Addis Ababa University

College of Natural and Computational Sciences

Department of Microbial, Cellular and Molecular Biology

Phenotypic, Biochemical and Molecular Diversity of Hexaploid Wheat (*Triticum aestivum* L.) Genotypes in Ethiopia

A PhD Dissertation Submitted to the School of Graduate Studies, Department of Microbial, Cellular, and Molecular Biology, Addis Ababa University, in Partial Fulfilment of the Requirements for the Degree of Doctor of Philosophy in Biology (Applied Genetics)

By

Abebe Tiruneh Tegegne

March/2019
Addis Ababa, Ethiopia

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SCHOOL OF GRADUATE STUDIES

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Dr. Kassahun Tesfaye **(Internal Examiner)** _____

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Dr. Gurja Belay **(Chairman)** _____

DECLARATION

I declare that the dissertation I hereby submitted for the Degree of Doctor of Philosophy (PhD) in Biology (Applied Genetics) to the School of Graduate Studies, Addis Ababa University, is my own independent work and has not previously been submitted by me or anybody else at Addis Ababa University or elsewhere.

To my knowledge, the materials obtained from other groups have been duly acknowledged in the dissertation.

	Name	Signature	Date
PhD Candidate:	Abebe Tiruneh	_____	_____

The PhD dissertation was done under the close supervision of the following supervisors and confirmed to be defendable

Supervisors:	Dr. Kifle Dagne	_____	_____
	Dr. Tileye Feyisa	_____	_____

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ACRONYMS

AAU	Addis Ababa University
AMOVA	Analysis of Molecular Variance
ANOVA	Analysis of Variance
ARARI	Amhara Region Agricultural Research Institute
AFLP	Amplified Fragment Length Polymorphism
BY	Biomass yield
CT	Correction Term
CGIAR	Consultative Group on International Agricultural Research
CSA	Central Statistical Agency, Ethiopia
CV	Coefficient of Variation
GY	Grain Yield
H	Genetic Diversity
HI	Harvest Index
HLW	Hectoliter Weight
I	Shannon information index
IBC	Institute of Biodiversity Conservation
ISSR	Inter Simple Sequence Repeat
Mo	Moisture Content
NJ	Neighbor-Joining
NPL	Number of Polymorphic Loci
NSB	Number of Storable Bands
NSLP	Number of Spike-lets per Plant
NSS	Number of Seeds per Spike
NT	Number of Tillers
NVT	National Variety Trial
PAGE	Poly Acrylamide Gel Electrophoresis
PH	Plant Height
PVT	Pre-National variety Trial
SSR	Simple Sequence Repeats
Sta	Starch Content
Zele	Zeleny/SDS volume content
TGW	Thousand Grain Weight
WGC	Wet Gluten Content
UPGMA	Unweight Pair Group Method with Arithmetic Mean
WHO	World Health Organization

ABSTRACT

Hexaploid Wheat (*Triticum aestivum* L.) is one of the most important food cereals worldwide. World population is set to increase by 2.6 billion in 2050. Ethiopia is one of the countries expected for an increase in food production. Few studies were on genetic diversity and in adequate evaluation of bread wheat genotypes. The objective of the project was to study genetic diversity of bread wheat genotypes using phenotypic, SSRs, good baking quality, seed storage protein performance across environments.

For phenotypic genetic diversity study, 121 bread wheat genotypes, arranged in 11x11 simple lattice design, at 3 locations of Ethiopia using 11 parameters were studied; there were highly significant difference among the genotypes in all traits at individual locations. Abola (9.77), Menze (9.69) and ETBW6696 (9.36) at Adet, Tusie (9.95), ETBW6845 (9.93) and ETBW6696 (9.90) at Debre Tabor and ETBW6114 (9.99), ETBW6212 (9.96) and TBW7693 (9.92) at Kulumsa were the best performing for grain yield in tons/ha.

Bread making quality of 121 bread wheat genotypes was assessed based on grain quality characteristics using seven parameters by NIRS analysis, and flour quality of fifty bread wheat genotypes based on SDS PAGE electrophoresis banding patterns. All characteristics of grain quality showed significant differences, higher PCV than GCV values, high heritability (>80%) in all genotypes; hence, selection could be effective for different quality characters or for inclusion in crossing program or creating variability in bread wheat genotypes. According to the results of flour SDS PAGE analysis, maximum bands (8) revealed by genotypes 8, 9, 13, 18, 46 & 48 and minimum (1) by genotype 34 using gliadin markers. Maximum bands (4) revealed by genotypes 3, 18, 26 &

46 and none band by genotype 4 using HMW GS markers. Maximum bands (4) revealed in the genotypes 10, 30, 37, 41, 43 & 48 and none band revealed in genotypes 17 &18 using LMW GS markers. Hence, flour containing large number of bands revealed by gliadin and glutenin (HMW- and LMW-GS) markers is generally of better quality than low contents for the preparation of bread.

Seed storage protein diversity of fifty selected bread wheat genotypes using SDS PAGE based on MAF and PIC values were evaluated; the mean value of MAF was highest at Adet followed by Kulumsa and lowest at Debre Tabor and the mean value of PIC was highest at Debre Tabor followed by Kulumsa and lowest at Adet for gliadin and glutenin (HMW- and LMW GS) loci. There was no environmental fluctuation for both quality and seed storage protein; hence, the composition of quality and seed storage protein traits are more dependent on genotypic than environmental factors.

SSR marker analysis of 96 genotypes showed highly informative percentage of polymorphic loci, an effective number of alleles and mean expected heterozygosity, and Shannon's information index. Nei's gene diversity among the groups showed a medium degree of variation. AMOVA showed allelic diversity to individual genotypes but not among groups, indicates there was no sharp distinct clusters among the groups which attributed to gene flow and the reproductive biology of the crop.

This research is of great interest and is in line with the current National Wheat Program. It will contribute to the increasing of food security, improve productivity and profitability of wheat farming and sustain natural resources in Ethiopia.

Key words: Genetic diversity, SSRs, *Triticum aestivum* L., Genotypes.

1. INTRODUCTION

1.1. Background and Justification

Wheat is one of the most important cereals world-wide and it is grown in many areas (Curtis, 2002). A rapid increase in global wheat production was realized over the last five decades, mainly due to increased productivity rather than an expansion of the cultivated area. The average global yields rose from 1 t/ha in the 1950s to about 2.5 t/ha at the turn of the 21st century (Curtis, 2002).

It is the world's leading source of cereal proteins in human food, with higher protein content than maize or rice. In total, 16% and 26% of total dietary calories in developing and developed countries, respectively, come from wheat (Ortiz *et al*., 2008). Its grain is a staple food used to make flour for leavened, flat and steamed breads, biscuits, cookies, breakfast cereal, noodles, biofuel, and for fermentation to make alcoholic beverages such as beer and liquors (Tsegaye & Berg, 2007).

In Sub-Saharan Africa, Ethiopia ranks 2nd next to South Africa, in terms of total wheat area and production. According to (CSA, 2015), wheat is an important cereal crop in Ethiopia, ranking third in total production next to teff and maize. It is largely grown in the highlands of the country constituting roughly 20-30% of the annual cereal production and playing an appreciable role of supplying the population with carbohydrates, proteins and minerals (Hayatullah K *et al.*, 2000).

Bread wheat is one of the staple foods and the main groups of calories in major producing regions of Ethiopia. It accounts for a little more than 20 percent of the total calorie supply. Sixty percent of the

total production is used for household consumption, 20 percent is sold to the market, while the balance is used for seed, in-kind wages, animal feed and other uses. Ethiopian wheat production self-sufficiency is only 75 percent while the remaining 25 percent is imported for trade or through food aid. The share of total cereal consumption has increased by 20% in recent year, making it the second most consumed cereal in Ethiopia after corn (USDA, 2016). Therefore, to meet the countries self-sufficiency and growing demand from manufacturing industries and increasing the yield potential is an important solution in the long-run. Furthermore, increasing wheat production is important to the economic stability and food security of Ethiopia.

Genetic diversity is one of the key factors for the improvement of many crop plants including wheat. Plant breeders rely on the availability of genetic diversity during selection in cultivar development. The efficiency of genetic gain by selection can be improved if the patterns of genetic diversity within a group of breeding lines are known. Genetic similarity/distance estimates among genotypes are helpful in the selection of parents to be used in a breeding program (van Becelaere *et al*. 2005). Genotypes developed with wider genetic base may be helpful in enhancing the yield under various agro-climatic conditions (Asif *et al*., 2005). Diverse genetic base may also resist the spread of diseases (Zonghua *et al*., 2000) in approved genotypes. The study of genetic diversity is also important for genotypes identification, proper purity maintenance, for the implementation of plant genotype protection rights and export under WTO regulations.

Agro-phenotypic characterization (phenotyping) is a first step towards diversity and conservation of plant genetic regroups. It provides greater complementary information to molecular markers

characterization (Gomez-Becerra *et al.*, 2010). Agro-phenotypic criteria such as the color and structure of seeds, days to heading, days to maturity and heading, plant height, grain yield, etc. can be used to study the variation among the hexaploid wheat genotypes. For successful diversity and conservation, knowledge on the nature and extent of the available variation is important. Different studies have dealt with the variability in the Ethiopian wheat for agronomic and phenotypic characters (Abinasa *et al*., 2011). In most cases the studies showed the presence of variation within and between groups and geographical regions.

Biochemical analysis is the investigation of variation that may exist within and between groups in wheat by the use of biochemical markers that involve the nutritional contents of the wheat like hectoliter weight, thousand grain weight, grain protein percentage, zeleny sedimentation, gluten content, grain starch percentage, grain hardness, and the seed storage proteins and isozymes (Takata *et al*., 2007). This information can be used to measure group subdivision, genetic diversity, gene flow, genetic structure of species, and comparisons among species out-crossing rates, group structure and group divergence, such as in the case of crop wild relatives.

The baking quality of flour is defined by the elasticity (strength) of the gluten, the volume and crust of the loaf, and the quantity of water absorbed. The volume of the loaf and the strength of the gluten may be considered together, as loaf volume depends on the elasticity of the wet gluten in the dough. The yeast acts on the starch and produces carbon dioxide (CO_2) and alcohol. The dough mass fills with CO_2, the volume of the dough increases, and the dough rises. If the dough is not subjected to the baking temperature, the elasticity of the walls around the gas-filled spaces reaches its limit, the

walls break, the gases are released, and the dough contracts and returns to its original volume (Dwivedi and Ortiz, 2013).

Seed storage proteins in wheat are the most important nutrient for humans and animals. The protein content of wheat grains varies between 10%-18% of the total dry matter. Wheat proteins are classified according to their extractability and solubility in various solvents. Classification is based on the classic work of Sladana *et al*., (2011). In their procedure, sequential extraction of ground wheat grains results in the following protein fractions: Albumins, which are soluble in water; globulins, which are soluble in dilute Sodium chloride ($NaCl_2$) solution, and insoluble at high $NaCl_2$ concentration; gliadins, which are soluble in 70% ethyl alcohol, and; glutenin, which are soluble in dilute acid or sodium hydroxide solutions.

Seed-storage proteins represent an important source of food and energy, being also involved in the determination of bread-making quality (Mohd *et al*., 2007). Wheat genotypes are qualified to different classes, which exhibit different applications and differ in quantity and quality of proteins, mainly gluten. Gluten, comprising roughly 78 to 85% of total wheat endosperm protein, is a very large complex composed mainly of polymeric (multiple polypeptide chains) and monomeric (single chain polypeptides) proteins known as glutenin and gliadins, respectively (Malik 2009). Glutenin confer elasticity to dough, whereas gliadins are viscous and give extensibility to dough (Kuktaite 2004).

The wheat plant stores proteins in this form for future use by the seedling. Storage proteins in wheat are unique because they are technologically active because they do not have enzymatic activity but

a function in the formation of dough as they retain gas, producing spongy baked products (Sladana *et al*., 2011).

Gliadins are heterogeneous mixtures of single-chained polypeptides with molecular weight range of 30,000 to 75,000Da. Due to extensive polymorphism, these proteins have been widely used for cultivar identification in hexaploid and tetraploid wheats (Malik, 2009). Allelic variants differ in the number, mobility, and intensity of their components and can be characterized through A-PAGE or even SDS-PAGE.

The pioneer studies of (Malik, 2009) showed that two types of glutenin subunits were present; the low molecular weight (10,000 – 70,000 Da) and the high molecular weight glutenin subunits (80, 000 – 130,000 Da). Electrophoretic studies have revealed appreciable polymorphism in the number and mobility of HMW-GS in bread wheat (Muhammad *et al*., 2016). The Low Molecular Weight-Gluten Subunits (LMW-GS) represents about one-third of the total seed protein and 60% of total gluten (Malik, 2009). Despite their abundance, they have received much less research attention than the HMW-GS. This has been mainly due to the difficulty in identifying them in one-dimensional sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels. The polyacrylamide-gel electrophoresis has been used to show that large size variation exists among LMW and HMW glutenin subunits, and it has been suggested that deletions and insertions within the repetitive region are responsible for these variations in length (Muhammad *et al*., 2009).

Molecular diversity is the divergence or similarity of crops based on the molecular markers by highlighting differences (polymorphisms) within a nucleic acid sequence between different

individuals. These differences include insertions, deletions, translocations, duplications and point mutations. They do not, however, encompass the activity of specific genes. In addition to being relatively impervious to environmental factor, molecular markers have the advantage of: (i) being applicable to any part of the genome; (ii) not possessing pleiotropic or epistatic effects; (iii) being able to distinguish polymorphisms which do not produce phenotypic variation and finally, (iv) some of them being co-dominant. The different techniques employed are based either on restriction-hybridization of nucleic acids or techniques based on Polymerase Chain Reaction (PCR), or both (Han *et al*., 2015).

Because SSRs are multiallelic, they have high potential for use in evolutionary studies and studies regarding genetic diversity and relationships. At present, microsatellites are one of the most promising molecular-marker types able to identify or differentiate genotypes within a species. Their co-dominant inheritance, high level of polymorphism and easy handling make them extremely useful for many different applications (Siddra, 2011).

1.2. Statement of the Problem

Ethiopia is one of the countries predicted to account for the increase in the world population. There is a pressing need for the increase in food production to feed this population. Wheat is among the major cereal crops grown in Ethiopia. It grows on an area of about 1.69 million hectares, and ranks third after teff and maize (FAO, 2019). It is an important commodity crop, which could contribute a major part in achieving the country's agricultural objective of food grain self-sufficiency (Negash, 2013). Despite the country having potential environments for wheat culture and being the center of diversity for wheats, the average national yield is low (1.8 t/ha) which is about 24% of South Africa’s

average national productivity, and (1.4t/ha) which is about 48% of the world's average productivity (FAO, 2019).

Moreover, the major wheat yield limiting factors in Ethiopia are diseases, weeds, poor soil fertility, lack of high yielding and resistant cultivar choice, frost occurrence in the highlands, terminal drought stress and water logging in the intermediate altitudes, and drought stress in the lowlands (Shewaye and Solomon, 2018). Few studies performed using microsatellites (Alamerew *et al*., 2004), isozymes (Malik, 2009), and glutenin and gliadin storage protein and AFLP (Messele 2001) considered either few accessions or focused mainly in the central highlands of Ethiopia. Thus, it was felt that because wheat genotypes have not been adequately evaluated, their genetic resource remains largely unexploited.

Hence, for successful breeding program, the presence of genetic diversity and seed storage protein plays a role as a genetic diversity indicator. Genetic diversity based on phenotypic and biochemical, seed storage protein and SSR are essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, and pest and disease resistance.

Research on Ethiopian bread wheat genotypes for genetic and molecular diversity studies based on seed storage protein and microsatellite markers are limited. Moreover, studies in baking quality of hexaploid wheat genotypes are scanty. Comparative studies on selected genotypes to show inter and intra group variation in Ethiopian bread wheat using morphologic and biochemical characters, seed storage protein and DNA markers have not been conducted.

Hence, this study is intended to fulfill the above gaps with the following objectives;

1.3. Objectives

1.3.1. General Objective

- To study the genetic diversity of bread wheat (*Triticum aestivum* L.*)* genotypes from Ethiopia using phenotypic, grain quality, seed storage protein, and SSR markers.

1.3.2. Specific Objectives

This experiment was designed with the following specific objectives:

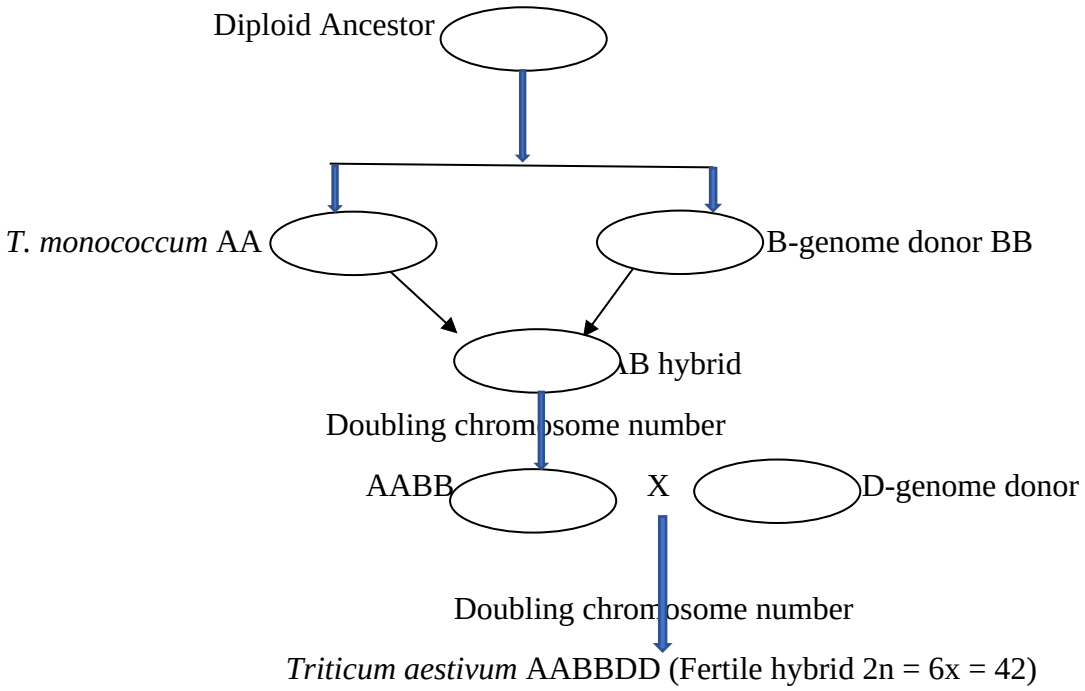
- To assess variation among genotypes using phenotypic/ agronomic traits**;**
- To assess the genetic diversity using SSR markers**;**
- To determine genotypes with good baking quality**;**
- To characterize the genotypes for their composition of high and low molecular weight glutenin subunits and gliadins;
- To investigate variation of genotypes in grain and flour quality traits performance across environments.

2. LITERATURE REVIEW

2.1. Origin, Taxonomy and Development of Wheat

Wheat (*Triticum* spp.) was one of the Neolithic founders' crops, and played an important role in the transition from hunter-gathering to a sedentary agrarian society approximately 12,000 years ago (Lev-Yadun *et al.*, 2000; Abbo *et al.*, 2013). It belongs to the genus *Triticum* and the tribe *Triticeae* of the family Poaceae (*Gramineae*) (Carl Linnaeus, 1753) and it evolved from wild grasses found in the Eastern Mediterranean and Near East regions. It was probably domesticated around 10,000 to 15,000 B.C. in the bordered areas of the countries known as Iran, Iraq, Syria, and Turkey (Feldman, 1976); a mountainous hilly region in the upper reaches of the Tigris and Euphrates drainage basin (Efrem *et al*., 2000).

There are fifteen recognized species within the genus *Triticum* (Rahel and Fekadu, 2016). About 90% of the world wheat production consists of three species: *Triticum aestivum* (common wheat), *Triticum compactum* (club wheat) and *Triticum durum* (durum or macaroni wheat). The species of the genus *Triticum* and their close relatives comprise of diploid, tetraploid and hexaploid groups, with chromosome numbers of 2n = 14, 28 and 42 respectively, in which the basic chromosome number is x = 7. The wild species are diploids (2n = 2x = 14), e.g. with the genome designation AA (*T. monococcum*), DD (*T. tauschii*, syn. *Aegilops squarossa*), and SS (*T. speltoids*), or tetraploids (2n = 2x = 28), e.g. with the genomes AABB (*T. durum* or *T. turigidum*) or AAGG (*T. timopheevii)*. The most common cultivated wheat, nowadays, is hexaploid (bread wheat), *T. aestivum*, AABBDD, (2n= 6X= 42) (Rahel and Fekadu, 2016).



(After Van Buren, 2001; Kerby & Kuspira, 1987). Each capital letter represents a genome composed of seven chromosomes

Figure 1: Possible origins of *Triticum aestivum*

The first wheat was diploid einkorn (*T. boeoticum* Boiss., genome A^bA^b), and grown in the Near-Eastern Fertile Crescent (Salamini *et al.*, 2002; Kilian *et al.*, 2007). Wild einkorn was then cultivated and produced the domesticated form (*T. monococcum L.*). Subsequently, a tetraploid wheat emmer (*T. dicoccum Schübl*. genome A^uA^u BB) became the most important crop in the Fertile Crescent.

Emmer was domesticated from its wild progenitor, *T. dicoccoides* Koern which was derived from the hybridization between a wild diploid wheat (*T. urartu* Thum. ex Gandil, genome A^uA^u) and a relative of goat grass (*Aegilops speltoides* Tausch., genome SS, as the donor of the B genome) occurring during 300,000–500,000 years ago (Bottley *et al.*, 2006; Peng *et al.*, 2011). Next,

expansion of domesticated tetraploid wheat resulted in sympatric with another goat grass (*Ae. tauschii* Coss., genome DD) and a spontaneous hybridization between them took place about 9,000 years ago that gave rise to the emergence of hexaploid spelt (*T. Spelta L*., genome A^uA^uBBDD) (Peng *et al.*, 2011). Free-threshing forms of bread wheat (*T. aestivum* L. and durum wheat (*T. durum* Desf.) are usually considered as a result of mutations in emmer and spelt, respectively, about 8,500 years ago (Peng *et al.*, 2011).

2.2. Wheat Ecosystem and Cultivation

Bread and durum wheat were cultivated worldwide and domesticated some 10000 years ago. However, the evolutionary sequence of bread and durum wheat is still debatable. It has been proposed that spelt was derived from hybridization between free-threshing hexaploid wheat and hulled emmer (Blatter *et al.*, 2004; Dvorak *et al.*, 2012).

During wheat evolution, domestication was largely responsible for the appearance of current wheat. This process was a series of events for genetic selection to alter some key traits such as rachis fragility, glume tenacity and thresh ability, for better harvesting performance (Salamini *et al.*, 2002). Wild einkorn and emmer have brittle spikes (spikes disarticulating into spike-lets at maturity), and transformation of a brittle into non-brittle spike gave rise to domesticated forms (Salamini *et al.*, 2002). The second domestication trait is tenacious glumes, which hinder the release of A^uA^u seeds from spike-lets. Einkorn and emmer (both wild and domesticated forms) as well as spelt, usually have tenacious glumes, whereas bread and durum wheat have soft ones. The free-threshing phenotype represents the final step of wheat domestication (Salamini *et al.*, 2002). The most crucial gene governing this trait is *Q*, which is pleiotropic, not only conferring the free-threshing

character but also influencing the threshing ability-related traits (e.g. glume tenacity and spike fragility) and spike morphology (e.g. number of spike-lets per spike) (Jantasuriyarat *et al.*, 2004).

Wide adaptation among the major cereal crops of the world has resulted from centuries of evolutionary processes and years of plant breeding and selection. Wheat is grown across a wide range of environments around the world. It is considered to be the most broadly adapted cereal crop (Curtis, 2002). Wheat is one of the major staples and strategic food security crop in Ethiopia. It is cultivated on 1,697,640.16 hectares of land and has the production of 46,430,051.02 quintals with productivity of 27.36 qt/ha in Ethiopia (CSA, 2019).

Within the total area of wheat under cultivation in Ethiopia, it has been reported that hexaploid and tetraploid species each occupy approximately 50% of the area (Gorfu, *et al.*, 2001). However, a change in the relative proportions of wheat types grown has been reported more recently, with e.g. hexaploid and tetraploid species occupying approximately 70% and 30%, respectively, of the total wheat area under cultivation (CSA, 2019).

Narrow genetic background has rendered improved varieties less tolerant to biotic and abiotic stress (Maqbool *et al*., 2010). Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes (Aremu, 2012). Therefore, precise information on the nature and degree of genetic variability and divergence present in wheat would help to select parents for evolving superior varieties.

2.3. Wheat Production in Ethiopia

In Ethiopia, large amount of soft wheat germplasm (about12,000 accessions) have been maintained in the Institute of Biodiversity Conservation (IBC). Landraces constitute the lion's share of these collections. Landraces, which are locally adapted genotypes that have evolved because of natural and artificial selection forces over the millennia, are one of the invaluable heritages that traditional farmers have given us (Myers, 1994). Landraces may be used as starting populations for cultivar development (Lakew *et al*., 1997) or as sources for the introgression of genes and quantitative trait loci conferring resistance to biotic (Huang *et al*., 1997) and abiotic stresses (Forster *et al*., 2000). Lakew *et al*. (1997) confirmed the presence of individual genotypes within landraces that have a yield potential comparable with the best breeding lines.

Various authors (Vavilov, 1951; Porceddu *et al*., 1973; Amri *et al*., 1990; Belay *et al*., 1993; Kubo *et al*., 2004) reported the uniqueness of the Ethiopian hexaploid wheat germplasm for different useful traits. However, it is felt that these collections have not been fully utilized in the breeding programs. Efficient utilization of the genetic potential held in the germplasm collections requires a better knowledge of the collected material including phenotypic and phenological characterizations. Although several authors (Jain *et al*., 1975; Bekele, 1984; Negassa, 1986; Bechere *et al*., 1996; Pecetti and Damania, 1996; Eticha *et al*., 2005; Hailu *et al*., 2006) have conducted variability studies in Ethiopian hexaploid and tetraploid wheat, there is still a need for more information on population structure and about their potential input for breeding.

Ethiopia is the second largest wheat producing country in Africa, after South Africa. Most wheat producers in Ethiopia are small holder farmers (CSA, 2019). Wheat production zones in Ethiopia lie between $6^{o}$and 16^{o} north, and $35^{o}$and 42^{o} east, at altitudes ranging from 1500m to 3000m. The most suitable areas for wheat production, however, fall between 1900m and 2700m. In the high lands' rainfall distribution is bimodal and ranges between 600mm and 2000mm. The rainy season is divided into the short rains (belg) falling from February to April and the main rains (meher) falling from June to September (Bekele *et al.*, 2000).

Table 1: Production of wheat world-wide and in Ethiopia during the period 2013/14-2017/18

Year	World-wide			Ethiopia		
	Area (million hectares)	Yield (metric tons per hectare)	Production (million metric tons)	Area (million hectares)	Yield (metric tons per hectare)	Production (million metric tons)
2017/18	220.06	3.47	763.18	1.697	2.736	4.643
2016/17	222.71	3.40	756.51	1.696	2.675	4.538
2015/16	224.05	3.30	738.42	1.665	2.535	4.219
2014/15	222.07	3.29	730.38	1.663	2.543	4.232
2013/14	220.02	3.26	716.52	1.61	2.445	3.925

(Sources: USDA, 2019; GMR, 2019; CSA, 2019)

Hexaploid wheat is widely grown by farmers on the heavy Nitosoil of the Ethiopian Highlands, at altitudes of 1500-3000 meter above sea level (m.a.s.l.) during the main cropping season. However, the most suitable range of altitude is 1900-2700 m.a.s.l., where the annual rainfall range is between 600 and 2000 mm (Bekele *et al*., (2018).

Eyob *et al.* (2015) reported that the area under wheat production in Ethiopia recorded an annual growth rate of 11% during 1991/92 to 2001/02, whereas production increased at a rate of 9.5% and yield witnessed a negative growth rate during the same period. During the period 2002/03 to 2012/13, the area of wheat production increased at a rate of 3.7%, while yield and production decreased at a rate of 5.4% and 9.3%, respectively. The yield of wheat increased at a rate of 3.3%, whereas production and the area recorded increased at a rate of 6.3% and 2.9%, respectively, during the overall period 1991/92 to 2017/18. Currently, wheat grows on 1.697 million hectares of production area with a total production of 4.64 million metric tons and ranks fourth in both area and production among cereal crops in Ethiopia (CSA, 2019). It is due to low production & productivity as a result of diseases (Rusts, Fusarium, Septoria, and Tan spot) frost drought, inefficient cultivar choice & poor soil fertility (Gebremariam, 1991) and, also due to insufficient area for cultivation as a result of an increase in the population of the country.

2.4. Yield and Yield Related Traits in Wheat

Grain yield and yield related traits are the principal characters of a cereal crop (Ullah *et al*., 2011). They are complex quantitative characters, which are influenced by a number of contributing characters. Hence, the selection for desirable genotypes should not only be based on yield but the other yield components should also be considered. Direct selection for yield is often misleading in wheat because wheat yield is polygenically controlled. For effective utilization of the genetic stock in crop improvement, information of mutual association between yield and yield components is necessary.

Grain yield is basically a complex trait being the consequence of several genes and their interaction in a particular environment. The main effort of a wheat breeder is the detection of genes and to merge them in a particular genotype using most suitable combination (Ullah *et al.*, 2011). Furthermore, grain yield is the most complex trait because it is influenced by all factors (known and unknown) that determine productivity (Araus *et al.*, 2001). Among those factors, yield related traits include days to heading, days to maturity, plant height, number of tillers per plant, thousand-kernel weight, hectoliter weight and number of kernels per tiller and they highly influence the amount of grain yield.

Harvest index (HI) appears to be approaching maximum because of increasing yield in wheat, which resulted from reduction in height (Richards *et al.*, 2001). The harvest index (HI) is expressed, for example for cereals, as the ratio of grain yield (GY) and the above ground biomass at maturity (BY): HI=GY/BY= GY/GY+S, where S denotes the straw weight at maturity of the crop (Sokoto *et al*., 2012). There is a clear advantage in the use of the harvest index ratio compared to an application of grain/straw ratios (Sokoto *et al*., 2012). First and foremost, harvest index links grain yield to the valuable measurement, biological yield and the determination of biological yield is a necessary step in the derivation of harvest index. A second advantage is that its value tends to be linear rather than exponential in their relationship to grain yield.

