GENETIC VARIABILITY AND ASSOCIATION OF YIELD AND YIELD RELATED CHARACTERS IN BREAD WHEAT (*Triticum aestivum L.*) VARIETIES

M.Sc Thesis

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June, 2012
JIMMA UNIVERSITY

GENETIC VARIABILITY AND ASSOCIATION OF YIELD AND

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BY
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A Thesis Submitted to the College of Agriculture and Veterinary Medicine
Department of Plant Science, School of Graduate Studies
JIMMA UNIVERSITY

In Partial Fulfillment of the requirements of the Degree of
MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING)

June, 2012
JIMMA

APPROVAL SHEET

SCHOOL OF GRADUATE STUDIES
JIMMA UNIVERSITY COLLEGE OF AGRICULTURE AND VETERINARY MEDICINE

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DEDICATION

I dedicate this thesis manuscript to **BIRTUKAN MEBRATE**, my wife and my daughter, **LUNA TADESSE**

STATEMENT OF THE AUTHOR

First, I declare that this thesis is my work and that all sources of materials used for this thesis have been acknowledged. This thesis has been submitted in partial fulfillment of the requirements for than M.Sc. degree at the Jimma University College of Agriculture and Veterinary Medicine Department of Plant Science and is deposited at the University Library to be available to borrowers under the rules of the Library. I declare that this thesis is not submitted to any other institution anywhere for the award of academic degree, diploma, or certificate.

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June, 2012

BIOGRAPHICAL SKETCH

The author was born on October 14, 1966 in Axum, Tigray region. He attended elementary school education at Saint Mary Junior Secondary and high school education at Adi-Ugri Comprehensive Secondary School at Axum (Tigray) and Asmara (Eritrea), respectively. After the completion of his high school education he joined then Addis Ababa University faculty of science and graduated with a BSc in Biology in 1984/85. After his graduation he served as a biology teacher in Holeta Comprehensive Secondary and Preparatory School. He has been serving since September 1985 until he left for this study in September 2010 to Jimma University College of Agriculture and Veterinary Medicine.

AKNOWLEDEGEMENTS

I am grateful to my major advisor, Dr. Sentayehu Alamerew, for his follow up, constructive comments, guidance, support, and concern from the inception up until the completion of the thesis writes up. My appreciation also goes to my co-advisor, Dr. Alemayehu Assefa for his provision of the necessary materials and for his valuable comments in the course of preparation of the thesis. My deepest gratitude goes to Ato Adane Meresa and Bogale for their help in the field and laboratory works.

I am greatly indebted to my father, Ghiday G/micheal and my mother Mebrat G/wahide for filling the gap associated with my family and encouragement. I am also thankful to my brother Beyene G/selasei and Silass Ghiday for their encouragement. I would like to thank the Holeta City Administration for sponsoring and supported me to join the post graduate study. I would like to thank Holeta Agricultural research center for all the support it provided me during my research work. The last but not least acknowledgement is for Jimma University College of Agriculture and Veterinary Medicine for financing the research work and all round support it provided me during the course of my study.

LIST OF ABBREVATIONS

ADARC	Adiet Agricultural Research Center
ANOVA	Analysis of Variance
ARARI	Ardita Agricultural Research Institute
cm	Centimeter
CSA	Central Statistics Authority
CYMMIT	International Maize and Wheat Improvement Center
DBARC	Debre Birhane Agricultural Research Center
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agriculture Organization
g	gram
HU	Haramaya University
HARC	Holeta Agricultural Research Center
KARC	Kulumsa Agricultural Research Center
kg	Kilogram
Kg/ha	Kilogram per hectare
LSD	Least significant difference
m	Meter
masl	Meters above sea level
OARI	Oromia Agricultural Research Institute
SARC	Sinana Agricultural Research Center
SRARC	Sirinka Agricultural Research Center

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GENETIC VARIABILITY AND ASSOCIATION OF YIELD AND YIELD RELATED CHARACTERS OF BREAD WHEAT (*Triticum aestivum. L*) GENOTYPES

BY

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ABSTRACT

Twenty one bread wheat (Triticum aestivum. L) varieties were evaluated for ten quantitative traits in RCBD at two locations, Holeta and Ginchi. The overall objective was to study the extent of genetic variation and association among grain yield and ten yield related traits. The genotypes differ significantly for all of the traits and the relatively wide range of the mean values for most of the characters indicated the existence of variation among the tested genotypes. Estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation were generally moderate for most of the characters. The PCV values were greater than the GCV values. Moderate PCV and GCV values were exhibited by 1000-grain weigh at both locations. Moderate to high PCV and GCV were observed for grain yield, number of tillers, days to heading, pant height, number of spiklets per spike, number of grains per spike and, harvest index at the two locations combined. Thousand grain weights showed high heritability at both locations. All studied characters showed high heritability at the two locations combined. In combined analysis estimate of GAPM was high for grain yield per plant, number of tillers, number of spikelets per spike, number of grains per spike, harvest index, days to heading and plant height and moderate for days to maturity and spike length. Thousand grain weight had high GAPM at Ginchi and Holeta. The D^2 analysis showed the 21 genotypes grouped into five clusters. This makes the genotypes to become moderately divergent. The principal component analysis revealed that five principal components PC1 to PC5 which are extracted from the original data and having latent roots greater than one accounting nearly for 86.01% of the total variation. Grain yield had significant and positive correlation with HI at Ginchi location. The same trait showed positive and significant phenotypic and genotypic correlation with, number of spikelets per spike, number of grains per spike and harvest index and it had positive and significant association with days to heading at genotypic level only at combine over locations. Path coefficient analysis showed that harvest index and number of tillers exerted positive direct effect at combined over locations. While these two characters can be considered for selection, these wheat genotypes need to be crossed and selected to develop high yielding pure line variety.

1. INTRODUCTION

Wheat crop is the promising cultivated crop to feed the over growing population of the world, and plays an appreciable role of supplying production carbohydrates, proteins and minerals (Schulthess *et al*., 2000). Wheat is one of the cereals used extensively in many parts of the world for the production of bread and many bakery products (Fincher and Stone, 1986; Reynolds and Borlaug 2006a). Only wheat flour is capable of producing dough with rheological properties that permits the baking of leavened bread. Wheat flour is an organic complex in which starch interacts with gluten and non-gluten proteins (albumins and globulins), lipids, and non-starch carbohydrates. A large portion of variation observed in flour quality may be attributed to variation in protein content and gluten composition.

The popularity of foods made from wheat flour creates a large demand for the grain, even in economies with significant food surpluses (Agricultural economics, 2010). Wheat is widely cultivated as a cash crop because it produces a good yield per unit area, grows well in a temperate climate even with a moderately short growing season, and yields versatile, high quality flour that is widely used in baking. Most bread is made with wheat flour, including many breads named for the other grains they contain like most rye and oat breads (Agricultural economics, 2010).

Wheat (*Triticum spp.)* belongs to the family Graminae. It is an annual temperate cereal crop but also it can grow in a wide range of environments around the world. Production is most successful between the latitudes of 30 and 60^{o}N, and longitudes of 27 to 40^{o}S, respectively (Heyne, 1987). The optimum growing temperature is about 25°C, with minimum and maximum growth temperatures of 3-4°C and 30-32°C, respectively (Briggle, 1980). Wheat is adapted to a broad range of moisture conditions from xerophytic to littoral. Although about three-fourths of the land area where wheat is grown receives an average of between 375 and 875 mm of annual precipitation, it can also grow in most locations where precipitation ranges from 250 to 1750 mm (Leonard and Martin, 1963).

Wheat (*Triticum spp.*) is the second major food crop of the world in its importance next to rice. In Ethiopia the crop ranks third in terms of total production next to teff and maize. It is largely grown in the highlands of the country and constitutes roughly 20-30 % of the annual cereal production (FAO, 2009).

Bread wheat is believed to be a relatively recent introduction to Ethiopia (Hailu et al., 1991); it exhibits wider adaptation and higher yield potential than durum wheat (Amsal, 2001). From 1991 on wards 22 bread wheat varieties were released and all of them are in production in different agro-ecological zone of the country (AIRO, 2004). Among these Simba is the best of all with respect to yielding potential in middle to high altitude areas. Similarly Digelu, Dodota, and Watera are best performing varieties for high altitude, low altitude and water logging areas respectively.

Wheat is grown on 217 million hectares throughout the world with a production of approximately 651 million tons of grain during the season 2009 (FAO, 2010). In Africa, wheat is grown on 9.5million hectares and is harvested with 22 million tons grain. In Ethiopia, wheat is the leading crop grown on 1.7 million hectares and with 3 million tons grain harvested in 2009 (FAO, 2010). This is attributed to shortage of improved varieties adapted to different agro-ecological zones, diseases, insects, drought, etc (FAO, 2010).Wheat has been one of the major cereals of choice, dominating the food habit and dietary practices and known to be a major source of energy and protein for the highland population (Abera, 1991).

Wheat compares well with other cereals in nutritive value. It has good nutrition profile with 12.1 per cent protein, 1.8 per cent lipids, 1.8 per cent ash, 2.0 per cent reducing sugars, 6.7 per cent pentosans, 59.2 per cent starch, 70 per cent total carbohydrates and provides 314K cal/100g of food. It is also a good source of minerals and vitamins *viz*., calcium (37 mg/100g), iron (4.1 mg/100g), thiamine (0.45mg/100g), riboflavin (0.13mg/100g) and nicotinic acid (5.4mg/100mg) (Lorenz and Kulp, 1991).

Unlike other cereals, wheat contains a high amount of gluten, the protein that provides the elasticity necessary for excellent bread making. Hard wheat is high in protein (10-17%) and yields a flour rich in gluten, making it particularly suitable for yeast breads. The low protein (6-10%) soft type yields flour lower in gluten and therefore better suited for tender baked products, such as biscuits, pastries and cakes. *Triticum durum* wheat, although high in gluten, is not suitable for baking, but suitable for semolina, the basis for excellent pasta, such as spaghetti and macaroni preparation (Souza. 2002).

Yield being a complex character is a function of several component characters and their inter relationship with environment. Probing of structure of yield involves assessment of mutual relationship among various characters contributing to yield. In this regard genotypic and phenotypic correlation shows the degree of association between different characters and thus aid in selection to improve the yield and yield attributing characters simultaneously. Farther, path coefficient analysis helps in partitioning of correlation coefficient into direct and indirect effects and in the assessment of relative contribution of each component character to the yield.

Genetic diversity plays an important role in plant breeding either to exploit heterosis or generate productive recombinants. The choice of parents is of paramount importance in breeding program. So, the knowledge of genetic diversity and relatedness in the germplasm is a pre-requisite for crop improvement programs. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes. Thus, precise information on the nature and degree of genetic diversity present in wheat collections from principal areas of cultivation would help to select parents for evolving superior varieties. For the genetic amelioration of this crop, diverse genotypes from existing germplasm should be selected and used in further breeding program. The objectives of the present study were therefore,

1. To estimate the extent of variability, heritability and genetic advance for yield, and yield components
2. To estimate the association among yield and yield related traits
3. To assess the level of genetic diversity through morphological traits

2. LITERATURE REVIEW

2.1 Taxonomy and morphology of wheat

Wheat is a member of the Gramineae (Poaceae) family of the angiosperms. Poaceae is an attractive group for comparative genomics because they include many important crops with diverse native distributions and at least 35-fold variation in genome size (Paterson *et al.,* 2005). Wheat consists of two genera, *Triticum* and *Aegilops* (Van Beem et al. 2005). Wheat can be divided into three groups based on ploidy level, diploid (2n = 2x = 14 chromosomes), tetraploid (2n = 4x = 28) and hexaploid (2n = 6x = 42), with the diploid and tetraploid groups including wild species. The wild wheat species *T. monococcum* ssp. *aegilopoides* (wild einkorn, diploid) and *T. turgidum* ssp. *dicoccoides* (wild emmer, tetraploid) are involved in domestication. The cultivated diploid is *T. monococcumm* ssp. *monococcum* (einkorn). Cultivated tetraploids are divided into two species, *T. timopheevii* and *T. turgidum*. Only the subspecies *timopheevii* within *T. timopheevii* is cultivated. Seven subspecies within *T. turgidum* are cultivated: ssp. *Dicoccum* (emmer), ssp. *paleocolchicum* (Georgian), ssp. *durum* (macaroni), ssp. *turgidum* (rivet or cone), ssp. *polonicum* (Polish), ssp. *turanicum* (Khorassan) and ssp. *carthlicum* (Persian). There are two cultivated hexaploids, *T. zhukovskyii* and *T. aestivum* (known as common, bread or dinkel wheat). According to Dubcovsky and Dvorák (2007), Simons *et al.* (2006) and Nevo *et al.* (2001) five subspecies within *T. aestivum* are cultivated: ssp. *aestivum* (common or bread wheat), ssp. *spelta* (dinkel or large spelt), ssp. *macha*, and ssp. *compactum* (club) and ssp. *sphaerococcum* (shot). Hexaploid bread wheat is the most prominent member of the tribe and is a highly variable group (Huang *et al.,* 2002). The shift from wild diploid and tetraploid genotypes to cultivated genotypes of hexaploid wheat includes changes in morphological characters related to seed dispersal. These changes have revealed spike dimensions, spike rachis fragility, spikelet disarticulation, awn development, pubescence, grain size, glume tenacity and threshability.

Genotypes with soft glumes that require limited mechanical action during the de-hulling process are considered free-threshing (Jantasuiyarat *et al.,* 2004). Bread wheat, with the exception of *T. spelta* and *T. macha*, has tough inflorescence stems that do not shatter

when harvested and the seeds are easily threshed after gathering (Simons *et al.*, 2006 and Hancock 2004). Spike morphology (shape, length and density) in hexaploid wheat is known to be influenced by three major genes *q*, *C* and *s-1* on chromosomes 5AL, 2DL and 3DL (Jantasuiyarat *et al.,* 2004 and Sourdille *et al.,* 2000a). The genetic changes responsible for the suite of traits that differentiate domesticated plants from their wild ancestors are referred to as the domestication syndrome (reviewed in Dubcovsky and Dvorák 2007). In wheat, as in other cereals, a primary component of this syndrome was the loss of spike shattering, preventing the grains from scattering by wind and facilitating harvesting (Nalam *et al.,* 2006). Another important trait for wheat domestication was the loss of tough glumes, converting hulled wheat into free-threshing wheat. Other traits shared by all domesticated wheat are increased seed size, reduced number of tillers, more erect growth and reduced seed dormancy (Simons *et al.,* 2006).

