



Diversity Analysis of Bread Wheat (*Triticum aestivum* L.) Genotypes Based on Yield and Yield Related Traits

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Abstract

The research was conducted during July–November in 2023 at Kulumsa Agricultural Research Center on 50 bread wheat genotypes to assess traits contributing to phenotypic variation, cluster genotypes into divergent groups, estimate genetic distances between clusters. The analysis of variance revealed significant genetic variability ($p < 0.01$) for all studied traits. The mean performance of the genotypes showed a wide range of values for traits. For instance, days to heading ranged from 62 to 74.5 days, and days to maturity ranged 112.5 to 122 days. Thousand kernel weight varied from 26 g to 40 g, with a promising aspect was that 34 genotypes exhibited superior thousand kernel weight compared to the check variety Boru. Hectoliter weight ranged from 65.73 to 73.15 hl kg⁻¹, and a positive sign was that 46 genotypes displayed superior hectoliter weight values than Boru. Grain yield ranged from 753.5 to 1751 kg ha⁻¹, all genotypes exhibited superior grain yield except 10 genotypes compared to Boru. Cluster analysis grouped the genotypes into four distinct clusters, indicating diversity within the wheat population. The inter cluster distance analysis revealed significant genetic differences between clusters, with the greatest genetic distance observed between Cluster I and Cluster IV. Crossing between genotypes from these clusters could lead to beneficial recombinants with improved traits. The first three principal components accounted 73.03% of the total observed phenotype variation with the major contributor of grain yield, thousand kernel weight, agronomic score and hectolitre weight. Generally, the findings underlined the potential for breeding high-yielding and disease-resistant wheat varieties.

Keywords: Bread wheat, diversity analysis, yield, yield related traits

1. Introduction

Wheat is a globally significant cereal crop, having been one of the first crops domesticated around 10,000 years ago (Feldmann, 2001). Today, global wheat production primarily relies on two modern species: common or hexaploid bread wheat (*Triticum aestivum* L., $2n=6x=42$, AABBDD) and durum or tetraploid wheat (*T. turgidum* subsp. durum, $2n=4x=28$, AABB) (Feldmann, 2001). Bread wheat (*Triticum aestivum* L.) belongs to the family Gramineae and is a monoecious plant with perfect flowers. It primarily reproduces sexually as an autogamous crop, although limited cross-pollination (approximately 3%) is possible (Mergoum et al., 2009).

In Ethiopia, wheat is one of the most important cereal crops, cultivated across a large portion of the country (Endale and Getaneh, 2015). Wheat production in Ethiopia for the

2021/22 season is projected to reach 5.18 mt, an increase of 1.6% over the estimated production for 2020/21. This growth is attributed to increased government involvement in irrigation, better input supply, and mechanized farming in the lowland and central regions of the country (Anonymus, 2021). However, wheat production and productivity in Ethiopia remain relatively low compared to global levels. This is primarily due to the fact that wheat is mostly grown by small-scale farmers using rain-fed systems with limited irrigation (Anteneh and Asrat, 2020). Production is further constrained by various infectious diseases, including rust and Septoria leaf blotch, which pose significant challenges to wheat cultivation in Ethiopia (Endale and Getaneh, 2015).

Genetic relationships among breeding materials can be identified and classified using multivariate grouping methods,



which categorize breeding materials into distinct and variable groups based on genotype performance (Aremu, 2012). Cluster analysis is a widely utilized and highly effective multivariate statistical method for grouping genotypes based on their characteristics. Among the various methods available for cluster analysis, Ward's method is particularly common and effective. Introduced by Ward (1963), essentially, it seeks to create clusters that are internally homogeneous, while simultaneously ensuring high heterogeneity between clusters (Karamanos et al., 1998). When plotted geometrically, individuals within a successful cluster analysis will appear closer together, while distinct clusters will be farther apart (Kumar and Kumar, 2005). A key aspect of cluster analysis is the concept of genetic distance, which refers to the degree of genetic difference between two entities. Genetic distance is often described by variations in alleles, which are different forms of a gene (Nei, 1973). The Mahalanobis generalized distance, introduced by Mahalanobis (1936), is a statistical measure that accounts for multiple variables simultaneously, providing a comprehensive measure of the distance between genotypes. This approach is particularly valuable for identifying genetically divergent genotypes, which can then be grouped based on their agronomic and morphological traits (Morishima and Oka, 1960). Understanding genetic distance is also critical in breeding programs, as it enables the selection of genetically diverse parents. These diverse parents are more likely to produce desirable recombinants, which are offspring that inherit favorable traits from both parents, in subsequent generations (Osiru et al., 2012).

