Journal of Agricultural Research Advances
ISSN: 2582-7227

Research Article
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Cluster and principal component analysis among bread wheat (*Triticum Aestivum L.*) accessions in west shewa, central Ethiopia

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Received on: 05/09/2023 Accepted on: 27/02/2024 Published on: 05/03/2024

ABSTRACT

Aim: The aim of this study was to assess the extent of clustering and identifypromising bread wheat genotypes for further breeding.

Materials and Methods: A total of 100 bread wheat genotypes were evaluated in alpha-lattice design with two replications in the 2022 main cropping season at Liban Jawi District, West Shewa, Ethiopia.

Results: Cluster I was the largest cluster, which consisted of 51 bread wheat genotypes (51%) followed by cluster IV. The maximum distance was observed between cluster II and cluster V (176.39), whereas the shortest distance was found between cluster III and clusterIV(39.2). Principal component analysisrevealed that the first five principal components with Eigen values greater than one accounted for 76% of the total variation among 100 bread wheat genotypes. Based on the present investigation among genotypes; genotypes viz 31790 (58.93 qt/ha), EBW192299 (57.97 qt/ha), 33682 (56.51 qt/ha) 34737 (55.38 qt/ha and Acc. 34159 (52.51 qt/ha) were identified as high yielders compared to another tested genotypes.

Conclusion: It was concluded that genotypes namely; 31790 (58.93 qt/ha), EBW192299 (57.97 qt/ha), 33682 (56.51 qt/ha), 34737 (55.38 qt/ha) and 34159 (52.51 qt/ha) were identified as high yielders genotypes compared to other tested genotypes.

Keywords: Bread Wheat, Cluster, Principal component

How to cite this article: Feyisa Gelgu, Gudeta Nepir and Singh BCS (2024). Cluster and principal component analysis among bread wheat (*Triticum Aestivum L.*) accessions in west shewa, central Ethiopia. J. Agri. Res. Adv., 06(01): 01-10.

Introduction

Bread wheat (*Triticum aestivum L.)* is a self-pollinated annual crop which belongs to the family Gramineae (Poaceae), tribe *Triticeae*, genus *Triticum* and species *aestivum* (Acquaah, 2007). It is an allohexaploid species with 3 different genome configurations (A, B, D) of 42 chromosomes (2n=6x= 42) and perfect flowers, whichareforced to reproduce as an autogamous crop with 1-4% natural cross- pollination (Hei *et al*., 2017). The bread wheat is one of the oldest cereal crop regarded as the 'king of cereals' since it shares a large area under production, high productivity, and holds a prominent position in the international food grain trade (Hazra *et al*., 2019).

Bread wheat accounts for about 95% of world-wide wheat production,and the remaining 5% being tetraploid durum wheat used in pasta and semolina products (Shewery, 2009). The report on wheat production reveals that the world annual production was 765.4 million metric tons with an average yields of 3.48 t/ha, and it accounts for nearly 30% of global cereal production. It was identified as the first in production area and second in total production after maize, and provides more nourishment than any other food crop (FAO, 2021).

In Ethiopia, wheatis produced under rain-fed conditions and nowadays broadly cultivated under irrigation. Wheat is widely grown in the high lands and mid-altitudes of Ethiopia. Inspite of existence of wide agro-ecological areas suitable for wheat production, demand for wheat is increasing because of population growth, urbanization, and expansion of agro-industries, in which wheat production is left behind by 25 - 30% of its demand in Ethiopia (Hodson *et al*., 2020).

Wheat is the major essential cereal crop, which occupying 1.79 million hectares of land with a total production of 5.8 million tons and a productivity was 3.046 t/ha in Ethiopia (CSA, 2021). Wheat is one of the main food crops and has been the basic staple food (Haas *et al*., 2018). Wheat has great importance for economic, commercial, industrial, diets for human beings and is also used for livestock feed (Shewry and Sandra, 2015). It is one of the staple foods and the main source of calories in the major producing areas (Shiferaw *et al*., 2013).