2.2 Production and utilization of wheat

Wheat is grown on 217 million hectares throughout the world with a production of approximately 651 million tons of grain during the season 2009 (FAO, 2010). In Africa, wheat is grown on 9.5 million hectares and is harvested with 22 million tons grain. In Ethiopia, wheat is the leading crop grown on 1.7 million hectares and with 3 million tons grain harvested in 2009 (FAO, 2010). World demand for wheat by 2020 is estimated at 840 to 1,000 million tons. Yield increases are essential to meet this demand, as expanding the wheat area is not feasible (Rajaram and Braun, 2008). Wheat is now extensively grown across the temperate, Mediterranean and subtropical parts of the world (Nevo *et al.,* 2002). Conventionally, bread wheat is classified into two types, winter and spring, based on its growth habit. Winter wheat is sown in fall. The plant needs a certain period of cold temperature or vernalisation, for the plant to flowering. Spring wheat is generally sown in the spring or in the fall without experiencing cold temperature during winter. Consequently, wheat can be grown in various climates all over the world and more of the world's farmland is devoted to wheat production than to any other food crop (Briggle and Curtis, 1987).

About 40% of the world population used wheat as feed and provided 20% of total food calories and protein in human nutrition. Wheat is used to produce starch, paste, malt, dextrose, gluten, alcohol and other products (Gupta *et al.,* 2008 and Nevo *et al.,* 2002). Wheat can also be classified into two types (hard and soft bread wheat) based on their grain texture and protein content (Giroux and Morris, 1998). Roughly 95% of the wheat crop is hexaploid common wheat, used for making bread, cookies and pastries, whereas the remaining 5% is tetraploid durum wheat, used for making pasta and other semolina products. Einkorn wheat and other hulled wheat, namely emmer and spelt, are today relic crops of minor economic importance (Dubcovsky and Dvorák, 2007).

2.3 Origin of Bread Wheat

Wheat is adapted to temperate regions of the world and was one of the first crops to be domesticated (Gupta *et al.,* 2008). The domestication of wheat occurred in South-Eastern Turkey near the Tigris and Euphrates rivers approximately 10,000 years before present (Dubcovsky and Dvorák, 2007; Luo *et al.,* 2007; Hancock, 2004 and Özkan *et al.,* 2002).

Allopolyploidy has played a major role in the evolution of crop plants sustaining mankind (Zhang *et al.,* 2008b). The allopolyploids arose from interspecific hybridization events followed by spontaneous chromosome doubling (Huang *et al.,* 2002). Amphiploids are the usually fertile products of spontaneous or induced chromosome doubling of sterile interspecific or intergeneric hybrids (Chen and Ni, 2006). Wheat has undergone sufficient divergence that the duplicated chromosomes normally do not pair and the sequences of gene pairs are usually distinguishable (Paterson, 2006). At the cytogenetic level, common wheat is a segmental allohexaploid having three closely related genomes A, B and D. Each genome has seven chromosomes (n = 21) that are organized in seven homologous groups. Each homologous group has three closely related chromosomes, one from each of the three related genomes (Gupta *et al.,* 2008). The expansion of agriculture lead to the dissemination of domesticated einkorn (*T. monococcum*) and domesticated emmer (*T. turgidum* ssp. *dicoccum*) across Asia, Europe and Africa. According to Luo *et al.* (2007) the domestication of hulled emmer was the

first step that ultimately resulted in the evolution of free-threshing tetraploid durum wheat (*T. turgidum* ssp. *durum*) and hexaploid bread wheat (*T. aestivum* ssp. *aestivum*). Bread wheat (*T. aestivum*) has the genome composition AABBDD, which arose from spontaneous hybridisation, meaning two polyploidisations (McFadden and Sears 1946 and Kihara 1944 cited in Zhang *et al.,* 2008b). Domestication of wheat resulted from mutations that gave rise to traits such as soft glumes, a nonfragile rachis and the free-threshing character (Simons *et al.,* 2006). The first polyploidisation produced *T. turgidum* with the genome composition of AABB, in which *T. urartu* donated the A genome (Gupta *et al.,* 2008).

The A and D genomes of allopolyploid wheat share a high degree of homology with the diploid genomes of *T. urartu* and *Ae. tauschii* (Feldman and Levy 2005). *Ae. tauschii* is the donor of D genome, this has recently been confirmed through analysis of DNA sequences of the two genes *Acc-1* (plastid acetyl-CoA carboxylase) and *Pgk-1* (plastid 3-phosphoglycerate kinase) and the *GluDy* allele variation (Giles and Brown 2006 and Huang *et al.,* 2002). *T. aestivum* was formed by the second polyploidisation after the crossing between cultivated *T. turgidum* and *Ae. Tauschii* followed by chromosome doubling (Huang *et al.,* 2002). The B genome donor is still controversial (Nevo *et al.,* 2002) and believed to be extinct, much modified or not yet detected, but it was probably an ancestor of *Ae. speltoid*es (Zhang *et al.,* 2008b and Huang *et al.,* 2002). DNA sequences of the above genes, *Acc-1* and *Pgk-1* also proved to be of no help in identifying of the progenitor of the B genome (Gupta *et al.,* 2008). However, it is not known which AB tetraploid (*qq* or *QQ* genotype) was involved in the hybridization with *Ae. tauschii* (D genome) that gave rise to hexaploid wheat. And, with regard to *q*, it has been a matter of speculation whether it first arose in the tetraploid progenitor of hexaploid wheat or if it arose independently in hexaploids and tetraploids (Simons *et al.,* 2006). However, it is likely that due to the outbreeding nature of *Ae. speltoides*, no modern *Ae. speltoides* lines have preserved the B genome donor genotype in its ancestral state (Gupta *et al.,* 2008).

2.4 Wheat breeding

Worldwide wheat breeding in the last 50 years had many priorities, of which yield increase, maintenance of biotic resistance and increased abiotic tolerance, especially manipulation of traits for drought and heat, have been given a lot of attention. In the last 40 years, many researchers have investigated yield increases in wheat. There have been constant increases in yield potential in many geographic regions of the world, both developed and developing countries (Rajaram and Braun 2008). In favourable environments, breeding for increased yield potential and biotic stress tolerance/resistance has been the norm for the last 100 years since Mendelian genetics were redetected. The genetic gains as a result of international wheat breeding efforts have been spectacular (Rajaram and Braun 2008).

Breeders have introgressed genes for disease resistance into high yielding and popular cultivars. There has not been a parallel phenomenon in relation to combining yield potential and tolerance to drought, heat and other abiotic environmental stresses. Breeders developing cultivars for abiotic stress environments have mostly ignored yield potential and focused on stress tolerance. However, there is a need for stress tolerant cultivars with high yield potential in years with high rainfall. In such years, tall cultivars lodge and yields are further reduced due to disease susceptibility (Rajaram and Braun 2008).

Bread wheat is believed to be a relatively recent introduction to Ethiopia (Hailu, 1991); it exhibits wider adaptation and higher yield potential than durum wheat (Amsal, 2001). In Ethiopia a number of improved bread wheat varieties were released; between 1967and 1974, 14 bread wheat varieties were recommended for release. Among these: Laketch, Kanga, Mamba, Dereselign, Enkoy and Romany BC were grown on large areas. From 1975 to 1990 16 bread wheat varieties were released among which 6290 Bulk, 6295-4A, ET13.A2, Pavon76 and Dashen are currently under production (Hailu, 1991). From 1991

on wards 17 bread wheat varieties were released and all of them are in production in different agro-ecological zone of the country. Among these Digelu is the best of all with respect to yielding potential in middle to high altitude areas. Similarly Digelu, Dodota, and Watera are best performing varieties for high altitude, low altitude and water logging areas respectively (Personal contact).

2.5 Nutritional composition of Bread Wheat

The ability of wheat flour to be processed into different foods is largely determined by the proteins. Mature wheat grains contain 8% to 20% proteins. Wheat proteins show high complexity and different interactions with each other, thus making them difficult to characterize. Usually, they are classified according to their solubility. Following the sequential Osborne extraction procedure, albumins, globulins, gliadins and glutenins are isolated. An alternative classification to that described above has been proposed based on composition and structure rather than solubility Shindo *et al.*, 2002. Albumins and globulins of wheat endosperm represent 20% to 25% of total grain proteins (Baresel *et al*., 2008, and Miflin *et al*., 2002). Nutritionally, the albumins and globulins (non-glutens) have a very good amino acid balance. Many of these proteins are enzymes involved in metabolic activity. However, several other proteins have unknown functions and are not well characterized. Some proteins, particularly those belonging to a family of trypsin and α-amylase inhibitors, are also implicated in plant defense(Charmet *et al.2005)*, but the role of α-amylase and trypsin inhibitors as wheat allergens in baker's asthma has been demonstrated (Prasad *et al.*,2003) Most of the physiologically active proteins also influence the processing and rheological properties of wheat flour. In recent years, the benefits of the use of amylases, xylanases, lipoxygenase, pentosanase, glucoseoxidase, has stimulated further interest in the bread-making industry (Khlestkina *et al.,* 2006).

Wheat is unique among the edible grains because wheat flour has the protein complex called "gluten" that can be formed into dough with the rheological properties required for the production of leavened bread (Weightman *et al.,* 2008). The rheological properties of gluten are needed not only for bread production, but also in the wider range of foods that can only be made from wheat, viz., noodles, pasta, pocket breads, pastries, cookies, and other products (Weightman *et al.,* 2008). The gluten proteins consist of monomeric

gliadins and polymeric glutenins. Glutenins and gliadins are recognized as the major wheat storage proteins, constituting about 75–85% of the total grain proteins with a ratio of about 1:1 in common or bread wheat (Baresel *et al*., 2008) and they tend to be rich in asparagine, glutamine, arginine or proline but very low in nutritionally important amino acids lysine, tryptophan and methionine (Shindo *et al*., 2007).

The gliadins constitute from 30 to 40% of total flour proteins and are polymorphic mixture of proteins soluble in 70% alcohol, and can be separated into α-, β-, γ-, and ω-gliadins with a molecular weight range of 30 to 80 kDa as determined by SDS-PAGE. The molecular weights of ω-gliadins are between 46 and 74 kDa, and the α-, β- and γ-gliadins have lower Mw, ranging from 30 to 45 kDa by SDS-PAGE and amino acid sequencing (Kato *et al*., 2003). The latter approach has shown that the α- and β-gliadins are closely related and thereby they are often referred to as α-type gliadins. α-Gliadins are thought to be responsible for gluten intolerance (Simmonds *et al.,* 1990) while γ-gliadins and glutenins are much less (Barton *et al*., 2008).

Glutenin polymers are made up of single polypeptides linked through intermolecular disulfide bonds that account for about 45% of the total proteins in the grain endosperm. Glutenins can be broadly classified into two groups, the high molecular weight (HMW) and the low molecular weight (LMW) subunits, with molecular weight (Mw) range of 100 to 140 kDa and 30 to 55 kDa, respectively, according to mobility on SDS-PAGE (Bietz JA, 1988). They link together and form heterogeneous mixtures of polymers by disulfide bonded linkages of polypeptides. The glutenin proteins, therefore, are among the largest protein molecules in nature with molecular weights up into tens of millions (Wrigley CW. *et al.,* 1996). Differences in glutenin subunits size, polarity, and number of cysteine residues influence the ability to form disulfide bonds necessary for building up the glutenin polymer structure. This variation in glutenin subunits is a critical factor in determining bread dough end-product quality, particularly through its influence on polymer size distribution (Kato *et al*., 2000). The LMW subunits most closely resemble γ-gliadins in sequence (Müller *et al.,* 1998) and comprise about 20% to 30% of the total proteins while the HMW subunits account for about 5 to 10% of the total proteins (Lookharts *et al.,* 1995).

2.6 Variability, heritability and Genetic Advance

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. The phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic component being the heritable part of the total variability, it's magnitude on yield and its component characters influences the selection strategies to be adopted by the breeders (Sharma *et al.,* 2005).

There is need for effective and quick selection of wheat strains that could possess desired traits. High value of heritability and predicted genetic advance clarifies that the selection among genotype would be effective for yield and yield components (Ghandorah & Shawaf, 1993). High heritability (broad sense) associated with high genetic advance reveals strong contribution of additive genetic variance for expression of the traits and the selection based on these traits could play a vital role in improving grain yield (Iqbal & Khan, 2003). The studies conducted by various researchers have shown that high heritability alone is not enough for selection in advance generations; it must be accompanied with substantial amount of genetic advance (Memon *et al*., 2007 and Mangi *et al*., 2008). However, if a character or trait is controlled by non additive gene action it gives high heritability but low genetic advance, while the character ruled by additive gene action, heritability and genetic advance both would be high (Ahmed *et al*., 2007).

Main quantitative traits associated with high heritability and high genetic advance has great importance in selection of genotype in early generations (Memon *et al*., 2005). Heritability values can be used as a measuring scale to determine genetic relationship between parents and progeny (Memon *et al*., 2007). Better heritability values recorded points to the possibility of improvement in the parameters; therefore, attention may be focused on important traits while synthesizing genotypes (Ahmed *et al*., 2007). Yield is a polygenic trait and attributed to its associated trait therefore for the higher yield the total genetic expression of all its component genes is needed. However, their expression is also influenced by environmental factors (Sial *et al*., 2003). Heritability and genetic advance

enables the breeders to use best genetic stock for improving the crop (Mangi *et al*., 2008). The success of any breeding programme depends upon amount of good knowledge of heritability and genetic advance present in different yield associated parameters (Waqar-ul Haq *et al*., 2008). Rambaugh *et al*., (1984). The same authors described that heritability study must be conducted in favorable environments rather than unfavorable environments; genetic parameters such as mean, genetic variance, broad sense heritability and genetic advance are decreased under unfavorable environments.

