CHARACTERIZATION AMONG BREAD WHEAT (*Triticum aestivum* L.) LANDRACES AT KAFFA ZONE, SOUTH WEST ETHIOPIA

MSc. THESIS

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CHARACTERIZATION AMONG BREAD WHEAT (*Triticum aestivum* L.) LANDRACES AT KAFFA ZONE, SOUTH WEST ETHIOPIA

MSc. Thesis

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DEDICATION

This thesis is dedicated to my parents who raised and directed me in every aspect of my journey.

STATEMENT OF THE AUTHOR

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LIST OF ABBREVIATIONS AND ACRONYMS

CA	Cluster Analysis
CSA	Central Statistical Agency
CIMMYT	International Maize and Wheat Improvement Center
CV	Coefficients of Variations
D^2	Squared Distance
E.C.	Ethiopian Calendar
EIAR	Ethiopian Institute of Agricultural Research
GAM	Genetic advance as percent of mean
GCV	Genotypic Coefficient of Variation
H’	Shannon Weaver Diversity Index
IBPGR	International Board for Plant Genetic Resources
M.a.s.l	Meter Above Sea Level
MoANR	Ministry of Agriculture and Natural Resources
PC	Principal Component
PCV	Phenotypic Coefficient of Variation
SAS	Statistical Analysis System
SNNPR	Southern Nations Nationalities and Peoples Region
SSA	Sub Saharan Africa
USDA	United States Department of Agriculture
^0C	Degree Celsius

BIOGRAPHICAL SKETCH

The author was born in January 1995 G.C. in Kobech Kebele, Gewata Woreda, Kaffa Zone, from his father Gebremariam Gebre and mother Tirunesh G/Michael. He started his primary school in 2001 G.C. He completed his elementary school at Kobech Primary School from 2001-2009 G.C. and continued his Secondary School in Konda High School from 2010-2011 G.C. He also continued his preparatory school in Gimbo Secondary and Preparatory School from 2012-2013 E.C. After completion of preparatory school, he joined Mizan Tepi University in 2014 E.C. After staying three years there in Mizan Tepi University, he graduated with B.Sc. Degree in Plant Science in June 21, 2016 G.C. Immediately after graduation, he was hired at Mizan Tepi University as a graduate Assistant I under College of Agriculture, Plant Science Department on August 11/2016 G.C. and worked there for one year. After one year’s service he joined Jimma University for postgraduate studies in 2017 G.C. to pursue a study leading to MSc degree in Plant Breeding.

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ABSTRACT

Bread wheat landraces have high level of genetic diversity which provides high degree of resistance to biotic and abiotic stresses. Despite the diversity of bread wheat in Ethiopia, the production of wheat in Kaffa Zone is very low compared to national average production. The low production of wheat is due to lack of adaptive high yielding variety. The present study was initiated with the overall objective of characterization of bread wheat for quantitative and qualitative traits and determination of genetic diversity. The study was conducted on hundred bread wheat landraces with three checks. The plots were laid out in an augmented design. The analysis of variance showed significant ($P< 0.05$) difference for all of the traits. This indicated the existence of variability and hence the potential for selection and improvement. The mean performance of the accessions indicated that accession number 29812 gave a higher grain yield than the other accessions. According to the mean performance, accessions 29812, 29811, 29813, 242427, 242429 and 243702 that performed better than the released check varieties for grain yield. Moderate genotypic and phenotypic coefficient of variation were observed for spike length, number of seeds per spike, biomass yield and harvest index. Number of productive tiller and grain yield were found to have a high phenotypic coefficient of variation. Moderate to high heritability coupled with moderate to high genetic advance as per cent of the mean were observed for spike length, number of seeds per spike, thousand seed weight, biomass yield and harvest index. This means effective and satisfactory selection for practical improvement of these important traits is possible. Grain yield showed positive and significant correlation with grain filling period, number of productive tillers, spike length, number of seeds per spike, thousand seed weight and biomass yield. Positive correlations of grain yield with the major yield components give an opportunity to simultaneously improve yield and yield contributing traits. Thousand seed weight and number of productive tillers exerted a favorable direct effect on grain yield at genotypic and phenotypic level. Selection for number of productive tiller and thousand seed weight would be very useful for grain yield improvement of bread wheat. The principal component analysis grouped all the traits into four principal components accounted a cumulative of 74% for total variation. The accessions were clustered into seven clusters and one ungrouped accession. Among the clustered groups, the highest inter cluster distance was observed between cluster IV and cluster VI (($D^2=104.77$)) indicating the possibility for selecting parental genotype for hybridization. The estimated diversity index showed the presence of polymorphism. The highest (0.99) diversity index was obtained for seed size, possibly indicating the differential responses of the accessions to the varying environment. However, the present result is only an indication and cannot draw definite conclusion. Thus, for more reliability the experiment should be repeated over location and seasons.

Key word: accessions, bread wheat, clusters, divergence, landraces and traits.

1. INTRODUCTION

Wheat is the first important and strategic cereal crop for the majority of the world's population. In Ethiopia, Wheat is used to make bread, porridge (*genfo*), local beer (*tela*), roasted grain (*kolo*), boiled grain (*nifro*), pasta (Morketa, 2017). Nutritionally, it is an important source of carbohydrates (Shewry and Hey, 2015). The principal use of wheat grain is the production of flour, which contains 13% water, 71% carbohydrates, and 1.5% fats. Its 13% protein content is mostly gluten (75-80% of the protein in wheat) (Shewry *et al.,* 2002).

Bread wheat (*Triticum aestivum* L.), is a self-pollinating annual C3 grass that belongs to the genus *Triticum* and the tribe *Triticeae* of the family *Poaceae* (MacKay, 1966). The earliest cultivated forms were diploid (genome AA) (einkorn) and tetraploid (genome AABB) (Emmer) wheat's and their genetic relationships indicate that they are originated from the southeastern part of Turkey (Heun *et al*., 1997; Nesbitt, 1998; Dubcovsky and Dvorak, 2007). Bread wheat is hexaploid with a total of 42 chromosomes, which is originated through a cross between tetraploid (*Triticum turgidum)* and *Triticum tauschii* (source of the "D" genome) (Shewry *et al*., 2003; Gustafson *et al*., 2009).

Wheat is the most important food security crop at the global level. It is currently grown on 215.44 million hectares annually and produced more than 730.9 million metric tons of grain in 2018/19, the second highest cereal production after maize (1,395.8 million metric tons). Wheat is also one of a food security crop in Africa. It is grown more than 7.94 million hectares and produced more than 24.23 million metric tons annually. The top three wheat producing African countries are Egypt (8.45 million metric tons), Morocco (7.34 million metric tons) and Ethiopia (4.50 million metric tons) (USDA, 2019).

Ethiopia is the first largest wheat producer in Sub-Saharan Africa followed by South Africa (USDA, 2019). The crop ranked fourth after, maize, teff and sorghum both in terms of area coverage (1,696,082.59 ha) and quantity of production (45,378,523.39 quintals) in 2016/17 cropping season (CSA, 2017).

In Ethiopia wheat has been one of the major cereals of choice, dominating the food habit and dietary practices next to tef 'injera' and known to be a major source of energy and protein for the highland population (Abera, 1991).

In Ethiopia, wheat grows under diverse environmental conditions ranging in an altitude from 1500 to 3200 m.a.s.l. (Faris *et al*., 2006) which makes possible for the existence of different wheat in Ethiopia. Knowledge about the extent of variability among bread wheat (*Triticum aestivum* L.) accessions is a high value for the genetic improvement programs and the efficient genetic diversity utilization of plant materials (Pasandi *et al.*, 2015). Since, landraces are important genotypes for crop breeding for their high potential to adapt to specific environmental conditions and the large source of genetic variability that they provide (Azeez *et al*., 2018).

Even though, several works have been done on genetic variability studies of bread wheat at the different regions of Ethiopia (Gezahegn *et al*., 2015; Negash *et al.,* 2015; Wondowosen, 2014; Ahmed *et al*., 2017). Despite the diversity of bread wheat in Ethiopia, wheat is grown in 7137.64 hectares per annually and the production is 19.02 quintals per hectare in Kaffa Zone which is lower than the national production (26.75 quintal per hectare) (CSA, 2017). The low production of wheat in Kaffa Zone is due to lack of adaptive high yielding variety. Therefore, assessing the variation present in collections conserved at the Ethiopian Biodiversity Institute is an important prerequisite for crop improvement. Keeping the above facts in view, the present investigation was undertaken with the following objectives:

- To characterize the accessions for quantitative and qualitative traits.
- To determine the genetic diversity of bread wheat
- To estimate the broad sense heritability and expected genetic advance of various important traits.

2. LITERATURE REVIEW

2.1. Bread Wheat Genetic and Botanical Description

The diploid einkorn wheat (*T. monococcum)* (2n = 2x = 14, AA), was domesticated directly from its wild form, *T. monococcum* (2n = 2x = 14, AA) in the Fertile Crescent, probably in the Karacadag mountain range in southeast Turkey (Heun *et al*., 1997). Einkorn wheat (*T. monococcum*) is diploid (AA, two complements of seven chromosomes, 2n=14) (Belderok *et al.*, 2000). Most tetraploid wheat (emmer and durum wheat) is derived from wild emmer, *T. dicoccoides*. Wild emmer is the result of hybridization between two diploid wild grasses, *T. urartu* and a wild goat grass such as *Aegilops searsii*. According to Nesbitt and Samuel (1996), einkorn wheat was basically replaced by cultivated tetraploid and hexaploid wheat during the last 5000 years, and currently it is a crop grown for feed only in a few Mediterranean countries.

The evolution of the common wheat (*Triticum aestivum*) (2n = 6x = 42, BBAADD), has been the subject of many investigations and intense discussions for several decades. It is now considered that hexaploid wheat was formed from a hybrid between the tetraploid wheat species *T. turgidum* (2n = 4x = 28, BBAA) and the diploid species *Aegilops tauchii var. strangulata* (2n = 2x = 14, DD) (Dvorak *et al*., 1998; Riley *et al*., 1958).

Botanically, it is an annual plant having spikelet inflorescence. The floret may be awned or awnless. The presence of awns also tends to influence transpiration rate, accelerating the drying of ripe grain. Consequently, the tips of awnless spikes tend to be blasted in hot dry weather. The grain may also be amber, red, purple, or creamy white in color (Acquaah, 2007). Bread wheat, as described by Lersten (1987) is a mid-tall annual or winter annual grass with flat leaf blades and a terminal floral spike consisting of perfect flowers.

2.2. Bread Wheat Distribution and Importance

According to Dixon *et al*. (2009), wheat crop is grown under a wide range of climatic conditions and geographical areas, and due to this; its distribution range is more than any other plant species. The top three wheat producing countries in the world are China (131.4 million metric tons), India (99.9 million metric tons) and Russia (71.7million metric tons) (USDA, 2019).

Wheat is one of the major cereal crops grown in the Ethiopian highlands. At present, bread wheat is produced solely under rain fed conditions. Of the current total wheat production area, 75% are located in Arsi, Bale and Shewa regions. A small amount is produced in the rest of the north and south regions (MoANR, 2016).

Altitude plays an important role in the distribution of wheat production through its influence on rainfall, temperature and the presence of diseases. In Arsi, Bale and Shewa regions, the soil, moisture and disease conditions within the range of 1900-2300 m altitude zone are favorable for the production of early and intermediate maturing varieties of bread wheat (Hailu *et al*., 1991). This is estimated to comprise 25% of the total wheat production area, while the remaining 75% falls in the 2300-2700 m altitude zone. There, early, intermediate and late varieties are grown. Soil types used for wheat production vary from well-drained, fertile soils to waterlogged heavy Vertisols (Hailu *et al*., 1991).

Wheat, in the form of bread, provides more nutrients to the world population than any other single food source. Bread is particularly important as a source of carbohydrates, proteins and vitamins B and E (Pomeranz, 1987). Bread consumption, particularly that of breads prepared from whole grain flours and with multigrain flours tends to increase in developed countries. This is mainly due to an increase in a nutritionally conscious population that wants to reduce the consumption of simple carbohydrates, fat and cholesterol while increasing the consumption of complex carbohydrates, dietary fiber and plant proteins (Seibel, 1995).

2.3. Challenges to Wheat Production

Wheat is one of cereal crops grown in Ethiopia both in rain-fed and irrigated environments. But the production of wheat in Ethiopia is low due to abiotic and biotic factors. In rain-fed area, the most serious abiotic factors which affect the crops growth are drought, soil acidity, erosion, poor soil fertility, water-logging, excessive rain during heading and maturity and climate change (Wuletaw *et al*., 2018). Associated with climate change, Lobell *et al*. (2011) reported high temperature during reproductive stages of wheat causes significant yield loss and grain quality reduction mainly because of reductions in the duration of developmental stages, early leaf senescence and adverse physiological and biochemical changes. Other factor affecting wheat productions are biotic factors which causes complete loss of wheat production in Ethiopia. The biotic factors which cause 100 per cent yield losses are disease, insect and pests. Admassu, (2010) reported that rusts are the most devastating disease of wheat in the world, in spite of great progress made in their control in many countries and considered as the major diseases of wheat since no other wheat disease could result in greater loss over large area in a given year.

2.4. Wheat Breeding History and Achievements in Ethiopia

Prior to 1930, wheat breeding basically started with the collection of germplasms followed by identification and characterization. Regarding to these, Koernicke and Werner (1885) made the first description of some Ethiopian wheat and identified five species and nine varieties. Likewise, Vavlov (1929) collected and identified Ethiopian wheat germplasms.

During the periods between 1930-1952 collection and evaluation of indigenous wheat and the introduction of exotic germplasm were done for testing under local conditions. A formal wheat improvement program started in 1949 at the Paradiso Government Station near Asmara for with the testing large number of indigenous and exotic varieties. Consequently, some promising local variety selections were performed and some were released during 1950s (Hailu *et al*., 1991).

Between the periods 1953-1966, wheat research continued at Paradiso, Debre Zeit, Alemaya and Kulumsa. Simultaneously, the station initiated hybridization program among local and exotic bread wheat genotypes to incorporate stem and leaf rust resistance genes to get high quality bread wheat cultivars (Nastasi, 1964). During this period germplasm screening, variety testing and crop management studies were performed. This effort resulted in the release of some bread wheat varieties plus multiplication and distribution of seed of the varieties (Kenya 1 and Kenya 5) in the Shewa and Arsi highlands (Tesfaye and Jamal, 1982).

During the periods between 1967-1990, the establishment of the Institute of Agricultural Research (IAR) expanded the breeding strategies and also establishment of several other research and development institutions, resulting in an effectively organized national wheat research program. The chain between research center and substation brought a satisfactory change in breeding program of wheat (Hailu *et al*., 1991).

Institute of Agricultural research in close collaboration with other organizations, have included: the use of international and national nurseries to identify desirable genotypes, the exploitation of the Ethiopian tetraploid wheat germplasm, the execution of an extensive national and regional variety testing program, the development of varieties through breeding, the coordination and execution of agronomic and crop management studies plus multiplication and distribution of breeder and basic seed (Hailu *et al* ., 1991).

Till 1974, the Debre Zeit Agricultural research center was responsible for coordinating the national wheat program. After 1975, the coordinating centers were classified into two; the Holetta research center was made responsible for the coordination of bread wheat research while the durum wheat program was assigned to Debre Zeit research center. Currently, the government assigned research headquarters at Kulumsa for bread wheat and at Debre Zeit for durum wheat (Hailu *et al*., 1991).