Knowledge ofthe genetic diversity of a crop helps the breeder in choosing desirable parents for the breeding program and gene introgression from distantly related germplasm (Rauf, 2012). Cluster analysis is very important to broaden the genetic basis through crossing of genotypes in the different cluster. Principal component analysis is a suitable multivariate technique for the identification and determination of independent principal components that are effective on plant traits separately. Principal component analysis also helps breeders improve genetic traits such as yield (Golparvar *et al*., 2006). Therefore, this research was conducted using one hundred different bread wheat genotypes to study the extent of clustering of bread wheat genotypes and to identify the important traits in distinguishing the genotypes

Materials and Methods

The experiment was conducted in Liban Jawi District, West Shewa Zone, Oromia Regional State, of Ethiopia. Liban Jawi is located at 173 km from Addis Ababa and 47 km from Ambo town. The altitude of the district ranges from 1800 to 3098 m.a.s.l. (meters above sea level) and receives an annual rain fall of 1000 mm to 1800 mm with an average temperature of 10.4-29^{0}c. It has three different agro-climatic conditions, namely high land, moderate altitude, and low land, constituting 27%, 65% and 8%, respectively. The district is bordered in north by Chaliya and MidaKegni district, in the south by Dire Inchini and Jibat district, in the east by TokeKutaye district and in the west by Dano, Chaliya and Jibat district. The dominant soil type at the test site is loamy soil with a PH of 6-7 (LJAO, 2021).

Planting Materials

A total of 100 wheat accessions were grown at Liban Jawi in 2021 cropping season. These bread wheat accessions were collected from different source, such as: Ethiopian Biodiversity Institute (EBI), Kulumsa Agricultural Research Center (KARC), and Holeta Agricultural Research Center (HARC). Nine released varieties (Alidoro, Dandaa, Digelu, Enkoy, Hidase, King bird, Kubsa, Ogolcho and Wane) were used as check varieties (Table 1).

Experimental Design and Trial Management

The field experiment was carried out in a 4x25 alpha lattice design with two replications during the main rainy season of 2022 at one location. The total area, including border, was 18.8 m x 17 m (319.6 m2) out of these effective trial area was 12.8 x 11 m (140.8 m2). The replication had four blocks, in which each block contained twenty-five plots, with two plots at the border to minimize the bordering effect. The plot per block dimension was 27 rows of 2 m length with 0.20 m row spacing. It means twenty-five (25) entries and two borders, with 27 rows applied per block. The width of the block was 0.2 m x 27, which was 5.4 m per replication. The dimension of an individual block area was 5.4 m width x 2 m length (10.8m2). The spacing between blocks was 1 m and space between plots was 0.2 m. Terraces were formed over the block to protect the plot from soil erosion. The experimental field was well ploughed four times before sowing, and then planting rows were ready by exploitation of hand forced row markers.

Planting was done by hand drilling at a depth of 5 cm with a seed rate of 150 kg/ha. Planting was carried out in the firstweek of July. NPS and urea fertilizers were applied at a rate of 100 kg/ha. Urea was applied in split applications: the first split (1/3) and the second split (2/3) of the total dose at planting and mid-tillering stages, respectively. Weeds were manually eradicated from the experimental field.

Data Collection

Data were collected both on a plant and plot basis by random sampling technique with the use of descriptors for wheat (IBPGR, 1985).

Plant basis

Ten plants were randomly taken from the central plants for recording the following observations and the mean values for the treatments were computed.

Plant height (cm): The distance in cm between the ground level to the tip of the spike of ten plants (excluding the awns) at maturity was measured.

Number of productive tillers per plant (PT): The actual count of the fertile numbers of tillers of ten plants (spike bearing) per plant.

Spike length (cm): Length measured in cm from base of spike to the tip of the highest spikelet of ten plants (excluding the awns) in cm at maturity.

Spikelet per spike (SPS): The total number of spikelets on the main spike of all ten plants was counted at the time of maturity and average was recorded.

Number of kernels per spike (KPS): Theaverage number of seeds was recorded from the ten sampled plants.

Flag Leaf length (cm): Average length of the uppermost leaf on ten randomly selected plants at physiological maturity.

Flag Leaf width (cm): Average width of the uppermost leaf at the widest point on ten randomly selected plants at physiological maturity.

Peduncle Length (cm): The length of peduncle from the last node to the tip of the peduncle during maturity on ten randomly tagged plants.

Awn Length (cm): Awn length from the end of the spike to the tip of the awn was measured and the average for ten randomly tagged plants was recorded.

Plot basis

The data on the following attributing traits were collected based on of the plots.

Days to 50% heading (DH): It was recorded by counting the number of days from sowing to the date when at least 50% of the heads in the plot fully exerted from the boom or flowered.

Grain filling period (GFP): It was the result obtained from the number of days to maturity minus the number of days to heading.