Sokoto *et al*., (2012) reported that grain yield/plant was negatively correlated with days to heading, maturity, grain filling period and plant height in Ethiopian tetraploid wheat landraces. They found positive correlation between days to heading and maturity. However, with the exception of plant height, these two traits showed a negative association with the rest of the traits. The same authors

indicated that tiller number was positively associated with grain yield, but showed a negative correlation with number of kernels/spike and 1000-grain weight.

Ghanbar *et al*., (2012) reported positive correlation of grain yield with number of seeds per spike, number of spike-lets per spike and biological yield in bread wheat genotypes. The same authors also indicated that number of spike-lets per spike was negatively correlated with number of spike length, number of tillers and grain yield while grain filling period was highly and significantly correlated with number of seeds per spike and grain yield. Shukla *et al*., (2005) reported high phenotypic and genotypic variation for number of tillers, number of seeds per spike and harvest index under rain fed and partially irrigated conditions.

Physiologically, yield is the result when plant biomass is divided by harvest index (HI). HI has been largely improved with the use of dwarfing genes, and closely associated with yield progress (Sadras and Lawson, 2011; Sanchez-Garcia *et al.*, 2013; Shearman *et al.*, 2005). HI currently reaches *c*. 0.45-0.50 in spring wheat and 0.50-0.55 in winter wheat, approaching its theoretical maximum value (*c*. 0.64 in winter wheat) (Foulkes *et al.*, 2011; Reynolds *et al.*, 2012). To further increase HI, biomass partitioning to different plant organs needs to be optimized. Genetic variation in biomass partitioning has been observed in elite wheat lines, and this variation can be broadened by introducing desirable traits from wild species existing in Triticeae (Foulkes *et al.*, 2011; Reynolds *et al.*, 2012).

Tillering in bread wheat determines plant canopy size, photosynthetic area, and, more importantly, the number of spikes bearing grains at maturity (fertile shoots), which is a key component of yield. Wheat plants undergo several events to form final fertile shoots: auxiliary bud initiation, first bud outgrowth, tillering cessation, tiller abortion, and the development of surviving tillers. Tiller buds are initiated from the auxiliary meristems in the axils of developing leaves on the main shoots, and bud number is associated with total number of leaves (Longenecker *et al.*, 1993). Early tillers can also be parent shoots producing secondary buds and tillers (Evers and Vos, 2013).

Tillering normally ceases just before stem elongation (Sylvester-Bradley *et al.*, 2008), and the remaining auxiliary buds become dormant. However, the dormancy is not definitive, and can be released in some cases like early lodging and damage to the apices of parent shoots (Rameau *et al.*, 2015). The timing of tillering cessation and number of total tillers initiated are regulated by number of genes; example, (gene (*tin1*) on chromosome 1AS) (Spielmeyer and Richards, 2004), physiological (biological hormones) (Rameau *et al.*, 2015) and by environmental factors (plant density, shade and nutrient supply) (Evers *et al.*, 2006; Sparkes *et al.*, 2006).

2.5. Grain Quality in Bread Wheat

Wheat grain quality is usually defined in terms of its suitability towards a particular product. Thus, quality of any kind of wheat can't be expressed in terms of a single property, but depends on several factors such as milling, chemical content, baking, processing and physical dough characteristics, each of which is important in the production of bread, pastry and pasta products. Grain quality is well known as one of the most important breeding objectives in many developed countries. It has a

great role in wheat markets because of the increased demand by consumers for high quality end products of bread wheat (Morgounov *et al*., 2013).

Wheat genotypes that produce dough with visco-elastic properties produce leavened bread provided that the protein is present in sufficient quantity and the initial wheat was in good condition. Such type of wheat is known as ‘strong’ wheat. On the contrary, genotypes that give rise to non-elastic but very extensible dough are not desirable for bread making but they are considered good for biscuit production and are categorized under ‘weak’ wheat (Makawi *et al*., 2013).

The quality of wheat is defined in terms of specific properties that determine suitability for milling and bread production (Makawi *et al*., 2013). Grain hardness is a grain quality trait that influences milling properties and baking quality in bread wheat (Morgounov *et al*., 2013). Milling time, milling energy requirements and the level of starch damage produced in the milled flour are all influenced by grain hardness. Hard wheat requires longer conditioning times in the preparation for milling and more milling energy, and produces a large amount of damaged starch granules.

The pigmentation level in wheat and absence of lipoxygenase enzyme during processing are some of the grain quality traits that determine the flour color quality in bread processing industries. Bread wheat genotypes were found to be different in their pigmentation, lipoxygenase activity, enzymes type, and levels during processing. The grain color in wheat can be extracted in a water saturated n-butanol or ethanol and the amount can be estimated by measuring the optical density by spectrophotometer.

The performances of many quality characteristics are influenced by environmental conditions, which result in differential expression of grain quality from site to site. Wheat quality is influenced by genotype (G), environmental factors (E) and the interaction between genotype and environment (G x E) (Uhlen, *et al*., 1998). But the relative effects on quality are a challenge that makes production of predictable quality bread wheat difficult (Peterson *et al*., 1992). Kaushik *et al*., (2014) investigated hexaploid wheat for diversity of most quality characters, and among which only gluten quality showed a low level of diversity.

Wheat genotypes are the result of extensive selection by breeders to meet both quality and agronomic requirements for the wide range of end products such as traditional pan, sponge and dough pan, flat or steamed breads, chapatti, frozen doughs, yellow alkaline or udo style noodles, confectionary, biscuits, and cakes (Gale, 2005). Nowadays, the most challenging task for wheat breeders is not only to increase grain yield but also to improve the grain quality for end products to meet the requirement of ever-increasing population (Duvalier *et al.*, 2007). Thus, wheat quality becomes a major target in wheat breeding program for the world wheat trade (Gross *et al.*, 2007).

The factors that influence the wheat grain quality have been broadly classified in two groups- physical and chemical characteristics. The physical characters include grain appearance score, kernel or grain hardness, virtuousness of kernel, thousand grain weight, hectoliter weight, and kernel size and shape, whereas chemical characters that determines bread making quality in bread wheat are protein content and quality, starch content, gluten content, moisture content and sedimentation volume found in the flour which can be determined from the grain using NIRS.

2.6. Flour Quality in Bread Wheat

The flour quality character that determines bread making quality in bread wheat is the flour protein gluten content that comprises different units such as gliadins and glutenin (HMW- and LMW-GS) content and quality found in the flour (Mac Ritchie, 1994).

2.6.1. Protein Content in Wheat

The quantity of protein is an important quality trait in bread wheat flour. The protein content in bread wheat varies between 8 and 17 % depending on genetic make-up and on external factors associated with the crop. The quality and quantity of protein can affect end use quality of bread wheat flour.

In bread making process, grain and flour proteins have a major role in dough visco-elastic properties and governing the technological and rheological properties of wheat flour (Simsek *et al*. 2014). Moreover, it is widely known that both protein content and protein composition are important factors to have a good baking process (Zhao *et al*. 2010).

Efrem *et al*. (2000) observed significant differences among genotypes of durum wheat for thousand grain weight, protein content, SDS-sedimentation volume and yellow berry kernels. Bread manufactured using vitreous, high protein grains had better cooking quality than that obtained from starchy, low protein grains. The baking potential of wheat flours is influenced by many factors, most notably protein content. While Novaro *et al*. (1997) indicated significant difference among genotypes for hectoliter weight and SDS sedimentation volume.

One of the major influencing factors for protein content is nitrogen fertilization, while the protein quality is determined primarily by the wheat genotype. On the other hand, both the quality and the

content of the bread wheat protein are affected by the climatic conditions during wheat maturation (Abboud and Charles, 2012).

2.6.2. Gluten Content in Wheat

An important property of wheat flour for bread making is the formation of a visco-elastic protein mass known as gluten, when water and the dilute salt protein are in contact with in the flour. Gluten is obtained after soluble protein and starch are removed by washing the dough in excess water. Gluten, comprising roughly 75 to 85 % of the total protein, is a very large complex composed of mainly polymeric and monomeric proteins known as glutenines and glidins, respectively.

Gluten is responsible for most of the visco-elastic properties of wheat flour dough and is the main factor dictating the use of a wheat genotype in bread making. Protein content in bread wheat has a high correlation with gluten content and in turn mechanical strength and cooking quality. Higher protein concentration and strong gluten of bread wheat has superior end use quality. Gluten protein largely consists of two groups of proteins, the sulfur reach glutenins, able to form polymeric networks, and the sulfur poor gliadins largely present as monomers (Ahmed, *et al*., 2016).

2.6.2.1. Gliadin Content in Wheat

Gliadins comprise a heterogeneous group of proteins. When these proteins are fractionated by one dimensional gel electrophoresis at low pH using aluminum lactate buffer, the components separate and are grouped in to α-, β-, ϒ-, ω- gliadins, the latter having the lowest mobility (Yadav and Singh 2011). The molecular masses of α-, β-, ϒ- gliadins vary between 30 – 40 KDa, whereas the ω-gliadins are larger, up to 78KDa (Yadav and Singh, 2011); α- gliadins contain six cysteine residues and form three inter-chain-disulfide bonds. Because gliadins are limited in sulfur containing amino

acids, they exclusively form intra-molecular disulfide bonds and they result in cohesiveness with poor resistance to extension.

2.6.2.2. Glutenin Content in Wheat

Glutenin macro- polymers consist of high molecular weight subunits (HMW-GS) with molecular masses between ca 80 and 145kDa and low molecular weight (LMW-GS) having molecular masses between ca 31 and 48kDa. HMW-GS are generally believed to exist as complex sub units linked by inter-chain disulfide bonds discovered a correlation between the presence of certain HMW-GS and gluten strength, measured by SDS- Sedimentation volume test (Horvath, (2014).

Protein quality in terms of polymeric/monomeric protein ratio and the molecular size of the protein polymer determined by the presence of specific glutenin subunits is also important (Clyde Don, 2005) also confirmed that wheat flours can contain different glutenin/gliadin ratio that may change its visco-elastic properties. The glutenin fraction is the major protein factor implicated for variations in dough strength among wheat genotypes. Many studies indicate the relationship between their genetic control and quality. Glutenins confer mainly viscous flow and extensibility to the gluten complex (Horvath, 2014).

The role of specific low molecular weight glutenin subunits on gluten have been determined in bread wheat; LMWG subunits, LMW-2 and its variants, confer stronger gluten character than LMW-1 (Clyde Don, 2005). The larger the number of components (up to 7) comprising a single LMW GS makes it practically impossible to distinguish them by using the conditions for determining high molecular weight glutenin subunits composition, particularly if the gliadins which

co-migrate with the low molecular weight glutenin subunits are present (Horvath, (2014). Two LMW-GS patterns, LMW-1 and LMW-2, largely explain quality differences between some bread wheat genotypes. Clyde Don, (2005) indicated that, in general, lines with the LMW-2 pattern had significantly greater SDS sedimentation volume and better mixograms than those with the LMW-1 patterns. The presence of ϒ- gliadin band 45 was associated with good bread making whereas that of ϒ- gliadin 42 implicated to give poor bread quality.

Protein levels in wheat are influenced by genotype, nitrogen management and environmental conditions (fertilizers, temperature, soil types, humidity, etc.). Growers may manipulate the first two factors through cultivar selection and N application. However, environmental conditions may work either in support or opposition to cultivar selection and diverse management. For instance, despite N management for high yield and low protein, a low rain fall season will tend to produce a crop with low yielding and high protein (Daniel and Toribio, 2000).

The lack of environmental predictability, and to a certain extent market conditions, has made the idea of dual-purpose hard wheat attractive. That is, if the grain does not meet quality specifications for one use, there is potential for placement of the grain in the alternative market. Daniel and Toribio (2000) also reported that the percentage of proteins in the flour increased with the increase of temperature and nitrogen supply, whereas the quantity of proteins per grain was affected negatively by high temperature and affected positively by N fertilizer.

2.6.2.3. Baking Quality in Wheat

The rheological properties of dough are often described in terms of resistance to extension and extensibility. Strong dough is one that gives a relatively high resistance as it is being extended, as well as a degree of elasticity, such that when released from moderate extension it will tend to regain its former shape. Weak dough will extend readily with little resistance and has no elastic tendency. The type of gluten influences dough rheological characters. Extensibility (plasticity) to dough is imparted by types and number of gliadins present, while the high molecular weight glutenin play major role in the resistance of dough to extension (Sliwinski, 2003).

Bread wheat physical dough properties have been determined using dough mixing instruments such as the mixograph or descriptive rheological methods such as the alveolograph. Gluten composition is a major factor in determining the dough mixing strength and processing characteristics. Of the several review articles have been published, Sliwinski, (2003) indicated, gluten imparts visco-elastic nature to dough. It has been established already that linear visco-elastic properties of bread wheat dough are related to dough mixing strength, baking characteristics and baking quality (Clyde Don, 2005; Edwards, *et al*., 2001), and that large deformation creep tests provide information on dough extensibility properties.

Measurement of fundamental linear visco-elastic properties of gluten and its building blocks, gliadin and glutenin, will help to better understand the underlying macro molecular structures in gluten that are responsible for its unique physical properties in influencing the bread quality.

2.7. Phenotypic Variation in Crop

Variation is the occurrence of differences among individuals due to differences in their genetic makeup and/or the environment in which they are raised (Falconer, 1990; Welsh, 1990).

2.7.1. Phenotypic and Genotypic Variability

Phenotypic variation is made of genotypic value and environmental deviation (Falconer, 1990; Welsh, 1990). Variation of phenotypic value is therefore determined by variance attributable genotypic values and environmental deviation (Falconer, 1990; Welsh, 1990; Singh and Ciccarelli, 1996). Vavilov (1951) observed a large phenotypic variation within and between groups in his study on Ethiopian wheat. Later on, several researchers too reported the presence of significant genetic variability among wheat genotypes in Ethiopia (Bekele, *et al.*, 1996, Awale, *et al.* 2013., Tesfaye, *et al.* 2014., Gezahegn, *et al.*, 2015). Similarly, Rajendra *et al.* (2015) reported the presence of a wide range of variability for grain yield, plant height, days to heading, number of grains/ spike, number of spike- lets/spike and yield/plant in the group of bread wheat.

If the character expression of two individuals could be measured in an environment exactly identical for both, differences in expression would result from genetic control and hence, such variation is called genetic variation (Falconer, 1990; Welsh, 1990). Information on the nature and magnitude of genetic variability greatly helps in formulating sound crop breeding program. Genetic variability is of prime interest to the plant breeder because proper management of this diversity can produce permanent gain in the performance of the plant (Welsh, 1990).

Environmental deviations contribute to the component of variation. Although some environmental variation can be reduced by proper experimentation, its total elimination is impossible because it includes, by definition, the non-genetic variance, and much of these are beyond experimental control (Gomez and Gomez, 1984).

2.7.2. Phenotypic and Genotypic Coefficient of Variation (PCV and GCV)

Majumder *et al.* (2008) reported that spike length, grains per spike, harvest index and grain yield displayed high variation at phenotypic level in spring wheat. Genotypic variability was high for number of seeds per spike, harvest index and grain yield. However, phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) in case of plant height and days to maturity, indicating presence of environmental influence on the expression of these characters. The other characters, such as spikes per plant, spike length, grains per spike and grain yield showed considerably high PCV than GCV which indicated marked influence of environment on the expression of these characters. Similarly, Desheva and Cholakov, (2014) and Navin *et al*. (2014) reported higher PCV than the GCV for all traits studied, indicating the influence of growing environments.

Generally, knowledge on the extent of genetic diversity, heritability and genetic relationships among genotypes is a prerequisite and of paramount importance for successful bread wheat breeding program. Developing bread wheat genotypes with desirable traits requires a thorough knowledge about the existing genetic variability in this crop (Maniee, *et al.*, 2009; Tesfaye, *et al.*, 2014).

2.8. Heritability and Genetic Advance

Heritability can be expressed as broad-sense or narrow sense value. Broad-sense heritability (h^2_b) is the ratio of the genotypic variance including additive, dominance and epistasis to the phenotypic variance ($\delta_g^2/ \delta_p^2 = \delta_g^2/ (\delta_g^2 + \delta_e^2 + \delta_{ge}^2)$), it expresses the extent to which individuals' phenotypes are determined by the genotypes. Narrow sense heritability is a ratio of the additive genetic variance to the phenotypic variance (δ^2_A/ δ_p^2), and it expresses the extent to which phenotypes are determined by the genes. Heritability, in theory, both h^2_b and h^2_n can vary from 0 to 1 determines the degree of resemblance between relatives and measures the relative importance of additive portion of the genetic variance that can be transmitted to the next generation of offspring (Fellahi *et al*., 2013).

Heritability estimates provide information about the expected response to selection in segregating groups. High estimates indicate how well evaluation of the parents will predict what the progenies will be like with a particular combination of breeding material and technique of evaluation. Characteristics with high h^2_b values can be improved more rapidly with less intensive evaluation than those with low values and hence, h^2_n is useful in calculating selection progress estimates. The h^2_n overestimates the response to selection as it includes non-additive effect (Fellahi *et al*., 2013).

Knowledge of heritability of a trait thus guides a plant breeder to predict performance of succeeding generations and helps in making desirable selections in wheat. Conventional analysis of variance and statistical parameters like phenotypic and genotypic coefficients of variability, heritability and genetic advance have been used to assess the nature and magnitude of variation in wheat breeding

material. Heritability combined with genetic advance is a more reliable index for selections of traits (Anshuman, *et al*., 2013). Desheva and Cholakov, (2014) reported high heritability accompanied with high expected genetic progress in the case of plant height, spike length and number of grains per spike indicated that heritability was due to additive gene effects and selection may be effective in early generations for these traits in bread wheat. Low to moderate heritability and genetic advance and moderate heritability with high genetic advance was reported for spike length (Firouzian, *et al.,* 2003; Safeer-ul-Hassan, 2003). Badran and Moustafa, (2015) reported low heritability values in narrow sense (0.029 and 0.195) was accompanied by low expected genetic advance as a percentage of each trait mean (0.97 and 5.64%) for the number of spike-lets per spike and plant height, respectively in wheat. Moderate heritability (Muhammad, *et al.,* 2001), low to moderate heritability and genetic advance (Safeer- ul-Hassan, 2003), moderate heritability and high genetic advance and high heritability with high genetic advance (Firouzian, *et al.,* 2003; Salim, *et al.,* 2003) were observed for number of grains/spikes. Low to moderate heritability and genetic advance (Safeer- ul-Hassan, 2003), high heritability (Muhammad, *et al.,* 2001), high heritability with high genetic advance (Shukla, *et al., 2000*) were reported for 1000-grain weight. Safeerul-Hassan (2003) observed low to moderate heritability with high genetic advance for grain yield/plant whereas Shukla *et al.* (2000), Firouzian *et al.* (2003) and Salim *et al.* (2003) reported high heritability with high genetic advance for this trait.

Tesfaye *et al.* (2014) reported that thousand grain weights had high heritability while grain yield, hectoliter weight, day to heading and plant height had medium heritability. Badran and Moustafa, (2015) in their study on wheat genotypes concluded the possibility of depending on additive variance through grain yield per plant and straw yield per plant in early generations' selection for

improvement in wheat yield and as the findings were consistent with results of both heritability and expected genetic advance. On the other hand, they concluded possibility of using dominance variance through number of grains/spikes, plant height and number of spike-lets/spikes in hybrid vigor in F1 generation. According to a report by Pramoda and Gangaprasad, (2007) heritability estimates on bread wheat can be low (<40%), medium (40-59%), moderately high (60-79%), and very high (≥80%). Accordingly, Awale *et al.* (2013) reported heritability estimates were very high for days to heading (89.08%) and grain yield plot^{-1}(84.64%), indicating the possibility of success in selection.

The value of the selected population over that of the original population indicating the genetic advance under selection, measures the difference between the mean genotypic values of the selected population over the mean genetic value of the original population for a given character (Allard, 1960). Heritability *per se* is not enough in predicting the effectiveness of selection unless and otherwise it is considered along with genetic advance (Allard, 1960; and Johansson *et al.*, 1955).

In an experiment on bread wheat done by Subhani and Khaliq (1994) & Chowdhry *et al.*, (1997) it is reported that days to heading, number of tillers, spike length, plant height & spike lets per spike has shown high heritability value and high genetic advance for all genotypes studied. Whereas, days to heading & harvest index showed high heritability coupled with low genetic advance. Jedynski (2001) reported high heritability estimates for plant height, intermediate for number of grains per spike and very low for grain yield per plant.

2.9. Correlation of Traits

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

Generally, three types of correlations are discussed in quantitative genetics and these are phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlations (r_p). Phenotypic correlations measure the extent to which the two observed characters are linearly related. It is determined from measurements of the two characters in a number of individuals of the groups. Genetic correlation (r_g) is the associations of breeding values (i.e. additive genetic variance) of the two characters. Genetic correlation measures the extent or degree to which the same genes or closely linked genes cause co-variation (simultaneous variations) in two different characters. The correlation of environmental deviations together with non-additive genetic deviations (i.e. dominance and epistatic genetic deviations) is referred to as an environmental correlation (r_e) (Falconer and Mackay, 1996; Sharma, 1998).

Studies on genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program (Amsal, 2001). Correlations between different characters of a crop plant may arise either

from genotypic factor or environmental factors. Environmental correlations arise from the effect of overall environmental factors and that varies at different environments. Correlations due to the genetic causes are mainly pleiotropic effects of genes and linkage (a phenomenon of genes inherited together) between genes affecting different characters. Pleiotropy is the property of a gene, which affects two or more characters; as a result, it causes simultaneous variations in the two characters when the gene segregates (Singh, 1993; Falconer and Mackay, 1996).

Correlation coefficients may range in value from -1 to +1. Phenotypic correlations can normally be estimated with a high degree of accuracy. Estimates of genetic correlations, however, usually have high standard errors because of difficulties to avoid the directional effects of confounding factors (i.e. dominance and epistatic genetic effects) on additive genetic correlation estimates (Lynch and Walsh, 1998 in Amsal, 2001). In addition, genetic correlations are strongly influenced by gene frequencies, and therefore, may differ markedly in different groups (Falconer and Mackay, 1996).

Estimate of correlations and significance test was previously discussed by several workers (Robertson, 1959; Singh and Chaudhary, 1977; Sharma, 1998). Depending on the sign genetic correlations between two characters can either facilitate or impede selection progress. Correlation value ($r = 1$) implies perfect (100%) correlation, where both traits vary hand in hand, $r = -1$ means there is 100 % correlation between two characters, but they vary in opposite direction, and $r = 0$ carries the implication that there is no correlation at all between the two characters (Falconer and Mackay, 1996; Sharma 1998).

Awale *et al*. (2013) reported that plant height displayed positive and highly significant association with number of spike-lets per spike at genotypic level of correlations. Spike length showed negative and highly significant association with number of spike-lets per spike and 1000-grain weight at genotypic level of correlations. Number of spike-lets per spike showed negative and highly significant association with 1000-grain weight at genotypic level of correlations.

Raza *et al.* (2013) observed that simple correlation between traits of grain yield with traits of biological yield, spike weight and spike number per meter square produced a positively significant correlation in bread wheat. The same author reported that the traits number of fertile tillers, days to maturity and harvest index had a positively insignificant relation with grain yield. Birhanu, (2010) reported biomass yield had positive and high correlation with grain yield (r= 0.8) and a positive significant association of plant height and biomass yield (r=0.34). Khan *et al*. (2013) reported significant and positive correlation of plant height with 1000-grain weight at both genotypic and phenotypic levels of correlations in bread wheat.

Primary yield components, namely spikes per meter square, grains per spike and thousand weight were negatively associated with each other. However, all the three components were highly significantly and positively correlated with grain yield. Awale *et al*. (2013) and Obsa (2014) reported that yield per plant had strong positive correlation with tillers per plant, spike length, kernels per spike-let and thousand grain weight.

Ali *et al.* (2008) reported that grain yield per plant had strong and positive genotypic correlation with number of productive tillers per plant and number of grains per spike with maximum direct effects in bread wheat. Those workers highlight the two traits were the key contributors to yield per plant suggesting the need for more emphasis on these components for increasing the grain yield in bread wheat. Number of spike-lets per spike and spike length although showed high correlation with grain yield, yet could not be considered in selection criteria due to their low direct effects and high indirect effects *via* number of productive tillers per plant and number of grains per spike in bread wheat.

Singh *et al.* (1998) reported that tillers per plant, yield per ear and biological yield per plant were significantly and positively correlated with grain yield per plant. Among other traits, biological yield per plant depicted significant positive correlation with tillers per plant, grains per ear and yield per ear. The results of these workers, likewise, revealed that yield per ear, as expected, were positively associated with grains per spike-let and grains per ear. Besides, they also noted significant negative correlations of grain weight with spike-lets per ear, grains per spike-let and grains per ear and of spike-lets per ear with tillers per plant. Camargo and Deo (1998) observed that grain number per ear was negatively correlated with 1000-grain weight ($r = -0.91$) in wheat.

Tesfaye *et al.* (2014) reported on bread wheat; thousand grain weight, as part of yield component, was positively correlated with yield but inversely related with days to maturity which are similar to the finding of Aycecik and Yildirim, (2006) who also observed positive association of Thousand Grain Weight (TGW) with grain yield.

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 in wheat.

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 grain weight in bread wheat. In addition, his result also depicted very weak positive correlations (Y_p=0.02, Yg=0.26) between grain yield and grain protein content, and strong positive association of grain protein content with hectoliter weight (Y_p =0.68, Y_g =0.91) and thousand grain weight (Y_p =0.54, Y_g =0.79) in bread wheat.

3. MATERIALS AND METHODS

This study comprises four sets of experiments:

I. Phenotypic diversity analysis in Ethiopian bread wheat genotypes. This experiment was conducted in three locations to evaluate the variation of genotypes performance at different locations and analyze the performance of released and pipe line genotypes in different environments based on agro-phenotypic characteristics.

II. Biochemical diversity of Ethiopian bread wheat genotypes. This experiment was conducted in a series of two sub experiments. These are: (1) identification of grain quality; (2) evaluation of flour quality; and hence, are used to identify bread making quality; to characterize the genotypes for their composition of high and low molecular weight glutenin subunits and gliadins; investigate variation of genotypes in grain quality traits performance across environments; evaluate genotypes of potential for further breeding and improvement of nutritional and baking quality wheat.

III. Seed storage protein diversity among Ethiopian bread wheat genotypes. This experiment was conducted for the investigation of the variation of genotypes using the most important seed storage protein unit, gluten, based on the analysis of the composition of gliadin, glutenin and HMW and LMW sub units of glutenin.

IV. Molecular diversity of Ethiopian bread wheat genotypes: to assess the genetic diversity and relationship among Ethiopian bread wheat genotypes using DNA figure printing, SSR marker analysis.

3.1. Phenotypic Diversity Study in Bread Wheat Genotypes from Ethiopia

3.1.1. Plant Materials

A total of one hundred twenty-one released and elite bread wheat genotypes (45 released and 76 pipe line genotypes) were characterized phenotypically at Adet, Debre Tabor, and Kulumsa Research Centers in (July-November, 2013/14) main cropping season. These locations are assumed to represent the major bread wheat production areas of Ethiopia.

The entry name, pedigree, origin, group and nature of the genotypes used in this study are indicated in Appendix 1; these genotypes were developed based on pedigree selection.

3.1.2. Experimental Locations

The phenotypic characterization was conducted at three sites viz., Adet Agricultural Research Center (West Gojam, Amhara Regional State), Debre Tabor Sub-center (North Gondar, Amhara Regional State) and Kulumsa Agricultural Research Center (Arsi zone, Oromia Regional State).

Adet site is situated in Amhara Region, Yilmana Densa district at 11°16´N latitude and 37°29´E longitude at an altitude of 2240 meters above sea level (m.a.s.l). This study area is located 45km east of Bahir Dar town and 485km north-west of Addis Ababa. The Adet sub-center is characterized by unimodal rainfall; which starts in April and extends to end of November, with maximum rainfall received in June, July, August, September, and October. The mean annual rainfall of the area is 1211.0 mm and the annual average temperatures varied from 11.57^{o}C to 26.89^{o}C (National Meteorological Service Agency, 2009). The major soil types found in the experiment area are Nitisols (source: Adet Agricultural Research Center).

Debre Tabor site is situated in Amhara Region, Farta district at 11°89´N latitude and 39°9´E longitude at an altitude of 2630 m.a.s.l. The study area is located 100 km north of Bahir Dar town and 630 km north of Addis Ababa. The Debre Tabor Sub-center is also characterized by unimodal rainfall; which starts in April and extends to end of October with maximum rainfall received in June, July, August, and September. The mean annual rainfall of the area is 1457.2 mm and the annual average temperatures varied from 9.71 ^{O}C to 21.82 ^{O}C (National Meteorological Service Agency, 2009). The major soil types found in the experiment area are Luvisols (source: Debre Tabor Agricultural Research Sub Center)**.**

Kulumsa Agricultural Research Center (KARC) is situated in Oromia National Regional State at 8.10'N latitude and 39.10'E longitude at an altitude of 2200 m.a.s.l. The study area is located in Arsi Zone about 160 km south of Addis Ababa, and 8 kms north of Assela. At KARC, in the main cropping season, the rain fall starts in June and extends to end of October and sometimes extends to mid of November. The average annual rainfall of the area is 832 mm and the mean annual minimum and maximum temperature is 10 ^{O}C and 22 ^{O}C, respectively (Kulumsa Agricultural Research Center, 2015). The major soil types found in the experimental area is Vertic-Luvisol (source: KARC).

Key: **Adet** **Debre Tabor** **Kulumsa**

Figure 2: Map of Ethiopia showing experimental locations for agro-morphologic study of the bread wheat genotypes

3.1.3. Field Experimental Design and Trail Management

The experiment was carried out in 11 x 11 Simple Lattice Design with two replications at each location. The genotypes were grown under uniform rain fed conditions. The plot/block dimension was four rows of 0.20m length with 0.20m row spacing. Planting was done by hand drilling in June, 2013/14 with the seed rate of 150 kg/ha (30g/plot).

Fertilizers (both N and P_2O_5) were applied at the rate of 150kg/ha and 100kg/ha, respectively, at the time of planting and tillering. Seed and fertilizer were drilled uniformly by hand. Weeding and other

agronomic practices were carried out as per the recommendations of respective locations. Neither herbicides nor insecticides were applied.

In total, 12 agro-morphometric (metric) traits were recorded at the correct growth stages. For all quantitative agro-phenotypic traits, data were collected on sample of ten plants from two middle rows of each plot, per replication, per site, which were randomly selected and tagged at all locations. The harvest was then dried, threshed and cleaned for scoring of the seeds grain yield and its components.

