOPM-099Y-099M-099Y-8WGY-0B	CIMMYT	-
17	Advanced line (A6)	SOKOLL/3/PASTOR// HXL7573/2*BAU/4/ WHEAR/SOKOLL	CMSA09Y00810S-050Y-050ZTM-0NJ-099NJ-19WGY-0B	CIMMYT	-
				Continued.	
18	Advanced line (A7)	MILAN//PRL/ 2*PASTOR/4/ CROC_1/ AE.SQUARROSA (213)//PGO/3/ BAV92/5/PAURAQ	CMSA09M00542S-050ZTM-0NJ-099NJ-15WGY-0B	CIMMYT	-
19	Advanced line (A8)	FRANCOLIN #1/BAJ #1	CMSS09B00490S-099M-099Y-2WGY-0B	CIMMYT	-
20	Advanced line (A9)	CROC_1/ AE.SQUARROSA (205)// BORL95/3/PRL/ SARA//TSI/VEE#5/4/ FRET2*2/5/WHEAR/ SOKOLL	CMSA09M00056T-077(SR25HET)Y-050ZTM-0NJ-099NJ-8WGY-0B	CIMMYT	-
21	Advanced line (A10)	TILHI/SOKOLL*2// KINGBIRD #1	CMSS10Y00766T-099TOPM-099Y-099M-10WGY-0B	CIMMYT	-
22	Advanced line (A11)	SUP152/BAJ #1	CMSS07Y00195S-0B-099Y-099M-099Y-16M-0WGY	CIMMYT	-
23	Advanced line (A12)	KACHU*2/3/ ND643//2*PRL/ 2*PASTOR	CMSS08B00712T-099TOPY-099M-099NJ-2WGY-0B	CIMMYT	-
24	Advanced line (A13)	CHIBIA//PRLII/ CM65531/3/MISR 2*2/4/ HUW234+LR34/ PRINIA//PBW343*2/ KUKUNA/3/ROLF07	CMSS09Y00853T-099TOPM-099Y-099M-099Y-10WGY-0B	CIMMYT	-
25	Advanced line (A14)	PREMIO/2*BAVIS	CMSA09Y00228T-050M-050Y-050BMX-0NJ-099NJ-13WGY-0B	CIMMYT	-
26	Advanced line (A15)	MILAN/KAUZ// PRINIA/3/BAV92/4/ BAVIS	CMSA09Y00896S-050Y-050ZTM-0NJ-099NJ-4WGY-0B	CIMMYT	-
27	Advanced line (A16)	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/ BAV92/4/BERKUT/5/ BAVIS	CMSA09M00547S-050ZTM-0NJ-099NJ-2WGY-0B	CIMMYT	-
28	Advanced line (A17)	SHA7//PRL/VEE#6/3/ FASAN/4/ HAAS8446/2*FASAN/ 5/CBRD/KAUZ/6/ MILAN/AMSEL/7/	CMSS09B00076S-099M-099Y-12WGY-0B	CIMMYT	-

		FRET2*2/KUKUNA/8/ KINGBIRD #1			
29	Advanced line (A18)	NAVJ07/ SHORTENED SR26 TRANSLOCATION/3/ ATTILA/BAV92// PASTOR	CMSA09M00047T-079(SR26POS)Y-050ZTM-0NJ-099NJ-3WGY-0B	CIMMYT	-
30	Advanced line (A19)	W15.92/4/PASTOR// HXL7573/2*BAU/3/ WBLL1*2/5/WHEAR/ SOKOLL	CMSA09M00092T-048(SR25HET)Y-050ZTM-0NJ-099NJ-6WGY-0B	CIMMYT	-
31	Advanced line (A20)	SERI.1B//KAUZ/ HEVO/3/AMAD/4/ ESDA/SHWA//BCN	AISBW05-0153-11AP-0AP-0AP-2AP-0SD-0TR	ICARDA	-
32	Advanced line (A21)	ATTILA 50Y// ATTILA/BCN/3/PFAU/ MILAN	ICW05-0632-12AP-0AP-0AP-2AP-0AP-0TR	ICARDA	-
33	Advanced line (A22)	SERI.1B//KAUZ/ HEVO/3/AMAD/4/ PFAU/MILAN	ICW06-00151-8AP-0AP -03 SD-0TR	ICARDA	-
34	Advanced line (A23)	KAUZ//ALTAR 84/AOS 3/KAUZ/3/ ATTILA 50Y// ATTILA/BCN/4/ PASTOR-6	ICW06-50246-7AP-0AP-0AP -1 SD-0TR	ICARDA	-
35	Advanced line (A24)	ANGI-1	ICW92-0326-12AP-0L-7AP-0L-2AP-0AP-0TR	ICARDA	-
36	Advanced line (A25)	ENKOY/FLAG-5	ICW06-00434-13AP/ 0KUL-0DZ/0AP-0DZ/ 0AP-1AP-0AP-0TR	ICARDA	-
Source: Kulum sa Agricultural Research Center.					