Days to 90% maturity: Recorded by counting the number of days from sowing to the days when 90% of the heads in the plot were physiologically matured.

Grain yield per plot (g): Moisture was adjusted to the standard moisture content at 12.5% moisture basis after threshing using moisture tester and the adjusted yield per plot was converted to quintal per hectare.

Thousand seed weight (g): The weight (g) of 1000 seeds from randomly sampled seeds per plot is measured by using sensitive balance.

Biological yield or biomass (g): Was determined by weighing the total air dried above ground biomass of the plot and converted to quintal per hectare.

Harvest index(%): It was calculated by dividing grain yield per plot to total above ground dry biomass yield per plot and then multiplied by hundred.

Data Analysis

Analysis of Variance (ANOVA)

All data were subjected to analyses of variance (ANOVA) using general linear model (GLM) a procedure of SAS statistical version 9.4 software (SAS, 2013). Least significance difference (LSD) was used to separate differences in parameters means of genotypes where significant variation was observed at a 5% probability level (Table 2).

Analysis of variance was done using the following model:-

$Yijl = \mu + \tau i + \gamma j + \rho l\ (j) + \varepsilon ijl$

Where; μ is the overall (grand) mean, τi is the effect due to the ith treatment, (i=1, 2, 3…, t), γj is the effect due to the jth replication, and (j=1, 2…, r), ρl (j) is block inside replicate effect, εijl is that the error term wherever the error terms, are independent observations from an approximately normal distribution with mean = 0 and constant variance $\sigma^2 \varepsilon$.

Genetic Diversity and Cluster Analysis

Clustering was done for 100 genotypes after standardization mean values of each trait.

Genetic distance: Phenotypic genetic distance was computed based on phenotypic data collected from 100 bread wheat genotypes using average linkage Euclidean distance (ED) as follows (Sneath and Sokal, 1973),

$$EDjk=\sqrt{\sum_{i=1}^{n}(xij - xik)^2}$$

Where EDjk = distance between genotypes j and k; xij and xik = value of phenotypic trait of the ith character for genotypes j and k, respectively; and n= number of phenotype characters used to compute the distance.

Principal Component Analysis (PCA)

Principal components were estimated based on original data using MINITAB 17 (MINITAB, 2016) software to identify the most important traits contributing to the total variation observed among the accessions.

The first PCA value (Y1) was given by the linear combination of the variables X1, X2… Xp Y1= a11X1+a12+…a1pXp, the second principal component was calculated in the same way, Y2= a21X1+a22X2+…a2pXp.

Table 1. List and source of 100 bread wheat accessions grown in 2022

S.N	Accession	Source	S.N	Accession	Source	S.N	Accession	Source
1	31169	Amara	35	33907	Amara	69	34737	Tigray
2	31224	Oromia	36	33909	Amara	70	34804	Amara
3	31257	Oromia	37	33911	Amara	71	34821	Oromia
4	31258	Oromia	38	33915	Tigray	72	34856	Amara
5	31296	Amara	39	33917	Amara	73	36255	Oromia
6	31394	Oromia	40	33919	Amara	74	36503	Amara
7	31395	Oromia	41	33921	Amara	75	EBW192364	KARC
8	31430	Amara	42	33924	Amara	76	EBW192398	KARC
9	31542	Oromia	43	33972	Oromia	77	EBW192299	KARC
10	31543	Oromia	44	34029	Amara	78	EBW192344	KARC
11	31600	Oromia	45	34037	Amara	79	EBW192345	KARC
12	31551	Oromia	46	34039	Amara	80	EBW192362	KARC
13	31554	Oromia	47	34043	Oromia	81	EBW192610	KARC
14	31593	Amara	48	34045	Amara	82	BW184033	KARC
15	31627	Oromia	49	34053	Oromia	83	EBW192875	KARC
16	31630	Oromia	50	34073	Amara	84	EBW192865	KARC
17	31632	Oromia	51	34086	Amara	85	EBW192348	KARC
18	31643	Oromia	52	34097	Oromia	86	EBW192489	KARC
19	31644	Oromia	53	34098	Oromia	87	EBW192872	KARC
20	31786	Amara	54	34137	Oromia	88	BWKU13383	KARC
21	31790	Amara	55	34145	Oromia	89	EBW192398	KARC
22	31813	Amara	56	34152	Amara	90	EBW194030	KARC
23	31818	Amara	57	34157	Amara	91	EBW192870	KARC
24	33206	Amara	58	34159	Amara	92	Alidoro	HARC
25	33387	Oromia	59	34161	Oromia	93	Danda,a	HARC
26	33389	Oromia	60	34169	Oromia	94	Digelu	KARC
27	33516	Amara	61	34190	Oromia	95	Enkoy	KARC
28	33556	Oromia	62	34239	SNNP	96	Hidase	KARC
29	33597	Amara	63	34280	Tigray	97	Kingbird	KARC
30	33682	Amara	64	34667	Oromia	98	Kubsa	KARC
31	33794	Amara	65	34706	Oromia	99	Ogolcho	KARC
32	33828	Amara	66	34720	Tigray	100	Wane	KARC
33	33893	Amara	67	34728	Tigray			
34	33901	Tigray	68	34735	Tigray			