In addition to cluster analysis, Principal Component Analysis (PCA) is another powerful tool used to study genetic diversity. PCA helps to identify the main contributors to variation within a dataset. By reducing the dimensionality of the data, PCA simplifies the complexity while retaining the maximum possible variation. Eigenvalues, which are derived from the PCA process, help determine the number of significant components or factors that should be retained (Jolliffe, 2002). Therefore, this research was conducted to identify traits that contributed significantly to total phenotypic variation, to cluster genotypes into genetically divergent groups, and to estimate the genetic distance between clusters of bread wheat genotypes.

2. Materials and Methods

2.1. Experimental site and year

The research was conducted during July–November in 2023 at Kulumsa Agricultural Research Center in 2023 main cropping season. The experimental site was located at 08°01'10"N longitude and 39°09'11"E latitude at an altitude of 2200 m above sea level. The mean annual rain fall of the site was 820 mm with an average annual temperature of 16.5°C.

2.2. Experimental materials and design

The experiment was laid out in an 8×5 simple lattice design

with two replications. Materials used for study were forty nine (49) bread wheat genotypes introduced from International Maize and Wheat Improvement Center (CIMMYT) and one (1) released variety (Boru) presented in Table 1.

2.3. Data collected

Data were collected characters such as days to heading, days to maturity, plant height, grain yield, hectoliter weight, thousand kernels weight, agronomic score, Yellow and stem rust severity.

3. Results and Discussion

3.1. Analysis of variance (ANOVA)

Analysis of variance (ANOVA) revealed significant genetic variation ($p < 0.01$) among the 50 wheat genotypes for all nine studied characters (Table 2). These characters included days to 50% heading, days to 90% maturity, Plant height, thousand kernel weight, grain yield, hectoliter weight, agronomic score, yellow rust severity, and stem rust severity. This finding aligned with previous research by Wani et al. (2018) and Zewdu et al., (2024b) who also reported significant genetic variability among wheat genotypes for days to heading, maturity, plant height, thousand kernel weight, and grain yield.

3.2. Mean performance of studied bread wheat genotypes

This section details the variation observed among 50 wheat genotypes for several key traits (Table 3).

3.2.1. Days to 50% Heading

This ranged from 62 to 74.5 days, with an average of 66.62 days. 17 genotypes head earlier and 32 genotypes heading later than the check variety Boru (66 days). 22 genotypes head earlier than the mean and 32 genotypes heading later than the mean (66.62 days).

3.2.2. Days to 90% maturity

This ranged from 112.5 to 12 days, with an average of 115.5 days. Here, a higher proportion (92%) of genotypes matured later than the check variety Boru. The only 3 genotypes had equal days to maturity with check variety Boru (112.5 days).

3.2.3. Thousand kernel weight

This ranged widely, from 26 g to 40 g, with an average of 32.62 g. Nearly half (54%) of the genotypes had lower than average kernel weight, while the remaining genotypes (46%) had higher values. Notably, only 8 genotypes had lower thousand kernel weight than the check variety Boru (30 g), while 7 genotypes matched the check Boru (30 g). However, a promising aspect was that 34 genotypes exhibited superior thousand kernel weight compared to Boru.

3.2.4. Hectoliter weight

This ranged from 65.73 to 73.15 hl kg⁻¹, with an average of 70.30 hl kg⁻¹. Here, 44% of the genotypes had lower than average hectoliter weight, while 56% had higher values. Compared to the check variety Boru (68.79 hl kg⁻¹), the only



