

## Assessing Genetic Diversity in Wheat Using Agro-Morphological Traits and the Association between Traits

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**Abstract:** Knowledge of the genetic variability in germplasm is critical for effective selection in breeding. To this effect, an experiment was conducted in 2014 and 2015 to assess the genetic diversity of 150 wheat genotypes based on agro-morphological traits. Highly significant differences ( $P < 0.001$ ) were observed among the genotypes in most of the traits studied. The PCA showed four principal components (PC) which accounted for 69.1% of the total variation. First principal component (PC1) accounted 30.6%, PC2 16.5%, PC3 11.3% and PC4 10.6% of the variation. Hectolitre weight, peduncle length, tiller/m<sup>2</sup> and grain yield were important traits for classifying the genotypes on PC1. For PC2, days to heading, days to maturity and plant height were important for classifying the genotypes. Cluster analysis of the traits based on Ward's method and squared Euclidean distance grouped the genotypes into five clusters. Genotypes within the same cluster displayed similarity in the traits studied. All clusters except cluster IA had a mixture of both local and exotic genotypes. The grouping of the genotypes into different clusters indicated that the genotypes had different genetic backgrounds which provide a great opportunity for genetic improvement. Furthermore, traits such as hectolitre weight, tiller/plant, thousand grain weight, grains/spike, peduncle length and tillers/m<sup>2</sup> could be effective selection criteria for high yield as they exhibited positive direct effects on yield and also positive and significant association with yield.

**Key words:** Cluster • Correlation • Path analysis • Variability • Breeding

### INTRODUCTION

Genetic diversity assessment is the foundation for crop improvement in a wide range of crop species including wheat [1]. Breeders rely on genetic variability for identification of diverse parental genotypes for variety development and selection of genotypes for different breeding purposes [2, 3]. However, modern intensive breeding narrowed the genetic diversity in wheat [4, 5, 6]. The narrow genetic base presents a problem in case of any disaster (disease or pest), as the entire crop could be lost as it becomes vulnerable to diseases or pests hence threatening food supplies [5, 7, 8]. Moreover, it presents difficulties in breeding crops for adaptation to biotic and abiotic stresses [9]. Exploring genetic diversity among wheat genotypes could help to

increase knowledge of the extent of genetic variability amongst the genotypes. In addition, this could assist in the development of plants resistant to abiotic and biotic stresses and adapted to various agro-climatic conditions [5, 10, 11, 12].

Morphological and agronomic traits have been used to assess genetic diversity in a wide range of crop species. According to [13, 14], morphological and agronomic traits provide a simple and direct way of determining genetic variations among genotypes while at the same time assessing their performance under normal growing conditions. Furthermore, the method is cheaper compared to use of molecular markers [14]. [15] reported that morphological data could effectively be used in estimating genetic diversity as morphological differences in plants were a result of genes controlling the trait.

Additionally, [16] reported that morphological traits were the most appropriate and practical tools for assessing genetic diversity in a large number of genotypes. However, use of morphological and agronomic traits has been reported to be unreliable as they are usually influenced by environment in the field, have low heritability, low polymorphism, late expression [17, 18], may be controlled by epistatic and pleiotropic gene effects [19] and are limited in number [20, 21]. In addition, the method is time consuming and requires extensive field trials making it more expensive than molecular markers [22, 23]. Despite that, morphological traits have been used successfully for genetic diversity assessments and development of cultivars [19]. [24] revealed that using detailed morphological descriptors for classification of genotypes was significant even in the presence of more precise DNA markers.

Essential morphological and phenological descriptors for evaluating and classifying wheat genotypes include plant height, spike length, tillers per plant, peduncle length, thousand grain weight, days to heading, days to maturity and yield (International Board for Plant Genetic Resources (IBPGR) [25]. [26] successfully used morphological traits to examine and select genetically diverse genotypes for breeding purposes from a large pool of genotypes. Efficiency in selection for genetically diverse superior genotypes also requires knowledge of the relationships between traits. Trait associations in wheat have been studied using simple correlation and path analysis [27]. Correlation coefficient measures the degree and direction of linear relationship between traits. The path coefficient measures direct effects of one trait upon another trait and also the indirect effect of the one trait via another trait [28]. The information on association between traits is important as they would help breeders in formulating effective selection strategies for breeding desired genotypes. The present study therefore, was conducted to assess genetic variability of 150 wheat genotypes using agro-morphological traits. The association between traits using correlation and path analysis is also reported.

