GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES AT JAMMA AND GEREGERA, ETHIOPIA

M. Sc. THESIS

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I have completed my thesis research work as per the approved proposal and it has been evaluated and accepted by my advisers. Hence I hereby kindly request the Department to allow me to present the findings of my work and submit the thesis.

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We, the thesis advisers have evaluated the contents of this thesis and found to be satisfactory, executed according to the approved proposal, written according to the standards and format of the University and is ready to be submitted. Hence, we recommend the thesis to be submitted.

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DEDICATION

I dedicate this thesis manuscript to my beloved mother Belay Adinew, my father Getachew Assen, my son Abubekr Ahmed and to my uncle Seid Hassen.

STATEMENT OF THE AUTHOR

First of all, I declare that this thesis is my original work and all sources of materials used for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for M.Sc. degree in plant breeding at Jimma University and is deposited at the University Library to be available to borrowers under the rules of the library. I solemnly declare that this thesis is not submitted to any other institution anywhere else for the award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

The author, Ahmed Getachew Assen, was born on April 19, 1988 in Wogdie Woreda, South Wollo Zone, Amhara Regional State, Ethiopia. He attended his primary education in Demasiko Elementary School from 1995 to 2001.He attended his Junior and secondary school education at Fita, from 2002 to 2003. He attended his Secondary School from 2004 to 2005 in Wogdie high School and he completed his Preparatory School in Borena preparatory School from 2006 to 2007 G.C.

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LIST of ACRONYMS and ABBREVIATIONS

ANOVA	Analysis of Variance
bp	base pair
CSA	Central Statistical Agency
CV	Coefficient of Variation
FAO	Food and Agricultural Organization of the United Nations
GAIN	Global Agricultural Information Network
GCV	Genotypic Coefficient of Variation
LSD	Least Significance Difference
PCA	Principal Component analysis
PCV	Phenotypic Coefficient of Variation
SARC	Sirinka Agricultural Research Center
SAS	Statistical Analysis System

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GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN BREAD WHEAT (Triticum aestivum L.) GENOTYPES AT JAMMA AND GEREGERA, ETHIOPIA

ABSTRACT

Continuous identification of the best genotypes that have wider genetic base, capable of producing better yield under a wide range of agro-climatic conditions and stresses increases production and productivity. Forty nine bread wheat genotypes were evaluated for 12 traits in simple lattice design at Jamma and Geregera to determine the extent of genetic variation and character association among grain yield and its related traits. Mean squares of the traits studied showed statistically significant differences among the genotypes listed ($P< 0.01$), indicating the presence of adequate variability. Maximum values of genotypic coefficient of variation were recorded for spike length (8.66%), number of productive tillers (8.4%), number of grains per spike (6.4%) and thousand seed weight (6.15%), whereas better value of phenotypic coefficient of variation were recorded for productive tillers, grain yield, spike length and harvest index with values of (13.3%, 11.35%, 10.3% and 9%), respectively. Heritability ranged from 29.1% for grain yield to 82% for days to heading. Relatively high genetic advance as percent of mean was obtained for spike length, productive tillers, number of grains per spike, thousand seed weight, heading date and plant height with values of (14.9%, 10.6%, 10%, 10%, 9.7%, and 9%), respectively. Grain yield had strong and positive genotypic correlation with harvest index (0.731), biological yield (0.617), thousand seed weight (0.395), plant height (384) and productive tillers (0.366). Path analysis indicated maximum positive direct effect obtained between grain yield and harvest index (0.731) and also grain yield and biological yield (0.731). The first five principal components, with eigenvalue greater than one, accounted for 80.4% of the total variation. Based on the average linkage cluster analysis, the 49 genotypes were classified into six clusters; indicating the genotypes were divergent. Thus, crossing program between members of cluster I with cluster III, and cluster II with III, and IV could possibly resulted in heterosis in the F_1, and a great deal of variability in the F_2. Plant selection based on plant height, higher number of grains per spikes, thousand seed weight, biological yield and higher harvest index will be most effective for future wheat yield improvement program.

***Key words**: Bread wheat genotypes, Character association, Genetic variability, Grain yield.*

1 INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a self-pollinating annual plant belonging to the family *Poaceae*, and it is an allohexaploid species with three different genomes configuration (A, B, D) of 42 chromosomes (2n = 6x = 42) (http://sundoc.). It is used as a domestic food consumption and industrial crop (Gashaw *et al*., 2014), manufacture of flour for making bread and other home made products (Negash *et al.*, 2013). It is also traded food crop internationally, and an emergency food in aid for developing countries (Hailu, 2011).

In 2014, 723.4 million ton wheat was produced from 222.3 million hectare (ha) with average yield of 3.25 ton/ha worldwide including the main wheat producing regions of European Union, China, India, Russian, United States, Canada, Australia, Pakistan and Ukraine (FAO, 2015, USAD, 2015). Whereas the national share of wheat in cereal area was around 13.25% (1.66m ha) in 2014, and share in production was 15.65% (4.23million metric ton) with average yield of 2.54 ton per ha (CSA, 2014/15). It was ranked third in total production as cereal behind maize and teff and forth in area coverage after teff, maize and sorghum.

In Ethiopia, an effectively organized national wheat research program started since 1967 and many varieties were released (Hailu, 1991). Attempts have been made so far to improve production and productivity of bread wheat considering it importance as a food and industrial crop, the ever increasing population, its high economic and nutritive value as well as its vast acreage devoted to its cultivation. However, the average yield at production fields has remained 2.54 t/ha, which is low compared to the experimental yield of above 5 t/ha in the country (Hailu, 1991); the world average of 3.25 ton per ha (FAO, 2015, USAID, 2015); other leading wheat producers in the world like Germany, France where average yields were 7.4 and 7.2 t/ha respectively (Yao *et al*., 2012).

This is primarily due to the consequence of interaction between various abiotic and biotic factors, shortage of high yielding genotype which are adapted to local conditions and stresses, wide seasonal variability and environmental fluctuation, low amount of rainfall, and poor soil moisture conservation (Hailu, 1991; Adem, 2013; Mideksa and Tadele, 2014). The important biotic stresses include diseases, such as rusts and weed causes maximum yield losses of 30-50 %

and 29%, respectively (Samuel *et al*., 2014; Sramková *et al*., 2009). Drought also causes maximum yield losses of 64%, which affects growth and development of plants through alterations in metabolism and gene expression (Nezhadahmadi *et al*., 2013).

As a result, to alleviate those constraints, effective breeding program for grain yield improvement to further yield increases, continue identification of best genotypes as donors of various genes of agronomic importance as well as the development of superior cultivars depends upon; various genetic and non-genetic factors, the amount of genetic variability present in the plant population, and association of agro-morphological traits with grain yield (Ali *et al.,* 2009). Besides this genetic variability with the help of suitable parameters such as genetic coefficient of variation, heritability estimates and genetic advance are necessary to start an efficient breeding program in any crop plants including bread wheat (Ali *et al*., 2009; Fellahi *et al*., 213; Kumar *et al*., 2014). With continuous phenotypic traits, in most cases the alleles that are present in the population or even the loci affect the trait are unknown, so we need to use the statistical measures of mean and variance (and later covariance) to characterize populations.

The characterization of this variability in a population is relevant since genetic diversity within population and within species determines the rates of adaptive evolution and the extent of response in bread wheat improvement. Knowledge of genetic diversity and the genetic relationship between genotypes is equally important consideration for efficient rationalization and utilization of germplasm resources. Information on genetic diversity is also needed for the optimal design of plant breeding programmes, influencing the choice of genotypes to cross for the development of new populations (http://sundoc.) Therefore, this study was conducted with the following objectives:

General objective

To estimate the extent of genetic variability, association of grain yield with other characters as well as direct and indirect effects of yield attributing traits on bread wheat grain yield.

Specific objectives

i. To determine variability, heritability and genetic advance

ii. To estimate the correlation and path coefficients among traits studied

2. LITERATURE REVIEW

2.1. Origin and Taxonomy of Bread Wheat

The probable origin of the genus *Triticum* is found in Asia, in the area known as the Fertile Crescent, and parts of Africa, in the area that stretches from Syria to Kashmir and southwards to Ethiopia (Singh and Kota, 2007; Sramkova *et al.,* 2009). The central Asia, Near East, Mediterranean and Ethiopian regions are origins and centers of diversity of wheat species, and had distributed to India, Great Britain, Ireland and Spain (Sramkova *et al.,* 2009*).*Taxonomically it belongs to the family Poaceae(grasses), tribe Triticeae, genus Triticum and species *aestivum (*Acquaah, 2007).

The genetic origin of wheat is a classic example how closely related species combine in nature to form a polyploidy series (Singh and Kota, 2007). The genome analysis, the determination of evolutionary relationships on the basis of chromosome pairing in hybrids indicated that allopolyploidy was involved and that wheat evolution followed a system of diploid divergence and polyploid convergence (http://www.oecd.org/ehs). All the species of wheat are grouped into three groups: diploid, tetraploid and hexaploid that form a polyploid series with chromosome numbers, a turning point in triticum classification, 14 (n=7), 28 (n=14) and 42 (n=21) (Sramková, *et al.,* 2009), respectively.

Evidences indicate that the hexaploid wheat (AABBDD) is believed to have arisen when genomes of diploid (2n = 14, AA) forms of *T. monococcum*(a) were naturally pollinated by weed species (2n = 14, BB). The subsequent genome duplication of hybrids by natural polyploidy gave rise to several wild and cultivated tetraploid species (2n = 28, AABB) like *T. dicoccum*(b) and *T. durum*; again, the natural pollination of the tetraploid *T. dicoccum*(b) by *Aegilops squarrosa L.(Ttiticum tauschii)* (2n =14, DD) gave rise to the hexaploid (2n = 42, AABBDD) species (c) (Singh *et al,* 2007; Sramková *et al.,* 2009*;* Velu and Singh, 2013).

The haploid DNA content of hexaploid wheat is approximately 1.7 x 10^{10}base pair (bp) genome size resulted from polyploidy and extensive duplications, such that over 80% of the genome consists of repetitive DNA sequences. This base pair is about 100 times larger than the *Arabidopsis* genome, 40 times that of rice and about 6 times that of maize(http://sundoc.).

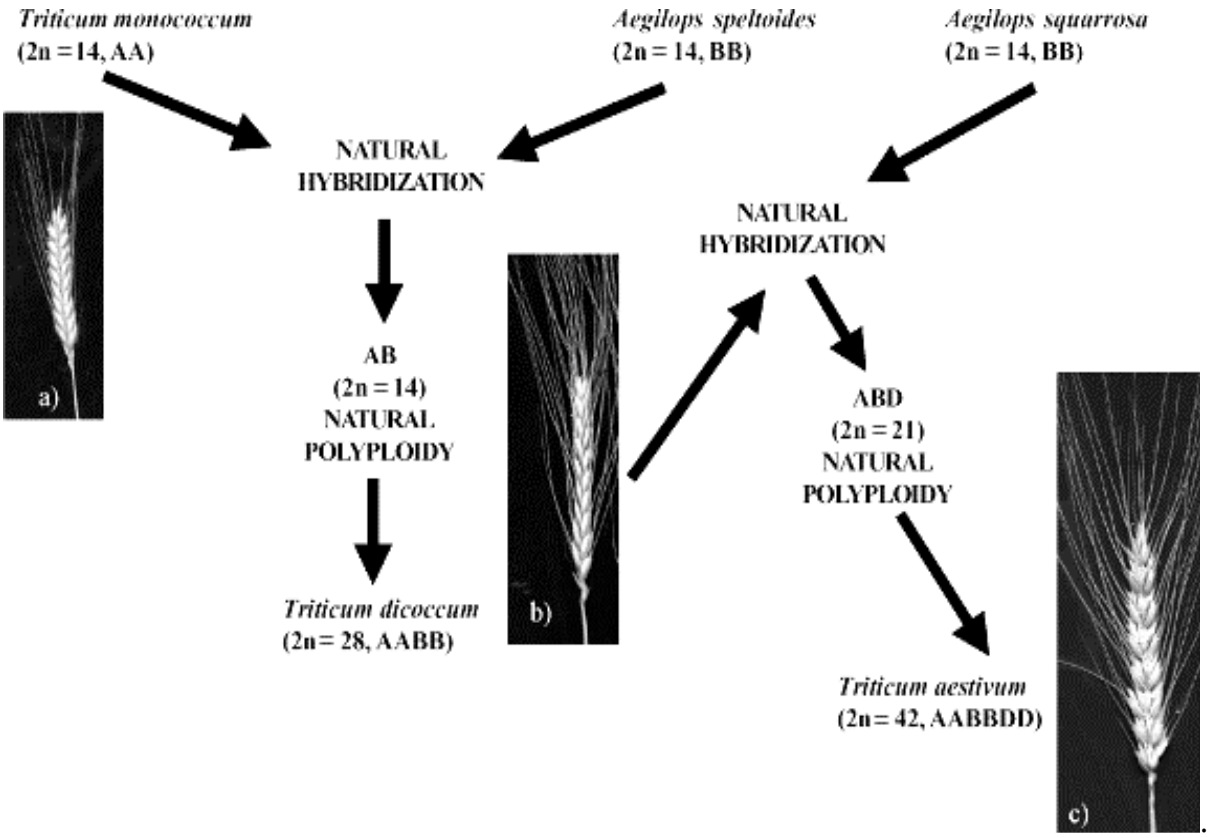

Figure 1. Evolution of Cultivated Wheat

Source: Sramkova *et al*. (2009).

2.1.1. Reproductive and Floral Biology

According to Acquaah (2007), wheat has a determinate, composite spike inflorescence. Each spike bears 10–30 spikelets, which are borne singly at nodes on alternate sides of a zigzag rachis. A spike may be awnless, awnleted, or awned. A spikelet consists of 1–5 flowers (or florets) attached alternatively to opposite sides of the rachilla (central axis). A spikelet is subtended by a pair of empty bracts and glumes (Singh and Kota, 2007).

A floret consists of a lemma and pale, which enclose these stamens and a pistil, plus two lodicules that regulate the opening of the flowers and anthers. Wheat flowers bloom under temperatures of 13–25°C. The flowering is usually diurnal, the highest peak occurring in the morning, and a lower peak in the afternoon. Blooming begins in the spikelets located above the middle of the spike and proceeds both upward and downward. It takes about 2–3 days for a

wheat spike to complete blooming, after the appearance of the first anthers. The flowering period may last from 14 to 21 days (Singh and Kota, 2007).

2.1.2. Pollination

Wheat is predominantly self-pollinated with about 1–4% natural cross-pollination (Singh and Kota, 2007). Pollen shed usually starts inside the floret, but about 80% of anther dehiscence occurs outside the floret. The primary and secondary florets produce larger and more viable pollen grains than other florets. Wheat pollen remains viable for up to about 30 minutes after shedding. Once pollinated, the pollen tube growth starts within 15–60 minutes. Even though the stigma remains receptive for up to 13 days, it is most receptive within 3 days of anthesis.

2. 2. Wheat Production

2.2.1. Wheat Production in the World

Wheat is the staple food of the 1/3rd of the world's population. Approximately 25 % of global agricultural land is utilized for wheat cultivation, making it the largest food crop worldwide in terms of area (Velu and Singh, (2013), and the productivity is increasing at less than 1% annually, while the annual productivity must increase at 2 % annually to meet the global demand. Because of its high economic and nutritive value, vast acreage devoted to its cultivation and its association with some of the earliest and most important civilizations of the world, wheat is known as the queen of cereals. It is also the first strategic, and the world's leading cereal grain (Chhibber *et. al.*, 2014*;* Saleem, *et al*, 2015*).* It is mostly a temperate crop, while it grows in a wide range of agro-climatic regions under several production systems worldwide (between latitudes 30° and 60° north and south) at altitudes from sea level to 3000 m.a.s.l with an optimum growing temperature of 25°C (Sramkova *et al.,* 2009).

Globally, wheat is the leading source of vegetable protein in human food, having a higher protein content than other major cereals, maize (corn) or rice. In terms of total production used for food, it is currently second to rice as the main human food crop and ahead of maize, after allowing for maize's more extensive use in animal feeds (Hailu, 2011).