Key: S.N =Serial Number, KARC=Kulumsa Agricultural Research, HARC = Holeta Agricultural Research Center

Table 1. Skeleton of analysis of variance table for alpha lattice design

SV	DF	Mean square	F values	Expected mean square
Replication(r)	r-1	Msr	Msr/Mse	$\sigma^2_r + \sigma^2_b + \sigma^2_g + \sigma^2_e$
Block(rep)	r(b-1)	Msb	Msb/Mse	$r\sigma^2_b + \sigma^2_g + \sigma^2_e$
Genotypes(g)	g-1	Msg	Msg/Mse	$rb\sigma^2_g + \sigma^2_e$
Error	rg-rb-g+1	Mse		σ^2_e
Total	rg-1	Mst		

Key: SV= source of variation, DF= degree of freedom, r= number of replication, b= block, g= genotypes, Msr= mean square of replication, Msg= mean square of genotypes, Msb= mean square of block with in replication, Mse= mean square of error, Mst= mean square of total.

This continues until a total of principal components have been calculated equals to the original number of variables. At this point, the sum of variances of allprincipal components is equal to the sum of the variances of all variables. As suggested by Johnson and Deutscher (1988), principal components with Eigen values greater than one are considered to determine the number of clusters.

Results and Discussion

Cluster Analysis

Clustering of Genotypes

Most breeding programs utilize diverse parents which are genetically far apart from one another; cluster analysis usually finds the extent of genetic diversity and groups the organisms with similar parents into one cluster (Mohammadi *et al*., 2015). The extent of genetic 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 (Birhanu *et al*., 2016).

The analysis of genetic diversity through the cluster analysis based on average linkage Euclidean distance of 100 bread wheat genotypes were grouped into five genetically distinct clusters suggesting a considerable amount of genetic diversity in the material (Table 3). It was indicated that the tested bread wheat genotypes were moderately divergent. Four of them were group clusters (I, II, III, and IV) and the remaining one is solitary (V). Cluster I was the largest cluster by having 51 bread wheat genotypes (51%), followed by cluster IV (18%). Cluster II and III consist of 16 and 14 genotypes respectively. Cluster V consisted of 1 genotype comparatively the smallest cluster.

This indicates that crossing between superior genotypes of the above various cluster pairs would possibly give fascinating recombinant for developing high-yielding bread wheat varieties. Genotypes from various clusters can be used in crossing programs to mix fascinating traits and might be used as donors in breeding programs.

Several authors previously reported the presence of genetic divergence among bread wheat genotypes indicating need to cluster them in to distinct group. Ajmal *et al*. (2013) classified 50 genotypes of bread wheat into 5 clusters. Salman *et al*. (2014) classified sixty-five bread wheat genotypes into half adozen clusters. Dargicho *et al*. (2015) also used 68 bread wheat germplasm and grouped into five clusters. Devesh *et al*. (2019) also classified 60 genotypes into five clusters.