## MATERIALS AND METHODS

**Experimental Sites:** The study was conducted during in 2014 (2013/14) and 2015 (2014/15) summer season of at three sites in each year. In 2013/14 season, the study was carried out at Mutanda Research Station located at 12°25.959' S and 26°12.620' E (Environment 1), Mt. Makulu

Research Station at 15°32.946' S and 28°15.078' E (Environment 2) and Golden valley Agricultural Research Trust (GART) at 14°58.185' S and 28°06.134' E (Environment 3). For 2014/15 season the experiment was evaluated at Mpongwe Seed-Co Research Farm located at 12°06.622' S and 3°114.660' E (Environment 4), Mt. Makulu Research Station at 13°32.831' S and 28°03.626' E (Environment 5) and GART at 14°58.056' S and 28°05.875' E (Environment 6).

### Experimental Material, Layout and Crop Management:

One hundred and fifty wheat genotypes from Zambia and International Maize and Wheat Improvement Centre (CIMMYT), Mexico were used in the study. The list of genotypes used for genetic diversity study is presented in Appendix 1. The experimental field was laid out in a 10 × 15 alpha lattice design. Each genotype was planted in 2.5 meters long plot of two rows, 20 cm between rows with a plant to plant distance of 10 cm. Spacing of 40 cm between plots was used. Standard agronomic practices were followed for good crop management.

**Measurements:** Evaluation of morphological characteristics was done using descriptors recommended by the International Board for Plant Genetic Resources (IBPGR) [25]. Observations were recorded on five plants per plot. Means for each trait were used for further statistical analysis. Data was recorded on plant height (cm), number of tillers per square meter, tillers per plant, days to heading, days to maturity, spike (ear) length (cm), number of grains per spike, grain yield per plot (g/plot), thousand grain weight (g), peduncle length (cm) and hectolitre weight ( $\text{kg h}^{-1}$ ).

**Data Analysis:** Analysis of variance was conducted using general linear model procedure (PROC GLM) in SAS version 9.3 [29]. Simple linear correlation coefficient was used to determine the degree of association between the traits. Path analysis was also performed using the correlation values to assess the direct and indirect effects of different traits on grain yield following the method in [30]. Path coefficient values proposed by [31] as cited by [32] were used in this study. Path coefficients of < 0.09 were considered as having negligible direct effects, 0.10 to 0.19 as low, 0.20 to 0.29 as moderate and 0.30 to 0.99 as high direct effect on grain yield. Residual effects which determine how the causal factor (independent variable) accounts for variability of the dependent factor (yield) were estimated using the formula below [30].

Residual effect (h) =  $\sqrt{1 - \sum P_{iy} r_{iy}}$

where,  $P_{iy}$  is the component of direct effect of independent  $i^{\text{th}}$  factor and the dependent factor  $y$  (yield) as determined by path analysis and  $r_{iy}$  is the correlation coefficient of  $i^{\text{th}}$  factor with  $y$  (yield) as measured by correlation.

Based on the mean values for each trait, the principal component analysis was performed in GenStat version 14 [33] to detect traits that explained the most variability in the data set and also to cluster genotypes based on the similarities. In this study, the trait with the coefficient equal to or greater than 0.3 was considered to discriminate the genotypes more than those with coefficient less than 0.3 [34, 35]. Cluster analysis based on Ward's method [36] using squared Euclidean distance was used to group genotypes in to clusters using Statistical Package for Social Scientists (SPSS) for windows version 16.0 [37].

## RESULTS

**Variation among the Genotypes:** Significant differences ( $P < 0.001$ ) (Table 1) were observed among the 150 genotypes for the characters studied. Location effect was significant for all the traits. The year effect was significant for all traits except for tiller/m<sup>2</sup>. Genotype  $\times$  location interactions were significant for all traits except for spike length and grains/spike (Table 1). Genotype  $\times$  year interaction was significant for all traits except for spike length, tillers/plant and hectolitre weight. Genotype  $\times$  year  $\times$  location interactions were not significant for spike length, tillers/plant and hectolitre weight but significant for all other traits.