Table 1: Materials used for study and pedigree

Entry	Genotype	Pedigree
1	Boru	Boru
2	EBW233032	Kakuru #1
3	EBW233033	Bonsu
4	EBW233034	Becard//Nd643/2*Wbll1*2/3/Borl14
5	EBW233035	Borl14*2/Blanca Grande 515
6	EBW233038	Kachu*2/3/Nd643//2*Prl/2*Pastor*2/4/Prl/2*Pastor*2//Vorb
7	EBW233043	Francolin #1/3/Pbw343*2/Kukuna*2//Yanac/4/Kingbird #1//Inqalab 91*2/Tukuru*2/5/Prl/2*Pastor*2//Vorb
8	EBW233045	Saua/Mutus/4/Kachu #1//Wbll1*2/Kukuna/3/Brbt1*2/Kiritati/5/2*Kachu/Saua*2//Copio
9	EBW233047	Kasuko/Nadi#2//Kasuko
10	EBW233048	Kasuko*2/5/Mutus/Danphe #1/4/C80.1/3*Batavia//2*Wbll1/3/C80.1/3*Qt4522//2*Pastor
11	EBW233050	Kasuko/4/Ciro16*2/3/Muu #1/Saua//Muu/5/Kasuko
12	EBW233052	Chipak/4/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
13	EBW233053	Kachu//Kiritati/2*Trch/3/Kasuko
14	EBW233054	Kachu//Kiritati/2*Trch/3/Kasuko
15	EBW233057	Kachu*2/3/Nd643//2*Prl/2*Pastor/4/Kasuko
16	EBW233059	Prl/2*Pastor//Kachu/3/Kasuko
17	EBW233061	Sup152/Ciro16//Kasuko
18	EBW233065	Becard/Akuri*2/3/Pbw343*2/Kukuna*2//Frtl/Pifed/4/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
19	EBW233067	Up2338*2/Shama/3/Milan/Kauz//Chil/Chum18/4/Up2338*2/Shama/5/Up2338*2/Vivitsi/3/Fret2/Tukuru//Fret2/4/Misr 1/6/Kasuko
20	EBW233068	Kachu/Kiritati//Borl14/3/Kasuko
21	EBW233070	Tc870344/Gui//Temporalera M87/Agr/3/2 *Wbll1/8/ Bow/Vee/5/ Nd/Vg9144 //Kal/Bb/3 /Yaco/ 4/ Chil/6/Caskor/ 3/ Croc _1/Ae. Squarrosa (224)//Opata/7/Pastor//Milan/Kauz/3/Bav92/9/Kasuko
22	EBW233071	Kfa/2*Kachu/4/Wbll1*2/Kuruku//Kronstad F2004/3/Wbll1*2/Brambling/5/Kasuko
23	EBW233073	Kfa/2*Kachu/4/Wbll1*2/Kuruku//Kronstad F2004/3/Wbll1*2/Brambling/5/Kutz//Kfa/2*Kachu
24	EBW233074	Tacupeto F2001/Brambling//Kiritati/3/Francolin #1/Blouk #1/4/Francolin #1/Blouk #1/5/Shortened Sr26 Translocation //2*Wbll1*2/Kkts/3/Becard
25	EBW233075	Tacupetof2001/6/Cndo/R143//Ente/Mexi_2/3/Aegilopssquarrosa(Taus)/4/Weaver/5/Pastor/7/Rolf07*2 /8/ Saua /Yanac//Saua/9/ Kasuko
26	EBW233077	Tacupeto F2001/6/Cndo/R143//Ente/Mexi_2/3/AegilopsSquarrosa (Taus)/4/ Weaver/5/ Pastor/7/Rolf07 *2/8/Saua/ Yanac//Saua/9/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
27	EBW233078	Tacupetof2001/6/Cndo/R143//Ente/Mexi_2/3/AegilopsSquarrosa (Taus)/4/Weaver/5/ Pastor/7/Rolf07*2/8/ Saua/ Yanac//Saua/9/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
28	EBW233079	Tacupetof2001/6/Cndo/R143//Ente/Mexi_2/3/AegilopsSquarrosa (Taus)/4/Weaver/5/ Pastor/7/Rolf07*2 /8/Saua /Yanac//Saua/9/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
29	EBW233085	Kasuko/Mokue #1
30	EBW233086	Nd643//2*Attila*2/Pastor/3/Wbll1*2/Kuruku/4/Wbll1*2/Brambling/6/Babax/Lr42//Babax*2/3/Kukuna/4/ Crosbill #1/5/Becard/7/Kasuko
31	EBW233087	Nd643//2*Attila*2/Pastor/3/Wbll1*2/Kuruku/4/Wbll1*2/Brambling/6/Babax/Lr42//Babax*2/3/Kukuna/4/ Crosbill #1/5/Becard/7/Kasuko

Table 1: Continue...