The bread wheat varieties improved during the 1970s and 1980s are Romany, Kanga, Penjamo 65, INIA 66, Mamba, Dereselge, K 6290 Bulk, Pavon-76, etc. (EIAR, 2004). To-date, more than 100 bread and durum wheat varieties were released in Ethiopia by different regional and national research centers. Some of them are Kakaba, Danda'a, Hoggana, Tsehay, Gambo, MeKelle-02, MeKelle-01, Shorima, Mekelle- 03, Hidase, Ogolcho, Hulluka, Jefferson, Mekel-4, Sorra, Sekota-1, AD EL-6, Lucy, Kingbird ,Lemu, Wane etc. (MoANR, 2016). The wheat breeding method in Ethiopia was mainly selection and hybridization (Tesfaye and Getachew, 1991).

2.5. Genetic Variability of Bread Wheat

Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1960; Falconer and Mackay, 1996). If the characteristic expression of two individuals could be measured in an environment identical for both, differences in expression would result from genetic control and hence such variables is called genetic variation (Welsh, 1990; Falconer and Mackay, 1996). Information on the nature and magnitude of genetic variability present in a crop species is important for developing effective crop improvement programs (Singh *et al*., 1980; Welsh, 1990; Dabholkar 1999).

Genetic variability, which is due to the genetic differences among individuals within a population is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can cop up against seasonal fluctuations (Welsh, 1990; Sharma, 1998). In addition, the estimation of the magnitude of variation within germplasm collections of important plant attributes will enable breeders to exploit genetic diversity more efficiently (Jahufer and Gawler, 2000).

Diversity in plant genetic resources provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (yield potential and large seed, etc.) and breeders preferred traits (pest and disease resistance etc.) (Govindaraj *et al.*, 2015).

Variability present in breeding populations can be assessed in the following three ways, (1) by using simple measures of variability, such as range, mean, variance, standard deviation, coefficient of variation and standard error (2) by estimating the various components of variance and (3) by measuring the genetic diversity. The utilization of genetic resources requires proper and systematic evaluation of such resources. Ali Mansouri *et al*. (2018) from Algeria, Wani *et al*. (2018) from India, Birhanu *et al*. (2016) from Ethiopia suggested that evaluation of bread wheat genotypes has revealed useful genetic variation.

Dargicho *et al*. (2016) studied genetic variability of bread wheat and observed the existence of significant variability in the genotypes. Gezahegn *et al*. (2015) evaluated genetic variability studies on bread wheat genotypes and suggested the presence of wide variation for days to heading, days to maturity, grain filling period, plant height, spike length and grain yield.

2.6. Morphological diversity of bread wheat

Studying morphological traits are the prerequisite for conservation of plant genetic resources and molecular characterization (Abebe *et al*., 2015). Accordingly, Messele (2001) studied agronomic and morphological traits of Ethiopian wheat landraces to observe the presence of variations among genotypes. Likewise, Mostafa *et al*. (2010) assessed the agro-morphological characterization of durum wheat accessions aimed to study the relationship among traits. Firdissa *et al*. (2005) also studied phenotypic diversity of tetraploid wheat collected from Bale and Wello area and observed the presence of agro-morphological traits variation. Solia *et al*., 2015; Dejene *et al*., 2015; Negash and Heinrich, 2013 also studied the agro-morphological traits diversity of wheat genotypes and suggested the presence of morphological variation among the genotypes.

2.7. Heritability and Genetic Advance on Traits of Bread Wheat

Heritability in a broad sense can be defined as the proportion of the total genetic variation to the total phenotypic variance (Allard, 1960). Estimation of heritability as a ratio of genotypes of phenotypic variance may vary greatly depending upon the unit for which variance is considered (Johnson *et al.*, 1955b). Heritability estimate is of greater value to the breeder, since it indicates the degree of dependence of genotypic values of phenotype value. Heritability indicates the effectiveness with which selection of genotypes can be based on phenotypic performance. If heritability were 100%, that is the genotypic variance (s^2g) is equal to phenotypic variance (s^2p), then phenotypic performance would be a perfect indication of genotypic value (Johnson *et al.*, 1955b); but, even in such a hypothetical situation, the heritability value in itself provides no indication of the amount of genetic progress that would result from selecting the best individuals. However, genetic progress would expect from selection increase with an increase in the genotypic variance. Therefore, the utility of estimates of heritability is increased when they are used in conjunction with the selection differential leading to concomitant estimate of genetic advance expectations from the selection.

Knowledge of the heritability of the traits is important to breeders since it indicates the possibility and extent to which improvement is possible through selection. Effective selection in plant breeding is based on the information about the extent to which observed differences in traits under the selection are heritable and to which they are correlated with each other (Johnson *et al*., 1955a).

Laird and Lange (2011) proposed the goal of heritability analysis is to estimate the overall genetic effect of the quantitative trait. This effect is defined as the proportion of the total variability in the phenotype explained by variation in all loci underlying the qualitative trait. Falconer and Mackay (1996) also proposed heritability as the ratio of additive genetic variance to phenotypic variance. Genetic advance is a measure of improvement that can be achieved by practicing selection in a population. The estimation of heritability along with genetic advance is generally more useful in predicting the result and in selecting the best individuals (Johnson *et al*., 1955a) the estimates of heritability give no indication of the amount of progress expected from the selection. The factors influencing genetic advance are selection intensity, heritability and phenotypic variance. High genetic advance coupled with high heritability is an indication of more additive gene action (Panse and Sukhatme, 1957).

Different researchers estimated heritability of different plant traits under normal and stressed conditions (Khan and Hassan, 2017; Obsa *et al.,* 2017; Sharaan *et al*., 2017; Lone *et al*., 2017) for days to maturity, days to heading, grain filling period, plant height, spike length and number of seeds per spike According to Kumar *et al*. (2017) high heritability estimates with moderate genetic advance were shown for days to flowering, number of productive tillers, grain yield and biomass yield while the plant height, spike length, number of spikelet per spike and 1000 grain weight, showed moderate value for heritability and highest value for genetic advance.

Din *et al*. (2018) reported high heritability with low genetic advance were observed for traits like number of productive tillers and the high heritability coupled with high genetic advance were observed for plant height while moderate heritability for kernel per spike and biomass yield with high genetic advance.

According to Iqbal *et al*. (2017), high heritability coupled with low genetic advance was observed for days to heading, days to maturity and spike length. Whereas, moderate broad sense heritability coupled with high genetic advance was recorded for biomass yield and grain yield while less broad sense heritability and genetic advance was displayed by grain weight per spike.

Berhanu *et al*. (2017) reported that high heritability was recorded for days to heading and days to maturity. Moderate heritability values were computed for the grain filling period, plant height, kernels per spike, spikelet's per spike, spike length, biomass yield, grain yield and thousand kernel weight. Low heritability estimated for a number of effective tillers per plant and harvest index. High heritability is coupled with moderate genetic advances as per cent of the mean was observed for days to heading and days to maturity.

Bhushan *et al*. (2013) pointed out the plant height were recorded highest heritability followed by days to heading, harvest index, biomass yield, spikelet's per spike, grain yield , productive tillers per plant and days to maturity. Moderate heritability was recorded for the grain filling period and test weight. High heritability coupled with high genetic advance as per cent of the mean were registered for plant height, harvest index, biomass yield and grain yield indicated a predominance of additive gene action in the expression of these traits. High heritability coupled with moderate genetic advance were observed for days to heading and days to maturity indicated a predominance of additive and non-additive gene action in the expression of these traits therefore, these traits can be improved by mass selection and other breeding methods based on progeny testing.

Ullah *et al.* (2018) also reported that high heritability with low genetic advance were recorded for days to heading, days to maturity, plant height; and low heritability coupled with low genetic advance was observed for Spike length low. Likewise, moderate heritability with low genetic advance was observed for thousand seed weight.

According to Nishant *et al*. (2018) high heritability estimate was exhibited for days to maturity 1000 grain weight and days to heading. The estimate of genetic advance as per cent of the mean was highest for yield per plant, thousand grain weight followed by yield per plot and the traits like days to heading, days to anthesis and days to maturity showed moderate genetic advance while high heritability coupled with high genetic advance as percent of mean was recorded for thousand grain weight and yield per plot indicating effectiveness of selection for the improvement of these traits.

2.8. Correlations among Traits of Bread Wheat

The various characteristics of crop plants are generally interrelated or correlated. Such correlations can be either negative or positive. In plant genetics and breeding studies, correlated traits are of prime importance because of genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes brought about by a natural or artificial selection (Singh, 1993; Falconer and Mackay 1996; Sharma 1998).

Falconer and Mackay (1996) proposed two causes of correlation between traits, genetic and environmental. The genetic cause of correlation is chiefly pleiotropy, though linkage is a cause of transient correlation, particularly in populations derived from crosses between divergent strains. Falconer and Mackay (1996) also proposed degree of correlation arising from pleiotropy expresses the extent to which two traits are influenced by the same genes. But the correlation resulting from pleiotropy is the overall, or net, effect of all the segregating genes that affect both traits. Some genes may increase both traits, while others increase one and reduce the other; the former tend to cause a positive correlation, the latter a negative one.

The environment is a cause of correlation in so far as two traits are influenced by the same differences of environmental conditions. Again, the correlation resulting from environmental causes is the overall effect of all the environmental factors that vary; some may tend to cause a positive correlation, others a negative one.

Phenotypic correlations measure the extent to which the two observed traits are linearly related. It is determined from measurements of the two traits in a number of individuals of the populations. Genetic correlation (rg) is the associations of breeding values (i.e additive genetic variance) of the two traits.

Genetic correlation measures the extent to which degree the same genes or closely linked genes cause co-variation (simultaneous variations) in two different traits. The correlation of environmental deviations together with non-additive genetic deviations (i.e. Dominance and epistatic genetic deviations) is referred to as environmental correlations (re) (Singh and Chaudhary 1977; Falconer and Mackay 1996; Sharma 1998).

When breeders attempt to improve an animal or plant they are generally interested in upgrading several attributes of the phenotype simultaneously. Thus, they may wish not only to increase the egg production of hens or seed yield of sunflower but also the size of the eggs or the oil content of the seed. The extent to which these traits are correlated will, therefore, influence the breeder's success. From these illustrations we can see that knowledge of the extent, direction and cause of the correlation between traits is important and we devote part of this chapter to their analysis (Kearsey and Pooni, 1996).

Both environmental and genetic correlations are important to a breeder because they collectively determine how effective the selection program would be. While the breeder can do little about the environmental correlations, except note their direction and try to minimize them or exploit them as the situation may demand, the genetic correlations would have to be manipulated to improve the efficiency of selection. It is therefore important to examine the underlying causes of the phenotypic correlation and identify and separate its causal components (Kearsey and Pooni, 1996).

According to Lynch and Walsh (1998) correlation coefficients may range in value from -1 to +1. Phenotypic correlations can normally be estimated with a high degree of accuracy. Estimates of genetic correlations, however, usually have high standard errors because of difficulties to avoid the directional effects of confounding factors (i.e. Dominance and epistatic genetic effects) on additive genetic correlation estimates.

Salehi *et al*. (2018) carried out an experiment on correlation, regression and path analysis, among yield and yield related traits in wheat and observed a significant correlation among bread wheat, strong positive and highly significant correlation between grain yield per plant and each of fertile tiller numbers and grain number, and grain weight, and thousand grain weights. Total tillers number had a positive, highly significant correlation with fertile tiller number and negative significant correlation with thousand grain weight. Productive tiller number had a positive significant correlation with grain number per spike and negative and highly significant correlation with thousand grain weight. The correlation between grain number and grain weight was positive and highly significant, and the same relationship was between grain weight and thousand grain weight.

Kandel *et al*. (2017) reported that harvest index, effective tiller and thousand kernel weights were highly positive significant correlation with grain yield. Whereas individual trait, exhibited a highly significant correlation with other traits *viz*., effective tiller, thousand grain weight and grain yield.

Din *et al*. (2018) concluded that days to maturity showed non-significant negative correlation with grain per spike while showed positive, non-significant correlation with productive tillers, leaf area index, plant height, 1000-grains weight, biomass yield and grain yield. Productive tillers showed positive significant correlation with grain yield and it had negative significant correlation with grain spike-1 while positive, non-significant correlation with leaf area index, plant height, 1000-grains weight, biomass yield and grains yield. 1000-grains weight had positive, non-significant correlation with grain yield and plant height, while it had negative non-significant correlation with productive tillers, leaf area index, and biomass yield. Plant height revealed a positive significant correlation with productive tillers, while showing negative non-significant correlation with grains per spike. Iqbal *et al*. (2017) reported that grain yield had significant positive phenotypic and genotypic correlation with days to heading, days to maturity, flag leaf area and biomass yield.

Berhanu *et al*. (2017) reported that grain yield had positive and highly significant genotypic correlation with biomass yield and harvest index. Grain yield also exhibited positive and significant genotypic correlation with plant height, thousand kernel weights.

Bhushan *et al*. (2018) found that there is strong genotypic and phenotypic correlation coefficient in test weight, biomass yield, spikelets per spike and grain filling period. While the days to heading, plant height and days to maturity has direct negative correlation with grain yield. Direct non-significant genotypic correlation was observed for harvest index.

Kabir *et al*. (2017) evaluated bread wheat genotypes for yield and its associated traits and observed correlation between yield and yield related traits strong correlation was found for days to flowering with plant height, followed by plant height and days to 50% maturity, grains per spike and total grain weight with plant height. Moderate correlation was noticed among straw weight with plant height and days to flowering, followed by days to 50% maturity. Hundred percent correlations were noticed for days to 50% maturity with days to flowering.

2.9. Path Coefficient Analysis of Traits

Path coefficient analysis is an important statistical tool that can be used to obtain an indication of which variables (causes) exert influence on other variables (effects), while recognizing the impacts of multicolinearity (Akanda and Mundt, 1996).

Partitioning of the cause and effect relationship of different traits will help to see what is contributing to the observed correlation. In some conditions, correlation alone does not give the exact picture of direct and indirect effect of traits upon each other; thus, path coefficient analysis is preferable, since it can identify the direct and indirect causes of associations and can measure the relative importance of each (Singh and Chaudhary, 1977)

Correlation analysis aided by path coefficient analysis is a powerful tool to study the trait associations. Grain yield of wheat is a complex character affected directly or indirectly by every gene present in the plant. Genotypic and phenotypic correlations are of value to indicate the degree to which various morpho-physiological traits are associated with economic productivity (Alam *et al*., 1992).

Knowledge of inter-trait relationship is very important in plant breeding for indirect selection for traits that are not easily measured and for those that exhibit low heritability. Correlation studies between traits have also been of great value in the determination of the most effective breeding procedures. As the number of independent traits affecting a dependent trait increases, there is bound to be some amount of interdependence. Under such a complex situation, correlation alone becomes insufficient to explain relationships among traits (Ariyo *et al*., 1987).

Path-coefficient analysis is one of the reliable statistical techniques, which allow quantifying the interrelationship of different components, and their direct and indirect effects on grain yield. Shelembi and Wright (1991) through correlation estimate the mutual relationship of different morpho-physiological traits and also the type and extent of their contribution to yield.

The correlation values explain only the nature and extent of the association existing between the pairs of traits. A dependent trait like grain yield is influenced by several component traits which are mutually associated. Each component has two path actions, direct effect on yield and indirect effects through components which are not revealed by correlation studies alone (Dewey and Lu, 1959).

Ali Mansouri *et al*. (2018) found the negative and significant correlation coefficients, relating grain yield to the number of days to heading, were made of sizeable negative indirect effects via other traits and high and significant correlation coefficients relating grain yield to aboveground biomass and to spike number were made of high direct effect for biomass yield and indirect effects for spike number. Indirect effects of biomass yield and direct effect of spike number, on grain yield.