Days to heading ranged between 49 to 86 days with the earliest being SB 50 (Sonalika) from Mexico with 49 days. Sonalika was also the earliest genotype to mature (68 days). Genotype 19HRWSN7 showed the highest number of days to head (86 days) as well as days to maturity (110 days). In addition, it also exhibited the lowest grain yield (0.1 t ha<sup>-1</sup>) and TGW (23.42 g). The highest yield was recorded in genotype 30SAWSN10 (2.0 t ha<sup>-1</sup>). Genotype 30SAWSN5 was second highest in grain yield per hectare (1.8 t ha<sup>-1</sup>) and recorded the highest hectolitre weight. Spike length was high in genotype SB9 (14.0 cm) with SB1 having shortest spikes length (6.0 cm). The highest number of grains per spike was recorded in genotype 20HRWYT7. Coucal a locally adapted genotype was the tallest (83.6 cm) among all the genotypes followed by Kwale also a locally adapted genotype. Number of tillers/plant was high in genotype

19HRWSN21 while the highest number of tillers/m<sup>2</sup> was recorded in genotype 19HWSN22 and Kwale. The longest peduncle length was recorded in genotypes 19HRWSN21, Coucal and Kwale. Among all the genotypes, genotype SB34 had the highest TGW compared to others.

**Correlation and Path Coefficient Analysis:** Negative and significant correlation coefficients were detected between days to heading with peduncle length ( $P < 0.001$ ), thousand grain weight (TGW) ( $P < 0.001$ ) and grain yield ( $P < 0.01$ ) (Table 2). Negative and non-significant correlations were observed between days to heading with hectolitre weight, tillers/m<sup>2</sup> and tillers/plant while days to heading showed positive and non-significant correlations with spike length, grains/spike and plant height. Days to maturity were negatively and significantly correlated with hectolitre weight, peduncle length, TGW and grain yield. Positive and highly significant correlation ( $P < 0.001$ ) was observed between grain yield with grains/ spike, hectoliter weight, thousand grain weight, peduncle length, tiller/m<sup>2</sup> and tillers/plant. Thousand grain weights was highly significantly and positively correlated with plant height, hectoliter weight and grain yield. Plant height was highly significant and positively associated with peduncle length, grains per spike, tillers/m<sup>2</sup> and grain yield ( $P < 0.001$ ). Significant association ( $P < 0.01$ ) was also observed between plant height and spike length, hectoliter weight, days to maturity and tillers/plant.

From the path analysis results (Table 3), hectolitre weight (0.46) and tillers/plant (0.34) exhibited the highest positive direct effect on grain yield, while moderate direct effects on grain yield were observed through TGW (0.21). Grains/spike (0.19) showed a low positive direct effect on grain yield. The direct effect of peduncle length and tillers/m<sup>2</sup> on grain yield was positive though not so pronounced. Direct effects of days to heading, days to maturity, plant height and spike length was negative and negligible  $< 0.09$ . The residual effect was 0.48.

**Principal Components Analysis for Agro-Morphological Traits:** Results from the principal component analysis for the two years combined, showed that the four principal components (PC1, PC2, PC3 and PC4) accounted for 69.1% of the total variation in the phenological and morphological traits (Table 4). The first principal component (PC1) contributed 30.6%, PC2 contributed 16.5%, PC3 and PC4 contributed 11.3% and 10.6%, respectively, of the total variation. The Eigen values (Table 4) showed that the relative discriminating power of the principal components was high for PC1 (3.37) followed

Table 1: Combined analysis of variance for 150 wheat genotypes evaluated in 2014 and 2015.