Entry	Genotype	Pedigree
32	EBW233089	Wbll1*2/Brambling//Juchi/3/Kingbird #1//Inqalab 91*2/Tukuru/4/Wbll1*2/Brambling//Kachu/5/Kasuko
33	EBW233090	Francolin #1//Wbll1*2/Kuruku/3/Wbll1*2/Brambling//Chyak/4/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
34	EBW233091	Francolin #1//Wbll1*2/Kuruku/3/Wbll1*2/Brambling//Chyak/4/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
35	EBW233096	Borl14*2/Fitis//Kasuko
36	EBW233098	Grack/Chyak/6/Rolf07*2/5/Fct/3/Gov/Az//Mus/4/Dove/Buc/7/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
37	EBW233104	Munal/Westonia//Sup152/Baj #1/4/Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
38	EBW233107	Mutus//Wbll1*2/Brambling/3/Wbll1*2/Brambling*2/4/Kachu/Kiritati/5/Kutz//Kfa/2*Kachu
39	EBW233116	Mutus//Nd643/2*Wbll1*2/3/Onix/Kbird*2//Kfa/2*Kachu
40	EBW233118	Francolin #1/3/Pbw343*2/Kukuna*2//Yanac/4/Kingbird #1//Inqalab 91*2/Tukuru/5/2* Sup152//Wbll1*2/ Brambling*2/3 /Ksw/Saua//Saua
41	EBW233122	Kauz//Altar84/Aos/3/Milan/Kauz/4/Saua/5/Trch/Srtu//Kachu/6/Kachu/Saua/7/2*Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
42	EBW233123	Saua/Mutus//Kingbird #1/3/Saua/Mutus/4/2*Kasuko
43	EBW233125	C80.1/3*Batavia//2*Wbll1/5/Reh/Hare//2*Bcn/3/Croc_1/Ae.Squarrosa (213)//Pgo/4/Huites/6/Pbw343*2/Kukuna*2//Frtl/Pifed/7/C80.1/3*Batavia//2*Wbll1/5/Reh/Hare//2*Bcn/3/Croc_ 1/Ae.Squarrosa (213)//Pgo/4/Huites/8/2*Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//S
44	EBW233128	Tacupetof2001/6/Cndo/R143//Ente/Mexi_2/3/AegilopsSquarrosa (Taus)/4/Weaver/5 /Pastor/7/Rolf07*2/ 8/Saua/Yanac//Saua*2/9/Kasuko
45	EBW233130	Kasuko*2/Mokue #1
46	EBW233132	Kasuko*2/3/Sup152/Quaiu #2//Becard/Quaiu #1
47	EBW233133	Tacupetof2001/Brambling//Kachu/8/Reh/Hare//2*Bcn/3/Croc_1/Ae.Squarrosa(213)//Pgo/4/Huites/5/T.Dicocconpi94 624/Ae.Squarrosa(409)//Bcn/6/Reh/Hare//2*Bcn/3/Croc_1/Ae.Squarrosa(213)//Pgo/4/Huites/7/Mutus*2/9/Borl14*2 //Kfa/2*Kachu
48	EBW233137	Kutz//Kfa/2*Kachu/4/2*Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua
49	EBW233139	Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua/4/Borl14*2//Kfa/2*Kachu/5/Borl14*2//Kfa/2*Kachu
50	EBW233140	Sup152//Wbll1*2/Brambling*2/3/Ksw/Saua//Saua*2/4/Prl/2*Pastor//Kachu

3 genotypes (6%) had lower hectoliter weight, but a positive sign was that 46 genotypes (92%) displayed superior values.

3.2.5. Agronomic score

This ranged from 1.5 to 2.75, with an average of 2.19. Compared to the check variety Boru, 28 genotypes had a higher agronomic score than the check and 7 genotypes had equal agronomic score with the check Boru (2). 14 genotypes had lower agronomic score than the check variety Boru.

3.2.6. Grain yield

This exhibited the widest range, varying from 2511.67 to 5836.67 kg ha⁻¹, with an average of 3971.97 kg ha⁻¹. Slight majority genotypes (54%) yielded less than the average, while the remaining genotypes (46%) produced more. The only ten genotypes yielded lower than the check variety Boru (2963.33 kg ha⁻¹), but all others exhibited superior grain yield

compared to Boru.

Generally, the study revealed substantial genetic diversity among the wheat genotypes for all measured traits. There's potential for breeding efforts to target earlier heading combined with faster maturity, improved kernel weight, and even higher grain yield. Many genotypes displayed superior performance compared to the check variety Boru, highlighting the potential for breeding advancements. These findings were consistent with previous research by Zewdu et al. (2024b) who also reported significant variations in grain yield and related traits among bread wheat genotypes.

3.3. Cluster analysis

Cluster analysis was conducted following the agglomerative hierarchical clustering ward's method, in order to categorize genotypes into different homogeneous groups (Ward, 1963).



