

# Genetic Variability, Principal Component and Cluster Analysis of Bread Wheat (*Triticum aestivum* L.) Genotypes in Enda Mehoni District, Northern Ethiopia

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**Abstract:** The experiment was laid out in 6x6 lattice design with three replications to evaluate 36 bread wheat genotypes. The objectives were to determine the extent of variability, heritability and genetic advance of traits and to assess the variability of bread wheat via multi variate analysis. Analysis of variance revealed highly significant differences ( $\leq 0.01$ ) among genotypes for all the traits considered, indicating the presence of adequate variability among the genotypes. In this study, the values for phenotypic coefficients of variance ranged from 4.49 % for days to heading to 16.19 % for grain yield while genotypic coefficients of variance ranged from 3.29 % days to heading to 14.52 % for grain yield. Phenotypic and genotypic coefficients of variance had moderate values for grain yield (16.19, 14.52) and grain filling period (12.59, 11.52) respectively. Heritability was high for most of the traits studied except days to heading (54%) and plant height (67%), which had moderate heritability values. High heritability values coupled with high genetic advance were recorded for grain yield and grain filling period which indicated that additive gene action plays a key role in controlling the expression and existence of high expected genetic gain through selection. Two principal components with eigenvalues greater than unity explained 68% of the total variation. Quantitative traits based cluster analysis classified the genotypes in to five distinct clusters. In general, existence of adequate genetic variation was revealed which can be used in bread wheat improvement.

**Keywords:** Cluster Analysis, Coefficients of Variances. Genetic Advance, Heritability, Principal Component Analysis.

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## 1. INTRODUCTION

Bread Wheat (*Triticum aestivum*,  $2n = 6x = 42$ , AABBDD), belongs to the family Poaceae, is one of the most important staple food amongst major cereals of the world. Globally, wheat (*Triticum* spp.) is grown in about 220.83 million hectares holding the position of highest acreage among all crops with annual production around 769.31 million tones (USDA, 2019). In Ethiopia, it is one of the most important food security crops cultivated in a wide range of agro-ecology, currently covering more than 90% of the total wheat production area (Hodson *et al.*, 2020). The demand for wheat in Ethiopia has been increasing over the years because of rapid population growth and urbanization. In Ethiopia, wheat is used for making Bread, Porridge, "Tela", "kolo" and "nifro". Despite the significant dietary and ecological importance, its productivity is far below its potential ( $7\text{ton ha}^{-1}$ ) and the world's average  $3.53\text{ ton ha}^{-1}$  (USDA, 2021), which is  $3\text{ ton ha}^{-1}$  during 2020/21 cropping season (CSA, 2021). Diseases (rusts, septoria, fusarium, etc.), soil acidity, declining soil fertility, terminal moisture stress, heat, mono-cropping, unavailability of improved varieties and climate change were often cited as the major reason for this gap (Wuletaw *et al.*, 2022).

The existence of genetic variability in a gene pool is the pre-requisite of a breeding programme. For genetic manipulation of grain yield in wheat, there is a need to examine the nature of genetic variability for the yield related traits. Various studies reported the existence of variability, heritability and genetic advance in bread wheat varieties (Almaz *et al.*, 2022 and Garome *et al.*, 2022). Besides, cluster and principal component analysis have also revealed the existence of variation in bread wheat (Urgaya *et al.*, 2022). The wheat breeding program in Ethiopia, like many other breeding programs in the developing world acquired bread wheat genotypes mainly from the IARCs (CIMMYT and ICARDA) and released varieties. More than 90 bread wheat varieties were released to-date by research centers and universities. However, only few of the varieties have been grown widely. Therefore, concise information on genetic variability helps to select parents for evolving superior varieties. Thus, the study was aimed with the objectives to determine the extent of variability, heritability and genetic advance of traits and to assess the variability of bread wheat via principal component and cluster analysis