Mean squares												
Source	Df	Days to heading	Days to maturity	Spike length (cm)	Grains/spike	Hectolitre weight (kg hl <sup>-1</sup> )	Plant height (cm)	Peduncle length(cm)	Thousand Grain weight (g)	Tillers/ plant	Tillers/m <sup>2</sup>	Grain yield (t ha <sup>-1</sup> )
Year (Y)	1	26719.01**	6268.27**	275.52**	6131.97***	165.01*	240.48***	1266.67***	1109340.38***	587.67*	255.16 <sup>ns</sup>	28344.69***
Location (L)	2	39588.56*	27835.79**	307.17*	14724.47*	453.62**	86361.17**	1459.13***	762116.64**	2479.56*	296000.5*	325280.60*
L x Y	2	35349.97**	16695.87**	642.57*	11593.9**	294.87*	95175.56*	1622.78*	559310.48*	4349.28**	2702355.35*	155182.23**
Rep (Y x L)	6	28.48	929.02	11.13	212.56	3.74	561.79	11.88	1041.12	43.91	15756.72	876.75
Genotype (G)	149	232.46***	302.72**	7.14**	178.36**	4.95***	233.45***	45.03***	597.46***	9.06**	2710.50***	2236.41***
G x Y	149	41.17**	103.16**	5.87 <sup>ns</sup>	71.18**	2.92 <sup>ns</sup>	70.49***	7.00**	318.34**	3.16 <sup>ns</sup>	2007.17***	591.56***
G x L	298	41.42**	95.17***	5.85 <sup>ns</sup>	81.18 <sup>ns</sup>	3.26**	77.27***	5.78**	328.78**	5.00**	1977.79**	1056.50**
G x Y x L	298	36.89**	81.27**	5.83 <sup>ns</sup>	83.53*	2.82 <sup>ns</sup>	64.53**	5.52**	306.29**	4.58 <sup>ns</sup>	2021.14**	697.98
Error	894	18.12	49.15	5.17	63.12	2.62	49.37	4.6	136.96	4.00	1533.45	463.10
Corrected total	1799											
CV		7.35	7.89	28.0	25.0	29.0	10.89	23.40	24.00	28.06	29.0	30
R <sup>2</sup> (%)		93.70	82.96	62.39	72.17	67.0	91.14	81.91	97.10	84.28	90.66	82.40
Mean		58	89	8	32	1	65	9	48	7	60	0.8
Maximum		86	110	14	40	7	84	17	79	10	140	2.0
Minimum		49	68	6	20	0	54	6	23	5	60	0.1

\*\*\*, \*\*, \* indicate significance at P&lt;0.001, P&lt;0.01 and P&lt;0.05, respectively, ns= non-significant, Df: Degree of freedom, Rep = replication

Table 2: The Pearson correlation coefficient matrix for agro-morphological traits evaluated in 150 wheat genotypes in six environments

	DH	DM	SL	GS	HL	PH	PL	TGW	TP	TM <sup>2</sup>	GYD
DH	1.00										
DM	0.62***	1.00									
SL	0.05 <sup>ns</sup>	0.09 <sup>ns</sup>	1.00								
GS	0.01 <sup>ns</sup>	0.00 <sup>ns</sup>	-0.01 <sup>ns</sup>	1.00							
HL	-0.16 <sup>ns</sup>	-0.17*	-0.06 <sup>ns</sup>	0.16*	1.00						
PH	0.11 <sup>ns</sup>	0.19*	0.26***	0.21**	0.21**	1.00					
PL	-0.32***	-0.35***	0.03 <sup>ns</sup>	0.13 <sup>ns</sup>	0.35***	0.42***	1.00				
TGW	-0.28***	-0.21**	-0.06 <sup>ns</sup>	-0.10 <sup>ns</sup>	0.37***	0.16*	0.22**	1.00			
TP	-0.09 <sup>ns</sup>	-0.09 <sup>ns</sup>	-0.10 <sup>ns</sup>	0.21**	0.45***	0.29***	0.47***	0.11 <sup>ns</sup>	1.00		
TM <sup>2</sup>	-0.02 <sup>ns</sup>	-0.01 <sup>ns</sup>	-0.03 <sup>ns</sup>	-0.04 <sup>ns</sup>	0.19*	0.10 <sup>ns</sup>	0.34***	-0.07 <sup>ns</sup>	0.53***	1.00	
GYD	-0.22**	-0.26***	-0.15 <sup>ns</sup>	0.32***	0.75***	0.24***	0.46***	0.43***	0.65***	0.27***	1.00

\*\*\*, \*\*, \* indicate significance at P<0.001, P<0.01, P<0.05 respectively, ns= non-significant, DH=days to heading, DM=days to maturity, SL=spike length, GS=grains/spike, HL=hectolitre weight, PH=plant height, PL=peduncle length, TGW=thousand grain weight, TM<sup>2</sup>=tillers/meter<sup>2</sup> square, TP=Tillers/plant, GYD=grain yield.