Sharma *et al*. (2018) revealed that number of effective tillers per plant had highest positive direct effects on grain yield followed by the number of grains per spike, hundred grain weights, spike weight, days to heading and spike length. The negative direct effect towards grain yield was recorded for grain weight per spike followed by peduncle length, number of spikelet's per spike and plant height. The number of grains per spike has indirect influence for grain yield via spike weight, grain weight per spike, spike length and tillers per plant. The indirect effect for tillers per plant in a positive direction towards yield per plant was observed via plant height, peduncle length, number of grains per spike and hundred grain weights. Similarly for spike weight the indirect effect in a positive direction was recorded through traits *viz*., grain weight per spike, number of grains per spike, hundred grain weight and spike length. The positive indirect effect was also recorded for hundred grain weight via grain weight per spike, spike weight, spike length, number of grains per spike. The negative indirect contribution towards grain yield has been mainly observed in the case of grain weight per spike *via* spike weight. Obsa *et al.* (2017) reported that harvest index exerted the highest positive direct effect on grain yield followed by biomass yield per plot and days to maturity.

2.10. Genetic Divergence and Clustering of Bread Wheat

The pattern and level of genetic diversity in a given crop gene pool can be measured in terms of genetic distances. Genetic distances are measures of the average genetic divergence between cultivars or populations (Souza and Sorrells, 1991). Moll *et al*. (1965) defined genetic divergence of two varieties as a function of their ancestry, geographic separation and adaptation to differing environments. Genetic distance is the extent of genetic differences between cultivars as measured by allele frequencies in a sample of loci (Nei, 1987). Genetic similarity is the converse of genetic distances, as it refers to the extent of gene similarities among cultivars (Smith, 1984).

Conservation of germplasm resources is fundamental to crop improvement programs. However, for practical exploitation of the apparent variability, grouping or classification of genetic stocks based on a suitable scale is quite imperative, similarly, choice of genetically divergent parents for hybridization, under the transgresive breeding program, is also dependent upon categorization of breeding materials based on appropriate criteria. To that end, D^2 statistic is now most frequently used for these purposes (Sharma, 1998).

A meaningful classification of experimental material that enables to distinguish genetically close and divergent type is a prerequisite for both theoretical as well as practical plant breeding. Eco-geographical diversity has been regarded as an index of genetic diversity (Vavilov, 1926). D^2 statistic was first applied by Nair and Mukherji (1960) in biomass populations to classify the natural and plantation teak trees based on four important traits such as specific gravity, nodule structure, nodule elasticity and maximum crushing stress. Its application was extended to plant breeding subsequently by Murty and Pavate (1962) that assessed that these techniques can be extended to situations where overlapping species are to be discriminated and also to the discrimination at the sub- species level specific and species levels in several crops.

Singh and Kumar (2017) studied 60 diverse genotypes of wheat for fifty traits using Cluster analysis and principal component analysis. They found that grain yield per plant, number of grains per spike and1000 grains weight were contributed maximum towards total divergence in forming the eight groups obtained by cluster analysis.

Santosh *et al*. (2019) also studied genetic divergence in 32 diverse genotypes of bread wheat for sixteen agronomic and three physiological traits. On the basis of D^2 analysis, the genotypes were grouped into six clusters. The Clusters V and VI showed the maximum inter-cluster distance (1924.88) suggested a genetically distant relationship between these two clusters and high degree of genetic diversity among the genotypes followed by clusters-I and IV (1879.23), clusters-II and IV (1518.53), clusters-III and VI (1325.23), clusters-I and IV (1163.56), clusters-III and V(1105.93), clusters-I and V (996.05), clusters-III and IV (970.10), clusters-IV and VI (957.17), clusters-II and III (665.03), clusters-II and IV (638.41), clusters-IV and V (614.64), clusters-I and III (597.46), clusters-II and IV (596.43) while the lowest inter-cluster distance was observed between clusters-I and II (410.95) suggested a closer relationship between these two clusters and low degree of genetic diversity among the genotypes.

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted in Kaffa zone, Gewata Woreda, Bonga agricultural research center, Shupa substation in 2010/11 E.C. main cropping season. The experimental site is found in Southern Nations, Nationalities, and Peoples Regional State in Kaffa Zone. It's found in the South west of Addis Abeba and 550 km far from the capital city of Ethiopia and 102 km from Bonga town. It has minimum and maximum temperatures of 11.69 ^{0}c and 23.52 ^{0}c respectively. Its mean annual rainfall is 2115.91 mm. It is located at the latitude of 07^{0}35'026"North and a longitude of 035^{0}52'058" East and at an altitude of 2240 meters above the sea level. The soil type of the experimental site is known to be Clay loam having a p^H of 5.5 which is moderately acidic.

3.2. Planting Material

The planting material used in the study comprised hundred accessions of bread wheat collected from different regions of Ethiopia, and obtained from the Ethiopian Biodiversity Institute. Three varieties were used as a check. The accessions were selected randomly from major wheat producing regions. The details of accessions are summarized on (Table 1).

Table 1. Accession code, region of collection and altitude of bread wheat accessions

S/ No	Accession Number	Region	Zone	Woreda	Latitude	Longitude	Altitude
1	5196	Amhara	Agew Awi	Banja	11-00-00-N	36-54-00-E	2489.00
2	5261	Oromiya	Semen Shewa	Berehna Aleltu	08-50-00-N	39-00-00-E	2420.00
3	5335	Amhara	Semen Shewa	Minjarna Shenkora	09-55-00-N	39-22-00-E	2270.00
4	5377	Oromiya	Mirab Shewa	Ambo	08-59-00-N	37-51-00-E	1772.00
5	5670	Oromiya	Misrak Shewa	Lome	08-47-00-N	39-15-00-E	2300.00
6	6859	Oromiya	Bale	Raytu	06-59-00-N	39-12-00-E	2510.00
7	6883	Oromiya	Bale	Sinanana Dinsho	07-04-00-N	40-11-00-E	2460.00
8	6884	Oromiya	Bale	Sinanana Dinsho	07-03-00-N	40-18-00-E	2250.00
9	6885	Oromiya	Bale	Goro	06-59-00-N	40-28-00-E	1900.00
10	6887	SNNPR	Bench Maji	Konso Special	05-18-00-N	37-20-00-E	1500.00
11	6991	Oromiya	Arsi	Chole	08-22-00-N	39-56-00-E	2800.00
12	6999	Oromiya	Arsi	Sude	07-59-00-N	39-55-00-E	2585.00
13	7010	Oromiya	Arsi	Munesa	08-19-00-N	39-42-00-E	2635.00
14	7028	Oromiya	Arsi	Chole	08-21-00-N	39-56-00-E	2880.00
15	7033	Oromiya	Arsi	Sude	07-59-00-N	39-55-00-E	2590.00
16	7248	Amhara	Agew Awi	Banja	10-55-00-N	36-58-00-E	2400.00
17	7253	Amhara	Misrak Gojam	Guzamn	10-21-00-N	37-40-00-E	2290.00
18	7257	Amhara	Misrak Gojam	Guzamn	10-15-00-N	37-51-00-E	2390.00

Table 1 (*Continued*)

S/ No	Accession Number	Region	Zone	Woreda	Latitude	Longitude	Altitude
19	7259	Amhara	Misrak Gojam	Guzamn	10-19-00-N	37-43-00-E	2450.00
20	7279	Amhara	Semen Gondar	Wegera	12-50-00-N	37-43-00-E	2850.00
21	7304	SNNPR	Semen Omo	Offa	06-33-00-N	37-41-00-E	2200.00
22	7341	Oromiya	Mirab Harerge	Tulo	09-15-00-N	40-08-00-E	2420.00
23	7506	Amhara	Semen Wello	Meket	11-38-00-N	38-50-00-E	2750.00
24	8285	SNNPR	Semen Omo	Arba Minch Zuria	06-08-00-N	37-35-00-E	2020.00
25	8313	SNNPR	Semen Omo	Chencha	06-19-00-N	37-31-00-E	2610.00
26	8314	SNNPR	Semen Omo	Chencha	06-19-00-N	37-31-00-E	2600.00
27	29808	SNNPR	Gamogofa	West Abaya	06-23-18-N	37-40-04-E	2470.00
28	29810	SNNPR	Gamogofa	Mirab Abaya	06-23-99-N	37-39-24-E	2515.00
29	29811	SNNPR	Gamogofa	Mirab Abaya	06-23-99-N	37-39-27-E	2498.00
30	29812	SNNPR	Gamogofa	Mirab Abaya	06-23-87-N	37-39-54-E	2519.00
31	29813	SNNPR	Gamogfa	Arbaminch Zuria	06-01-56-N	37-27-41-E	2195.00
32	29814	SNNPR	Gamogofa	Arbaminch Zuria	06-01-56-N	37-27-41-E	2196.00
33	203754	Amhara	Agew Awi	Banja	11-00-00-N	36-54-00-E	2489.00
34	203755	Amhara	Agew Awi	Banja	11-00-00-N	36-54-00-E	2489.00
35	203915	Tigray	Debubawi	Enderta	13-30-00-N	39-33-00-E	2687.00
36	204362	Amhara	Debub Gondar	Farta	11-48-00-N	38-13-00-E	2970.00
37	204585	Amhara	Agew Awi	Dangela	11-15-00-N	36-50-00-E	2400.00

Table 1 (*Continued*)

S/ No	Accession Number	Region	Zone	Woreda	Latitude	Longitude	Altitude
38	204586	Amhara	Agew Awi	Dangela	11-15-00-N	36-50-00-E	2500.00
39	206544	Tigray	Debubawi	Enderta	13-30-00-N	39-33-00-E	2200.00
40	207845	Tigray	Debubawi	Endamehoni	12-47-00-N	39-31-00-E	2050.00
41	207855	Tigray	Debubawi	Alaje	NA	NA	2300.00
42	211488	SNNPR	Bench Maji	Konso Special	05-19-00-N	37-23-00-E	1860.00
43	212653	Amhara	Semen Wello	Dawuntna Delant	11-44-00-N	39-16-00-E	2760.00
44	213037	SNNPR	Hadiya	Limo	NA	NA	2290.00
45	213309	Tigray	Debubawi	Enderta	13-30-00-N	39-33-00-E	2520.00
46	214115	SNNPR	Semen Omo	Ela	NA	NA	2450.00
47	214116	SNNPR	NA	Yem Special Woreda	05-18-00-N	37-20-00-E	2300.00
48	214264	Amhara	Semen Gondar	Debark	13-08-00-N	37-56-00-E	2860.00
49	216669	SNNPR	Gedeo	Wenago	06-15-00-N	38-10-00-E	2140.00
50	216670	SNNPR	Gedeo	Wenago	06-15-00-N	38-10-00-E	2250.00
51	219348	Oromiya	Borena	Yabelo	04-16-00-N	38-11-00-E	1550.00
52	219354	Oromiya	Borena	Liben	05-19-00-N	39-35-00-E	1460.00
53	221735	Tigray	Debubawi	Enderta	13-28-00-N	39-32-00-E	2170.00
54	2217340	Tigray	Debubawi	Enderta	13-31-00-N	39-29-00-E	1990.00
55	222194	SNNPR	Hadiya	Soro	07-26-00-N	37-49-00-E	2440.00
56	222300	Oromiya	Bale	Agarfa	07-13-00-N	39-50-00-E	2460.00

Table 1 (*Continued*)

S/ No	Accession Number	Region	Zone	Woreda	Latitude	Longitude	Altitude
57	222384	Oromiya	Arsi	Jeju	08-04-00-N	39-35-00-E	1660.00
58	222385	Oromiya	Arsi	Jeju	08-04-00-N	39-35-00-E	1660.00
59	222388	Oromiya	Arsi	Amigna	07-40-00-N	39-56-00-E	2490.00
60	222389	Oromiya	Arsi	Amigna	07-40-00-N	39-56-00-E	2490.00
61	222476	Oromiya	Misrak Wellega	Limu	09-55-00-N	36-37-00-E	2090.00
62	222482	Oromiya	Misrak Wellega	Guto Wayu	09-08-00-N	36-41-00-E	2470.00
63	222494	Amhara	Mirab Gojam	Dega Damot	10-42-00-N	37-09-00-E	2000.00
64	222518	Amhara	Semen Gondar	Wegera	12-50-00-N	37-43-00-E	2850.00
65	222520	Amhara	Semen Gondar	Wegera	12-50-00-N	37-43-00-E	2850.00
66	222686	Amhara	Semen Wello	Wadla	11-32-00-N	39-05-00-E	2840.00
67	222691	Amhara	Semen Wello	Wadla	11-35-00-N	39-04-00-E	2250.00
68	222705	Amhara	Semen Wello	Dawuntna Delant	11-35-00-N	39-13-00-E	2865.00
69	222761	SNNPR	Bench Maji	Konso Special	05-18-00-N	37-20-00-E	1500.00
70	222783	SNNPR	Gedeo	Wenago	06-15-00-N	38-10-00-E	2140.00
71	222784	SNNPR	Gedeo	Wenago	06-15-00-N	38-10-00-E	2140.00
72	222785	SNNPR	Gedeo	Wenago	06-15-00-N	38-10-00-E	2140.00
73	222800	Oromiya	Bale	Goro	07-00-00-N	40-27-00-E	1900.00
74	222823	SNNPR	NA	Yem Special Woreda	05-18-00-N	37-20-00-E	2300.00
75	222837	Amhara	Semen Gondar	Debark	13-08-00-N	37-56-00-E	2860.00

Table 1 (*Continued*)

S/ No	Accession Number	Region	Zone	Woreda	Latitude	Longitude	Altitude
76	226246	Tigray	Debubawi	Enderta	13-30-00-N	39-33-00-E	2687.00
77	226259	SNNPR	Hadiya	Soro	07-31-00-N	37-52-00-E	2250.00
78	226261	SNNPR	Hadiya	Soro	07-31-00-N	37-52-00-E	2250.00
79	227072	SNNPR	Semen Omo	Gofa Zuria	NA	NA	2530.00
80	227073	SNNPR	Semen Omo	Gofa Zuria	NA	NA	2445.00
81	228124	SNNPR	Hadiya	Limo	NA	NA	2340.00
82	228138	SNNPR	Hadiya	Limo	NA	NA	2022.00
83	228756	Oromiya	Mirab Shewa	Ambo	NA	NA	1500.00
84	222674	Amhara	Debub Gondar	Farta	NA	NA	2670.00
85	231578	Amhara	Debub Gondar	Lay Gayint	11-44-00-N	38-25-00-E	2980.00
86	240507	SNNPR	Kaffa	Chena	07-35-00-N	35-52-00-E	2550.00
87	240508	SNNPR	Kaffa	Chena	07-35-00-N	35-52-00-E	2340.00
88	240509	SNNPR	Kaffa	Chena	07-35-00-N	35-52-00-E	2645.00
89	240510	SNNPR	Kaffa	Chena	07-35-00-N	35-52-00-E	2247.00
90	240511	SNNPR	Kaffa	Chena	07-35-00-N	35-52-00-E	2457.00
91	242425	Oromiya	Mirab Harerge	Chiro	09-06-00-N	40-58-00-E	2206.00
92	242426	Oromiya	Mirab Harerge	Chiro	09-06-00-N	40-58-00-E	2213.00
93	242427	Oromiya	Mirab Harerge	Chiro	09-06-00-N	40-58-00-E	2220.00
94	242428	Oromiya	Mirab Harerge	Chiro	09-06-00-N	40-58-00-E	2206.00

Table 1 (*Continued*)

S/ No	Accession Number	Region	Zone	Woreda	Latitude	Longitude	Altitude
95	242429	Oromiya	Mirab Harerge	Chiro	09-06-00-N	40-58-00-E	2229.00
96	243702	Amhara	Semen Wello	Dawuntna Delant	11-34-00-N	39-14-00-E	2950.00
97	243704	Amhara	Semen Wello	Dawuntna Delant	11-34-00-N	39-14-00-E	2950.00
98	243710	Tigray	Debubawi	Endamehoni	12-47-00-N	39-31-00-E	2455.00
99	243711	Tigray	Debubawi	Endamehoni	12-45-00-N	39-27-00-E	2330.00
100	243726	Amhara	Semen Gondar	Debark	13-08-00-N	37-56-00-E	3115.00

NA: Not available, Source: *Ethiopian Biodiversity Institute*

3.3. Experimental Design and Trial Management

This experiment was conducted in 2018/19 cropping season. The experiment was laid out in an Augmented Design (AD) with ten blocks. Each block comprised ten accessions and three checks, a total of thirteen accessions in one block. All the checks were repeated in all the blocks randomly, while the accessions were un-replicated. Each accession was sown in two rows with 1.50 m long and 0.4 m width. Spacing between blocks and the plots were 1m and 0.5m respectively. The total area required for an experiment was 364 m^2. The recommended seed rate/ha of 150 kg was used and the NPS were applied at the rate of 100 kg/ha. All the normal recommended agronomic practices and plant protection measures were carried out during the crop growth period as per EIAR (2004) recommendation.