## 2. MATERIALS AND METHODS

### Experimental Site, Plant Materials and Experimental Design

The study was conducted at southern Tigray National Regional State at Mekan Farmers' Training Center (FTC), which is 660 km from Addis Ababa, Ethiopia during 2015. The testing site is located at 12°44'N latitude and 39° 32' E longitude with an altitude of 2423 m.a.s.l. The area receives annual mean rainfall of 485 mm. The soil type in the testing field is Vertisols. The plant materials used in this study comprised of 36 released bread wheat genotypes were obtained from Kulumsa Agricultural Research Center (Table 1). The experiment was laid out in 6x6 lattice design with three replications and each experimental plot had six rows of 2.5 m long spaced 20 cm apart with a plot area of 1.2 m x 2.5 m (3 m<sup>2</sup>). The seed rate was maintained at 150 Kg ha<sup>-1</sup>. The fertilizer was applied at a rate of 100 kg ha<sup>-1</sup> DAP and 100 kg ha<sup>-1</sup> of Urea. Urea was applied twice at planting and tillering time.

**Table 1: List of 36 bread wheat genotypes**

No	Genotypes	No	Genotypes	No	Genotypes
1	ETBW 5879	13	Mekelle-2	25	King Bird
2	ETBW 6095	14	Ga'ambo	26	Hawi
3	WORRAKATTA/PASTOR	15	Kakaba	27	tusie
4	UTQUE96/3/PYN/BAU//MILLAN	16	Danda'a	28	ET-13A2
5	Hidasse	17	Gassay	29	K6295-4A
6	Ogolcho	18	Alidoro	30	Senkegna
7	Hoggana	19	Digelu	31	Menze
8	Hulluka	20	Tay	32	Bolo
9	Mekelle-3	21	Sofumar	33	Dinknesh
10	Mekelle-4	22	Mada-Wolabu	34	Tossa
11	Shorima	23	Pavon-76	35	Kulukulu
12	Mekelle-1	24	Geferson	36	ETBW 6848

### Data Collected

Data were collected from the middle four central rows in each plot on plant and plot basis. Data were collected on Days to heading (DH), Days to maturity (MD), Grain filling period (GFP), Grain yield (YLD) at 12.5% moisture and Thousand-kernel weight (TKW) on plot basis, whereas Plant height (PH) were collected from 10 randomly selected plants.

### Data Analyses

Data of the 36 bread wheat genotypes were subjected to Analysis of variance using Proc lattice and Proc GLM procedures of SAS 9.2 software. The expected mean squares from the analysis of variance were used to estimate the phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability (H<sup>2</sup>) and genetic advance (GAM) using Micro Soft Excel 2010 program. Principal Component Analysis (PCA) and Cluster Analysis were carried out using proc princomp and Proc cluster procedure of SAS 9.2 software respectively. Appropriate numbers of clusters were determined from the values of pseudo F and pseudo T<sup>2</sup> statistics

### 3. RESULTS AND DISCUSSION

The analysis of variance (Table 2) showed highly significant ( $p \leq 0.01$ ) differences among the genotypes of the traits considered. Indicating the existence of variability in the genotypes, which can be exploited through selection for further breeding programs. Similar results were reported by several authors for those traits (Destaw *et al.*, 2020; Garome *et al.*, 2022 and Almaz *et al.*, 2022).

#### Variations, Coefficient of Variations, Heritability and Genetic Advance

The estimates of variances, heritability and genetic advance are presented in Table 2. Significant range of variation was observed among the genotypes indicating enough scope for bringing about improvement in the desire direction. Grain yield ranged from (1.96–4.75 ton ha<sup>-1</sup>) with the mean value 3.42 ton ha<sup>-1</sup>. Days to heading and days to maturity ranged from 60-69 and 105-130 days respectively with a mean of 68 for days to heading and 117 for days to maturity. Grain filling period ranged from 36-65 days with a mean of 49 days. For plant height the minimum and maximum values were 57 cm and 96 cm with an average value of 80 cm. The other key yield component, thousand-kernel weight ranged from 32g–55g with an average value of 43 g. Similar results were reported by Almaz *et al.* (2022) and Garome *et al.* (2022) for those traits. Such variations are very essential to develop varieties fitting to various agro-ecologies and cropping systems.