Table 3: Estimates of direct (diagonal bold) and indirect effect of 10 traits under study on grain yield.

	DH	DM	SL	GS	HL	PH	PL	TGW	TP	T/M <sup>2</sup>	GYD
DH	-0.02	-0.05	0.00	0.02	-0.07	0.00	-0.01	-0.06	-0.03	0.00	-0.22
DM	-0.01	-0.08	-0.01	0.00	-0.08	0.00	-0.01	-0.04	-0.03	0.00	-0.26
SL	0.00	-0.01	-0.06	0.00	-0.03	0.00	0.00	-0.01	-0.03	0.00	-0.15
GS	0.00	0.00	0.00	0.19	0.07	0.00	0.00	-0.02	0.07	0.00	0.32
HL	0.00	0.01	0.00	0.03	0.46	0.00	0.01	0.08	0.15	0.00	0.75
PH	0.00	-0.01	-0.02	0.04	0.09	-0.01	0.02	0.03	0.10	0.00	0.24
PL	0.01	0.03	0.00	0.02	0.16	-0.01	0.04	0.05	0.16	0.00	0.46
TGW	0.00	0.02	0.00	-0.02	0.17	0.00	0.01	0.21	0.04	0.00	0.43
TP	0.00	0.01	0.01	0.04	0.21	0.00	0.02	0.02	0.34	0.00	0.65
T/M <sup>2</sup>	0.00	0.00	0.00	-0.01	0.09	0.00	0.01	-0.02	0.18	0.01	0.27

DH=days to heading, DM=days to maturity, SL=spike length, GS=grains/spike, HL=hectolitre weight, PH=plant height, PL=peduncle length, TGW=thousand grain weight, TM<sup>2</sup>=tillers/meter<sup>2</sup> square, TP=Tillers/plant, GYD=grain yield. <sup>†</sup>Residual effect= 0.48

Table 4: Eigenvectors of the first four principal components (PC1, PC2, PC3 and PC4) axes for 150 wheat genotypes evaluated in 2013 and 2014.

Trait	PC1	PC2	PC3	PC4
Days to heading	-0.22	0.54	-0.10	0.22
Days to maturity	-0.22	0.53	-0.01	0.16
Spike length	-0.05	0.19	0.57	-0.43
Grains/spike	0.14	0.27	0.04	0.36
Hectolitre weight	0.41	0.04	0.04	0.30
Plant height	0.21	0.41	0.45	-0.14
Peduncle length	0.40	0.01	0.11	-0.35
TGW	0.25	-0.23	0.37	0.28
Tiller/m <sup>2</sup>	0.41	0.23	-0.29	-0.10
Tillers/plant	0.24	0.20	-0.48	-0.46
Grain yield	0.48	0.04	-0.04	0.28
Eigen value	3.37	1.82	1.25	1.17
Percent variation	30.63	16.52	11.33	10.65
Cumulative	30.63	47.15	58.48	69.13

Table 5: Grouping genotypes based on cluster analysis and the members present in each cluster based on Ward's method.

Cluster	Frequency	Cluster membership
IA	16	56, 134, 31, 42, 50, 59, 24 82, 3, 47, 118, 106, 123, 142, 7,
IB	35	32, 66, 29, 89, 25, 83, 57, 113, 126, 8, 6, 64, 30, 26, 78, 62, 74, 107, 61, 72, 43, 138, 120, 41, 79, 39, 94, 99, 13, 21, 9, 44, 69, 130, 80
II	12	81, 84, 14, 88, 148, 95, 97, 147, 67, 71, 144, 5
III	14	15, 16, 73, 55, 75, 11, 19, 70, 77, 90, 91, 92, 86
IV	43	10, 63, 129, 103, 1, 150, 115, 11, 96, 111, 140, 141, 143, 2, 45, 135, 33, 12, 34, 105, 116, 137, 51, 133, 22, 20, 85, 37, 124, 128, 122, 87, 108, 136, 109, 117, 18, 56, 112, 27, 28, 76, 46
V	30	98, 104, 132, 100, 125, 35, 36, 93, 52, 68, 53, 114, 60, 102, 145, 149, 49, 38, 65, 4, 40, 127, 54, 139, 101, 146, 131, 119, 23