Wheat requirement is increasing continuously due to ever increasing population of the world (Waqas *et al*., 2014), while the yield is generally insufficient to fulfill the domestic requirements

(GAIN, 2014), which calls for improved and high-yielding varieties to be developed by plant breeders. Therefore, it is necessary to develop new wheat cultivars, as well as to enhance the existing ones, that are genetically more stable, having wider genetic base, capable of producing better yield under a wide range of agro-climatic conditions and stresses to improve the yield potential and enhance the grain yield (Ali *et al.*, 2008; Laghari *et al.*, 2010; El-Mohsen *et al.*, 2012; Farshadfar *et al.*, 2013; Fellahi *et al*, 2013; Kumar *et al*, 2014).

Table1. Harvested area, production and average yields for major wheat producing countries during 2014

SN	Country	Area harvested (million ha)	Production (million ton)	Yield (Metric ton/ha)
		Worldwide		
1	European Union	26.8	155.6	5.81
2	China	24.1	126.2	5.23
3	India	30.6	95.80	3.13
4	Russia	23.4	59.0	2.23
5	U.S.A	18.8	55.1	2.94
6	Canada	9.46	29.3	3.10
7	Australia	13,8	26.50	1.74
8	Pakistan	-	25.3	-
9	Ukrine	6.3	24.5	3.89
		In Africa		
1	Egypt		8.8	
2	Morocco		5.1	
3	Ethiopia	1.665	4.23	2.54
	Total Worldwide	222.288	723.384	3.25

Sources: CSA (2014/2015), FAO (2015), USDA (2015).

2.2.2. Wheat Production in Ethiopia

In Ethiopia, it contributes a major part in achieving the millennium goal of the country, food grain self-sufficiency (Mathewos and Tewodros, 2012; Tewodros *et al.*, 2014). The most suitable

areas fall between 1800-2800 m.a.s.l with average temperature and rain fall ranges from 15-25 ^{0}C and 400-1200 mm, respectively (Adem, 2013). Almost all wheat production (more than 99%) comes from four major wheat producing regions; Oromia, Amhara, SNNPR and Tigray regions (CSA, 2013). From 1995/96 to 2012/13 wheat production area and yield increased by double from 0.8 million ton to 1.6 million ton, and from 1.2 t/ha to 2.1 t/ha, respectively (CSA, 2013).

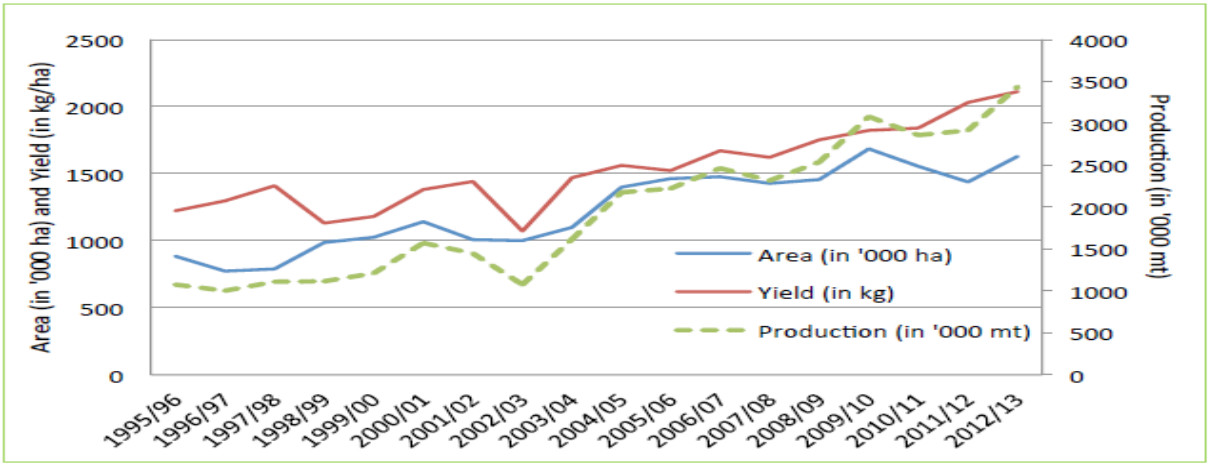

Figure 2. Wheat Production, Area Cultivated and Yield in Ethiopia.

Source: FAOSTAT (2014) cited in Gashaw *et al*. (2014).

2.2.3. Importance of Bread Wheat

Wheat is one of the major staple crops in the country in terms of both production and consumption (Gashaw *et al.,* 2014). It is used for the manufacture of flour for bread, biscuits and industrial products (Mathewos and Tewodros, 2012; Negash *et al.,* 2013). Wheat grain is a staple food used to make flour for leavened, flat and steamed breads, biscuits, cookies, cakes, breakfast cereal, couscous and for fermentation to make beer, other alcoholic beverages and biofuel (https://en.wikipedia.org/wi). Traditionally the crop is used for making *dabo, dabokolo, ganfo, kinche* and other types of foods (Mathewos and Tewodros, 2012; Negash *et al.,* 2013). The straw is good source for animal feed and is also used for thatching roofs (Mathewos and Tewodros, 2012; GAIN, 2014). The basic ingredients of bread wheat grain are carbohydrate (70%), water (12%), protein (12%), vitamins and minerals (2%), lipid (2%) and crude fiber (2%) (White and Edwards, 2008).

2. 2.4. Grain Yield in Bread Wheat

The wheat grain is caryopsis, a small dry, indehiscent; one seeded fruit with a thin pericarp consisting of a germ or embryo and an endosperm (Singh and Kota, 2007), as well as seed is the reproductive unit and the end-use product. Grain yield in wheat is a complexly inherited trait of low to moderate heritability and is strongly influenced by the environmental conditions (Velu and Prakash, 2013). A wheat grain can be broadly divided into three components: seed coat and aleurone layer (or bran) (14%), endosperm (83%), embryo (germ) (3%). Grain development is the period from flowering to physiological maturity when fertilized florets fill and ripen to form grain. The wheat grain has three growth stages; grain enlargement, grain fill and physiological maturity (White and Edwards, 2008).

In many crops, a variation of genotypes in time to reproductive stage is a source of a combination of genetic and environmental constraints and requires appropriate consideration. In general, unfavorable conditions in time to reproductive stage differently affects productivity and growing of commercial cultivars in production areas. Thus, genotypes least effected from changed environmental conditions especially in reproductive stage can remain present in yield performance (Nezhadahmadi *et al*., 2013).

To attain maximum yield, it is important to achieve a balance between biomass and resources. The inputs that can be managed are: plant population, fertilizer, sowing date, diseases and insects, row spacing, surface stubble. Yield is determined by four components: number of heads/m^2, number of spikelet per head, number of grains per spikelet, weight per grain (White and Edwards, 2008). Yield potential is generally assessed through grain yield and yield components, which themselves are complex characters and are considered to be the cumulative result of different physiologic processes (Ali *et al*., 2009).

2.3. History of Wheat Breeding and Genetics in Ethiopia

In fact research on wheat in Ethiopia has been active for more than six decades, it has passed through different phases and has never fully satisfied the needs of farmers in the different wheat production systems. Wheat research in Ethiopia prior to 1930, dealt mainly with germplasm collection, identification and characterization. From 1930-52, introduction, hybridization and

selection began, culminating in the release of Kenya 1 and 5. This work continued at Debre Zeit and other stations during the period 1953-66 when 6 cultivars were released. The organized national wheat improvement program has been started most effectively from 1967 and from 1967 up to 1990, thirty improved wheat varieties have been released (Hailu, 1991).

2.3.1. Breeding Methods of Bread Wheat

The choice and key success in plant breeding work mainly depends on knowledge of the crops; mode of reproduction (sexual reproduction, asexual reproduction), system of pollination (self-pollinated, cross-pollinated), gene action of the desired characters (additive, dominance, epistasis), sufficient genetic variations; types of variation (non-heritable and heritable variation) and kinds of variation (qualitative and quantitative variation), appropriate method of selection (related to gene action of the characters, types of variety going to develop), selection criteria being developed (single character being bred and multiple selection criteria) and breeding objective of crop species (Acquaah, 2007). The main structures of the wheat plant are the coleoptiles, leaves, tillers, stem, roots and head (White and Edwards, 2008), and growth is determined by number of tillers/plant, root and shoot lengths and fresh and dry weights (Shahzad *et al*., 2012).

Being self- pollinated crop, the basic methods of wheat improvement include pure line, pedigree, bulk, single-seed descent and back cross method (Baenziger and DePauw, 2009). The first phase for development of improved wheat genotypes is the adoption of pure line selection from indigenous landraces and then introduction of improved exotic types. Later hybridization program involving inter crossing of systematically selected genotypes in a system of single, double or complex multiple crossing schemes followed by various forms of pedigree selection.

2. 4. Genetic Variability, Heritability in Broad sense and Genetic Advance in Bread Wheat

2.4.1. Variability in Wheat

Variation is differences between parents and their offspring or among individuals in a population. It is an important aspect of breeding, for if all organism look alike there will be no

bases for breeding work. Variation in a population or among a group of individual therefore is important to the breeder (http://www.unaab.edu.ng).

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variability in a population is important for biodiversity, because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction (http://www.unaab.edu.ng).

Variability is an important factor in evolution as it affects an individual's response to environmental stress and thus can lead to differential survival of organisms within a population due to natural selection of the fit variants. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they have grown. The quantitative measurement of individual character provides the basis for an interpretation of different variability parameters. The phenotypic variability which is observable includes both genotypic and environmental variation and changes under different environmental conditions (Farshadfar *et al.,* 2013).

Thus, separating the total variation into heritable and non-heritable components with the help of genetic parameters i.e. genotypic and phenotypic co-efficient of variation, heritability and genetic gain is necessary (Kahrizi *et al*., 2010; Farshadfar *et al.,* 2013). Often, it is not feasible to determine the number of genes affecting a particular trait, and the individual effects of genes on the phenotype. The extent to which variation in yield components are responsible for differences in yield among various genotypes, it must be borne in mind that overall variability depends on heritable and non-heritable components (Tabbal, 2012).

Biological variation exist in the plant population are phenotypic, genotypic and environmental, but a primary step in wheat cultivar improvement is to generate heritable genetic variation, which remains unaltered by environmental conditions and is more useful to a plant breeder for exploitation in selection or hybridization (Farshadfar *et al*., 2013; Kumar *et al*., 2014). The development of an effective plant breeding program and the efficiency of selection mainly

depends upon the magnitude of genetic variability existed in plant material under study, because it is pre-requisite for finding nature and extent of association among various yield and yield components (Ali *et al.,* 2008; Laghari *et al.,* 2010; El-Mohsen *et al.,* 2012; Farshadfar *et al.,* 2013; Fellahi *et al,* 2013; Kumar *et al*, 2014; Adhiena *et al*., 2016).

Many studies have investigated on the extent of genetic variability available in bread wheat. Genetic variability studies conducted to investigate diversity for various traits in bread wheat showed the existence of wide trait diversity that would respond positively to selection (Moghaddam *et al*., 997; Laghari *et al*., 2010; Mathewos and Tewodros, 2012; El-Mohsen *et al*, 2012; Awale *et al*., 2013; Karim *et al*., 2013; Farshadfar *et al*., 2013; Fellahi *et al*., 2013; Kumar *et al*., 2014; Adhiena *et al*., 2016).

Moghaddam *et al*. (1997) conducted an experiment to estimate genetic variation and heritability for 13 developmental and quantitative characters in fifty-three pure lines of bread wheat and reported highly significant variations among the materials for all characters like days to heading ranged from (102–129), plant height (cm) 81–118), number of tillers per plant (5–11), number of spikes per plant (4–8), main spike length (7–12 cm), number of grains per spike (20–54), 1000-grain weight (21–47g), shoot biomass per plant (15–29g), grain yield per plant (3–10g), straw biomass per plant (7–20g), harvest index (20–52(%)).

Ali *et al*. (2008) conducted the experiment to evaluate variability parameters, correlations and path coefficients in seventy bread wheat genotypes for eight metric traits i.e., plant height, which ranged from (64.57–120.17 cm), number of productive tillers per plant (5.33–24), number of spikelets per spike (8.50–25.67), spike length (7.47–17 cm), number of grains per spike (22–85.67), fertility % (80.15–97.83), 1000 grain weight (32.3–56.9 g), yield per plant (5.67–36.45 g). Thus he concluded that significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each character, which provided a good opportunity for yield improvement.

Mohibullah *et al*. (2011) conducted a study for five quantitative characters in hundred breed wheat germplasm to test the variation with correlation and reported a wide range of variation and highly significant variation for characters studied like spike length (6.9 -22.4 cm), number of spikelets per spike (10.5- 31.8), grain yield per plan (1.35 -4.6), 1000-grain weight (16.8- 46.2),

grain yield (2701- 5185 kg /ha). Mathewos and Tewodros (2012) found large variation for morphological traits such as plant height ranged from (72.8-120.6 cm), spike length (3.9-9.95 cm), number of seeds per spike (25.5-70.2), number of days to mature (83-167) and yield (0.46 to 12.4 t/ha) over locations.

El-Mohsen *et al*. (2012) studied eight quantitative characters of ten wheat varieties and reported a wide range of variation and highly significant variation for characters studied like days to (50%) heading (80.1-95.44), plant height (70.6-122.3), number of tillers per plant (5.89-20.36), spike length (8.65-14.22), number of spikelet's per spike (15.4-25.7), number of grains per spike (33.56-71.27), thousand grain weight (35.27-58.42g) and grain yield per plant (10.22-39.25g).

Studies of Awale *et al*. (2013) conducted to estimate the extent of genetic variability and traits association in bread wheat genotypes , reported a wide range of variation for characters studied like days to heading (32 to 71 days), grain filling period (11 to 66 days), days to maturity (59 to 105 days), plant height (35 to 68 cm), number of tillers per plant (1 to 8), spike length (1 to 13 cm), number of spikelet's per spike (2.2 to 17), number of grains per spike (31.7 to 59), 1000-grain weight (10.6 to 54g) and grain yield per plot (12.1-48.2 qt/ha) indicating good opportunity for grain yield improvement.

Studies conducted at Ofla district, North Ethiopian, in 2014 with the objective of estimating nature and magnitude of variation existing in twenty six bread wheat genotypes (Adhiena *et al*., 2016), reported highly significant variations among genotypes ranged for days to heading (49.33-66), days to maturity(102.7-129.7), grain filling period (47.67-66.67), number of tillers (1.53-3.27), spike length (5.87-8.87), number of kernels per spike (34.27-46.7), 1000-kernel weight (68.53-95.20), biological yield (6.46-16.17), grain yield (2.96-6.35 qt/ha).

2.4.2. Genotypic and Phenotypic Coefficients of Variation

Coefficients of variation measure the magnitude of variability present in a population. The success or failure in breeding program largely depends on the extent of variability in the base population which is measured by different population parameters including genotypic and phenotypic coefficients of variation (Usmani *et al*., 2014).

Several researchers have estimated the genotypic and phenotypic coefficient of variation between different yield attributing characters and their effects on yield in bread wheat. The high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicate the high variability of characters in the germplasm that selection may be effective based on these traits and their phenotypic expression would be good indication of the genotypic potential (Ali *et al*., 2008; El-Mohsen *et al*., 2012; Awale *et al*., 2013; Kumar *et al*., 2014; Adhiena *et al*., 2016). Many workers demonstrated higher phenotypic coefficient of variation than the corresponding genotypic coefficient of variation which indicates less effect of environment on the expression of characters studied (Moghaddam *et al*., 1997; Kashif *et al*., 2004; Ali *et al*., 2008; Atta *et al*., 2008; Laghari *et al*., 2010; Kalimullah *et al*., 2012; Farshadfar *et al*., 2014).

On an average, higher magnitude of GCV and PCV were recorded for grain yield per plant, harvest index, tillers per plant, spike length, number of kernels per spike, biomass yield and test weight suggesting sufficient variability and thus scope for genetic improvement through selection for these traits (Moghaddam *et al*., 1997; Kashif *et al*., 2004; Ali *et al*., 2008; Atta *et al*., 2008; Laghari *et al*., 2010; Kalimullah *et al*., 2012; Farshadfar *et al*., 2014).