The GCV and PCV were categorized as low (0-10%), moderate (10-20%) and high (> 20%) (Burton and devane 1953) In this study, the values for PCV ranged from 4.49 % for days to heading to 16.19 % for grain yield while GCV ranged from 3.29 % days to heading to 14.52 % for grain yield. PCV and GCV had moderate values for grain yield (16.19, 14.52) and grain filling period (12.59, 11.52) respectively. The result obtained was in agreement with the findings of Jagdish *et al.* (20220) and Almaz *et al.* (2022) for grain yield, indicating that the effectiveness of selection based on the phenotypic performance of grain yield. Thousand -kernel weights had moderate PCV (11.07) and low GCV (9.9). .PCV and GCV had low values for days to heading (4.49, 3.29), days to maturity (4.97, 4.74) and plant height (9.21, 7.53) respectively. This indicates the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these traits through direct selection for better performing genotypes.

Heritability and genetic advance are important factors determining the success of selection in breeding programs. Singh (2001) classified heritability values as high (>80%), moderate (40-80%) and low (<40%). In view of that, heritability was high for most of the traits studied except days to heading (54%) and plant height (67%), which had moderate heritability values. High heritability values were observed for days to maturity (91%) followed by grain filling period (84%), grain yield (80%) and thousand-kernel weights (80%).The results were in agreement with the findings of Kabir *et al.* (2017) for thousand-kernel weight and grain yield and Garome *et al.* (2022) for days to maturity, grain filling period, grain yield and thousand-kernel weights. Such high heritability indicates high proportion of genetic variance that could be inherited. and would be exploited by breeders to select superior genotypes based on phenotypic performance.

It has been emphasized that without genetic advance, the heritability values would not be of practical importance in selection based on phenotypic appearance. So, genetic advance should be considered along with heritability in coherent selection breeding program. Genetic advance as percent of mean (GAM) was categorized as low (0-10%), moderate (10-20%) and high >20% (Johnson *et al.*, 1955). Among the traits higher values of genetic advance as percent of means were observed for grain yield (26.68 %) and grain filling period (21.76%). High heritability values coupled with high genetic advance were recorded for grain yield and grain filling period, which indicated the additive nature of genetic variation was transmitted from the parents to the progeny.

**Table 2: Variations, heritability, coefficient of variations and genetic advance of 36 bread wheat genotypes**

Traits	MST	Range (ton h <sup>-1</sup> )	Mean	GCV (%)	PCV (%)	H <sup>2</sup> (%)	GAM
YLD	0.80**	1.96-4.75	3.42	14.52	16.19	80%	26.68
DH	19.35 **	60-69	68	3.29	4.49	54 %	4.99
DM	95.34 **	105-130	117	4.74	4.97	0.91	9.34
GFP	101.85 **	36-65	49	11.52	12.59	0.84	21.76
PH	126.94 **	57-96	80	7.53	9.21	0.67	12.70
TKW	58.83 **	32-55	43	9.89	11.07	0.80	18.23

\*\*=Significant 1%, MST=Mean square of Treatment, GCV=genotypic coefficient of variance, PCV=phenotypic coefficient of variance, H<sup>2</sup>=heritability GAM=genetic advance as % of mean, YLD= Grain yield, DH =Days to heading, DM =Days to maturity, GFP= Grain-filling period, PH =Plant height and Thousand-kernel weight