3.4. Data Collection

3.4.1. Quantitative traits

3.4.1.1. Data taken on plant basis

All the data were recorded based on the wheat descriptor list (IBPGR, 1985)

Plant height (cm): Height of five randomly taken plants from each experimental unit was measured from the ground level to tip excluding awn and the mean was recorded as plant height at maturity.

Number of productive tillers per plant: Number of tillers which bear mature spike of five randomly taken plants from each experimental unit was counted and the mean was recorded as productive tillers per plant.

Spike length (cm): The length of spikes of five randomly taken plants was measured excluding awns in centimeter and the mean was taken as spike length.

Number seed per spike: The seed of five randomly selected spikes was counted and the mean was taken as number of kernels/seeds per spike.

3.4.1.2. Data taken on plot basis

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

Days to maturity (DM): The numbers of days from seedling emergence to the stage when 90% of the plants in a plot have reached physiological maturity were recorded.

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

Thousand seed weights (g): Thousand seed weight was measured when the grains attained 12-15% moisture content.

Grain yield (t/ha): Harvested and threshed grain yield from each experimental plot was taken and measured when the grain attained 12-15% moisture content.

Biomass yield: The above ground biomass yield at the time of harvesting was measured for each experimental unit.

Harvest index: it was recorded as the ratio of grain yield to the above ground biomass yield per plot.

3.4.2. Qualitative traits

Qualitative traits were recorded as per bread wheat descriptor list (IBPGR, 1985)

Glume color was recorded 1 as white, 2 as red to brown and 3 as purple to black

Awnedness was recorded 3 as awnless, 5 as awnletted and 7 as awned

Awn roughness was recorded 3 as smooth, 5 as intermediate and 7 as rough

Spike density was recorded 1 as very lax, 3 as Lax, 5 as intermediate, 7 as dense and 9 as very dense

Seed color was recorded 1 as white, 2 as red and 3 as purple

Seed size was recorded 3 as small, 5 as intermediate, 7 as large and 9 as very large

Seed shape was recorded 3 as ovoid, 5 as semi-elongated and 7 as Elongated

3.5. Statistical Analysis

The statistical analysis of the data on individual plant traits were carried out by using the mean values of five plants from each accession. The data were analyzed using SAS version 9.3 (SAS, 2014) software.

3.5.1. Quantitative traits

3.5.1.1. Analysis of variance

The analysis of variance for traits was carried out following the Augmented Design suggested by Sapra and Agarwal (1991) (Table 2).

Table 2. ANOVA table for Augmented Design

Source of variation	Df	SS	MS	F-value
Block	(b-1)	SSb	MSb	MSB/MSE
Treatment	(c+g)-1	SSt	MSt	$\frac{MSt}{MSe}$
Among-controls	(c-1)	SSc	MSc	$\frac{MSc}{MSe}$
Among-accessions	(g-1)	SSg	MSg	$\frac{MSg}{MSe}$
Accessions-vs-Control	1		$\frac{SSe}{(c-1)(b-1)}$	
Error	(b-1)(c-1)			

Where, g = Number of accessions tested

c= Number of check varieties

b = Number of blocks

Quantitative data were analyzed by using SAS version 9.3 (SAS, 2014). A PROC GLM model procedure was used as adopted as:

$$\mathbf{Y_{ij} = \mu + \beta_j + C_j + \tau_{k(i)}\ e_{ij}}$$

Where: Y_{ij} is the response variable, μ is general mean, β_j is the effect of jth block, C_j the effect of jth check, τk(i) the effect of ith new entries and eij is random errors.

3.5.1.2. Estimation of variance components

Genotypic and phenotypic variances were estimated using the following formula suggested by Burton and De Vane (1953).

Genotypic variance $= \frac{\textbf{TMS}-\textbf{MSE}}{\textbf{Block}}$

Where TMS = Mean square of treatment, MSE= Mean square of error

Phenotypic variance = Genotypic variance + error MS

Where σ^2g= Genotypic variation; MS = mean square

Coefficients of variation for quantitative traits were computed by the following formula as suggested by Burton and De Vane (1953).

Phenotypic Coefficient of Variation (PCV) $= \frac{\sqrt{\sigma^2 p}}{\bar{x}} x100$

Genotypic Coefficient of Variation (GCV) = $\frac{\sqrt{\sigma^2 \mathrm{g}}}{\bar{x}} \boldsymbol{x}100$

Where:

σ^2p =Phenotypic variation;

σ^2g= Genotypic variation and

$\bar{x}$= Grand mean of the trait

The PCV and GCV were classified as suggested by Burton and Devane (1953**)** into the following classes.

0 – 10%	Low
10 – 20%	Moderate
20 and above	High

3.5.1.3. Heritability and genetic advance

Heritability in broad sense for all traits were calculated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage according to the method suggested by Falconer and Mackay (1996).

$$H= \frac{\sigma^2 \mathrm{g}}{\sigma^2 \mathrm{p}} x100$$

Where, H = heritability in a broad sense

σ^2g = the genotypic variance, where $\sigma^2g = \frac{\textbf{Mean square treatment} - \textbf{Mean square of error}}{\textbf{Block}}$

σ^2p = phenotypic variance, where σ^2p = Genotypic variance + mean square of error

Heritability was classified as suggested by Robinson *et al*. (1949) into different classes as follows

0 – 30%	Low
30 – 60%	Moderate
60 and above	High

Genetic advance

Genetic advance was calculated by assuming selection of superior 5% of the genotypes was estimated as suggested by (Falconer and Mackey, 1996) as:

$$GA = K * \sigma p * H$$

Where, GA = expected genetic advance,

H = heritability in the broad sense,

K = the selection differential which k constant is 2.063

σp= phenotypic standard deviation on mean basis

Genetic advance as % of the mean (GAM) was computed as:

$$GAM = \frac{GA}{\bar{x}} x100$$

Where,

GA = genetic advance under selection,

GAM = the genetic advance as % of mean

$\overline{X}$= mean of population

Genetic advance as per cent of the mean was categorized as suggested by Johnson *et al*. 1955a, into following cases

0 - 10%	Low
10 – 20%	Moderate
20 and above	High

3.5.1.4. Genotypic path coefficient analysis

The direct and indirect effect of component traits on yield and among themselves were estimated following the method suggested by Dewey and Lu, (1959) and is given as follows:

$$r_{ij} = p_{ij} + \sum r_{ik}\, p_{kj}$$

Where: - r_{ij} = Mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient. Pij = Component of direct effects of the independent trait (i) on the dependent variable (j) as measured by the path coefficient and, $\sum r_{ik}\, p_{kj}$ = Summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) via all other independent traits (k). Residual effect estimated by the formula

$$\text{Residual effect} = \sqrt{1 - R^2}$$

Where: - $R^2 = \sum r_{ik}\, p_{kj}$ Where, R^2 is the residual factor, Pij is the direct effect of yield by ith trait, and rij is the correlation of yield with the ith trait.

3.5.1.5. Cluster analysis

Clustering were performed using the proc cluster procedure of SAS version 9.3 (SAS Institute, 2014) by employing the method of average linkage clustering strategy of the observation. The numbers of clusters were determined by following the approach suggested by Cooper and Miligan (1988) by looking into three statistics namely Pseudo F, Pseudo t^2 and cubic clustering criteria. The dendrogram were constructed on the basis of paired group and Euclidean distance used as a measure of dissimilarity technique. Mahalanobis's D^2 statistics (1936) were also used to examine the genetic distance between populations. The generalized distance between any two populations is expressed as:

$D^2_{ij} = (x_i - x_j)\, cov^{-1}\, (x_i - x_j)$; where, D^2_{ij} =the distance between cases i and j; xi and xj =vectors of the values of the variables for cases i and j; and cov^{-1} = the pooled within group variance covariance matrix.

3.5.1.6. Principal component analysis

The principal component analysis (PCA) was computed to reduce the number of variables into a few correlated components that can explain much of the variability. It was performed using the correlation matrix to define the patterns of variation among landraces based on the mean of quantitative traits. Principal component analysis was performed by using SAS version 9.3 (SAS, 2014). The contribution of observation i to component l is denoted by and obtained using the formula suggested by Saporta and Niang, 2009.

$$Ctr_{i,l} = \frac{\mathrm{f}^2{}_{i,l}}{\lambda \mathrm{l}} \times 100$$

Where, $f^2{}_{i,l}$ squared factor scores of each observation, λl are the eigenvalue of the l-th component.

3.5.2. Qualitative traits

3.5.2.1. Phenotypic frequency

Phenotypic frequency of qualitative traits were calculated using computer excel program. Phenotypic frequency is the proportion of observed value for a give trait to all the sample of the accessions.

3.5.2.2. Shannon Weaver diversity index

Shannon-Weaver diversity index was used to evaluate variation within all accessions. The Shannon-Weaver diversity index was calculated as suggested by Hutchenson (1970).

$$H' = -\sum_{i-1}^{n} pi \ln \; pi$$

Where, **H'** = Shannon-Weaver diversity index; ***Pi* =** is the proportion of accessions in the ith class of an n-class trait and n = is the number of phenotypic classes for a trait.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance (ANOVA)

Mean square of all the traits studied shown significant difference ($P< 0.05$) among the tested accessions (Table 3) indicating existence of sufficient genetic variations in the studied breeding materials for all the traits, which can be exploited through selection.

Table 3. Mean squares from the analysis of variance for eleven quantitative traits of bread wheat landraces

Source of variation	Df	Mean squares					
		DH	DM	GFP	NPT	PH(cm)	SPL (cm)
Block	9	1.35 ^{ns}	39.56 ^{ns}	39.37 ^{ns}	1.17 ^{ns}	60.38 ^{ns}	0.93 ^{ns}
Entries	102	47.67**	122.55**	74.87*	4.25**	280.07**	21.97**
New accessions	99	30.87**	97.47**	40.23 ^{ns}	1.34**	126.27**	3.32 ^{ns}
Checks	2	150.03**	27.03 ^{ns}	51.03 ^{ns}	0.16 ^{ns}	95.21 ^{ns}	0.95 ^{ns}
Checks *vs* accessions	1	77.85**	961.05**	491.85**	5.76**	9144.20**	16.28**
Error	18	1.18	2.7	9.70	0.33	10.89	1.04
CV (%)		1.60	4.93	11.45	15.79	6.85	10.18
Total	129						

*=Significant at probability level of 0.05 and **=Significant at probability level of 0.01; ns= non-significant, df= Degree of freedom, CV%=Coefficient of variation in percentage, DH= Days to heading, DM = Days to maturity, GFP = Grain filling period, NPT = Number of productive tiller, PH = Plant height in centimeter, SPL = Spike length in centimeter

Table 3 (*Continued*)

Source of variation	Df	Mean squares				
		NSPS	TSW(g)	GY (t ha^{-1})	BY (t ha^{-1})	HI
Block	9	3.12^{ns}	0.08^{ns}	0.29^{ns}	0.44^{ns}	0.0036^{ns}
Entries	102	230.44**	32.1**	2.82**	3.88**	0.0694**
New accessions	99	96.04**	0.56**	0.91**	1.09**	0.00697**
Checks	2	248.44**	1.04^{ns}	1.29**	1.74**	0.0013^{ns}
Checks *vs* accessions	1	1260.28**	4.80**	4.08**	4.89**	0.015**
Error	18	3.38	1.3	0.20	0.22	0.0018
CV (%)		7.10	15.70	13.39	12.85	6.20
Total	129					

**=Significant at probability level of 0.01; df= Degree of freedom, CV%=Coefficient of variation in percentage, NSPS= Number of seeds per spike, TSW= Thousand seed weight, GY (t ha^{-1}) = Grain yield in ton per hectare, BY (t ha^{-1}) = biomass yield in ton per hectare, HI = Harvest index

4.2. Range and Mean Values

All the bread wheat accessions showed a wide range of variability for most of the traits (Table 4). Days to heading ranged from 57 to 84 with a mean of 67.95 whereas the early check had 60 days. Days to maturity ranged from 95 to 136 with a mean of 112.39 indicating that there was accession which mature 41 days later than the checks. The result of the present study agrees with the finding of (Habtamu and Ahadu, 2019) who reported high variation among the genotype for days to heading and days to maturity. The accession number 222785 was the earliest to fill grain with 26 days, which is 37 days earlier than late grain filling period while accession number 214115 was late to fill grain with 63 days (Appendix I). The mean value of all the accession for number of productive tiller was 4.1 with a range from 1.5 to 7.2. The lowest number of productive tiller was observed in accession number 7341, whereas accession number 29812 recorded the highest number of productive tillers while the check had 3.6 & 5.4 minimum and maximum tiller number, respectively. The high range of variation for number of plant height was reported by (Arya *et al.*, 2017: Kumar *et al.*, 2017; Berhanu *et al.*, 2016). The mean plant height was 113.89 cm with a range of 77.6 cm to 154.2 cm. The check had lowest plant height of 77.6 cm and the highest plant height of 154.2 cm was observed for accession number 214116. The mean value of all the accession for number of seeds per spike was 40.78 with a range from 16.2 to 66.8. In line with the present study, Yakoob (2016) reported high range of variation for plant height. The lowest number of seeds per spike was observed in accession number 213037, whereas the highest numbers of seeds per spike were recorded in accession number 240507 while the check had 42 and 55.6 minimum and maximum number of seeds per spike respectively. The overall mean value for this trait was 23g. The range value of thousand seed weight was 7 g to 39.5 g. The lowest seed weight was exhibited by the accession number 213309 while highest thousand seed weight was recorded in accession number 6885. The minimum grain yield recorded was 1.047 tons ha^{-1} for accession number 7341, whereas a maximum of 5.70 tons was for accession number 29812 with a mean value of 3.35 tons ha^{-1}. The checks had 2.791 and 4.678 tons ha^{-1} lowest and highest grain yield respectively (Appendix I). Some accessions: 6883, 6884, 29811, 29813, 242429 and 243702 exhibited higher grain yield than the check variety (Shorima). Astawus *et al*. (2018) who reported high range of variation among genotypes for grain yield. In support of the present study (Alemu *et al*., 2017; Habtamu and Ahadu, 2019; Assefa *et al*., 2014) reported a high range of variation for grain yield. In general, higher range of variation among accession for days to heading, days to maturity, grain filling period, number of productive tillers, plant height, **s**pike length, number of seeds per spike, thousand seed weight and grain yield was due to genetic and environmental variation.