2.4.3. Heritability in Broad sense (H^2)

Quantitative traits are influenced by genetic and environmental factors. The gross variation in a population is the result of the combination of genotypic and environmental effects. Most of this dissimilarity caused by the genotype is called heritability (Kumar *et al*., 2014). The genotypic component being the heritable part of the total variability, its magnitude on yield and its component characters affects the selection strategies to be adopted by the breeders (Ahmed *et al*., 2007). A useful thing for breeders to know is, for any trait of interest, how much of the phenotypic variability of that trait is due to genetic variance, and how much is due to non-genetic environmental factors (http://www.unaab.edu.ng). Complex traits show a low heritability because their expression is highly influenced by environmental factors, i.e. the conditions in which the genotype is grown. First, there is no one heritability for given trait in a given species, because heritability can and often does differ among populations and among environments. It can differ among populations because additive variance (VA) depends on allele frequencies (http://www.unaab.edu.ng).

The heritability (H^2) of a character, which is the proportion of phenotypic variance due to variance in genes ($H^2 = V_G/V_P$ x100), could vary from 0-100% (Baenziger and DePauw, 2009). The heritability value of 0% indicates that genes do not contribute at all to phenotypic individual differences, and the heritability value of 100% indicates genes are the only reason for individual differences (heritability/heritability.intro.html). Heritability plays an important role in deciding the suitability and strategy for selection of a trait. Heritability estimates show the efficiency in which selection of genotypes can be based on phenotypic performance of quantitative traits (Acquaah, 2007). Heritability estimates under stress conditions were found to be lower than under controlled conditions which indicated that heritability is not constant and varies with changes in environment (Shahzad *et al*., 2012). Characteristics of tolerant varieties grown in stress environments relative to their performance without stress(Hailu,1991) are; the maturity period is reduced by 20 %, plant height is reduced by less than 30%, harvest index ranges between 0.3 - 0.5, kernel weight exhibits a low variance, and grain yield is reduced by less than 50%.

Studies have been conducted to estimate heritability in bread wheat and the higher the heritability estimates, the simpler are the selection procedures (Moghaddam *et al*., 1997; Ali *et al*., 2008; Laghari *et al.*, 2010; Kalimullah *et al*., 2012; Awale *et al*., (2013); Karim *et a.*, 2013; Farshadfar *et al*., 2013; Fellahi *et al*., 2013; Kumar *et al*., 2014; Tewodros *et al*., 2014; Adhiena *et al*., 2016). According to Kumar *et al*. (2014), traits closely associated with yield should be more heritable than *per se* to serve as better indicators of the genetic yield potential of a line.

Estimating of heritability was conducted in grain yield of bread wheat and high heritability were reported (Moghaddam *et al*.,1997; Kashif *et al*., 2004; Ali *et al*., 2008; Kalimullah *et al*., 2012; Awale *et al*., 2013; Farshadfar *et al*., 2014; Kumar *et al*., 2014). However, Laghari *et al*. (2010) reported moderate heritability in grain yield. Moreover, Mohammadi *et al*. (2011), Mollasadeghi *et al*. (2012); Tesfaye *et al*. (2014) and Adhiena *et al*. (2016) reported low heritability in grain yield such as (7.4%), (12.27%), 19% and 25%, respectively, indicating the limited scope of improvement of this trait through selection.

Estimating of heritability was made in characters like heading date, maturity date, number of tillers per plant, plant height and high heritability were recorded and reported (Moghaddam *et*

al., 1997; Laghari *et al.*, 2010; Awale *et al*., 2013; Farshadfar *et al*., 2014; Kumar *et al*., 2014; Adhiena *et al*., 2016). However, Ali *et al*., (2008) and Mollasadeghi *et al*. (2012) reported moderate heritability in number of productive tillers, and Adhiena *et al*. (2016) reported low heritability in tillers per plant (4.45%). Laghari *et al.* (2010) also reported low heritability in plant height.

Moderate high to high heritability for traits like spike length, number of spike lets per spike, number of grains per spike, 1000-grain weight due to smaller phenotypic variances were reported (Moghaddam *et al*., 1997; Kashif *et al*., 2004; Ali *et al*., 2008; Atta *et al*., 2008; Laghari *et al*., 2010; Kalimullah *et al*., 2012; Awale *et al*., 2013; Karim *et al*., 2013; Farshadfar *et al*., 2014; Adhiena *et al*., 2016). However, Laghari *et al*. (2010) reported moderate heritability for number of grains per spike, and Awale *et al*. (2013) reported moderate heritability for number of spikelets per spike (57.40%) and low heritability for spike length (23.48%).

High heritability was observed in harvest index (Moghaddam *et al*., 1997; Kumar *et al*., 2014) and biological yield (Kumar *et al*., 2014). On the other hand, Adhiena *et al*. (2016) reported moderate heritability and low heritability for harvest index and biological yield, respectively.

2.4.4. Genetic Advance

Genetic advance (GA) is the superiority of selected individuals over the base (original) population. Genetic advance under selection is a genotypic value, which depends on three things (Allard, 1960): genetic variability, heritability or masking effect of non-genetic variability on the genetic variability and the selection intensity applied. Genetic progress would increase with increase in the variance. Level of improvement in one or more measured traits as compared to natural or unimproved populations usually expressed as a percentage, and usually improvement (GA) is determined by heritability of the trait (h^2), selection and phenotypic standard deviation. Because of the cyclic nature of a breeding program, the majority of parents in any given cycle are represented by the best lines selected from the previous cycle (Kumar *et al*., 2014).

Moghaddam *et al*. (1997), Laghari *et al*. (2010) and Awale *et al*. (2013) reported high genetic advance as percentage of mean in bread wheat for characters like number of tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, 1000-seed

weight, harvest index, biological yield and grain yield, and also low genetic advance as a percentage of mean for heading date and maturity date were reported. However, Moghaddam *et al*. (1997), Laghari *et al.* (2010) and Awale *et al*. (2013) reported high genetic advance as a percentage of mean for heading date and maturity date. On the other hand, Adhiena *et al*. (2016) computed moderate genetic advance as percent of mean for most of traits studied except for number of fertile tillers per plant, which refers to improvement of these traits in genotypic value for the new population compared with the base population with one cycle of selection is not rewarding.

2. 5. Association among Characters

2.5.1. Genotypic and Phenotypic Correlation Coefficients

A correlation coefficient gives a numerical summary of the degree of association between two variables for example, to what degree do high values of one variable go with high values of the other one? Correlation coefficient vary from -1 to +1, with positive values indicating an increasing relationship and negative values indicating a decreasing relationship.

Correlation coefficient is an important statistical method, which can help breeders in selection for higher yields. The correlation coefficient, the degree of association between two characters, measures the magnitude and direction of mutual relationship between various plant characters and helpful in determining the component characters of a complex trait, like yield (Mohammadi *et al*., 2012; Laghari *et al*., 2010). The phenotypic and genotypic correlation coefficients are measures of the degree of closeness of the linear relationship between pairs of variables and also a value to indicate the degree to which various morpho-physiological characters are associated with economic productivity (El-Mohsen *et al*., 2012).

The existence of correlation between a complex trait and its components is an indication of gene association or pleiotropism. Correlations in phenotype may be due to genetic or environmental causes and may be positive or negative. Genetic causes may be due to pleiotropy, linkage, gametic phase disequilibrium. At genetic level, a positive correlation occurs due to coupling phase of linkage and negative correlation occurs due to repulsive phase of linkage of genes controlling two different traits.

Correlation coefficients (r) were estimated to study the relationships among the traits (Usmani *et al*., 2014) ranged from -1 to +1 and r value of -1 or +1 indicates perfect correlation; values close to -1 indicate high negative correlation. In opposition, values close to +1 indicate high positive correlation. If there is no linear association between variables, the correlation is zero (Fellahi *et al*., 2013). Statistical analysis showed that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits which reflect the influence of environment on the expression of traits (Ali *et al*., 2008; Laghari *et al*., 2010; El-Mohsen *et al*., 2012; Kalimullah *et al*., 2012; Farshadfar *et al*., 2014).

Results of positive associations of grain yield per plant with number of tillers per plant, number of spikelet's per spike, spike length, number of grains per spike and 1000-grain weight at genotypic and phenotypic levels were reported, but days to 50% heading and plant height contributed negatively towards grain yield at both levels (Kashif *et al.,* 2004; Ali *et al*., 2008; Khan *et al*., 2010; El-Mohsen *et al*., 2012; Irfaq *et al*., 2012; Awale *et al*., 2013; Gelalch and Hanchinal, (2013). However, Kashif *et al*., (2004) reported positive association between plant height and grain yield.

2.5.2. Path Coefficient Analysis

In plant breeding program, direct selection for yield as such could be misleading. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield (Ali *et al*., 2008). The correlation coefficient may not give sufficient information about the relationship between different variables as much as statistical multivariate methods give (Fellahi *et al*., 2013). Therefore, correlation studies along with path analysis provide a better understanding and an exact picture of the association of different characters with grain yield (Ali *et al*., 2008). Path coefficient analysis provides an effective way of finding out direct and indirect sources of correlations, using genotypic correlations of different plant attributes (Kashif *et al*., 2004).

Path coefficient analysis is an efficient statistical technique especially designed to determine the direct effect of one character on another character and permits the separation of a correlation coefficient in to components of direct and indirect influences for a set of *a priori* cause and effect

interrelationships (Ali *et al*., 2008; Fellahi *et al*., 2013). Path coefficient analysis is a reliable statistical technique, which provides means to quantify the interrelationship of different yield components and indicate whether the influence is directly reflected in the yield or take some other path ways to produce an effect. Grain yield per plant was selected as resultant variable and plant height, flag leaf area, fertile tillers per plant, spike length, spikelets per spike, grains per spike and 1000-grain weight as casual variables (Kashif *et al*., 2004).

Studies have been conducted to estimate direct and indirect effects of different traits on grain yield in bread wheat. Khan *et al*. (2010) reported the highest direct effect of grains per spike on grain yield followed by spike length and days to maturity whereas 1000-grain weight and plant height had negative direct effect on the same parameter, and characters such as days to maturity and grains per spike exerted positive direct effect along with positive genotypic correlation on grain yield.

In a study conducted by Ali *et al*. (2008), number of grains per spike exhibited the highest positive direct effect followed by number of productive tillers per plant and 1000-grain weight. Furthermore, El-Mohsen *et al*. (2012) reported maximum positive direct effects of number of grains per spike, followed by number of tillers per plant and 1000-grain weight on grain yield per plant.

Path coefficient analysis study in bread wheat displayed maximum positive direct effect on grain yield per plot mostly exerted by days to heading, grain filling period, number of tillers per plant and grains per spike on grain yield per plot (Awale *et al*., 2013). Gelalcha and Hanchinal (2013) also reported biomass, harvest index and plant height imparted significant direct influence on grain yield in bread wheat.

2. 6. Principal Component Analysis

Principal component analysis (PCA) is defined as a method of data reduction to clarify the relationships between two or more characters and to divide the total variance of the original characters into a limited number of uncorrelated new variables (Fellahi *et al*., 2013). This will allow visualization of the differences among the individuals and identify possible groups. The reduction is achieved by linear transformation of the original variables into a new set of

uncorrelated variables known as principal components (PCs). The first step in PCA is to calculate Eigen values, which define the amount of total variation that is displayed on the PC axis.

Azeb (2016) noted the first PC generalizes most of the variability present in the original data relative to all remaining PCs and a study conducted at Atsbi, Ofla and Quiha environments revealed that four principal components PC1, PC2, PC3 and PC4 with eigenvalues 3.87, 2.87, 1.26 and 1.04, respectively have accounted for 82.16% of the total variation among genotypes for the 11 quantitative traits considered at Atsbi. This holds true for Ofla site, where the first three principal components PC1, PC2 and PC3 with eigenvalues of 4.08, 2.07 and 1.47 resulted in 69.27% total variation and, the first three principal components PC1, PC2 and PC3 with eigenvalues 4.64, 1.93 and 1.35, respectively, have accounted for 72.04% of the total variation where the first two principal components PC1 and PC2 contributed values of 42.20% and 17.58%, respectively to the total variation at Quiha environment..

Different levels of diversity were observed in different accessions/populations on the basis of agro-morphological traits. The Eigen values are often used to determine how many factors to retain and the sum of the Eigen values is usually equal to the number of variables (Fellahi *et al*., 2013). According to the results of Fellahi *et al*. (2013), the estimated wheat variables had grouped into three principal component factors with Eigen values more than one which all together explained 77.44% of total variability.

Mideksa *et al*. (2014) reported principal component analysis explained better the variation among varieties and land races which showed that the first four components with Eigen values more than one accounted 74% (22, 21, 18 and 12%, respectively) plant height, ear shape, days to maturity, grain yield, biological yield, ear color and grain color being the most important factors in contributing to the total variability. The study of Awale and Sentayehu (2013) demonstrated that characters having relatively higher value in the first principal component like number of tillers per plant, grain yield per plot, grains per plot which accounted 27.9% from the total variation (91.87%) of the six principal components had more contribution to the total variation and they were the ones that most differentiated the clusters.

Daniel *et al*. (2011) assessed the genetic diversity for yield and yield related traits in 49 bread wheat genotypes for 17 characters and showed wide variability for the components studied. Accordingly, the result of the principal components analysis revealed that nine principal

components accounted nearly 80 % of the total variation. Out of the total principal components retained, PC1, PC3, PC8 and PC 4 with values of 18.71 %, 9.68 %, 9.22 % and 8.15 %, respectively, contributed more to the total variation. Hence, the first principal component had high positive component loading from protein content, sedimentation volume and wet gluten content; and high negative loading from grain yield, biomass yield and starch content contributed more to the diversity and they were the ones that most differentiated the clusters. More over the major contributing characters for the diversity in the third principal component (PC3) were days to maturity, harvest index and days to heading; whereas grain filling period and days to heading in principal component four (PC4); and biological yield, days to heading, grain yield and starch content in principal component eight (PC8).

2. 7. Genetic Divergence (Distance) and Cluster Analysis

Genetic divergence is one of the important biometrical techniques used for estimating the extent of diversity existed among selected genotypes present in a population (Mahalanobis, 1936). The pattern and level of genetic diversity in a given crop gene pool can be measured in terms of genetic distances which is the extent of gene differences between cultivars as measured by allele frequencies at sample loci.

Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization since it is necessary that the varieties should be genetically divergent especially for quantitative characters that contribute towards yield (Daniel *et al*., 2011). The analysis of genetic diversity through the cluster analysis of cluster diagram (dendrogram) based on different dissimilarity/similarity measures using various clustering algorithms categorize genotypes in to different clusters at a certain percentage of dissimilarity/similarity level. Knowledge of genetic diversity and relationships among elite breeding materials is important for the improvement of crop plants. Genetic diversity is different from genetic variability in a way that the former measures the number of the actual variation of species in a population whereas the latter measures how much the trait or the genotype will tend to vary. Genetic diversity refers to any variation in the nucleotides, genes, chromosomes, or whole genomes of organisms (http://www.unaab.edu.ng).

Cluster analysis is a multivariate method or technique, which aims to classify a sample genotypes based on a set of measured variables into a number of different groups such that

similar genotypes are placed in the same group and arranging variables into different clusters to find the clusters that their cases within are more similar and correlated to one another comparing to other clusters (Fellahi *et al.,* 2013).

Clustering is also defined as the process of organizing genotypes into homogeneous groups and is performed to study the patterns of groupings of genotypes whose members are similar in some way (Chahal *et al*., 2002). It operate on a matrix of dissimilarity (or similarity) indexes for all possible pairs of genotypes depending on which is being clustered (Ghaderi *et al*., 1980).

In a study conducted by Ali *et al*. (2008), cluster analysis grouped 70 wheat genotypes into 4 different clusters at 30% linkage distance. Cluster analysis was performed by Tewodros *et al*. (2014) to study the patterns of groupings of fourteen bread wheat genotypes and grouped into three clusters.

Cluster analysis based on agro-morphological traits of modern varieties and land races revealed that the local varieties (land races) had the highest thousand-seed weight and unique phenotypic characteristics in terms of ear shape and awn conditions as compared to other bread wheat varieties (Mideksa *et al*., 2014). Awale and Sentayehu (2013) grouped twenty-six bread wheat genotypes into six clusters using D^2 analysis.