**Principal Components (PCs)**

Principal components analysis (PCA) represents the largest contributor to the total variation at each axis of differentiation. The first principal component accounts for as much of the variability and each succeeding component accounts for as much of the remaining variability. According to Kaisers criterion (Kaiser, 1960; Zalewski *et al.*, 2015), only those principal components (PCs) that showed the eigenvalue >1 were taken into account. Two PCs with eigenvalues greater than unity explained 68% of the total variation (Table 3). PC1 explained the most variation (42%) and PC2 accounted 26% of the total variation. Grain-filling period (0.56), days to maturity (0.55) and thousand-kernel weight (0.42) contributed for most of the variation in PC1. The results were in agreement with the findings of Pavan *et al.* (2019) for thousand-kernel weight and Urgaya *et al.* (2022) for days to maturity. The variation in PC2 was mainly due to days to heading (0.71), grain yield (0.55) and plant height (0.37).

**Table 3: Eigenvectors and eigenvalues of the first two principal components (PCs) for traits of bread wheat genotypes.**

Traits	Eigenvectors	
	PC1	PC2
Grain yield	0.31	-0.55
Days to heading	0.07	0.71
Days to maturity	-0.55	0.19
Grain-filling period	-0.56	-0.16
Plant height	0.33	0.37
Thousand-kernel weight	0.42	0.04
Eigen value	2.52	1.56
differences	0.96	0.64
Percent of total variance explained	42%	26%
Cumulative percent of total variance explained	42%	68%

**Clusters**

The cluster analysis resulted in classifying the 36 genotypes in to five distinct clusters (Table 4, Fig. 1). Cluster I comprised of 15 genotypes, whereas 8, 6,4 and 3 genotypes were included in Cluster II, Cluster III, Cluster IV and Cluster V, respectively. The mean value of traits within each cluster was presented in Table 5. Based on cluster mean, genotypes in cluster IV had the highest yield (4.41 ton h<sup>-1</sup>), grain-filling period (50) and thousand- kernel weight (47.25g). Cluster III was identified with relatively early maturing (113 days), lowest plant height (74.56 cm) and high yield (3.95 ton ha<sup>-1</sup>) whereas genotypes of cluster V were identified with least performances for grain yield (2.42 ton ha<sup>-1</sup>), thousand-kernel weight (39.11 g) and late maturity (129 days). Cluster I was the biggest cluster comprising 15 genotypes, which had the highest plant Height (81.69 cm), moderate yield (3.37 ton h<sup>-1</sup>), late to heading (69 days), high grain filling period (49 days ) and good value of thousand-kernel weight (43.33 g). Cluster II had low grain yield (2.94 ton h<sup>-1</sup>), low thousand-kernel weight (41.71g) and relatively moderate maturity date (115 days). Thus, breeders dealing with high grain yield should use genotypes in cluster IV whereas those dealing with early maturity genotypes should focus on genotypes in cluster III.

**Table 4: Distribution of 36 bread wheat genotypes in to five clusters**

Cluster	Number	Genotypes
I	15	Gassay, Hidasse, Digelu, Sofumar, Alidoro, Ga'ambo, Danda'a, Senkegna, Mekelle-2, Ogolcho, Shorima, Mekelle-3, Tay, Hulluka and Kulukulu
II	8	WORRAKATTA/PASTOR, Hoggana, Mekelle-1, King Bird, K6295-4A, ETBW 5879, Geferson and ETBW 6848
III	6	ETBW 6095, Tossa, Mada-Wolabu, Pavon-76, Dinknesh and tusie
IV	4	Kakaba, UTQUE96/3/PYN/BAU//MILLAN, Mekelle-4 and Hawi
V	3	ET-13A2, Bolo and Menze