Table 1: Description of the tested bread wheat genotypes.

Data collection

Data were collected on plot and plant basis.

Data recorded on plot basis: Data were collected on plot basis from central rows of each plot in each replication.

Days to heading: The number of days from date of emergence to the stage where 75% of the spikes have fully emerged.

Days to maturity: The number of days from date of emergence to the stage when 90% the plants in a plot have reached physiological maturity.

Grain filling period: The number of days from heading to maturity, *i.e.* the number of days to maturity minus the number of days to heading.

Effective tillers per meter square: Number of tillers per meter square was counted in the square meter frame area. Tillers were recorded by counting the number of tillers of one meter length in four central rows of each sub plot and then converted to tiller per meter square.

Grain yield/ha (t ha^{-1}): Grain yield t ha^{-1} was estimated from grain yield (g/plot). Grain yield in grams estimated from plants in the central 4 rows of each plot was adjusted to 12.5% moisture content. Plants grown in 20 cm at the outer most of the plot left as border plants and yield per plot was estimated from 2.5 m × 0.8 m total harvestable area (2 m^2). Therefore, grain yield (g/plot) of each plot was used to estimate grain yield per hectare in tons.

1000 kernel weight (g): Weight of 1000 seeds in gram adjusted to 12.5% moisture content.

Biomass yields (g/plot): The plants with in the four central rows (that was harvested for yield estimate) were harvested at the point where they are attached to the ground, collected, sun dried until the constant weight attained and weighed in grams to obtain the biomass yield per plot.

Harvest index (%): was calculated on a plot basis, as the ratio of dried grain weight adjusted to 12.5% moisture content to the dried total above ground biomass weight.

Data recorded on plant basis

Ten plants were selected randomly from the four central rows of the plots before heading and were tagged for recording the following characters.

Plant height (cm): The average height in cm of ten plants in each plot which has been measured from ground level to the tip of the spike excluding the awns.

Kernels per spike: The average number of kernels per spike of ten plants in each plot.

Spikelet per spike: The average number of spikelet per spike of ten plants in each plot.

Peduncle length (cm): The average length of the peduncle of the main culm of ten plants in each plot was recorded in centimeters from the top most nodes to the base of the spike.

Spike length (cm): The average spike length of ten plants on the main culm from the base of the spike to the top of the last spikelet excluding awns was recorded in centimeter.

Awn length (cm): the average awn length of ten plants from the tip of the spike to the tip of the longest awn was recorded in centimeter.

Physiological measurements

Relative leaf water contents (%): was measured at flowering stage using Turner and Kramer (1980) method:

$$RWC\% = \frac{FW - DW}{TW - DW} X100$$

Where, FW=Fresh leaf Weight; DW=Dry Weight (In Oven for 48 h); TW=Tumescent Weight.

Leaf water content (%) was calculated using Clarke and McCaig method [13]:

$$LWC\% = \frac{FW - DW}{FW} X100$$

Where, FW=Fresh leaf Weight; DW=leaves placed in an oven at 50°C for 24 h and re-weighed.