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The field experiment was conducted at Sirinka Agricultural Research Center (SARC) testing sites of Jamma and Geregera

1. Jamma which lies between the geographical coordinates 10^{o} 23' to 10^{o} 27' N latitudes and 39^{0} 7' to 39^{0} 24' E longitudes in South Wollo Zone of the Amhara National Regional State, which is 260 km away from the capital city, Addis Ababa, in the north east direction and at geographical coordinates of 10^{0} 27' N latitude and 39^{0} 15' E longitudes at an altitude of 2600 m.a.s.l. The dominant soil type is of P^{H} 6.0 with total rainfall of 720.5 mm, and minimum and maximum temperatures of 10.0 and 21.1 ^{0}C, respectively.

2. Geregera is found 651 km away from Addis Abeba and located at an altitude of 2650-2855 m.a.s.l, which lies between 39 ^{o} N longitude and 12^{o} E latitude with annual rainfall of 1105 mm. The soil type is characterized as *Lithosol*, brown colour and p^{H} of 5.6. Rainfall is erratic in distribution, often unpredictable and is uni-modal, which starts in the first week of July and stops at the end of August.

3.2. Planting Materials

Forty-nine bread wheat genotypes which are released varieties and elite materials taken from Sinana and Kulumsa Agricultural Research Centers were used in the study. Description of the genotypes are presented in Table 2.

Table 2. Description of bread wheat genotypes used in the study

SN	Genotype	Code	Pedigree	Source center	Year of release
1	Honqolo	-	-	Kulumsa	-
2	Biqa	-	-	Kulumsa	-
3	WORRAKATTA/PASTOR	-	-	Sinana	2014
4	UTQUE96/3/PYN/BAU//MILLAN			Sinana	2014
5	Hidasse	ETBW5795	YANAC/3/PRL/SARA//TSI/VEE#5/4	Kulumsa	2012
6	Ogolcho	ETBW 5520	WORRAKATTA/2*PASTOR	Kulumsa	2012
7	Hoggana	ETBW 5780	PYN/BAU//MILAN	Kulumsa	2011
8	Hulluka	ETBW5496		Kulumsa	2012
9	Mekelle-3	M17SAWSN79	-	Mekele	2012
10	Mekelle-4	-	-	Mekele	2013
11	Shorima	ETBW 5483	UTQUE96/3/PYN/BAU//MILAN	Kulumsa	2011
12	Kakaba	Picaflor#1	KIRITATI//SERI/RAYON	Kulumsa	2010
13	Danda'a	Danphe#1	KIRITATI//2*PBW65/2*SERI.1B	Kulumsa	2010
14	Gassay	HAR 3730	PASTOR	Adet	2007
15	Alidoro	HK14R251	HK-14-R251	Holeta	2007
16	Digelu	HAR3116	SHA7/KAUZ	Kulumsa	2005
17	Tay	ET12/604	ET12D4/4777(2)//FKN/GB/3/PVN"S"	Adet	2005
18	Sofumar	HAR 1889	LIRA 'S'/TAN"S"	Sinana	1999
19	Mada-Wolabu	HAR 1480	TI/3/Fn/Th/Nar 59 *2/4/Bol'S'	Sinana	1999
20	Pavon-76	-	VCM//CNO"S"/7C/3/KAL/BB	Kulumsa	1982
21	Jeferson	-	-	Kulumsa	2012
22	King Bird	-	(300/SM+501M)/HAR 1709	Kulumsa	2014
23	ETBW 6861	-	WAXWING*2/HEILO	Kulumsa	Pipe line
24	ETBW 8506	-	AGUILAL/FLAG-3	Kulumsa	Pipe line
25	ETBW 8507	-	DURRA-4	Kulumsa	Pipe line

26	ETBW 7120	-	QAFZAH-23/SOMAMA-3	Kulumsa	Pipe line
27	ETBW 8508	-	REYNA-8	Kulumsa	Pipe line
28	ETBW 7213	-	CHAM4/SHUHA'S'/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB	Kulumsa	Pipe line
29	ETBW 8509	-	REYNA-29	Kulumsa	Pipe line
30	ETBW 7038	-	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA//TSI/VEE#5/4/CROC_1/AE.SQUARROSA (224)//2*OPATA	Kulumsa	Pipe line
31	ETBW 8510	-	HIJLEEJ-1	Kulumsa	Pipe line
32	ETBW 7058	-	ROLF07//TAM200/TUI/6/WBLL1/4/HD2281/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/TACUPETO F2001	Kulumsa	Pipe line
33	ETBW 8511	-	BOW#1/FENGKANG 15/3/HYS//DRC*2/7C	Kulumsa	Pipe line
34	ETBW 7147	-	CROC-1/AE.SQUARROSA(224)//OPATA/3/QAFZAH21/4/SOMAMA-3	Kulumsa	Pipe line
35	ETBW 8512	-	BABAX/LR42//BABAX*2/3/KURUKU/4/KINGBIRD #1	Kulumsa	Pipe line
36	ETBW 7871	-	PAURAQ/4/PFAU/SERI.1B//AMAD/3/WAXWING	Kulumsa	Pipe line
37	ETBW 8513	-	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING	Kulumsa	Pipe line
38	ETBW 6940	-	UTIQUE 96/FLAG-1	Kulumsa	Pipe line
39	ETBW 8514	-	TUKURU//BAV92/RAYON/3/WBLL1*2/BRAMBLING/4/	Kulumsa	Pipe line
40	ETBW 7368	-	D. 56455	Kulumsa	Pipe line
41	ETBW 8515	-	BECARD/3/PASTOR//MUNIA/ALTAR84	Kulumsa	Pipe line
42	ETBW 7364	-	ACSAD1115	Kulumsa	Pipe line

43	ETBW 8516	-	KACHU/KIRITATI	Kulumsa	Pipe line
44	ETBW 7194	-	VAN'S'/3/CNDR'S'/ANA//CNDR'S'/ MUS'S'/4/TEVEE-5	Kulumsa	Pipe line
45	ETBW 8517	-	FRNCLN*2/TECUE #1	Kulumsa	Pipe line
46	ETBW 7101	-	KAMB2/PANDION	Kulumsa	Pipe line
47	ETBW 8518	-	SUP152/AKURI//SUP152	Kulumsa	Pipe line
48	ETBW 7872	-	QUAIU/5/FRET2*2/4/SNI/TRAP#1/3 /KAUZ*2/TRAP//KAUZ	Kulumsa	Pipe line
49	ETBW 8519	-	ATTILA/3*BCN*2//BAV92/3/KIRIT ATI/WBLL1/4/DANPHE	Kulumsa	Pipe line

Source: Kulumsa Agricultural Research Center, 2015.

3.3. Experimental Design, and Trial Management

The experiment was laid out in 7x7 simple lattice design with two replications. The dimension of an individual plot area was 1.2m width x 2.5 m length ($3m^2$) with six rows for each entry. The spacing between blocks, plots and rows were 1.5m, 0.4m and 0.2m, respectively. The experimental field was well tilled and planting rows were prepared using hand pulled row-marker. Planting was done with the seed rate of 150 kg/ha (45 g/plot). Diammoniumphosphate (DAP) and Urea fertilizers were applied at the rate of 100 kg/ha. Urea in splits: first split (1/3) and the second split (2/3) of the total dose at planting and mid tiller stages, respectively. All the cultural and agronomic practices were applied as recommended and kept constant. Weeds were removed manually as and when required. The data for characters studied were collected from the four central rows for each plot.

3.4. Data collected

For quantitative characters, AGROVOC descriptors: Cereal crops, plant developmental stages, plant physiology, agronomic characters, yield components, measurement, sampling was adopted and data were recorded on plant and plot basis as described below.

3.4.1. Plant basis

Ten plants were randomly taken from the four central rows for recording the following observations and the mean values for the treatment were computed:

1. **Plant height (PH)**: The distance in cm between the ground level to the tip of the terminal spikelet of ten plants (excluding the awns) at maturity.
2. **Number of productive tillers per plant (NPP):** The actual count of the fertile numbers of tillers of ten plants (spike bearing) per plant.
3. **Spike length (SL):** Length measured in cm from base of spike to the tip of the highest spikelet of ten plants (excluding the awns) in cm at maturity.
4. **Number of spikelets per spike (NSPS):** Total numbers of spikelet's on main spike of all ten plants from four rows were counted at the time of maturity and average was recorded.
5. **Number of grains per spike (NGS):** The actual count of the number of kernel per spike of all ten plants after threshed manually at the time of harvest.

3.4.2. Plot basis

The data on the following attributing traits were collected on the basis of the central four rows ($2m^2$) in each plot.

1. **Days to heading (DH):** The number of days from date of sowing to the stage where 50% of the spikes have fully emerged.
2. **Days to maturity (DM):** The number of days from sowing to the stage when 75% of the plants in a plot have reached physiological maturity.
3. **Grain filling period (GFP):** The number of days from heading to maturity, i.e. the number of days to maturity minus the number of days to heading.
4. **Thousand Seed weight (TSW)**: Weight of 1000 seeds randomly taken from each plot in gram.

5. **Biological yield (BY) (kg/m^2):** The representative plants within the four central rows or from 2m^2/ plot were harvested and weighed in kilograms at maturity, after drying at 70°C for 24 hours in a well-ventilated oven.
6. **Grain yield (GY) (qt/ha):** Grain yield in grams (**g/m^2**) obtained from the central four rows (2m^2) of each plot and converted to quintals per hectare after moisture of the seed is adjusted to 12.5% moisture content.
7. **Harvest index (%):** The ratio of yield of dried grain weight to the dried above ground biomass weight of the harvestable plot (2m^2 /plot) multiplied by 100.

3.5. Statistical Analysis

3.5.1. Analysis of Variance (ANOVA)

Analysis of variance was applied in order to test the significance differences of traits. The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) for simple lattice design using Proc lattice and Proc GLM procedures of SAS version 9.2, (SAS Institute, 2008). Then after testing the ANOVA assumptions, Fisher's protected least significant difference (LSD) test at 5% level of significance was used for genotypes mean comparisons, whenever genotype differences were significant. To perform a combined statistical analysis across locations, test of homogeneity of error variances of each character for the two locations were performed by using F- test (the ratio of the largest to the smallest error variance) to the characters, and the test showed homogeneity of the two locations for all characters that involved in the study. The ANOVA was also run for the two locations separately and combined over the two locations since all characters showed homogeneity of error variance. The difference between treatment means was compared using Fisher's protected least significant difference (LSD) test at 5% probability levels. GENRES Version 7.01, (Pascal Institute, 1994) was employed for estimation of correlation between traits, and path coefficient analysis.

The model for lattice design is:

$$Yil(j) = \mu + ti + rj + (b \mid r)l(j) + eil(j)$$

Where; $Y_{il(j)}$ is the observation of the treatment i (i = 1, ..., v = k^2), in the block l (l = 1, ..., k) of the replication j (j = 1, ..., m);

μ is a constant common to all observations;

t_i is the effect of the treatment i;

r_j is the effect of the replication j;

$(b|r)_{l(j)}$ is the effect of the block l of the replication j;

$e_{il(j)}$ is the error associated to the observation $Y_{il(j)}$, where $e_{il(j)} \sim N(0, s)$, independent.

Table 3. Skeleton for individual location analysis of variance for simple lattice design

Source of variance	**Df**	**Sum of squares**	**Expected Mean Squares**	**F-Values**
Replication (r)	r-1	SSR	MSr	MS_R/ MSe
Genotypes (g) - [Un adj.]	g^2-1	SSg	MSg	MSg/ MSe
- [adj.]	g^2-1	SSg	MSg	MSg/ MSe
Block within replication (b) [adj.]	r(b-1)	SSB	MSb	MSb/MSe
Intra-block error (Ebe)	(b-1) (rb-b-1)	SSE	MSe	
Total	rb^2-1	SSt		

Table 4. Analysis of variance in the case of a series of genotypes evaluated across environments

Source of variation	Degrees of freedom	Mean Squares	Expected Mean Squares
Environment	e-1	MS_E	$\sigma^2_e + g\,\sigma^2_{r(E)} + r\,\sigma^2_{GE} + rg\,\sigma^2_E$
Rep(block)	(r-1)e	MS_R	$\sigma^2_e + g\,\sigma^2_{r(E)}$
Genotype	g-1	MS_G	$\sigma^2_e + r\,\sigma^2_{GE} + re\,\sigma^2_G$
Genotype × Environment	(g-1)(e-1)	MS_{GE}	$\sigma^2_e + r\,\sigma^2_{GE}$
Error	(g-1)(e-1)e	MS_E	σ^2_e

Notes; Total phenotypic variance: Var $(Y_{ijk}) = \sigma^2_p + \sigma^2_e + \sigma^2_{GE} + \sigma^2_G$

Phenotypic variance of genotypic means: Var $(\bar{Y}_{ijk}) = \sigma^2_p = \frac{\sigma^2_e}{re} + \frac{\sigma^2_{GE}}{e} + \sigma^2_G = \frac{MS_G}{re}$

Genotypic variance = $\sigma^2_G = (MS_G - MS_{GE})/re$

Heritability on individual experimental unit basis: $H^2 = \frac{\sigma^2_G}{\sigma^2_G + \sigma^2_{GE} + \sigma^2_e}$

Heritability on a genotypic-mean basis: $H^2 = \frac{\sigma^2_G}{\sigma^2_G + \frac{\sigma^2_{GE}}{e} + \frac{\sigma^2_e}{re}}$

The above calculations were done according to Comstock and Robinson, (1952).

Source; FAO, (2009).

where: r = number of replication, G = number of genotypes, df = degree of freedom, b = block, e= environment, Ebe= Intra-block error, SS = Sum of squares, MS = mean squares, SSR and MSR are sums of squares and mean squares of replication, respectively; SSG and MSG are sums of squares and mean squares of genotypes, respectively; SSb and MSb are sums of squares and mean squares of blocks within replication, respectively; SSe and MSe are sums of squares and mean squres of intra-block error, respectively; and SSt is sum of squares of the total; σ^2_g=variance due to genotypes, σ^2 Ge= variance due to genotypes with environment interaction, σ^2_e=variance due to environments.

3.5.2. Genotypic and Phenotypic Coefficients of Variation

Phenotypic and genotypic coefficients of variation were estimated according to Singh and Chaudhary (1985).

$$\mathbf{GCV} = \frac{\sqrt{\sigma^2 \mathbf{g}}}{\bar{\mathbf{X}}} * \mathbf{100} \qquad \mathbf{PCV} = \frac{\sqrt{\sigma^2 \mathbf{P}}}{\bar{\mathbf{X}}} * \mathbf{100}$$

Where; GCV = Genotypic coefficient of variation;

PCV =Phenotypic coefficient of variation

$\bar{x}$= Grand mean of the characters under study

The mean values were used for genetic analyses to determine genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Singh and Chaudhury, 1985).

3.5.3. Genetic Advance (GA)

Genetic advance (GA) was calculated with the method suggested by Allard (1960); Singh and Chaudhury (1985):

$GA = k.\ \sigma^2_p.\ H^2$

Where; GA: genetic advance.

K: constant = 2.06 at 5% selection intensity.

σ^2_p: square root of phenotypic variance.

H^2: Heritability in broad sense

3.5.3.2. Genetic advance as percent of mean

Genetic advance as percent of the mean was calculated to compare the extent of predicted advance of different traits under selection, using the following formula:

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where; GAM=Genetic advance as percent of mean

GA=Genetic advance under selection, and $\bar{x}$=Grand mean of the trait

3.5.4. Correlation Analysis

Estimation of correlation coefficients (r) was computed using GENRES statistical software (Pascal Intl Software Solutions, 1994). Phenotypic and genotypic correlations were estimated using the standard procedure suggested by Miller *et al*. (1958) and Kashiani and Saleh (2010) from the corresponding variance and covariance components.

$$\mathbf{r_g} = \frac{\mathit{g}\mathbf{covx.y}}{\sqrt{\delta^2\mathbf{gx}.\delta^2\mathbf{gy}}} \qquad \mathbf{r_p} = \frac{\mathbf{pcovx.y}}{\sqrt{\delta^2\mathbf{px}.\delta^2\mathbf{py}}}$$

Where: r_g = Genotypic correlation coefficient

r_p = Phenotypic correlation coefficient

$Gcov_{xy}$ = Genotypic covariance between variables x and y

$Pcov_{xy}$ = Phenotypic covariance between variables x and y

$\sigma^2_g x$ = Genotypic variance for variables x

$\sigma^2_g y$ = Genotypic variance for variables y

$\sigma^2_p x$ = Phenotypic variance for variables x

$\sigma^2_p y$= Phenotypic variance for variables y

To test the significance of correlation coefficients, the following formula was used (Sharma, 1998):

$t = r / SE(r)$

Where; $SE(r) = 1-r^2$

Where; *r* is correlation coefficient

n is number of genotypes.