Names of the genotypes are given in Appendix 1.

by PC2 then PC3 and least for PC4. Table 4 shows that much of the variation in PC1 was contributed by grain yield (0.45), peduncle length (0.40), tillers /m<sup>2</sup> (0.41) and hectolitre weight (0.41). Thousand grain weight (TGW), grains/spike and tillers / plant contributed less to PC1. Days to heading, days to maturity and spike length contributed negatively and less to PC1. The traits which contributed more to PC2 were days to heading (0.54), days to maturity (0.53) and plant height (0.41). All other traits, except TGW, contributed positively but less to PC2. Spike length (0.57), peduncle length (0.45) and TGW (0.37) contributed more to PC3 while hectolitre weight (0.30), grains/spike (0.36), spike length (-0.43), peduncle length (-0.35) and tillers/plant (-0.46) contributed more to PC4. The traits that loaded more on PC1 and PC2 were used to cluster the 150 genotypes into closely related groups.

**Cluster Analysis:** The dendrogram (Fig. 1) revealed five major clusters I, II, III, IV and V. Cluster I had two sub groups A and B. Members of each cluster are presented in Table 5. Sub-cluster I A consisted of sixteen genotypes (10.7%) mostly from Mexico-CIMMYT. The genotypes in this cluster were late maturing with average grain yield. The date of maturity for this group ranged between 91–99 days. Sub-cluster I B grouped thirty-five genotypes (23.3%) that were intermediate in days to maturity and

grain yield. It had one local genotype 94 (Mampolyo). Cluster II grouped twelve genotypes (8.0%) which were short, early heading and early maturing. The shortest being genotype 147 from CIMMYT-Mexico with 53.6 cm while the earliest was genotype SB 50 also from CIMMYT-Mexico with 68 days to maturity. Cluster II contained two local genotypes 95 (Nkhanga) and 97 (Pwele). Cluster III contained fourteen genotypes (9.3%) of which two were local genotypes, 91 (Coucal) and 92 (Kwale). The genotypes in this cluster were high yielding, high tillering, had long peduncle length, high TGW, tall as well as late maturing. The yield ranged between 1.5 t ha<sup>-1</sup>-2.0 t ha<sup>-1</sup>. The tallest genotype in this cluster was genotype 91 (Coucal) from Zambia with 83.6 cm. High tillering genotypes included genotype 15, 92, 77 and 73. Number of tillers/m<sup>2</sup> for these genotype ranged between 131 and 140 tillers. Forty-three genotypes in cluster IV were characterized by being intermediate in plant height, hectolitre weight and peduncle length. Among the forty-three, genotype 150 (UNZAWV2) and 96 (Nseba) were local genotypes. Cluster V grouped thirty genotypes (20%). This cluster included three local genotypes, 98 (Sahai), 93 (LoerrieII) and 149 (UNZAWV1). The wheat genotypes in this cluster were low tillering with short peduncle length, low TGW and low yielding. Number of tillers ranged between 60 and 72 tiller/m<sup>2</sup>. The hectolitre weight ranged between 0.5 to 1.23 kg h<sup>-1</sup>.