3.1.4. Data Collection

The data for three locations on the following attributes were collected from the central two rows of each plot of each replication and the average values were recorded:

Plant Height (PH): is the average height of 10 randomly selected plants from each plot in (cm).

Days to Maturity (DM): The number of days from sowing to physiological maturity.

Days to Heading (DH): The number of days from date of sowing to the stage where 75% of the spikes have fully emerged.

Number of Tillers Per Plant (NT): The average number of fertile tillers of 10 randomly selected plants.

Stand Percent (ST %): The percentage value of erect or properly grown plants without including logged plants from the total plants in a plot. It was scored first, by calculating the percentage value of logged plants through counting the number of lodged plants and dividing by the total number of plants in each plot and multiplied by 100. Second, ST% was calculated, by subtracting logged plants

percentage value calculated that was calculated earlier from the total plants in the plot and then multiplied by 100.

Spike Length (SL): The average length of the spike of 10 randomly selected plants in cm.

Number of Seeds Per Spike (NSS): The average number of seeds per spike from 10 randomly selected spikes determined by taking randomly selected spikes into head thresher that counts the number of seeds from each spike.

Septoria Disease Occurrence (SDO): There are two major Septoria diseases in wheat. These are Septoria tritici blotch, incited by the fungus *Septoria tritici* (teleomorph: *Mycophaerella graminicola*), and Septoria nodorum blotch, caused by the fungus *Septoria nodorum* (teleomorph: *Leptosphaeria nodorum*). Both diseases cause serious yield losses reported to range from 31 to 53 percent (Eyal, 1981; Babadoost and Herbert, 1984). The data was recorded as of UPOV descriptor (UPOV, 1985). This is done to see whether the yield difference is due to these diseases or its inherent difference. Based on an eye observation on the leaf of the genotypes after maturity.

Grain Yield (GY) Kg/plot: The average weight of grains determined by harvesting 10 randomly selected plants from the middle two rows of a plot and threshed, cleaned, adjusted to 14% moisture content by using wheat moisture tester and then weighed using an electronic sensitive balance. The yield per harvested area was calculated in tons per hectare bases.

Biomass Yield (BY) Kg/plot: at maturity plants were harvested from above the ground, dried and weighted and the biomass was converted in tons per hectare bases.

Harvest Index: is the proportion of grain yield to biomass yield calculated as:

HI = GY/ BY, Where, HI is harvest index, GY is grain dry weight, and BY is total biomass dry weight.

Number of Spike-Lets Per Plant (NSLP): The average number of spike-lets per spike from five typical spikes of selected plants in an individual plot.

3.1.5. Data Analysis

3.1.5.1. Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) was performed using the SAS version 9.1.3 software for Simple-Lattice Design. ANOVA was done for the data of three locations and combined data over locations, using the mean of ten plants per plot for the following characters: plant height, number of tillers per plant, number of spike-lets per plant, spike length, and number of seeds per spike.

However, plot values were used for the ANOVA of the characters such as days to heading and days to maturity, grain yield and above ground biomass yield per hectare, harvest index and stand percent, and Septoria disease occurrence. The Least Significant Difference (LSD) was used to compare two means at the 5% and 1% level of significance.

ANOVA for individual locations were computed using the following mathematical model:

$$P_{ijk} = \mu + \tau_j + \beta_{k(j)} + \pi_j + \varepsilon_{ijk}$$

Where: P_{ijk} = Phenotypic value of i^{th} treatment under j^{th} replication and k^{th} incomplete block, μ = Grand mean of trait, τ_j = The effect of j^{th} treatments, $\beta_{k(j)}$= The effect of incomplete block k within replication and π_j = The effect of replication j and ε_{ijk} = experimental error (pooled error).

Table 2: ANOVA Model for Individual Locations

Source of Variation	DF	SS	MS	Expected Mean Square
Replication	r-1	SS_r	MSr	$\sigma^2_e + g\sigma^2 r$
Block within replication	r(b-1)	SS_b	MS_b	$\sigma^2_e + b\sigma^2 r$
Treatment	t-1	SS_t	MS_t	$\sigma^2_e + r\sigma^2_g$
Residual	r(t-b)-t+1	SS_e	MS_e	σ^2_e
Total	tr-1	-	-	-

Where, r = Number of replications; b = number of blocks; g = number of genotypes (treatment); SSr = Sum square of replication, SSt = sum square of treatment; SSe = sum square of error; MSr = mean square due to replication; MSt = mean square due to treatment; σ2e = environmental variance; σ2g = genotypic variance.

Before computing the combined analysis, error variance homogeneity test was performed using Hartley`s test (F-max test) (Gomez and Gomez, 1984). There were only three error variances per traits (three locations) and hence, error variance for the test location were found to be homogeneous (F-ratio less than or equal to three times the error variances). In the combined location analysis of variance, locations were considered as random variable and genotypes were considered as fixed variables.

The Combined ANOVA of the traits was done using the following mathematical model:

$$P_{ijks} = \mu + \tau_j + \beta\, k(j)(s) + \pi j(s) + L_s + (\tau xl)_{is} + \xi_{ijks}$$

Where, $\mathbf{P_{ijks}}$ = Phenotypic value of i^{th} treatment (collection) under j^{th} replication at s^{th} location and k^{th} incomplete block within replication j and location s; $\boldsymbol{\mu}$ = Grand mean; τ_i = the effect of i^{th} treatment; $\boldsymbol{\beta_{k(j)(s)}}$ = the effect of incomplete block k within replication j and location s; $\boldsymbol{\pi_{j(s)}}$ = the effect of replication j within location s; $\mathbf{L_s}$ = the effect of location; $(\boldsymbol{\tau xl})_{is}$ = the interaction effects between treatment and location; and $\boldsymbol{\xi_{ijks}}$ = pooled error.

Table 3: ANOVA Model for Combined Data Over Locations

Source of Variation	DF	SS	MS	Expected Mean Square
Location	l-1	SSl	MSl	$\sigma^2_e + g\sigma^2$ l
Replication within location	l(r-1)	SSrl	MSrl	$\sigma^2_e + gl\sigma^2$ r
Genotype	g-1	SSg	MSg	σ^2e + rσ^2g*l* + r*l*σ^2g
Genotype x Location	(*l*-1) (g-1)	SSgl	MSgl	σ^2_e+ rσ^2_{gl}
Residuals	l(g-1) (r-1)	SSE	MSe	σ^2_e
Total	gr*l*-1	-	-	-

Where, **r** = number of replication; **b** = number of blocks; **g** = number of genotype (treatment); **l** = location; $\mathbf{SS_l}$ = Sum square of location; **SSg** = sum square of genotype; **SSe** = sum square of error; $\mathbf{MS_l}$ = mean square due to location; **MSg** = mean square due to genotype; **MSgl** = mean square due to genotype by location; **MSe** = mean square due to error; $\boldsymbol{\sigma^2_e}$ = environmental variance; $\boldsymbol{\sigma^2_g}$ = genotypic variance; $\boldsymbol{\sigma^2_{gl}}$ =Variance for treatment by location interaction

3.1.5.2. Estimating Phenotypic and Genotypic Variance

The genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability were estimated according to statistical procedure, by using the formula, adopted by Burton and De Vane (1953) as follows:

❖ Genotypic variance (δ^2_g) = $\frac{MSg-MSe}{r}$

Where: MS_g = mean square due to genotypes, MS_e = error mean square, r = the number of replications

❖ Environmental variance (δ^2_e) = error mean square = *MSe*

❖ Phenotypic variance (δ^2_p) = $\delta^2_g + \delta^2_e$

Variance components for the data combined over locations were computed in a similar fashion as for the individual locations by using the formulae (Johnson *et al*., 1955)

$$\delta^2_e = Ms_e$$

$$\delta^2_{gl} = \frac{MSgl-MSe}{r}$$

$$\delta^2_g = \frac{MSg-MSgl}{rl}$$

$$\delta^2_p = \delta^2_g + \frac{\delta^2}{l}gl + \frac{\delta^2 e}{lr}$$

Where: $\boldsymbol{\delta^2_{gl}}$ = Gene by location interaction, $\mathbf{MS_e}$ = Error mean square, $\mathbf{MS_{gl}}$ = Genotype by location interaction mean square, $\mathbf{MS_g}$ = Genotype mean square, **r** = Replication and **l** = Location.

Coefficients of variation at phenotypic, genotypic and environmental levels were estimated using the following formula:

- ❖ Phenotypic coefficient of variation (PCV) per location = $\frac{\sqrt{\delta^2 p}}{m}$ x 100
- ❖ Genotypic coefficient of variation (GCV) per location = $\frac{\sqrt{\delta^2 g}}{m}$ x 100

Where: m = group mean for the traits considered

3.1.5.3. Estimation of Heritability in Broad Sense

Broad sense heritability per location were estimated according to Allard (1960) as

Heritability per location (H^2) = $\frac{\delta^2 g}{\delta^2 p}$ x 100

Where, $\delta^2 g$ = genotypic variance and; $\delta^2 p$ = phenotypic variance.

Similarly, broad sense heritability combined over locations were estimated according to Allard (1960) as:

$$\mathbf{H^2 = \frac{\delta^2 g}{\delta^2 p} x\ 100} \quad \text{Where, } \delta^2 p = \delta^2 g + (\delta^2 gl/l) + (\delta^2 e/rl)$$

3.1.5.4. Estimation of Genetic Advance

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al.*, (1955) as:

$$GA = K\delta^2_p H$$

Where, K = the standard selection differential at 5% selection intensity (K = 2.063), δ_p = phenotypic standard deviation on mean basis and H = heritability in broad sense.

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

$$GAM = \frac{GA}{m} \times 100$$

Where: GAM= genetic advance as percent of mean, GA = genetic advance under selection and m = group mean of the traits considered.

3.1.5.5. Estimation of Phenotypic and Genotypic Correlation Coefficients

Correlation coefficient measures the mutual relationship between various traits and determines the component character on which selection can be based for improvement in yield (Singh and Chaudhary, 1985). The phenotypic and genotypic coefficients of correlation for the traits measured in the study were estimated using Pearson Simple Correlation which deals with association between any two traits. Phenotypic correlation is the observable correlation between two variables, which include both genotypic and environmental effects, and genotypic correlation is the inherent association between two variables.

Phenotypic and genotypic correlation coefficients between two traits were determined by using PROC CANDISC procedure of SAS software following the variance and covariance components (Singh and Chaudhary, 1985; Sharma, 1998).

$$\Upsilon_{Pxy} = \frac{Covp(x.y)}{\sqrt{(\delta^2 px)(\delta^2 py)}} \quad \text{and} \quad \Upsilon g_{xy} = \frac{Covg(x,y)}{\sqrt{(\delta^2 gx)(\delta^2 gy)}}$$

Where: $\mathbf{Cov_{p\ (x,\ y)}}$ = Phenotypic covariance between traits x and y, $\mathbf{\Upsilon_{Pxy}}$ = phenotypic coefficient between traits x and y, $\mathbf{\sigma^2 p_x}$ = Phenotypic variance of trait X; $\mathbf{\sigma^2 p_y}$ = Phenotypic variance of trait Y, $\mathbf{Cov_{g\ (x,\ y)}}$ = Genotypic covariance between traits x and y, $\mathbf{\Upsilon g_{xy}}$ = Genotypic correlation coefficient between traits x and y, and $\mathbf{\delta^2 g_x}$ = Genotypic variance of trait x and X; $\mathbf{\sigma^2 g_y}$ = Genotypic variance of trait Y

Phenotypic and genotypic correlation coefficients were tested for their significance using the formula suggested by Robertson (1959), using the t- table at (g-2) degrees of freedom at 5% and 1% level of significance; g is the number of genotypes (treatments) used in the study.

$$t = \frac{\Upsilon pxy}{SEpxy} \text{ and } t = \frac{\Upsilon gxy}{SEgxy} \quad \text{respectively,}$$

Where, $\mathbf{SE_{pxy}}$ and $\mathbf{SE_{gxy}}$ = Standard error for phenotypic and genotypic correlation respectively

$$SE_{pxy} = \sqrt{\frac{(1-\Upsilon pxy)^2}{2Hx*Hy}} \text{ and } SE_{gxy} = \sqrt{\frac{(1-\Upsilon gxy)^2}{2Hx*Hy}}$$

Where, H_x = Heritability of trait x and H_y = Heritability of trait y

3.2. Genetic Diversity Study of Bread Wheat Genotypes from Ethiopia Based on Grain and Flour Baking Quality

In this study there were two sub experiments; one for the identification of grain quality and the other for identification of flour quality in bread making performance of genotypes. These experiments were done at Amhara Region Agricultural Research Institute (ARARI) Grain Quality Analyses Laboratory, Bahir Dar and ICARDA Biodiversity and Integrated Gene Management Program (BIGM) Biotechnology Laboratory in Cairo, Egypt, respectively, to score the data for analysis in the following manner:

3.2.1. Grain Quality Identification

3.2.1.1. Plant Materials

Grain was harvested from 121 bread wheat genotypes phenotyped at each location Adet, Debre Tabor and Kulumsa (Appendix 1). These genotypes were selected mainly randomly to study genetic diversity for bread making performances. The grains were cleaned manually to remove soil particles, broken and foreign seeds.

3.2.1.2. Data Collection

Data was collected for both grain physical quality characteristics such as thousand grain weight and hectoliter weight, and grain chemical parameters included protein content, starch content, gluten content, moisture content and SDS test.

Both physical (TGW and HLW) and chemical (the rest) characteristics of grain quality data indicated below were measured using Near Infrared Spectroscopy (NIRS) analyzer in such a way that the whole grain meal was used according to the AACC method 39–70A and reading the mechanical system (Williams and Sobering, 2002). This work was done at Amhara Region Agricultural Research Institute (ARARI) Grain Quality Analyses Laboratory, Bahir Dar, Ethiopia in 2015 for the following characters:

Thousand Grain Weight (TGW): One thousand clean and sun-dried grains were collected from ten plants randomly from the middle two rows of each plot. The moisture content of the grain yield was adjusted at 14% moisture content and weighed by using a sensitive balance. Thousand grains of each genotype are expressed in grams.

Hectoliter Weight (HLW): a measure of the volume of grain per unit. The weight of grain samples was taken into a hectoliter (an apparatus which was calibrated to hold one liter) then the one-liter grain samples were weighed. It is a good indication of grain-soundness usually millers use as an expected flour yield.

Moisture Content: is the amount of water in a product measured by a specific method, and it allows certain general statements to be made about grain deterioration. It affects the quantity of grain, price

discounts and premiums, as well as grain storability. Therefore, moisture content can affect economic return. It was expressed in percentage

Grain Protein Percentage (GP%): is determined by Near Infra-red Spectroscopy (NIRS) when 300 to 500gm of seed samples were put in to the NIR machine to give a result in percentiles.

Grain Starch Percentage (STA%): the starch contents of the seed sample of the genotypes were determined using near infra - red reflecting spectroscopy (NIRS) by putting 100gm seed samples in the NIR apparatus and calibrating the NIR to provide the information by the infra-red as percent starch content.

Wet Gluten Content (GLUE): the wet gluten content of the sample of 100gm seed samples was determined using NIRS. It was expressed in percentage

Zeleny Sedimentation (SDSZ) test: describes the degree of sedimentation of flour suspensions when dissolved in lactic acid solution during a standard time interval and this is taken as a measure of baking quality. However, here harvested genotypes from three different environments were determined using NIR.

N.B. Wheat genotypes were tempered to 12.5% moisture content for 48 h to determine all the above grain physical as well as chemical characteristics of the data. About 300-500gm of seed samples were used to determine the contents of the last five characteristics or the chemical parameters of the grain quality in the NIRS analysis and their unit of measurements was in percentiles**.**

3.2.1.3. Data Analysis

The plant materials (Page 42-44) and all the statistical analytical methods (Page 49-54) used here are described in details in the phenotypic analysis part of this paper above, including the following

procedures: Analysis of Variance (ANOVA), estimation of phenotypic and genotypic parameters, estimation of heritability in broad sense, estimation of genetic advance and correlation studies.

3.2.2. Flour Quality Identification Based on SDS-PAGE Banding Patterns.

The study was intended to analyze genetic diversity and similarity of bread making quality in their flours using composition of gliadins, glutenin and HLW- and LMW-GS analyzed by SDS PAGE banding patterns method. The bands formed during electrophoresis by the genotypes were compared to the standard protein markers. For gliadin composition the protein markers used were 21, 23, 38, 41, 42, 43, 48, 49, 50, 51, 52, 53 and 54 in KDa, for the analysis of glutenin composition markers used were 35, 45, 50, 55, 65, 130, 140, 150 and 160 in KDa, and the protein markers 35, 45, 50, 55 and 65in KDa were used to investigate HMW GS and 130, 140, 150 and 160 in KDa protein markers were used for the analysis of LMW GS (Malike, 2009).

3.2.2.1. Plant Materials

A total of 363 (121 from each 3 locations) bread wheat samples were taken to ICARDA Biodiversity and Integrated Gene Management Program (BIGM), Biotechnology Laboratory Cairo, Egypt during 2017/18 for the study of diversity of flour bread making quality and seed storage protein composition based on SDS-PAGE analyses (Table 4).

It was intended to check if there might be an environmental effect on flour quality and seed storage protein diversity among the genotypes, which was a very large number. But due to lack of chemicals, laboratory equipment and time factor; it was only allowed to work with a total of 150 samples (50 for each 3 locations).

Table 4: List of 50 bread wheat genotypes used for flour quality and seed storage protein diversity study collected at three locations based on SDS PAGE analyses

S. N	Genotype	Pedigree	Origin	Source/Group	Nature
1	K 6290-bulk	-	KARC/EIAR	Commercial genotype	Released
2	Hawii	HAR2501	KARC/EIAR	Commercial genotype	Released
3	Hoggana	ETBW 5780	KARC/EIAR	Commercial genotype	Released
4	Tay	ET-12D4/HAR604(1)	KARC/EIAR	Commercial genotype	Released
5	Kakaba	Picaflor #1	KARC/EIAR	Commercial genotype	Released
6	Menze	HAR 3008	KARC/EIAR	Commercial genotype	Released
7	Dereselign	-	KARC/EIAR	Commercial genotype	Released
8	GAMBO	QUIA#2	KARC/EIAR	Commercial genotype	Released
9	Bobitcho	HAR 2419	KARC/EIAR	Commercial genotype	Released
10	Bolo	HAR3816	DBARC/ARARI	Commercial genotype	Released
11	Ogolcho	ETBW 5520	KARC/EIAR	Commercial genotype	Released
12	Simba	HAR2536	KARC/EIAR	Commercial genotype	Released
13	Kulkulu	HAR 4621	HU	Commercial genotype	Released
14	Mitike	HAR 1709	KARC/EIAR	Commercial genotype	Released
15	Danda'a	Danphe#1	KARC/EIAR	Commercial genotype	Released
16	Sulla	710/RBC	AwARC/SARI	Commercial genotype	Released
17	Shorima	ETBW 5483	KARC/EIAR	Commercial genotype	Released
18	ETBW 6095	ASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	KARC/EIAR	New Genotype	Released
19	K 6290-4A	-	KARC/EIAR	Commercial genotype	Released
20	Enkoy	-	KARC/EIAR	Commercial genotype	Released
21	Katar	HAR1899	KARC/EIAR	Commercial genotype	Released
22	ET-13A2		KARC/EIAR	Commercial genotype	Released
23	Sirbo	HAR2192	KARC/EIAR	Commercial genotype	Released
24	Abola	HAR 1522	KARC/EIAR	Commercial genotype	Released
25	Dinknesh	HAR3919	SRARC/ARARI	Commercial genotype	Released
26	Gasay	HAR3730	ADARC/ARARI	Commercial genotype	Released

Table 4: Continued…

27	Honqollo (ETBW5879)	NJORO SD-7	KARC/EIAR	New genotype	Released
28	Dashen	-	KARC/EIAR	Commercial genotype	Released
29	Mada Walabu	HAR1480	SARC/OARI	Commercial genotype	Released
30	Meraro	11-6-24	KARC/EIAR	Commercial genotype	Released
31	KBG-01	FH-1-7A or Line 8 3 8	KARC/EIAR	Commercial genotype	Released
32	Glema	HAR604	KARC/EIAR	Commercial genotype	Released
33	Laketch	-	ADARC/ARARI	Commercial genotype	Released
34	Sofumar	HAR1889	SARC/ORI	Commercial genotype	Released
35	Pavon-76	VCMIICNO17C/3/KALIBB	KARC/EIAR	Commercial genotype	Released
36	Doddota	HAR2508	KARC/EIAR	Commercial genotype	Released
37	Digelu	SHA 7/KAUZ or HAR3116	KARC/EIAR	Commercial genotype	Released
38	Galil	Galil	KARC/EIAR	Commercial genotype	Released
39	Hidasie	ETBW5795	KARC/EIAR	Commercial genotype	Released
40	Kubsa	HAR1685	KARC/EIAR	Commercial genotype	Released
41	Dure	HAR 1008	SARC/OARI	Commercial genotype	Released
42	Tossa	HAR3123	SRARC/ARARI	Commercial genotype	Released
43	Huluka	ETBW 5496	KARC/EIAR	Commercial genotype	Released
44	ETBW6406	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
45	ETBW 6953	CROW'S'/BOW'S'-3-1994/95//TEVEE'S'/TADINIA	-	BWPVT-II-2013	Pipe line
46	ETBW 6114	SOKOLL//SUNCO/2*PASTOR	-	BWNVT-II-13-14	Pipe line
47	Millennium	ETBW4921	KARC/EIAR	Commercial genotype	Released
48	ETBW 6107	KLDR/PEWIT1//MILAN/DUCULA	-	BWNVT-II-13-14	Pipe line
49	ETBW 6212	QAFZAH-23/SOMAMA-3	-	BWNVT-II-13-14	Pipe line
50	Tusie	HAR1407	KARC/EIAR	Commercial genotype	Released

So, it was decided to include all the advanced lines (all 43 commercial and all 2 newly released genotypes) and only 5 pipe line genotypes selected from the total of 76 pipe line genotypes and a total of 50 genotypes by 3 locations were analyzed. These pipe line genotypes were chosen based on their group and pedigree to include different genotypes as much as possible from different groups.

All the procedures such as protein sample and gel preparation, and the procedures followed during SDS PAGE in this study are discussed below:

3.2.2.2. SDS-PAGE Procedure

Mature, clean and undamaged seeds of plants were collected from the field which were grown for phenotypic variation study at each location and taken to ICARDA Biodiversity and Integrated Gene Management Program (BIGM) Biotechnology Laboratory in Cairo, Egypt for the purpose of flour quality analyses of bread making based on gliadin and glutenin (HMW and LMW) sub units composition of 50 bread wheat genotypes, based on the following methodologies:

3.2.2.2.1. SDS PAGE Preparation

Preparation of 10% SDS- PAGE and running buffer (2lt), Coomassie stain (200ml) and APS (Ammonium Per Sulfate) (200ml), 1.5M Tries solutions and loading dye (10ml), 50ml resolving gel and other necessary chemicals for SDS PAGE were done following Osborne (Osborne, 1907) and Damiana (Damiana, *et al*., 1983) with little modifications.

3.2.2.2.2 Protein Extraction

Seven to eight matured seeds were selected and ground in tissue lyzer for 10 to 20 min at 30 vibrations per second, and then the powder (100-150mg) was placed in microtubes.

The powder in the tubes were washed in series of steps (about 4x) to remove the water-soluble albumen component (using deionized water) and then to remove the salt soluble globulin component (using 0.5 M NaCl aqueous solution) of the protein components with the supernatants. The residue was conserved for the analysis of gliadin, glutenin and its subunit components of interest.

The conserved residue was treated with Isopropanol for incubation (3x), with an interval vertexing and centrifugation to settle the residue at the bottom and milky solution (supernatant) at the top, i.e., the first collection of gliadin component and transferred in to new microtubes.

The residue was treated again with Isopropanol to collect the second dissolved gliadin solution in the supernatant and added on to the same microtube of the first solution.

This step was repeated to dissolve and collect the third supernatant that contains gliadin to be added on to the new tube collections of the first and the second gliadin supernatants.

Finally, the new microtube contained the collection of gliadin contents from the three series of steps. This solution was ready for electrophoresis. After all the above three steps of extraction of gliadin, the final residue was treated to extract glutenin (HMW & LMM) components with the following steps:

The first step was dissolution of the residue of the gliadin, and then was treated by alcohol and Polyvinyl Phosphate (PVP) solution. The series of steps were the same as the steps followed in gliadin isolation, in which incubation was followed by an interval vertexing (3-times) and final centrifugation to collect the glutenin extracts in the supernatant to a new test tube for later electrophoresis.

The HMW- and LMW glutenin sub units were finally identified based on their weight from the gel bands during electrophoresis of the glutenin extracts.

NB. For further detailed reference of the protocol to extract protein from each genotype, please refer to Appendix 19.

3.2.2.2.3. Preparation of Separating and stacking gels as of Laemmle (Laemmle, 1970)

For the gel electrophoresis to run two types of gels were used, the stacking gel whose purpose was with its lower pH and low acrylamide percentage, to "stack" all of the proteins in the sample into as narrow of a band as possible, so that they all enter the resolving gel at essentially the same time and separating gel was used to separate a mixture of proteins based on their size in order to identify proteins by size, protein standards of a known size were loaded along with samples and run under the same conditions.

In order to prepare 15% separating gel, after 20ml of stock acrylamide solution and 1.4ml water were mixed with 8.0ml Tris HCl at pH of 8.9. Subsequently, a mixture of 0.2ml ammonium per sulphate solution, 0.4 ml 10% SDS with 20µl Tetramethyl ethylenediamine (TEMED) solution was added.

While, 10% gel was prepared by mixing 13.3ml of stock acrylamide solution and 8ml Tris HCl at pH of 8.9 with 18.1ml distilled water, with subsequent addition of 0.2ml ammonium per sulphate solution in a mixture of 0.4ml 10% SDS and 20µl TEMED solution.

To prepare 3% stacking gel 4.0 ml of stock acrylamide solution and 2.0ml Tris HCl (pH of 6.7) were mixed with 2.0ml riboflavin solution and 8.0ml water. This solution was mixed with 0.1ml 10% SDS and 20µl TEMED solution.

3.2.2.2.4. Preparation of Protein Samples and Casting of Gel

Protein sample (48µl) was mixed with 12µl 4x sample buffer (0.25M Tris-HCl pH 6.8 added with 8% SDS, 40% glycerol, 20% β-mercaptoethanol, 0.5% bromophenol blue) and heated in water bath containing boiling water for 2-3 min to ensure complete interaction between protein and SDS. Samples were cooled at room temperature. Protein samples were run in the SDS-PAGE chamber and taken to the documentation room for reading. Pictures were taken then the bands were scored for analysis (Shuaib and Alam Zeb, 2007)

3.2.2.2.5. Protein Markers Used for Screening

Molecular weight of different bands was calibrated with a mixture of standard protein markers 21kda to 54kda, 35kda to 160kda, 130kda to 160kda and 35kda to 65kda for the assessment of bread wheat genotypes based on gliadin, glutenin, HMW and LMW glutenin composition of these genotypes, respectively (Malik, 2009).

3.2.2.2.6. Running the Gel

Protein electrode buffer solution was poured into the bottom pool of the apparatus. Gel plates were placed in the apparatus carefully so as to prevent bubble formation at the bottom of gel plated. Equal quantity of extracted protein from each sample along with protein molecular weight marker (PAGE mark) was loaded with the micropipette into each wells of the gel. The apparatus was connected with constant electric supply. Electrophoresis was carried out at 20mA current for 3-4 hours till the tracking dye reached the bottom of the gel. After electrophoresis, the protein bands were visualized by staining with Coomassie brilliant blue G-250 and distained with methanol, acetic acid and water (4:1:5).

3.2.2.3. Data Scoring

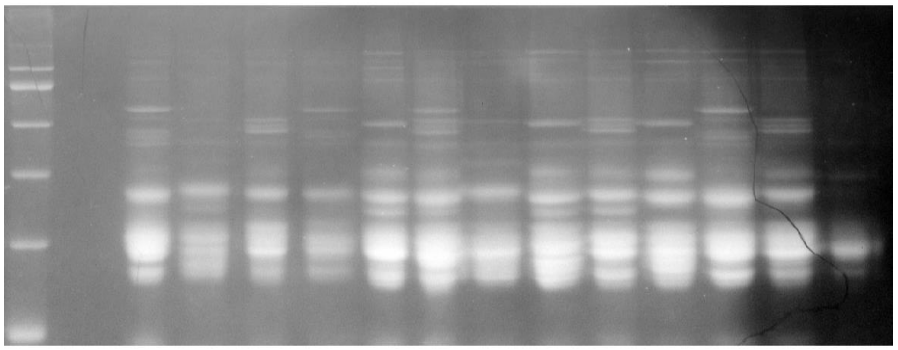
The data gained based on presence or absence of bands formed by the genotypes in reference to the protein markers were used for data analysis.

3.2.2.4. Data Analysis

The photographs of SDS-PAGE were used to study the protein profile of all the genotypes. The bands were designated on the basis of their molecular weight of the markers. The presence of protein band was scored as "1" and its absence as "0". In the present study, the group diversity based on SDS PAGE banding patterns was calculated using POPGENE 1.31 (Yeh *et al*., 1999) software. The data matrices were then entered into NTSYS-PC (Numerical Taxonomy and Multivariate Analysis System Program) developed by Rholf (2000). The data were analyzed using SIMUQUAL Jaccard's Similarity Coefficients formula (Sneath and Sokal, 1973). The matrix of similarity coefficients generated from data of 50 wheat genotypes was subjected to unweight pair group method for arithmetic average (UPGMA) using NTSYS-PC, version 2.02 (Exeter software, New York).