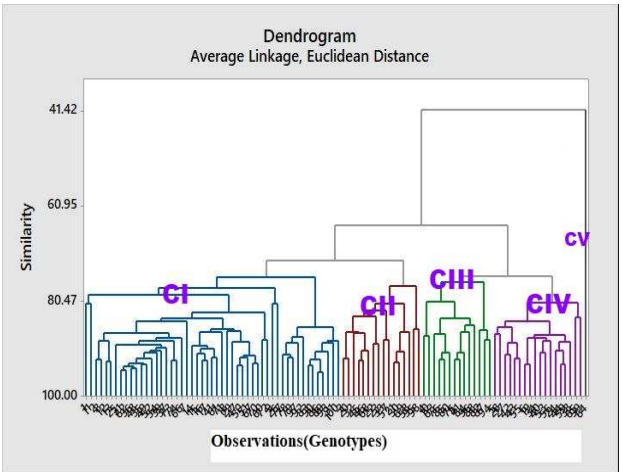

Fig 1. Dendrogram on the basis of 16 traits of 100 bread wheat genotypes

Cluster Distance of Bread Wheat Genotypes

The intra and inter-cluster distances of genotypes were presented (Table 4). The intra-cluster distance was highest in cluster I (27.96) followed by cluster III (26.84) and the lowest intra cluster distances were recorded in cluster V (0.00) which shows the absence of genetic variability within the cluster. The inter-cluster distance was ranged from176.39 to 39.20 between clusters. Maximum inter-cluster distance was observed between cluster II and cluster V (176.39) followed by cluster I and cluster V (130.83) and cluster II and cluster III (105.97).

This revealed that these clusters were genetically more divergent from each other and had the tendency of obtaining promising parents for crossing. The maximum quantity of heterosis is predicted from the crosses of parents belonging to the most divergent clusters (Katiyar and Singh, 1990). Parents from these groups might be used for selection for hybridization because the diversity gives a chance for isolating useful recombinants in the segregating generation.

The shortest inter-distance was found between cluster III and cluster IV (39.20) followed by cluster I and cluster II (46.76) and between cluster I and cluster IV(50.13). The genotypes in this cluster were closely related or there was little existence of genetic variability between the clusters. Thus, the crossing of genotypes from these clusters may not produce high heterotic

values in the (F1) and broad spectrum of variability in segregating (F2) populations. According to Hazra *et al*. (2019b) who showed that the hybrids of genotypes with maximum distance resulted in high yield, cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Therefore, more emphasis should be given to cluster II and cluster V for selecting germplasm as parents for crossing with germplasm of cluster, which may produce new recombinant with desirable traits.

Cluster Mean Analysis

The cluster mean values revealed considerable differences among the clusters for different characters. The mean value of five clusters across 16 traits of 100 bread wheat genotypes was listed (Table 5). Thousand seed weight was maximum in cluster-I (42.02) followed by cluster-II (40.37) while it was minimum in genotypes included in cluster -V (33.89). Maximum awn length was recorded from genotypes grouped in cluster-I (9.09) and minimum awn length was recorded from genotypes grouped in cluster-V (0) which indicated it was awn less genotypes group. The highest biomass yield was measured from genotypes included in cluster-II (206.64) while the lowest biomass yield was measured from genotypes grouped in cluster-V (36.25).

The maximum leaf length was obtained from genotypes grouped in cluster-II (30.17) followed by cluster-IV (29.86) while minimum in cluster III- (24.26). Genotypes of cluster-II (5.78) had the highest number of productive tillers followed by cluster –I (5.22) while it was lowest in cluster-V (2.1). Cluster-II consists of the tallest accessions with a mean plant height of (113.58 cm), while the shortest plant height was measured from genotypes grouped in cluster–III (83.41 cm). Maximum grain yield was measured from genotypes grouped in cluster-II (44.21) followed by cluster–I (34.01) but lower yield was measured from genotypes grouped in cluster-V (6.86).

The highest grain yield and productive tillers were observed in cluster-II and selection for these traits will be very effective from cluster-II. The highest mean performances of the number of kernels per spike were recorded for cluster –III (60.84) followed by cluster–II (55.76) while the smallest numbers of kernels per spike were obtained in cluster–V (46.05).

The highest cluster means for days to heading (80.82 days) were observed in cluster –III while the lowest cluster means for days to heading where clustered in cluster–IV (76.17 days) that were thought to be the first heading accessions found in this cluster. Cluster–III (49 days) also exhibited the highest grain filling period against the lowest of cluster–V (42.5 days). The Early maturing accessions were represented in cluster–V (117.5 days) and selection for early maturity can be made more effectively from cluster–V whereas late maturing with mean days to maturity of 124.94 days was found in cluster–II. Maximum peduncle length was also recorded from genotypes grouped in cluster-V (56.28) while minimum peduncle length was recorded from genotypes grouped in cluster-III (36.06).