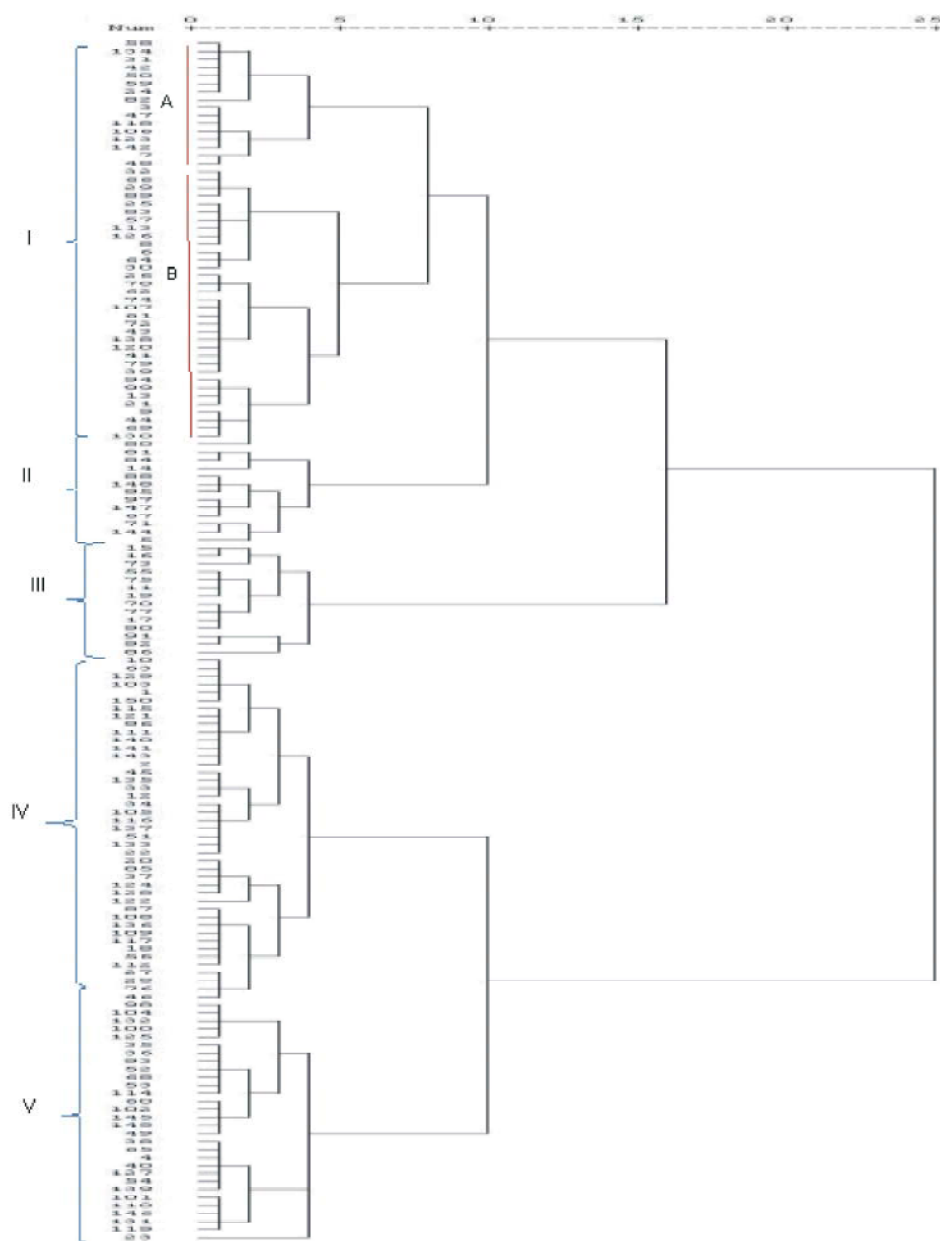


Fig. 1: Dendrogram of 150 wheat genotypes based on agro-morphological traits using hierarchical cluster analysis (Ward's method and squared Euclidean distance). Genotypes are labelled 1 to 150. Names of genotypes are given in Appendix 1.

## DISCUSSION

Variations observed amongst the 150 wheat genotypes with respect to all the traits under study, gives an opportunity to plant breeders to select genotypes with desired traits for genetic improvement through breeding. The significant genotype  $\times$  location interaction (GLI) on most traits suggests the differential expression of

genotypes across locations, hence confirming the presence of genetic differences among the genotypes. Nonetheless, the existence of GLI complicates selection of superior genotypes [38]. The non-significant GLI on traits such as spike length and grains/spike implies that these traits were non-responsive to changes in the environment. The genotype  $\times$  year interaction on traits such as spike length, grains/spike and hectolitre weight were not

significant indicating that the performance of these traits was consistent over the years [39]. Significant year  $\times$  location and genotype  $\times$  year  $\times$  location interactions on most traits shows that there was inconsistency in the performance of the genotypes in different locations in both years. Similar findings were reported by [40].