Among several factors, yield related traits highly influence the amount of grain yield that can be obtained. Some of the yield related traits include days to heading, days to maturity, plant height, and tillers per plant, thousand-kernel weight and number of kernels per tiller. These traits affect yield positively and/or negatively; and their effect on yield depends on the influence of environment on these traits. High temperature during the grain filling stage reduced grain weight via reduction of grain filling duration (Tahir *et al.,* 2006). Wheat exhibits considerable genetic variation for yield and yield related traits.

Heritability, a measure of the phenotypic variance attributable to genetic causes, has predictive function of breeding crops (Songsri *et al*., 2008). It provides an estimate of the genetic advance a breeder can expect from selection applied to a population under certain environment. The higher the heritability estimates, the simpler are the selection procedures (Khan *et al*., 2008). High genetic advance coupled with high heritability estimates offers the most effective selection criteria for selection (Larik *et al*., 2000). The magnitude of genetic inheritance and expected genetic advance are important for the prediction of response to selection in diverse environments and provide the basis for planning and evaluating breeding programs (Ahmad *et al*., 2006, 2007).

Kumar *et al.* (2003) reported high heritability coupled with high genetic advance for plant height, number of spikelets per spike, thousand grain weight (TGW) and number of days to 50% heading in wheat. The grain yield was significantly and positively correlated with thousand-kernel weight (TKW) and the number of spikes per meter (Korkut *et al.,* 2001).

Khan *et al*. 2008 reported high heritability for days to heading, days to maturity, plant height, number of tillers, number of spikelets, number of grains, harvest index and grain yield but genetic advance were observed only at days to heading, plant height, number of tillers, number of spikelets, number of kernel per spike, harvest index and grains yield

2.7 Correlation Coefficients

In genetics studies, it is necessary to distinguish two causes of correlation between characters, genetic and environmental. The two possible causes of correlation are attributed to pleiotropism and/or linkage disequilibrium (Allard, 1960). Pleiotropy, particularly in a population derived from crosses between divergent strains. The degree of correlation arises from pleiotropy expresses the extent to which two characters are influenced by the same genes. Some genes may increase both characters, while others increase one and reduce the other; the former tend to cause a positive correlation, the latter a negative one.

The association between two characters that can be directly observed is the correlation of phenotypic values, or the phenotypic correlation. This is determined from measurements of the two characters in a number of individuals of the population. The genotypic correlation is the correlation of breeding values, and the environmental correlation, the correlation of environmental deviations together with non-additive genetic deviations (Falconer and Mackay, 1996).

A highly significant and positive correlation of grain yield per plant was observed with effective tillers per plant, spike length, spikelets per spike, plant height and main spike weight (Khan *et al*., 2008) in wheat. Shekhawat et al. (2006) obtained positive correlation of grain yield with heads per plant, kernel weight, and kernels per head. On the other hand, ear length and days to anthesis were found to be negatively correlated (Solanki and Bakish, 1973). Bhatt (1973) reported that kernel weight correlated positively with plant height and negatively with heading time. And also spike number and kernel weight

showed high and positive correlation with grain yield, while heading time was negatively correlated with grain yield.

Nass (1973) observed that harvest index; kernels per ear and yield per year were associated with plot yield. Kernels per ear and kernel weight also were associated with yield per year. It was concluded that ears per plant, yield per ear and harvest index together would be effective in selection for increased grain yield. Das *et. al.* (2005) found that harvest index was positively correlated with grain yield, spikes per plant and grain weight. Primary yield components, namely spikes per meter, grains per spike and test weight were negatively associated with each other. However, all the three components were highly significantly and positively correlated with grain yield (Sastry, 1979). Chand (1978) reported that yield per plant had strong positive correlation with tillers per plant, spike length, kernels per spikelet and thousand-kernel weight.

Singh *et al*. (1995) observed that wheat grain yield was positively correlated with productive tillers and flag leaf area. Similarly, Singh and Dewivedi (2002) reported significant positive association of grain yield per plant with number of spikes bearing tillers per plant both at genotypic and phenotypic levels. Tammam *et al.* (2000) reported that grain yield per plant had a positive genetic correlation with number of spikes per plant and 1000-kernel weight. Shahid *et al.* (2002) observed that spike length had significant positive genotypic correlation with grain yield. Lad *et al.* (2003) reported that grain yield exhibited highly significant and positive correlation with tillering capacity, spikelets per spike at both the genotypic and phenotypic levels. Khaliq. (2004) reported that plant heights, spike length, spikelets per spike and thousand grain weights were positively and significantly correlated with grain yield at genotypic level.

There was a non significant and positive correlation between days to heading and number of spikelets per spike as in conformity with the findings of Bhullar *et al*. (1982). There was a non significant and negative correlation between days to heading and 1000-grain weight as also reported by Ahmad *et al*. (2006). There was a non significant and positive correlation between days to maturity number of spikelets per spike as reported Bhullar *et*

al. (1982). There was a positive and significant correlation between plant height and spike length similar with the findings of Bhutta & Chaudhary (1984). Plant height was negatively and non significantly correlated with number of spikes per plant. A highly significant and positive correlation was observed between number of spikelets per spike and number of grains per spike in accordance with the findings of Ahmad & Chaudhry (1987) and Mohammad *et al*. (2001). There was a positive and significant correlation between numbers of spikelets per spike and grain yield per plant in accordance with the findings of Bahadur *et al*., (1993), Khaliq *et al*. (2004) and Khaliq (2004). Number of grains per spike was positively and non significantly correlated with number of tillers per spike. A positive and significant correlation was observed between number of grains per spike and grain yield per plant in conformity with the finding of Shahid *et al*., (2002). Results of the study showed that these genotypes may provide good source of material for further breeding program. It can also be concluded that grain yield per plant can be improved by utilizing these conditions among different characters of plant populations.

Desalegn *et al*. (2000) reported positive correlation of grain yield with days to anthesis and maturity, grain filling period and plant height, but negative correlation of days to anthesis with grain filling period and plant height. They also observed that grain size and grain yield had strong positive correlation. Likewise, Balcha (2002) observed that grain yield was positively correlated with grain filling period, spike length and harvest index, but negatively correlated with days to heading and maturity, plant height, and thousand kernel weights. In addition, his result also depicted very weak positive correlations (rp=0.02, rg=0.26) between grain yield and grain protein content, and strong positive association of grain protein content with hectoliter weight (rp=0.68, rg=0.91) and thousand-kernel weight (rp=0.54, rg=0.79).

Thousand kernel weights showed positive association with yield both at genotypic and phenotypic level. This result is in agreement with the results of Mondal *et al*. (1997), Dokuyucu and Akaya (1999), Mondal and Khajuria (2001). Khaliq (2004) observed number of spikelets per spike as significantly and positively correlated with grain yield.

2.8 Path Coefficient Analysis

Path coefficient analysis is a very important statistical tool that indicate which variables (causes) exert influence on other variables (effects), while recognizing the impacts of multicolinearity (Albayrak *et al.,* 2005). A path coefficient is simply a standardized partial regression coefficient and, as such, estimates the direct influence of one variable upon another (Dewey and Lu, 1959; Albayrak *et al.,* 2003; Türk and Çelik, 2006), and permits the separation of correlation coefficients into components of direct and indirect effects (Akanda and Mundt, 1996; Albayrak *et al.,* 2004; Kara and Akman, 2007). It requires a cause and effect situation among variables. Path coefficient analysis can be defined as "the ratio of standard deviation of the total effect" in a phenotypic or genotypic correlation of multi correlated trait (Falconer and Mackay, 1996).

Albayrak *et al.* (2003) illustrated the following concluding remarks:

a) If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then the correlation explains the true relationship and a direct selection through this trait will be effective;

b) If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be reason of correlation. In such situations, the indirect causal factors must be considered simultaneously, and

c) Correlation coefficient can be negative, but the direct effect may be positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed, that is, restrictions are to be imposed to nullify the undesirable indirect effects, to make use of the direct effect.

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

of associations and can measure the relative importance of each (Sharma, 1998; Kara and Akman, 2007).

Correlation analysis aided by path coefficient analysis is a powerful tool to study the character associations. He Zhong-hu and Rajaram (1994) observed that the magnitude and significance of correlation coefficients varied with different groups of genotypes and different seasons. However, the results exhibited that grain yield was consistently positively associated with grains per spike and harvest index regardless of the difference in genotypes and seasons, and also were yield and biomass were also positively correlated. They, thus, suggested that seeds per spike (fertility), biomass and harvest index could influence the yield under high temperatures.

Several workers have studied character associations using path coefficient analysis for several crops, in bread wheat, Bhatt (1973); Ariyo *et al.* (1973); Dokuyucu (2002). Kashif and Khaliq *et al*. (2004) found out that the three primary components of grain yield (i.e. grains per spike, thousand-kernel weight and spikes per plant) had larger direct effect on grain yield than harvest index, days to anthesis and plant height. However, spikes per plant and grains per spike were significantly and negatively correlated with thousand-kernel weight and the former two characters (spikes per plant and grains per spike) had negative association. Therefore, the positive effect of number of spikes per plant on grain yield was completely counterbalanced by its indirect effects mainly via thousand-kernel weight and to some extent through grains per spike.

Getachew *et al*. (1993) reported high direct effect of tiller number (0.92) and thousand kernel weight (0.66) on grain yield; however, these two traits exhibited substantial indirect counter-balancing effect via one another. These workers also found that days to maturity had a very strong negative correlation (r = -0.82) with grain yield per plant and showed a negative and negligible direct effect on grain yield. Its negative correlation with grain yield was largely due to the negative indirect effects via days to maturity, tillers number and thousand-kernel weight. They also found that kernel number per spike

showed an intermediate direct effect and a negative indirect effect via tiller number, and a small but positive indirect effect via thousand-kernel weight.

2.9 Genetic Divergence

Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, pest and disease resistance. Genetic divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal, 2003). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Lyons, 2005b).

Crosses involving parents belonging to more divergent clusters would be expected to manifest maximum hetrosis and wide variability in genetic architecture (Singh *et al*., 1987). The D^2 values represent the index of genetic diversity among the clusters, it would be most appropriate to make cross between genotypes belonging to cluster separated by high estimates of statistical distances. Hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety and also suggested to create variability for developing the varieties involving a large number of different lines instead of closely instead of closely related ones.

Based on Mahalanobis' D^2 analysis, genotypes were grouped into clusters with variables number of genotypes, suggesting considerable amount of genetic diversity in the material. The highest mean value for number of effective tillers per plant was recorded by of Sharma *et. al.* (1998) for grains per spike and for tiller per plant, thousand grain weight and grain yield per plant and the same was also reported by Bergale *et al.* (2001).

Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Plant uniformity, which can be resulted by the use of modern plant breeding techniques, can

produce plants, which are more efficient by means of different goals including enhanced resistance under stress, however much more research must be performed to indicate the most optimized methods that can be used for the production of efficient plants. This is of significance for the production of food for the world increasing population (Fu and Somers, 2009). Accordingly, the increased attention to the production of resistant plant species for prolonged food production under different conditions indicate the necessity of performing breeding experiments (Martin *et al.,* 2008; Van de Wouw *et al.,* 2010). One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to benefit transgressive segregation, genetic distance between parents is necessary (Joshi *et al.,* 2004). The higher genetic distance between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966; Anand and Murrty, 1968).

Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety (Benadeki, 1992). Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004). Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Bhatt, 1970; Carves *et al.,* 1987; Mohammadi and Prasanna, 2003; Eivazi *et al.,* 2007).Usually before calculating the genetic distance, the variables are standardized so that all variables are of similar importance in determining the distance. Unfortunately, standardization decreases the differences among groups. The results of cluster analysis and PCA may have relative differences with each other. Therefore, before using cluster analysis, the principle components may be avoided. On the other hand, when the two first principal components account for high variation percentage, grouping according to these two components, can certainly be a useful method to find the clusters (Fotokian *et al.,* 2002). Various algorithms have been used in studying of genetic diversity in cluster analysis of which, UPGMA and Ward's methods are the most popular approaches. Of the

algorithms, UPGMA, Ward's, SLINK, and CLINK, applied for cluster analysis and exploring genetic diversity and grouping of plant materials in the past, the UPGMA is the most valid method in accordance with the relationship of family based on their genetic material (Mohammadi and Prasanna, 2003). Chaining effect in UPGMA model is considered as the major drawback on application of this approach in cluster analysis and results in confusions in interpretation of the results (Mohammadi and Prasanna, 2003). Ward's approach is similar to UPGMA method but it without having chain effect issues.

Benadeki (1992) investigated the genetic diversity of five local geographical regions across central provinces of Iran for bread wheat. It has been proposed that the differences for studied traits across regions were significantly (P=0.01) different and resulted in nine classes discriminated by geographical regions (Benadeki, 1992). Narouee Rad (2006) determined the genetic diversity of wheat landraces in the west of Iran and by using cluster analysis, six clusters were determined for different areas. Fang et al. (1996) clustered 120 genotypes of durum wheat into five groups based on maturity date, plant height, spike length, number of seed per spike, 1000-seed weight and spike seed yield. Jain *et al.* (1975) investigated the geographical patterns of phenotypic diversity of durum wheat using the world collection and achieved a developed program for the protection of genetic resources to identify and assess inter variation and intra societies. Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety (Benadeki, 1992). Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase.

Generalized genetic distance by using multiple measurements that are subjected to multivariate statistical analysis can provide such measure based on generalized distance as indicated by D^2 statistics (Mahalanobis, 1936; Rao, 1952). A number of workers observed that Mahalanobis D^2 statistics was a powerful tool in describing divergence among lines based on multiple characters (Deshmukh *et al*., 1999; Amsal, 2001; Debebe *et al*., 2000).

2.10 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 eigenvalues are often used to determine how many factors to retain. The sum of the eigenvalues is usually equal to the number of variables.

According to Chahal and Gosal (2002) characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. The differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character. Characters which load high positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters.

Results of using PCA showed that this method is limited when the pattern of variation is not based on a 0 and 1 scores. Therefore, combined PCA and other techniques can be appropriately used for grouping (Mohammadi and Prasanna, 2003). The cluster analysis is an appropriate method for determining family relationships (Mellingers, 1972). The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). One of the issues with breeding projects based on hybridization is to estimate the relationship between parents before initiating the crossing. Euclidean distance can theoretically estimated the genetic distance between parents to maximize the trangressive segregation (Hoque and Rahman, 2006). Determination of genetic diversity is useful for plant breeding and hence production of more efficient plant species under different conditions.