In general, Cluster-I exhibited highest values of thousand seed weight (42.02 g/plot) and awn length (9.09 cm) while intermediate for rest characters. Cluster II was characterized by longest value of days to maturity, highest plant height, highest spike length, large number of spikelet per spike, highest grain yield, highest biomass yield, highest productive tillers and flag leaf length having intermediate values for rest traits. Cluster III had longest grain filling period, longest days to heading, highest kernels per spike and large number of spikelet per spike followed by cluster - II whereas these cluster exhibited shortest plant height, lowest harvest index, shortest flag leaf length and peduncle length while it was medium for other characters.

This indicates that accessions present in cluster-III and II may be used as parents in hybridization programs for developing high-yielding wheat varieties. Cluster-IV was characterized by highest value of harvest index whereas lowest value of days to heading being intermediate values for rest characters. Cluster-V was characterized by having highest peduncle length and flag leaf width whereas lowest for days to maturity, grain filling period, spike length, spikelet per spike, kernel per spike, grain yield, biomass yield, thousand seed weight, productive tillers and awn length having intermediate values for the rest traits. This result implies that sufficient scope for genetic improvement through hybridization between the accessions from divergent clusters.

Principal Components Analysis (PCA)

The principal component analysis showed that only first five principal components showed Eigen values of more than one and cumulatively explained 76% of entire variability available

among accessions (Table 6). According to Chahal and Gosal, (2002) characters with largest absolute values nearer to unity at intervals primary principal element influences clustering more than those with lower absolute values nearer to zero.

From results of principal component analysis first two principal components PC1 and PC2 with values of 32.9% and 16% respectively, contributed more to total variation. The principal component analysis revealed that 32.9 % of total variation in genotype for traits was explained by PC1. The higher contribution of PC1 was loaded by plant height, flag leaf length, peduncle length, harvest index and days to heading. PC2 contributed 16% to variation of the accessions.

The 16% contribution of PC2 was due to high variation for kernels per spike, spikelet per spike, grain yield, thousand seed weight and biomass yield. PC3 accounted for 11.2% of the variation of the accessions. The 11.2% contribution of PC3 variation was chiefly attributed due to days to maturity, grain yield and awn length.

PC4 accounted for 8.6% of the total variation, which the variation was mainly due to productive tillers, biomass yield, grain yield and thousand seed weight. The last and fifth principal component analysis (PC5) accounted for 7.3 % of the total variation. In principal component (PC5) variation chiefly originated from harvest index and days to heading. Therefore, during this study, complete differentiation of the genotypes into different clusters was because of a cumulative effect of several characters instead of the contribution of a specific few characters. Similar works have been reported previously by (Girma, 2018; Devesh *et al*., 2019) for grouping of genotypes by principal component analysis.

Table 3. Distribution of 100 bread wheat genotypes in to five cluster groups

Clusters	Number of genotypes	%	Genotypes
I	51	51%	31169, 31600, 31224, 31430, 31551, 31554, 33387, 33794, 34190, 33909, 34045, 33907, 34053, 34097, 34137, 33917, 33911, 36255, 36503, 34720, 31395, 31593, 31627, 31630, 31632, 33921, 34190, 34821, 31643, 33597, 34043, 34073, 34086, 34728, 34804, 34169, 34856, 31542, 33389, Enkoy, EBW192344, EBW192345, King bird, Kubsa, EBW192875, EBW194030, EBW192489, EBW192398, Danda,a, EBW192870, Wane
II	16	16%	31257, 31786, 33828, 34037, 34039, 34735, 31813, 31818, 33893, 34157, Alidoro, 33682, 34737, 34159, EBW192299, 31790
III	14	14%	31258, 31543, 34280, EBW192398, EBW192348, EBW192362, EBW192364, EBW192610, EBW19286, Hidase, BWKU13383, BW184033, EBW192872, Digelu
IV	18	18%	31296, 33556, 33516, 33924, 33972, 34145, 31394, 31644, 3390, 33919, 34098, 34152, 33206, 34029, 34161, 33915, 34706, Ogolcho
V	1	1%	34667

Table 4. Euclidean distance between clusters based on 16 phenotypic traits in bread wheat

Clusters	I	II	III	IV	V
I	**27.96**	46.76	61.30	50.13	130.83
II		**25.97**	105.97	95.40	176.39
III			**26.84**	39.20	85.80
IV				**21.63**	81.92
V					**0.00**