Then, calculated 't' value was compared with standard value at *n*-2 degrees of freedom and a levels of probability (where t is 0.05 and 0.01).

3.5.5. Path Coefficient Analysis

The analysis was done following the method suggested by Dewey and Lu (1959):

$Rij = pij + \sum rik + pkj$

Where rij = mutual association between the dependent character, i (yield-related trait) and independent character, j (grain yield) as measured by the correlation coefficients; Pij is the components of direct effects of the independent character (i), Σ *rik pkj* = summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k). Whereas the contribution of the remaining unknown characters is measured as the residual effect (R^2) which is calculated as: $\sqrt{(1-R^2)}$

Where, $R^2=\sum pij + rij$

3.6. Principal Component Analysis

Principal component analysis was performed using correlation matrix by employing PAST 1.93 (Palaeontological Statistics; Hammer *et al.*, 2001) to evaluate the contribution of each quantitative character in the total variation of genotypes. Number of factors retained was decided by looking at the Eigen values (values > 1.0) (Fellahi *et al*., 2013). Those traits that had load coefficient values > 0.40 (ignoring the sign) were considered as relevant scores for the PCAs. The general formula to compute scores on the first component extracted (created) in a principal component analysis is described as:

$$C1 = b11(X1) + b12 + \cdots b1p(Xp)$$

Where, C1 = the subject's score on principal component 1 (the first component extracted)

b1p = the regression coefficient (or weight) for observed variable p, as used in creating principal component one.

Xp = the subject's score on observed variable p.

3.7. Genetic Divergence and Cluster Analysis

Mahalanobis (1936) statistics was used to estimate the genotypic divergence between clusters. All the genotypes used were clustered into different groups based on D^2 statistics. The D^2 values of all the combinations were arranged in descending order. D^2 statistics is defined by the following formula:

$$D^2ij = (Xi - Xj)\, S^{-1}\, (Xi - Xj)$$

Where; D^2ij = the square distance between any two genotypes i and j;

Xi and Xj = the vectors for the values for genotypes ith and jth genotypes;

S^{-1} = the inverse of pooled variance covariance matrix within groups.

Testing the significance of the squared distance values obtained for a pair of clusters was taken as the calculated value of c^2 (chi-square) and tested against the tabulated c^2 values at p-1 degree of freedom at 1% and 5% probability levels, where p = number of traits used for clustering genotypes.

The proc cluster of SAS system with average linkage method of clustering strategy version 9.2 (SAS Institute, 2008), which grouped and sorted the genotypes into clusters to form Dendrogam. Cubic clustering criterion (CCC), pseudo F (PSF), and pseudo t2 (PST2) statistics were used in determining the number of clusters in the data.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

The analysis of variance for different characters at Jamma and Geregera locations are presented in Appendix table 2, and 3 respectively. There was significant differences at (P< 0.01 and P< 0.05) levels among genotypes for all characters considered the two environments except for grain filling period at Geregera, which was non-significant.

Since the relative efficiency of simple lattice design is less than complete randomized block design (RCBD) for most characters (Appendix table 2 and 3), which showed under 105% and also blocks within replication sum of squares were non-significant. Therefore analysis of variance were performed using complete randomized block design (RCBD) model. Similar findings were reported by Azeb *et al*. (2016). Before pooling the data across environments, test of homogeneity using F-test for error of variance was done. Therefore, the hypothesis of homogeneous variance is accepted, and analysis of variance and other statistical analysis were run for combined over the two locations.

Combined analysis of variance results for different studied traits is shown in (Table 5). The location effect was significant for all traits, indicating the different climatic conditions in two locations. The location × genotype interaction effect was significant for all traits except number of spikelets per spike indicating different performance of bread wheat genotypes across the two locations. Furthermore, Mean square of genotypes for all characters studied were significant (P<0.05 and P<0.01) differences among the bread wheat genotypes, indicating the existence of sufficient genetic variability within different genotypes to be exploited in the breeding programs that was also reflected in the broad ranges observed for each traits as presented in (Table 5), representing the genetic diversity for further selection procedures in the experimental material under study. The present investigation are in confirmation with early findings of (Ashamo *et al*., 2012; Awale *et al*., 2013; Kumar *et al*., 2014; Tewodros *et al*., 2014; Zeeshan *et al*., 2014; Adhiena *et al*., 2016).

Table 5. Estimated values of mean squares C.V (%) and R-square (%) for 11 traits of 49 bread wheat genotypes combined over across locations

Traits	Sources of Variance							
	E	Re(b)	G	E x G	error	C.V (%)	LSD at 5%	R-Square (%)
DF	1	1	48	48	96			
DH	65.15**	5.45ns	58.12**	10.5**	3.110	2.65	2.480	0.92
DM	650.3**	0.785ns	34.67**	11.70*	5.900	1.90	3.410	0.84
PHT	4662**	348.6**	117.4**	44.7**	25.50	6.45	7.090	0.84
NPTP	9.48**	1.77**	0.163**	0.10**	0.060	16.3	0.350	0.81
SL	99.26**	13.17**	2.40**	0.710*	0.460	8.97	0.940	0.86
NSPS	321.4**	9.130*	3.50**	1.30ns	1.130	7.30	1.480	0.84
NGS	922.4**	2.800ns	40.5**	17.00*	11.27	8.90	4.710	0.77
TSW	9839**	15.00ns	41.30**	16.15*	6.800	7.11	3.900	0.94
BY	23.40**	0.020ns	0.140**	0.088**	0.045	10.0	0.299	0.89
HI	1.070**	0.006*	0.00311**	0.0021*	0.0014	9.66	0.043	0.94
GY	35311.8**	75.60*	61.72**	43.75**	22.50	13.7	6.66	0.95

NB: E=environment, Re(b)= replication within a block, E x G= environment with Genotype interaction mean square, CV=coefficient of Variation, DF=degrees of freedom, DH=Days to heading, DM=Days to maturity, PHT=plant height, NPT=number of productive tillers plant, SL =Spike length, NSPS=Number of spike lets per spike, NGS=Number of grains per spike, BY=Biological yield, HI=Harvest index, TSW=Thousand seed weight, and GY=Grain yield per hectare.

4.2. Genetic Variability and Mean Performance of Genotypes

The success of a breeding program depends largely upon the amount of genetic variability present in the population and the extent to which the desired traits are heritable. Based on

combined over location the mean performance of genotypes for studied traits showed a wide range of variation (Table 6). Days to heading ranged from (61-79.5 days), with mean value of 66.6 days, days to maturity (124-136 days) with mean value of 127.6 days, plant height ranged from 68-93.75 cm with mean value of 78.3 cm, productive tillers per plant(1.2-1.9) with mean value of 1.5, spike length (6.4-10.9 cm) with mean value of 7.5 cm, number of spikelets per spike(13-17.4) with mean value of 14.6, number of grains per spike (29.45-7) with mean value of 37.8, , thousand seed weight (34.8-48 g) with mean value of 40.8 g, biological yield (1.8-2.7 kg) with mean value of 2.12 kg, harvest index (0.26-0.36) with mean value of 0.31, grain yield per hectare (26.5-43.8 qt/ha) with mean value of 34.6 qt/ha, indicating good opportunity for grain yield improvement. A wide range of variation among bread wheat genotypes in yield and yield related traits reported (Ashamo *et al*., 2012; Awale *et al*., 2013; Kumar *et al*., 2014; Tewodros *et al*., 2014; Adhiena *et al*., 2016).

Based on mean performance of genotypes the response of grain yield for separate and across location was discussed below. At Jamma environment, grain yield ranged from Genotypes such as ETBW 8518 (60), Mada-wollabo (58.5), ETBW 8506 (57), Hoggana (56.25), Ogolcho (55) were better grain yielder in Qt/ ha respectively. Whereas genotypes such as Gassay (32.5), ETBW 7058 (32), Biqa (29.25), Mekele-3 (27.5) and Mada-wollabo (27.5) were better grain yielder in Qt/ ha under Geregera respectively. Genotypes such as Gassay (44.75), Mada-wollabo (43.00), Biqa (41.5), Mekele-3 (40), UTQUE96/3/PYN/BAU//MILLAN (39.9) were the top grain yielder genotypes across location. Thus it was observed that the overall mean for grain yield was the lowest (21.17 qt/ha) at Geregera environment, whereas Jamma seems to be ideal for cultivation of bread wheat as the overall mean grain yield of the location was (48 qt/ha) as data presented in appendix (Table 2 and 3).

4.3. Genotypic and Phenotypic Coefficients of Variation

Because of high genotype-environment (G × E) interactions, estimates of GCV, H^2 and GA for most of the characteristics using combined over location analysis were generally lower than the estimates computed from the variance analyses made separately for each location as presented in (Table 6 and Appendix table 2, 3) respectively.

Low genotypic as well as phenotypic coefficient of variation in the characters observed may be due to presence of both positive and negative alleles in the population (Majumder *et al*., 2008). The genotypic coefficient of variation ranged from 1.88 % for maturity date to 8.66 % for spike length; and phenotypic coefficient of variation ranged from 2.3% for maturity date to 13.3% for number of productive tillers per plot (Table 6). Maximum values of genotypic coefficient of variation were recorded for spike length (8.66 %), followed by number of productive tillers per plant (8.4%), number of grains per spike (6.4 %), and thousand seed weight (6.15 %), whereas better value of phenotypic coefficient of variation were recorded for productive tillers followed by grain yield, spike length, and harvest index with a value of 13.3%, 11.35 %, 10.3%, 9% respectively in the study.

The magnitude of phenotypic coefficient of variation (PCV) is much higher than the genotypic coefficient of variation (GCV) for number of productive tillers per plant, grain yield, harvest index and biological yield indicating that apparent variation for the characters was not only due to genotypes but also due to influence of wide range of phenotypic (V_P or σ^2_P) and genotypic variance (V_G or σ^2_g) observed in the experimental material for all the traits studied. This result is related with the findings of other similar works (Kashif *et al.,* 2004*;* Subhani *et al.,* 2010*;* Mohammedi *et al.,* 2011; Asaye *et al*., 2013). Likewise, the phenotypic variances for plant height and days to heading were also high, indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these traits.

4.4. Estimation of Heritability in Broad Sense

The concept of heritability explains whether differences observed among individuals arose as a result of differences in genetic makeup or due to environmental forces (Azeb *et al*., 2016). More effective in breeding of homozygous lines. Heritability estimate for characters under study is indicated in (table 6). In this study heritability in broad sense ranged from 29% for grain yield to 82% for heading date. The heritability is categorized as low (0-30%), moderate (30-60%) and high (60% and above) as given by Comstock and Robinson, (1949). Accordingly, high heritability was estimated for days to heading (82%), maturity date (66.2%), spike length (70.4%), plant height (63.6), number of spikelets per spike (62.5) and thousand-seed weight (61%). Similar results were reported by Laghari *et al.* (2010); and also Ali *et al*. (2008) and

Karim *et al*. (2013) reported high estimates of heritability for spike length and number of spikelets per spike in bred wheat.

Moderate heritability was obtained for number of grains per spike, number of productive tillers, harvest index and biological yield, indicating that the characters were more influenced by environment. Although high heritability estimate have been found to be effective in the selection of superior genotypes on the basis of phenotypic performance, Kumar *et al*., (2014), suggested that heritability estimates along with genetic advance will be more useful in predicting the effect for selecting the best individual.

Related findings were reported by Laghari *et al.* (2010). Low heritability was obtained for yield per hectare (29%) which is in agreement with the results obtained by (Mollasadeghi *et al*., 2012; Mohammadi *et al*., 2011; Tesfaye *et al*., 2014; Mesele *et al*., 2016) with a value of (12.27%, 7.4%, 19% and 25%) respectively. Opposed to this study, Awale *et al*. (2013) reported low estimates of heritability for spike length, while Tewodros *et al*., (2014) reported low estimates of heritability for heading date (13%), maturity date (7.79%), plant height (12.8%) and thousand-seed weight (32.8%). The main difference in the findings may be due to the difference in the genetic material used and environmental conditions (Kashif *et al*., 2004; Mohammadi *et al*., 2011; Adhiena *et al*., 2016).

Heritability determine the choice of plant breeding method/technique. High h^2 use mass and pure line selection whereas low h^2 use recurrent selection. For traits with low h^2 selection in early segregating generation (F2) would be effective because of in subsequent generation's variation decreases due to increase of homozygosis. High heritability accompanied with relatively high genetic advance in case of, plant height, spike length, and thousands seed weight indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. High heritability for days to heading, days to maturity, number of spikelets per spike coupled with low genetic advance indicates non-additive gene effects. Therefore, there seems a limited scope for improvement in this trait.

4.5. Estimates of Expected Genetic Advance (GA)

Genetic advance as a percent mean ranged from 3.15% for maturity date to 14.9% for spike length (Table 6). Relatively high genetic advance as a percent mean were recorded for spike length followed by number of productive tillers per plant, number of grains per spike, thousand seed weight, heading date and plant height with values of 14.9%, 10.6%, 10%, 10%, 9.7%, and 9.07%respectively, indicating good response to selection.The present study was in close agreement with the findings of (Mohammadi *et al*., 2011; Asaye *et al*., 2013; Adhiena *et al*, 2016; Rahman *et al.,* 2016).

It was suggested that the importance of considering both the genetic advance and heritability of traits rather than considering separately in determine how much can progress to be made via selection (Kumar *et al*., 2014). As a result, traits like spike length, number of grains per spike, and thousand seed weight showed high heritability accompanied with better genetic advance as percent of mean and genetic and phenotypic coefficient of variation in this study. The high heritability estimates along with low genetic advance indicates that non additive type of gene action and genotype-environment interaction plays a significant role in the expression of the traits as observed in days to maturity in the present study, which agrees with the findings of (Majumder *et al*., 2008).

Plant height, spike length, grains per spike and thousand seed weight weight had relatively high heritability along with high genetic advance in percentage of mean making them most important in the selection of modern wheat. High GCV, PCV, heritability and GA% of mean for spike length suggested that it could be transmitted to the hybrid progeny and phenotypic selection based on this would be effective.

Table 6. Estimates of range, means, genotypic and phenotypic variances, broad sense heritability, genetic advance, and genetic advance as a percentage of mean for 11 characteristics of 49 bread wheat genotypes, combined across the locations

Traits	Range	Mean ± SE	δ^2_g	δ^2_p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM
DH	61-79.5	66.6±0.04	11.90	14.53	5.20	5.72	82.0	6.45	9.70
DM	124-136	127.6±0.22	5.74	8.67	1.88	2.30	66.2	4.02	3.15
PHT	68-93.75	78.3±0.084	18.7	29.35	5.50	6.90	63.6	7.10	9.07
NPT	1.2-1.95	1.5±0.214	0.016	0.040	8.40	13.3	38.7	0.16	10.6
SL	6.4-10.9	7.5±0.104	0.422	0.600	8.66	10.3	70.4	1.12	14.9
NSPS	13 -17.4	14.6±0.78	0.550	0.880	5.10	6.44	63.0	1.21	8.30
NGS	29-45.7	37.8±0.11	5.850	10.12	6.40	8.42	57.8	3.80	10.0
TSW	34.8-48	40.8±0.10	6.29	10.32	6.15	7.86	61.0	4.04	10.0
BY	1.8-2.70	2.12±0.123	0.013	0.035	5.38	8.82	37.0	0.143	6.73
HI	0.26-0.36	0.31±0.16	0.00025	0.00078	5.10	9.00	32.0	0.018	5.95
GYP	26.5-43.8	34.6±0.20	4.50	15.43	6.13	11.35	29.1	2.360	6.80

NB: σ^2_g = genotypic variance, σ^2_p=phenotypic variance, GCV (%) = genotypic coefficient of variation, PCV (%) = phenotypic coefficient of variation, H^2 (%) =broad sense heritability, GA =genetic advance, GAM % =genetic advance as percentage of mean, DF=degrees of freedom, DH=days heading, DM=days maturity, PH=plant height, NPTP=number of productive tillers per plant, SL =spike length, NSPS=number of spikelets per spike, NGS=Number of grains per spike, TSW= thousand seed weight, BY=biological yield, HI=harvest index, and GY= Grain yield.