Table 2: Mean squares, coefficient of variation and R- square for 9 traits of 50 bread wheat genotypes evaluated at Kulumsa Agricultural Research center in 2023

Traits	Replication (DF=1)	Block (Replication) (DF=8)	Genotype MS (DF=49)	Error MS (DF=41)	CV (%)	R ²
DTH	1.00	1.01	21.30**	1.58	1.89	0.94
DTM	0.40	1.43	10.55**	1.23	1.23	0.91
PHT	9.61	52.17	64.00**	19.48	5.76	0.82
YrS	13.69	65.03	599.56**	42.38	31.43	0.95
TKW	17.64	7.94	32.15**	10.66	10.01	0.79
HLW	6.61	3.59	9.53**	2.50	2.25	0.83
AgrSc	0.72	0.14	0.49**	0.16	18.22	0.80
SrS	31.36	25.55	153.26**	16.27	32.97	0.92
GYLD	1093418.78	1104466.97	1794907.19**	454497.4	16.97	0.84

Note: * and ** indicates significant at ($p=0.05$) and highly significant at ($p=0.01$) probability levels respectively. DTH: days to heading; DTM: days to Maturity; PHT; plant height; AgrSc: agronomic score; TKW: thousand kernel weight; HLW; hectoliter weight; YrS: yellow rust severity; SrS: stem rust severity; GYLD; grain yield; MS: mean square; CV: coefficient of variations; DF: degree of freedom and R²: Coefficient of determination.

Table 3: Ranges, means and standard errors of the means for 7 quantitative traits among 50 bread wheat genotypes

Traits	Range	Mean	Standard error
DTH	62–74.5	66.62	0.96
DTM	112.5–122	115.50	0.85
PHT	65–85	76.61	3.36
AgrSc	1.5–2.75	2.19	0.30
TKW	26–40	32.62	2.49
HLW	65.73–73.15	70.30	1.20
GYLD	2511.67–5836.67	3971.97	513.43

DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; AgrSc: Agronomic score; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield

Cluster analysis classified the 50 bread wheat genotypes into four distinct clusters (Table 4). This indicated the presence of

diversity among the tested bread wheat genotypes. Cluster I and Cluster II had the largest clusters which consisted equal 17 genotypes (34% of the studied genotypes) of each cluster followed by cluster III and V contained 12 genotypes (24% of the studied genotypes) and 4 (8% of the studied genotypes) respectively.

Similarly clustering of wheat genotypes were studied by different researchers, Zemedet et al. (2019) reported that 64 wheat genotypes grouped into five distinct clusters with cluster-I contain 7 genotypes, cluster-II contain 4 genotypes, cluster-III contain 35 genotypes cluster-IV contain 8 genotypes and cluster-V contain 10 genotypes. Kumar et al. (2016) also reported the 55 wheat genotypes were grouped into eight clusters and 50 wheat genotypes were grouped into eight clusters (Poudel et al., 2017). 127 wheat genotypes clustered into four distinct groups (Mohi-Ud-Din et al., 2021) and 25 bread wheat genotypes clustered into four diverse groups (Adilova et al., 2020).

Table 4: Distribution of 50 bread wheat genotypes in to four different cluster groups

Cluster No	No of genotypes	Percentage (%)	Genotypes
I	17	34	Boru, EBW233035, EBW233038, EBW233048, EBW233050, EBW233053, EBW233054, EBW233068, EBW233070, EBW233085, EBW233086, EBW233087, EBW233107, EBW233116, EBW233130, EBW233137, EBW233140
II	17	34	EBW233032, EBW233033, EBW233045, EBW233061, EBW233065, EBW233067, EBW233077, EBW233078, EBW233079, EBW233091, EBW233098, EBW233118, EBW233122, EBW233125, EBW233132, EBW233133, EBW233139
III	12	24	EBW233034, EBW233043, EBW233047, EBW233052, EBW233057, EBW233071, EBW233073, EBW233075, EBW233089, EBW233090, EBW233123, EBW233128
IV	4	8	EBW233059, EBW233074, EBW233096, EBW233104



3.3.1. Analysis of inter and intra cluster distance

The analysis of intra- and inter-cluster distances revealed significant genetic variation among the wheat genotypes (table 5). All inter-cluster distances were found to be highly significant ($p < 0.01$) compared to the chi-square value ($\chi^2 = 21.67$), and these distances were greater than the intra-cluster distances (Table 5). Among the clusters, Cluster III exhibited the smallest intra-cluster distance ($D^2 = 50.93$), followed by Cluster II ($D^2 = 61.61$). The largest intra-cluster distance was observed in Cluster I ($D^2 = 74.45$), with Cluster IV showing the second largest ($D^2 = 63.21$).

Regarding inter-cluster distances, the greatest genetic distance

Table 5: Intra (diagonal) cluster distance and Inter (off diagonal) cluster distance of 50 bread wheat genotypes

Cluster	I	II	III	IV
I	74.45	232.85**	443.02**	710.46**
II		61.61	210.19**	477.65**
III			50.93	267.68**
IV				63.21

* and **: Indicated significant at ($p = 0.05$) = 16.92 and highly significant at ($p = 0.01$) = 21.67 probability levels respectively; ns = Non-significant

was recorded between Cluster I and Cluster IV ($D^2 = 710.46$), followed by Cluster II and Cluster IV ($D^2 = 477.65$). On the other hand, the smallest inter-cluster distance was found between Cluster II and Cluster III ($D^2 = 210.19$), followed closely by Cluster I and Cluster II ($D^2 = 232.85$).