Leaf area (cm^2): From the fully developed flag leaf of selected mother shoots, the maximum length and width was measured in centimeters. Plants' leaves diameter was measured with a ruler and leaves areas were calculated using the following equation [14]: Leaf area (cm^2)=maximum leaf length × leaf width × 0.75.

Chlorophyll content: A flag leaf per plant from 10 sample plants per plot was measured using portable chlorophyll meter Minolta SPAD-502 at flowering [15]. The averages of the SPAD values from sample plants at flowering stage were used for analysis in each genotype [16,17].

Data analyses

Analysis of variance: The data collected for each trait were subjected to Analysis of Variance (ANOVA) for simple lattice design. Analysis of variance was done using Proclattice and Proc GLM procedures of SAS version 9.0 [18]. The difference between treatment means was compared using DMRT at 5% probability levels.

Multivariate analysis

Cluster analysis: The analysis was based on all yield and yield contributing traits. Clustering of genotypes was done using the PROC clustering strategy of SAS 9.0 and appropriate numbers of clusters were determined from the values of pseudo F and pseudo T2 statistics [17].

Principal component analysis: Principal component analysis was computed by using SAS (computer software from correlation matrix). Standardized quantitative data was used for the analysis.

Results and Discussion

Analysis of variance

Analysis of variance by GLM and lattice for 18 characters are presented in (Table 2). The result showed the existence of highly significant ($P \leq 0.01$) variation among genotypes for days to heading, days to maturity, grain yield, harvest index, plant height, number of kernels per spike, number of spikelet's per spike, peduncle length, spike length, leaf area and awn length. Similar results were reported by several investigators [19-24]. These authors reported the presence of highly significant differences among the studied wheat genotypes for days to maturity, days to heading, plant height, spike length, spikes per plant, grains per spike, harvest index and grain yield per plant. Also reported highly significant ($P \leq 0.01$) differences among bread wheat genotypes for days to heading, days to maturity, number of kernels per spike, spike length and biomass yield [25]. There was also significant difference ($P \leq 0.05$) among genotypes for grain filling period, thousand kernel weight, biomass yield and chlorophyll content. However, there is no significant difference among genotypes for effective tillers per meter square, relative leaf water content and leaf water content. The presence of appreciable differences among genotypes for most of the characters studied makes the possibility to carry out further breeding and genetic analysis.

Traits	Mean Squares			CV	± SE	Efficiency (%)	R^2
	Genotype (df=35)	Replication (df=1)	Error (df=25)				
DH	12.377**	6.12ns	3.86	3.87	1.39	101.22	0.87
DM	20.2**	55.12**	4.23	2.1	1.45	112.06	0.898
GFP	14.28*	36.12*	6.13	6.25	1.75	113.22	0.846
ETPM	7143.09ns	2910.20ns	5182.64	31.03	50.91	104.76	0.71
GY	1.14**	10.89**	0.331	14.41	0.41	193.69	0.893
TKW	16.64*	2.88ns	8.06	7.09	2.01	98.12	0.825
BY	100999.5*	1034401.00*	45361	16.29	150.6	167.1	0.853

HI	134.27**	25.83ns	53.16	11.82	5.16	53.158	0.809
PH	117.08**	353.76ns	26.83	7.14	3.66	162.1	0.894
NKPS	42.26**	11.92ns	11.86	8.91	2.44	108.4	0.863
NSPS	3.34**	0.016ns	0.45	3.94	0.48	126.93	0.938
PL	26.4**	19.11ns	4.85	7.94	1.56	125.09	0.91
SL	1.28**	7.27**	0.14	4.47	0.26	100.79	0.941
RLWC	113.37ns	1231.32**	87.91	11	6.63	93.97	0.76
LWC	21.84ns	11.77ns	14.87	5.39	2.73	100.25	0.72
LA	25.36**	0.31ns	9.16	21.36	2.14	99.25	0.843
CC	10.90*	5.39ns	5.19	4.47	1.61	133.28	0.841
AL	0.86**	9.86**	0.1	7.98	0.22	3.924	0.956