4.6. Correlations Analysis of Quantitative Traits

Genotypic and phenotypic correlations of all possible combinations for traits under study are presented in (Table 7), provided that in most of the cases the genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficient indicating strong inherent relation between the traits but suppressing effect of the environment, which modified the phenotypic expression of these characters by reducing phenotypic coefficient values.

A positive value of r (correlation) shows that the changes of two variables are in the same direction, that is, high values of one variable are associated with high values of other and vice versa (El-Mohsen *et al*., 2012). In general the magnitude of genotypic correlations (r_g) is higher than those of phenotypic correlations (r_p). This revealed that association among characters is under genetic control and indicating the preponderance of genetic variance in expression of characters. It might be due to depressing effect of environment on character association as reported earlier for wheat crop (Laghari *et al*., 2010; El-Mohsen *et al*., 2012). When value of r_p is greater than r_g, it shows apparent association of two traits is not only due to genes but also due to favorable influence of environment. By contrast, if value of r is zero or insignificant, this shows that the two traits are independent.

Thus from the study, positively and significantly correlation of characters studied with grain yield per hectare both at genotypic and phenotypic levels, suggests that yield per hectare would increase with increase of those characters and vice versa.

Days to heading: Days to heading showed negative non-significant association at genotypic and at phenotypic levels (r_g = -0.184, r_p = -0.102) with grain yield per hectare. El-Mohsen *et al*. (2012) and Awale *et al*. (2013) reported negative associations between days to heading and grain yield per plot at genotypic and phenotypic levels. While Moghaddam *et al*. (1997) and Ali *et al*. (2009) reported positive association between days to heading and grain yield per plot. Days to heading highly significant positive association at genotypic and at phenotypic levels with maturity date and highly negative associated with number of productive tillers per plant at genotypic level.

Days to Maturity: Days to maturity showed negative association at genotypic levels (r_g = -0.252) and at phenotypic level (r_p =-0.021) with grain yield per hectare. This finding is in agreement with the findings of Awale *et al*. (2013) and contradicted with the findings of Ali *et al*. (2009). The findings of Khan *et al*. (2010) showed positive association at genotypic levels and negative association at phenotypic levels. Days to maturity negative significant associated with biological yield per plot at genotypic level. On the other hand it was positive non-significant associated with spike length, number of spike lets per spike, and thousand seed weight at both

levels. While negatively non-significant associated with other traits at both levels, except harvest index at phenotypic level.

Plant height: The correlation between plant height and grain yield per hectare was positive and significant at both genotypic and phenotypic levels (r_g = 0.384**, r_p = 0.354*) which indicates that an increase in plant height leads to an increase grain yield. Similar results have been found (Moghaddam *et al*., 1997; Kashif and Khaliq, 2004; Aydin *et al*., 2010; Fellahi *et al*., 2013; Farshadfar *et al*., 2014; Awale *et al*., 2013; Gelalcha and Hanchinal, 2013). However, El-Mohsen *et al*. (2012) reported negative correlation of plant height and grain yield. Plant height showed negative non-significant association at genotypic and at phenotypic levels with days to heading and days to maturity. However it was positive non-significant associated with number of productive tillers per plant and harvest index at both correlation types. Moreover it was highly associated with spike length, number of spikelets per spike, number of grains per spike, thousand seed weight and biological yield.

Number of productive tillers per plant: The correlation between number of tillers per plant and grain yield per hectare was positive and significant at both genotypic and phenotypic levels (r_g = 0.366*, r_p = 0.226). Number of tillers per plant was negatively and highly significant associated with number of spikes per spike at genotypic level (r_g = -0.381**), and also non-significant negative correlation with spike length, suggesting that increase in tiller number reduce , number of spikes per spike and spike length, which are similar with El-Mohsen *et al*. (2012). Number of productive tillers per plant displayed positive and significant relationship at genotypic level with thousand seed weight, and positive and non-significant relationship at genotypic level with number of grains per spike, biological yield and harvest index, suggesting that increase in tiller number adds the value of those traits, indicated that number of tillers per plant may be an effective trait to select higher yielding genotypes.

Spike length: Spike length was in negative relationship at genotypic levels and in positive phenotypic with grain yield per hectare (r_g = -0.047, r_p = 0.014). These results are supported by the findings of earlier researchers like Khan *et al.* (2010). A positive and highly significant correlation was observed between spike length and number of spikelets per spike. It means that with the increase in spike length there was a significant increase in number of spikelets per spike

as discussed by Ul-haq *et al*. (2010). There was a positive correlation between spike length and thousand seed weight at genetic level and also positive and highly significant correlation was observed between spike length and plant height.

Number of spikelets per spike: Number of spikelets per spike was in positive relationship at genotypic level (r_g = 0.004) and in negative relationship at phenotypic level (r_p = -0.124) with grain yield per hectare. A significant and positive phenotypic correlation was observed between numbers of spikelets per spike and plant height, number of productive tillers per plant and at genotypic level highly correlated with numbers of grains per spike. Kashif and Khaliq (2004) and El-Mohsen *et al*. (2012) also observed number of spikelets per spike as significantly and positively correlated with grain yield at genotypic level.

The number of spikelets per spike showed negative and highly significant correlation with spike length and number of grains per spike at the genotypic level which agrees with the findings of (Awale *et al*., 2013, Ali *et al*., 2009), while positive highly significant correlation with spike length at the phenotypic level also agrees with (Ali *et al*., 2009).

Number of grains per spike: It had positive association with grain yield per hectare at genotypic level (r_g = 0.176**), and at phenotypic level (r_p = 0.136). It had highly significant positive relationship with plant height at genotypic and phenotypic level. The perusal of both the correlation coefficient results suggested that number of grains per spike should be given prime importance regarding its contribution to yield. These results suggest that selections should be based on number of grains per spike for developing new high yielding wheat varieties. These results are substantiated with those of Kashif and Khaliq (2004) and El-Mohsen *et al*. (2012).

Thousand seed weight: Thousand seed weight showed positive and significant association at genotypic and phenotypic levels (r_g = 0.395*, r_p = 0.365) with grain yield per hectare. This result is in agreement with a number of works in wheat (Kashif *et al*., 2004; Khaliq *et al*., 2004; Mohibullah *et al*., 2011; Iftikhar *et al*., 2012; Kalimullah *et al*.,2012; Laei *et al*., 2012; Zafarnaderi *et al*., 2013), but contradicted with the findings of Khan *et al*.(2010) and Awale *et al*. (2013). The interrelation between yield contributing characters exhibits that thousand seed weight was positively correlated with harvest index which indicated high portion of photosynthesis was due to increase thousand seed weight.

Biological yield: It was in positive and highly significant relationship at both phenotypic and genotypic levels with grain yield per hectare (r_g = 0.617**, r_p = 0.624**). These results are supported by the findings of Chowdhry *et al*. (1991), Laei *et al*. (2012) and Chimber *et al*. (2014). Also, it was highly and positively correlated with plant height at both genotypic and phenotypic levels. The results corroborate the findings of Moghaddam *et al*. (1997).

Harvest Index: Harvest index had positive and significant relationship at both genotypic and phenotypic levels with grain yield per hectare (r_g = 0.731**, r_p = 0.625*). These results are supported by the findings of Chowdhry *et al*. (1991), Laei *et al*. (2012) and Zafarnaderi *et al*. (2013). It was negatively correlated with days to heading, days to maturity, spike length and thousand seed weight at genotypic level, and the result is supported by the findings of Moghaddam *et al*., (1997), but contradicted with the findings of Zafarnaderi *et al*., (2013).

The significant correlation suggests that these traits could be used as indirect selection traits for grain yield, i.e., increase of these traits would increase grain yield per hectare (Asaye *et al*., 2013). The study of correlation among yield and yield contributing traits suggests that plant height, number of productive tillers per plant thousand seed weight, harvest index and biological yield were the most important characters which possessed highly positive association with grain yield per plant. Therefore, these characters could be utilized in breeding program to improve varieties for higher yield.

Table 7. Genotypic correlation coefficient (rg) (upper diagonal) and phenotypic correlation coefficient (rp) (below diagonal) of 11 traits of 49 bread wheat genotypes

Traits	DH	DM	PH	NPTP	SL	NSPS	NGS	TSW	BY	HI	GY
DH		0.946**	-0.165	-0.386**	0.148	0.095	-0.092	0.207	-0.168	-0.122	-0.184
DM	0.767**		-0.064	-0.099	0.155	0.107	-0.017	0.096	-0.306*	-0.033	-0.252
PH	-0.113	-0.039		0.26	0.565**	0.575**	0.625**	0.377**	0.363*	0.232	0.384**
NPTP	-0.132	-0.033	0.18		-0.261	-0.381**	0.159	0.288*	0.268	0.248	0.366*
SL	0.087	0.107	0.474**	-0.132		0.743**	0.032	0.218	-0.047	0.06	-0.047
NSPS	0.038	0.033	0.38**	-0.039	0.662**		0.248	-0.012	0.046	-0.014	0.004
NGS	-0.09	0.005	0.39**	0.064	0.007	0.188		0.019	0.061	0.177	0.176
TSW	0.154	0.161	0.372**	0.214	0.213	0.03	0.012		0.109	0.396**	0.395**
B	-0.123	-0.057	0.375**	0.169	0.038	0.046	0.118	0.194		-0.067	0.617**
HI	-0.031	0.031	0.161	0.15	0.021	-0.165	0.064	0.322*	-0.144		0.731**
GY	-0.102	-0.021	0.354*	0.226	-0.014	-0.124	0.136	0.365*	0.624**	0.625**	

X^2 =0.288, 0.372 (*, **) at 5 % and 1% probability level respective, DH=days to heading, DM=days to maturity, PH=plant height, NPTP=number of productive tillers per plant, SL =spike length, NSPS=number of spikelets per spike, NGS=Number of grains per spike, BYP=biological yield, HI=harvest index, TSW= thousand seed weight, and GY= Grain yield.

4.7. Path Coefficient Analysis

Knowledge of correlation alone is often misleading as the correlation observed may not be always true. Two characters may show correlation just because they are correlated with a common third one. In such cases, it becomes necessary to use a method which takes into account the causal relationship between the variables, in addition to the degree of such relationship. Path coefficient analysis measures the direct influence of one variable upon the other, and permits separation of correlation coefficients into components of direct and indirect effects. Partitioning of total correlation into direct and indirect effects provide actual information on contribution of characters and thus form the basis for selection to improve the yield.

Estimates of path coefficient analysis, direct and indirect effects of yield contributing characters on grain yield per hectare using genotypic correlation, which showed significant association with grain yield were presented in (Table 8). Maximum positive direct effect on grain yield per hectare was exerted by harvest index (0.753), followed by biomass yield (0.753). The high direct effects of these characters on grain yield could be considered as causes of such high correlation. This means that a slight increase in one of these traits may directly contribute to grain yield. Chowdhry *et al*. (1991) also reported positive direct effect of harvest index (0.443) and biological yield (0.327) on grain yield per plant. On the other hand, negative direct effect was exhibited by plant height (-0.215), number of productive tillers per plant (-0.078),

Plant height and number of productive tillers per plant showed negative direct effect on grain yield by displaying a value of (-0.215, -0.078) respectively. Since the direct effect were negative, so the direct selection for these trait to improve yield will be undesirable (Ali *et al*., 2008), and positive indirect effect through biological yield per plot, thousand seed weight and harvest index.

Thousand-seed weight vs. grain yield: Positive direct effect in case of thousand-seed weight on grain yield was estimated by displaying a value of (0.161) on grain yield and in addition to this thousand seed weight affected grain yield indirectly through harvest index (0.298*).

Biological yield and Harvest index showed positive direct effect on grain yield by displaying a value of (0.753)

Dramatic increase in the grain yield of major world cereal crops is due mainly to increases in the harvest index and to a lesser extent the biological yield (Acquaah, 2007). In this study both harvest index and biological yield showed high genotypic correlation and positively significant direct effect on grain yield. Thus plant breeder should practice selection through those most favorable traits for future wheat yield improvement programs.

On the basis of estimates of path coefficients, it could be suggested that harvest index followed by biological yield and thousand seed weight are the main contributors to grain yield in the present investigation. The result agrees with Arega *et al*. (2007) and Gelalcha and Hanchinal (2013), reported that traits such as biomass and harvest index, which showed highly significant correlation with grain yield, can be used as selection indices in grain yield improvement. Therefore, selection for characters will possibly improve other component characters thereby improving grain yield.

The residual effect in path analysis determines how best the resultant component (independent) variables account for the variability of the causal (dependent variable), grain yield per plant (Singh and Chaudhary, 1985). To this end, residual effect in the present study was 0.126 showing that 87.4 % of the variability in grain yield was explained by the component factors. This further indicates the interventions of environmental factors on the expression of the characters for the choice of yield attributing traits. This result was related with the findings of Gelalcha and Hanchinal (2013) and Arega *et al*. (2007), who reported residual effects 0.065 and 0.0083, respectively, indicating that characters included in the study explained high percentage of variation in grain yield per plot. It also indicate that in addition to the studied characters, there are also other factors to justify grain yield per plot changes (El-Mohsen *et al*., 2012).

Table 8. Estimate of direct (bold face and diagonal) and indirect (off diagonal) effects at genotypic level in 10 traits of 49 bread wheat genotypes

Traits	PH	NPTP	TSW	BY	HI	rg
PH	**-0.215**	-0.020	0.061	0.273	0.174	0.384**
NPTP	-0.056	**-0.078**	0.046	0.202	0.187	0.366*
TSW	-0.081	-0.023	**0.161**	0.082	0.298*	0.395**
BY	-0.078	-0.021	0.018	**0.753****	-0.050	0.617**
HI	-0.050	-0.019	0.064	-0.050	**0.753****	0.731**

Residual effect= 0.126 *, ** indicate significance at 0.05 and 0.01 probability levels, PH=plant height, NPTP=number of productive tillers per plant, TSW= thousand seed weight, BY=biological yield, HI=harvest index, rg=genotypic correlation.

4.8. Principal Components Analysis

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma, 1998). The main advantage of principal component analysis is reducing the number of dimensions without much loss of information (Fellahi *et al*., 2013). The eigenvalues are used to determine how many factors to retain and the sum is usually equal to the number of variables (Daniel *et al*., 2011; Awale and Sentayehu, 2013 and Fellahi *et al*., 2013). The first step in PCA was to calculate eigenvalues, which all together explained total variability that is displayed on the PC axes. The PCs with eigenvalue > 1.0 are used as criteria to determine the number of PCs (Fellahi *et al*., 2013).

Data presented in Table 9 demonstrated that an increase in the number of components was associated with a decrease in Eigen values. According to the results, the estimated wheat variable had grouped into five principal components (PCs) such as PC1 (25.48%), PC2 (20.85%), PC3 (16.8%), PC4 (10.0), and PC5 (7.73) with Eigen values more than one (2.79, 2.18, 1.96, 1.15, 1.01) respectively, which all together explained 80.4% of total variability, leaving the remaining 19.4% in the last six principal components (Table 9).

Daniel *et al*., (2011) taken characters which load high positively or negatively with a value of greater than ±3.0, contribute more to the variability and they are the ones that most differentiated

the clusters. Hence, data presented in Table 7 and graphically shown in Appendix figure 1 showed the most contributing characters are found in the first principal component which were plant height, biomass yield, thousand seed weight and grain yield; whereas in the second PC were days to heading, days to maturity, spike length and number of spikelets per spike; in the third PC were harvest index, spikelets per spike, biological yield, grain yield; and in the fourth PC were biological yield, number of grains per spike, harvest index and thousand seed weight were the major contributing characters for variability to those principal components.