This analysis underscored the importance of genetic distance in assessing diversity among genotypes. In genetic studies, the distance between clusters represented the degree of variation or similarity between groups of genotypes. Larger inter-cluster distances indicated a greater genetic difference between the clusters, which reflected wider genetic diversity among the genotypes they contain. When clusters exhibited large genetic distances from one another, it suggested that the genotypes in these clusters have accumulated a variety of genetic differences over time. This variation was valuable in plant breeding because it created opportunities for introducing new traits and increasing genetic variability in offspring. The wider the genetic diversity between genotypes, the greater the potential for producing novel, advantageous combinations of traits when these genotypes were crossed.

Consequently, the largest inter-cluster distances in this analysis point to clusters with highly diverse genotypes. Crosses between genotypes from these distant clusters were more likely to result in superior genetic recombinants, offspring that inherit beneficial traits from both parents, potentially leading to improved yield, disease resistance, or other desirable agronomic traits. This made these distant clusters ideal candidates for crossing in breeding programs aimed at enhancing genetic gain and achieving higher crop

performance.

In contrast, the smallest inter-cluster distances indicated lower genetic diversity between the clusters, with the genotypes being relatively similar. As a result, crossing genotypes from closely related clusters was less likely to produce genetically diverse recombinants and was generally not recommended (Allard, 1960).

Kumar et al., (2016) Reported the existence of genetic divergence among the fifty five wheat genotypes clustered into eight different clusters in which the maximum inter cluster distance was observed between cluster VI and cluster VIII followed by cluster VI and VI which exhibited high degree of genetic diversity. The minimum intra cluster distance was observed within cluster VI and cluster III followed by cluster I and VIII, which exhibited less genetic diversity and thus might be utilized under population improvement of wheat genotypes.

Thirty wheat genotypes clustered into seven clusters in which the maximum intra cluster distance observed in cluster III (162.58) followed by cluster II (102.15) and minimum in cluster IV–VII and maximum inter cluster distance found between cluster VI and VII ($D^2 = 1627.88$) followed by cluster V and cluster VII ($D^2 = 1270.68$) and between cluster IV and VI ($D^2 = 943.23$) and significant difference observed between all inter cluster distances (Kumar et al., 2013).

In general, Crossing between genotypes from this significant inter clusters distance would be enhancing the yield and chances of getting better recombinants in segregating generations might be utilized in hybridization in wheat breeding program (Adilova et al., 2020).

3.3.2. Cluster mean analysis

The mean values of four clusters for 9 different traits revealed considerable differences among the clusters of 50 bread wheat genotypes (Table 6). For most all quantitative traits genotypes grouped in cluster IV had the maximum cluster mean values except for plant height (second maximum for plant height), this indicated that genotypes in this cluster were the late heading and late maturing genotypes, and Genotypes grouped in this cluster (cluster IV) were the best resistance for both yellow and stem rust diseases. Genotypes grouped in cluster III characterized by the tallest in plant height (80 cm), had the second maximum value for days to maturity, agronomic score, thousand kernel weight, hectolitre weight, grain yield the second best resistance genotypes for yellow and stem rust.

Genotypes in cluster I were characterized by the early maturity genotypes (115.05 days to 90% to matured), the minimum cluster mean values for most traits viz. plant height, agronomic score, thousand kernel weight, hectolitre weight and grain yield ($1738.56 \text{ kg ha}^{-1}$) and genotypes in this cluster were the most susceptible for both yellow and stem rust. While genotypes in cluster II characterized by the second minimum cluster mean values for all characters except day to 50%



Table 6: the four clusters mean for 9 traits of 50 tested bread wheat genotypes

Class	DTH	DTM	PHT	YrS	SrS	AgrSc	TKW	HLW	GYLD
I	66.56	115.06	74.56	32.94	8.65	1.90	29.59	69.00	949.32
II	66.50	115.12	76.21	30.00	7.88	2.10	32.77	70.34	1182.12
III	66.29	115.92	80.00	30.00	6.92	2.52	35.25	71.42	1392.25
IV	68.38	117.75	76.88	16.25	2.50	2.75	37.00	72.29	1659.50

DTH: Days to heading; DTM: Days to Maturity; PHT: Plant height; AgrSc: Agronomic score; TKW: Thousand kernel weight; HLW; hectoliter weight; GYLD; grain yield

heading, and the second early maturing and the second most susceptible genotypes for both yellow and stem rust.