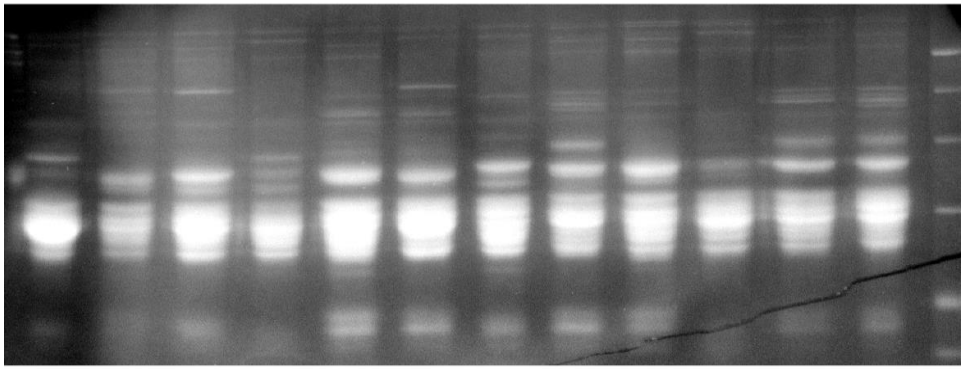
Gel Documentation and Analysis: Molecular weight of protein bands was estimated by their relative mobility. Pairing affinity or Similarity index was calculated by the method described by the formula.

$$PA = \frac{Bands\ common\ to\ variety\ I\ and\ variety\ II}{Total\ bands\ of\ the\ variety\ I\ and\ variety\ II}$$



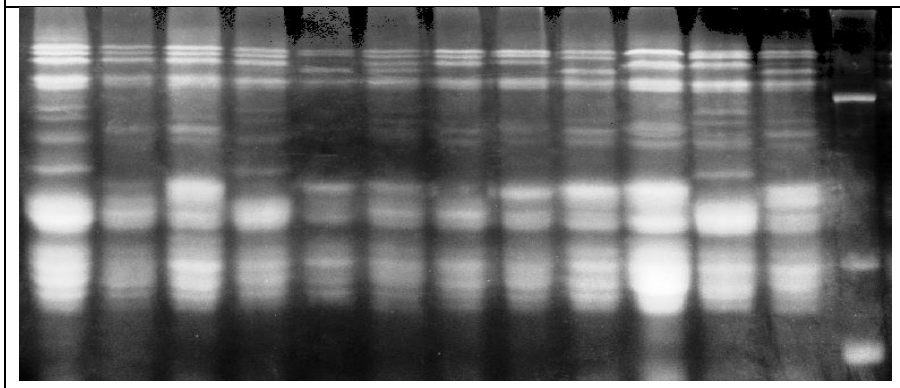
M	13	14	15	16	17	18	19	20	21	22	23	24

The above number 13-24 represent the genotypes with respect to thier bands for their gliadin composition



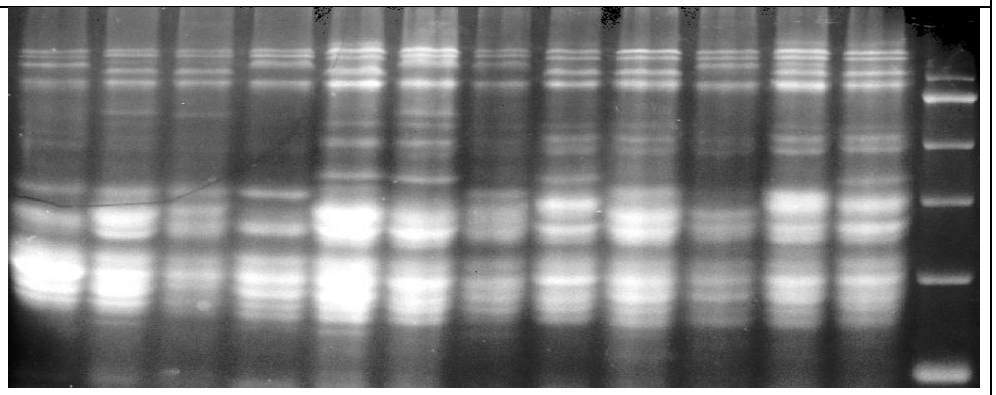
25	26	27	28	29	30	31	32	33	34	35	36	M

The above number 25-36 represent the genotypes with respect to thier bands for their gliadin composition



13	14	15	16	17	18	19	20	21	22	23	24	M

Number 13-24 represent the genotypes with respect to thier bandsfor their glutenin composition



25	26	27	28	29	30	31	32	33	34	35	36	M

Number 25-36 represent the genotypes with respect to thier bands for their glutenin composition

NB. 13 Gliadin markers (M) 21 to 54 in KDa and 9 glutenin markers 35 to 160 were used for screening of the genotypes

Figure 3: Extracted protein sample run on SDS PAGE.

3.3. Seed Storage Protein Diversity Study in Bread Wheat (*Triticum aestivum* L.) Genotypes from Ethiopian Using SDS-PAGE

This investigation was aimed at the determination of seed storage protein diversity among 50 bread wheat genotypes, which were selected based on their group and nature (from commercial, newly released and pipe line groups), using gliadin and glutenin (HMW- and LMW-GS) markers. The study was intended to analyze the seed storage protein genetic diversity and similarity among the genotypes. It is also useful to provide clue to have certain similarity or difference that may exist between the flour quality diversity and seed storage protein diversity in bread wheat genotypes from Ethiopia.

3.3.1. Plant Materials

The plant materials (Table 4) and all the data analytical methods used here are described in details in the bread making quality analysis part of this paper, page (50 - 59), including the following procedures:

3.3.2. SDS-PAGE Procedure

The following Procedure was followed for the flour quality analysis

3.3.2.1. SDS PAGE Preparation and Electrophoresis

It is described in details in the bread making quality analysis part of this paper

3.3.2.2. Protein Extraction

It is described in details in the bread making quality analysis part of this paper

3.3.2.3. Preparation of Separating and Stacking Gels

It is described in details in the bread making quality analysis part of this paper

3.3.2.4. Preparation of Protein Samples

It is described in details in the bread making quality analysis part of this paper

3.3.2.5. Protein Marker Calibration

It is described in details in the bread making quality analysis part of this paper

3.3.2.6. Running of the Gel

It is described in details in the bread making quality analysis part of this paper

3.3.3. Scored Data

It is described in details in the bread making quality analysis part of this paper

3.3.4. Data Analysis

The 50 bread wheat genotypes were analyzed using genetic diversity indices, group differentiation test, and genetic relationships analysis in the following manner:

3.3.4.1. Genetic Diversity Indices and Group Differentiation Test

The genotypic data were subjected to various statistical tools. Accordingly, Power Marker version 3.25 (Liu and Muse, 2005) was used to measure genetic diversity indices at each seeds storage locus, including the total number of alleles (NA), major allele frequency (MAF), polymorphism information content (PIC) and others.

3.3.4.2. Genetic Relationships Analysis

Genetic distances between each pair of genotypes and between pre-grouped groups were measured based on both shared allele frequencies and Nei's genetic distance (Nei *et al*., 1983) using Power Marker (Liu and Muse, 2005). Genetic distance matrices for each locus were summed across loci assuming statistical independence. Pair-wise genetic frequency-based dissimilarity or distance matrix between individuals were calculated according to Nei *et al*. (1983) as implemented in Power Marker. The resulting dissimilarity matrix was subjected to tree construction using the un-weighted pair group method with arithmetic mean (UPGMA) analysis using the same software.

3.4. Genetic Diversity Study in Bread Wheat Genotypes from Ethiopia Using SSR Markers

3.4.1. Plant Materials

A total of 96 bread wheat genotypes included all 43 commercials, all 2 newly released and 51 pipe line genotypes selected based on their group and pedigrees, for the SSR study (Appendix 2). The seeds collected from the phenotypic study, from three locations, were taken to the ICARDA Biodiversity and Integrated Gene Management Program (BIGM) Biotechnology Laboratory in Cairo, Egypt for simple sequence repeat (SSR) analyses.

3.4.2. DNA Extraction

Leaves from two to three-week-old plants grown in a greenhouse were collected into separate microtubes and allowed to dry at room temperature in a glass box to protect them from the dust. The dried leaf samples were pulverized using mortar and pestle. Genomic DNA was extracted following a CTAB protocol with slight modifications (Saghai-Maroof *et al*., 1984).

A total of 850µl CTAB solution was added to the leaf powder (about 0.5gm) in the microtube and incubated at 65^{o}C in water bath for 30min to 1h. Then the mixture was cooled on ice for 5min and chloroform-iso-amyl was added in the proportion of 24:1. Acetate and iso-propanol solution was added to precipitate the DNA pallet and the supernatant/clear solution removed. Finally, the collected pallet/residue was washed with 70% ethanol and dissolved in 1x TE buffer, and made ready for later gel electrophoresis.

Table 5: Transferred and functional *T. aestivum* SSR primers used for screening in *T. aestivum* diversity study {Raman *et al.,* (2014) and Phan *et al.* (2007)}

SN.	Primer code	Forward primer sequence	Reverse primer sequence	Annealing temp.
1	Xgwm_3*****	GCA GCG GCA CTG GTA CAT TT	AAT ATC GCA TCA CTA TCC CA	55
2	Xgwm_129*****	TCA GTG GGC AAG CTA CAC AG	AAA ACT TAG TAG CCG CGT	50
3	Xgwm_165*****	TGC AGT GGT CAG ATG TTT CC	CTT TTC TTT CAG ATT GCG CC	60
4	Xgwm285*	ATG ACC CTT CTG CCA AAC AC	ATC GAC CGG GAT CTA GCC	60
5	Xgwm456	TCT GAA CAT TAC ACA ACC CTG A	TGC TCT CTC TGA ACC TGA AGC	55
6	Xgwm458	AAT GGC AAT TGG AAG ACA TAG C	TTC GCA ATG TTG ATT TGG C	60
7	Xgwm459	ATG GAG TGG TCA CAC TTT GAA	AGC TTC TCT GAC CAA CTT CTC G	55
8	Xgwm471	CGG CCC TAT CAT GGC TG	GCT TGC AAG TTC CAT TTT GC	60
9	Xgwm642	ACG GCG AGA AGG TGC TC	CAT GAA AGG CAA GTT CGT CA	60
10	WMC_24*****	GTGAGCAATTTTGATTATACTG	TACCCTGATGCTGTAATATGTG	51
11	WMC25	TCTGGCCAGGATCAATATTACT	TAAGATACATAGATCCAACACC	51
12	WMC_44*****	GGTCTTCTGGGCTTTGATCCTG	TGTTGCTAGGGACCCGTAGTGG	61
13	WMC_216*****	ACGTATCCAGACACTGTGGTAA	TAATGGTGGATCCATGATAGCC	51
14	WMC243	CGTCATTTCCTCAAACACACCT	ACCGGCAGATGTTGACAATAGT	61
15	WMC256	CCAAATCTTCGAACAAGAACCC	ACCGATCGATGGTGTATACTGA	61

NB. Seven markers (* labelled) showed highly polymorphic bands

3.4.3 SSR Markers Assay and PCR Amplification

For SSR assays, a total of 15 polymorphic SSR markers based on reports by Raman *et al*. (2014) and Phan *et al*. (2007) were selected for screening. Under optimized PCR conditions, seven of the 15 primer pairs consistently amplified their targets and hence were selected for use on the whole samples. PCR amplification reactions were carried out using Gene Amp PCR system 9700 thermos cycler in a total reaction volume of 10µl lyophilized negative dye Bioneer 96 well plate, 1.5 - 2.5µl of genomic DNA template, 0.4µl of each primer at concentrations of 0.2µM, 0.2µlMg buffer at a concentration of 0.5mM to top-up the one present in the Bioneer premix tubes, and 6.5 - 7.5µl demineralized distilled water was added. PCR amplification was carried out at 94^{o}C for 3min, followed by 30 cycles at 94^{o}C for 30s, 55^{o}C-65^{o}C (depending on the particular primer) for 30s to 1min and 72^{o}C for 2min; and a final extension at 72^{o}C for 15min. Annealing temperatures of each primer were determined by primer digital software (primerdigital.com). PCR products of

contrasting florescent labels were pooled based on dye color and band intensities to have uniform signal strength. The pooled PCR amplicons were denatured with Hi-Di formamide at 95^{o}C for 3min and then separated by capillary electrophoresis using an ABI3730 DNA genetic analyzer (Applied Biosystems, Foster City, CA) using GeneScan-500 Internal LIZ and 1200 Internal LIZ Size Standards based on size of amplicons. The fragment analysis data from ABI3730 system were analyzed and allele sizes scored with GENEMAPPER V 4.1 software (Applied Biosystems).

3.4.4. Data Analysis

3.4.4.1 Genetic Diversity Indices and Group Differentiation Tests

The genotypic data were subjected to various statistical tools. Accordingly, Power Marker version 3.25 (Liu and Muse, 2005) was used to measure genetic diversity indices at each SSR locus, including the total number of alleles (NA), major allele frequency (MAF), accession-specific alleles, observed heterozygosity (Ho), number of genotypes (NG), polymorphism information content (PIC) and expected heterozygosity (He). GenAlEx version 6.5 (Peakall and Smouse, 2012) was used to compute the numbers of rare alleles (RA), common alleles (CA) and abundant alleles (AA), partitioning of total genetic variation into within and among pre-grouped groups through molecular analysis of variance (AMOVA), pairwise Fst and gene flow.

3.4.4.2. Genetic Relationships Analysis

Genetic distances between each pair of accessions and between pre-grouped groups were measured based on both shared allele frequencies and Nei's genetic distance (Nei *et al.*, 1983) using Power Marker (Liu and Muse, 2005). Genetic distance matrices for each locus were summed across loci assuming statistical independence. Pair-wise genetic frequency-based dissimilarity or distance matrix between individuals were calculated according to Nei *et al.* (1983) as

implemented in Power Marker. The resulting dissimilarity matrix was subjected to tree construction using the un-weighted pair group method with arithmetic mean (UPGMA) analysis using the same software.

3.4.4.3. Group Structure Analysis

A Bayesian model-based software called Structure 2.3.4 (Pritchard *et al*., 2000; Falush *et al*., 2003) was used to infer the group structure of the sampled genotypes set using a burn-in of 10,000, a run length of 100,000, and a model allowing for admixture and correlated allele frequencies. Five runs of Structure were conducted by setting the number of groups (K) from 1 to 20. The model choice criterion to detect the most probable value of K was, both the LnP(D) value for each given K and ΔK, an ad hoc quantity related to the second-order change of the log probability of data with respect to the number of clusters inferred by Structure (Evanno *et al*., 2005). Once the best K was found, the analysis was re-run in the same software using a burn-in of 10,000, a run length of 500,000 with the same aforementioned model. CLUMPAK: "a program for identifying clustering modes and packaging group structure inferences across K" (CLUMPAKserver) was used.

4. RESULTS AND DISCUSSION

The main results obtained and discussion regarding phenotypic traits, biochemical and microsatellites (SSRs) markers system analysis in the diversity study in bread wheat genotypes from Ethiopia are presented below:

4.1. Phenotypic Diversity Study in Bread Wheat Genotypes from Ethiopia

Phenotypic traits variations in121 genotypes from Ethiopia were investigated during the main growing seasons of the crop (July– November) in 2013 / 2014. The main results of the study are presented below under separate headings:

4.1.1. Analysis of Variance of the Studied Traits

ANOVA was carried out using 12 characters recorded at Adet, Debre Tabor and Kulumsa on the basis of individual locations (Appendix 4, 5 and 6) and across locations (Table 6). Coefficients of variation (CV %) were used to compare the precision of the experimentation, i.e. means with lower CV% for most of the characters revealed existence of reliability of the data (Gomez and Gomez, 1984).

According to the results of ANOVA (Table 6), there was a highly significant difference among the genotypes for all the studied traits including DH, DM, SDO, NT, PH, GY, BY, HI, NSLP, SL, ST and NSS studied at individual locations, confirming the existence of genetic variability for yield and its components. Similarly, the previous study of Awale *et al.*, (2013) and Obsa (2014) reported considerable genetic variability for grain yield and its component characters of studied bread wheat genotypes from Ethiopia. Other authors also reported considerable genetic variability for grain yield and its component characters in durum wheat (Khan *et al.*, 2013 and Mohammed *et al.*, 2011).

Gezahegn *et al*. (2015) reported highly significant differences among genotypes (P<0.01) for DH, DM, PH, SL, NT, NSLP, BY and GY per plot, HI. The significant and wide range of genetic variation obtained in the present study signposts the existence of large genetic variability among the tested genotypes and could be used as baseline information for further work in preservation and breeding of the crop. However, the non-significant variation was observed for the traits PH, NT and SL by other researcher (Adhiena, 2015), may be due to the influence of location-treatment interactions and the negligible (nearly zero) analysis of variability suggested by the presence of stronger genetic base of variations than the environmental effect. Hence, effectiveness of testing the genotypes at multiple sites, and efficiency in selection for the traits on the bases of non-significant values could be likely the reasons.

Table 6: Mean square of the 12 traits of bread wheat genotypes tested at Adet, Debre Tabor and Kulumsa experimental locations

	Source							
	Loc.	Rep * (Loc)	Block (Loc * Rep)	Genotype	Genotype * Location	Error		
Traits	**DF = 2**	**DF = 3**	**DF = 20**	**DF = 120**	**DF = 239**	**DF= 340**	**Mean**	**CV%**
DH	3232.81***	0.08ns	0.32***	186.76***	5.17***	0.21	54.42	0.84
DM	12452.53***	0.46ns	0.28ns	161.16***	12.79***	0.23	103.75	0.49
SDO	149.68***	1.47**	0.53**	49.03***	1.31***	0.23	79.62	0.61
ST	1227.76***	0.18ns	0.58**	72.18***	22.82***	0.27	85.38	0.61
PH	1015.83***	0.43ns	0.70*	247.64***	19.20***	0.42	83.69	0.77
BY	16894.30***	19.98ns	11.02ns	3020.69***	652.66***	9.57	209.58	1.48
NT	2.44***	0.09ns	0.28***	0.88***	0.03ns	0.05	2.44	9.33
SL	63.03***	0.02ns	0.13ns	1.65***	0.25***	0.08	7.49	3.87
NSLP	63.23***	0.01 ns	0.24*	6.60***	0.94***	0.14	16.02	2.31
NSS	136.32***	0.07ns	0.46ns	105.58***	25.83***	0.32	38.79	1.47
GY	16639.92***	3.45**	0.92ns	470.85***	141.30***	0.67	78.73	1.05
HI	0.28***	0.000056*	0.0000059ns	0.006***	0.003***	0.000014	0.38	1.000008

Note, ns, ** and * indicates non-significant, highly significant at 1% and significant at 5% probability levels, respectively. Rep=Replication, Loc = Location, CV = Coefficient of variations and DF= degree of freedom. DH=days to heading, DM=days to maturity, SDO=Septoria disease occurrence, ST=stand percent, PH=plant height, BY=biomass yield, NT=number of tillers, SL=spike length, NSLP=number of spike-lets per plant, NSS=number of seeds per spike, GY=grain yield and HI=harvest index.

The high value of variance detected, particularly, in most of the yield contributing traits, also suggests a favorable condition to identify superior genotypes with respect to direct selection of the traits.

Twelve quantitative characters which had homogeneous error variances were subjected for combined ANOVA over locations (Table 6). Significant location effects were observed for all the traits indicating the differences in growth conditions exhibited at the three locations.

Mean squares of genotypes were significant ($P \leq 0.01$) for all characters studied except number of tillers per plant (Table 6) indicating variability in studied genotypes. Hence, selection could be effective for different quantitative characters or for inclusion in crossing program for creating variability. Such variability with in studied genotypes was also reported by Navin *et al*. (2014).

The location × genotype interaction was significant for DH, DM, PH, GY, SDO, ST, SL, NSLP, BY and NSS except NT and HI indicating different performance of bread wheat genotypes across the three locations or genotypes responded differently to different environmental conditions suggesting the importance of the assessment of genotypes under different environments in order to identify better performing genotypes for a particular environment. The current finding is similar to the previous work of Tesfaye *et al*. (2014) who reported significant differences among genotypes for most of the traits including DH, DM, PH, SDO, TGW and HLW across environments.

4.1.2. Mean and Range of Grain Yield and Yield Related Traits

Phenotypic traits-based univariate analysis in bread wheat genotypes from Ethiopia evaluated at three experimental locations, are presented in combined analysis in the following sections:

Summary of the ranges and the means together with their standard errors, obtained on the basis of quantitative traits data combined over the experimental locations, are shown (Table 7). In general, the bread wheat genotypes from Ethiopia considered in this study showed wide ranges of variation

and wide ranges between the maximum and minimum mean values in most of the 12 quantitative traits considered.

Table 7: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as of mean for the 12 characters of bread wheat genotypes tested across locations in 2015/16.

Traits	Range	Mean	δ^2_g	δ^2_p	H^2	GCV %	PCV %	GA	GAM
DH	43.83-69	54.42	93.28	93.49	99.78	17.75	17.77	19.90	36.57
DM	95.5-118.33	103.75	80.47	80.69	99.72	8.65	8.66	18.48	17.81
SD	72-83.33	79.61	24.4	24.63	99.05	6.20	6.23	10.14	12.74
ST	73.83-92.98	85.38	35.96	36.22	99.26	7.02	7.049	12.33	14.44
PH	69.77-104.08	83.69	123.61	124.03	99.66	13.29	13.31	22.89	27.36
BY	150.76-271.26	209.58	1505.56	1515.13	99.39	18.51	18.57	79.79	38.07
NT	1.467-4.00	2.44	0.41	0.47	88.82	26.30	27.92	1.25	51.17
SL	5.74-9.01	7.49	0.29	0.51	88.50	7.17	9.56	0.94	12.50
NSLP	13.35-19.45	16.02	3.23	3.37	95.96	11.22	11.46	3.64	22.68
NSS	22.53-51.2	38.81	52.63	52.95	99.39	18.7	18.76	14.92	38.46
GY	55.45-97.37	78.73	235.08	235.77	99.71	19.48	19.50	31.59	40.12
HI	0.29-0.47	0.38	0.00299	0.003	99.53	14.50	14.53	0.11	29.83

σ^2_{gl}=genotype by environment interaction variance, σ^2_g= genotypic variance, σ^2_p= phenotypic variance H^2 = broad sense heritability, GCV= Coefficient of genotypic variance, CV= coefficient of phenotypic variance, GA= genetic advance and GAM= genetic advance as a percent of mean

Accordingly, BY revealed the widest range (150.76 – 271.26), about six hundred and sixty nine folds of the minimum range, with average mean performance value of 209.58q/ha, followed by GY (55.45 - 97.37), PH (69.77 – 104.08), NSS (22.53 – 51.2), DH (43.83- 69), DM (95.5-118.33), ST (73.83 – 92.98) and NSLP (13.35-19.45), each with 209.58q/ha, 78.73q/ha, 83.69cm, 38.81, 54.42days, 103.75days, 85.38% and 16.02 in mean performance, in that order. On the other hand, HI showed the least range (0.29 – 0.47), with a mean performance value of 0.38, followed by spike SL (5.74-9.01) with a mean trait value of 7.49. NT revealed a moderate range (1.47-4) about niteen-folds of the minimum range, with average yield of around 2.44.

The tested genotypes were early to medium days to heading and maturing category. Hence, the early maturing genotypes such as ETBW 6841, Laketch and those genotypes at least with a mean value below average in their order are suggested for selection during breeding.

Similarly, the difference in PH and ST showed highly significant difference ($p<0.01$) among the studied genotypes, it is due to genetic differences between genotypes, as plant height is a quantitative trait controlled by many genes (Yao, *et al*., 2011). However, the mean value results were not influenced environmentally, supported by the work of Shahzad *et al*., (2007), that height and stand percent of the crop is mainly controlled by the genetic makeup of a genotype but not by the environmental factors. Hence, genotypes with higher PH and ST are somehow susceptible for lodging and hence are not rewarding for further breeding due to higher PH.

Biological Yield, GY, NSS, and NSLP showed a wide range of variation and higher mean values compared to other traits. This is BY is the sum total of the grain yield and the straw in which one can guess the height of the plant, NSLP and GY can result in such large amount of BY and hence a big difference among genotypes. So, it is suggested to harvest higher biological yield relative to other traits.

The presence of higher NSLP may influence the grain yield production equally which were not influenced environmentally, this result indicates that there was a wider variation or difference among the studied genotypes. Since the higher BY, GY, NSS and NSLP are expected to have a positive effect on economic value or grain yield and hence the genotypes had higher genetic diversity among themselves. Then the higher value of these traits plays a vital role in bread wheat towards the identification of high yielding genotypes which is similar to the previous work of (Shahzad et *al.*, 2007), as far as phenotypic diversity is concerned, these traits showed significant ($P>0.05$) effect among the studied genotypes. In his previous study, the data showed that all the genotypes are statistically significant. So, it can be concluded from the current results that these characters are the

results of genetic character of the genotypes, which is less influenced by agronomic practices. Hence, analyses of BY, GY, NSS and NSLP in yield and associated changes in agronomic traits in bread wheat are useful to develop breeding strategies and to prioritize traits for enhancement. Similar to the previous work of Khan *et al*. (2001) reported that genotypes have different genetic potential regarding the BY, GY, NSS and NSLP.

Moreover, these results indicate the objective and direction of selection and the genetic inheritance of the phenotypic associations. Hence, varieties with large amount of grain yield, larger spikes and spike-lets per spike, higher number of tillers and relatively shorter days to maturity and heading and less susceptible to septoria disease should be given special attention in the efforts towards yield improvement.

Generally, according to the results of analysis (Table 7) of the traits, highest mean and wider range values were scored in the genotypes Hoggana and Huluka and lowest for ETBW6839, ETBW 6939 and ETBW 6848 at individual as well as combined locations, with slight variation in values. Hence it is suggested that the improvement of these traits is possible through intelligent selection in early generations for the genotypes like Hoggana and Huluka but not for the genotypes ETBW6839, ETBW 6939 and ETBW 6848. Similar results were also reported by Subhani *et al*. (2000) while he was doing on wheat study.

Comparison of Some of the Major Phenotypic Traits Among Genotypes

In the current study, based on the result of range and mean values (Appendix 3) and for HI and GY in addition with range, mean and top 3 performers (Table 8). Some of the major phenotypic traits (DM, PH, BY, HI and GY) were considered for comparison about the status (how they are varied)

among 121 bread wheat genotypes, so that, it is possible to sort out the top performers for further breeding and the least 2 (needs further analysis for validation) based on their phenotypic performance as follows:

Table 8: Range and mean values of harvest index and grain yield, and the top three grain yield performer genotypes at three test sites/locations

	Harvest index		Grain yield values		
Location	Range	Mean	Range	Mean	Best grain yield performing genotypes (tons/ha)
Adet	0.23-0.43	0.34	4.32-9.77	6.92	Abola (9.77), Menze (9.69) and ETBW6696(9.36)
Debre Tabor	0.29-0.48	0.38	5.54-9.95	8.36	Tusie (9.95), ETBW6845 (9.93) and ETBW6696 (9.90)
Kulumsa	0.26-0.52	0.41	4.32-9.99	8.35	ETBW6114(9.99), ETBW6212 (9.96) andTBW7693(9.92)

NB. Value of the performance is in parenthesis

Biological Yield

According to the results of this comparison (Appendix 3) at Adet, highest BY recorded in their order for genotypes Menze (287.5), Abola (285.72), ETBW6506 (268.75) and ETBW6439 (268.75) but lowest for ETBW6869 (137.5) and ETBW6847 (125), and all other genotypes scored between these highest and lowest values. However, DM, PH and GY showed almost similar values among the genotypes. This shows that the genotypes responded differently for BY. Indicates that this location was favorable for the production of animal feed due to high variability observed in BY production. Hence, high straw production can be suggested through selection of the genotypes like Menze (287.5), Abola (285.72), ETBW6506 (268.75) and ETBW6439 (268.75) for high production of biological yield and it is not rewarding for selection of the genotypes ETBW6869 (137.5) and ETBW6847 (125) as they were with the lowest By.

Accordingly, the results of comparison of five traits (Appendix 3) at Debre Tabor, the top four BY performer genotypes were ETBW6928 (274), Abola (273.5), ETBW6696 (268.83) and Quiau (263.54), and the lowest BY value was scored by ETBW6850 (164) and K629 bulk (159.66).

However, all other genotypes for their BY values were distributed between the highest and lowest values.

Likewise, at Kulumsa all other traits DM, SDO, PH and GY showed similar mean value for all genotypes, and Enkoy (292.64), Menze (286.41) and ETBW6459 (275.9) were the top three genotypes for BY, whereas ETBW6393 (154) and ETBW6847 (136.07) were the least value recorded. These traits; DM, PH and GY showed almost similar values by the genotypes and by locations.

Generally, from the results of individual locations, the highest BY (292.64kg) was recorded by Enkoy and lowest by ETBW6847 (136.07) at Kulumsa. Hence, due to the highest value of BY yield at this location, it will be suggested that Enkoy is the best genotype to be selected for the purpose of forage production. However, all other traits showed the same values at all and across locations among the studied genotypes; hence, it is possible for the selection of the genotypes for further study at any environment for the traits other than BY.

Grain Yield

In the present study of comparison of the studied traits among 121 genotypes tested (Appendix 3**),** the top 4 genotypes for grain yield (Table 8), varied from 4.32 ton/ha to 9.77 ton/ha (mean of 6.92 tons/ha), 5.54 tons/ha to 9.95 tons/ha (mean of 8.36 tons/ha) and 4.32 tons/ha to 9.99 tons/ha (mean of 8.35 ton/ha) at Adet, Debre Tabor, Kulumsa and across locations, respectively. Since, the genotypes Tusie (9.95 ton/ha), ETBW 6845 (9.93 ton/ha), ETBW 6696 (9.9 ton/ha), Abola (9.77 ton/ha), Menze (9.69 ton/ha) and ETBW 6696 (9.36 ton/ha) at Adet, and at Debre Tabor and ETBW

6114 (9.99 ton/ha), ETBW 6212 (9.96 ton/ha) and ETBW 7693 (9.92 ton/ha) at Kulumsa found to be the top 4 yielders; then, genotypes with top grain yielding capability at least from two locations are suggested to be selected for further multiplication and breeding program, however, further multi-location study is needed for validation. Similar work was done by Gezahegn *et al.* (2015) as reported on the variation of grain yield of bread wheat genotypes per hectare with a range of 2.115 tons/ha (Menze) to 5.955 tons/ha (Alidoro).

Generally, the results of grain yield mean performance at all locations, showed similarity among the genotypes. However, it was better at Debre Tabor and Kulumsa relatively to Adet; hence, better grain yield potential of genotypes for bread wheat breeding is suggested to be at two locations compared to Adet.

Harvest Index (HI)

According to the current result of top performance list of genotypes (Table 8), harvest index ranged from 0.23 to 0.43 with an average value of 0.34 at Adet, ranged from 0.29 to 0.48 with an average value of 0.38 at Debre Tabor and ranged from 0.26 to 0.52 with an average value of 0.41 at Kulumsa. The score of the variable was lower than its theoretical maximum value (0.64) at all locations (Table 8). Hence, the current study showed less harvestability of the biomass by the locations and by the genotypes (with few exceptions) under study, similar to the work of (Foulkes *et al.*, 2011; Reynolds *et al.*, 2012), harvest index has been used to describe the proportion of harvestable biomass; and wheat genotypes have HI of c. 0.45-0.50 (spring type) and 0.50-0.55 (winter type), approaching its theoretical maximum value (c. 0.64 in winter wheat).