4.3. Estimates of Genetic Parameters

4.3.1. Genotypic and phenotypic coefficients of variation

In the present study, GCV ranged from 3.173 for days to heading to 15.279 for grain yield. PCV ranged from 3.553 for days to heading to 21.818 for number of productive tillers (Table 4). According to Burton and Devane (1953), GCV and PCV are classified as high (>20%), medium (10-20%) and low (<10%). Thus, high PCV values were observed for number of productive tillers (21.81%) and grain yield (20.28).

Medium PCV values were observed for spike length (17.66%), number of seeds per spike (12.52%), biomass yield (17.31%) and harvest index (12.33%). Low PCV estimates were observed for days to heading (3.55%), days to maturity (3.40%), grain filling period (9.13%) and plant height (5.39).

Moderate GCV was also observed for grain yield (15.279 %), number of productive tillers (14.965%), biomass yield (13.499%) and harvest index (10.938%).

The present result revealed that the magnitude of the difference was relatively low for days to heading, days to maturity, plant height, spike length, thousand seed weight, number of seeds per spike and thousand seed weight. This suggested that the marked influence of environmental factors for the phenotype expression of genotypes was low and the higher chance of improvement of these traits through selection. In support of present result, Arya *et al*. (2017) and Adhiena *et al*. (2016) reported low magnitude of differences of PCV and GCV were observed for days to heading, days to maturity, plant height, spike length, thousand seed weight and harvest index

In the present study, magnitude of difference between PCV and GCV was high for grain filling period, number of tillers, grain yield and biomass yield. This implies greater influence of environmental factors for the phenotypic expression of these traits that enhances breeder to use heterosis/ hybridization/ breeding strategy. In relation with present result, (Obsa *et al*., 2017; Alemayehu *et al*., 2019; Desheva and Kyosev, 2015) reported high magnitude of differences of the PCV and GCV was observed for number of productive tillers, grain yield and biomass yield.

Table 4. Mean, range, phenotypic and genotypic variances and coefficient of variations; heritability in broad sense and genetic advance for eleven quantitative traits of bread wheat landraces

Traits	Min	Max	Range	Mean	SE	s^2g	s^2p	GCV%	PCV%	H^2 (%)	GA	GAM (%)
DH	57	84	27.00	67.95	1.086	4.649	5.829	3.173	3.553	79.756	3.972	5.846
DM	95	136	41.00	112.39	5.692	11.985	14.685	3.080	3.409	81.614	6.452	5.740
GFP	26	63	37.00	44.10	5.449	6.517	16.217	5.788	9.131	40.186	3.338	7.570
NPT	1.5	7.2	5.70	4.13	0.652	0.382	0.812	14.965	21.818	47.044	0.874	21.175
PH	77.6	154.2	76.60	113.89	7.803	26.918	37.808	4.555	5.39	71.196	9.031	7.929
SPL	6.2	15.4	9.20	10.02	1.019	2.093	3.133	14.438	17.664	66.804	2.439	24.345
NSPS	16.2	66.8	50.60	40.78	2.895	22.706	26.086	11.684	12.524	87.042	9.171	22.489
TSW	7	39.5	32.5	23	0.362	3.08	4.38	7.630	9.099	70.319	3.036	13.20
GY	1.0474	5.7012	4.65	3.35	0.448	0.262	0.462	15.279	20.289	56.710	0.795	23.737
BY	2.0129	6.7884	4.78	4.42	0.568	0.366	0.586	13.687	17.319	62.457	0.986	22.315
HI	0.4488	0.9692	0.52	0.75	0.046	0.00676	0.00856	10.962	12.336	78.971	0.150	20.097

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NPT: Number of productive tillers , PH: Plant height (cm), SPL: Spike length (cm), NSPS: Number of seed per spike, TSW: Thousand seed weight (g), GY: Grain yield (t ha^{-1}), BY: biomass yield (t ha^{-1}), HI: Harvest index, SE: Standard error s^2g: Genotypic variance, s^2p: Phenotypic variance, PCV: Phenotypic coefficient of variations, GCV: Genotypic coefficient of variations, H^2: Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as percent of mean

4.3.2. Estimation of heritability in broad sense and genetic advance

The effectiveness of selection for any traits depends not only on the amount of phenotypic and genotypic variability, but also on the magnitude of heritability.

The estimated heritability was studied for all traits (Table 4). The heritability values ranged from 40.186 for grain filling period to 87.042% for number of seeds per spike. According to Robinson *et al*. (1949) classified heritability values as: Low (0 – 30%); moderate ((30 – 60%) and high (60 and above). Thus, high heritability was observed for days to heading (79.75%), days to maturity (81.61%), plant height (71.19%), spike length (66.80%), number of seeds per spike (87.04%), thousand seed weight (70.31%), biomass yield (62.45%) and harvest index (76.21%) which indicates that environment had low influence on the expression of the traits suggesting direct selection for improvement. In support of the present study, Alemu *et al*. (2019) reported high heritability for days to heading and spike length. Moderate broad sense heritability was observed for the grain filling period (40.18%), number of productive tillers (47.04%) and grain yield (56.71%) which may be due to influence of the environment on the expression of the traits. In relation with present the finding Gezahegn *et al*. (2015) reported moderate heritability for grain yield. Din *et al*. (2018) also reported high heritability estimate for plant height and grain per spike. Iqbal *et al*. (2017) reported high heritability for days to heading, days to maturity and spike length. In support of the present finding, Kumar *et al*. (2016) reported moderate heritability for number of productive tillers.

The estimates of heritability, however, indicate only the effectiveness with which selection of genotypes can be based on their phenotypic performance, but it provides inadequate information on the amount of progress expected from selection (Johnson *et al*., 1955a). Therefore, heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance. In the present study, high heritability coupled with high genetic advance as per cent of the mean was observed for spike length, number of seeds per spike, biomass yield and harvest index (Table 4). This suggests that these traits are not much influenced by environmental factors and substantial improvement for these traits could be achieved through direct selection and also these traits are considered to be governed by additive genes. In support of the present finding Arya *et al*. (2017) found high heritability coupled with high genetic advance as percent of the mean for spike length, number of seeds per spike, biomass yield and harvest index.

Moderate heritability coupled with high genetic advance as per cent of the mean were observed for number of productive tiller and grain yield indicating improving these traits through selection would be effective. In agreement with these Din *et al*. (2017) reported moderate heritability with high genetic advance as percent of mean for grain yield. Kumar *et al*. (2017) reported moderate heritability coupled with high genetic advance as percent of mean for number of productive tillers. Alemayehu *et al*. (2019) reported moderate heritability coupled with high GAM for grain yield.

High heritability values associated with low genetic advances as per cent on mean were observed for days to heading, days to maturity and plant height, indicating non-addictive gene expression of these traits. Hence, the selection may not be effective, but heterosis breeding might be important for improvement of these traits. These findings were supported by Alemu *et al.* (2019) who reported high heritability associated with low GAM for days to maturity. Ibrahim, (2019) also pointed out high heritability coupled with low genetic advances as a percent of mean for days to heading and days to maturity. In addition, Kumar *et al*. (2016), Birhanu *et al*. (2016) and Gaur (2019) also reported high heritability coupled with low genetic advance as percent of mean for days to heading and days to maturity.

4.4. Correlation Studies

4.4.1. Correlation of grain yield with other traits at genotypic and phenotypic level

Grain yield exhibited positive significant correlation with the grain filling period, number of productive tillers, spike length, number of seeds per spike, thousand seed weight and biomass yield both at phenotypic and genotypic level (Table 5). Therefore, any improvement of these traits would result in a substantial increment on grain yield. This also implies that selection of accessions on the basis of the grain filling period, number of productive tillers, number of seeds per spike and biomass yield would be beneficial for increasing wheat grain yield. In support of the present findings Alemu *et al*. (2016) who reported grain filling period, number of tillers, spike length, thousand seed weight and biomass yield had positive correlation with grain yield. In agreement with the present Din *et al.* (2018) also pointed out that grain yield had positive significant correlation with number of productive tillers. In line with the present study, Salehi *et al*. (2018) also reported that grain yield had strong positive and highly significant correlation between number of productive tillers, number seed per spike and thousand grain weights. On the other hand, grain yield exhibited negative correlation with days to heading and days to maturity which were due to the nature of the accessions. This finding is in agreement with the findings of Mohammadi *et al*. (2012) who found the presence of negative correlation between days to maturity and grain yield under irrigated condition. The significant correlation of yield related traits with grain yield can be either due to pleiotropy or linkage or both.

4.4.2. Correlation between major traits at genotypic and phenotypic level

Number of productive tillers had positive significant correlation with days to heading and days to maturity; these results suggested the importance of considering these traits due to their contribution to number to productive tiller. While number of productive tillers had negative significant correlation with grain filling period, number of seeds per spike and thousand seed weight both at genotypic and phenotypic level. In support of the present study, Din *et al.* (2018) reported that productive tillers showed negative significant correlation with seed per spike.

At genotypic level, spike length had negative significant correlation with number of productive tillers. At phenotypic level, plant height and biomass yield had positive significant correlation with number of productive tillers. The negative correlation of number of productive tillers with number of seeds per spike and thousand seed weight suggested that the low number of tiller has a high number of seeds per spike and higher seed weight. In close agreement with the present study, Singh and Kumar, (2017) reported that spike length had negative correlation with spike length at genotypic level.

At both genotypic and phenotypic level, the correlation of spike length with a grain filling period, the number of seeds per spike and thousand seed weight was positive and significant which indicated increasing spike length increases the number of seeds per spike while negative correlation with days to heading, days to maturity and number of productive tiller this suggests increasing these traits might decreases spike length. In line with the present study, Singh and Kumar, (2017) also reported significant and positive correlation of spike length with number of seeds per spike and thousand seed weight. In close agreement with the present study, Rathod *et al*. (2019) reported that the number of seeds per spike had positive significant correlation with spike length and negative significant correlation with number of productive tillers.

At both genotypic and phenotypic level, number of seeds per spike showed positive significant correlation with grain filling period, spike length and thousand seed weight (Table 5). In support of the present findings, Arain *et al*. (2018) who reported thousand seed weight and spike length showed positive significant correlation with the number of seeds per spike. In close agreement with the present findings, Rathod *et al*. (2019) reported that the number of seeds per spike had positive significant correlation with spike length and negative significant correlation with number of productive tillers.

At both genotypic and phenotypic level, thousand seed weight showed positive significant correlation with a grain filling period, spike length, number of spikes per spike and biomass yield. However, negative significant correlation of thousand seed weight with days heading, days to maturity and number of productive tillers (Table 5). The present results are similar to that of Zulkiffal *et al*. (2018) who reported positive correlation of thousand seed weight with spike length and number of seeds per spike. Birhanu *et al*. (2017) also found a strong negative correlation with days to heading, days to maturity and strong negative correlation of thousand seed weight with days to heading, days to maturity and strong positive correlation with grain filling period.

Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of the eleven bread wheat traits

Traits	DH	DM	GFP	NPT	PH	SPL	NSPS	TSW	GY	BY	HI
DH	1	0.811**	-0.659**	0.646**	0.327	-0.658**	-0.766**	-0.660**	-0.679**	-0.213	0.318
DM	0.834**	1	-0.506**	0.511**	0.194	-0.527**	-0.641**	-0.487*	-0.574**	-0.089	0.163
GFP	-0.562**	-0.551**	1	-0.628**	-0.014	0.681**	0.714**	0.992**	0.921**	0.467*	-0.367
NPT	0.567**	0.520**	-0.584**	1	0.360	-0.647*	-0.483*	-0.655**	0.627**	0.301	-0.130
PH	0.136	-0.003	-0.028	0.271**	1	0.044	-0.217	-0.043	0.018	-0.148	0.309
SPL	-0.387**	-0.226	0.412**	-0.217	0.061	1	0.624**	0.689**	0.748**	0.099	-0.104
NSPS	-0.485**	-0.384**	0.681**	-0.402**	-0.151	0.433**	1	0.704**	0.791**	0.142	-0.479**
TSW	-0.561**	-0.538**	0.992**	-0.589**	-0.020	0.413**	0.672**	1	0.925**	0.495**	-0.353
GY	-0.599**	-0.576	0.938**	0.567**	0.002	0.473**	0.773**	0.939**	1	0.220**	-0.378
BY	-0.282	-0.313**	0.674**	0.420**	-0.080	0.076	0.234	0.703**	0.458**	1	-0.072
HI	0.303*	0.269*	-0.334**	-0.239	0.150	-0.050	-0.072	-0.325	-0.252	-0.371**	1

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NPT: Number of productive tillers, PH: Plant height (cm), SPL: Spike length (cm), NSPS: Number of seeds per spike, TSW: Thousand seed weight (g), GY: Grain yield (t ha^{-1}), BY: biomass yield (t ha^{-1}), HI: Harvest index, P: phenotypic and G: genotypic correlation coefficient

4.5. Path coefficient analysis of different traits on grain yield at genotypic level

Path coefficient analysis was carried at genotypic levels taking grain yield as dependent traits and all the traits which exhibited significant correlation with grain yield were considered as independent traits.

Among the traits studied, thousand seed weight (1.18), exhibited the highest direct and positive effect on grain yield, followed by a number of productive tillers (0.18) and spike length (0.13) (Table 6). Hence, favorable direct effects of thousand seed weight, number of productive tiller and spike length on grain yield indicate that, with other variables kept constant, improvement of these traits will increase grain yield. However, days to heading (-0.67), days to maturity (-0.07), grain filling period (-1.01), number of seeds per spike (-1.96) and biomass yield (-0.92) (Table 6) had a negative direct effect on grain yield. This suggests that these traits don’t show true correlation with grain yield. Therefore, thousand seed weight, number of productive tiller and spike length could be used as an indirect selection criterion to improve grain yield. Hence emphasis should be given to thousand seed weight, number of productive tiller and spike length. In support of the present study, Arya *et al*. (2017) revealed the direct effect of number of productive tillers per plant, and thousand grain weights towards grain yield. Ibrahim, (2019) who reported thousand seed weight had a genotypic positive direct effect on grain yield. Rajput, (2019) who reported that day to maturity and grain per spike had exhibited negative direct effect on grain yield.

The indirect effect of spike length (0.52), number of seeds per spike (0.61), thousand seed weight (0.53) and biomass yield (0.17) on grain yield was positive *via* days to heading, which suggests the merit of days to heading for improving grain yield. On the other hand, days to maturity (-0.52), grain filling period (-0.82) and a number of productive tillers (-0.66) had considerable negative indirect effects via days to heading. Hence, they could not be used for indirect selection for improving grain yield.

Table 6. Genotypic path coefficients of direct (diagonal) and indirect (off diagonal) effects of eight traits of bread wheat

Traits	DH	DM	GFP	NPT	SPL	NSPS	TSW	BY	rg
DH	**-0.67**	-0.52	-0.82	-0.65	0.52	0.66	0.53	0.17	-0.679**
DM	-0.85	**-0.07**	0.28	-0.69	0.29	0.15	0.27	0.05	-0.574**
GFP	4.51	4.64	**-1.01**	0.39	-1.63	-1.91	-3.42	-2.49	0.921**
NPT	2.04	1.62	-1.98	**0.18**	-0.94	-1.03	-0.14	0.87	0.627**
SPL	-0.62	-0.36	0.53	-0.08	**0.13**	0.44	0.61	0.09	0.748**
NSPS	0.47	0.62	-0.29	1.41	-0.25	**-1.96**	0.97	-0.18	0.791**
TSW	-0.91	-0.19	0.02	-0.31	0.19	0.11	**1.18**	0.83	0.925**
BY	0.31	0.78	-0.04	0.15	-0.02	-0.03	-0.01	**-0.92**	0.220**

Residual effect = 0.198

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NPT: Number of productive tillers, SPL: Spike length, NSPS: Number of seeds per spike, TSW: Thousand seed weight, GY: Grain yield, BY: biomass yield, rg: genotypic correlation coefficient

The residual effect of the present study was 0.198) which indicated that the trait included in the genotypic path analysis explained 80.2% of the total genetic variations in grain yield. Thus, thousand seed weight, spike length and number of productive tillers could be used as indirect criteria for bread wheat improvement.