Adilova et al. (2020) reported the cluster analysis revealed the classification of 25 accessions into four diverse groups. The maximum average values for grain yield (742.2 kg ha⁻¹), biomass (1756.7 kg ha⁻¹), and grains per spike (45.3) were higher in cluster III compared to other clusters. Cluster IV exhibited the maximum thousand-kernel weight (46.6)

Zemedet et al. (2019) reported that 64 wheat genotypes grouped into five clusters in which the first cluster genotypes had highest in grain yield associated to high number of kernels and long spike. The second cluster genotypes produced relatively low grain yield and biomass yield. Ten genotypes were found in cluster V which had shortest in their height associated with low biomass yield and high harvest index.

Poudel et al. (2017) Studied 50 bread wheat genotypes clustered in to four groups in which cluster I genotypes having highest value of thousand kernel weight, plant height and grain yield, Cluster 2 had the highest value of days to heading and lowest yield in comparison to other clusters. This cluster had shown moderate value of plant height, number of grains spike⁻¹ and days to maturity. Cluster III showed moderate values for all traits and cluster IV genotypes had the highest number of grains spike⁻¹. Ali et al. (2008) The mean number of effective tillers plant⁻¹ (14.89), number of spikelets spike⁻¹ (22.20), spike length (11.49), number of grains spike⁻¹ (73.67) and yield plant⁻¹ (31.23) were highest in cluster I. The plant height (113.18) and 1000 grain weight (48.55) were maximum in cluster II.

Yadav et al. (2014) clustered 50 wheat genotypes in to eight clusters in which cluster IV (119.75) was characterized by highest mean performance for days to 50 heading (96.50 days), days to maturity (134.50 days), spike length (12.38) and lowest for plant height (81.00) followed by cluster I with cluster mean values highest for plant height (95.90), cluster VIII with highest cluster mean values for thousand kernel weight (56.58 g), while cluster VI had highest cluster mean values for grains spike⁻¹ (56.70) and remaining cluster VII, cluster II, cluster V and cluster III were characterised average mean values for all traits.

3.4. Principal component analysis

The results of principal component analysis for nine traits of

50 bread wheat genotypes were presented in Table 7 and figure 1: Scree plot. The first three principal components (PCs) accounted 73.03% of the total observed phenotype variation. Among the three principal components the first principal component (PC) contributed for 37.43% of the total variation with the eigenvalue of 3.37. This was due to the positive loading effect of all studied traits except days to heading, yellow rust and stem rust severity, mainly grain yield (0.50), thousand kernel weight (0.47), agronomic score (0.46) and hectolitre weight (0.41).

Table 7: Principal component analysis for ten traits of Three components of 50 bread wheat genotypes evaluated at Kulumsa Agricultural Research Center in 2023

Traits	PC1	PC2	PC3
DTH	-0.01	0.68	0.07
DTM	0.21	0.56	0.26
PHT	0.29	0.04	-0.09
YrS	-0.13	-0.13	0.68
SrS	-0.09	0.22	-0.65
AgrSc	0.46	0.16	0.13
TKW	0.47	-0.22	-0.13
HLW	0.41	-0.30	0.02
GYLD	0.50	0.06	-0.03
Eigenvalue	3.37	1.87	1.33
Proportion (%)	37.43	20.78	14.83
Cumulative (%)	37.43	58.21	73.03

The second principal component shared about 20.78% of the total variation with the eigenvalue of 1.87 and the major contributing characters were days to heading (0.68), days to maturity (0.56) and hectolitre weight (0.30). The third principal component had proportion variability of 14.83% from the total variation with the eigenvalue of 1.33. The main loading effect of yellow rust (-0.68), stem rust severity (-0.65) and days to maturity (0.26).

Wani et al. (2018) studied on twenty-four bread wheat genotypes for principal component analysis the first three principal components based on the Euclidean similarity matrix explained 76.67% of the total variation and had eigenvalue