3. MATERIALS AND METHOD

3.1 Descriptions of the Study Areas

The experiment was conducted in the 2011/12 main crop season at two locations, namely, Holeta and Ginchi. Holeta Agricultural Research Center is located between latitude 09^0 05' N and longitude 38^0 30' E, altitude 2400 masl and 34km west of Addis Ababa. The soil type is red clay loam with PH of 4.88. The annual rainfall, maximum and minimum temperatures were 935.7mm, 21.98 ^{0}C and 6.5 ^{0}C, respectively. Ginchi Agricultural Research Sub Center is located between latitude 09^0 03'N and longitude 38^0 15'E, altitude 2250 masl and 84west of Addis Ababa. The soil type is black (vertisol) clay loam with PH of 5.98.The annual rainfall and average maximum and minimum temperatures of the area were 1027.4 mm, 24.72 ^{0}C and 8.76 ^{0}C, respectively. The soil of Holeta well drained, 1-3% organic matter, 0.12-0.24%N and 3-13 ppm available P. The soil of Ginchi is Vertisol (Black soil), with organic matter 0.91-32%, 0.09-0.14% N and 4.2-9.9 ppm available P. (Gebreyes et al.,2010). The total annual rainfall and temperature data of both locations for the years 2001-2011 are presented in the appendix figures I-VII.

3.2 Experimental Materials

Twenty one diverse bread wheat genotypes released by the national research system were used in the experiment (Table 1). The genotypes were obtained kindly from Holeta Agricultural Research Center (HARC).

Table 1. Varieties name, pedigree, breeder/maintainer and year of release for the 21 bread wheat genotypes used in this study (2011/2012).

No	Variety	Pedigree	Breeder /maintainer	Year of release
1	Danda'a	Danphe#1	KARC/EIAR	2010
2	Kakaba	Picaflor #1	KARC/EIAR	2010
3	Hawi	HAR2501	KARC/EIAR	1999
4	Tusie	HAR1407	KARC/EIAR	1997
5	Pavon 76	CM8399-D-4M-3Y-1M-1Y-1M-0Y		1983
6	ET13.A2	ET13A.2.L.3.L		1981
7	K6295.4A	6295-4A		1980
8	ETBW5483			2005
9	ETBW5496			2005
10	Digelu	SHA-7/KAUZorHAR3116	KRRC/EIAR	2005
11	Sofumar	HAR1889	SARC/OARI	1999
12	Mad-walabu	HAR1480	SARC/OARI	1999
13	Tay	ET-12D4/HAR604(1)	ADARC/ARARI	2005
14	Senkegna	HAR3646	ADARC/ARARI	2005
15	Gossay	HAR3730	ADARC/ARARI	2007
16	Menze	HAR3008	DBARC/ARARI	2007
17	Bolo	HAR-3816	DBARC	2009
18	Alidero	HK-14-R251	HARC/EIAR	2007
19	Denknesh	HAR3919	SRARC/ARARI	2007
20	Tossa	HAR3123	SRARC/ARARI	2004
21	Kulkulu	ETBW4621	HU	2009

3.3 Experimental Design and Trial Management

The experiment was laid out in RBCD design with three replications. The plot size was six rows of 2.5m length with 0.2m row spacing. That is 1.2m x 2.5m = $3m^2$. Planting was done by hand drilling on June 21, 2011 at Holeta and July 6, 2011 at Ginchi. Seed rate was 150kg/ha (45g/plot) at both locations. DAP and UREA were applied at the rate of 150kg/ha and 71kg/ha, respectively, at Holeta. At Ginchi DAP and UREA were applied at the rate of 130kg/ha and 100kg/ha, respectively. Phosphorus was applied in the form of DAP at sowing. Nitrogen was applied in the form of urea, in two splits, 1/3 at planting and the remaining 2/3dressed at tillering at Ginchi only. All the other management practices such as land preparation, weeding, etc. were uniformly applied to all plots using recommended practices of HARC (Hailu *et al*.1985). Harvesting date for Holeta and Ginchi were November 27, 2011 and November 25, 2011 respectively.

3.4. Data Collected

The traits such as plant height, number of effective tillers per plant, spike length, number of spikelets per spike, number of seeds per spike and grain yield per plant were recorded from 10 randomly taken plants and then the average is taken to represent the genotype. The remaining traits were recorded on plot basis. Data were collected on the following agronomic characteristics.

3.4.1. Days for heading (DH): Counted as the number of days from sowing to 50 % heading stage i.e., 50% of the heads fully emerged from the flag leaf sheath.

3.4.2. Days for maturity (DM): Number of days from emergence to 75% of plants attained physiological maturity *i.e.* when the plant loss chlorophyll

3.4.3. Plant height (PH): The height of ten randomly sampled plants from the central rows of each plot was measured (from the base of the ground to the top of the spike excluding awns) and the average of the ten observations was used for analysis.

3.4.4. Number of effective tillers per plant (NT): Average number of productive tillers per plant were counted from the ten randomly taken plants.

3.4.5. Spike length (SL): Average lengths of the central spikes in cm excluding awn were measured at maturity from ten randomly taken plants.

3.4.6. Number of spikelets per spike (NSl): Were counted from the main tiller of each of the spike of ten randomly taken plants and expressed as average.

3.4.7. Number of seeds per spike (NGS): Were counted from the main tiller of each of the spike of ten randomly taken plants and expressed as average.

3.4.8.1000-seed weight (TGW): Weight (g) of 1000 kernel was estimated by counting 1000 seeds randomly drawn from the grain yield of each plot.

3.4.9. Harvest index (HI): Was estimated by dividing grain yield to biological yield

3.4.10. Grain yield (g/plant) (GY): Grain yield per plant is the average seed yield of ten randomly selected plant of each plot

3.5. Statistical Analyses and Procedures

3.5.1 Analysis of variance (ANOVA)

The variability among accessions was assessed by employing analysis of variance (ANOVA) using SAS version 9.2 (SAS Institute, 2008). The statistical tools like range for means, mean, phenotypic and genotypic variance and coefficient of variation were computed. Least Significant Difference (LSD) test was employed for mean separation among the accessions. Bartley model was used to test homogeneity of variance and RCBD design model for analysis of variance.

Individual location analysis of variance was the first step towards combined analysis of variance. In order to combine the data the error with which each mean is measured should be tested for homogeneity which is one of the basic assumptions of analysis of variance. A quick test of homogeneity of variance is provided by the ratio of the largest means square errors to the smallest mean square error. The ratio shows heterogeneous for thousand grain weight, but homogenous for all the rest traits. For the heterogeneous trait thousand grain

weight variance component analysis was made at each location. For the traits which were homogenous combined over the two locations. Analysis of variance model:

$Y_{ij} = \mu + T_i + \beta_j + \epsilon_{ij}$ **(**Gomez and Gomez. 1984**)**

Where:

μ = Population mean

T_i = Treatment effect

βj = Block effect

ϵ_{ij} = Error effect

Table 2A. ANOVA skeleton for individual location

Source of variation	degree of freedom	Mean square	Expected mean square
Replication	r-1	Msr	$\sigma^2 e + g\,\sigma^2 r$
Genotypes	g-1	Msg	$\sigma^2 e + r\,\sigma^2 g$
Error	(r-1) (g-1)	Mse	$\sigma^2 e$
Total	gr-1		

Table 2B. ANOVA skeleton for combined over location

Source of variation	degree of freedom	Mean square	Expected mean square
Location	L-1		
Rep within location	L(r-1)	Msr	$\sigma^2 e + gL\,\sigma^2 r$
Genotypes	g-1	Msg	$\sigma^2 e + r\,\sigma^2 gL + rL\,\sigma^2 g$
Genotype x location	(g-1)(L-1)	Msgl	$\sigma^2 e + r\,\sigma^2 gL$
Error	r(g-1)(r-1)	Mse	$\sigma^2 e$
Total	grL-1		

Where:

r = number of replication

g = number of genotypes

Msr = mean square due to replications

Msg = mean square due to genotypes

$\sigma^2 g$ = genetic variance

$\sigma^2 e$ = environmental variance

$\sigma^2 gL$ = genotype by location interaction variance

MsgL= mean square due to genotype by location interaction

Mse = mean square of error

3.5.2 Estimation of phenotypic and genotypic variability

The variability present in the population was estimated by simple measures, namely range, mean, standard error, and phenotypic and genotypic variances and coefficients of variations. The phenotypic and genotypic variance and coefficients of variations were also estimated as per the procedure suggested by Burton and De Vane (1953) as follows: at

$$ó^2 p = ó^2 g + ó^2 e \quad \text{at single location}$$

$$ó^2 g = \frac{MSg - MSgl}{lr} \quad \text{at combined over two locations}$$

$$ó^2 g = \frac{MSg - MSe}{r}$$

Where, $ó^2 g$ =Genotypic variance

$ó^2 P$ = Phenotypic variance

$ó^2 e$ = Environmental (error) variance or Error mean square

MSg = mean sum square due genotypes (accessions)

MSe =mean sum square of error (environmental variance)

r = number of replications

Phenotypic Coefficient of variation (PCV), $PCV = \frac{\sqrt{ó^2 p}}{\bar{x}} x100$

Genotypic Coefficient of variation (GCV), $GCV = \frac{\sqrt{ó^2 g}}{\bar{x}} x100$

$\bar{x}$ = Population mean of the character being evaluated

3.5.3 Heritability (in broad sense)

Heritability in the broad sense for quantitative characters was computed using the formula suggested by Singh and Chaudhary (1985):

$$H = \frac{ó^2 g}{ó^2 p} x100$$

Where, H= heritability in the broad sense.

$(ó^2 g)$ = Genotypic variance and

$(ó^2 p)$ = Phenotypic variance.

3.5.4 Expected genetic advance (GA)

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960) as:

$$GA = K * ó_P * H$$

Where, GA = expected genetic advance, $ó_p$ =phenotypic standard deviation on mean basis, H= Heritability in broad sense, K =selection differential (k=2.06 at 5% selection intensity)

Genetic advance (as percent of mean) (GA) was computed to compare the extent of predicted genetic advance of different traits under selection using the formula:

$$GA = \frac{GA}{\bar{X}} * 100$$

Where, $\bar{x}$ =population mean of the quantitative character, GA =genetic advance as percent of mean.

3.5.5 Correlation coefficient

3.5.5.1 Phenotypic and genotypic correlation coefficients

The character associations represented by correlation coefficient between different pairs of characters at the genotypic and phenotypic levels were calculated from the genotypic, phenotypic and environmental co-variances obtained by covariance analysis as shown in Table3.

Table 3. Analysis of covariance between any two characters

Source of variation	Degree of freedom	MSP	EMSP
Replication	(r-1)	MSPr	$ó^2exy + gó^2rxy$
Genotype	(g-1)	MSPg	$ó^2exy + gó^2rxy$
Error	(r-1)(g-1)	MSPe	$ó^2exy$

Where,

MSPg= mean sum products due to genotypes for characters x and y,

MSPe= mean sum product of environment (error) for characters x and y,

EMSP=expected mean sum product,

r= number of replications

These covariance components were substituted in the following formula to calculate the genotypic and phenotypic correlation as described by Sharma (1998).

$$Cov_{gxy} = \frac{MSPg - MSPE}{r}$$

$$Cov_{pxy} = Cov_{(gxy)} + Cov_{(exy)}$$

Where, Cov_{gxy} = genotypic covariance between characters x and y

Cov_{pxy} = Phenotypic covariance between characters x and y

Cov_{exy} = Environmental covariance between character x and y

The correlation was estimated using the formula suggested by Miller *et al.* (1958):

$$r_p = \frac{P_{\text{cov } xy}}{\sqrt{(ó^2 p_x * p_y)}}$$

Where, r_p =phenotypic correlation coefficient

$P_{\text{cov } xy}$ = Phenotypic covariance between character x and y

$$r_g = \frac{g_{\text{cov } xy}}{\sqrt{(ó^2 g_x * g_y)}}$$

Where, gcoxy= genotypic covariance between character x and y,

rg = genotypic correlation coefficient,

$ó^2 gx$= Genotypic variance of x character

$ó^2 gy$ = Genotypic variance of y character

$ó^2 px$ = Phenotypic variance of x character

$ó^2 py$ =Phenotypic variance of y character

the coefficients of correlation were tested using "r" tabulated value at n-2 degree of freedom, at 5% and 1% probability level, where n is the number of treatments (accessions).

3.5.6 Path coefficient analysis

In this analysis, grain yield per plant was taken as the resultant (dependent) variable while the rest of the characters were considered as casual (independent) variables. The direct and indirect effects of the independent characters on grain yield per plant were estimated by the simultaneous solution of the following general formula suggested by Dewey and Lu (1959) and with statistical package developed by Wright (1991).

$$r_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where, r_{ij} = mutual association between the independent character i (yield related trait) and dependent character, j grain yield as measured by the genotypic correlation coefficient; P_{ij} is components of direct effect of the independent character (i) on the dependent character (j) as measured by the genotypic path coefficients; and $\Sigma\, r_{ik}\, p_{jk}$ =summation of components of indirect effects of a given independent characters (i) on the given dependent character (j) via all other independent characters (k). Whereas the contributions of the remaining unknown characters are measured as the residual which is calculated as:

$$R_R = \sqrt{\left(1 - \sum P_{IJ} - RIJ\right)}$$

3.5.7 Cluster analysis for quantitative traits

Cluster analysis is a multivariate statistical analysis technique involving partitioning a set of objects into groups so that objects within a group are more similar and objects in different groups are more dissimilar (Gupta *et at.*,2007). This analysis was performed by canonical roots method using procedures of SAS version 9.2 (SAS Institute, 2008).

3.5.8 Genetic distance between clusters

The genetic distances between clusters were estimated by Mahalanobis's statistics (1936) for the 22 quantitative characters and were analyzed using the procedure proc discrim of SAS version 9.2 (SAS Institute, 2008).

D^2 statistics is defined by the following formula:

$$D^2 ij = \left(\overline{X}_i - \overline{X}_j\right)^1 COV^{-1} \left(\overline{X}_i - \overline{X}_j\right)$$

Where, $D^2 ij$ = Total generalized distance between class i and j,

$\left(\overline{X}_i - \overline{X}_j\right)$ =The difference between the mean vectors of i^{th} and j^{th}; and

COV^{-1} = the pooled variance-covariance matrix within groups.