Grain filling period (0.28), spike length (0.29), number of seeds per spike (0.15), thousand seed weight (0.27) and biomass yield (0.05) had indirect positive effects on grain yield through days to maturity. On the other hand, days to heading (-0.85) and a number of productive tillers (-0.69) had negative indirect effect on grain yield through days to maturity.

Days to heading (2.04), days to maturity (1.62) and biomass yield (0.87) exerted positive and indirect effect *via* number of productive tillers on grain yield. It is also suggested that selecting days to heading and days to maturity had an important role in grain yield improvement. While, grain filling period (-1.98), spike length (-0.94), number of seeds per spike (-1.03), and thousand seed weight (-0.14) had negative indirect effect on grain yield.

Spike length influenced grain yield through positive indirect effect via grain filling period (0.53), number of seeds per spike (0.44), thousand seed weight (0.61) and biomass yield (0.09) while the negative indirect effect *via* days to heading (-0.62), days to maturity (-0.62) and a number of productive tillers (-0.08).

Number of seeds per spike had positive indirect effects on grain yield through days of heading (0.47) days to maturity (0.62), number of productive tillers (1.41) and thousand seeds (0.97). On the other hand, it had negative indirect effects through grain filling period (-0.02), spike length (-0.25) and biomass yield (-0.18). Shyam *et al*. (2018) reported the number of seeds per spike showed a positive indirect effect on seed yield per plant through days to maturity.

Thousand seed weight exhibited the positive indirect effect *via* grain filling period (0.02), spike length (0.19), number of seeds per spike (0.11) and biomass yield (0.83) which suggests that increasing this all traits indirectly increases grain yield through thousand seed weight, while days to heading (-0.91), days to maturity (-0.19) and a number of productive tillers (-0.31) showed a negative indirect effect on grain yield *via* thousand seed weight. This further clarifies late heading, late maturing and high number of productive tillers decreases thousand seed weight which indirectly affects grain yield.

4.6. Principal Component Analysis

In the present investigation, only the first four principal components showed Eigen values more than one and cumulatively they explained 73.77% of the entire variability available among the accessions (Table 7).

According to Chahal and Gosal (2002) traits with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in the present study, differentiation of the accessions into a different cluster was because of a cumulative effect of a number of traits rather to the small contribution of each trait.

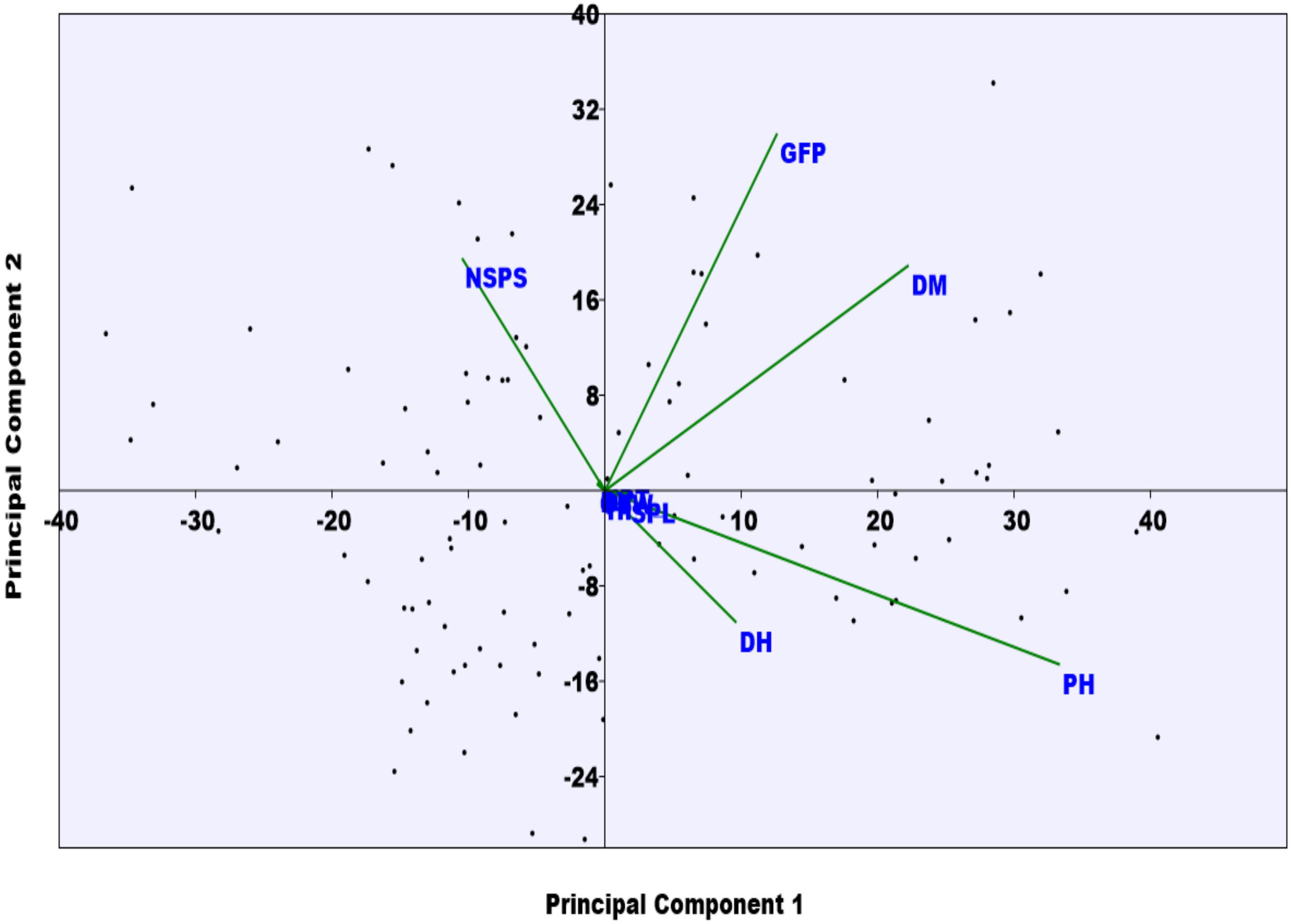
The first two principal components are more important as revealed by their higher Eigenvalues. The principal component analysis showed that 31.96% of the total variation in the landraces for the traits was explained by PC1. The higher contribution of PC1 were loaded by grain yield, biomass yield, thousand seed weight, number of productive tiller, number of seed per spike and days to heading. PC2 contributed 17.96% for total variation of the accessions. The 17.96% contribution of PC2 were due to high variation for days to maturity, plant height and spike length. Around 14.14% variation was accounted by PC3 which were loaded by grain filling period. PC4 accounted 9.71% for total variation which were loaded by harvest index (Table 7). Alemayehu *et al*. (2019) found the most contributing traits were above ground biomass, spike length and plant height in durum wheat. Poudel *et al*. (2017) reported days to heading, maturity and grain filling period contributed more to the total diversity.

Table 7. Eigenvectors and eigenvalues of four principal components (PCs) for eleven quantitative traits of bread wheat landraces

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
DH	-0.469	0.422	-0.547	0.191
DM	-0.365	0.791	0.400	0.029
GFP	-0.061	0.542	0.799	-0.100
NPT	0.692	0.306	-0.072	0.039
PH	-0.345	0.634	-0.251	-0.107
SPL	-0.052	0.635	-0.330	-0.034
NSPS	0.595	-0.040	0.259	-0.461
TSW	0.750	0.109	0.018	-0.266
GY	0.903	0.227	-0.064	0.247
BY	0.871	0.250	-0.073	0.010
HI	0.570	0.079	-0.040	0.693
Eigenvalue	3.834	2.155	1.697	1.165
Percent of total variance explained	31.96	17.96	14.14	9.71
Cumulative percent of total variance explained	31.96	49.92	64.06	73.77

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NPT: Number of productive tillers, PH: Plant height, SPL: Spike length, NSPS: Number of seeds per spike, TSW: Thousand seed weight, GY: Grain yield, BY: biomass yield, HI: Harvest index

The traits far from the origin contributed more to the total diversity. Accordingly, the primary traits contributed more for total diversity are plant height, days to maturity, days to heading, number of seeds per spike and grain filling period (Figure 1). In other way, the trait nearest to the x-axis contributed for PC1 and nearest to y-axis contributed to PC2. The traits which lie on the origin (spike length, number of productive tillers, thousand seed weight, grain yield, biomass yield and harvest index) contributed less for total diversity.



DH: days to heading, DM: days to maturity, GFP: grain filling period, PH: plant height, NSPS: number of seed per spike, Dot symbol= accession code

Figure 1. Principal component’s Biplot of all studied traits of bread wheat landraces

4.7. Multivariate Analysis of Genetic Diversity

In the crop improvement program genetic diversity is an important factor which is an essential pre-requisite for hybridization program for obtaining high yielding progenies. Quantitative measurements of genetic divergence among individual trait have enabled plant breeders to understand the racial affinities and evolutionary pattern in various species of cultivated plants as well as in making decision for the selection of best parental combination in hybridization programs (Morishima and Aka, 1960).

4.7.1. Clustering of accessions

The cluster analysis based on mean of the quantitative data classified the accessions into seven clusters and ungrouped accession indicating the tested accessions are moderately divergent (Table 8).

Clusters I (30.10%) was the largest cluster containing 31 accessions, of which 10 accessions were from Amhara, 9 accessions from SNNP, 6 accessions from Oromiya, 3 accessions from Tigray and three checks (Table 8). Cluster II (23.30%) consisted of 24 accessions, originating 10 accessions from Oromiya, 8 accessions from SNNPR, 4 accessions from Amhara and 2 accessions from Tigray. Cluster III (21.36%) consisted of 22 accessions, of which 8 accessions wre from SNNP, 7 accessions from Amhara, 5 accessions from Oromiya, and 2 accessions from Tigray. Cluster V (8.74%) had 9 accessions, of which 3 accessions from Amhara, 2 accessios from SNNP, 2 accessions from Oromiya and 2 accessions from Tigray. Cluster VII (8.74%) contains 9 accessions, of which 4 accessions were from Oromiya, 2 accessions from SNNPR 1 accession from Amhara, and 1 accession from Tigray. Cluster IV (4.85%) comprised 5 accessions, of which 2 accessions were from Amhara, 2 accessions from SNNP, 1 accession from Oromiya; Cluster VI (1.94%) had 2 accessions, originating 1 accession from Oromia and 1 accession from SNNPR. This result revealed that accession of different origin were grouped into one cluster and accession of the same origin were grouped into different cluster indicating that the geographical distribution is not the criteria for the genetic diversity.

Table 8. Distribution of accessions into eight clusters based on squared distance analysis for 103 bread wheat accessions

Cluster	Number of accessions	Regional State	Accessions
Cluster I	31	Amhara	5335, 7253, 7259, 203754, 203755, 204362, 212653, 222674, 243702,
		Oromia	243726
		SNNPR	6884, 6991, 7341, 228756, 242427, 242429
		Tigray	6887, 29811, 29812, 29813, 29814, 216669, 222194, 226259, 240510
			206544, 207845, 221735
			CH1, CH2,CH3
Cluster II	24	Amhara	5196, 7506, 214264, 222494
		Oromia	5377, 5670, 6885, 219354, 222384, 222385, 222388, 222476, 222800,
		SNNPR	242428
		Tigray	7304, 8285, 8313, 8314, 211488, 216670, 227072, 227073
			207855, 221740
Cluster III	22	Amhara	7257, 204585, 204586, 222518, 222691, 222837, 231578
		Oromia	6859, 6883, 6999, 7010, 222300
		SNNPR	29808, 214116, 222761, 222783, 222784, 222785, 222823, 240508
		Tigray	203915, 226246
Cluster IV	5	Amhara	7248, 243704
		Oromia	242425
		SNNPR	228124, 240507

Table 8 (*Continued*)

Cluster V	9	Amhara	222520, 222686, 222705
		Oromia	226261, 228138
		SNNPR	222389,242426
		Tigray	243710, 243711
Cluster VI	2	Oromia	7033
		SNNPR	240509
Cluster VII	9	Amhara	7279
		Oromia	5261, 7028, 219348, 222482
		SNNPR	29810, 213037, 240511
		Tigray	213309

4.7.2. Cluster mean analysis of the major contributed traits for diversity

In the present study, cluster IV was characterized as lowest cluster means for days of heading which considered to be the early heading accessions were found in this cluster. The early maturing accessions were represented in cluster II, with recorded mean days to maturity of 95 days, whereas late maturing with mean days to maturity of 131 days found in cluster VI (Table 9). Cluster II (26.) exhibited the lowest grain filing period against the highest of cluster V (58.67). Cluster VI consists of tallest accessions with mean plant height of (139 cm), whereas the shortest with a mean height of 98.91 cm was found in cluster VII. Highest mean performances of a number of seeds per spike were recorded for cluster IV (56.24), while smallest numbers of seed per spike for cluster VII (29.16). This result implies that sufficient scope for genotypic improvement through hybridization between the accessions from divergent clusters. In general, cluster IV exhibited highest cluster mean value for number of productive tiller, number of seed per spike and thousand seed weight, whereas cluster V exhibited highest grain yield which indicates the accessions present in cluster IV and V may be used as parents in hybridization programs for developing high yielding wheat varieties.

Table 9. Cluster mean values for eleven traits in bread wheat accessions

Traits	Clusters						
	I	II	III	IV	V	VI	VII
DH	67.10	68.21	76.36	61.40	63.44	73.00	71.22
DM	110.61	95.00	124.05	101.40	122.11	131.50	107.78
GFP	43.52	26.00	47.68	40.00	58.67	58.50	36.56
NPT	4.75	4.09	4.23	6.00	4.89	5.50	4.69
PH	115.01	114.88	135.13	87.68	105.64	139.00	98.91
SPL	9.95	9.38	11.42	9.72	9.80	12.70	10.62
NSPS	46.42	35.09	31.46	56.24	43.91	51.80	29.16
TSW	2.58	2.10	1.83	2.77	2.48	2.00	1.85
GY	3.61	3.11	2.82	3.59	3.64	2.69	3.15
BY	4.87	4.06	3.87	4.49	4.65	3.63	4.18
HI	0.74	0.76	0.72	0.79	0.77	0.75	0.75

DH: Days to heading, DM: Days to maturity, GFP: Grain filling period, NPT: Number of productive tillers, PH: Plant height (cm), SPL: Spike length (cm), NSPS: Number of seeds per spike, TSW: Thousand seed weight (g), GY: Grain yield (t ha-1), BY: biomass yield (t ha^{-1}), HI: Harvest index

4.7.3. Genetic distance (squared distance) analysis

4.7.3.1. Intra and inter-cluster distances

The highest average inter-cluster D^2 was recorded between cluster IV and cluster VI (D^2=104.77) followed by between cluster II and cluster VI (D^2=103.880), cluster IV and cluster VII (D^2=92.492), cluster III and cluster IV (D^2=74.423) (Table 10). This revealed that these clusters were genetically more divergent from each other and the tendency of obtaining promising parent for crossing.