4.1.3. Estimates of Genetic Parameters

The amount of genotypic and phenotypic variability that exist in a genotype is of utmost importance in breeding to select better genotypes and initiate a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given genotype.

Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability as well as genetic advance for selection of the traits were studied at individual and presented across locations (Tables 7) in the following manner:

4.1.3.1. Components of Variance and Coefficients of Variation

According to the results obtained (Table 7) across locations, phenotypic variance ranged from 0.003 (HI) to 151.19 tons/ha (BY) and the values for genotypic variances ranged between 0.00299 (HI) and 151.56 tons/ha (BY). Maximum phenotypic variance 151.19 tons/ha and 23.58 tons/ha revealed by the traits BY and GY, respectively, and minimum phenotypic variance was recorded by HI. A wide genotypic variability was also recorded for the character BY (151.19 tons/ha), GY (23.58 tons/ha), PH (124.03), DH (93.49), DM (80.69), and NSS (52.95). Similarly, with the same value order of the traits, higher phenotypic variance was recorded than the genotypic variance. This indicates the effectiveness of selection based on the phenotypic performance for these characters. The rest of the characters showed smaller genotypic variability. The finding is in agreement with Obsa (2014), Majumder *et al*. (2008) and with Obsa (2014) and Majumder *et al*. (2008) and Gezahegn *et al.* (2015) who worked with bread wheat variability analysis.

Similarly, according to the current results in the combined analysis (Table 7), PCV ranged from 6.23% (SDO) to 19.50% (GY). GCV ranged from 6.20% (SDO) to 19.48% (GY). Generally, the

PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. Gezahegn *et al*. (2015), Gergana and Bozhidar (2015) reported similar results observed for all the studied characters for the work on diversity study of wheat. Moderate GCV and PCV values (>10%) were observed for DH (17.75% and 17.77%), PH (13.29% and 13.31%), BY (18.51% and 18.57%), NSLP (11.22% and 11.46%), NSS (18.7% and 18.76%), GY (19.48% and 19.50%), and HI (14.50% and 14.53%), respectively. Adhiena, (2015) reported moderate PCV and GCV for SL, NSS and HI. Similarly, Gezahegn *et al*. (2015) noted moderate phenotypic and genotypic coefficients of variation for thousand grain weight, GY and HI in sixty-four bread wheat genotypes from Ethiopia which are in line with this finding for PCV. The lowest GCV and PCV value (<10%) were observed for DM (8.65% and 8.66%), SDO (6.20% and 6.23%), ST (7.23% and 7.05%), and SL (7.17% and 9.56%), respectively, indicating less scope of selection as they were under the influence of environment. The highest GCV and PCV values (>20%) were observed for a single trait, NT (26.30% and 27.92%), respectively. The result is in line with the finding of Gezahegn *et al*. (2015) and Arati *et al*. (2015).

Therefore, in this study results for the individual as well as combined locations, value of PCV was higher than their corresponding GCV, indicating that the influence of environment on the expression of these characters. Hence, narrower differences between the values of GCV and PCV indicated that the environmental effect was small for the expression and selection for these characters during breeding and selection. Which is similar to the previous work of Deshmukh *et al.* (1986) and Navin *et al.* (2014) reported high and moderate magnitude of GCV and PCV for grain yield and related traits.

The rest of the characters were grouped under low PCV and GCV, indicating less scope of selection as they were under the influence of environment. Suggesting the indication of sufficient information for variability based on these traits among genotypes and hence, help to scale up the scope for genetic improvement of genotypes through selection using these traits, as the previous work of Navin *et al.* (2014) reported higher magnitude of GCV and PCV for grain yield per plant, harvest index, tillers per plant, spike length and test weight which support this finding. The rest of the characters were grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment.

This indicated that selection will be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Similar results of moderate PCV and GCV has been reported for thousand grain weight and grain yield in wheat (Gezahegn *et al*., 2015). The characters days to maturity, septoria disease occurrence, plant height, spike length, and number of spike- lets per spike were grouped under low PCV and GCV. The result is in line with the finding of Mohammed *et al*. (2011) and Gezahegn *et al*. (2015) for characters days to maturity, number of spike-lets per spike and test weight showed low PCV and GCV (<5%) values. Mitsiwa, (2013) also reported low PCV and GCV for grain filling period (1.82%, 1.59%) and days to maturity (3.63%, 3.50%), respectively. Indicating that selection of these traits for improvement of genotypes is less rewarding due to environmental effect.

Generally, from the results observed during the current study at individual as well as combined analysis, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously during conducting an experiment, and hence genotypes and

hybrid development will go a long way with the breeding programs especially in case of wheat. In addition, the variability observed under studied traits may be due to only the environmental factor by the time the research conducted in the experiment by chance to result with high PCV but not with high GCV. So, the high PCV and GCV observed under studied traits are likely to indicate their high variability to in turn offer good scope for selection while breeding.

4.1.3.2 Estimates of Heritability

Among the traits studied, estimate of heritability in broad sense (Hb %) revealed a wide range of variation (88.5%) in spike length to (99.78%) in days to heading. Moreover, all of the traits exhibited high estimate (>80%) of such parameters (Table 7). According to Pramoda and Gangaprasad, (2007), heritability estimates categorized as low (<40%), medium (40-59%), moderately high (60-79%), and very high (≥80). The use of breeding will likely be successful in improving of the studied traits or wheat genotypes selection based on genotype than phenotype.

From this observation then, the high heritability at individual as well as across locations in the genotypes was unaffected by environmental factors but by genetic factors. Hence, selection with high heritable characters could be fairly easy because there would be a close association between genotype and phenotype due to a relatively smaller contribution of environment to phenotype or the high heritability of the traits was due to the influence of genotypic rather than environmental factors and hence, selection of the same genotypes for the traits with high heritability may not be rewarding at different environments.

4.1.3.3. Estimates of Expected Genetic Advance

Genetic advance as per cent of mean (GAM), categorized as low (0-10%), moderate (10-20%) and high 20% and above (Johnson *et al.,* 1955).

According to the current results of GAM (Table 7), all the traits categorized form medium to high GAM with a range of 12.50% in SL to 51.17% in NT. Highest GAM was recorded in NT (51.17%), GY (40.12%), NSS (38.46%), BY (38.07%), DH (36.57%), PH (27.36) and NSLP (22.68), in their order. But all other traits were grouped under moderate level of GAM. This indicates that selecting of the top 5% of the base group could result in an advance of 7.30% to 23.50% percent over the respective group mean. This result is in agreement with the findings of Arati *et al*. (2015), who did on similar work.

GAM was moderate for HI(19.21%) followed by PH, NSLP, and DM, indicating that selecting the top 5% of the base group could result in an advance of 6.97% to 37.69% percent over the respective group mean, which is in conformity with the findings by Gezahegn *et al.* (2015) and Awale *et al.* (2013) for the traits, TGW (20.13%), GY (14.85%), days to 50% heading (14.70%) and number of grains per plant (14.65%) except for HI (15.68%).

GAM was high for most of the findings such as HI (37.69%) followed by NT, NSLP, GY, BY and DH, respectively. This result was moderate for PH (15.28%) followed by NSLP and SL in conformity with the findings by Gezahegn *et al.* (2015) and Awale *et al.* (2013) for the traits, GY (14.85%), days to 50% heading (14.70%) and number of grains per plant (14.65%) except for HI (15.68%). However, the value of GAM was low for DM (9.93%) and septoria disease occurrence (6.97%).

Generally, according to the results of combined analysis (Table 7), GAM was categorized as moderate to high for all the studied traits.

The category of GAM from moderate to high in phenotypic traits indicates the correlation of GAM with high genetically heritability of the traits for each individual as well as combined locations as in the current work, similar to the work of Gergana and Bozhidar (2015) with moderate GAM for SL (31.83%), and for Mohammed *et al*. (2011) high GAM for GY and related traits, and also Awale *et al*. (2013) reported high genetic advance for the traits DH, NT, PH and SL.

So, from the results observed in the current finding, it is suggested that selection could be effective in genotypes for the traits with high to moderate GAM for the purpose of great possibility of improving bread wheat genotypes through direct selection based on the heritability of the traits at these values concerning grain yield and related traits.

In addition, characters like DH, PH, BY, NT, NSLP, NSS, GY and HI showed high heritability coupled with high genetic advance in the current work. Therefore, these characters should be given top priority during selection breeding in wheat, which is similar to Desheva and Cholakov (2014) for SL and similar grain yield and related traits indicated heritability was due to additive gene effects, and selection may be effective in early generations for these traits. This result was also supported by Gezahegn *et al*. (2015) as he reported that high heritability coupled with moderate GAM for PH (69.43%, 10.27%), SL (63.66%, 10.34%), and with similar other phenotypic traits.

The association of high heritability with moderate genetic advance exhibited by DM (99.72, 17.812), septoria disease occurrence (99.05, 12.738), ST (99.263, 14.435) and SL (88.5, 12.5), respectively; may be because of the predominance of non-additive gene action in the expression of this character.

Therefore, from the current results observed, the couple occurrence of high to moderate heritability and GAM, indicated presence of significant genetic variation among the studied genotypes. Thus, there is an opportunity to select superior genotypes among advanced bread wheat genotypes through direct selection at the study locations as short-term strategy rather than a lengthy crossing program.

4.1.3.4. Estimation of Association of Phenotypic Traits

In this part of the study association among traits was analyzed using two methods; based on correlation coefficients and based on biplot and clustering in the following manner:

A. Analysis Using Correlation Coefficients

Analysis of correlation coefficients was performed to find out the inter-relationships among the studied pairs of traits. In this regard, genotypic and phenotypic correlation coefficients between yield and yield related traits are presented below:

Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between each pairs of characters were studied at three locations and presented as over locations (Table 9). In most of the traits studied, the phenotypic correlation coefficients were less in magnitude than the genotypic correlation coefficients that revealed the presence of inherent genetic relationships among various characters and less dependent on environment. Similarly, genotypic correlation coefficients were found to be higher in magnitude than that of phenotypic correlation coefficients in most of the traits, indicated the presence of inherent association among the studied characters.

Table 9 Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of the 12 quantitative traits of bread wheat genotypes across locations 2014/15 cropping season

Trait	DH	DM	SD	ST	PH	BY	NT	SL	NSLP	NSS	GY	HI
DH	1	**0.76*** **	**-0.07ns**	**0.39*** **	**0.28***	**0.27***	**-0.09ns**	**-0.05ns**	**0.42*** **	**0.33*** **	**0.05ns**	**-0.34*** **
DM	0.76***	1	**-0.03ns**	**0.22***	**0.18ns**	**0.15ns**	**-0.05ns**	**-0.13ns**	**0.44*** **	**0.34*** **	**0.008ns**	**-0.23***
SDO	-0.07ns	-0.02ns	1	**0.14ns**	**0.06ns**	**0.13ns**	**0.04ns**	**-0.20***	**-0.08ns**	**0.07ns**	**0.16ns**	**0.08ns**
ST	0.39***	0.22***	0.14*	1	**0.28****	**0.47*** **	**-0.20***	**-0.22***	**0.02ns**	**-0.08ns**	**0.37*** **	**-0.09ns**
PH	0.27***	0.18**	0.06ns	0.28***	1	**0.54*** **	**-0.04ns**	**-0.07ns**	**0.11ns**	**0.26****	**0.38*** **	**-0.13ns**
BY	0.27***	0.15*	0.13*	0.47***	0.54***	1	**-0.09ns**	**-0.20***	**-0.03ns**	**0.12ns**	**0.80*** **	**-0.10ns**
NT	-0.08ns	-0.04ns	0.03ns	-0.19**	-0.04ns	-0.08ns	1	**0.28****	**0.19***	**0.14ns**	**0.009ns**	**0.15ns**
SL	-0.05ns	-0.12ns	-0.20**	-0.21***	-0.066ns	-0.19**	0.27***	1	**0.43*** **	**0.37*** **	**-0.09ns**	**0.12ns**
NSLP	0.40***	0.43***	-0.07ns	0.013*	0.108ns	-0.03ns	0.175**	0.42***	1	**0.65*** **	**-0.052ns**	**-0.076ns**
NSS	0.33***	0.34***	0.069**	-0.076ns	0.26***	0.12*	0.14*	0.37***	0.63***	1	**0.15ns**	**0.0ns8**
GY	0.047*	0.008ns	0.16*	0.37***	0.38***	0.80***	0.007**	-0.09ns	-0.052ns	0.15*	1	**0.52*** **
HI	-0.34***	-0.23***	0.082ns	-0.092ns	-0.13*	-0.10ns	0.13*	0.12*	-0.075ns	0.077ns	0.51***	1

Note, ** and * indicates highly significant at 1% and significant at 5% probability levels, respectively. DH: days to heading, DM: days to maturity, SDO: Septoria disease occurrence, ST: stand percent, NT: number of tillers, GY: grain yield, BY: biomass yield, HI: harvest index, NSLP: number of spike-lets per plant, PH: plant height (cm), NSS: number of seeds per spike, and SL: spike length

Accordingly, GY per hectare of land showed a highly significant ($p<0.001$) and positive genotypic correlation with ST (0.37), PH (0.38), BY (0.80), HI (0.52) whereas, the correlation with all the remaining traits were non-significant. In addition, the extents of correlation sound higher ($r > 0.5$) for BY and HI, in that order (Table 9).

Likewise, GY per hectare of land showed a highly significant positive phenotypic correlation with ST (0.37), PH (0.38), BY (0.80), HI (0.51) ($p<0.001$), NT (0.007) ($p<0.01$), DH (00.05), SDO (0.16), NSS (0.15) ($p<0.05$) and positive non-significant with DM (0.008) but negative non-significant with SL(-0.009) correlation (Table 9). Moreover, BY and HI revealed a strong correlation ($r>0.5$) in their order of magnitude. Indicates, the objective and direction of selection and the genetic inheritance of the phenotypic associations. Which is similar to the works of Wasif *et al*. (2015), reported significant positive phenotypic correlations of BY, NSS and PH with GY. The same author reported non-significant correlation of NSS and HI with GY which contradicted with this finding. Quan (2015) also reported positive correlations of GY with BY, HI, NSS, which is in agreement with the present study for those traits. Foulkes *et al.*, (2011) reported high biomass is an especially valuable trait to raise yield potential of bread wheat, because HI is approaching the limit of approximately 0.64, and

there has been no significant progress since the early 1990s (0.50-0.55). Recent yield improvement has shown an association with increased biomass (Sadras and Lawson, 2011).

Among the studied characters (Table 9), positive correlations of BY and HI are the most important physiological traits, Majumder *et al.* (2008) indicating improvement of these characters can increase the GY of bread wheat. However, in the current study, GY showed non-significant positive phenotypic correlations with the rest of the characters contradicting the previous work of Majumder and others; however, further study is necessary for validation. The result is in agreement with Awale *et al.* (2013) for the association of DH with DM and grains filling period. Wasif *et al*. (2015) reported significant positive phenotypic association of PH with SL, BY, NT and grains, and also reported significant positive phenotypic correlations of BY, NSS and PH with GY in addition to correlation among BY and SL.

On the other hand, the current finding contradicted with Quan (2015) and Ali *et al.* (2008) who reported weak BY association with PH, indicating that more biomass can be achieved in short plants, which is essential for lodging resistance. However, the same author reported non-significant correlation of thousand kernel weight and harvest index with grain yield which contradicted with this finding. Quan (2015) also reported positive correlations of GY with BY, HI, NSS, which is in agreement with the current study for those traits. Foulkes *et al.*, (2011) reported high biomass is an especially valuable trait to raise yield potential of bread wheat, because HI is approaching the limit of approximately similar to the value 0.64, and there has been no significant progress since the early 1990s (0.50-0.55). Recent yield improvement has showed a negative association with increased biomass (Sadras and Lawson, 2011).

Similar association in winter wheat was also reported by Majumder *et al.,* (2008) in spring wheat indicating improvement of these characters can increase the grain yield of wheat.

Days to maturity showed week positive significant correlation with stand percent (r=0.17), plant height (r=0.47), biological yield (r=0.49), number of seeds per spike (r=0.30), spike length (r=0.02), grain yield (r=0.06) and number of spike lets per plant (r=0.43) and negative significant correlation with Septoria disease occurrence (r=-0.08), number of tillers per plant (r=-0.04) and harvest index (r=-0.08)).

So, from the results observed in the study of individual as well as combined analysis, characters that had positive correlations with each other are likely to occur together for the purpose of breeding with two or more traits in a program, while those characters showing negative correlations are not to be considered together for breeding purposes. Hence, it is suggested for simultaneous selection and breeding of those traits that showed positive significant correlations for the purpose of inclusion of two or more traits in a breeding program.

Similarly, Adhiena (2015) and Birhanu (2010) reported biomass yield (r= 0.8) had positive and high correlation with grain yield. Obsa (2014) also reported highly significant positive phenotypic correlation of grain yield with above ground biomass and harvest index which support the current finding, in which grain yield showed significant positive correlation with days to heading, plant height, spike length and number of seeds per spike. Hence, selection based on these characters could be suggested for the valid and simultaneous improvement two or more traits for economic or grain yield in bread wheat.

Days to heading showed significant positive correlation with DM, PH, BY, NSLP and NSS at both genotypic and phenotypic level. However, its association with SDO, SL and HI were negative, this implied that increasing the DH would increase DM, BY, PH, NSLP and NSS as the expense of SDO, SL and HI. This association is similar with the difference of correlation coefficient value. Awale *et al*. (2013) and Navin *et al*. (2014) reported highly significant association of DH with DM and NSLP.

Days to maturity showed positive significant correlation with PH, BY, NSLP and NSS at both genotypic and phenotypic level. This probably indicated that longer phonological period could result in large biomass accumulation with the maximum contribution to NSS and GY. Its association with SDO, SL and HI were negative similar to the trait occurred in DH.

Septoria disease occurrence showed significant and positive correlation with PH, BY, NSS, and NSLP but negatively correlated with SL and HI at phenotypic level. At the genotypic level PH, BY, SL and HI showed negative correlation with SDO showing that these traits are environmentally influenced.

Harvest index had significant negative correlation with all the studied traits but it showed highly positive correlation with GY at both genotypic and phenotypic level. Naeem *et al.* (2006) reported BY showed positive and highly significant correlation coefficients with GY and negative association with HI on his experiment in titled with estimation of genetic and phenotypic correlation coefficients among grain yield and its components in bread wheat. Adhiena (2015) and Wasif *et al*. (2015) also reported negative association of BY and HI. This indicates that increments in the BY reduce the HI ratio.

Plant height showed significant positive correlation with BY, NSLP and NSS and significant negative correlation with SL and HI at both genotypic and phenotypic level. This clearly indicated that larger BY is the result of increment in PH. Similarly, Birhanu (2010) reported a positive significant association of PH and BY (r=0.34). NSS exhibited significant and positive correlation with all the traits studied. Similar report was indicated by Quan (2015), 1000 kernel weight was consistently negatively associated with grains per spike.

Spike length revealed significant positive association with NSLP and NSS and significant negative correlation with PH, SDO, DM and DH at both phenotypic and genotypic levels. Obsa (2014) reported positive and significant correlation of peduncle length with PH and NSS, suggesting the genotypes with longer peduncle length may also be longer in PH with a greater NSS. It also showed significant positive correlation at genotypic level with PH and NSLP.

Biological yield showed significant positive association with number of NSLP and NSS and negatively correlated with SL and HI at both phenotypic and genotypic level. NSLP showed positive correlation with NSS at both phenotypic and genotypic level, but NSLP and NSS showed negative association with HI.

Tiller per plant and spike per plant had highly significant and positive association at both genotypic level and phenotypic level indicating an increasing the number of tillers per plant could result in high number of spikes per plant. This indicates a key function of tillering is to establish final spike number per plant Quan (2015).

Generally, from the results at individual as well as combined locations, those characters in which grain yield showed positive and significant correlations, there were component interactions in which a gene conditioning that can increase in one character will also influence another character provided other conditions are kept constant.

Similarly, the results showed that yield per hectare had a positive phenotypic as well as genotypic correlation with other traits except for unfilled grain per panicle and plant height. Grain yield trait does not exist in isolation but rather as a result of an association with other traits that form a complex relationship that ultimately affects the yield. So, selection based on the correlated components is effective due to their equal contribution towards grain yield increment.

B. Estimation of Morphological Traits Relationships and Profiles Using Dendrogram and Biplots Methods

Traits relationships and their profile was analyzed using the dendrogram (Figure 3a, 4a, 5a and 6a) and biplot/ trait vector projectile (Figures 3b, 4b, 5b and 6b) for individual and over locations, respectively. Both phenotypic and grain quality traits were analyzed together, however, they were treated separately with respect to their parts of the thesis.

For the phenotypic study, traits were investigated based on dendrogram and biplot methods, how the traits were related/different to each other at individual as well as across locations in the following manner:

According to the results of dendrogram-based relationships among the 12 traits studied, at Adet (Figure 3a), there were 4 main cluster groups; the first cluster included a solitary trait SL, the second cluster consisted of SDO and HI. The third cluster included two sub clusters consisting of NSLP and

NSS in one sub cluster and DH, DM and ST in the other. The fourth cluster consisted of two sub clusters in one solitary trait PH was found and in the other two traits BY and GY found.

During the study of traits relationships based on biplot method (Figure 3b); a solitary trait SL was found in the 1st quadrant in opposite direction to the traits GY and PH in the 3rd quadrant. In the 2nd quadrant similarly a solitary trait HI was found in opposite direction to the largest member of traits DH, DM, PH, BY, NSLP and NSS in the 4th quadrant.

Based on the direction they follow/arrow using vector methods, the traits analyzed showed similar results to dendrogram analysis for Adet. Since, the similarity in the vector direction of the traits follow is important indication for the association of the traits to occur simultaneously and, hence to consider together during breeding and to occur together and cultivar development programs.

So, traits followed the same direction/similarly and or in the same cluster groups are expected to be considered together during breeding programs and cultivar development. Two traits are positively correlated if the angle between the vectors is acute (<90°); negatively correlated if the angle is obtuse (>90°); and not correlated if the angle is right angle (Yan and Tinker, 2006).

At Debre Tabor, relationships among 12 traits using dendrogram (Figure 4a) studied during phenotypic study 4 main clusters found. The first cluster included a solitary trait ST and the second cluster composed of two sub clusters a solitary trait NSS in the first sub cluster and PH, BY, NSLP, DH and DM in the second sub cluster. The third cluster composed of traits GY and HI. The fourth cluster composed of two sub clusters in which the first includes traits SD and NT and the other includes a solitary trait SL.

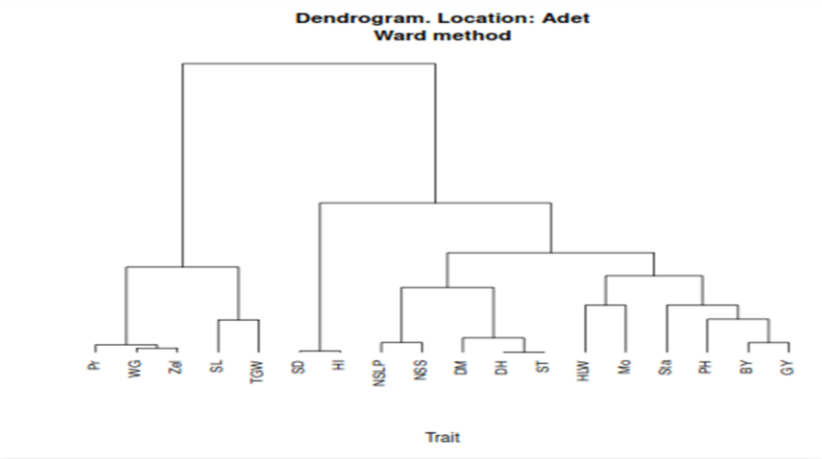


Figure 3a: Dendrogram of 12 traits studied for Ethiopian bread wheat genotypes based on Wards method at Adet**.**

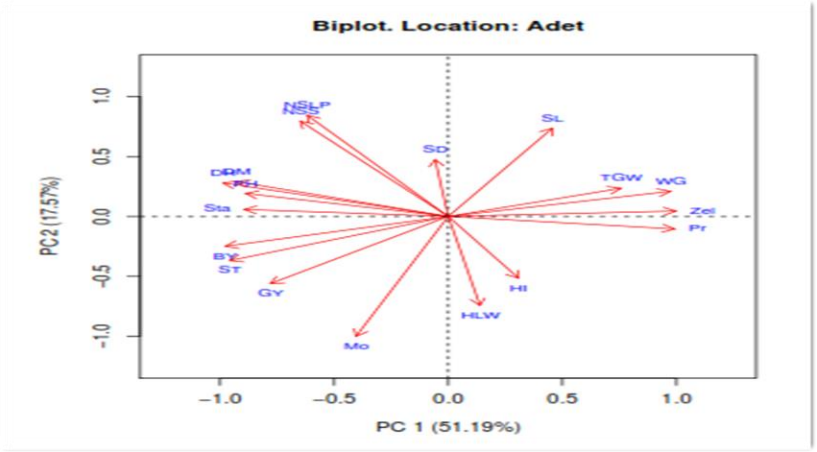


Figure 3b: Biplots showing the interrelationships among different traits for bread wheat evaluated in different scenarios at Adet

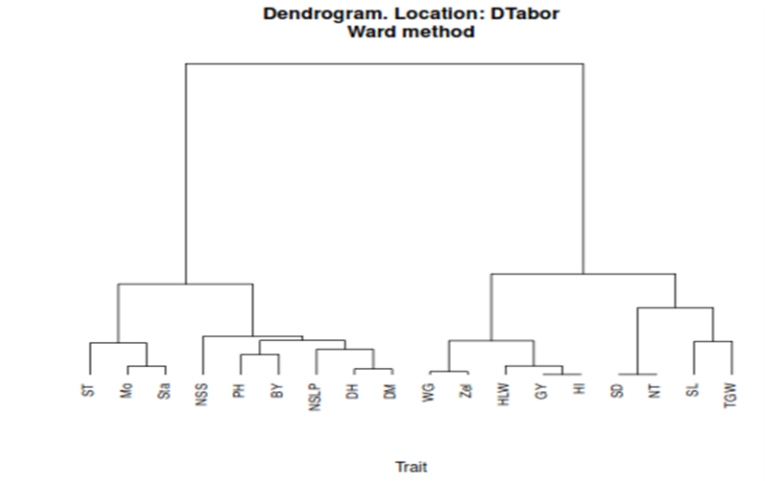


Figure 4a: Dendrogram of 12 traits studied for Ethiopian bread wheat genotypes based on Wards method at Debre Tabor

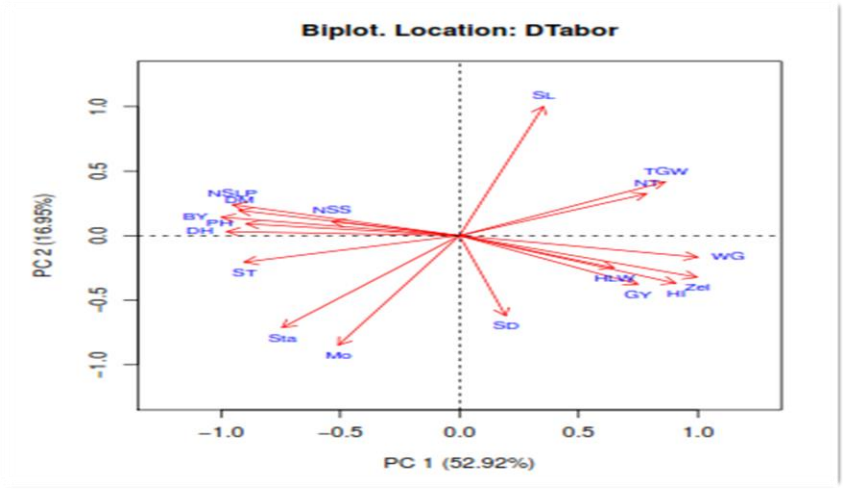


Figure 4b: Biplots showing the interrelationships among different traits for bread wheat evaluated in different scenarios at Debre Tabor

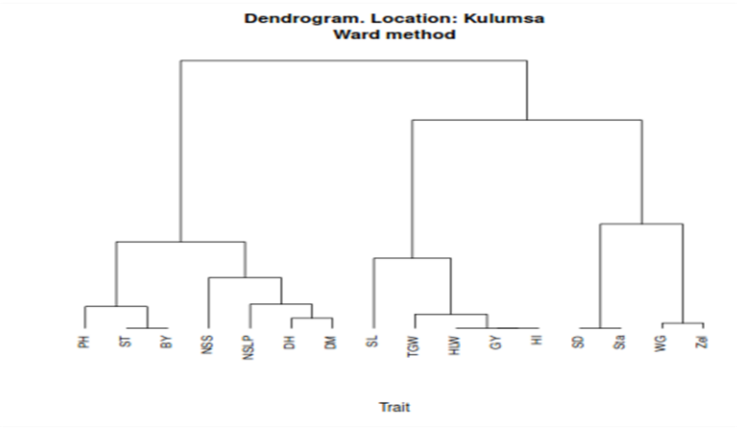


Figure 5a: Dendrogram of 12 traits studied for Ethiopian bread wheat genotypes based on Wards method at Kulumsa**.**

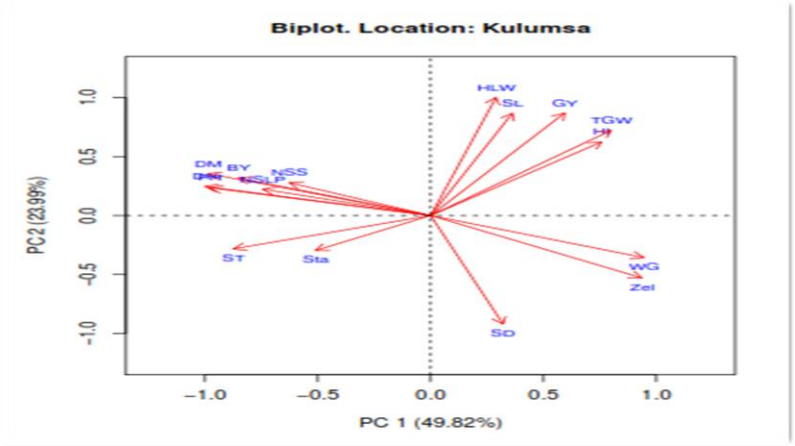


Figure 5b: Biplots showing the interrelationships among different traits for bread wheat evaluated in different scenarios at Kulumsa

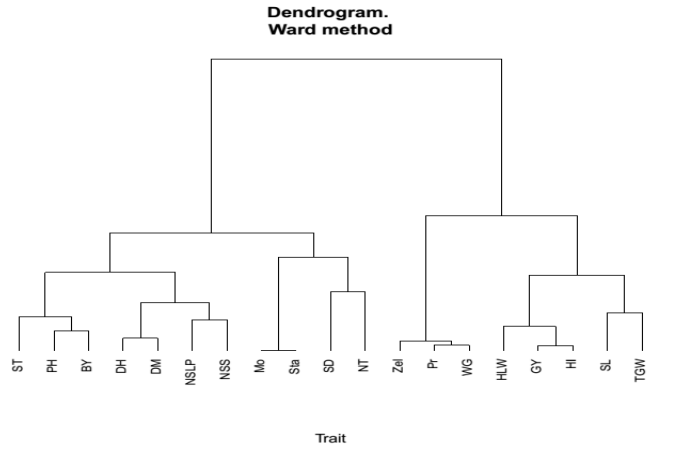


Figure 6a: Dendrogram for 7 traits studied for 50 Ethiopian bread wheat genotypes evaluated based on Wards method across locations

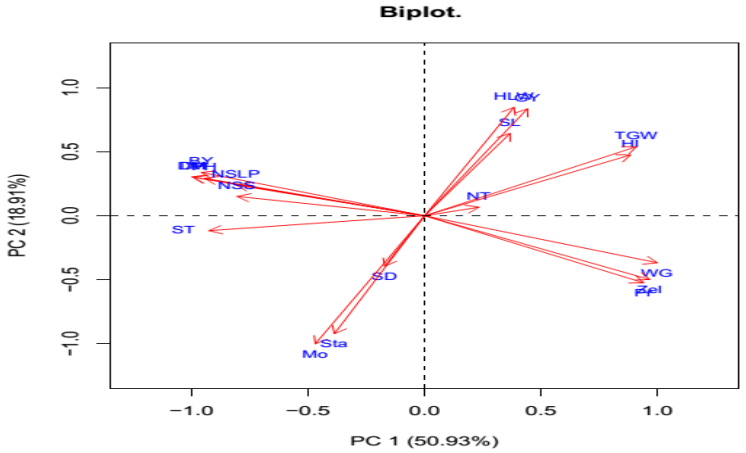


Figure 6b: Biplots showing the interrelationships among different traits for 50 bread wheat genotypes evaluated in different scenarios across locations

During the study of traits at Debre Tabor, relationships based on their direction using biplot method (Figure 4b); SL and NT were found in the same direction in the 1st quadrant in opposite direction to the solitary trait ST found in the 3rd quadrant. In the 2nd quadrant traits GY, HI and SD were found in opposite direction to the largest member of traits DH, DM, PH, BY, NSLP and NSS in the 4th quadrant.