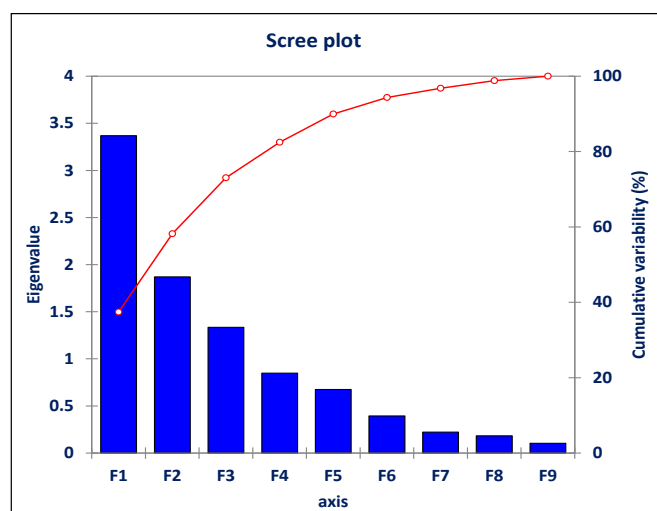


Figure 1: Scree plot for 9 traits of 50 bread wheat genotypes

greater than one (eigen value <1) which was PC1, PC2 and PC3 had eigenvalue of 12.32, 1.25 and 1.03 respectively. It was revealed that days to heading, biological yield, and grain yield contribute significantly to the quantum of variation as explained by principal component 1 (PCA1) and it was further observed that days to maturity, plant height and thousand grain weight were the main components of the PCA2.

Zewdu et al. (2024c) reported the first four Principal Components (PCs) accounted 76.76% of the total observed variation. Among the five principal components the first Principal Component (PC) contributed for 42.55% of the total variation, this was due to the positive loading effect of all studied traits mainly plant height (0.28), number of kernel spike⁻¹ (0.25), head weight (0.33), yield head⁻¹ (0.36), biomass yield (0.32), grain yield (0.35), hectolitre weight (0.34), thousand kernel weight (0.33) and harvest index (0.29). The second principal component shared about 14.69% of the total variation and the major positively contributing characters were days to heading (0.45), days to maturity (0.38), number of spikelet spike⁻¹ (0.31), number of kernel perspike (0.23), spike length (0.10) and head weight (0.09). Whereas, all the rest traits were observed negative loading effect, among these number of tillers plant⁻¹ (-0.37), number of effective tillers plant⁻¹ (-0.41), peduncle length (-0.36) and thousand kernel weight (-0.18) had highest negative loading effect in PC II. Kumar et al. (2016) study on principal component analysis the first six principal components showed Eigen values more than one and explained 81.75% variability. The first principal component explained 20.83% of the total variation and the second and third principal components explained 19.428% and 10.39% variation, respectively. And Zewdu et al. (2024c) had studied on Principal component analysis indicated that the first four Principal Components (PCs) accounted 76.76% of the total observed variation among sixteen traits of 64 bread wheat genotypes. Among the four principal components the first Principal Component (PC) contributed for 42.55% of the total variation, this was due to the positive loading effect of all studied traits mainly plant height (0.28), number of

kernel spike⁻¹ (0.25), head weight (0.33), yield head⁻¹ (0.36), biomass yield (0.32), grain yield (0.35), hectolitre weight (0.34), thousand kernel weight (0.33) and harvest index (0.29). The second principal component shared about 14.69% of the total variation and the major positively contributing characters were days to heading (0.45), days to maturity (0.38), number of spikelet spike⁻¹ (0.31), number of kernel spike⁻¹ (0.23), spike length (0.10) and head weight (0.09). Whereas, all the rest traits were observed negative loading effect, among these number of tillers plant⁻¹ (-0.37), number of effective tillers plant⁻¹ (-0.41), peduncle length (-0.36) and thousand kernel weight (-0.18) had highest negative loading effect in PC II.

The third principal component had proportion variability of 10.98% from the total variation. The main positive loading effect of days to heading (0.32), days to maturity (0.25), plant height (0.15), number of tillers plant⁻¹ (0.55), number of effective tillers plant⁻¹ (0.50), number of spikelet spike⁻¹ (0.34) and spike length (0.25), while the rest traits had negative loading effect to PCIII. The fourth principal component accounted for 8.55% from the total variation. variation was chiefly attributed due to number of spikelet spike⁻¹ (0.44), number of kernel spike⁻¹ (0.11), spike length (0.61) and peduncle length (0.29) and days to maturity (-0.37) followed by days to heading (-0.28) had highest negative loading effect for PC IV.

4. Conclusion

The analysis revealed significant genetic variability ($p < 0.01$) across all traits, particularly in grain yield (2511.67–5836.67 kg ha⁻¹). Cluster analysis categorized genotypes into four groups, with the maximum genetic distance found between Clusters I and IV. Principal component analysis showed that the first three PCs explained 73.03% of total phenotypic variation. Substantial diversity exists for improving maturity, kernel weight, and yield, with several genotypes outperforming the check variety Boru, suggesting strong potential for future wheat breeding advancements.

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