*, ** ns, significant at P ≤ 0.05, P ≤ 0.01 and non-significant, respectively

Key: DF=Degrees of Freedom, CV=Coefficient of Variation, SE=Standard Error, Efficiency (%)=Relative efficiency to Randomized complete block design, R^2=Coefficient of determinations, DH=Days to Heading (days), DM=Days to Maturity (days), GFP=Grain Filling Period (days), PH=Plant Height (cm), SL=Spike Length (cm), NSPS=No. of Spikelet Per Spike, NKPS=No. of Kernel Per Spike^{-1}, TKW=Thousand Kernel Weight (g), BY=Biomass Yield g plot^{-1}, HI=Harvest Index, ETPM=Effective Tiller per m^2, PL=Peduncle Length (cm), GY=Grain Yield (t/ha), RLWC=Relative Leaf Water Content (%), LWC=Leaf Water Content (%), LA=Leaf Area (cm^2), CC=Chlorophyll Content and AL=Awn Length (cm)

Table 2: Mean squares from analysis of variance by GLM and Lattice for the 18 characters of 36 bread wheat genotypes grown at ATARC (2017).

Multivariate analysis

Cluster analysis: Cluster analysis revealed that the 36 bread wheat genotypes were grouped into 4 clusters (Table 3 and Figure 1). The genotypes were distributed in such way that 18 genotypes were grouped into cluster I (50%), 10 genotypes in cluster II (27.77%), 5 genotypes in cluster III (13.88%) and 3 genotypes in cluster IV (8.33%). Cluster I contains the highest mean values of chlorophyll content (51.53) (Table 4). Cluster II contains high mean values of grain yield (4.52 ton) but the least in thousand kernel weight (39.52 g), relatively high in plant height (78.23 cm), number of kernels per spike (40.39), number of spikelet per spike (17.40), spike length (8.51 cm), leaf water content (72.18), and awn length (4.23 cm). The third cluster is characterized by high mean values of biomass yield (1625 g), late in heading date (53.30), late maturing (101.40), higher effective tiller per meter square (310.07), longer peduncle length (30.79 cm), higher relative leaf water content (88.11) and relatively the highest in leaf area (16.09 cm^2). Cluster IV is distinguished by the highest in thousand kernel weight (40.60 g) and harvest index (68.26) but the shortest in plant height (61.77 cm), least in relative water content (71.14), relatively early maturing (95.67) and relatively low values for all other traits. Clustered 108 wheat genotypes in four groups [26]. Also classified 300 wheat genotypes in seven clusters based on agronomic performance [27].

In general, cluster analysis portrayed the presence of wider genetic variability among genotypes and the possibility to broaden the genetic basis through crossing of genotypes in the different cluster. For instance, genotypes in cluster IV are characterized by early maturing but low yielder, whereas, genotypes in cluster III are late maturing and high yielder. A cross made between selected genotypes in those cluster could possibly create high yielding and early maturing variety that can escape late season moisture deficit.

Cluster	No of genotypes	Percentage (%)	Genotypes
I	18	50	14, 23, 20, 28, 16, 27, 21, 24, 18, 32, 7, 12, 34, 36, 19, 33, 11, 15
II	10	27.77	13, 31, 3, 17, 2, 9, 29, 1, 4, 30
III	5	13.88	25, 26, 35, 5, 6
IV	3	8.33	8, 10, 22

Table 3: The distribution of genotypes into 4 clusters for 36 bread wheat genotypes tested at ATARC (2017).