According to phenotypic relationship studies among 12 traits based on dendrogram as of Ward method (Figure 5a), there were 5 main clusters. The first cluster composed of two sub clusters, the first sub cluster included a solitary trait PH and the second sub cluster was with traits ST and BY. The second cluster also composed of two sub clusters in which NSS was found alone in the first sub cluster while traits NSLP, DH and DM were included in the second sub. The third cluster included a solitary trait SL. The fourth cluster included traits GY and HI. The fifth cluster included a solitary trait SD.

Similarly, relationships study based on their vector/direction using biplot method (Figure 5b); SL, GY and HI were in the same direction found in the 1st quadrant but opposite in direction to the solitary trait ST which was in the 3rd quadrant. In the 2nd quadrant a solitary trait SD was found in opposite direction to the largest member of traits DH, DM, PH, BY, NSLP and NSS in the 4th quadrant.

Generally, in the current study, at individual locations (Figure 3a &b, 4a&b, and 5a&b) as well as across locations (Figure 6a & b), similar results were observed, i.e., SL, GY, NT and HI were found in the same direction in the 1st quadrant in opposite direction to the solitary trait ST found in the 3rd quadrant. In the 2nd quadrant a solitary trait SD was found in opposite direction to the largest member of traits DH, DM, PH, BY, NSLP and NSS in the 4th quadrant. Hence, those traits that were occurring

together in a cluster and following the same direction/vector projections are expected to go together during breeding and cultivar development than traits found on different clusters and direction of their projections.

4.2. Genetic Diversity Study in Bread Wheat Genotypes from Ethiopia Using Grain and Flour Baking Quality

Various quality tests need to be carried out to evaluate the bread making potential of wheat genotypes. Baking test has been found to be one of the most reliable methods for assessment the bread making quality of wheat flour. However, this test is time consuming and labor intensive. Thus, simpler and rapid indirect tests, such as thousand grain weight, hectoliter weight, the SDS sedimentation volume, protein content and similar other tests have been devised and widely adopted, but it does not always differentiate effectively wheats of medium strong quality. Hence, other methods are needed to test the suitability of flours in terms of bread making quality in a shorter period of time. The determination of rheological properties of wheat flour dough is essential for the successful manufacturing of bread because they affect the behavior of dough during mechanical handling, thereby, influencing the quality of the finished product (Khatkar, 2002).

4.2.1. Estimation of Variation in Grain Physical and Chemical Quality Traits of the Bread Wheat Genotypes

In this study 121 bread wheat genotypes for their bread making performance were analyzed based on grain physical quality such as thousand grain weight (TGW) and hectoliter weight (HLW) and grain chemical quality like protein, moisture, starch, gluten and zeleny contents in the following manner:

4.2.1.1. Analysis of Variance for Studied Traits

ANOVA was carried out for individual locations (Appendix 11, 12 and 13) and across locations (Table 10) for seven characters. Accordingly, there was a highly significant difference among the genotypes for all the traits studied at individual as well as combined locations confirming the genetic variability for grain quality characteristics. Obsa, (2014) and Awale *et al.,* (2013) also reported considerable genetic variability for grain quality characters in studied bread wheat genotypes from Ethiopia. Other authors also reported considerable genetic variability for grain quality characters in durum wheat (Khan *et al.,* 2013) and Mohammed *et al.* (2011). Gezahegn *et al*., (2015) reported significant differences among genotypes ($P<0.01$) for hectoliter weight, thousand grain weight, protein and starch contents, wet gluten and sedimentation volume contents. Coefficients of variation (CV %) was used to compare the precision of the experimentation, i.e. means with lower CV% for most of the characters revealed existence of reliability of the data (Gomez and Gomez, 1984).

In the current study, all the seven grain quality characteristics had homogeneous error variances. The traits were subjected to combined ANOVA analysis over locations (Table 10). Significant location effects were observed for all the traits indicating the differences in grain quality conditions exhibited at the three and combined locations. Mean squares of genotypes were significant ($P\leq0.01$) for all characters, indicating variability for these traits in studied genotypes. Hence, selection could be effective for different quality characters or for inclusion in crossing program for creating variability. Such variability within studied genotypes was also reported in a previous study by Navin *et al*., (2014).

Table 10: Mean squares of seven traits of bread wheat genotypes tested at Kulumsa, Debre Tabor and Adet in 2014/15.

	Groups							
	Loc.	Rep * (Loc)	Block (Loc * Rep)	Genotype	Genotype * Location	Error	Mean	CV
Traits	**DF = 2**	**DF = 3**	**DF = 20**	**DF =120**	**DF = 240**	**DF = 340**		
TGW	59804.32	0.23	0.34	71.29	46.49	0.34	39.86	1.46
HLW	186226.53	0.94	8.80	18.85	10.13	0.22	55.25	0.85
MOC	726.81	0.13	0.17	1.29	1.36	0.15	12.01	3.19
Prot.	302.05	0.44	0.24	1.70	1.43	0.11	11.68	2.87
Sta	123.41	0.27	0.20	22.51	18.56	0.18	65.16	0.66
WG	2446.27	0.78	0.35	17.81	7.10	0.21	22.62	2.01
Zele	3800.67	1.31	0.29	60.92	19.36	0.24	29.39	1.67

Note, all the traits studied were highly significant at 1% probability levels. Rep =Replication, Loc = Location, CV = Coefficient of variations and DF= degree of freedom

4.2.1.2. Mean and Range of Grain Quality Traits

Grain quality traits-based univariate analysis in bread wheat genotypes from Ethiopia evaluated at three experimental locations, are presented in combined analysis in the following sections:

Summary of the ranges and the means together with their standard errors, obtained on the basis of quanlitative traits data for each location (Appendix 4, 5 and 6) and combined over the experimental locations (Table 11) are presented. In general, bread wheat genotypes from Ethiopia considered in this study showed wide ranges of variability and wide ranges between the maximum and minimum mean values in most of the 7 qualitative traits considered in the following manner:

Thousand Grain Weight (TGW)

In the present study for individual locations, TGW, ranged from 22.5 to 42.35g in genotypes Hoganna and ETBW6529, respectively, and had average value of 33.33g. For TGW 54. 55.0% of

the genotypes were above and 53.72% of the genotypes were below the grand mean (33.33g) at Adet. At Debre Tabor, TGW ranged from 20.8 to 37.5 in genotypes KBG01 (20.8g) and ETBW6529 (37.5g) respectively, with a mean value of 28.49g. Similarly, 54.55% of the genotypes were below and 53.72% of the genotypes were above the grand mean (28.49g) in a way as in the Adet location. At Kulumsa, the range for TGW was 13.47 to 29.03g in genotypes KBG01 (13.47g) and ETBW6529 (29.03g), respectively with a mean value of 23.41gm, and the genotypes that were below the mean value were 43.80% and the genotypes that were above the grand mean were 56.20%. The genotype (KBG01) scored minimum value and genotype (ETBW6529) that scored maximum value were the same in the Debre Tabor and Kulumsa locations, however, the two extreme values were larger at Adet than at Kulumsa. But the maximum value, with a slight difference in values, was scored by genotype (ETBW6529) collected from the three locations.

Since, TGW measures the mass of the wheat kernel and used by wheat breeders and flour millers as a complement to test weight to better describe wheat kernel composition and potential for flour extraction. Hence, wheat genotypes with a higher TGW such as KBG01 and ETBW6529 are suggested to have a greater potential in flour extraction in bread making capability.

However, the previous study of Estifanos, *et al*., (2007) and Gelalcha, *et al.,* (2000) stated that the TGW values of 20 advanced bread wheat lines grown at Haramaya and ten bread wheat genotypes from Ethiopia grown at Kulumsa ranged between 33.2-44.8 g and 32.0-45.9 g, respectively; which is slightly different to the results of the present study. In some previous studies (Abubaker *et al*., 2013) it was shown that genotypes have significant effect among the studied genotypes for TGW in agreement with the current study. Hence, from these results, it is possible to suggest that the previous

workers result with a slight difference to the current may be due to variation in the environment of test sites, whereas, the agreement of the previous workers to the current study may be due to genetic factors rather than environmental factors. So, selection can be due to the direction of genetic than phenotypic factors.

Thousand grains weight is an important indication of flour yield where wheat can be classified according to grain weight as 15-25 g (very small), 26-35 g (small), 36-45 g (medium), 46-55 g (large) and over 55 g (very large) (Williams, *et al.* 1993). Accordingly, 82.6% of the wheat genotypes in the current study fall under small grain category while the rest 17.4% of the genotypes were in medium sized kernels. So, the bread wheat genotypes Madawalabu, Dinkinesh, Galil and Gassay with relatively higher TGW (>35g) are suggested to be explored by breeders for the improvement of grain yield and hence, for better flour extraction during milling. Similarly, as of Dhaka *et al*., (2012), TGW is a useful trait for the assessment of the potential milling quality. Hence, variability of the kernel size (which has direct relation with TGW) contributes directly towards the improvement of grain yield as well as milling yield. The present study suggests that the wheat genotypes possessing higher grain weight (TGW) offer great potential for better milling yield and hence wide variation in grain weight could be an indication for exploitation by the wheat breeders to incorporate this trait in the new genotypes.

Hectoliter Weight (HLW)

HLW depends on the shape, size and soundness of grains and should be more than 76kg/l for industrial use and the difference in the HLW may be attributed to the difference in climatic conditions, cropping practices and genetic makeup of the genotypes (Dhaka *et al*., 2012).

In the current study, the range for hectoliter weight at Adet was 67.77 (ETBW 6876) to 78.54 (ETBW 6169) which was with a similar narrow range as that of Debre Tabor location from 60.2E (TBW 6911) to 74.3 (Millennium). Relatively, the range at Kulumsa was wider from Kulkulu (25.16) to Millennium (67.36). This trait was with highest mean value at Adet (74.22) followed by 68.12 at Debre Tabor and then 57.79g at Kulumsa.

Hectoliter weight provides a rough estimate of flour yield potential in wheat and is important to millers just as grain yield is important to wheat producers. This variable ranged from 67.77 kg/hl (ETBW 6876) to 78.54.9 kg/hl (ETBW 6169) with an average value of 74.22 kg/hl at Adet, a range of 60.2kg/hl (ETBW 6911) to 74.3 kg/hl (Millennium) with an average value of 68.123 kg/hl at Debre Tabor and ranged from 25.16 kg/hl (Kulkulu) to 67.36 kg/hl (Millennium) with an average value of 57.79 kg/hl at Kulumsa.

The hectoliter weight, which depends on both grain size and shape, is considered to be one of the most important physical criteria in all wheat grading systems as it highly influences milling quality for the flour yield and baking quality. So, from the current finding, across locations (Appendix 8) all genotypes performed below the standard value 76kg/l (Dhaka *et al*., 2012) for industrial use, hence the trait is not rewarding for further breeding and preservation of genetic potential of genotypes in any environment. However, at a single location, Adet, for about 13 genotypes out of all the studied genotypes were equal or greater to the standard value (76kg/l) of HLW as Dhaka and others work indicated, in close agreement with the previous work of Cornish *et al*. (2001) who reported that HLW of 130 hard red spring bread wheat grown at different locations of USA varied from 66.2 to 80.20 kg /hl, and 77.91 kg/hl to 82.15 kg/hl in 20 bread wheat genotypes from Ethiopia, respectively; and similar to the previous findings of Muhammad *et al*. (2009) who reported the range of HLW from

68.30 to 81.00 kg/hl in different bread wheat genotypes studied from Pakistan. This may be due to the influence of an environment for the influence; however, it needs further study for validation.

Protein Content

In a previous study of Dhaka, *et al*., (2012), the protein content of wheat genotypes ranged from 8.61 to 14.7% with an average value of 12.22%, similar to the present findings. Flours suitable for bread making are those made from hard wheat and have high protein content in the range of 11 to 14% (Ktenioudaki, *et al*., 2010). Protein content and composition of wheat is the most important criteria in the determination of wheat quality (Bilgin and Korkut, 2005). Protein content determines water absorbing ability, dough stability, dough resistance and elasticity. The importance of protein content also lies in the ability of gluten to produce dough with the desired rheological properties. Moreover, higher amount of good quality protein is required for gas retention and dough rise during fermentation or early stages of baking of bread.

In the present study, the protein content at Adet ranged from 10.15 to 14.85% with a minimum value in genotype ETBW 6492 and maximum value in genotype Dinknesh, respectively, with an average value of 12.72% in which genotypes that were below the mean value (12.72%) were 53.72% and those genotypes that were above the mean value were 46.28%. At Debre Tabor, protein content ranged from 7.81% in genotype ETBW 6427 to 12.91% in genotype Simba (12.91%) with the average value of 10.5%. Regarding this trait, 46.28% of the genotypes were below mean value and those 53.72% of the genotypes were above the grand mean at Debre Tabor in a similar way as in the Adet location. At Kulumsa, the range for protein content was 7.28% in genotype QUIA#2 (GAMBO) to 12.45% in genotype Doddota, in which 15.7% of the genotypes were below and 84.30% of the

genotypes were above the grand mean. This difference between the minimum and maximum values at Kulumsa was very large compared to the other two locations, with a mean value of 11.82%.

Protein is one of the primary quality parameters that influence most of the wheat grain baking quality characteristics. In hard wheat, variation in loaf volume of bread can be attributed directly to differences in protein concentration (Fowler, 2002). The results of the present study are in consistent with the results reported by Gelalcha, *et al*. (2000) who found significant difference in grain protein contents of ten Ethiopian bread wheat genotypes grown under Kulumsa, in Arsi, Oromia condition to vary from 7.7% to 13.2%. Anjum, *et al*. (2008) reported variation in protein content from 9.68% to 13.45% among Pakistani wheat genotypes. Wilson, *et al*. (2008) also reported that the protein contents of six bread wheat genotypes grown over three years vary from 8.7 to 12.9%, which is in similar range with the results of the current study.

So, in most of the current findings, the value of protein content was within the range of (11% to 15%) that exhibited high protein content, hence, the bread making quality in the mentioned genotypes of the study are with the best bread making performance though that needs further analysis in multi-locations and years for validation.

Higher protein content (>12%) is the property of hard bread wheat and it is suitable for leavened bread preparation Williams and Sobering, (1993). Qarooni, *et al*. (1988) described that flour with protein content ranging from 10% to 12% is more suitable for the production of Arabic bread. Lower protein content (<10%) on the other hand is suitable for the production of soft wheat products like nodules, cookies, and cakes. From this, it is possible to suggest that wheat genotypes Gassay,

Kakaba, Katar, Pavon76, Simba and Tay got high protein content, because their values were with the high protein wheat class, which make them suitable for leavened bread production.

Starch Content

The range of starch content at Adet was from 60.6% in the genotypes ETBE 6861 to 70.445% in the genotype Bolo in which genotypes that were below and above the grand mean value 65.42% were 49.59% and 50.41%, respectively. Almost all the genotypes distributed equally with similar protein content values, i.e., almost 50-50% of the genotypes were found above and below the value of the grand mean. At Debre Tabor, the range for starch content was from 49.75% in genotype Dinknesh to 70.05% in genotype Bolo with the average value of 65.71% in which genotypes distribution that were below and above the grand mean were 42.98% and 57.02%, respectively. The range of starch content at Kulumsa was from 47.30 in genotype ETBW 6839 to 68.73% in genotype ETBW 7724 in which 15.7% of the genotypes were below and 84.30% of the genotypes were above the grand mean 64.351.

From this result, variation observed in the distribution of genotypes above and below mean values, at two locations Adet and Debre Tabor, there was equal number of genotypes distributed above and below their corresponding mean values. At Kulumsa, the distribution of genotypes above its mean value was about 6 times higher than the distribution of genotypes below the average value. So, Kulumsa location may be the ideal site for further breeding of genotypes in starch content for bread making; though further research is needed for validation.

Wet Gluten Content

At Adet, the wet gluten content ranged from 21.83% in genotype Bolo to 31.95% in genotype ETBW 6529 with an average value of 26.28% in which genotypes that were below and above the average

value were 52.07% and 47.93%, respectively. The range of gluten content at Debre Tabor was 14.425% in genotype ETBW 6314 to 28.384% in genotype ETBW 6837. Genotypes that need below and above the average value (21.054%) were 48.76% and 51.24% respectively. At Kulumsa, the range of gluten content was 14.7% in genotype QUIA#2 (GAMBO) to 26.3% in genotype ETBW 6850 in which genotypes that were below and above the average values were 44.63% and 55.37%, respectively; this difference between the minimum and maximum values in Kulumsa was very similar to the other two locations, with a mean value of the traits 20.53.

Different researches worked on bread wheat genotypes wet gluten content (GC): Sadowski *et al*., (2001) observed variation of GC from 17.1% to 33.60% on twenty-four bread wheat genotypes from Poland; Miralbes, (2003) found variation from 15.6% to 39.3% in different wheat genotypes and Paliwal and Singh, (1985) also reported that GC in the range of 12.77% to 44.06% in Uttar Pradesh wheat genotypes that all were similar to the current study.

Hence, the variation in wet gluten among bread wheat genotypes of the present study may be attributed to the differences in genotypes and the environmental conditions like temperature and rainfall as was reported by Wrigley *et al*., (1991).

Sedimentation Volume (SDS-volume or Zeleny) Content

The sedimentation volume (SDS-volume or Zeleny) content at Adet ranged from 23.55ml in the genotype ETBE 6492 to 47.45ml in the genotype ETBW 6529 in which genotypes that were below and above the grand mean value (34 ml) were 54.55% and 45.45%, respectively. At Debre Tabor, the range for sedimentation volume (SDS-volume or Zeleny) content ranged from 10.46 ml in genotype Sulla to 42.15 ml in genotype ETBW 6841 with the average value being 27.37 ml in which genotypes that were below and above the grand mean were 42.15% and 57.85%, respectively. The

range of sedimentation volume (SDS-volume or Zeleny) at Kulumsa, ranged from 15.85 ml in genotype ETBW 6427 to 39.6 ml in genotype KG6290 with the average value being 26.85 ml in which genotypes that were below and above the grand mean were 47.93% and 52.07%, respectively.

The SDS-sedimentation volume is an estimate of the protein strength relating to the wheat quality, which depends on the degree of hydration and degree of oxidation of proteins in the wheat. Sedimentation values can be in the range of 20ml or less for low-protein wheat with weak gluten to as high as 70ml or more for high-protein wheat with strong gluten (USWA, 2007). More SDS-sedimentation volume (>30 ml) indicates more gluten strength of protein as Williams (1986) and will be better for bread making. Coskuner and Karababa, (2005) reported the range of SDS sedimentation value from 42.5ml to 59.6ml. According to the previous report of Narasimha (2008), SDS sedimentation volumes of three wheat genotypes grown under different environmental conditions ranged from 59ml to 90ml which is contradictory to the current study, in contrary to the current study that SDS sedimentation volume varied from 10.462ml to 47.45ml; this difference might be due to the differences in the genetic makeup of the bread wheat genotypes or similar other factor that further study is necessary. However, based on the SDS sedimentation volume results it is possible to classify bread wheat genotypes in to strong, medium and low strength gluten classes.

Generally, in the present study, for the range TGW at Kulumsa, was 13.47 to 29.03 relatively narrower than HLW at Adet with minimum values in genotypes ETBW 6876 and the maximum in ETBW 6169 with an average value of 57.02% of the genotypes were above the grand mean (50.41%) of starch content. TGW at Debre Tabor and Kulumsa also ranged from 20.8 (KBG01) to 37.5 (ETBW 6529) and 13.47 (KBG01) to 29.03g (ETBW 6529), respectively, with an average value of 28.49 and

23.41g, respectively, indicating that the tested genotypes were similar with respect to their performance in the TGW, HLW and Sta content at three locations, hence, genotypic factors should be given top priority for selection of the genotypes for breeding and development than phenotypic factors considering TGW, HLW and starch contents. Wet gluten content ranged from 21.83 to 31.95, 14.43 to 28.38 and 14.7 to 26.3 at Debre Tabor, Kulumsa and Adet, respectively, indicating that larger protein is required at Debre Tabor followed by Kulumsa and last at Adet. The implication is that the trait is stable.

4.2.1.3 Estimates of Genetic Parameters

The amount of genotypic and phenotypic variability that exist in a genotype is of utmost importance in breeding to select better genotypes and initiate a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given genotype. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability (H) as well as genetic advance for selection (GAM) of the traits were studied across locations (Table 11).

Table 11: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as of mean for the seven characters of bread wheat genotypes tested across location in 2015/16

Traits	Range	Mean	δ^2_g	δ^2_p	H^2	GCV %	PCV %	GA	GAM%
TGW	26.04-47.89	39.86	35.48	35.81	99.06	14.94	15.01	12.23	30.68
HLW	50.03-59.94	55.25	9.31	9.53	97.70	5.52	5.59	6.22	11.26
Prot.	10-14.85	11.68	0.79	0.90	87.5	7.62	8.14	1.716	14.70
MoC	9.83-12.81	11.678	0.545	0.658	71.45	5.41	6.077	1.66	14.54
Starch	57.03-69.27	65.16	11.17	11.35	98.37	5.13	5.17	6.84	10.49
Gluten	23.03-27.09	22.62	8.80	9.01	97.72	13.36	13.52	6.05	26.75
Zele	18.73-38.04	29.39	30.34	30.58	99.21	18.74	18.81	8.88	30.2

σ^2_{gl}=genotype by environment interaction variance, σ^2_g= genotypic variance, σ^2_p= phenotypic variance H^2 = broad sense heritability, GCV= Coefficient of genotypic variance, CV= coefficient of phenotypic variance, GA= genetic advance.

Grain quality traits-based univariate analysis in bread wheat genotypes from Ethiopia evaluated at three experimental locations, are presented in combined analysis in the following sections:

4.2.1.3.1. Analysis of Variance Components and Coefficients of Variation

Summary of the ranges and the means together with their standard errors, obtained on the basis of qualitative traits data combined over the experimental locations, are shown in Table 11. In general, bread wheat genotypes from Ethiopia considered in this study showed wide ranges of variability and wide ranges between the maximum and minimum mean values in most of the 7 qualitative traits considered.

According to the results obtained across locations (Table 11), phenotypic variance ranged from 0.66 (MOC) to 35.81 (TGW) and the values for genotypic variances ranged between 0.55 (MOC) and 35.48 (TGW). Maximum phenotypic variance 35.81 and genotypic variance 34.48 was recorded by the trait TGW for both, and minimum phenotypic variance 0.66 and genotypic variance 0.55 was recorded by the same trait MOC. A wide range of phenotypic and genotypic variance was recorded for the characters TGW (35.81, 35.48), Zele (30.58, 30.34), Starch (11.35, 11.17), HLW (9.53, 9.31) and Gluten (9.01, 8.80), respectively. Similarly, with the same value of order in the traits, higher phenotypic variance was recorded than the genotypic variance. This indicates that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. The rest characters showed smaller phenotypic and genotypic variance. This finding is in agreement with Obsa (2014), Majumder *et al*. (2008) and with Obsa (2014) and Majumder *et al*. (2008) and Gezahegn *et al.* (2015) who worked with bread wheat variability analysis. Similarly, in conformity with finding of Gezahegn *et al.* (2015), minimum phenotypic variance was recorded for the variable's gluten content (4.8) and Protein content (0.68) and a wide

genotypic variability also recorded for the characters HLW (57.999), Starch content (20.476), Zeleny (12.09), TGW (8.251), gluten content (4.74) and protein content (0.66) on their research on bread wheat genetic diversity study.

According to the results of combined analysis (Table 11), PCV ranged from 5.17% (starch content) to 18.81% (SDS), whereas GCV ranged from 5.13% (starch content) to 18.74% (SDS). So, PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. Gezahegn *et al*. (2015), Gergana and Bozhidar (2015) and Navin *et al*. (2014) reported similar result during genetic diversity study of bread wheat genotypes. Moderate GCV and PCV (>10%) values were observed for wet gluten content (13.36% and 13.52%), TGW (14.94% and 15.01%) and SDS (18.74% and 18.81%), respectively. Similarly, Gezahegn *et al*. (2015) noted moderate phenotypic and genotypic coefficients of variation for thousand kernel weight, grain yield and harvest index in sixty-four bread wheat genotypes in Ethiopia which are in line with this finding for PCV. The lowest GCV and PCV (<10) values were observed for starch content (5.13% and 5.17%), hectoliter weight (5.52% and 5.59%) and protein content (7.62% and 8.14%), respectively, indicating less scope of selection characters as they were under the influence of environment. The result is in line with the finding of Gezahegn, *et al*., (2015) and Arati, *et al*., (2015). Navin, *et al*., (2014) reported higher PCV for thousands of kernels weight (28.43), hectoliter weight (25.027), protein content (23.038), starch content (23.03) and test weight (18.64) which contradicted this finding.

Likewise, the values of PCV was higher than their corresponding GCV, indicating that the influence of environment on the expression of these characters. Hence, narrower differences between the

values of GCV and PCV indicated that the environmental effect was small for the expression and selection for these characters during breeding and selection. Similar to the previous work of Deshmukh *et al.* (1986) and Navin *et al.* (2014) reported high and moderate magnitude of GCV and PCV for grain quality in bread wheat and related traits.

The rest of the characters are grouped under low PCV and GCV, indicating less scope of selection as they were under the influence of environment. Suggesting the indication of sufficient information for variability based on these traits among genotypes and can help to scale up the scope for genetic improvement of genotypes through selection using these traits, as the previous work of Navin *et al.* (2014) reported higher magnitude of GCV and PCV for grain quality traits. The rest of the characters are grouped under low PCV and GCV, indicating less scope of selection as they were under the influence of environment.

This indicated that selection will be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Similar results of moderate PCV and GCV has been reported for thousand grain weight and similar to grain yield in wheat (Gezahegn *et al*., 2015).

Generally, from the results observed in the current study at individual as well as combined analysis, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously during conducting an experiment, and hence genotypes and hybrid development will go a long way with the breeding programs especially in case of wheat. In addition, the variability observed under studied traits may be due to only the environmental factor by the time

the research conducted in the experiment by chance to result with high PCV but not with high GCV. So, the high PCV and GCV observed under studied traits are likely to indicate their high variability to in turn offer good scope for selection while breeding.

Similarly, the result indicates that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. The rest characters showed smaller genotypic variability. The finding is in agreement with Obsa (2014) and Majumder *et al*. (2008) and Gezahegn *et al.* (2015). The minimum phenotypic variance was recorded for the variable's gluten content (4.8) and Protein content (0.68). A wide genotypic variability was also recorded for the characters HLW (57.999), Starch content (20.476), Zeleny (12.09), TGW (8.251), gluten content (4.74) and protein content (0.66).

The estimates of PCV in this study were higher than their corresponding GCV indicating the influence of environment on the expression of these characters, although the differences were small at individual as well as combined locations analysis. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these characters. According to Deshmukh *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 moderate.

Among all characters, moderate GCV and PCV values (>10%) were observed for zeleny (10.83 and 10.99) and thousand seed weight (10.16% and 10.28%), respectively, suggesting sufficient variability and thus scope for genetic improvement through selection for these traits. Navin, *et al.*,

(2014) reported higher magnitude of GCV and PCV for thousand seed weight, hectoliter weight, starch content, protein content and test weight which support this finding. The rest of the characters grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment.

This indicated that selection will be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential for breeding. Similar results of moderate PCV and GCV has been reported for HLW, Zeleny, TGW and WG in wheat (Gezahegn *et al*., 2015). The characters' protein content and starch content were grouped under low phenotypic and genotypic coefficients of variation which is in line with the finding of Mohammed *et al*. (2011) and Gezahegn *et al*. (2015). Hence, selection of both physical (TGW and HLW) and chemical grain (others) quality traits for breading programs should be based on genotypic than phenotypic factors.

Finally, varieties with large amount of grain protein, like- Gassay, Kakaba, Katar, Pavon76, Simba and Tay, and large amount of starch & gluten content, lower SDS contents could be given special attention towards grain quality improvement

4.2.1.3.2. Estimates of Heritability

According to Pramod and Gang Prasad, (2007 broad sense heritability (H^2)) are categorized as low (<40%), medium (40-59%), moderately high (60-79%), and very high ($\geq$80).