Table 5. Mean values of five clusters for 16 traits in 100 bread wheat genotypes

Traits Clusters	I	II	III	IV	V
DH	77.49	77.12	80.82	76.17	80.50
DM	123.16	124.94	120.21	121.25	117.50
GFP	44.19	44.84	49.00	44.22	42.50
PH	106.03	113.58	83.41	110.04	103.15
SL	9.83	10.48	8.98	9.23	5.55
SPS	18.43	19.25	18.58	17.76	16.60
KPS	54.49	55.76	60.84	46.96	46.05
BY	161.86	206.64	108.75	114.31	36.25
HI	22.11	22.75	18.39	23.31	19.82
TSW	42.02	40.37	40.09	39.09	33.89
PT	5.22	5.78	3.80	4.74	2.10
FLL	29.27	30.17	24.26	29.86	27.05
FLW	1.48	1.55	1.25	1.51	1.75
AL	9.09	8.75	5.59	8.28	0.0
PEL	49.50	51.97	36.06	53.28	56.28
GY	34.01	44.21	29.51	23.21	6.86

Key: DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height SL= spike length, SPS= spikelet per spike, KPS= kernel per spike, BY= biomass yield, HI = harvest index,TSW= thousand seed weight, PT= productive tillers, FLL= flag leaf length, FLW= flag leaf width, AL= awn length, PEL= peduncle length, GY= grain yield

Table 6. Principal component analysis of 16 quantitative traits in 100 bread wheat genotypes

Traits	PC1	PC2	PC3	PC4	PC5
DH	-0.25	0.009	-0.099	-0.076	-0.618
DM	0.217	0.205	0.437	0.012	-0.18
GFP	-0.236	0.047	0.022	0.062	-0.064
PH	0.357	-0.042	-0.098	-0.057	-0.077
SL	0.194	0.292	0.231	0.213	-0.009
SPS	0.09	0.35	0.240	-0.21	-0.066
KPS	-0.174	0.382	-0.143	-0.035	0.244
BY	0.158	0.305	-0.161	0.426	-0.181
HI	0.275	-0.02	0.063	0.078	0.57
TSW	0.063	0.315	-0.159	-0.395	-0.047
PT	0.20	-0.029	-0.168	0.494	-0.039
FLL	0.345	0.004	0.004	-0.071	-0.153
FLW	0.238	0.006	-0.121	-0.224	-0.209
AL	0.208	0.086	-0.306	-0.105	0.119
PEL	0.327	-0.133	-0.252	-0.13	-0.085
GY	-0.044	0.336	-0.36	0.357	-0.107
Eigen value	6.24	3.04	2.13	1.64	1.38
Proportion	32.9 %	16%	11.2%	8.6%	7.3%
Cumulative	32.9%	48.9%	60.1%	68.7%	76%

Key:DH= days to heading, DM= days to maturity, GFP= grain filling period, PH= plant height, SL= spike length,SPS= spikelet per spike, KPS= kernel per spike, BY= biomass yield, HI= harvest index, TSW= thousand seed weight, PT= productive tiller, FLL= flag leaf length, FLW= flag leaf width, AL= awn length, PEL= peduncle length, GY= grain yield

Conclusions

In this research, a total of 100 bread wheat genotypes were evaluated for their diversity during the main cropping season of 2022 in West Shewa, central Ethiopia. The experiments were laid out using an alpha lattice design with two replications. A total of 100 bread wheat genotypes were grouped into five clusters. Among these cluster I was the largest cluster which consisted of 51 bread wheat genotypes (51%), followed by cluster IV(18%). The maximum inter-cluster distance was observed between clusters II and V (176.39). Thus, the genotypes belonging to the distant clusters could be used for breeding programs to obtain a wider

range of variability. Selection of parents from such clusters for hybridization programs would be helpful to achieve novel recombinant. The principal component analysis revealed that the first five PCs with Eigen values greater than one accounted for 76% of the total genotypic variation among the 100 bread wheat genotypes.

Genotypes that showed high genetic divergence from different clusters may be used as sourc of good characters for future bread wheat breeding programs. Based on the current results, genotypes namely; 31790 (58.93 qt/ha), EBW192299 (57.97 qt/ha), 33682 (56.51 qt/ha), 34737 (55.38 qt/ha) and 34159 (52.51 qt/ha) were identified as high yielders genotypes compared to other tested genotypes. However, it is important to emphasize that the results and conclusions made are based on the data obtained from one-year field evaluation at a single location. Therefore, evaluation of these genotypes in three to four replications across at least six locations would be necessary to get comprehensive results.

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