The significance of D^2ij values for pairs of clusters was tested using the calculated values of chi-square(x^2) at 1% and 5% probability level. The test was done against the tabulated values of x^2 for 'P' degrees of freedom, where P is the number of quantitative characters considered (Singh and Chaundhary, 1985).

3.5.9 Principal component analysis (PCA)

Principal component analysis was performed by using correlation matrix by employing procedure printcomp corr of SAS version 9.2 (SAS Institute, 2008) in order to examine the relationships among the 22 quantitative characters that are correlated among each other's by converting into uncorrelated characters called principal components.

4. RESULTS AND DISCUSSION

4.1. Variability Assessment

4.1.1 Analysis of variance

Mean squares of the 10 characters from analysis of variance (ANOVA) at individual locations and combined over the two locations are presented in Tables 4 and 5. At Holeta and Ginchi significant differences among genotypes (P<0.01) were observed for 1000-grain weight. The combined analyses of variances revealed highly significant (P<0.01) differences among the 21genotypes for 9 of the traits studied (Table 5), indicating the presence of inherent variation among the materials. Desirable genes from this germplasm can effectively be utilized to develop high performing pure line varieties after crossing. The present study agrees with earlier findings of Kumar *et al.* (2003) in wheat.

Table 4. Analysis of variance (mean squares) for 1000-grain weight of 21 bread wheat genotypes grown at Holeta and Ginchi (2011/12)

	LOCATION							
	HOLETA				GINCHI			
TRAIT	REP D.F=2	GEN D.F=20	ERROR D.F=40	CV%	REP D.F=2	GEN D.F=20	ERROR D.F=40	CV%
TGW	0.146	70.915**	0.003	0.155	5.762ns	72.155**	0.7619	2.7

TGW=1000-grain weight

D.F = Degree of freedom

*, **, P<0.05,P<0.01 respectively

ns =not significant

CV = Coefficient of variation

Table 5. Combined analysis of variance (mean squares) for 9 traits of 21 bread wheat genotypes grown at Holeta and Ginchi (2011/12)

TRAITS	REPLICATION WITHIN LOCATION (df=2)	LOCATION (L) (df=1)	GENOTYPES (G) (df=20)	ERROR (df=82)	CV %
DH	3.87*	271.63**	196.97**	0.60	1.06
DM	1.79ns	9086.51**	126.19**	0.85	0.86
PH	230.95**	4705.56**	394.64**	20.18	4.64
NT	0.40**	0.14**	2.54**	0.0002	0.34
SL	0.30**	0.08**	1.69**	0.002	0.41
NSl	11.18**	314.93**	148.12**	1.49	3.33
NGS	4.17**	3.08**	128.64**	0.17	1.14
HI	10.37**	79.38**	66.91**	0.48	2.36
GY	0.77**	4.054**	4.59**	0.04	4.44

CV%= coefficient of variation df= degree of freedom

DH = days to heading, DM = days to maturity, PH = plant height, NT = number of effective tillers, SL = spike length, NSl = number of spikelets per spike, NGS = number of grains per spike, HI = harvest index, GY = grain yield

4.1.1.2 Range and mean values

Range and mean values for thousand grain weight were shown in Table 6 for Holeta and Ginchi and in Table 6, combined over locations. The mean performance of thousand grain weights at Holeta and Ginchi; and the mean performance of nine traits of 21 bread wheat genotypes combined over location are presented in the Appendix Tables I and II, respectively.

The grand mean for thousand grain weight was 32.28g at Ginchi while its range was 24g to 44g. At Holeta, the grand mean was 32.58g and the range was 25.9g to 43.1g.The grand means were almost the same between the two locations at Holeta and Ginchi had the same some sort of rain fall shower, relative humidity and temperature in the season particularly during the grain filling period.

At combined over location (Appendix Table II), days to heading was ranged between 62.833 days (Denknesh) to 82.5days (ETBW5496), with an average of 73 days, and days to maturity between 100.17 days (ETBW5483) to 118.5 days (Senkegna) with an average of 107 days, and plant height ranged between 86.67cm (Hawi) to 118.33 cm (ET13.2A) with an average of 96.9 cm, and number of effective tillers between 2.8 (Denknesh and Tossa) to 4.9 (ETBW5483), with an average of 3.64, and spike length between 8.58 cm (ET13.2A) to 10.5 cm (ETBW5496), with an average of 9.52 cm, and number of spikelets per spike27.73 (Sofumar) to 47 (Digelu), with an average of 36.57, and number of grains per spike between 26.83 (Sofumar) to 46.67 (Digelu) with average of 36.27, and harvest index between 23.84 (Pavon76) to 36.34(Digelu), with an average of 29.34 and grain yield between 3.1g (Tossa) to 6.85g (Digelu) and with an average of 4.48g, these all variations occur because of the different response of the genotypes to these locations and as the same time the two locations were different.

4.1.3 Variance components and coefficients of variation

Estimates of Phenotypic (δ^2p), genotypic (δ^2g) and environmental (δ^2e) variances and phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 6 and 7 for Holeta and Ginchi, and combined over two locations, respectively. The PCV values were higher than that GCV values for each and combined locations.

At Holeta, genotypic and phenotypic variances of 1000-grain weight were high (23.637 and 23.640). Similarly, at Ginchi, genotypic and phenotypic variances of 1000-grain weight were high (23.798 and 24.560).These observed high values of genotypic and phenotypic variances indicating the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for 1000-grain weight. The present findings corroborate the earlier reports of Kumar et al. (2003) in wheat.

According to Deshmuk *et al*., (1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Accordingly at Holeta, the GCV and PCV were meduim (14.923% and 14.924%) for thousand grain weight. Similarly, at Ginchi, the GCV and PCV were also medium (15.112% and (15.352%) for the same trait, indicating the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for 1000-grain weight at both locations.

In combined analysis across locations (Table 7), high GCV and PCV were recorded for grain yield (27.502%, 27.862%) and number of effective tillers (25.250%, 25.253%). Yousaf Ali *el at*.(2008) observed from his study high PCV and GCV in grain yield per plant, number of effective tillers, number of grains per spike. Number of spikelets per spike (19.117%, 19.407%), number of grains per spike (18.042%, 18.078%), harvest index (16.038%, 16.211%), plant height (11.53%, 12.427%) and days to heading (11.106%, 11.157%), exhibited medium genotypic as well as phenotypic coefficient of variation in the present study. It indicates that selection may be effective based on these

characters and their phenotypic expression would be a good indication of the genotypic potential. Days to maturity (6.041%, 6.102%) and spike length (7.883%, 7.897%) exhibited low genotypic as well as phenotypic coefficient of variation in the present study. This trait offered less scope of selection, as it was under the influence of environment. The findings were supported by Mohammad *et al*., (2001); who observed low coefficients of variation for days to maturity.

Table 6. Estimate of range, mean, standard error (SE), genotypic (δ^2g), phenotypic (δ^2p).environmental (δ^2e) components of variance, genotypic (GCV) and phenotypic (PCV) coefficient of variability, broad sense heritability (H^2b), expected genetic advance (GA) and genetic advance as percentage of mean (GAPM) for one character at each location in Holeta and Ginchi2011/2012.

Location	Trait	Range	Mean	SE	δ^2g	δ^2e	δ^2p	GCV	PCV	ECV	H^2b	GA	GAPM
Holeta	TGW	25.9-43.1	32.58	0.002	23.637	0.003	23.640	14.923	14.924	0.155	99.989	10.012	30.740
Ginchi	TGW	25-44	32.28	0.873	23.798	0.762	24.560	15.112	15.352	2.704	96.898	9.892	30.645

TGW= 1000-grain weight

Table 7. Estimate of range, mean, standard error (SE), genotypic (δ^2g), phenotypic (δ^2p), environmental (δ^2e) components of variance, genotypic (GCV) and phenotypic (PCV) coefficient of variability, broad sense heritability (H^2b), expected genetic advance (GA) and genetic advance as percentage of mean (GAPM) for nine character from combined ANOVA over location, Holeta and Ginchi (2011/12)

TRAIT	RANGE	MEAN	δ^2p	δ^2g	δ^2e	GCV	PCV	H^2b	GA	GAPM
DH	62.83-82.5	72.85	66.057	65.457	0.6	11.106	11.157	99.092	16.591	22.774
DM	100.17-118.5	107	42.63	41.78	0.85	6.041	6.102	98.006	13.182	12.320
PH	86.67-118.33	96.9	145	124.82	20.18	11.530	12.427	86.083	21.353	22.037
NT	2.8-4.9	3.644	0.8468	0.8466	0.0002	25.250	25.253	99.976	1.895	52.003
SL	8.58-10.5	9.518	0.565	0.563	0.002	7.883	7.897	99.646	1.543	16.211
NSl	27.73-47	36.57	50.367	48.877	1.49	19.117	19.407	97.042	14.187	38.795
NGS	26.83-46.67	36.27	42.993	42.823	0.17	18.042	18.078	99.605	13.454	37.094
HI	23.84-36.34	29.34	22.623	22.143	0.48	16.038	16.211	97.878	9.590	32.687
GY	3.1-6.85	4.478	1.557	1.517	0.04	27.502	27.862	97.430	2.504	55.921

DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, SL=spike length, NSl=number of spikelets per spike, NGS=number of grains per spike, HI=harvest index, GY=grain yield

4.1.4 Heritability and genetic advance

Heritability is a significant parameter for the selection of an efficient population improvement method. Single plant selection in earlier generation may be much effective for a character that is highly heritable. Furthermore, environment may also interact with genotypic constitution to influence heritability (Raiz, 2003).

Heritability estimate for characters under study at Holeta & Ginch, and combined over location are indicated in Table 6 and 7, respectively. According to Robinson *et al.* (1949) heritability values are categorized as high (≥60%), moderate (30-60%) and low (0-30%). Based on these, at Holeta, 1000-grain weight (99.99%) had high heritability (Table 6). At Ginchi, 1000-grain weight (96.898%), recorded also high heritability. Kumar *et al*. (2003), in wheat reported high heritability for 1000-grain weight. There was no as such appreciable difference between the two locations for this trait as far as heritability and genetic advance as percentage of mean were concerned.

In combined analysis over locations, number of effective tillers (99.976%), spike length (99.646%), number of grains per spike (99.605%), days to heading (99.09%), days to maturity (98.006%), harvest index (97.878%), grain yield per plant (97.43%), number of spikelets per spike (97.042%) and plant height (86.083%) had high heritability values (Table 7). Larik *et al*. (2000) also reported high heritability for these traits.

Genetic advance as per cent mean was categorized as high (≥20%), moderate (10-20%) and low (0-10%) (Johnson *et al*. (1955). Accordingly at Holeta & Ginchi (Table 6), high genetic advance as percent of mean was observed for 1000-grain weight. Similar findings were reported by Dwived *et al*. (2002) and Yousaf e*t al*. (2008).

In combined analyses over locations, genetic advance as percent of mean ranged from 12.32% for days to maturity to 55.921% for grain yield per plant (Table 7). High genetic advance as percent of mean was observed for grain yield per plant (55.921%), number of effective tillers (52.003%), number of spikelets per spike (38.795%), number

of grains per spike (37.095%), harvest index (32.687%), days to heading (22.774%) and plant height (22.037%). Days to maturity (12.32%) and spike length (16.211%) had moderate genetic advance as percent of mean. These traits also had high heritability values. Selection based on those traits with high and moderate genetic advance as percent of mean will result in the improvement of the performance of the genotypes for the traits. Similar findings have been reported by Songsri *et al*. (2008).

4.2 Genetic Divergence

Differences in morphological and quantitative traits have been considered as simple indicator of genetic variability in crop species and varieties. Divergence analysis is a technique used to categorize genotypes that are similar as possible into one group and the other into different. D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization.

Table 8. The distribution of genotypes into 5 clusters based on D2 analysis for 21 bread wheat genotypes tested at Holeta and Ginchi; combined over two locations (2011/12)

CLUSTER	No	GENOTYPES
I	6	Kakaba, Hawi, Denkenes, Pavon76, Tossa, Sofumar
II	11	Mada-Walabu, Gossay, Tusei, ETBW5483, Tay, Bolo, Menze, Danda'a, ETBW5496, Senkegna, Alidero
III	2	ET13.A2, K6295-4A
IV	1	Kulkulu
V	1	Digelu

Table 9. Mean value of 10 characters for the 5 cluster of 21 bread wheat genotypes tested at Holeta and Ginchi, combined over two locations (2011/12)

	CLUSTER I	CLUSTER II	CLUSTER III	CLUSTER IV	CLUSTER V
DH	65.89*	75.06	75.17	77.33	81.17**
DM	105.89	107.61	109.84**	101.17*	106.17
PH	91.11	96.90	117.08**	89.17*	99.17
NT	3.58	3.74	3.13	3.35*	4.3**
SL	9.32	9.64	9.19*	10**	9.6
NSl	33.27	37.41	40.19	30.77*	47**
NGS	32.5	37.58	38.5	29.6*	46.67**
TGW	35.52	30.43	34.5	27.78*	36.4**
HI	28.24*	29.35	29.41	36.26	33.49**
GY	3.96	4.61	4.475	3.75*	6.85**

DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, SL=spike length, NSl=number of spikelets per spike, NGS=number of grains per spike, TGW=thousand grain weight, spike, HI=harvest index, GY=grain yield

The cluster analysis based on the pooled mean of genotypes resulted in classifying the 21 genotypes three groups and two solitaries (Table 8) (Appendix figure 4). This indicates the tested bread wheat genotypes were highly divergent. The chi-test for the five clusters indicated that there was statistically accepted difference between clusters (Table 10). The genotypes were distributed (Table 8 and 9) in such a way that 6 genotypes where grouped into Cluster-I (28.57%), 11 genotypes in to Cluster-II

(52.38%), 2 genotypes into Cluster-III (9.52%), one genotype to each of Cluster-IV and Cluster-V. Cluster-I contains low days to heading (65.89days) and harvest index (28.24). Cluster-II contains moderate value of characters. Cluster-III contains high days to maturity (109.83days) that is late maturing and plant height (117.08cm). In Cluster-III there were characters such as number of effective tillers (3.13) and spike length (9.19cm) of lower value. Cluster-IV contains high spike length (10cm) and harvest index (36.26); and cluster IV contains low days to maturity (101.17days), plant height (89.17cm), number of spikelets per spike (30.77), number of grains per spike (29.6), thousand grain weight (27.78 g) and grain yield (3.75g). The maximum inter cluster was between Cluster-III and IV (436.08) followed by Cluster I and III (208.77) and Cluster V and III (188.57) (Table9).The minimum being Cluster I and II (36.74) followed by Cluster II and V (45.90). Generally this study showed that the genotypes included in this study are moderately divergent.