Accordingly, the results of combined analysis, heritability of the studied traits (Table 11), ranged from 87.50 % in protein content to 99.21 % in SDS. High heritability (>80%) was computed for all the traits studied, indicating that the variation observed were mainly under genetic control and less

influenced by the environment and the possibility of progress from selection could be fairly easy and improvement is possible using these traits in breeding. Similar to the previous work of Gergana and Bozhidar (2015), high heritability (above 60%) for characters like TGW (67.47%) and HLW (73.51%) in their study on variability, heritability, genetic advance and associations among characters in emmer wheat genotypes. Arati *et al*. (2015), Navin *et al*. (2014) and Ali *et al*. (2008) also reported high heritability estimates for TGW which support the present findings.

It is not obvious that the differences due to environment obscure differences due to inheritance. The greater the proportion of the total variability that is due to the environment, the more difficult it would be to select for inherent differences. On the other hand, if environmental variability is small in relation to genotypic differences, selections were efficient, because the selected characters were transmitted to the progeny. Because the inherent portion of the variability is termed as heritability (Allard, 1960).

4.2.1.3.3. Estimates of Expected Genetic Advance

Genetic advance as percent of mean (GAM) categorized as low (0-10%), moderate (10-20%) and high 20% and above (Johnson *et al.,* 1955).

In the current study based on combined analysis (Table 11), GAM was highest in TGW (30.68), SDS (30.2%) and WG (26.75%), and moderate in protein content (14.70%), HLW (11.26%) and starch content (10.49%) in their order. The high value of TGW has a great potential in flour extraction in bread wheat, while SDS and WG (which are positively correlated to each other) to provide an information on protein quantity and quality of ground wheat and flour samples and hence are used as a screening tool in wheat breeding as well as in milling applications. Which is similar to the

previous work of Mohammed *et al*. (2011)) and Awale *et al*. (2013) of bread wheat baking quality analysis.

So, selection of genotypes with higher values of the physical as well as chemical grain quality characteristics could be effective for the interest of development, conservation and direction of selection during improvement of wheat in bread making.

Similarly, in the current work, high heritability was coupled with moderate GAM for the traits starch content (98.37, 10.49), hectoliter weight (99.06, 11.26) and protein content (87.5, 14.70), in accordance with the previous results of Navin *et al*. (2014) and Desheva and Cholakov (2014) with similar work which indicated that heritability was due to additive gene effects and selection may be effective in early generations for these traits.

Gezahegn *et al*. (2015) also reported that high heritability coupled with moderate and high GAM for all traits studied is similar to the present study. It may be because of the predominance of non-additive gene action in the expression of the current traits studied. Hence, high heritability of these traits can be due to the influence of the environment rather than genotypic factors, and selection for these traits may not be rewarding.

Generally, due to the occurrence of GAM in the range of high to moderate level for the grain physical and chemical quality traits and the occurrence of high heritability coupled with high and moderate GAM, these traits should be given top priority during selection breeding in bread baking quality.

4.2.1.3.4. Estimation of Association Among the Grain Quality Traits

In this study, association among grain quality traits was analyzed using two methods; based on correlation coefficients and biplot and clustering as follows:

A. Analysis Using Correlation Coefficients

Analyses of genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program and to find out the inter-relationship between the studied traits.

In this study, estimates of genotypic and phenotypic correlation coefficients for each pair of among traits were studied at individual and presented in a combined form (Table 12) in the following manner:

Table 12. Estimates of genotypic (*above diagonal*) and phenotypic (*below diagonal*) correlation coefficients computed using data from the 7 qualitative traits combined over the three locations.

Traits	HLW	TGW	Pro	Mo	Sta	WG	Zel
HLW	1	**0.44ns**	**0.08ns**	**-0.15ns**	**0.05ns**	**0.10ns**	**0.028ns**
TGW	0.43ns	1	**0.24ns**	**-0.28ns**	**-0.23***	**0.29ns**	**0.23ns**
Pro	-0.003*	0.12ns	1	**0.32ns**	**0.22*****	**0.91*****	**0.87*****
Mo	-0.22ns	-0.08*	0.19ns	1	**0.99****	**-0.17ns**	**0.098ns**
Sta	0.00072*	-0.20***	0.40***	0.39***	1	**0.089ns**	**0.16ns**
WG	0.0058ns	0.16ns	0.89***	0.038ns	0.29ns	1	**0.86*****
Zele	-0.017ns	0.13ns	0.82***	0.082ns	0.26ns	0.82***	1

Note, ** and * indicates highly significant at 1% and significant at 5% probability levels, respectively. DH: days to heading, DM: days to maturity, GFP: grain filling period, GY: grain yield, TKW: 1000 kernel weight, AGB: above ground biomass (kg/ha, HI: harvest index, HW: hectoliter weight, TPP: tillers per plant, PH: plant height (cm), SPS: spike-lets per spike, KPS: kernels per spike, SL: spike length, SPP, spikes per plant.

Accordingly, protein content showed a highly significant ($p<0.001$) and positive genotypic correlation with WG (0.91), Zele (0.87), Starch (0.22), whereas, the correlation with all the remaining traits were non-significant. In addition, the extents of correlation sound higher ($r > 0.5$) for WG and

Zeleny content, in that order (Table 12). Similarly, HLW showed highly significant positive genotypic association with protein content and gluten content. It may be due to less influence of the environmental impact on the traits than their genetic makeup, hence suggesting the potential for selecting the best genotypes in terms of these grain quantity and quality traits. However, further study is needed for validation. Similar to the previous works of Wasif *et al*. (2015) and Quan (2015), (Sadras and Lawson, 2011) and Majumder *et al.* (2008) and Shahin Nia *et al*. (2002) who have reported existence of significant positive correlations among most of the grain quality traits.

Likewise, grain protein content showed a highly significant positive phenotypic correlation with WG (0.89), Zeleny (0.82), moisture content (0.80), negative significant ($p<0.05$) (HLW-0.003) and positive non-significant correlation with TGW (0.008) (Table 12). Moreover, WG and Zeleny content revealed a strong correlation ($r>0.5$) in their order of magnitude. Indicates, the objective and direction of selection and the genetic inheritance of the phenotypic associations. Which is supported by the previous workers of Wasif *et al*. (2015) who reported significant positive phenotypic correlations of protein content with hectoliter weight, thousands of seed weight, gluten content and Zeleny content of grain quality traits. Awale *et al.* (2013) also reported that the association of Hectoliter weight showed negative significant correlation with 1000 kernels weight ($r=-0.32$) and he reported the non-significant correlation of thousand kernel weight and hectoliter weight with grain protein content similar to the current finding. Quan (2015) also reported positive correlations of grain protein with other quality traits, which is in agreement with the present study for those traits. Foulkes *et al.*, (2011) similar to the current work as reported high WG and Zeleny content are especially valuable traits to raise protein content potential for bread making in wheat. Similarly, this finding is in agreement with the finding of Carter (1999) as of protein content had strong association with

gluten and zeleny contents, hence this association is important to sort out useful genotypes to provide good bread making quality in bread wheat.

Moreover, most of the phenotypic correlation coefficients were less in magnitude than the genotypic correlation coefficients, that revealed the presence of inherent genetic relationships among various characters and less dependent on environment. Similarly, analysis of genotypic correlation coefficients was found to be higher in magnitude than that of phenotypic correlation coefficients in most of the traits, which indicated the presence of inherent association among various characters. Similar to the previous finding of Eivazi *et al* (2005) and Wasif *et al*. (2015), an increase in the amount of starch stored in seeds and a decrease in the amount of protein, TGW and the grain yield increase, is in agreement with the current finding. On the other hand, the previous work of Quan (2015) and Ali *et al.* (2008) reported to be in weak association in contradictory to the current study, indicating that additional research work has to be done for validation.

B. Estimation of Grain Quality Traits Relationships and Profiles Using Dendrogram and Biplots Methods

From the dendrogram (Figure 3a for Adet, 4a- Debre Tabor and 5a- Kulumsa and Figure 6a- across locations) and biplot/ trait vector projection (Figures 3b, 4b and 5b and across locations 6b) were analyzed, both the phenotypic and grain quality traits were analyzed together. However, they were treated separately with respect to their parts of the thesis.

In the grain quality study, traits were investigated based on dendrogram and biplot methods, how they were related/differ to each other at individual as well as combined locations in the following manner:

Accordingly, dendrogram-based relationships of 7 grain quality traits studied at Adet (Figure 3a), there were 4 main clusters groups; the first cluster includes traits Pro, WG and Zele. The second cluster consists of solitary trait TGW. The third cluster included traits HLW and Mo, and the fourth cluster consisted of a solitary trait Sta. During the study of traits relationships based on biplot method (Figure 3b); traits TGW, WG and Zele found in the 1st quadrant in opposite direction to solitary trait Mo in the 3rd quadrant. In the 2nd quadrant traits HLW and Pro were found in opposite direction to the trait Sta in the 4th quadrant.

Traits were analyzed based on the similarity/differences in the direction vector projections (the arrow direction) they follow and based on dendrogram to suggest genetic similarity or variation of the traits, if they are in the same direction or in different clusters the genotypes occur, it is possible to predict how they are diverse or similar in their performance.

Hence, the similarity in the vector direction the traits follow and the presence of the traits within the same cluster in the dendrogram were assumed to be bread together in breeding and cultivar development programs; and those traits that can found in different clusters and/or occur in the opposite direction of the vector projections are unlikely to be bread together. According to Yan and Tinker, (2006) two traits are positively correlated if the angle between the vectors is acute (<90°) and negatively correlated if the angle is obtuse (>90°), and not correlated if the angle is right angle.

At Debre Tabor, dendrogram-based relationships among 6 traits studied (Figure 4a), there were 3 main clusters groups. The first cluster includes traits Mo and Sta and the second cluster included

traits WG and Zele. The third and the fourth clusters consisted of solitary traits HLW and TGW, respectively. In the study of traits relationships based on their direction using biplot method (Figure 4b), a solitary trait TGW found in the 1st quadrant was in opposite direction to the traits Mo and Sta in the 3rd quadrant. In the 2nd quadrant traits WG, Zele and HLW found in in the same direction without any trait opposite to its direction in the 4th quadrant.

At Kulumsa, dendrogram-based relationships among 5 traits studied during grain quality study (Figure 5a), there were 3 main clusters. The first cluster includes two sub clusters, trait TGW found in the first sub cluster and HLW in the other. The second cluster composed of a solitary trait Sta. The third cluster consisted of two sub clusters in which WG was found in one and Zele in the other sub cluster. During the study of traits, relationships based on their vector/direction using biplot method (Figure 5b) traits HLW and TGW were found in the same direction in the 1st quadrant but opposite to the solitary trait Sta at the 3rd quadrant. In the 2nd quadrant traits WG and Zele were found in the same direction without any trait in opposite direction in the 4th quadrant.

Similarly, the study results across location (Figure 6a and b) were similar to that of the individual locations when traits relationship and profiles were analyzed as that of individual locations.

Generally, from the result of the individual as well as combined analysis, estimates of (correlation studies or trait relationships and trait profiles) in grain quality of bread wheat genotypes, those traits that were occurring together (in a given cluster following the dendrogram) and in the same direction/vector projections are expected to go together during breeding and cultivar development compared to the traits that are found on different clusters and vector projectiles.

4.2.2. Estimation of Flour Quality Using Seed Storage Protein SDS PAGE Banding Patterns.

Improvement in quality and quantity of wheat has always been on the top priority of wheat breeders and geneticists. It has been proposed that variation within wheat genotypes is due to the occurrence of diverse allelic combinations in each genotype (Mayakovski, *et al*., 1997). Genetic diversity is routinely used for getting success in wheat enhancement and their diversity can be estimated by different methods (Fufa, *et al*., 2005). Different banding patterns in wheat proteins through SDS-PAGE analysis were previously determined (Shuaib, *et al*., 2007).

In SDS-PAGE, separation of protein subunits is achieved depending upon their molecular weight i.e. subunits of smaller molecular weight moving faster than the larger ones. The unknown molecular weight of proteins can be determined by comparing the migration of unknown to that of proteins of known molecular weight in the same gel. Stability is an important feature of total seed proteins profile. Due to this reason, it has been suggested as an important tool for addressing the problems of origin and evolution of crop plants (Muhammad *et al*., 2009).

Flour containing a large amount of gluten- which is composed of gliadin, glutenin and its components HMW- and LMW- GS (high and low glutenin sub units), is generally of better quality than flour with low gluten content and is thus suitable for the preparation of bread and pasta (Ruiz & Carrillo, 1995; Clarke *et al*., 1993; Payne & Lawrence, 1983). The disappearance of one band or the presence of a new and the observation of a noticeable change in band intensity help to define qualitative and quantitative effects, respectively (Payne *et al*., 1984).

In the present study, the protein markers were successful in screening of the bands formed by the genotypes during SDS PAGE. The protein markers developed were ranging from 21 to 54KDa for gliadin, 35 to 160KDa for glutenin, 130 to 160KDa for HMW- GS, and 35 to 65KDa for LMW- GS compositions, is similar to the previous work of (Muhammad *et al*., 2009) provided evidence on the good quality bread wheats in fact have more glutenin than poor quality wheats. So do gliadins (MW 21-54 kDa) monomeric, non-aggregating proteins and responsible for the extensibility in dough. Glutenin (MW 35-160 kDa) is polymeric, an aggregate protein involved in dough strength and quality; and it is divided in to HMW-GS 130-160kDa which forms the macro molecules and LMW-GS (35-65kDa) which form the gluten complex useful for the estimation of genetic diversity of bread wheat (*Triticum aestivum* L.) genotypes using SDS-PAGE.

In this study, a total of 50 bread wheat genotypes were compared for flour quality diversity of the genotypes by comparing their mean values analyzed using gliadin and glutenin (HMW and LMW) markers (Figure 7,8,9 and 10), respectively, following the number of bands formed relative to each marker (Table 13) discussed in the following steps:

4.2.2.1. Estimation of Variation of Genotypes for Gliadin Composition

Gliadins are complex structures linked with LMW- GS and inheritance in blocks (not individual alleles) are the main bottlenecks to dissecting the functional properties of individual gliadin genes in wheat (D'Oridio and Masci, 2004) and are little to resistance in extension for dough and are mainly related to dough cohesiveness to contribute for viscosity property.

These protein parts accounts for 40-50% of total wheat storage proteins and have impact on the processing and nutritional quality, but the effect of gliadin on processing quality is less significant than the HMW- and LMW- GS (Schmid, .2018).

In the current investigation, bread making flour quality among 50 bread wheat genotypes assessed using 13 gliadin markers in KDa (a molecular weight of 21, 23, 38, 41, 42, 43, 48, 49, 50, 51, 52, 53, and 54) (Table 13 and Figure 7) from the data harvested based on present/absent of bands formed (Appendix 18) in the genotypes SDS PAGE profiles. The highest number of bands (8) were observed in genotypes 8, 9, 13, 18, 46 and 48 followed by 7 bands observed in genotypes (20, 21, 23, 29, 37, 40, and 41). The third highest bands (6) were observed in genotypes (6, 11, 17, 24, 26, 36, 43 and 49), then followed by 5 bands observed in genotypes 1, 10, 14, 15, 16, 25, 27, 31, 32, 33, 44, 45, 47 and 50. In the 5^{th} position 5 bands were observed in genotypes 3, 4, 5, 12, 19, 22, 30, 35, 38, 39 and 42; in the sixth position 3 bands were observed in genotypes 2, 7 and 28. Among the fifty genotypes studied, genotype 34 showed single band. However, there was no any genotype without gliadin band formation (Table 12 and Figure 7).

The genotypes that had the same number of bands were expected to have genetic similarity, (i.e., those genotypes scored similar number of bands were similar) and those which scored different number of bands were different. In addition to that the more the number of the bands possessed by the genotypes, the more the composition of the gliadin in their stored protein.

Table 13: Summary of the total number of bands scored for gliadin, glutenin and HMW- and LMW-GS composition by the genotypes at three locations

S. N	Gliadin		Glutenin			
			HMW		LMW	
	Genotypes	**Bands**	**Genotypes**	**Bands**	**Genotypes**	**Bands**
1	8,9,13,18,46 & 48	8	3,18,26&46	4	10,30,37,41,43&48	4
2	20,21,23,29, 37,40 & 41	7	5,6,7,9,10,12,13,16,23,24,27,30,35,37,38,45,47&50	3	1,2,6,8,11,13,15,21,23,24,29,32,33,35,36,39,42,44,46&49	3
3	6,11,17,24,26,36,43,44 &49	6	1,2,8,14,15,17,19,20,21,25,28,29,31,32,33,34,36,39 ,40,41,42,44,48&49	2	3,4,5,9,14,16,18,19,20,22,34,38,40,45&47	2
4	1,10,14,15,16,25,27,31,32,33,45, 47&50	5	11,22	1	7,26,28,31&50	1
5	3,4,5,12,19,22,30,35,38,39, &42	4	4	0	12,17,25&27	0
6	2,7, &28	3				
7	34	1				
	Total 50	**34**	**50**	**10**	**50**	**10**

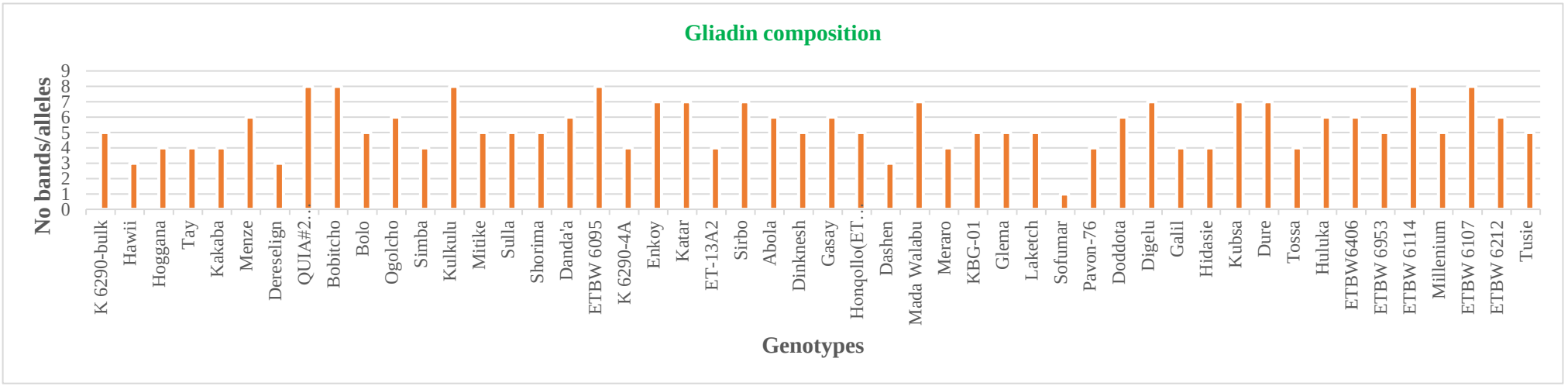


Figure 7: Mean value comparison of gliadin composition among fifty bread wheat genotypes

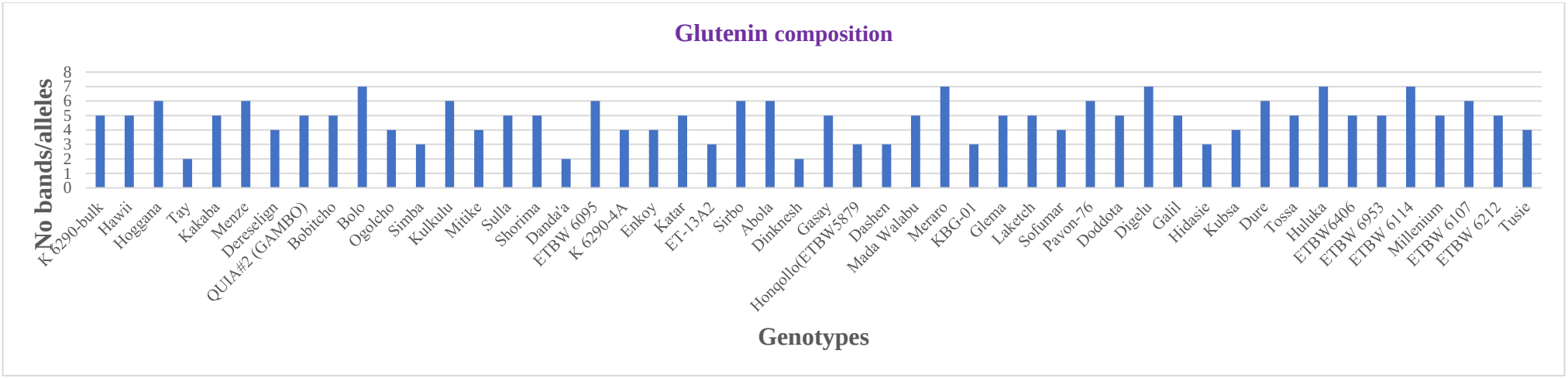


Figure 8: Mean value comparison of glutenin composition among fifty bread wheat genotypes

Therefore, those genotypes with higher number of gliadin banding pattern are expected to have little resistance and extension in dough and are mainly related to dough cohesiveness, and contribute to viscosity property in their order of number of bands formed. According to Payne *et al*., (1984) the disappearance of one band or the presence of a new and the observation of a noticeable change in band intensity help to define qualitative and quantitative effects, respectively. These genotypes with similar number of bands were more similar in their gliadin composition than any other genotypes compared to the other genotypes under this investigation and hence they were expected to have the highest gliadin composition in their seed stored protein if they do score high in their banding patterns.

Hence, it is advisable to select the genotypes such as represented by numbers 8,9,13,18,46 & 48, if one is interested in the development of genotypes for their gliadin components for their dough in the bread making for their flour quality.

Generally, the products in gliadin composition (Table 12 and Figure 7) were equal and the same for each of the three environments Adet, Debre Tabor and Kulumsa. Similar result was observed in the previous studies of Murat *et al*., (2013); Huebner and Bietz, 1988; Johansson *et al*., (2013). These authors reported specific gliadin composition of genotypes is free from environmental factors making this an easy and convenient method in evaluation of genotypes variability, and for pure seed productions in hexaploid wheat (Murat *et al*., 2013). Thus, one of the reasons to use variation in gliadin composition for evaluation of genetic diversity is that these proteins are highly polymorphic, while their composition is not influenced by the environment but only by genetic variation (Huebner and Bietz, 1988). The information from gliadin analyses can also be combined for a better understanding of bread-making quality in the material (Johansson *et al*., 2013).

Presence of broad genetic diversity and the information of genetic regroups is a pre-requisite for genetic improvement of any crop. It is, therefore, necessary to evaluate and characterize available genotypes, its conservation and utilization in crop breeding and improvement programs. Evaluation of genotypes using SDS-PAGE is simple, widely used and inexpensive. The SDS-PAGE is one of the methods to investigate genetic variability and classify crop genotypes (Isemura *et al*., 2001). Variation in total seed proteins and its analysis is also helpful to identify centers of diversity and centers of origin of different crop plants.

In the current study, genotypes Qui#2 (GAMBO), Bobitcho, Kulkulu, ETBW6095, ETBW6114 and ETBW6107 were the top 6 performing genotypes for gliadin composition, whereas the lowest performer was genotype Sofumar. Hence selection of the top 6 genotypes is suggested for the interest of high cohesive & viscos property to dough in bread wheat breeding for bread baking.

4.2.2.2. Estimation Variation of Genotypes for Glutenin Composition

In the current investigation (Table 13 and Figure 8), genotypes 10, 30, 37, 43 and 46 showed seven bands, this is the maximum number. Genotypes 17 and 25 showed the lowest number of bands, which is two. The second largest number of bands (6) was observed in the genotypes 3, 4, 6, 13, 18, 23, 24, 35, 41 and 48, the third largest bands (5) was observed in the genotypes 1, 2, 5, 8, 9, 15, 16, 21, 26, 29, 32, 33, 36, 38, 42, 44, 45, 47 and 49 in which the highest number of genotypes included. In the fourth position 4 bands were scored by eight genotypes 7, 11, 14, 19, 20, 34, 40 and 25. At the fifth position 3 bands were observed in six genotypes 12, 22, 27, 28, 31 and 39. Similarly, there was no any genotype without glutenin band.

So, those genotypes such as Hoggana, ETBW 6095, Gasay & ETBW6114 showed the highest HMW, & Bolo, Meraro, Digelu, Dure, Huluka & ETBW 6107 the highest LMW GS with seven number of bands were the first choice to provide rigidity and elastic property to dough during bread making, followed by those having 6 bands then the third choice of those varieties with 5 bands and last by those genotypes with 3 bands, and hence according to their order and based on their functions are suggested for further preservation and breeding purpose for bread making.

4.2.2.3. Estimation of Variation of Genotypes for The Ratio of The Glutenin/ Gliadin Composition

Here in this study the ratio of glutenin and gliadin composition was assessed based on the result of division of glutenin bands scored to that of gliadin bands; the result was counted as the possible number of bands that can be scored after the fraction, so the result showed the presence of higher number of bands in the glutenin composition than the score value of the gliadin in all genotypes studied. Similar to the previous studies of Autran *et al*., (1988), Belitz *et al*., (1988) and MacRitchie, (1984) who reported that good quality of durum wheat does in fact have more glutenin than poor quality durum wheats, however, further studies with bread wheats for index ratio (the ratio of glutenin to gliadin) seem to be necessary.

4.2.2.4. Estimation of Variation of Genotypes for HMW- and LMW-GS Composition

The molecular markers used for the estimation of LMW-GS were 35, 45, 50, 55 and 65 KDa and for HMW-GS were 130, 145, 150 and 160 KDa.

In the current investigation (Table 13 and Figure 9), using HMW-GS, maximum number of bands (3) scored by the genotypes 3, 9, 18, 24, 26, 35, 38, 45, 46, 47 and 50. Whereas, the minimum number

of bands observed by genotypes 2, 11, 22, 44 and 49 was one. There were no genotypes without HMW- GS, gliadin and glutenin bands. Similarly, Shuaib *et al*. (2007) reported genetic diversity results based on SDS-PAGE analysis of the grain HMW-GS storage proteins performed in order to analyze the molecular weight of sixty wheat genotypes.

In the present electrophoretic analysis for LMW- GS (Table 13 and Figure 10), five bands, which is the maximum number was scored in 4 genotypes and no band was shown in genotypes 17 and 18. Similar to the current study, the previous work of Salcedo *et al*. (1979) to fractionate the LMW-GS bands profiling as in our results the bands observed were with similar molecular weight ranges. Ghasemzade *et al*. (2008) and Chaparzadeh *et al*. (2008) have also reported similar findings in wheat genotypes and/or lines.

According to the present study on composition of gliadin, glutenin (HMW- and LMW- GS) in the flour bread making quality and seeds stored protein diversity were highly independent of environmental fluctuations but were strictly dependent on their genetic factors, which are similar to the previous work of (Javid, 2004).

Wheat improvement activities for wheat-based cropping systems and to study genetic behavior on the basis of protein profiles can be used for development of high yielding wheat genotypes, developing and releasing superior-quality wheat genotypes.

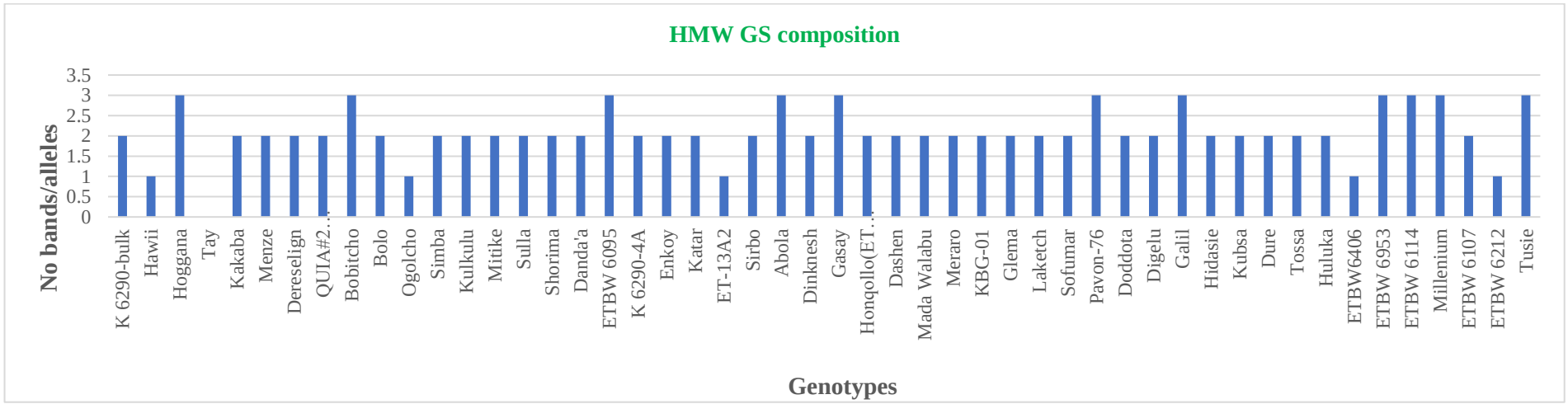


Figure 9: Mean value comparison of HMW GS composition among fifty bread wheat genotypes

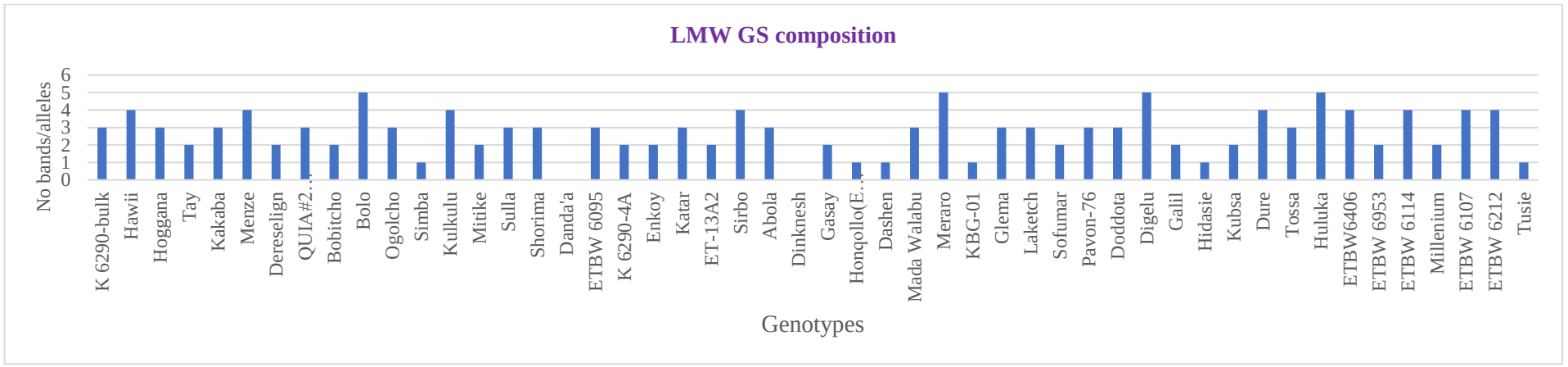


Figure 10: Mean value comparison of LMW GS composition among fifty bread wheat genotypes

Generally, from the results of current study, genotypes with maximum number of revealed bands should be given top priority for selection of bread wheat genotypes breeding for flour quality during bread making. Similarly, it is also possible to select genotypes in their order of the number of bands formed in the analysis of the flour quality for bread dough property.