Minimum inter-cluster distance was observed between cluster II and cluster VII (D^2=14.91223) (Table 10) indicating that accessions of these two clusters were closely related which suggests that the presence of gene flow. Thus, crossing of accession belonging to the same cluster is not expected to yield superior hybrids.

Table 10. Average intra (bold) and inter cluster divergence value for bread wheat accessions

Cluster	I	II	III	IV	V	VI	VII
I	**2.401**	18.212^{ns}	19.745*	27.198**	16.825^{ns}	51.029**	18.390*
II		**2.913**	46.320**	31.983**	52.980**	103.880**	14.912^{ns}
III			**3.087**	74.423**	24.390**	26.179**	44.821**
IV				**6.050**	39.416**	104.775**	21.226**
V					**4.875**	38.322**	35.618**
VI						**7.883**	92.492**
VII							**4.875**

x^2 at 5% = 18.31; x^2 at 1% = 23.21**= *highly significant*

The Chi-square test for the eight clusters indicated that there was statistically acceptable difference between all the clusters except between cluster I and II, I and V, and II and VII, However, the Chi-square test for within (intra) clusters was not significant for all clusters (Ta ble 10). Crossing cluster III to cluster IV, cluster IV to VII, cluster V with II, cluster VI with IV, cluster VII with II would be recommendable (Figure 2). Generally, the higher the cluster distance the higher the chance to select parents for hybridization.

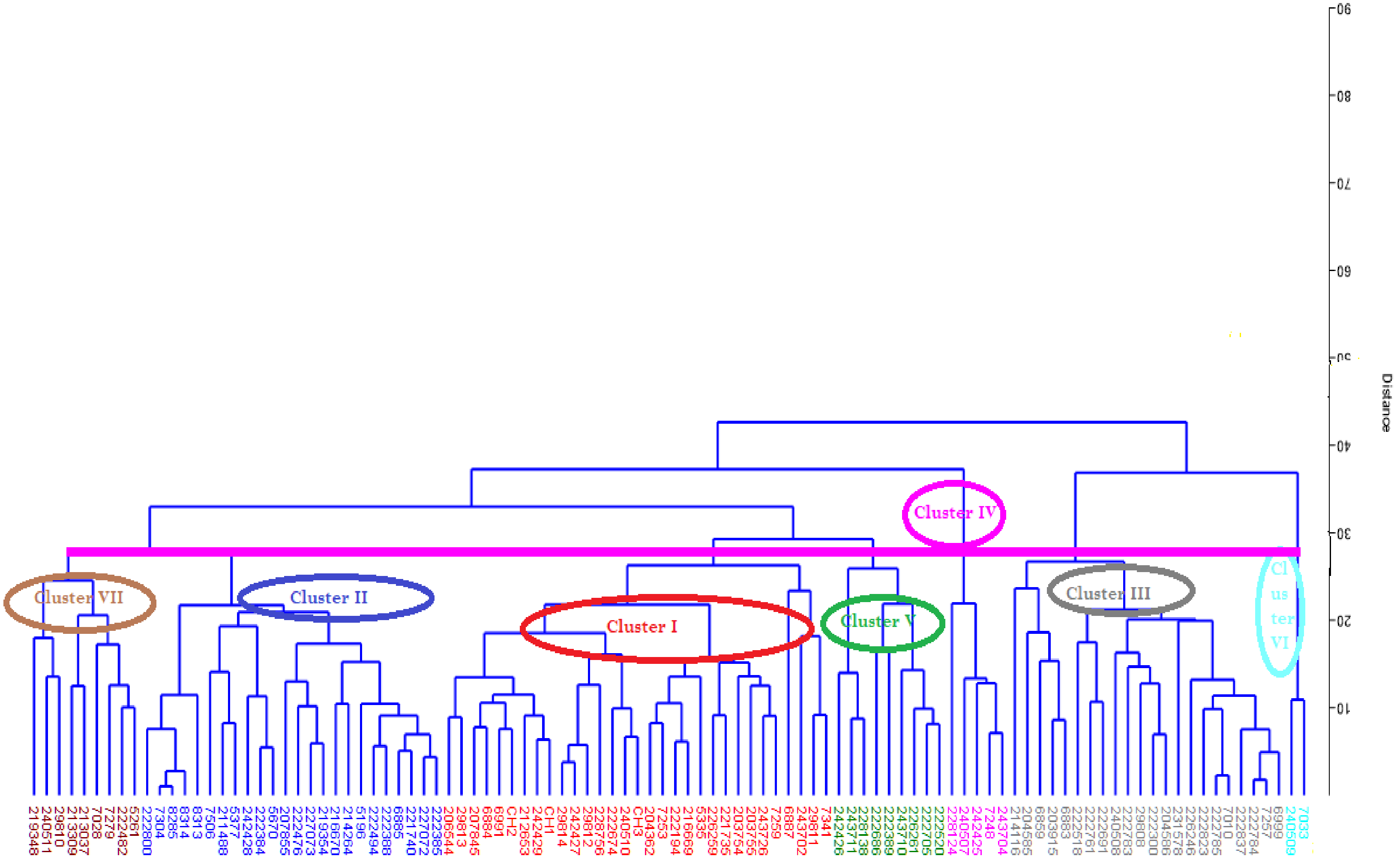


Figure 2. Hierarchical dendrogram generalized from Euclidean distance using a cluster method of paired group

4.8. Qualitative Trait Diversity

4.8.1. Phenotypic frequency

The frequency distributions of phenotypic classes showed high variability (Table 11). Glume color is one of the traits used for wheat classification. Therefore, white glume was the most frequent (65 %) within the accessions, whereas those with brown color were less frequent (35%). Awned accessions are the most common within the accession with a phenotypic frequency of 85%, while awnless and awnlettd were 12% and 3%, respectively. Most of the farmers claimed that the frequency of awnless accessions has diminished, and they are being replaced by awned types, which they regarded as easier for threshing. Rough awned accessions are predominant with a phenotypic frequency of 79%, while smooth and intermediate were 10% and 11%, respectively. Accessions having small seed size were 37%, followed by intermediate (33%) and large (30%). Seed color of the accessions was categorized under three classes. About 70% of the accessions were white colored followed by brown (27%) and purple (3%). The seed shapes of most accessions were semi-elongated (54%) followed by ovoid (26%) and elongated (20%). Likewise, most of them have an intermediate spike density (47.5%) followed by dense (35%) and very dense (18%) (Appendix II). The notable phenotypic diversity observed in landraces may be attributed to high agro-ecological heterogeneity and suitability for the cultivation of crops. In agreement with present study, Dejene *et al*. (2015) observed high phenotypic diversity for glume color, seed color, spike density and seed size.

Table 11. Qualitative traits, phenotypic classes, phenotypic frequencies and obtained chi square value

Qualitative Traits	Observed Phenotypic Class	Code	Proportion (%)	Obtained Chi square (χ2)
Glume color	White	1	65	9**
	Brown	2	35	
Awnedness	Awnless	0	12	121.46**
	Awnletted	3	3	
	Awned	7	85	
Awn roughness	Smooth	3	10	93.95**
	Intermediate	5	11	
	Rough	7	79	
Seed size	Small	3	37	0.7427**
	Intermediate	5	33	
	Large	7	30	
Seed color	White	1	70	69.21**
	Brown	2	27	
	Purple	3	3	
Seed shape	Ovoid	3	26	19.78**
	Semi elongated	5	54	
	Elongated	7	20	
SPD	Intermediate	5	47	12.76**
	Dense	7	35	
	Very dense	9	18	

****:** highly significant; H’: Shannon diversity index, SPD: Spike density

4.8.2. Shannon diversity index

All the recorded morphological traits were polymorphic, which ranged from intermediate to high (Table 12). This suggests the existence of wide range of variation in the accessions. Glume color, awnedness, awn roughness, seed color, seed size and spike density showed highly significant differences among the accessions. The diversity index was classified as high (H′ ≥ 0.60), intermediate (0.40 ≤ H′ ≤ 0.60), or low (0.10 ≤ H′ ≤ 0.40 (Firdissa *et al*., 2005). The highest Shannon diversity index was observed for seed size (H' = 0.995), followed by spike density (H'= 0.939), glume color (H'= 0.927), and seed shape (H' = 0.921), seed color (H' = 0.70), awn roughness (H' = 0.65). Intermediate Shannon diversity index was observed for awnedness (H' = 0.49). Similar findings to the present study were reported by Dejene *et al*. (2015) who observed high Shannon diversity index for spike density, glume color, seed color and seed size. The highest value of Shannon diversity index indicates the presence of polymorphism. This information can be used for the conservation of these germplasm resources, and future improvement of bread wheat crop.

Table 12. Shannon Weaver diversity index

Qualitative Traits	Diversity Index (H')
Glume color	0.927
Awnedness	0.497
Awn roughness	0.659
Seed size	0.995
Seed color	0.708
Seed shape	0.921
SPD	0.939

SPD: Spike density

5. SUMMARY AND CONCLUSION

The present experiment dealt with **“**characterization among bread wheat (*Triticum aestivum* L.) landraces at Kaffa Zone, South West Ethiopia” during 2018 /19 cropping season with the objective of characterizing the bread wheat accessions for quantitative and qualitative traits, determining the genetic diversity, and estimating the broad sense heritability and expected genetic advance of various important traits. One hundred germplasm accessions of bread wheat were sown during August 15, 2018 growing season following Augmented Design, having ten blocks comprising thirteen accessions each (10 accessions + 3 checks).

A wide range of significant variation was observed for all the traits. High PCV with moderate GCV values were observed for number of productive tiller and grain yield. Moderate values of PCV and GCV were observed for spike length, number of seeds per spike, biomass yield and harvest index. Low PCV and GCV were observed for days to heading, days to maturity, grain filling period, plant height and thousand seed weight. High magnitude of differences of PCV and GCV were observed for grain filling, number of productive tillers and grain yield.

Heritability in broad sense was high for days to heading, days to maturity, plant height, spike length, number of seeds per spike, thousand seed weight, biomass yield and harvest index while moderate values were observed for grain filling period, number of productive tillers and grain yield. The genetic advance as per cent of the mean was highest for number of productive tillers, spike length, number of seeds per spike, grain yield, biomass yield and harvest index, while moderate values were observed for days to heading, days to maturity, grain filling period, plant height and thousand seed weight. High heritability coupled with high genetic advance as percent of means were observed for number of productive tillers, spike length, biomass yield and harvest index. Moderate heritability with high genetic advance was observed for grain yield.

Grain yield was found to correlate significantly and positively at both phenotypic and genotypic level with grain filling period, the number of productive tillers, spike length, number of seeds per spike, thousand seed weight and biomass yield while, negative and significant correlations were found with days to heading and days to maturity. At genotypic level, thousand seed weight exhibited the highest direct effect on grain yield. At a phenotypic level, number of productive tillers exhibited the highest direct effect on grain yield.

The major contributor traits for the diversity of the accessions are days to heading, days to maturity, grain filling period, plant height, spike length and number of seeds per spike. Thus, the accessions should be screened for important traits like days to heading, days to maturity, grain filling and number of productive tillers in order to select genetically diverse accessions for hybridization.

The accessions were grouped into seven clusters and one ungrouped accessions. Cluster I was the largest with thirty one accessions, followed by cluster II (24 accessions), cluster III (22 accessions), cluster V (9 accessions), cluster VII (9 accessions), cluster IV (5 accessions), cluster VI (2 accessions).

The highest inter-cluster distance was observed between cluster IV and cluster VI (D^2=104.775), which indicates the presence of considerable diversity among the accessions. On the other hand, Minimum inter-cluster distance was observed between cluster II and cluster VII (D2=14.91223) which indicates that the accessions of these two clusters has close genetic associations. Cluster V was distantly placed from cluster VI, which was divergent for grain yield. Therefore, Parents from divergent clusters can be used for hybridization in order to isolate useful recombinants.

The highest diversity index was observed for seed size, spike density, glume color, seed shape, seed color, awn roughness, and awnedness. The presence of this higher diversity index indicates that there is ample opportunity for improving bread wheat.

In conclusion, the present study indicated the presence of variability among the tested accessions that can be exploited in the wheat improvement program. The existence of variability among accessions for both quantitative and qualitative traits shows direction for direct selection of parental genotypes to develop hybrids. The top five accessions that performed better than the released check varieties for grain yield were 29812, 29811, 29813, 242427, 242429 and 243702. Therefore, for grain yield production direct selection of those accessions can be possible. In general, the presence of genetic variability creates enormous opportunity in the improvement of bread wheat genotypes. Therefore, the information generated from this study needs to be used by breeders who are interested in different traits. However, the present result is only an indication and cannot draw definite conclusion. Since the experiment was carried out at one location and in one season, it is recommended to further evaluate high yielding accessions over locations and seasons to check the stability of the accession.

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APPENDICES

Appendix Table I. Mean values of the eleven traits of 103 accessions tested at Shupa in 2018/19

Accession number	Traits										
	DH	DM	GFP	NPT	PH(cm)	SPL(cm)	NSPS	TSW(g)	GY(ton ha^{-1})	BM(ton ha^{-1})	HI (%)
CH1	66	110	44	4.4	110.4	10.4	45.2	28.7	3.5518	5.7536	0.76
CH 2	68	95	27	3.6	105.8	9.6	42	25	2.7916	3.5762	0.78
CH 3	62	107	45	5	107.2	10.2	55.6	33.9	4.2644	5.7328	0.85
5196	63	108	45	3.4	112.4	9.6	46	26.1	2.6632	3.5745	0.75
5261	65	103	38	3.8	100	11.6	31	24.1	3.108	4.6421	0.67
5335	65	115	50	3	117.6	7.8	36	20	2.3666	3.3896	0.70
5377	72	115	43	3.6	116.2	10	17.8	24	2.864	3.7573	0.76
5670	72	112	40	2.6	119.8	10.2	37.8	18	1.9898	2.832	0.70
6859	70	109	39	4.2	128.2	13.2	50	28	3.4316	4.789	0.72
6883	64	112	48	6.4	111	14	38.6	38.5	5.0522	6.5678	0.77
6884	68	119	51	6.4	107.2	8.2	45	37.6	5.1033	6.6469	0.77
6885	68	110	42	5.2	127.4	8.2	38.6	39.5	4.4146	6.0269	0.73
6887	65	112	47	4.2	126.6	11.8	58.8	25	3.4426	4.8435	0.71
6991	69	118	49	2.8	109.6	11	37.2	25.4	2.075	3.8783	0.54
6999	63	114	51	2.4	132.6	10	31	9.7	1.975	2.8675	0.69
7010	78	119	41	3.4	135	13	32.2	21.2	2.7408	3.9546	0.69

CH1= Local check, CH2 = Danda’a, CH 3= Shorma

Appendix table I (*Continued*)