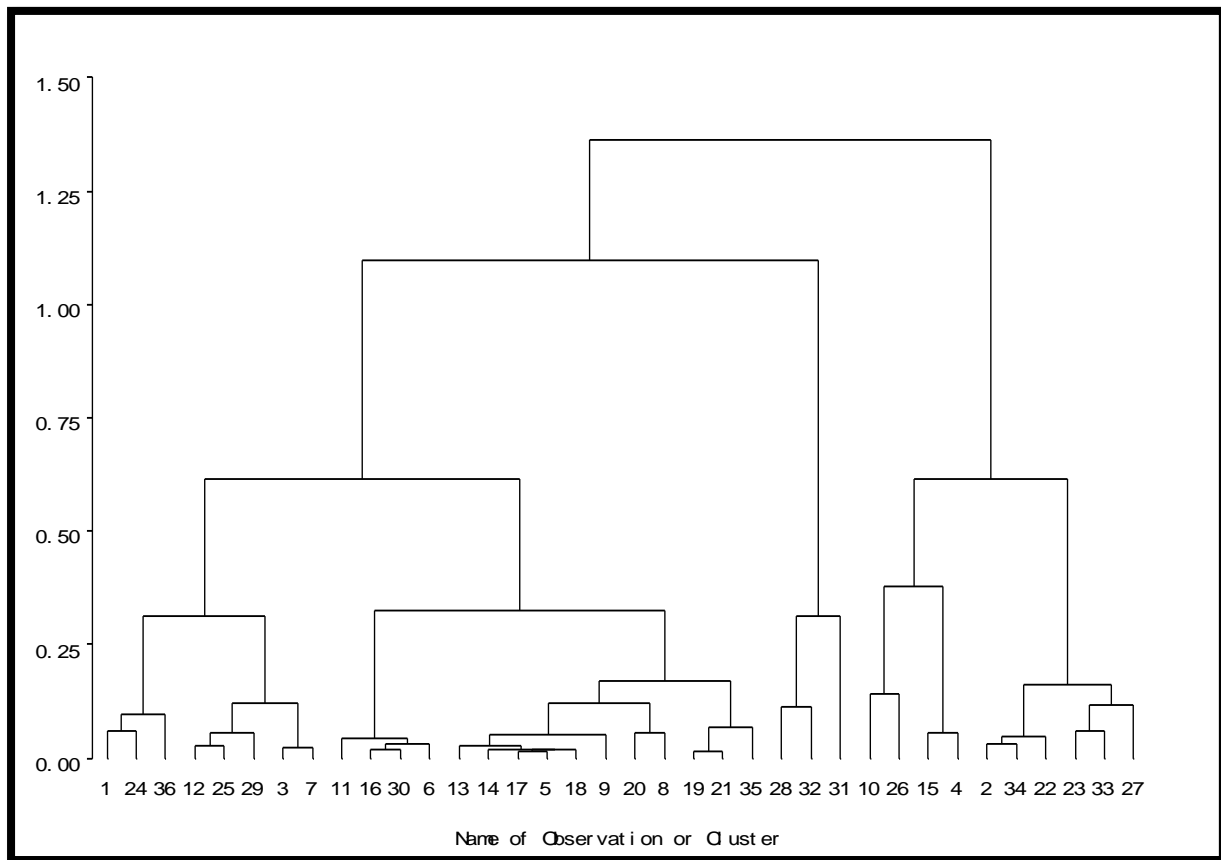


Figure 1: Dendrogram of thirty six bread wheat genotypes

Table 5: Mean values of traits within each cluster

cluster	YLD (ton h <sup>-1</sup> )	HD	MD	GFP	PTH (cm)	TKW (g)
I	3.37	69	117.48	49	69	43.33
II	2.94	69	115.33	47	80.38	41.71
III	3.95	66.44	113	47	74.56	42.39
IV	4.41	65.67	115	50	81.00	47.25
V	2.42	69	129.23	59.94	75.22	39.11

YLD= Grain yield, DH =Days to heading, DM =Days to maturity, GFP= Grain-filling period, PH =Plant height and Thousand-kernel weight

REFERENCES

[1] Almaz Bedada, Bulti Tesso, Ermias Habte. 2022. Genetic Variability for Yield and Yield Related Traits in Advanced Bread Wheat (*Triticum aestivum* L.) Lines in Eastern Ethiopia. *Journal of Plant Sciences*. 10(1): 12-18.