Table 10. Pair wise Generalized Squared Distance (D^2) among 21 bread wheat genotypes (*Triticum aestivum L.*) in five clusters at Holeta and Ginchi, combined over two locations (2011/12)

CLUSTER	I	II	III	IV	V
I		36.73913**	208.7661**	126.9046**	149.5315**
II			146.8624**	114.7859**	45.89932**
III				436.0773**	188.5736**
IV					154.4026**
V					

x^2= 16.92 and 21.67 at 5%, 1% probability level respectively

4.2.1 Principal component analysis

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma *et al.* 1998). The Eigen values are often used to determine how many factors to retain. The sum of the Eigen values is usually equal to the number of variables. The principal components of these data are given in Table 11.

Five principal components PC1 to PC5 which are extracted from the original data and having latent roots greater than one accounted nearly 86.01% of the total variation (Table 11). Suggesting these principal component scores might be used to summarize the original 10 variables in any further analysis of the data. Out of the total principal components retained, PC1, PC2, PC3, PC4 and PC5 with values of 29.85%, 17.18%, 16.01%, 12.76%, and10.2% respectively contributed more to the total variation. According to Chahal *et al*. (2002) characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character.

At (Table 11), the first principal component had high positive component loading from grain yield (0.505), number of grains per spike (0.489), number of spikelets per spike (0.441), and days to heading (0.360). The positive loading shows the presence of positive correlation trends between the components and the variables. Therefore, the above mentioned characters which load high positive contributed more to the diversity and they were the ones that most differentiated the clusters. The major contributing characters for the diversity in the second principal component (PC2) have high positive component loading from thousand grain weight (0.675) and harvest index (0.539). The major contributing characters for the diversity in the third principal component (PC3) had high positive component loading from days to maturity (0.626)and plant height (0.512); and negative loading from number of effective tillers (-0.333) and spike length

(-0.388). In principal component four (PC4) high positive component loading from spike length (0.637) and days to heading (0.394) and high negative loading from number of effective tillers (-0.550).In principal component five (PC5) high positive component loading from number of effective tillers (0.530) and days to heading (0.496); and high negative loading from number of spikelets per spike (-0.422) and number of grains per spike (-0.387). The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables. Therefore, the above mentioned characters which load high positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters.

Usually it is customary to choose one variable from these identified groups. Hence, at combined of Holeta and Ginchi (Table11), for the first group grain yield (0.505) is best choice, which had the largest loading from component ones, thousand grain weight (0.675) for the second, days to maturity period (0.626)for the third group, spike length (0.637) for the fourth group and number of effective tillers (0.529) for the fifth group.

Table11**.** Eigen vectors and Eigen values of the first five principal components of 21 bread wheat genotypes (*Triticum aestivum L.*) evaluated at combined of Holeta and Ginchi (2011/2012)

	PC1	PC2	PC3	PC4	PC5
DH	0.360	-0.212	0.120	0.394	0.496
DM	0.037	0.036	0.626	0.044	0.080
PH	0.271	-0.111	0.512	0.004	0.158
NT	0.122	-0.058	-0.333	-0.550	0.529
SL	0.026	-0.131	-0.389	0.637	-0.086
NSl	0.441	-0.255	-0.001	-0.260	-0.422
NGS	0.488	-0.227	-0.066	0.007	-0.387
TGW	0.091	0.675	0.118	-0.055	-0.256
HI	0.289	0.539	-0.106	0.237	0.157
GY	0.505	0.241	-0.203	-0.091	0.132
Eigen Value	2.985	1.718	1.601	1.276	1.020
Difference	1.267	0.117	0.325	0.256	0.297
Proportion	0.2985	0.1718	0.1601	0.1276	0.102
Cumulative	0.2985	0.4703	0.6304	0.7580	0.8600

DH = days to heading, DM = days to maturity, PH = plant height, NT = number of effective tillers, SL = spike length, NSl = number of spikelets per spike, NGS = number of grains per spike, TGW = thousand grain weight, spike, HI = harvest index, GY = grain yield

4.3. Association Studies

4.3.1 Correlation of grain yield with other traits

Grain yield is the end product of interactions of many factors known as contributing components hence it is complex trait. Understanding of the interaction of characters among themselves and with the environment has been of great use in the plant breeding. Correlation between different characters of plant could arise because of linkage, pleiotrophy or developmentally influenced functional relationships. Correlation studies provide information on the nature and extent of association between any two pairs of metric characters. From this it could be possible to bring about genetic up gradation in one character by selection of the other pair.

In general, the genotypic correlation coefficient values were higher than the phenotypic values. This indicated that strong intrinsic associations were some what masked at phenotypic level due to environmental effects.

At Holeta & Ginchi and combined over locations genotypic and phenotypic correlations for all possible combinations for traits under study are presented in Tables 12 and 13, respectively. At both locations grain yield had positive non significant correlation with thousand grain weights at both genotypic and genotypic levels. This non significant correlation between yield and 1000–grain is in harmony with the findings of Ihsanaullah *et al.* (2001) in wheat.

.Phenotypic (r_p) and genotypic (r_g) correlation estimates between grain yield and the various characters are presented in Table 13 for the two locations combined. At genotypic and phenotypic levels grain yield had highly significant positive correlations with number of grains per spike (r_g=0.615**, r_p=0.584**). It had highly significant and significant association with harvest index (0.671** and 0.533*) at genotypic and phenotypic levels. The same character had also positive and significant correlation with number of spikelets per spike (r_g=0.509*) at genotypic level, and positive and highly significant relationship at phenotypic level (r_p=0.565**). Grain yield had positive and

significant correlation with days to heading (r_g=0.454*) only at genotypic level and at phenotypic level no such association was noticed indicating influence of environment on association. These results agree with the report of Inamullah *et al.* (2006) in bread wheat. Grain yield have negative and non significant correlation with days to maturity (r_g= -0.095, r_p= -0.0760). Similar report, have come from Nirmala and Jha (1996) in segregating population of bread wheat. In contrast, Jadhav (1994) noticed positive and significant correlation of days to maturity with grain yield. Yield per plant had positive non significant correlation with plant height (r_g=0.217, r_p=0.175), number of effective tillers (r_g=0.42, r_p=0.379) and spike length (r_g=0.064, r_p=0.028) at both genotypic and genotypic levels. Khaliq *et al.,* (2004) reported similar results.

Table12. Phenotypic (r_p) and genotypic (r_g) correlation coefficient of the thousand grain weight character in 21 bread wheat genotypes grown at Holeta and Ginchi (2011/12)

Locations	Traits	DH		DM		PH		NT		SL		NSl		NGS		TGW		HI		GY	
		r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p
Holeta	TGW	-0.266	-0.265	0.224	0.223	0.071	0.066	-0.027	-0.027	-0.098	-0.098	0.047	0.046	0.065	0.042	1	1	0.371	0.368	0.194	0.193
Ginchi	TGW	-0.296	-0.287	0.205	0.195	-0.093	-0.066	-0.225	-0.221	-0.164	-0.164	-0.103	-0.099	-0.083	-0.078	1	1	0.527*	0.516*	0.424	0.414

Tabular r=0.433 at 5%; r=0.549 at 1%

DH = days to heading, DM = days to maturity, PH = plant height, NT = number of effective tillers, SL = spike length, NSl = number of spikelets per spike, NGS = number of grains per spike, TGW = thousand grain weight, spike, HI = harvest index, GY = grain yield

Table 13. Phenotypic (r_p) and genotypic (r_g) correlation coefficient of the 10 characters in 21 bread wheat genotypes combined over the two locations Holeta and Ginchi (2011/12)

		DH	DM	PH	NT	SL	NSl	NGS	HI	GY
DH	r_g	1	0.217	0.444*	0.05	0.212	0.245	0.463*	0.305	0.454*
	r_p	1	0.211	0.341	0.053	0.227	0.18	0.282	0.244	0.344
DM	r_g		1	0.315	-0.174	-0.213	0.018	-0.027	-0.112	-0.095
	r_p		1	0.259	-0.153	-0.205	0.013	-0.017	-0.084	-0.076
PH	r_g			1	-0.132	-0.264	0.346	0.337	0.072	0.217
	r_p			1	-0.026	-0.218	0.167	0.111	0.104	0.175
NT	r_g				1	-0.132	0.148	0.024	-0.049	0.42
	r_p				1	-0.131	0.161	0.042	-0.021	0.379
SL	r_g					1	-0.083	0.17	0.036	0.064
	r_p					1	-0.046	0.105	0.004	0.028
NSl	r_g						1	0.902**	0.009	0.509*
	r_p						1	0.848**	0.039	0.565**
NGS	r_g							1	0.2	0.615**
	r_p							1	0.085	0.584**
HI	r_g								1	0.671**
	r_p								1	0.533*
GY	r_g									1
	r_p									1

Tabular r=0.433 at 5%; r=0.549 at 1%

DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, SL=spike length, NSl=number of spikelets per spike, NGS=number of grains per spike, TGW=thousand grain weight, spike, HI=harvest index, GY=grain yield

4.2.2 Correlation among other traits

4.2.2.1 Genotypic and phenotypic correlation

At Holeta (Table12), thousand grain weights had positive and non significant correlation with all the characters. At Ginchi (Table12), thousand grain weight had positive and significant correlation with harvest index (r_g=0.527*, rp=0.516*). It had non significant correlation with the rest of the characters. This result was in agreement with the finding of Jat and Dhakar (2003) who reported positive and significant association of grain yield with 1000-grain weight.

At combined location (Table13), days to heading had positive and significant genotypic correlation with plant height (r_g=0.444*) and number of grains per spike (r_g=0.463*). It had non significant correlation with the rest of the characters at genotypic and phenotypic levels.

Plant height had negative non significant correlation with number of effective tillers and (r_g=-0.153, r_p=-0.132) and spike length (r_g= -0.205, r_p=-0.264) at both genotypic and phenotypic levels. It had positive non significant correlation with number of spikelets per spike (r_g=0.346, r_p=0.167), number of grains per spike (r_g=0.337, r_p=0.111) and harvest index (r_g=0.072, r_p=0.104) at both genotypic and phenotypic levels. This result contradicts with the finding by Lad *et al.* (2003), who reported positive significant association between plant height and number of grains per spike.

Number of spikelets per spike had positive and highly significant correlation with number of grains per spike (r_g=0.902**, r_p=0.848**) at both phenotypic and genotypic levels. Number of spikelets per spike had non significant correlation with the rest of the traits. There were non significant associations among the rest of the traits considered in this study.

4.2.3. Path coefficient analysis

The correlation coefficient indicated the relationship existing between pair of characters. But, a dependent character is an interaction of product of many mutually associated component characters and change in any one component will disturb whole network of cause and effect system. The path coefficient analysis, a statistical device developed by Wright (1921), which takes into account the cause and effect relationship between the variables which is unique in partitioning the association into direct and indirect effects through other dependent variables. The path coefficient analysis also measure the relative importance of causal factors involved. This is simply standardized regression analysis, wherein total correlation value is subdivided into causal scheme. Yağdı et al, (2009).emphasized the importance of path diagram which facilitates the understanding of the nature of cause and effect system. The path analysis suggested by Dewey and Lu (1959) helps to resolve these correlations further and throws more light on the way in which component traits contribute towards specifically identifying important component traits. Estimates of direct and indirect effects of yield contributing characters on grain yield per plant using genotypic correlation are presented in Table 14 and 15 for Holeta & Ginchi and combined location, respectively.

Genotypic path coefficient analysis at Holeta (Table 14) and Ginchi, showed that thousand grain weight (0.16747, 0.56775 in that order) had positive direct effect on grain yield. The correlation coefficients of these characters were (0.194 and 0.424) which are equivalent to the direct effects. This shows the correlation explains the true relationship.

Table 14. Estimates of direct (bold) and indirect (off bold) at genotypic level of thousand grain weight character on grain yield in 21 bread wheat genotypes tested at Holeta and Ginchi (2011/12)

location	Trait	DH	DM	PH	NT	SL	NSl	NGS	TGW	HI	rg
Holeta	TGW	-0.06008	-0.05063	0.01693	-0.00825	-0.0058	0.05581	-0.03373	**0.16747**	0.11239	0.194
Ginchi	TGW	-0.062	-0.0043	0.01803	-0.095	0.01469	-0.0154	-0.045	**0.56775**	0.04551	0.424

Holeta Residual effect=0.2646565
Ginchi Residual effect=0.2125289

DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, SL=spike length, NSl=number of spikelets per spike, NGS=number of grains per spike, TGW=thousand grain weight, spike, HI=harvest index, GY=grain yield

Table 15. Estimates of direct (bold diagonal) and indirect (off diagonal) at genotypic level of 10 characters on grain yield in 21 bread wheat genotypes combined over the two locations, Holeta and Ginchi (2011/12).