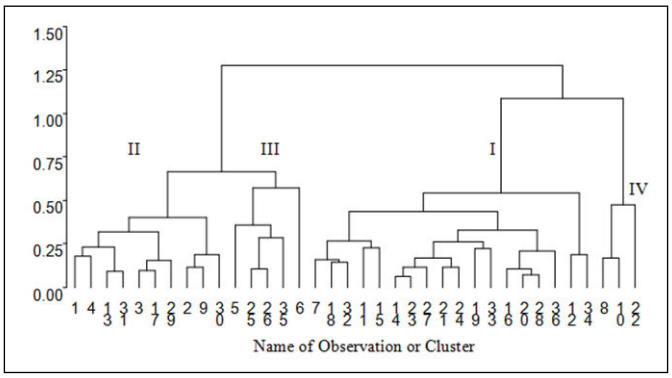

Figure 1: Clusters to which the genotypes belong and average distances between clusters.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV
DH	50.42	51.6	53.30**	45.50*
DM	96.86	99.1	101.40**	95.67*
GFP	38.94*	39.8	40.4	41.83**
ETPM	221.15	209.19*	310.07**	242.95
GY	3.72	4.52**	4.51	3.03*
TKW	40.22	39.52**	40.2	40.60**
BY	1200.56	1473	1625.00**	866.67*
HI	62.24	61.59	56.06*	68.26**
PH	69.7	78.23**	77.44	61.77*
NKPS	38.04	40.39**	38.35	36.77*
NSPS	17.2	17.40**	16.85	15.95*
PL	26.66	29.18	30.79**	24.47*
SL	8.5	8.51**	8.36	7.30*
RLWC	84.97	84.59	88.11**	79.71*
LWC	70.92*	72.18**	72.16	71.14
LA	13.07*	14.95	16.09**	14.92
CC	51.53**	50.99	50.01	49.83*
AL	3.78	4.23**	4.11	3.50*

*and **low and high value of the trait respectively.

Key: DH=Days to Heading (days), DM=Days to Maturity (days), GFP=Grain Filling Period (days), PH=Plant Height (cm), SL=Spike Length (cm), NSPS=No. of Spikelet Per Spike, NKPS=No. of Kernel Per Spike [1], TKW=Thousand Kernel Weight (g), BY=Biomass Yield G Plot[1], HI=Harvest Index, ETPM=Effective Tiller/m^2, PL=Ped uncle Length (cm), GY=Grain Yield (t/ha), RLWC=Relative Leaf Water Content (%), LWC=Leaf Water Content (%), LA=Leaf Area (cm^2), CC=Chlorophyll Content, and AL=Awn Length (cm)

Table 4: Mean values of 18 traits for 4 clusters of 36 bread wheat genotypes at ATARC (2017).

Principal component analysis: Principal component analysis is suitable multivariate technique in identification and determination of independent principal components that are effective on plant traits separately and it helps breeders to genetic improvement of traits such as yield that have low heritability specifically in early generations *via* indirect selection for traits effective on this [6]. Principal Component Analysis (PCA) indicated that the first seven vectors with Eigen values greater than one combined explained about 82.83% of the gross variation (Table 5). The first PC accounted for 20.27% of the total variation, whereas the corresponding values for the second to the seventh PCs were 17.11%, 12.99%, 10.64%, 8.9%, 7.15% and 5.72%, respectively. The results are in line with the finding

of which reported four principal components for explained relation of traits in 18 bread wheat genotypes studied, which account for 76% of the total variance [28].

Biomass yield, plant height, peduncle length and days to maturity were the major contributor for the variation recorded in the first PC. According to 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 [29]. The variation in the second PC was mainly due to spike length, leaf area, awn length, number of spike per spikelet and chlorophyll content. Relative leaf water content and grain yield was among the major contributor for the variability recorded in the third PC (Table 5). Grain filling period, effective tiller number and grain yield for the fourth PC; number of kernel per spike and effective tiller number for the fifth PC; harvest index, leaf water content and days to maturity for the 6th PC; and leaf water content and chlorophyll content was the major contributor for the 7th principal component.

Usually it is customary to choose one variable from these identified groups. Hence for the first group biomass yield (0.447), is best choice, which had the largest loading from component ones, spike length (0.409) for the second, grain yield (0.334) for the third, grain filling period (0.463) for the fourth, effective tiller per meter square (0.479) for the fifth, harvest index (0.444) for the sixth, and leaf water content (0.334) for the seventh group. Principal component analysis reflects the importance of the largest contributor to the total variation at each axis of differentiation [30].