The negative correlation observed in this study between days to heading with grain yield suggests that selection for very early heading would give lower yields. Similar findings were reported by [41]. The negative and highly significant association between days to maturity with yield implies that selection for very late maturing varieties (>95 days) could result in decrease grain yield. [41] found negative and non-significant correlation between days to maturity with grain yield. [42] reported that the complex modulation of days to heading and days to maturity of genotypes in response to photoperiod and temperatures under diverse environments, usually bring about the opposite effect observed on grain yield. Number of tillers/m<sup>2</sup>, tillers/plant, grains per spike, peduncle length, thousand grain weight (TGW), plant height, peduncle length and hectoliter weight had a significant and positive association with grain yield. This shows that grain yield potential can efficiently be improved by selecting for these traits. Selecting for high number of tillers indicates that there could be more spikes and grains resulting in increased yield. These results are in agreement with [43, 44, 45]. The negative and non-significant correlation between spike lengths with grain yield obtained in this study means that selection of this character may not be helpful in yield improvement. However, indirect selection for this trait for yield improvement could be through plant height.

The highly significant and positive association observed between tillers/m<sup>2</sup> with grains per spike, hectolitre weight, plant height and peduncle length indicates that the improvement on tillers/m<sup>2</sup> may hasten the per se performance of aforementioned characters. The highly significant positive association between plant height with peduncle length, spike length, grains per spike and TGW means that while selecting for plant height, spike length, grains per spike TGW and the length of the peduncle should also be considered. This suggests that the improvement of plant height would see the improvement in performance of these other characters. This is in agreement with the study by Daoura *et al.* [46]. Besides, the results revealed that peduncle length was not only an important component of grain yield for providing photosynthates to the developing grain but also a major contributor to the height of wheat plants a desired character for high straw yield [47]. Similar results were

reported by [27]. Negative and non-significant correlation, which was observed between grains/spike with thousand grain weight, implies that grains/spike had negligible effects on TGW. This indicates that the selection for this character may not be helpful in improving TGW. [44, 48] also reported negative and significant correlations between grains per spike with TGW.

The positive direct effects exhibited by hectolitre weight, tiller/plant and TGW to yield, entails that direct selection of these traits could increase the grain yield per hectare. [27] revealed that during selection for yield increases all traits with positive effects on yield though with less correlation magnitude should not be ignored. As such in this study, traits like grains/spike, tillers/m<sup>2</sup> and peduncle length with positive but low direct effects should be considered during selection for high yield. The residual factor value was found to be 0.48. This explains that the traits used in this study explained only 52% of the variability observed in the yield [30], which implies that there are some other factors not included in this study which were causing variation in grain yield.

From the principal component analysis, traits which were responsible for the separation of genotypes for PC1 included grain yield, tillers/m<sup>2</sup>, hectolitre weight and peduncle length; implying that PC1 was related to yield and its contributing components. This component reflected on yield potential of genotypes through some yield components. For PC2, days to heading, days to maturity and plant height were identified as major traits for genotype separation. This axis therefore could be named as phenological and plant height axis. Two principal components (PC1 and PC2) were used to cluster genotypes to observe the relationship that existed between genotypes since they contributed more than half of the total variation [49]. Furthermore, the traits that loaded more on PC1 and PC2 showed the strongest discriminatory power in separating genotypes hence were used to classify genotypes [34]. In this study, five clusters were identified and these clusters showed a clear separation among themselves. The improvement of any trait of importance among genotypes could easily be done by sampling and utilizing genotypes from appropriate contrasting clusters. For example, the early maturing genotypes (cluster II) could be selected to breed for early maturing type of genotype (68 days). Genotypes such as 91 and 92, both locally adapted genotypes were in the same cluster indicating that they were closely related in terms of the studied traits. Genotypes 93, 98 and 149 belonged to the same cluster revealing some similarities among them. Genotypes 95 and 97 were grouped in the same cluster. All in all, the results of this study showed

that a high level of variability existed among genotypes which could further be exploited and used in wheat breeding programme. According to [50], genetic improvements largely depend on the presence of genetic diversity in the genotypes.

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