	DH	DM	PH	NT	SL	NSl	NGS	HI	rg
DH	**-0.03414**	0.01326	0.04393	0.02368	0.01793	0.01075	0.19008	0.18884	**0.454***
DM	-0.0074	**0.06119**	0.03119	-0.08205	-0.01799	0.00077	-0.011	-0.06938	-0.095
PH	-0.01514	0.01927	**0.09903**	-0.06208	-0.02227	0.01518	0.1381	0.04461	0.217
NT	-0.00172	-0.01066	-0.01305	**0.47112**	-0.01112	0.00651	0.00964	-0.03027	0.42
SL	-0.00725	-0.01304	-0.02613	-0.06208	**0.08441**	-0.00365	0.06992	0.02216	0.064
NSl	-0.00836	0.00108	0.03422	0.06986	-0.00701	**0.04391**	0.36983	0.00583	**0.509***
NGS	-0.01582	-0.00164	0.03335	0.01108	0.01439	0.0396	**0.41013**	0.12351	**0.615****
HI	-0.01042	-0.00686	0.00714	-0.02305	0.00302	0.00041	0.08188	**0.61862**	**0.671****

Residual effect=**0.3270564**

DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, SL=spike length, NSl=number of spikelets per spike, NGS=number of grains per spike, spike, HI=harvest index, GY=grain yield

Harvest index that had positive and highly significant correlation (0.671) with grain yield had the highest positive direct effect (0.61862).The magnitude of the direct effect was equivalent to that of genotypic correlation coefficient. This justifies that the correlation explains the true relationship and direct selection through this trait will be effective. The result of the highest direct positive effect of harvest index on grain yield is supported by works of Gupta *et al. (*2002).

Days to heading had negative direct effect. The positive correlation it had with grain yield was positive and significant. The indirect effects via other traits were favorable. Hence the correlation with grain yield it had was largely due to the indirect effects. More over, even if it had positive association with grain yield its direct effect was negative, indicating that early heading is desirable.

Days to maturity had positive direct effect. The genotypic correlation with grain yield it had was negative. This implies restricted simultaneous selection has to be followed, restriction are to be imposed to nullify the undesirable indirect effects inured to make use of the direct effects of this trait.

Number of effective tillers and spike length which also had positive correlation with grain yield had positive direct effect. The respective indirect effects of these characters through other characters were negative. Hence, the correlation coefficient they had with grain yield was largely their direct effects.

Number of grains per spike which also had highly significant and positive correlation with grain yield had the third highest and positive direct effect. The indirect effects via other characters were mostly positive. Therefore, the association it had with grain yield was because of the indirect effects.

Number of spikelets per spike and plant height had positive direct effects. The genotypic correlation they had with grain yield were positive. Their indirect effect via other characters was mostly positive and negligible therefore, their positive correlation coefficient with grain yield was mainly due to their direct effects.

The residual effects of the present study were 0.2646565, 0.2125289 and 0.3270564 at Holeta, Ginchi and combined over the two locations, respectively which means the characters in the path analysis expressed the variability in grain yield by 73.53435%, 78.74711% and 67.29436%, respectively.

5. SUMMARY AND CONCLUSSIONS

The progress of crop improvement program depends on the choices of material, the extent of genetic variability present and the knowledge of quantitative characters with grain yield and among themselves. The present study comprises 21 bread wheat genotypes that were evaluated at two locations, namely Holeta and Ginchi with the objective of assessing the genetic variability and character association for 10 characters.

The analysis of variation for each location showed the genotypes were highly significantly different at ($P<0.01$) for 1000-grain weight. The combined analysis of variance across the two locations showed that the genotypes were highly significant for all the characters. The ranges of mean values for most of the characters were larger showing the existence of variations among the tested genotypes. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were generally high at the combined analysis over locations.

According to Deshmuk *et al*., (1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Accordingly at moderate PCV and GCV were recorded for thousand grain weight at both Holeta and Ginchi locations. At the combined location high PCV and GCV were recorded for number of effective tillers and grain yield per plant, moderate PCV and GCV were recorded for days to heading, plant height, number of spikelets per spike, number of grains per spike and harvest index. The lowest PCV values were observed at the combined location in days to maturity and spike length.

According to Robinson *et al.* (1949) heritability values are categorized as high (≥60%), moderate (30-60%) and low (0-30%). Based on these, the highest heritability values were recorded for all traits at each location as well as at the combined location.

Genetic advance as per cent mean was categorized as high (≥20%), moderate (10-20%) and low (0-10%) (Johnson *et al*, 1955). Accordingly, the expected mean as percent of mean ranges from 12.32% for days to maturity and 55.921% for grain yield per plant at combined location. At each location thousand grain weights had 30.645% genetic advance as percent of mean.

The cluster analysis based on D^2 analysis on pooled mean of genotypes classified the 21 genotypes into five clusters, which makes them to be moderately divergent. There was statistically significant difference between all of the clusters. The principal component analysis extracted five principal components PC1 to PC5 from the original data and having Eigen value greater than one accounting nearly 86.00% of the total variation. Characters with largest absolute value closer to unity within the first principal component such as days to heading, number of spikelets per spike, numbers of grains per spike and grain yield per plant influence the clustering. The differentiation of the genotypes into different clusters was because of relatively high contribution of these characters. Therefore, the above mentioned characters which load high positive contributed more to the diversity and they were the ones that most differentiated the clusters.

At Ginchi, grain yield was positively and significantly correlated with number of harvest index. At Holeta, grain yield was negative non significantly correlated with days to heading, number of effective tillers and spike length, and positive non significantly correlated with rest traits. Combined over the two locations, grain yield was positively and significant correlated with number of grains per spike, number of spikelets per spike and harvest index both at genotypic and phenotypic levels. Grain yield was correlated with days to heading positively and significantly at genotypic level only. By selecting for these traits showing positive and significant correlation coefficient with grain yield there is a possibility to increase grain yield of bread wheat.

Path coefficient analysis based on grain yield as a dependent variable showed that harvest index had the highest positive direct effect at genotypic level when the two locations are combined. Number of effective tillers also showed positive direct effect in the analysis combined over the two locations. Since harvest index and number of effective tillers had positive correlation with grain yield in the process of selection much attention could be given to them as these characters are helpful for indirect selections.

The following conclusions can be drawn from the present study:
There were differences in the performance of the genotypes as there were statistically supported significant differences among genotypes for most of the 10 characters at both locations and relatively wide range of the mean values for most of the characters. Nevertheless, the level of the genetic differences for many traits, including grain yield, may not be sufficient to expect progress in selection. Therefore, in order to improve the diversity of bread wheat in Ethiopia, subsequent crossing program aimed at developing bread wheat varieties of better diversity by crossing between highly divergent genotypic varieties needs to be carried out.

Harvest index showing positive and significant correlation and positive direct effect at Ginchi and combined over the two locations, it will be a useful trait for direct selection to increase grain yield.

Number of grains per spike, number of spikelets per spike and number of tillers showed high heritability, better genetic advance as percent of mean, positive correlation coefficient and direct effect on grain yield, this character may be included as component of indirect selection.

Days to heading had negative direct effect and positive significant correlation with grain yield. The correlation with grain yield it had was largely due to the indirect effects. This shows that early heading genotypes should be selected.

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7. APPENDICES

Appendix-I Mean value of thousand grain weight character of 21 genotypes grown at Holeta and Ginchi 2011/12.

		Location	
		Holeta	Ginchi
	GENOT YPES	TGW	TGW
1	Danda'a	30.2m	30.2gh
2	Kakaba	37.3d	37.3c
3	Hawi	43a	43a
4	Tusei	26s	26l
5	Pavon76	32.5667i	32.5f
6	ET13.A2	31.2j	31.2fg
7	K6295-4A	37.8c	37.8c
8	ETBW5483	30.7l	30.7g
9	ETBW5496	31.1k	31.1fg
10	Digelu	36.4e	36.4cd
11	Sofumar	29o	29hij
12	Mada-Walabu	26.8q	26.8kl
13	Tay	34.9g	28.6ij
14	Senkegna	34.9g	34.9de
15	Gossay	26.7r	26.7kl
16	Menze	34.6h	34.6e
17	Bolo	26.7r	26.7kl
18	Alidero	35.3f	35.3de
19	Denkenesh	41.3b	41.3b
20	Tossa	30n	30ghi
21	Kulkulu	27.7667p	27.8jk
	MEAN	32.5825	32.28
	CV%	0.2	2.7
	LSD (5%)	0.08316	1.44

Legend: TGW = Thousand grain weight,

Appendix-II Mean value of 9 characters of 21 genotypes combined over two locations (Holeta and Ginchi) 2011/12

	GENOTYPES	DH	DM	PH	NT	SL	NSl	NGS	HI	GY
1	Danda'a	79c	110.167c	92.5efghi	3.9g	9.3i	36.233ef	36.433i	28.265g	4.7c
2	Kakaba	65.667k	106.167f	89.167hi	2.9q	9.1k	36.133ef	36.267i	28.467g	3.9g
3	Hawi	65.5kl	106.5f	86.667i	3.8i	10c	34.3ghi	34.333kl	30.225ef	4.65c
4	Tusie	72.333g	101.167hi	90.833fghi	3.6j	10c	40.55cd	40.45d	26.995h	3.8gh
5	Pavon76	68.333j	106.167f	91.667efghi	4.8b	9.4h	35.217fgh	31.75n	23.835j	4.25f
6	ET13.A2	79c	110.167c	118.333a	3.05o	8.583n	45.133b	42.433b	27.86g	4.35df
7	K6295.4A	71.333h	109.5cd	115.833a	3.2n	9.8d	35.25fgh	34.567k	30.955e	4.6cde
8	ETBW5483	69.833i	100.167i	92.5efghi	4.9a	9.5g	40.633cd	39.2ef	32.07d	5.85b
9	ETBW5496	82.5a	106.167f	97.5bcde	3.2n	10.5a	29.5k	38.5g	32.405cd	4.75c
10	Digelu	81.167b	106.167f	99.167bcd	4.3e	9.6f	47a	46.667a	36.34a	6.85a
11	Sofumar	68.333j	106.167f	97.5bcde	4.4d	8.6n	27.733l	26.833p	28.168g	3.55h
12	Mada-Walabu	68.5j	110.167c	95.833cdefg	4.1f	9l	40.117d	39f	25.255i	3.7gh
13	Tay	76.333e	108.5de	103.333b	4.5c	9.7e	35.883efg	35.2j	28.13g	4.6cd
14	Senkegna	77.667d	118.5a	96.667cdef	3.5k	9.5g	33.04i	32.633m	29.56f	4.35f

	GENOTYPES	DH	DM	PH	NT	SL	NSl	NGS	HI	GY
15	Gossay	74.167f	114.167b	95defgh	3p	10.3b	41.133cd	39.583e	24.66i	3.783gh
16	Menze	74.833f	103.5g	99.167bcd	3.833h	9.5g	41.717c	41.417c	30f	5.95b
17	Bolo	74.333f	101.167hi	100.833bcd	3.3m	10c	37.35e	37.117h	27.595gh	4.4g
18	Alidero	76.167e	110c	101.667bc	3.3m	8.7m	34.133hi	33.833l	33.065c	4.85c
19	Denknesh	62.833m	108.167e	91.667efghi	2.8r	9.2j	34.8fgh	34l	34.373b	4.3f
20	Tossa	64.667l	102.167h	90ghi	2.8r	9.6f	31.433j	31.817n	25.095i	3.1i
21	Kulkulu	77.333d	101.167hi	89.167hi	3.35l	10c	30.767jk	29.6o	32.76cd	3.75gh
	MEAN	72.849	106.952	96.905	3.644	9.518	36.574	36.268	29.337	4.478
	CV%	1.060	0.862	4.636	0.342	0.413	3.3323	1.1433	2.362	4.439
	LSD (5%)	0.887	1.059	5.159	0.014	0.045	1.434	0.476	0.796	0.228

Legend: DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, NSl=number of spikelets per spike, NGS=number of grains per spike, SL=spike length, HI=harvest index, GY=grain yield

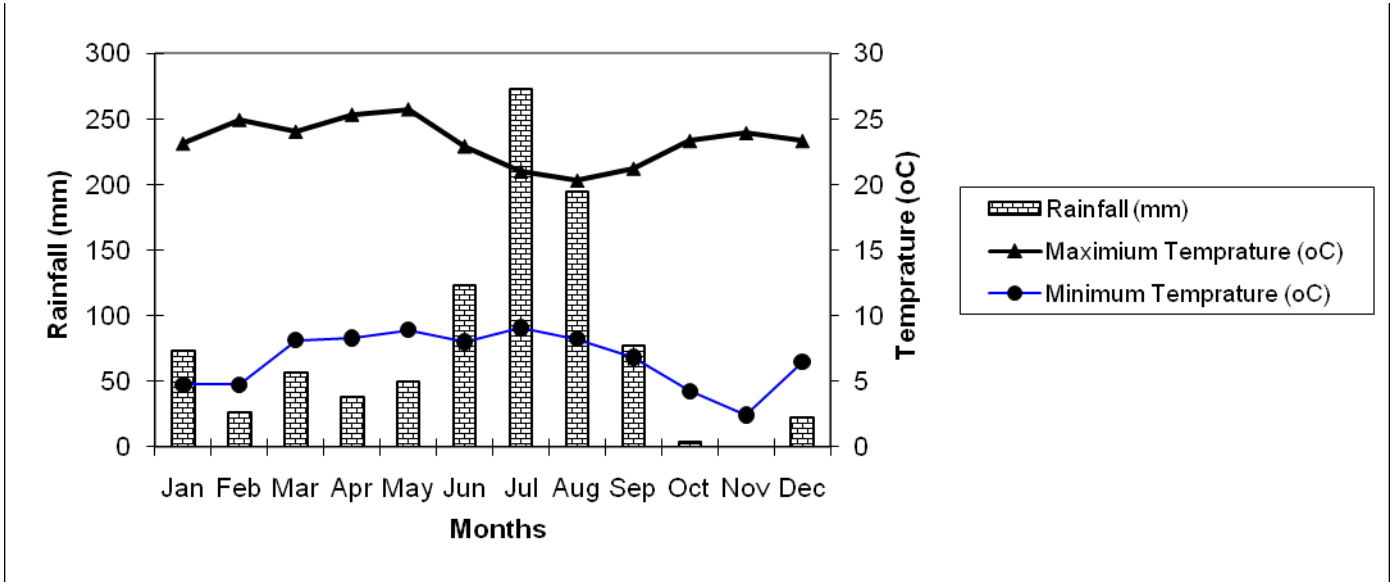
Appendix III. Analysis of variance (mean squares) for 10 characters of 21 bread wheat genotypes grown at Holeta and Ginchi (2011/12).