Principal Component Analysis (PCA)							
Traits	**PC 1**	**PC 2**	**PC 3**	**PC 4**	**PC 5**	**PC 6**	**PC 7**
DH	0.222	0.239	-0.052	-0.35	0.228	-0.364	0.075
DM	0.332	0.224	-0.263	0.165	0.023	-0.034	0.046
GFP	0.16	0.122	-0.266	0.463	-0.204	0.309	-0.134
ETPM	0.089	0.055	0.155	0.321	0.479	0.072	-0.072
GY	0.237	0.144	0.334	-0.32	-0.117	0.28	0.041
TKW	-0.165	0.288	-0.016	0.154	0.249	0.364	-0.314
BY	0.447	0.009	0.125	-0.138	0.099	-0.115	-0.116
HI	-0.185	0.157	0.281	-0.2	-0.289	0.444	0.15
PH	0.373	-0.103	0.215	0.024	0.116	0.21	-0.121
NKPS	0.177	0.235	0.146	0.118	-0.52	-0.024	0.099
NSPS	0.162	0.35	-0.083	0.083	-0.291	-0.321	0.016
PL	0.336	-0.226	0.266	0.11	0.079	0.091	-0.052
SL	0.128	0.409	0.146	0.142	0.013	-0.01	-0.155
RLWC	0.188	-0.026	-0.392	-0.299	0.081	0.23	0.223
LWC	0.23	-0.007	-0.392	0.031	0.096	0.36	0.334
LA	0.12	-0.373	0.245	0.232	-0.039	-0.013	-0.014
CC	-0.122	0.304	0.225	0.08	0.311	0.002	0.305
AL	0.21	-0.362	0.063	-0.282	-0.092	-0.063	0.154
Eigen Value	3.8509	3.2516	2.4674	2.02194	1.7005	1.35821	1.08596
Difference	0.59934	0.78414	0.4455	0.32134	0.34238	0.27224	0.29813
Proportion	0.2027	0.1711	0.1299	0.1064	0.0895	0.0715	0.0572
Cumulative	0.2027	0.3738	0.5037	0.6101	0.6996	0.7711	0.8282

Key: DH=Days to Heading (days), DM=Days to Maturity (days), GFP=Grain Filling Period (days), ETPM=Effective Tiller Per m^2, GY=Grain Yield (t/ha), TKW=Thousand Kernel Weight (g), BY=Biomass Yield g $plot^{-1}$, HI=Harvest Index, PH=Plant Height (cm), NKPS=No. of Kernel Per $Spike^{-1}$, NSPS=No. of Spikelet Per Spike, PL=Peduncle Length (cm), SL=Spike Length (cm), RLWC=Relative Leaf Water Content (%), LWC=Leaf Water Content (%), LA=Leaf Area (cm^2), CC=Chlorophyll Content and AL=Awn Length (cm)

Table 5: Eigen vectors and Eigen Values of the first seven principal components of 36 bread wheat genotypes evaluated at ATARC (2017).

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Conclusion

The analysis of variance revealed that there were sufficient variations among bread wheat genotypes for grain yield and yield related traits. The results showed the presence of significant differences ($P \leq 0.01/0.05$) among the tested genotypes for almost all traits indicating the presence of appreciable level of variability among the tested 36 bread wheat genotypes. Cluster analysis revealed that the 36 bread wheat genotypes were grouped into 4 clusters. The principal component analysis extracted seven principal components PCA1 to PCA7 from the original data having Eigen values greater than one accounting nearly 82.83% of the total variation.

The present study showed the presence of possibility of improving yield and other desirable characters through selection. The study also revealed the importance of considering other characters in the process of selection of genotypes for yield. However, this study was conducted at Adami Tulu District for one growing season, therefore, it may not be sufficient to make strong conclusion and recommendation. This indicates the need to conduct further study by considering many wheat growing areas of the district for more than one cropping season.

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