Accession	Traits									
number	DH	DM	GFP	NPT	PH(cm)	SPL(cm)	NSPS	TSW(g)	GY(ton	BM(ton	HI (%)
7028	66	113	47	3.4	117.6	13.2	43.4	21.8	2.609	3.852	0.68
7033	73	118	45	3.4	139.2	10	53.8	26	2.6752	3.875	0.69
7248	64	116	52	3	122.2	9.8	55.6	28	2.3972	3.598	0.67
7253	71	115	44	4.6	111.4	9.4	33.4	36	3.6532	5.389	0.68
7257	72	119	47	4.6	135.8	11.2	28.6	14	3.762	4.8593	0.77
7259	65	109	44	5.4	125.4	12	39.2	28.9	4.657	6.1345	0.76
7279	70	116	46	4.6	107.4	11.4	29.4	16.7	3.945	5.0567	0.78
7304	65	105	40	5.2	103	13.8	46.6	22.3	4.348	4.486	0.97
7341	68	119	51	1.5	132.2	11.4	47.6	7.4	1.0474	2.334	0.45
7506	70	113	43	4.8	122.8	7.6	30.2	12.3	4.0486	5.0679	0.80
8285	64	114	50	3	120.2	9.4	45.6	19.2	2.3262	3.5892	0.65
8313	66	109	43	5	118.6	10	40.6	22.7	4.176	5.1994	0.80
8314	74	119	45	4.8	116.8	11	43	20	3.9684	4.7335	0.84
29808	78	113	35	4.4	134.2	14	30.4	12	3.546	4.5981	0.77
29810	66	105	39	6.2	91.2	11.2	39.8	30.3	4.78	5.913	0.81
29811	67	105	38	6.4	132.8	11.6	53.4	29.2	5.11	6.7884	0.75
29812	65	108	43	7.2	112.4	11.8	59	34.2	5.7012	6.7732	0.84
29813	69	106	37	6.6	103.6	9.6	48.8	24	5.1748	6.3683	0.81
29814	66	109	43	4.8	115.2	9.4	59.6	26.5	3.979	4.5665	0.87
203754	71	107	36	5	121.4	10.8	44.2	35.1	4.238	5.2357	0.81

Appendix table I (*Continued*)

Accession number	Traits									
	DH	DM	GFP	NPT	PH(cm)	SPL(cm)	NSPS	TSW(g)	GY(ton	BM(ton	HI (%)
203755	64	107	43	4.8	116.4	10.2	37.2	32.5	4.0502	5.0319	0.80
203915	76	121	45	2.6	151	9.4	39.6	22	2.0046	2.9795	0.67
204362	75	109	34	2.4	113.2	11.4	35.6	10.3	1.7842	2.7217	0.66
204585	80	115	35	2.2	147.4	12.8	31.8	14.7	1.7544	2.28395	0.77
204586	75	127	52	4.2	129.2	9.6	30.2	19	3.4246	4.2124	0.81
206544	65	106	41	3.8	106.8	8.6	53.4	22	2.9254	3.7643	0.78
207845	64	102	38	4.2	107.4	7.4	42	12.9	3.4204	4.3047	0.79
207855	66	106	40	4	117.2	7.2	27.6	19	3.2736	4.1548	0.79
211488	77	120	43	2.8	122	9.4	22.8	18	2.0358	2.8831	0.71
212653	70	116	46	3.8	113	10.4	41.6	18	3.0708	3.874	0.79
213037	77	127	50	2	128.8	9.2	16.2	12.1	1.584	2.0129	0.79
213309	70	117	47	3	117.2	10.4	16.8	7	2.371	3.5163	0.67
214115	73	136	63	3.6	121.6	8.6	34.8	18	2.8544	3.7785	0.76
214116	75	112	37	4.4	154.2	12.8	19.6	29.8	3.449	4.5352	0.76
214264	73	113	40	4.2	117	12.6	30.4	19	3.342	4.6844	0.71
216669	70	116	46	4	118.4	11.8	34.8	28.8	3.3096	4.5652	0.72
216670	70	115	45	3.6	114.2	9	24.8	12.1	2.8596	3.3426	0.86
219348	62	106	44	4.4	106	11.2	23.2	16	3.568	4.4874	0.80
219354	64	105	41	4	112	11.4	21.2	10.3	3.226	4.1627	0.77
221735	66	111	45	4.2	116.8	7.6	45.6	31.9	3.415	5.2234	0.65

Appendix table I (*Continued*)

Accession number	Traits										
	DH	DM	GFP	NPT	PH(cm)	SPL(cm)	NSPS	TSW(g)	GY(ton	BM(ton	HI (%)
221740	65	109	44	4	105.2	9.4	36.6	32.9	3.202	5.0345	0.64
222194	70	115	45	4	117.2	8.2	32.2	19.4	3.242	4.1313	0.78
222300	78	105	27	2.6	129.8	10.4	34.2	23.9	2.0022	3.9461	0.51
222384	79	119	40	2.2	127.2	8.4	38.4	16	1.6724	2.3886	0.70
222385	67	119	52	2.8	109.8	7.6	39.4	9.4	2.1534	2.8125	0.77
222388	71	125	54	3.8	112	8	41.2	29.6	3.008	3.982	0.76
222389	61	106	45	4.2	115.6	7.2	49.2	30.2	3.3974	4.4394	0.77
222476	59	101	42	3.2	126.8	7.2	29.4	20.8	2.608	3.3615	0.78
222482	67	112	45	4.6	102.8	9.2	31.2	26.4	3.8592	4.8338	0.80
222494	68	111	43	4.2	111.8	6.2	38.4	26.4	3.386	4.0783	0.83
222518	65	125	60	2	129.4	12.8	28.2	11	1.586	2.7643	0.57
222520	69	119	50	3.6	120.4	12.6	37.8	24.2	2.7706	3.7139	0.75
222686	59	108	49	5.2	122.2	12.2	43.4	31.2	4.5574	5.7232	0.80
222691	73	125	52	2.6	129	9.6	21.2	7.6	1.9776	2.9751	0.66
222705	70	122	52	2.2	132.6	8.8	42.4	16	1.6182	2.9985	0.54
222761	70	120	50	2.8	131.4	9.2	19	11.3	2.1624	2.9417	0.74
222783	78	134	56	3	120.8	10	26.8	24	2.3666	3.4933	0.68
222784	76	122	46	4.4	118	12.6	35	22	3.6448	4.532	0.80
222785	78	104	26	4.4	118.8	10	47.6	16	3.6152	4.5673	0.79
222800	57	99	42	5.4	115.2	9.6	42.4	31.3	4.5855	5.753	0.80

Appendix table I (*Continued*)

Accession number	Traits									
	DH	DM	GFP	NPT	PH(cm)	SPL(cm)	NSPS	TSW(g)	GY(ton	BM(ton	HI (%)
222823	73	109	36	4	130.4	13.2	36.2	15.2	3.2922	3.823	0.86
222837	74	108	34	2.6	134	9	25.2	9.9	2.028	2.915	0.70
226246	71	105	34	3.6	140.6	11	35.4	25	2.7688	3.675	0.75
226259	70	104	34	5	111.8	10.6	47.4	19.7	4.1148	4.9568	0.83
226261	69	120	51	4.6	110.2	9.2	32.8	24	3.9322	4.9629	0.79
227072	66	103	37	2.4	129.6	10.8	37	16.1	1.9054	3.1876	0.60
227073	63	105	42	4	112.4	7.4	25	25	3.2194	3.9739	0.81
228124	66	108	42	3	126.6	8.6	53.6	22.1	2.4724	3.0916	0.80
228138	58	102	44	6.2	101.2	6.6	45.6	34.1	4.9698	6.0962	0.82
228756	60	112	52	2.8	127.2	10	60.8	24.2	2.1288	4.3873	0.49
222674	64	112	48	3	121.2	8.6	53.2	25.6	2.279	4.3816	0.52
231578	79	133	54	3.6	124.2	10.6	21.2	19.8	2.874	4.2459	0.68
240507	57	101	44	5.4	98.4	10.2	66.8	24	4.5676	5.6985	0.80
240508	75	107	32	3.2	126.8	12.8	30.2	8.9	2.6447	3.5421	0.75
240509	73	106	33	3.4	125.8	15.4	49.8	14	2.712	3.3878	0.80
240510	65	118	53	2.2	105.4	6.4	54.2	22	1.7734	2.7686	0.64
240511	59	108	49	3.2	119.2	8.2	31.4	12.4	2.5228	3.2854	0.77
242425	57	105	48	5.4	85.8	9	55	31.1	4.5899	5.1222	0.90
242426	63	118	55	5.2	91.8	8.8	57.4	26.1	4.5096	5.0344	0.90
242427	67	119	52	4.8	108.6	8.6	61.6	26.1	5.5702	6.5873	0.85

Appendix table I (*Continued*)

Accession number	Traits										
	DH	DM	GFP	NPT	PH(cm)	SPL(cm)	NSPS	TSW(g)	GY(ton	BM(ton	HI (%)
242428	84	116	32	4.2	115.4	11	41.4	12.8	3.339	4.4377	0.75
242429	67	112	45	6.6	107.4	11	47.2	26.8	5.1168	6.165	0.83
243702	59	103	44	6.8	109.8	10.4	53.2	33.2	5.186	6.258	0.83
243704	60	104	44	4.8	105.4	11	50.2	33.4	3.9464	4.9569	0.80
243710	68	115	47	4.8	107.6	12.6	42.6	19.8	3.9742	4.9482	0.80
243711	63	108	45	3.8	104.2	10.2	44	17.8	3.0116	3.8893	0.83
243726	63	110	47	4.4	114.8	12.4	34	28	3.5084	4.4226	0.79

Appendix table II. Characterization of 100 bread wheat accessions for qualitative traits

Character		**Accessions for different qualitative traits.**
Glume color	White	5261, 5335, 5377, 5670, 6883, 6884, 6885, 6887, 6991, 7010, 7028, 7033, 7248, 7253, 7257, 7259, 7279, 7304, 7341, 8313, 8314, 29810, 29813, 203915, 204585, 204586, 206544, 207845, 207855, 211488, 212653, 213037, 214116, 216669, 219348, 221735, 222384, 222385, 222476, 222494, 222518, 222686, 222705, 222761, 222784, 222800, 222823, 222837, 226246, 227072, 227073, 228124, 228138, 231578, 240508, 240509, 240510, 242426, 242427, 242428, 242429, 243704, 243710, 243711,243726
	Red/brown	5196, 6859, 6999, 7506, 8285, 29808, 29811, 29812, 29814, 203754, 203755, 204362, 213309, 214115, 214264, 216670, 219354, 221740, 222194, 222300, 222388, 222389, 222482, 222520, 222691, 222783, 222785, 226259, 226261, 228756, 222674, 240507, 240511, 242425, 243702
Awnedness	Awnless	7257, 203915, 204585, 204586, 214116, 216669, 222384, 222518, 222783, 222800, 226246, 243704
	Awnletted	222389, 222686, 226259
	Awned	5196, 5261, 5335, 5377, 5670, 6859, 6883, 6884, 6885, 6887, 6991, 6999, 7010, 7028, 7033, 7248, 7253, 7259, 7279, 7304, 7341, 7506, 8285, 8313, 8314, 29808, 29810, 29811, 29812, 29813, 29814, 203754, 203755, 204362, 221740, 222194, 222300, 222385, 222388, 222476, 222482, 222494, 222520, 222691, 222705, 222761, 222784, 222785, 222823, 222837, 226261, 227072, 227073, 228124, 228138, 228756, 222674, 231578, 240507, 240508, 240509, 240510, 240511, 242425, 242426, 242427, 242428, 242429, 243702, 243710, 243711, 243726

Appendix table II (*Continued*)

Awn roughness	Smooth	7257, 203915, 214116, 216669, 222518, 222783, 240507,
	Intermediate	29808, 222800, 226246, 227072, 228124, 228756, 222674, 240511, 242428, 243704, 243711
	Rough	5196, 5261, 5335, 5377, 5670, 6859, 6883, 6884, 6885, 6887, 6991, 6999, 7010,7028, 7033, 7248, 7253, 7259, 7279, 7304, 7341, 7506, 8285, 8313, 8314, 29810, 29811, 29812, 29813, 29814, 203754, 203755, 204362, 204585, 204586, 206544, 207845, 207855, 211488, 212653, 213037, 213309, 214115, 214264, 216670, 219348, 219354, 221735, 221740, 222194, 222300, 222384, 222385, 222388, 222389, 222476, 222482, 222494, 222520, 222686, 222691, 222705, 222761, 222784, 222785, 222823, 222837, 226259, 226261, 227073, 228138, 231578, 240508, 240509, 240510, 242425, 242426, 242427, 242429, 243702, 243710, 243726
Seed size	Small	5377, 6999, 7010, 7279, 7506, 29808, 203915, 204362, 204585, 204586, 207845, 207855, 211488, 212653, 213037, 213309, 214116, 214264, 216670, 219348, 219354, 222194, 222384, 222385, 222476, 222518, 222691, 222705, 222761, 222783, 222784, 222785, 222837, 226246, 226261, 227072, 240508,
	Intermediate	5196, 5261, 5335, 5670, 6991, 7028, 7257, 7304, 7341, 8285, 8313, 8314, 203755, 206544, 214115, 216669, 222300, 222388, 222482, 222494, 222520, 222823, 226259, 227073, 228124, 228138, 228756, 231578, 240507,
	Large	6859, 6883, 6884, 6885, 6887, 7033, 7248, 7253, 7259, 29810, 29811, 29812, 29813, 29814, 203754, 221735, 221740, 222389, 222686, 222800, 222674, 240510, 242425, 242426, 242427, 242429, 243702, 243704
Seed color	White	5196, 5261, 5377, 6991, 7248, 7253, 7259, 7279, 7506, 29808, 29813, 203755, 203915, 204585, 204586, 206544, 207855, 211488, 213037, 213309, 214115, 214264, 216669, 216670, 219348, 219354, 221735, 222300, 222384, 222388, 222476, 222482, 222494, 222686, 222691, 222705, 222783, 222784, 222785, 222800, 222823, 222837, 226261, 227072, 227073, 228124, 228756, 222674, 231578, 240507, 240508, 240509, 240510, 240511, 242425, 242427, 242428, 242429, 243704, 243710, 243711, 243726
	Red/brown	5335, 5670, 6859, 6883, 6884, 6885, 6887, 6999, 7010, 7257, 7304, 7341, 8285, 8314, 29810, 29811, 29812, 29814, 203754, 204362, 212653, 214116, 221740, 222194, 222389, 222518, 222520, 222761, 226259, 228138, 243702
	Purple	7028, 7033, 8313

Appendix table II (*Continued*)

Seed shape	Ovoid	6883, 7033, 7248, 7253, 29810, 29811, 29812, 29813, 29814, 216669, 216670, 219354, 222389, 222476, 222686, 222783, 222800, 228124, 228138, 240510, 240511, 242426, 242427, 242429, 243702, 243704
	Semi elongated	5261, 5377, 5670, 6859, 6884, 6885, 6999, 7010, 7257, 7259, 7279, 7506, 29808, 203754, 203755, 203915, 204585, 204586, 206544, 207845, 207855, 211488, 212653, 213037, 214115, 214116, 214264, 219348, 222194, 222300, 222384, 222385, 222482, 222494, 222518, 222520, 222691, 222761, 222784, 222785, 222823, 222837, 226246, 226261, 227072,
	Elongated	5196, 5335, 6887, 6991, 7028, 7304, 7341, 8285, 8313, 8314, 204362, 213309, 221735, 221740, 222388, 222705, 226259, 222674, 231578, 242425
SPD	Intermediate	5196, 5261, 5335, 5377, 6991, 6999, 7010, 7028, 7257, 7304, 7506, 8285, 8314, 29808, 203915, 204362, 204585, 204586, 207845, 207855, 211488, 212653, 213037, 213309, 214116, 214264, 216669, 216670, 219348, 222194, 222300, 222384, 222482, 222518, 222705, 222761, 222783, 222823, 222837, 226246, 226261, 227073, 231578, 240508, 243704, 243711
	Dense	5670, 6859, 6883, 6885, 6887, 7033, 7259, 7279, 7341, 8313, 203754, 203755, 214115, 219354, 221735, 221740, 222388, 222476, 222494, 222520, 222686, 222691, 222784, 222785, 226259, 227072, 228138, 228756, 222674, 240507, 240509, 242425, 243710
	Very dense	6884, 7248, 7253, 29810, 29811, 29812, 29813, 29814, 222800, 228124, 240510, 242426, 242427, 242428, 242429, 243726

SPD = spike density

Appendix figure I. Climatic data of the experimental site