	LOCATION							
	HOLETA				GINCHI			
	REPLICATION	GENOTYPES	ERROR	CV%	REPLICATION	GENOTYPES	ERROR	CV%
TRAIT	D.F=2	D.F=20	D.F=40		D.F=2	D.F=20	D.F=40	
DH	3.349ns	97.449**	0.449	0.902	1.000ns	105.443**	0.75	1.213
DM	10.111**	62.944**	0.411	0.555	10.349ns	63.250**	0.400	0.642
PH	26.587ns	249.680**	12.004	3.363	302.78ns	211.35**	24.44	5.446
NT	0.200**	1.480**	0.0002	0.343	0.200**	1.607**	0.0002	0.349
SL	0.181**	1.0265**	0.001	0.350	0.122**	0.737**	0.0019	0.457
NSl	1.656ns	100.350**	0.902	2.714	34.519ns	134.619**	0.893	2.477
NGS	2.006**	95.537**	0.104	0.893	3.281ns	150.786**	0.193	1.205
TGW	0.146	70.915**	0.003	0.155	5.762ns	72.155**	0.762	2.7
HI	0.951ns	48.118**	0.302	1.824	13.872**	51.75**	0.460	2.376
GY	0.1546**	2.3576**	0.002	1.150	0.724ns	3.917**	0.073	5.081

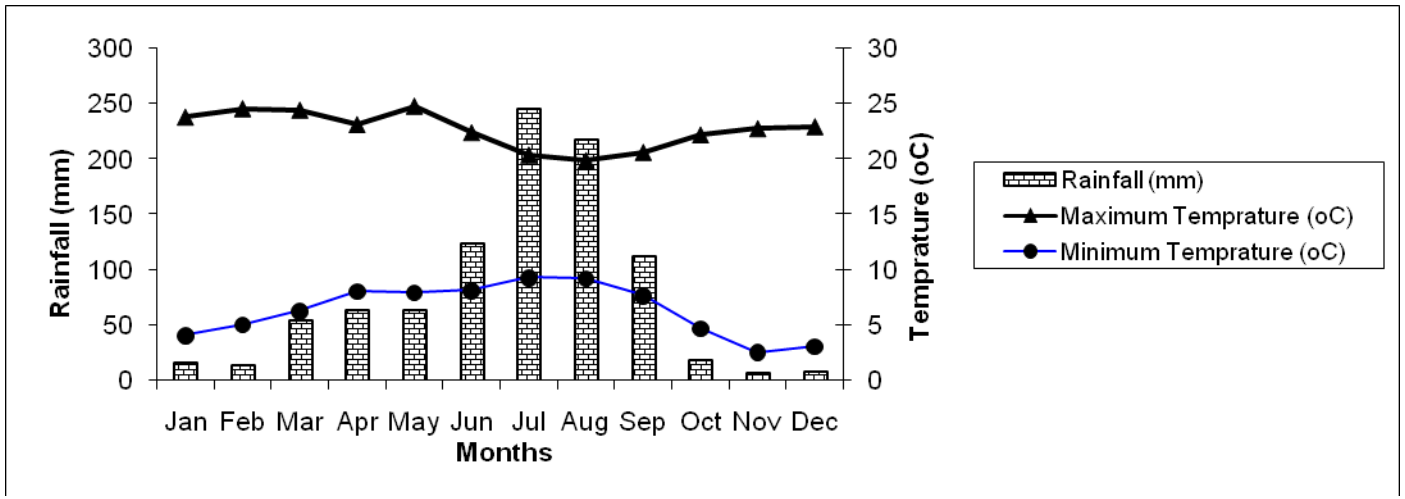
Legend: DH=days to heading, DM=days to maturity, PH=plant height, NT=number of effective tillers, NSl=number of spikelets per spike, NGS=number of grains per spike, SL=spike length, TGW=thousand grain weight, HI=harvest index, GY=grain yield

APPENDIX FIGURE

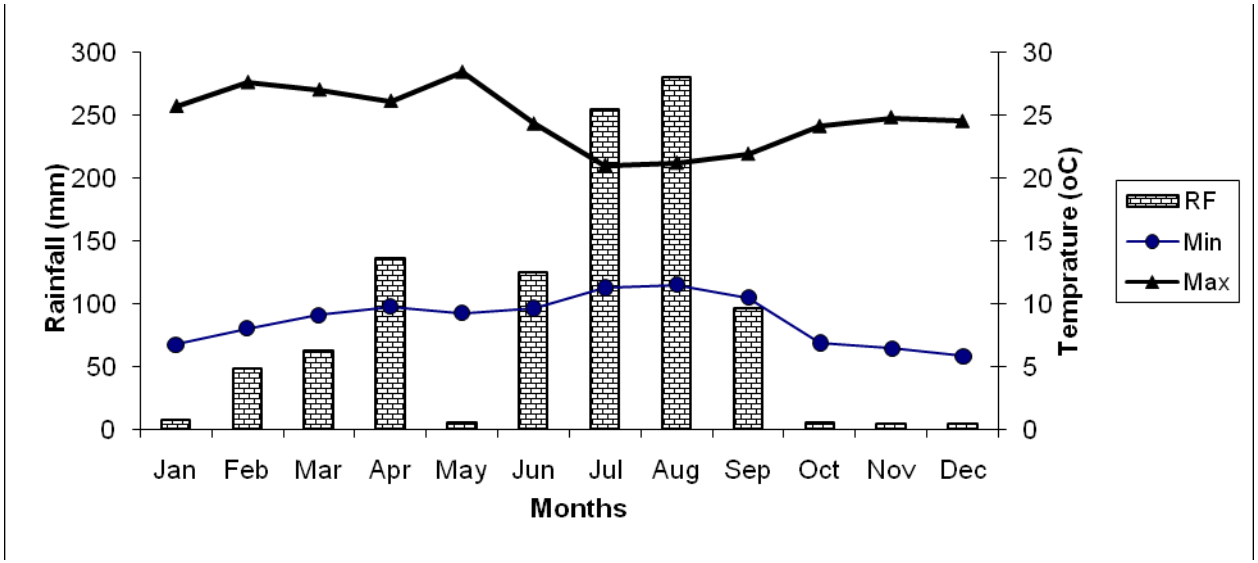
Appendix Figure I. Monthly total rain fall (mm) and average maximum & minimum temperatures (C^o) of Holeta Research Center, 2011/12.



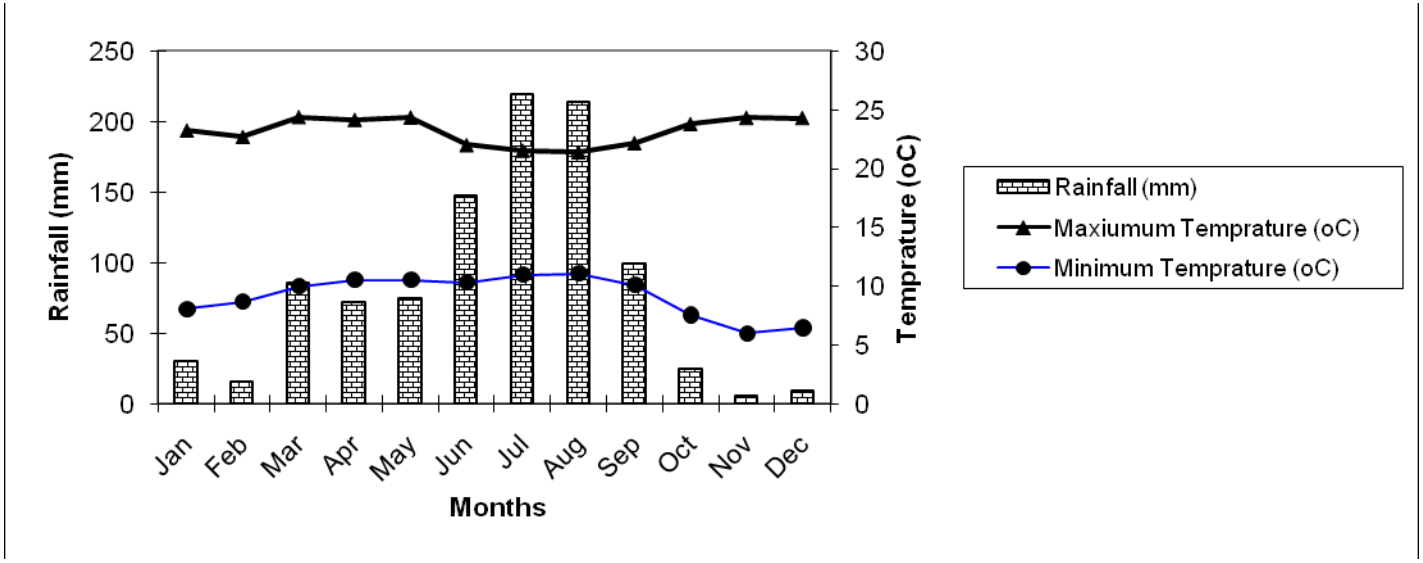
Appendix Figure II. Monthly average rainfall (mm) and average maximum and minimum temperature (C^{o}) of Holeta Research Center, (2000-2010).



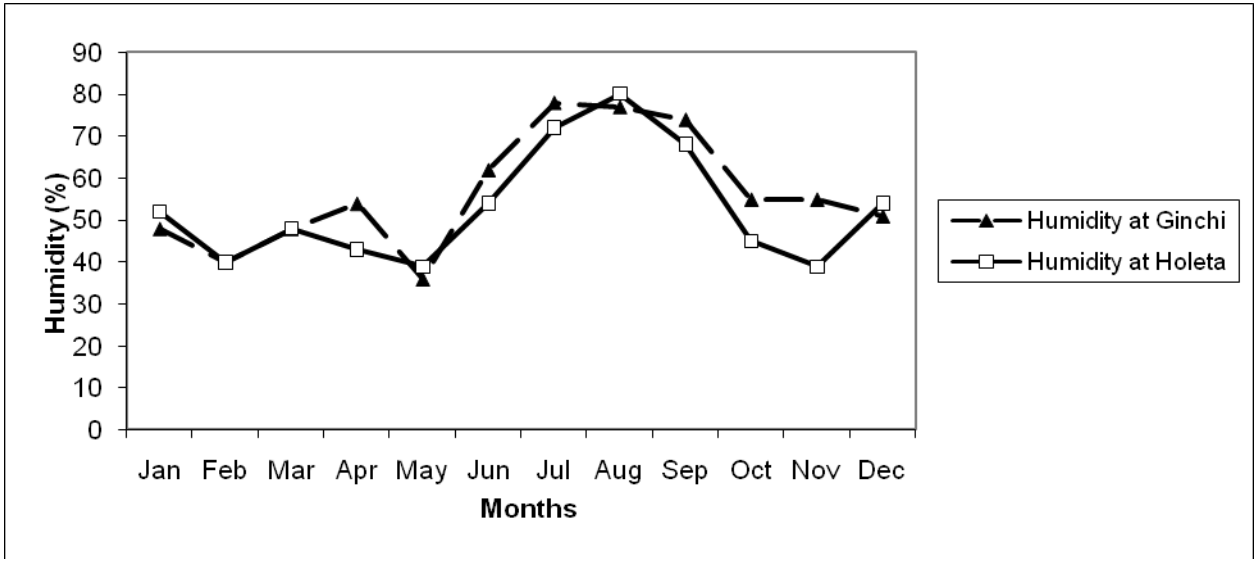
Appendix Figure III. Monthly total rain fall (mm) and average maximum & minimum temperatures (C^{o}) of Ginchi Research Sub-Center, 2011/12.



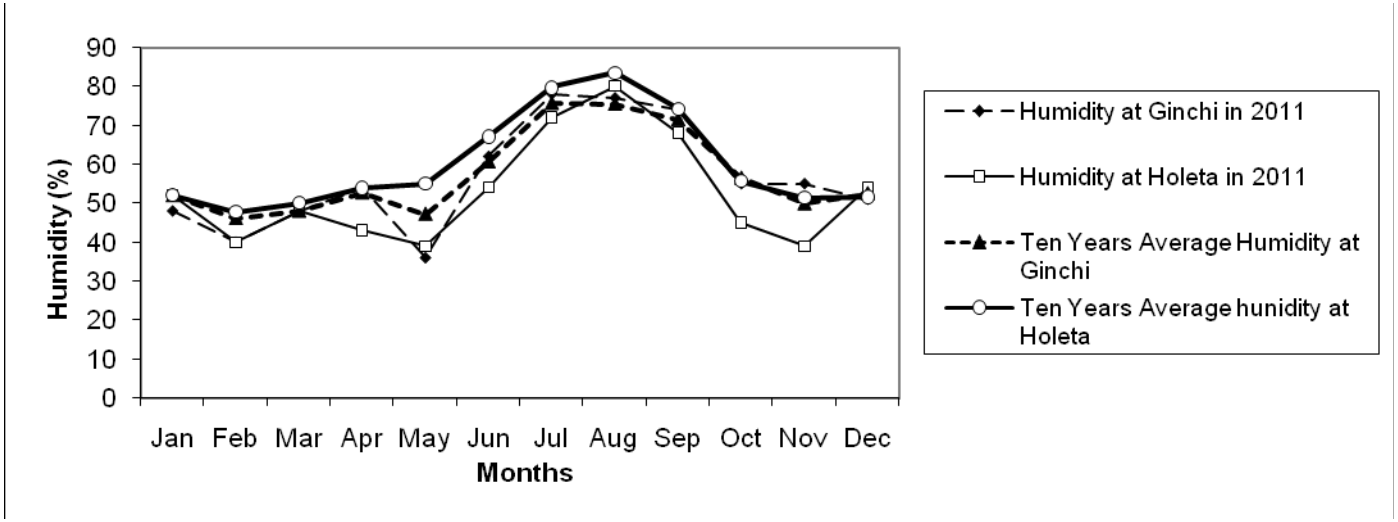
Appendix Figure VI. Monthly average rainfall (mm) and average maximum and minimum temperature (C^{o}) of Ginchi Research Sub-Center, 2011/12.



Appendix Figure V. Monthly average of relative humidity (%) of Holeta Research Center and Ginchi Research Sub-Center, 2011/12.



Appendix Figure VI. Monthly average of 2011 relative humidity (%), and monthly average of ten years relative humidity (%) of Holeta Research Center and Ginchi Research Sub-Center, 2001-2010.



Appendix Figure VII. Figure showing the clusters to which the genotypes belong and average distance between clusters (2011/12).