The factor loadings refer to the coefficients in each principle component or the correlation between the component and the variables. A high correlation between PC1 and a variable indicates that the variable is associated with the direction of the maximum amount of variation in the data set. The components and their contributions in the variables are graphically shown in Appendix figures 1. The present study confirmed the bread wheat genotypes showed wide variations for the character studied and it suggests ample opportunities for genetic improvement of bread wheat through direct selection from the genotypes, and conservation of the germplasm for future utilization. Similar findings of grouping bread wheat genotypes by principal component analysis were reported (Daniel *et al*., 2011; Awale and Sentayehu, 2013; Fellahi *et al*., 2013).

Table 9. Vector loadings and percentage of explained variation by the first four PCs

Character	PCA1	PCA2	PCA3	PCA 4	PCA 5
Hd	-0.165	0.451	0.434	0.212	0.117
Md	-0.112	0.432	0.456	0.158	0.223
PHT	0.483	0.204	-0.184	0.020	0.157
NPT	0.249	-0.259	0.141	0.057	0.221
SL	0.212	0.479	-0.245	-0.096	-0.332
NSPP	0.194	0.446	-0.364	-0.072	-0.081
NGS	0.255	0.055	-0.147	-0.096	0.811
TSW	0.319	0.122	0.357	-0.058	-0.201
BYP	0.337	-0.133	-0.023	0.7281	-0.126
HI	0.296	-0.082	0.364	-0.601	-0.097
GYP	0.461	-0.174	0.273	0.088	-0.153
Eigen value	2.800	2.260	1.800	1.100	1.010
% proportion	25.48	20.85	16.36	10.00	7.730
Cumulative%	25.48	45.22	63.04	73.49	80.40

NB: PCA=Principal component axis, DH=days to heading, DM=days to maturity, PH=plant height, NPTP=number of productive tillers plant, SL =spike length, NSPS=number of spikelets per spike, NGS=Number of grains per spike, BYP=biological yield, HI=harvest index, TSW= thousand seed weight, and GY= Grain yield.

4.9. Genetic Divergence (Distance) Analysis

Divergence analysis is performed using Mahalanobis (1936) D^2 distance to classify the diverse genotypes for hybridization purpose (Table 10 and 11). The genetic improvement through hybridization and selection depends on the extent of genetic diversity between parents. Chi-square values were tested for significance using P-1 degrees of freedom where, P is the number of characters used in the study (Singh and Chaudhary, 1985).

Inter cluster divergence values (D^2) between and within seven clusters are presented in the (table 10). The highest inter-cluster distance was exhibited between cluster I and III (D^2 = 25.79**), followed by cluster II and IV (D^2 = 22.82), and cluster II and III (D^2 = 22.75), indicating wider genetic divergence among the clusters. Thus, crossing of genotypes between members of cluster I with members of cluster IV, and members of cluster II with members of cluster III, and IV may produce a high amount of heterotic expression in the F1's and broad spectrum of variability in segregating (F_2) populations. Genetic divergence in bread wheat genotypes reported by earlier workers (Kashif *et al*., 2004; Ali *et al*., 2008; Daniel *et al*., 2011; Degewione and Alamerew, 2013; Fellahi *et al*., 2013).

Table 10. Inter and intra (bold) cluster D^2 values among six clusters in 49 bread wheat genotypes

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**
I		10.29	25.79**	7.36	13.31	16.07
II			22.75*	22.82*	17.00	19.78*
III				8.910	12.22	15.68
IV					7.060	17.00
V						14.58
VI						

X^2 =18.3, 23.2 (*, **) at 5 % and 1% probability level respective

4.10. Clustering of Genotypes

The dendrogram obtained from the cluster analysis through average linkage technique grouped the 49 genotypes into six clusters at about 47% similarity level based on D^2 values considering their pooled mean as data presented in (Table 11) and, as shown in (appendix figure 2) which makes them moderately divergent. Related findings were reported by earlier workers (Daniel *et al*., 2011; Awale and Sentayehu, 2013; Fellahi *et al*., 2013; Mideksa *et al*., 2014). Similarity between clusters is the average distance between all objects in one cluster and all objects in other cluster, where by individuals within any cluster were more closely related than individuals in different clusters. The distribution of genotypes into different diversity classes of cluster membership indicated that the genotypes are moderately divergent.

The genotypes were grouped in such a way that cluster I had the largest member of all clusters, included 27 (55%) genotypes, followed by cluster III included 15 (30.6%), cluster IV included 3 (6.04%) genotypes. In contrast cluster V and cluster VI had the smallest member, constituted of 1 (2.04%) genotype each. This cluster analysis revealed that bread wheat genotypes originated from different sources.

In the present study, genotypes gained from different source center clustered in the same category together, for instance, in cluster I genotypes released from Adet, Holeta, Mekele, Kulumsa, and Sinnana grouped together. In support of this Ali *et al*., 2008; Hailegiorgis *et al*., 2011; Fellahi *et al*., 2013 noted morphological diversity is more important factor rather than variation in geographical or origin as an indicator of genetic diversity. Moreover, genotypes collected from the same source of center (Gassay and Tay from Adet) were clustered in to different clusters, suggesting the existence of genetic diversity within each collection sources.

Table 11. Distribution and grouping of 49 bread wheat genotypes into different diversity classes of cluster membership based on D^2 analysis

Cluster	Number of genotypes	Name of genotypes	Proportions (%)
I	27	Mekelle-3, Shorima, ETBW 7368, Hidasse, ETBW 8517, ETBW 7120, Sofumar, ETBW 7038, Kakaba, Pavon-76, ETBW 8512, ETBW 7871, Millan, ETBW 6861, ETBW 8506, Mekele-4, Biqa, ETBW 8513, ETBW 7058, ETBW 8519, ETBW 7101, ETBW 8515, Alidoro, Mada-Wolabu, Gassay, Ogolcho, Dandaa	55.1
II	2	Tay, ETBW 7872	4.08
III	15	ETBW 8507, Jeferson, ETBW 8510, Honqolo, Hulluka, Pastor, ETBW 7194, ETBW 7364, ETBW 8507, ETBW 8514, ETBW 8509, ETBW 8516, King Bird, ETBW 8518, Hoggana	30.6
IV	3	ETBW 8511, ETBW 6940, ETBW 7213	6.12
V	1	Digelu	2.04
VI	1	ETBW 7147	2.04

4.11. Cluster Mean Analysis

The mean value of the 11 quantitative characteristic feature are presented in (Table 12). Cluster I had a characteristics feature of short in days to heading, high values in terms grain yield per hectare, and moderate high values in terms of harvest index. Cluster II had a characteristics feature of short in days to maturity, high values in terms of plant height, spike length, number of spike lets per spike, biological yield and grain yield, while relatively low in harvest index as compared to other clusters. Cluster III showed short in days to heading and days to maturity as well as grain yield.

Cluster IV had a characteristics feature of relatively low values of biological yield, and grain yield per hectare and relatively moderate values in terms of characters studied. Cluster V had a characteristics feature of long in days to heading and days to maturity, high values in terms of number of grains per spike, thousand seed weight, and harvest index. On the other hand had low value in terms of spike length, biological yield, and grain yield per hectare. Cluster VI had a characteristics feature of long in days to heading and days to maturity, short in plant height, moderate high values in terms of spike length, and thousand seed weight, and also characterized by high harvest index and grain yield per hectare.

Therefore, as presented in the table below low and high mean value recorded between cluster (I, II, III) and cluster (V, VI) for days to heading, between (II, III, V) and (VI) for days to maturity, between VI and II for plant height, cluster VI and I for number of productive tillers per plant, cluster V and II for spike length, cluster VI and II for number of spikelets per spike, cluster VI and V for number of grains per spike, cluster IV and VI for thousand seed weight, cluster V and II for biological yield, and for harvest index observed between cluster II and VI respectively. In addition to these the highest grain yield obtained from cluster II, II, VI, and the low grain yield obtained from cluster III, IV, and V.

Table 12. Mean values of seven clusters for 11 characters of 49 bread wheat genotypes

	Cluster Means										
Cluster	**HD**	**MD**	**PH**	**NPTP**	**SL**	**NSPS**	**NGS**	**TSW**	**BY**	**HI**	**GY**
I	65.50	127.33	81.22	1.55	7.69	14.64	38.14	41.83	2.16	0.326	36.02
II	66.38	126.15	91.8	1.45	8.75	16.3	41.25	41.15	2.48	0.285	36.31
III	65.87	126.41	72.40	1.45	7.07	14.24	36.43	39.29	2.07	0.301	32.51
IV	71.33	132.67	75.73	1.48	8.07	14.93	39.60	38.50	2.00	0.300	30.96
V	79.50	136.30	80.9	1.45	6.80	15.00	45.70	43.10	1.78	0.330	31.75
VI	79.00	136.50	69.2	1.30	7.20	13.30	29.10	43.30	2.05	0.340	36.00

NB: DH=days to heading, DM=days to maturity, PH=plant height, NPTP=number of productive tillers per plant, SL =spike length, NSPS=number of spikelets per spike, NGS=Number of grains per spike, BY=biological yield, HI=harvest index, TSW= thousand seed weight, and GY= grain yield.

5. SUMMARY AND CONCLUSION

Overall variability within a crop is due to heritable and non-heritable components. The present study comprised 49 bread wheat genotypes that were evaluated at Jamma and Geregera environments with the overall objective of studying genetic variation and character associations for 12 traits. The analysis of variance revealed highly significant differences at ($P< 0.01$ and $p<0.05$) levels among the genotypes for all traits except grain filling period at Geregera, which indicated the existence of variation among the tested genotypes.

Maximum values of genotypic coefficient of variation were recorded for spike length (8.66%), followed by number of productive tillers per plot (8.4%), number of grains per spike (6.4%) and thousand seed weight (6.15%), whereas higher values of phenotypic coefficient of variation were recorded for productive tillers followed by grain yield, spike length and harvest index with a values of (13.3%, 11.35%, 10.3%, 9%), respectively. Heritability ranged from 29.1% for grain yield to 82 % for heading date. Relatively high genetic advance as percent of the mean were recorded for spike length followed by number of productive tillers per plant, number of grains per spike, thousand-seed weight, days to heading and plant height with values of (14.9%, 10.6%, 10%, 10%, 9.7%, and 9.07%), respectively.

Because of high genotype-environment (G × E) interactions, estimates of GCV, H^2 and GA for most of the characteristics using combined over location analysis were generally lower than the estimates computed from the variance analyses made separately for each location.

Grain yield displayed positive and significant association with plant height, number of tillers per plant, thousand seed weight, biological yield, and harvest index at genotypic and phenotypic level. The estimated ranges of mean values revealed that bread wheat genotypes reflect good amount of genetic variability, and out of the 49 genotypes, 12 released varieties and 12 pipelines were characterized by relatively better yield performance as each scored above the overall mean of 34.6 qt/ha.

Based on the results of the individual and combined analysis of variance, high estimates of genotypic coefficient of variation, heritability and genetic advance as percent of mean observed for spike length and thousand seed weight.

The principal component analysis revealed that five principal components, with Eigen values greater than unity, explained 80.4% of the total variability, and hence, grain yield, biological yield, number of grains per spike, harvest index, and thousand seed weight were the major contributing characters for variability contained in the bread wheat genotypes.

The highest inter-cluster distance was exhibited between cluster I and III (D^2 = 25.79**), followed by cluster II and IV (D^2 = 22.82), cluster II and III (D^2 = 22.75), indicating wider genetic among the clusters. Therefore, initiating crossing program between members of cluster I with members of cluster III, and members of cluster II with members of cluster III, and IV may produce a high amount of heterotic expression in the F1's and broad spectrum of variability in segregating (F_2) populations.

The genetic parameters of the present study revealed that plant height, spike length, number of grains per spike, and thousand seed weight showed moderate to high heritability and genetic advance in percentage of mean. High significant positive correlation along with maximum positive direct effects on grain yield were achieved for harvest index and biological yield, may be identified as a best selection criterion (trait) for the development of modern wheat variety.

Thus, the results suggest that plant height, higher number of grains per spikes, thousand seed weight (bold size grains), biological yield and higher harvest index are the important yield contributing traits and thus plant selection based on these traits will be most effective for future wheat yield improvement program.

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7. APPENDIX

Appendix Table 1. Mean value of 11 quantitative traits of 49 tested bread wheat genotypes

SN	Genotype	DH	DM	PH	NPTP	SL	NSPP	NGS	TSW	BY	HI	GY
1	Mekelle-3	63.50	124.0	83.8	1.45	6.7	14.7	40.9	37.3	2.20	0.355	40.00
2	Mada-Wolabu	67.25	127.0	82.1	1.68	8.0	14.1	38.6	44.6	2.35	0.353	43.00
3	ETBW 8508	64.75	125.2	69.5	1.25	7.0	14.6	36.9	36.1	2.13	0.278	30.63
4	Shorima	67.25	128.2	78.3	1.25	7.3	14.5	35.4	39.9	1.93	0.320	31.38
5	Danda'a	70.00	133.3	83.8	1.7	6.9	14.0	41.6	44.9	2.23	0.328	37.50
6	ETBW 7871	67.00	129.5	79.1	1.5	8.2	15.3	40.1	39.3	2.20	0.323	37.50
7	ETBW 8517	64.00	127.3	78.5	1.25	8.2	13.6	35.6	40.4	1.95	0.358	33.75
8	ETBW 6861	70.00	131.0	78.7	1.3	8.4	15.5	35.7	39.2	2.05	0.345	36.25
9	ETBW 7120	66.75	127.3	82.7	1.55	8.3	15.1	36.9	40.2	2.05	0.283	32.50
10	MILLAN	68.00	128.5	79.3	1.25	7.8	13.9	37.2	39.7	2.45	0.313	39.88
11	ETBW 8506	63.00	125.5	77.7	1.45	7.3	14.1	35.6	42.1	2.13	0.335	38.25
12	Mekelle-4	66.00	125.8	79.1	1.25	7.9	14.3	37.8	43.9	2.13	0.345	37.50
13	ETBW 7147	79.00	136.5	69.2	1.3	7.2	13.3	29.1	43.3	2.05	0.335	36.00
14	ETBW 8510	65.25	125.2	71.4	1.25	7.3	14.7	33.9	38.1	2.05	0.290	32.13
15	TAY	67.50	126.5	89.8	1.5	8.0	16.3	40.3	39.2	2.45	0.298	37.63
16	Sofumar	64.00	126.7	83.6	1.7	8.0	16.1	35.6	40.2	2.08	0.310	32.88
17	ETBW 7038	61.25	126.5	78.1	1.65	7.2	14.6	41.1	37.4	2.03	0.328	35.00
18	Hulluka	65.75	127.7	72.6	1.45	6.8	13.7	39.6	35.9	1.95	0.290	30.00
19	ETBW 8511	70.00	134.0	75.7	1.7	8.1	15.0	37.4	36.1	2.20	0.263	29.63
20	ETBW 7368	65.75	128.0	79.9	1.4	8.3	14.6	36.5	39.7	2.05	0.275	29.25
21	Ogolcho	67.00	125.7	86.0	1.35	7.7	15.1	42.1	48.1	2.25	0.328	38.63
22	ETBW 7872	65.25	125.8	93.8	1.4	9.5	16.3	42.2	43.1	2.50	0.268	35.00