[2] Birhanu Mecha, Sentayehu Alamerew, Alemayehu Assefa, Ermias Assefa and DargichoDutamo. 2016. Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes. *Global Journal of Frontier Science Research* 16(7):12-15.

[3] Burton, G.W. and DeVane, E.H. 1953. Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material, *Agronomy journal* 45:478-481

[4] CSA (Central Statistics Agency). 2021. Agricultural sample survey report on area, production and grain yield of major crops (Meher season).Volume I Addis Ababa, Ethiopia.

- [5] Destaw Mullualem Atinafu, Shiferaw Alemu Alayachew and Kifle Zerga Heterat. 2020. Study of Genetic Variability in Some Bread Wheat Accessions (*Triticum aestivum* L.) in Gurage Zone, Ethiopia. *Asian Journal of Biological Sciences* 13: 309-317
- [6] Garome Shifaraw Geneti, Sentayehu Alamerew Kebede and Techale Birhan Mekonnen. 2022. Genetic Variability and Association of Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes in Gechi District, South West Ethiopia. *Advances in Agriculture* Article ID 7132424, 17 pages
- [7] Hodson, D.P., Jaleta, M., Tesfaye, K., Yirga, C., Beyene, H. and Kilian, A. 2020. Ethiopia's transforming wheat landscape: tracking variety use through DNA fingerprinting. *Sci Rep.* 10(1):18532.
- [8] Jagdish Prasad, Abhay Dashora, Deeksha Chauhan, Sandeep Kumar Bangarwa and Nesara, K. 2020. Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences*, 9 (10).
- [9] Johnson, H.W., Robinson, H.F. and Comstock, R.F. 1955. Genotypic and Phenotypic correlation in soybean and their implication in selection. *Agronomy Journal* 47:477-483.
- [10] Kaiser, H.F. 1960. The application of electronic computers to factor analysis. *Educational and Psychological Measurement* 20:141-151
- [11] Kabir, R., Ahmed, I., Rehman, A.U., Qamar, M., Intikhab, A., Rasheed, A., Zakriya, M., Atif, M.M. and Nisa, Z.U. 2017. Evaluation of bread wheat genotypes for variability and association among yield and yield related traits. *International Journal of Biosciences* 11(1):7-14.
- [12] Pavan Devesh, P.K., Moitra, R.S. Shukla and Suneeta Pandey 2019. Genetic diversity and principal component analyses for yield, yield components and quality traits of advanced lines of wheat. *Journal of Pharmacognosy and Phytochemistry.* 8(3): 4834-4839
- [13] Singh, B.D. 2001. Plant Breeding Principles and methods. Kalyani publishers, New Delhi.896p
- [14] Urgaya Balcha, Firew Mekbib and Dagnachew Lule. 2022. Cluster and Principal Component Analysis among Bread Wheat (*Triticum aestivum* L) Genotypes in Mid Rift Valley of Oromia, Ethiopia. *Adv Crop Sci Tech* 10:525
- [15] USDA (United States Department of Agriculture). 2021. World Agricultural production Foreign Agricultural Service/office of Global Analysis, International Production Assessment Division, USA.
- [16] USDA (United States Department of Agriculture). 2019. <https://apps.fas.usda.gov/psclonline/circulars/production.pdf>
- [17] Wuletaw Tadesse, Habte Zegeye, Tolesa Debele, Daniel Kassa, Wondwosen Shiferaw, Tafesse Solomon, Tamrat Negash, Negash Geleta, Zewdie Bishaw and Solomon Assefa 2022. Wheat Production and Breeding in Ethiopia: Retrospect and Prospects. *Crop Breed Genet Genom* 4(3):e220003.
- [18] Zalewski, D., Galek, R., Kozak, B. and Sawicka-Sienkiewicz, E. 2015. Pheno-morphological and agronomic diversity in a collection of wild and domesticated species of the genus *Lupinus*. *Turkish Journal of Field Crops* 20(1):43-48.