23	Digelu	79.50	136.3	80.9	1.45	6.8	15.0	45.7	43.1	1.78	0.330	31.75
24	ETBW 7194	71.25	128.0	70.0	1.3	6.4	13.7	34.4	41.8	2.03	0.278	30.63
25	PASTOR	66.00	126.8	76.2	1.35	6.9	13.9	42.0	34.8	2.13	0.278	30.00
26	Kakaba	62.25	124.7	81.2	1.95	7.4	14.1	36.6	39.0	2.03	0.348	35.25
27	ETBW 7364	67.75	127.0	72.8	1.5	7.4	14.1	36.9	42.9	2.05	0.303	31.88
28	ETBW 8512	63.00	125.0	83.0	1.4	7.3	14.1	42.0	38.3	1.85	0.315	31.75
29	Honqolo	66.50	127.0	73.8	1.72	6.8	13.8	32.4	37.2	2.18	0.300	33.75
30	ETBW 8516	61.50	124.5	74.5	1.4	7.1	14.4	40.3	41.4	1.90	0.352	35.00
31	ETBW 6940	72.25	131.8	75.1	1.4	7.8	13.8	37.0	40.8	1.85	0.328	32.00
32	Hidasse	65.00	127.2	79.8	2.0	7.0	13.3	38.1	42.1	2.10	0.313	31.00
33	ETBW 8513	64.00	128.2	83.4	1.9	7.3	14.1	37.0	47.2	2.25	0.335	38.00
34	ETBW 8515	63.50	126.0	79.9	1.65	7.1	14.1	38.5	46.2	2.10	0.290	32.13
35	ETBW 8514	65.25	125.7	68.1	1.72	6.5	13.1	36.6	42.0	2.08	0.270	29.50
36	ETBW 8509	67.25	128.2	72.9	1.2	7.9	16.9	34.0	39.6	2.05	0.258	26.50
37	Alidoro	69.00	129.3	85.1	1.4	10.3	17.7	36.4	45.2	1.78	0.340	30.63
38	Pavon-76	66.25	126.5	79.2	1.35	7.3	13.8	38.4	37.2	2.43	0.275	34.13
39	ETBW 8519	62.50	126.5	83.3	1.85	7.5	15.0	38.8	43.8	2.05	0.345	37.50
40	Jeferson	63.25	124.3	72.8	1.5	7.1	14.6	35.5	35.3	2.03	0.285	30.88
41	Hoggana	71.50	128.8	72.1	1.6	7.6	14.6	32.6	41.8	2.15	0.325	38.25
42	King Bird	62.50	125.8	73.5	1.5	6.7	13.7	37.9	38.6	2.13	0.335	36.63
43	ETBW 8518	62.25	124.2	70.9	1.55	6.8	14.1	38.5	39.5	2.15	0.343	39.38
44	ETBW 7213	71.75	132.2	76.4	1.35	8.3	16.0	44.4	38.6	1.95	0.313	31.25
45	ETBW 7101	64.75	125.5	84.1	1.55	7.9	15.5	36.8	41.5	2.15	0.323	35.95
46	ETBW 7058	66.75	130.0	81.8	1.55	7.3	14.2	35.3	44.7	2.48	0.303	37.75
47	Biqa	64.00	128.0	77.8	1.9	7.3	14.6	39.8	44.0	2.33	0.350	41.50
48	Gassay	66.75	126.8	83.8	1.7	7.6	15.3	41.5	43.4	2.65	0.325	43.75
49	ETBW 8507	67.25	127.8	74.8	1.4	7.7	13.7	34.9	44.4	2.10	0.318	32.50

Appendix Table 2. Estimated values of mean squares and f values of 49 bread wheat genotypes for 12 traits tested at Jamma, using Simple lattice design

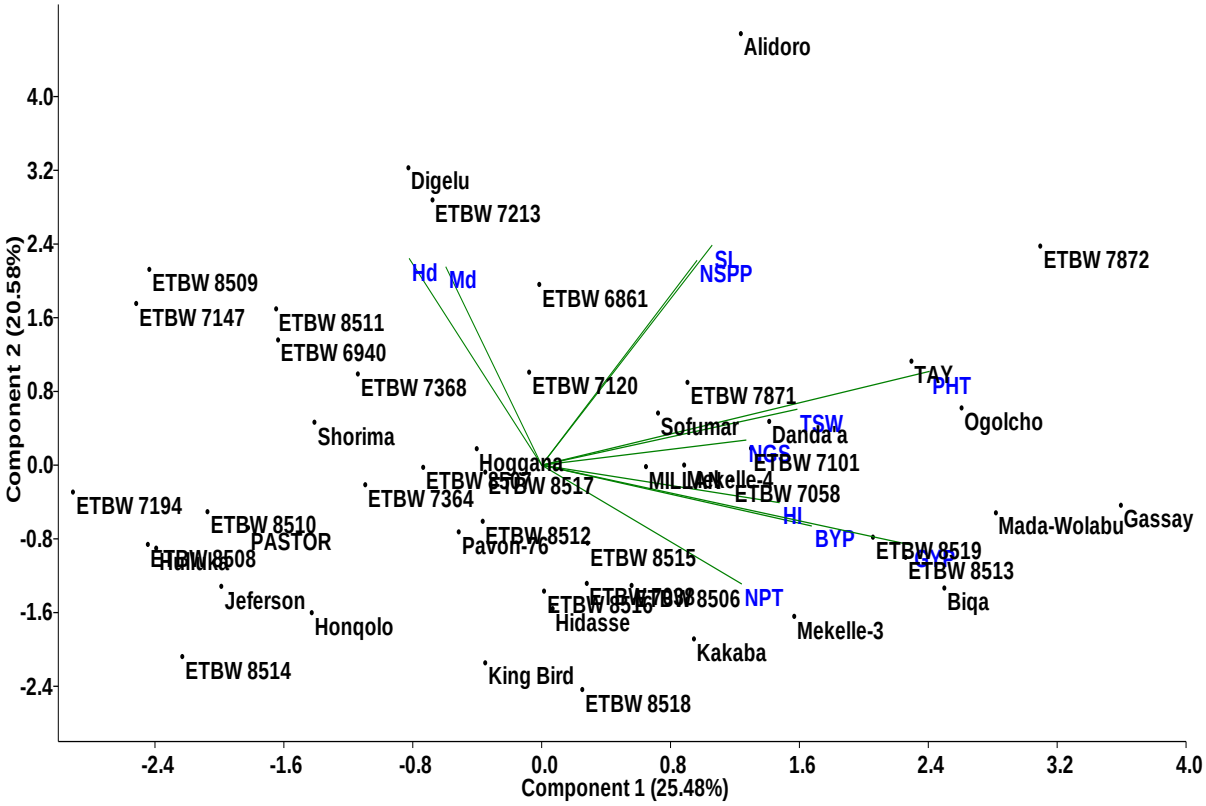
Source of variance	DF	Mean square of characters											
		HD	MD	GFP	PHT	NPTP	SL	NSPS	NGS	TSW	BY	HI	GY
Replication	1	9.2	0.09	2.95	73.6	3.2	24.9	16.7	0.79	28.1	0.007	0.009	140.2
Blocks (rep)	12	2.7	3.34	7.00	27.4	0.07	0.81	1.39	7.93	4.58	0.028	0.0005	20.6
Genotype	48	38.5**	15**	16.2*	67**	0.16*	2.1**	1.93*	21.8*	32**	0.063*	0.0026**	64.0**
Intra-b error	36	2.77	2.26	8.24	20.6	0.075	0.66	0.89	6.87	6.66	0.031	0.0008	26.75
RCBD	48	2.75	2.53	7.93	22.3	0.073	0.70	1.01	11.1	6.14	0.030	0.074	25.20
CV (%)		2.47	1.23	7.50	5.70	15.7	10.1	6.36	8.00	5.20	7.08	6.89	10.45
R^2 (%)		0.93	0.85	0.67	0.76	0.75	0.79	0.69	0.69	0.84	0.674	0.794	0.73
Mean		67.1	129	62.5	83.0	1.72	8.24	15.9	40.0	48.0	2.470	0.388	48.0
E.R RCBD		99.0	104	96.2	102	97.5	101	104	91.4	92.2	97.00	91.00	94.2
LSD at 1%		4.460	4.03	7.7	12.2	0.73	2.18	2.50	9.30	6.90	0.480	0.075	13.9
LSD at 5%		3.34	3.02	5.8	9.10	0.55	1.63	1.90	7.00	5.20	0.360	0.056	10.4
δ^2_g		17.87	6.37	3.98	23.2	0.042	0.72	0.52	7.47	12.7	0.0160	0.0009	18.6
δ^2_p		19.25	7.50	8.10	33.5	0.08	1.05	0.97	10.9	16.0	0.0315	0.0013	32.0
GCV (%)		6.30	1.96	3.20	5.80	11.9	10.3	4.54	6.83	7.42	5.120	7.6920	9.00
PCV (%)		6.54	2.12	4.55	6.97	16.5	12.4	6.12	8.25	8.33	7.186	9.2450	11.8
H^2 (%)		92.8	84.9	49.0	69.25	53.0	68.6	54.0	68.5	79.2	50.79	69.230	58.0
GA		8.40	0.10	2.88	8.27	0.31	1.45	1.10	4.67	6.54	0.172	0.1860	6.77
GAM		12.52	0.08	4.60	9.96	18.0	17.6	6.90	11.7	13.6	7.034	7.5300	14.1

NB: *, ** Indicates significance at 0.05 and 0.01 probability levels, respectively, σ^2_g = genotypic variance, σ^2_p=phenotypic variance, GCV (%) = genotypic coefficient of variation, PCV (%) = phenotypic coefficient of variation, H^2 (%) =broad sense heritability, GA =genetic advance, GAM % =genetic advance as percentage of mean, DF=degrees of freedom, DH=days to heading, DM=days to maturity, GFP= grain filling period, PH=plant height, NPTP=number of productive tillers per plant, SL =spike length, NSPS=number of spikelets per spike, NGS=Number of grains per spike, BY=biological yield, HI=harvest index, TSW= thousand seed weight, and GY= grain yield.

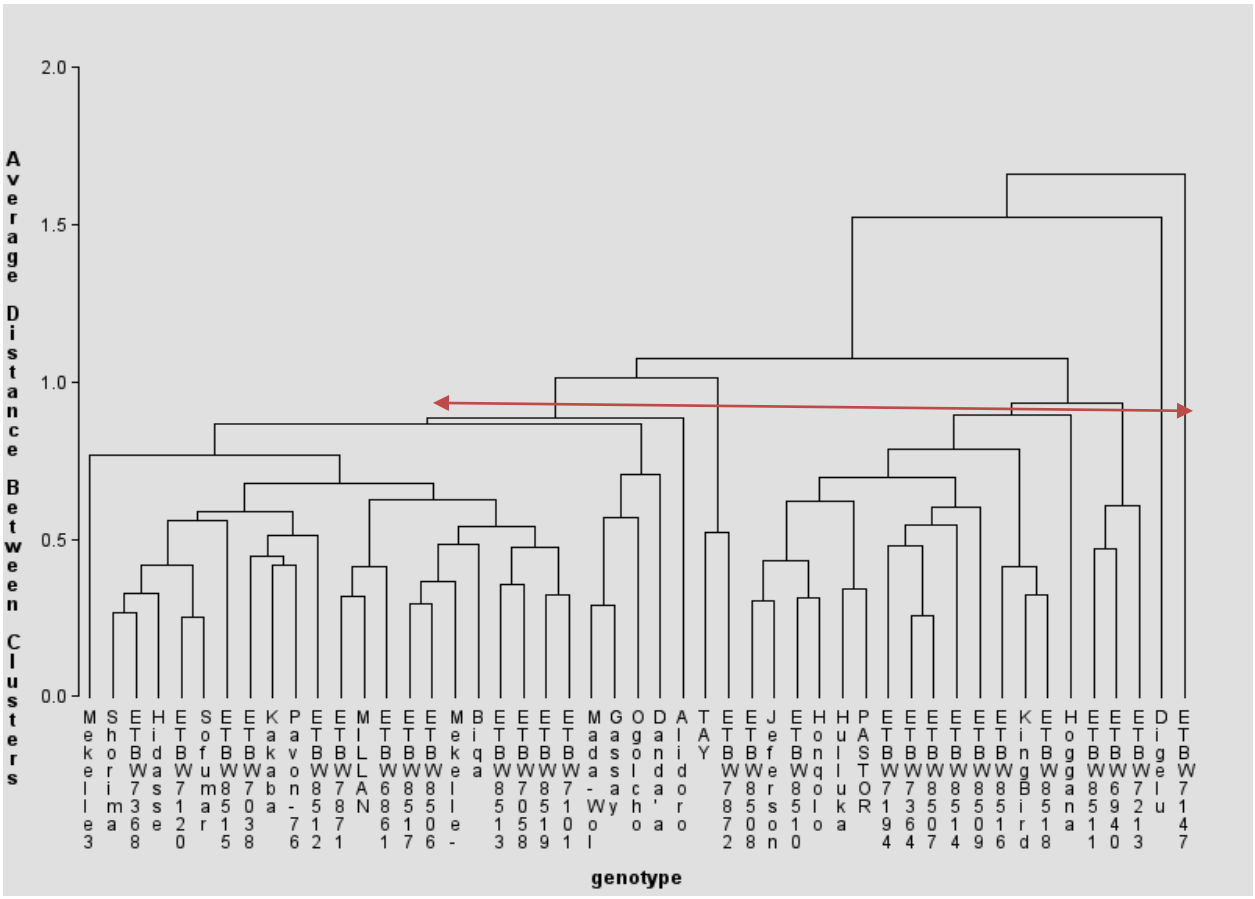
Appendix Table 3. Estimated values of mean squares and f values of 49 bread wheat genotypes for 12 traits tested at Geregera, using Simple lattice design

Source of variance	DF	Mean square of characters											
		HD	MD	GFP	PHT	NPTP	SL	NSPS	NGS	TSW	BY	HI	GY
Replication	1	1.72	1.47	2.90	624	0.276	1.47	1.62	4.76	2.30	0.037	0.002	11.1
Blocks (rep)	12	3.40	9.10	10.5	27.0	0.014	0.15	1.00	6.74	10.3	0.044	0.0008	16.0
Genotype	48	30**	32**	18.6^{ns}	95**	0.11*	1.0**	2.7*	33**	26*	0.165*	0.0027*	41.42*
Intra-b error	36	3.33	9.34	12.5	29.3	0.06	0.23	1.20	13.0	9.0	0.066	0.0012	21.02
RCBD	48	3.47	9.28	12.0	28.8	0.05	0.21	1.24	11.5	9.3	0.060	0.0011	19.78
CV (%)		2.82	2.42	5.77	7.30	17.1	6.76	8.37	7.94	9.0	13.83	14.00	21.00
R^2 (%)		0.89	0.77	0.61	0.79	0.70	0.83	0.70	0.80	0.73	0.733	0.708	0.678
Mean		66.0	126	60.0	73.4	1.28	6.82	13.3	35.7	33.8	1.780	0.240	21.17
E.R RCBD		100	99.0	96.0	98.0	81.0	90.7	94.0	88.0	100	91.70	90.40	94.10
LSD at 1%		4.90	8.20	9.7	14.5	0.65	1.30	3.10	9.7	8.00	0.688	0.095	13.30
LSD at 5%		3.67	6.10	7.1	11.0	0.49	0.97	2.30	7.2	6.00	0.516	0.071	9.220
δ^2_g		13.34	11.3	0.00	32.9	0.025	0.39	0.75	10.0	8.50	0.050	0.0008	10.21
δ^2_p		15.00	16.0	0.00	45.0	0.055	0.50	1.35	16.5	13.0	0.082	0.0013	20.71
GCV (%)		5.530	2.67	0.00	7.80	12.4	9.10	6.51	8.86	8.63	12.56	11.78	15.10
PCV (%)		5.870	3.17	0.00	9.14	18.3	10.4	8.74	11.4	10.7	16.13	15.00	21.50
H^2 (%)		88.90	70.8	0.00	73.0	45.5	77.0	55.6	60.6	65.4	60.00	55.55	49.30
GA		7.100	5.84	0.00	10.1	4.02	1.12	1.33	5.08	4.86	0.350	0.041	4.630
GAM		10.76	4.50	0.00	13.8	31.4	16.5	10.0	14.2	14.4	20.00	17.21	21.86

NB: *, ** Indicates significance at 0.05 and 0.01 probability levels, respectively, σ^2_g = genotypic variance, σ^2_p=phenotypic variance, GCV (%) = genotypic coefficient of variation, PCV (%) = phenotypic coefficient of variation, H^2 (%) =broad sense heritability, GA =genetic advance, GAM % =genetic advance as percentage of mean, DF=degrees of freedom, DH=days to heading, DM=days to maturity, GFP= grain filling period, PH=plant height, NPTP=number of productive tillers per plant, SL =spike length, NSPS=number of spikelets per spike, NGS=Number of grains per spike, BY=biological yield, HI=harvest index, TSW= thousand seed weight, and GY= grain yield.



Appendix Figure 1. Principal components plot of bread wheat genotypes based on 11 agronomic and phenotypic traits.



Appendix Figure 2. Tree diagram of genetic relationships among 49 bread wheat genotypes.