4.3. Seed Storage Protein Diversity Study in Bread Wheat (*Triticum aestivum* L.) Genotypes from Ethiopia Using SDS-PAGE

Electrophoretic analysis of the seed storage proteins had direct relationship to the genetic background of the proteins that reveal genetic diversity. Such analysis can be used to certify the genetic makeup of germplasm (Javid *et al*., 2004; Iqbal *et al*., 2005). Thus, profiling of total seed storage proteins through SDS-PAGE for differentiating rice genotypes is well established (Saruyama and Shinbasi, 1993; Montalvan *et al*., 1998; Thanh and Hirata, 2002). It also estimates the extent of genetic variation and its geographical distribution in rice germplasm (Asghar, 2004).

In the current study, a wide range of protein peptides (low to high molecular weights) showed the potential for discriminating 50 bread wheat genotypes and can create additional variability to supplement existing genotypes. Seed storage proteins polymorphism can be used as a potential molecular marker for genotypes identification and economic characterization of bread wheat genotypes as reported earlier (Netra and Prasad, 2007) in rice.

Presence of broad genetic diversity and the information of genetic regroups is a pre-requisite for genetic improvement of any crop. It is, therefore, necessary to evaluate and characterize available genotypes, its utilization in crop breeding and improvement programs. Evaluation of genotypes using sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) is simple, widely used and inexpensive. The SDS-PAGE is one of the methods to investigate genetic variability and classify crop genotypes (Isemura *et al*., 2001). Moreover, variation in total seed proteins and its analysis is also helpful to identify centers of diversity and centers of origin of different crop plants.

4.3.1. Seed Storage Protein Diversity Among Bread Wheat Genotypes

In this study, the divergence indices, Major Allele Frequency (MAF) and Polymorphic Information Content (PIC) were used for the estimation of seed storage protein diversity among genotypes based on gliadin and glutenin (HMW- and LMW-GS) markers in the following sections:

4.3.1.1. Seed Storage Protein Diversity Among Genotypes Using Gliadin Markers

The study of gliadin markers could be a key role in genotype identification and purity (Branlard *et al*., 2001; Sozinov, 2001).

The proportion of glutenin in the protein was highly dependent on cultivar, whereas, although cultivar was still important, environmental variation was greater than cultivar variation for gliadin. Environmental variation was greater than cultivar variation for instance the dough rheological characters (Panozzo, J.F. and Eagles, H.A. 2000).

In this study, twenty-two protein markers were checked for medium to high polymorphism before embarking for further analysis. These protein markers revealed a total of 175 alleles (Table 14). The

major allele frequency (MAF) per locus varied from 0.56 (52KDa) to 1 (42KDa), with an average of 0.7 per marker. Among 13 gliadin protein markers, overall Polymorphism Information Content (PIC) values ranged from 0 (42KDa) to 0.37 (52KDa), with an average value of 0.304 and the allele number, unlike the other two locations (Debre Tabor and Kulumsa) a single locus was only found at this location, that ranged from 1(42KDa) to 2 (for all other locus) with an average value of 1.92 (Table 14) at Adet. At Debre Tabor, major allele frequency (MAF) per locus varied from 0.56 (52KDa) to 1 (42KDa), with an average value of 0.7per marker. Among the 13 gliadin protein markers, the overall PIC value ranged from 0 (42KDa) to 0.37 (52KDa), with an average of 0.30 and with allele number 1(42KDa) to 2 for all other markers 0 with an average of 1.92 (Table 13). Mmajor Allele Frequency (MAF) per locus varied from 0.52 (21 and 38KDa) to 0.82 (43KDa), with an average of 0.64 per marker. Among the 13 protein markers, the overall PIC values ranged from 0.27 (43KDa) to 0.43 (21KDa), with an average of 0.37 (Table 13) at Kulumsa.

Table 14: Genetic diversity indices across the thirteen gliadin protein markers used for 50 bread wheat genotypes at three locations

	Adet		Debre Tabor		Kulumsa	
Markers (KDa)	**MAF**	**PIC**	**MAF**	**PIC**	**MAF**	**PIC**
54	0.68	0.3405	0.56	0.4797	0.6	0.3908
53	0.68	0.3405	0.68	0.4242	0.76	0.3172
52	0.56	0.3713	0.5	0.4918	0.64	0.3793
51	0.58	0.3685	0.6	0.4662	0.56	0.399
50	0.64	0.3546	0.44	0.5276	0.64	0.3793
49	0.84	0.2327	0.86	0.2316	0.74	0.3308
48	0.62	0.3602	0.68	0.4317	0.76	0.3172
43	0.6	0.3648	0.5	0.5076	0.82	0.2666
42	1	0	0.56	0.4934	0.56	0.3986
41	0.88	0.1889	0.6	0.4662	0.58	0.3952
38	0.62	0.3602	0.48	0.4938	0.52	0.4028
23	0.64	0.3546	0.6	0.4781	0.58	0.4189
21	0.74	0.3108	0.5	0.5076	0.52	0.4282
Mean	0.6984	0.3037	0.5815	0.4615	0.6369	0.3710

MAF= Major Allele Frequency, NA= number of alleles and PIC = polymorphic information content.

According to the mean value of MAF using gliadin markers among genotypes (Table 14), the highest score (0.7) was at Adet followed by (0.64) at Kulumsa and lowest (0.58) at Debre Tabor, however; the numerical values were almost similar. Similar to the previous work of Liu *et al*., (2007) as the frequency of the allele (allele with the highest frequency of the allele in the one locus) with an average of 0.56, were ranged from 0.33 to 0.72. Implies that there was highest variability among the studied genotypes, so seed storage protein diversity was significant among genotypes and, hence selection would be based on their performance to genetic potential for further breeding programs but not based on location or environmental factors, and it is also possible to preserve the genetic potential of the genotypes in any environmental conditions. However, it is recommended to undergo with further multi-location study for validation.

Likewise, the mean value of PIC (Table 14) was largest (0.46) at Debre Tabor followed by Kulumsa (0.37) and lowest at Adet (0.30), this rank order for locations was similar to the MAF, with minor numerical value differences, in conformity with the previous work of Botstein *et al*. (1980); the PIC value > 0.5 is considered as a highly informative marker, 0.5 > PIC > 0.25 is just informative marker, and PIC≤0.25 is a slightly informative marker, and also in agreement with the previous work of Liu *et al*., (2007) and Sud *et al*., (2005) who worked on and found a genetic diversity or PIC value per locus across the tested loci. Since, the present finding was at the range of informative level of the PIC value, indicated the presence of seed storage protein diversity among the studied genotypes. So, the PIC values increased commensurate with increasing heterozygosity at a locus that the scarce alleles have less effect on PIC values than common alleles, this trend was not consistent (Hokanson *et al*., 1998). Hence, these screening indices being informative can be suggested to study genetic diversity and group structures in bread wheat genotypes. In addition, polymorphism among

individual genotypes is observed due to variation in gliadin sequences present in their seed storage protein. So, higher polymorphic bands of the screening indices indicate their efficiency to study genetic diversity and discrimination of genotypes as (Pradhan *et al*., 2004) indicated. Similarly, these genotypes were less influenced by the environment so less affected by the phenotypic than genetically factors.

4.3.1.2. Seed Storage Protein Diversity Among Genotypes Based on Glutenin Markers

Nine glutenin markers (160Kda, 150Kda, 145Kda, 130Kda, 65Kda, 55Kda, 50kda, 45Kda and 35Kda) were used for the estimation of genotypes collected from three locations. Comparison was based on to MAF and PIC (Table 15) values.

Table 15: Major allele frequency and polymorphic information content used for glutenin genome of bread wheat loci at each location

	Adet		**Debre Tabor**		**Kulumsa**	
Markers (KDa)	**MAF**	**PIC**	**MAF**	**PIC**	**MAF**	**PIC**
160	0.72	0.321915	0.52	0.516752	0.56	0.444535
150	0.84	0.232673	0.64	0.464797	0.66	0.410397
145	0.7	0.3318	0.48	0.524368	0.62	0.42737
130	0.5	0.375	0.48	0.524368	0.52	0.450986
65	0.62	0.360185	0.52	0.516752	0.5	0.452806
55	0.6	0.3648	0.74	0.380599	0.78	0.326685
50	0.76	0.29826	0.52	0.516752	0.7	0.388409
45	0.8	0.2688	0.48	0.524368	0.7	0.388409
35	0.82	0.321915	0.54	0.511236	0.78	0.326685
Mean	0.706667	0.232673	0.546667	0.497777	0.646667	0.401809

MAF= Major Allele Frequency, NA= number of alleles and PIC = polymorphic information content

According to the results of the current study using glutenin markers (Table 15), MAF ranged from 0.84 by 150KDa to 0.5 by 130KDa marker with an average value of 0.71, and PIC value ranged from 0.36 by 55KDa marker to 0.23 by 42KDa marker with an average value of 0.31 at Adet. At Debre Tabor, MAF ranged from 0.74 by 55kda marker to 0.48 by 45kda marker with a mean value of 0.55, and PIC value ranged from 0.52 by both 130kda and 145kda markers to 0.38by 55kda marker with a

mean value of 0.5. While MAF ranged from 0.78 by 35kda and 55kda markers to 0.5 by 65kda marker with a mean value of 0.65, and PIC value ranged from 0.45 in 65kda marker to 0.34 by 35kda and 55kda markers with a mean value of 0.40, at Kulumsa.

Likewise, based on the result of MAF, the highest mean value (0.71) was scored at Adet followed by Kulumsa 0.64 and lowest at Debre Tabor 0.55, similar to the previous work of (Liu *et al*., 2007), as the frequency of the allele (allele with the highest frequency of the allele in the one locus) with an average value of 0.56 were ranged from 0.33 to 0.72. So, seed storage protein diversity based on glutenin marker was highly varied among genotypes due to genetic than environmental factors, and hence it is advisable to select genotypes for further breeding based on genetic factors.

According to the result of PIC value (Table 15), highest mean value 0.5 was recorded by genotypes from Debre Tabor, followed by Kulumsa 0.40 and lowest at Adet 0.31 similar to the order as MAF values. It is in accordance with the previous work of Botstein *et al*. (1980) and reported that PIC value>0.5 is considered as being highly informative marker while 0.5>PIC>0.25 is just informative marker, while PIC≤0.25 is a slightly informative marker. Implies that the glutenin markers were informative for the presence of seed storage protein diversity among the studied genotypes, similar to the previous work of (Liu *et al*., 2007) and (Sud *et al*., 2005) with the same experiment on wheat.

From this observation, PIC values increased commensurate with increasing heterozygosity at a locus. Hence, scarce alleles have less effect on PIC values than common alleles; this trend was not consistent (Hokanson *et al*., 1998). So, these primers being informative, can be recommended to study genetic diversity and group structures in bread wheat genotypes. Polymorphism among

individual genotypes is observed due to variation in glutenin seed storage protein present in their chromosomes. Higher polymorphic bands of glutenin indicate their efficiency to study genetic diversity and discrimination of genotypes (Pradhan *et al*., 2004). Similarly, these genotypes were less influenced by the environment and hence less affected by the phenotypic than genetic factors.

4.3.1.3. Seed Storage Protein Diversity Among Genotypes Estimated Using HMW Markers

Seed storage protein diversity among genotypes was studied using four HMW protein markers (160Kda, 150Kda, 145Kda, and 130Kda) which were collected from three locations. Comparison of genotypes was according to MAF and PIC values.

Table 16: Major allele frequency and polymorphic information content used for HMW & LMW glutenin sub-units genome study in bread wheat loci

	Adet		Debre Tabor		Kulumsa	
Markers (KDa)	**MAF**	**PIC**	**MAF**	**PIC**	**MAF**	**PIC**
Estimated HMW GS (a)						
160	0.72	0.322	0.52	0.517	0.56	0.445
150	0.84	0.233	0.64	0.465	0.66	0.4103
145	0.7	0.332	0.48	0.524	0.62	0.427
130	0.5	0.375	0.48	0.524	0.52	0.451
Mean	**0.69**	**0.315**	**0.53**	**0.506**	**0.59**	**0.433**
Estimated LMW GS (b)						
65	0.62	0.360	0.52	0.517	0.5	0.452
55	0.6	0.3648	0.74	0.381	0.78	0.327
50	0.76	0.298	0.52	0.517	0.7	0.388
45	0.8	0.2688	0.48	0.524	0.7	0.388
35	0.82	0.2516	0.54	0.511	0.78	0.327
Mean	**0.72**	**0.3087**	**0.56**	**0.499**	**0.692**	**0.377**

MAF= Major Allele Frequency, NA= number of alleles and PIC = polymorphic information content

According to the results based on HMW glutenin markers (Table 16a), in the current study, MAF ranged from 0.84 using 150kda to 0.5 by 130kda marker with a mean value of 0.69, and PIC value ranged from 0.3219 by160kda to 0.23 by150kda with a mean value of 0.32 at Adet. MAF ranged from 0.64 by 150kda to 0.48 by both 145 and 130kda markers with the mean value of 0.53 at Debre Tabor, and PIC value ranged from 0.52 by 145Kkda and 130kda markers to 0.46 by 150kda HMW marker with the mean

value of 0.51. At Kulumsa, MAF ranged from 0.66 by 150kda to 0.52 by 130kda marker with a mean value of 0.59, and PIC value ranged from 0.45 by 130kda marker to 0.41 by 150kda HMW marker with a mean value of 0.43.

The mean value 0.69 of MAF was highest at Adet, followed by 0.59 at Kulumsa and lowest 0.53 at Debre Tabor, similar to the finding of the previous work of Liu *et al*., (2007) as the frequency of the allele (allele with the highest frequency of the allele in the one locus) with an average of 0.56 were ranged from 0.33 to 0.72. Whereas, mean PIC value was highest 0.51 at Debre Tabor followed by Kulumsa 0.43 and lowest at Adet 0.32 with a similar rank order for all locations for MAF, similar to the previous work of Botstein *et al*. (1980), PIC value>0.5 is considered as being highly informative marker while 0.5>PIC>0.25 is just informative marker, while PIC≤0.25 is a slightly informative marker. Since, the values in the current study are at the informative level, seed storage protein diversity among genotypes was due to genetical than environmental factor. Similarly, it is in conformity with the previous work of (Liu *et al*., 2007) and (Sud *et al*., 2005) who worked with and found genetic diversity or PIC value per locus was observed across the tested loci.

From this observation, PIC values increased commensurate with increasing heterozygosity at a locus. Hence, scarce alleles have less effect on PIC values than common alleles; this trend was not consistent (Hokanson *et al*., 1998). So, HMW loci were informative in the current study and the markers are suggested to study genetic diversity and group structures in bread wheat genotypes. Polymorphism among individual genotypes is observed due to variation in HMW GS sequences present in their stored proteins. Higher polymorphic bands of HMW indicates their efficiency to study genetic diversity and discrimination of genotypes (Pradhan *et al*., 2004). In addition, these

genotypes were less influenced by the environment so less affected by the phenotypic then are genetically influenced.

4.3.1.4. Seed Storage Protein Diversity Among Genotypes Estimated Using LMW Markers

In this study, five LMW markers (65KDa, 55KDa, 50KDa, 45KDa and 35KDa) were used to analyze seed storage protein diversity among genotypes based on MAF and PIC values.

Accordingly, mean value of MAF (Table 16b) ranged from 0.82 revealed by 35kda to 0.6 by 55kda marker with a mean value of 0.72, and PIC value ranged from 0.36 by 55kda marker to 0.25 by 35kda with a mean value of 0.31, at Adet. Likewise, mean value of MAF ranged from 0.74 by 55kda to 0.48 by 45kda marker with a mean value of 0.56, and mean value of PIC ranged from 0.52 recorded by 45kda marker to 0.38 by 55kda with a mean value of 0.49 at Debre Tabor. Similarly, mean value of MAF ranged from 0.78 by 55kda and 35kda to 0.5 by 65kda marker with a mean value of 0.69, and PIC value ranged from 0.45 by 65kda marker to 0.33 by both 55kda and 35kda with a mean value of 0.38, at Kulumsa.

From these observations, the highest mean value of MAF (0.72) was at Adet, followed by Kulumsa 0.69 and lowest value 0.56 at Debre Tabor, similar to the previous work of Liu *et al*., (2007) as the frequency of the allele (allele with the highest frequency of the allele in the one locus) with an average of 0.56, indicates presence of highest genetical variability among the studied genotypes. Hence, seed storage protein diversity among genotypes was highly variable genetically than environmental factors, so it is possible to preserserve the genetic stalk of genotypes for further breading. Similarly, the highest mean value of PIC (0.50) recorded at Debre Tabor was followed by

Kulumsa (0.38) and lowest at Adet 0.31; similar to the order observed in the MAF result of current result. This result is supported by the previous works of Botstein *et al*. (1980), Liu *et al*., (2007) and Sud *et al*., (2005), equally as the current work was implying the values were in the informative level for the indication of genetic diversity among the studied genotypes, hence, seed storage protein diversity observed among genotypes, can help breeders to preserve the genotypic potential of genotypes at any environment. However, further study is needed for validation.

From this observation, PIC values increased commensurate with increasing heterozygosity at a locus. Since scarce alleles have less effect on PIC values than common alleles, this trend was not consistent (Hokanson *et al*., 1998). So, these LMW GS being informative, can be recommended to study genetic diversity among genotypes and group structures of bread wheat genotypes. Polymorphism among individual genotypes is observed due to variation in LMW GS sequences present in their seed storage protein. In addition, higher polymorphic bands of LMW markers indicate their efficiency for the study of genetic diversity among genotypes for seed storage diversity analysis among genotypes and discrimination of genotypes for further study as suggested by (Pradhan *et al*., 2004).

Generally, genotypes varied due to genetic than environmental factors, for the composition of gliadin and glutenin (HMW- and LMW GS). Hence, selection & further breeding of the genotypes is suggested based on the performance of genetic potential, and also it is possible to preserve the genetic potential of the varieties in any environment. However, further multilocation study is important for conformity.

4.3.2. Estimation of Seed Storage Protein Relationships Among Genotypes and Groups

In current study, dendrogram and cluster analyses were used for genetic similarity estimation among groups and within genotypes.

Dendrogram was generated using UPGMA cluster analyses based on Jaccard's similarity coefficient to study the relationship among groups and within genotypes based on seed storage protein gluten components; gliadin, glutenin and its sub units.

The ultimate goal of plant breeding programs is to improve the plant traits for seed storage protein and economic superiority. The knowledge of nature and extent of genetic variation and diversity available in the genotypes or breeding materials help the breeder for planning sound breeding programs. Hence, the present investigation was undertaken to evaluate 50 bread wheat genotypes (numbered 1 to 50, Appendix 1, used instead of their names for simplicity) collected from three locations.

4.3.2.1. Estimation Seed Storage Protein Similarity Among Groups Using Gliadin and Glutenin (HMW- & LMW-GS) Markers/Loci

Genetic similarity for seed storage protein among groups was analyzed using UPGMA based dendrogram generated by genetic distance matrix that revealed a complex genotypes distribution pattern with no clear grouping on the genotypes or their sources.

(a) **(b)**

Figure 11: Dendrogram generated for groups using UPGMA cluster analysis based on Jaccard similarity coefficient using gliadin (a) and glutenin (b) markers

According to the results of dendrogram analysis, for seed storage protein relationships among the groups, using gliadin and glutenin markers (Figure 11a &b), groups BWPVT-II-2013 and New varieties originated far back with a common point and similar back history in their origin with little time difference, compared to the other two groups BWNVT-II-2014 and Commercial variety with slight time gap variation.

In conformity with the previous study of Sharma *et al*. (1998) who reported that the genotypes of heterogenous origin/place of release and of different ploidy levels often grouped together, suggesting some degree of ancestral relationship between the genotypes. Similarly, Murthy and Arunachalam (1966) suggested with the opinion that the wide adaptability would be possible due to factors like heterogeneity, genetic architecture of groups, past selection history, developmental traits and degrees of general combining ability. It appeared that genotypes having same geographical origin differed and possessed wide divergence factors, since rapid ecotype differentiation was taking place even in the absence of reproductive isolation (Bennet, 1970).

From this observation, environmental factors were not responsible for the similarity/dissimilarity in the composition of seed storage protein among the groups, but genetic factors. So, it was observed that non-parallelism between groups for genetic diversity and relationship. Hence, the study of similarity/dissimilarity for the composition of seed storage protein among studied groups using gliadin and glutenin loci will help to select out the common genetic stalk (groups) for the composition of seed storage protein to create genetic similarity/dissimilarity based on the genetic makeup for the efficient breeding purposes.

4.3.2.2. Estimation of Seed Storage Protein Relationships Among Genotypes Using Gliadin and Glutenin (HMW- & LMW-GS) Markers/Loci

In the current study, seed storage protein relationship among genotypes studied based on Dendrogram- generated using UPGMA cluster analysis based on Jaccard similarity coefficient and cluster analysis using gliadin and glutenin markers (Table 17 and Figure 12a, b and c) as indicated below:

According to the results of the dendrogram (Figure 12) and cluster analysis (Table 17), only two genotypes (49 and 50) found common in a given cluster II at all locations. Single genotype 12 found in cluster II, three genotypes 28, 31 and 34 in cluster III, single genotype 21 in cluster IV and genotype 13 in cluster VI were common to both Adet and Kulumsa locations. Genotype 4, 6 and 7 in cluster III, 20 and 42 in cluster IV and genotype 30, 36 and 37 in cluster VI were common to locations Adet and Debre Tabor.

Table 17: Cluster analysis of genotypes as revealed by gliadin and glutenin markers

Adet		Debre Tabor		Kulumsa	
Clusters	**genotypes**	**Clusters**	**genotypes**	**Clusters**	**genotypes**
I	1, 19 and 35	I	32 and 33	I	7, 16, 21 and 30
II	12, 22, 25, 38, 39, 47, 49 and 50	II	27, 34, 47, 48, 49, and 50	II	6, 12, 49, and 50
III	2, 3, 4, 6, 7, 28, 31, and 34	III	1, 4, 5, 6, 7, 8, 12, 15, 18, 19, 21, 22 and 23	III	9, 10, 11, 15, 25, 26, 28, 31, 32, 33, 34, and 35
IV	8, 9, 15, 17, 18, 20, 21, 24, 40, 41, 42, and 45	IV	11, 13, 14, 16, 20, 35, 38, and 42	IV	3, 5, 14, and 21
V	5, 10, 11, 14, 26, 27, 33, and 46	V	25 and 31	V	39, 40, 42, 43, 44, and 45
VI	13, 16, 23, 29, 30, 32, 36, 37, 43, 44, and 48	VI	2, 17, 24, 26, 30, 36, 37 and 41	VI	1 and 13
		VII	3, 9, 39, and 40	VII	2, 20, 22, 37, 38, 41, and 48
		VIII	10, 28, 29, 43, 44, 45 and 46	VIII	4, 8, 17, 18, 19, 23, 24, 29, 36, 46, and 47

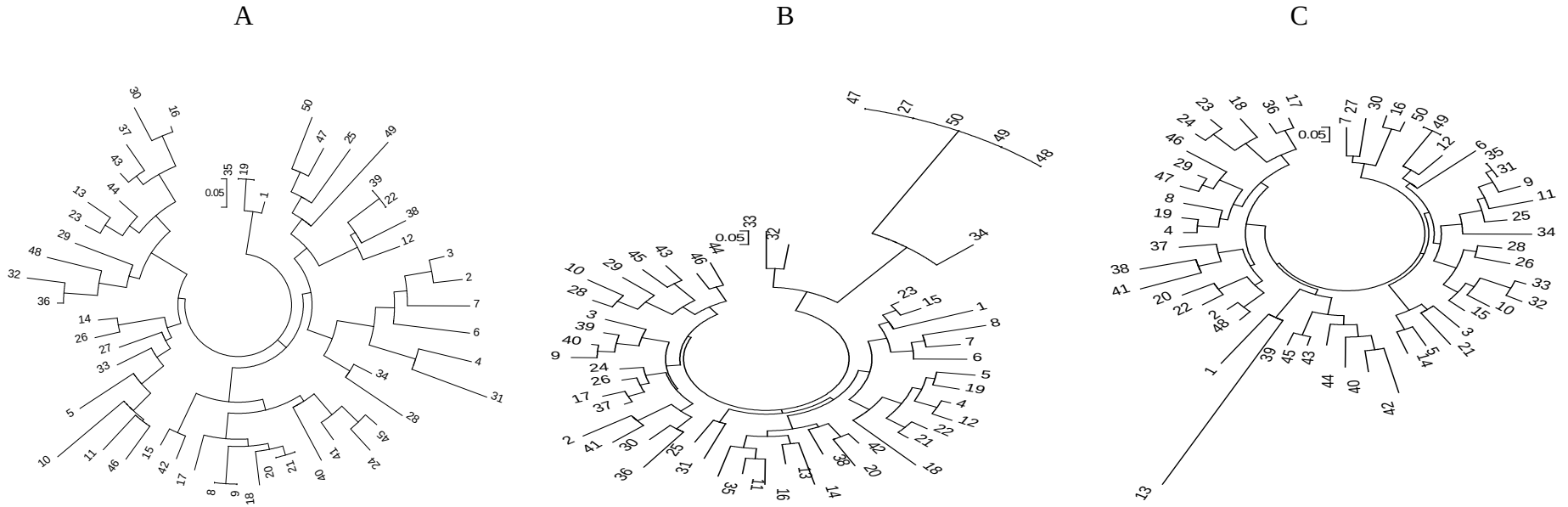


Figure 12: Dendrogram generated for each genotype using UPGMA cluster analysis based on Jaccard similarity coefficient at Adet (A), Debre Tabor (B) and Kulumsa (C) for gliadin and glutenin composition.

Solitary genotype 15 in cluster III and genotype 14 in cluster IV, two genotypes 29 and 46 in cluster VIII were common to Debre Tabor and Kulumsa locations. It was observed that those varieties coming from d/t groups were found to be in a given cluster, and those which were from the same group found to be in different clusters when analyzed based on both gliadin and glutenin (HMW & LMW GS) markers for the genotypes which were collected from all locations.

Similar results observed by the previous works of Walia and Garg (1996), Dotlacil *et al*. (2000), Bergale *et al*. (2001), who reported non-parallelism between geographic and genetic diversity. It was evident from the results that the genotypes of different ploidy levels viz., tetraploid (T. *durum*, T. *dicoccum*) and hexaploid (T. *aestivum*) also grouped in a same cluster (I, II, III, IV, V, VI and VII). This indicated that diversity is not only concerned with geographic origin or ploidy levels of genotypes but also with other characters. In conformity with the current result, earlier study of Sharma *et al*. (1998) also reported that the genotypes of heterogenous origin/place of release and of different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes.

Murthy and Arunachalam (1966) suggested also similar opinion with the current result that the wide adaptability would be possible due to factors like heterogeneity, genetic architecture of groups, past selection history, developmental traits and degrees of general combining ability. It appeared that genotypes having same geographical origin differed and possessed wide divergence factors, since rapid ecotype differentiation was taking place even in the absence of reproductive isolation (Bennet, 1970). Most genotypes, unlike to the genotypes found in common clusters above, found from different cluster groups are most important to provide superior hybrid genotype production and can

be used in future breeding programs for improvement of the concerned traits. And those genotypes found common in all at most and at two of the locations can be useful for the production of improved products at the mentioned locations.

From this observation, varieties from heterogenous population & place of release were grouped in the same cluster, so some degree of ancestral relationship is existed between studied varieties. Even though their area of adoption is different, this distribution of genotypes was due to unidirectional selection practiced by plant breeders of different states as of (Singh and Bains, 1968) as the current finding. Hence, it is possible to identify genotypes with similar genetic makeup to identify superior genotypes with similar genetic characteristics for further breading purpose.

4.4. Genetic Diversity in Bread Wheat Genotypes from Ethiopia Using SSR Markers

4.4.1. Markers Polymorphism Evaluation

Microsatellite markers are informative descriptors of the genetic variability of studied genotypes for the purpose of identification. The study on the use of microsatellite markers has further confirmed this marker as a powerful tool for identification and characterization of intra specific variations among wheat genotypes and landraces. SSR or microsatellite markers are often of multi-allelic nature, co-dominant inheritance, relative abundance, and extensive genome coverage were observed (Gupta & Varshney, 2000). Microsatellite markers are useful and becoming popular for different applications in wheat breeding due to their high level of polymorphism and easy handling (Devos *et al*., 1995; Roder *et al*., 1995; Bryan *et al*., 1997; Roy *et al*., 1999; Lelley *et al*., 2000) and are used to evaluate genetic diversity of hexaploid wheat (Al Khanjari *et al*., 2007).

In the previous studies, SSR markers almost succeeded in discrimination of wheat genotypes. But these markers could not separate wheat genotypes with different growth types completely. One reason could be that these genotypes had similar genetic resource, in addition that wheat is a self-pollinated crop and it has a narrow genetic base. Most of the primers that have been used in the studies revealed a high polymorphism. So, they can be used for screening, evaluation of genetic diversity and molecular mapping studies in bread wheat. In general, diversity measurements were higher in the genotypes at which such a high level of genetic similarity may be used for selection of the materials in the breeding programs where genotypes with high genetic distance can be used for this purpose. It can be concluded that more polymorphic wheat SSR markers could be used for efficient screening of the germplasm by saturating more regions of wheat genome (Roder, M.S., *et al*., 2002)

Based on molecular data, in the previous study employed twenty genic SSRs markers for molecular characterization of sixteen genotypes, the gene diversity was reported in the range from 0.11 (Xgwm247) to 0.70 (Xgwm257) with a mean value of 0.50. A similar approach was employed in a study involving molecular characterization of sixteen durum wheat accessions which were analyzed using nine microsatellite markers. The microsatellite markers studied amplified each one single locus. A total of 24 alleles were amplified with a range of 2 to 3 alleles per locus, with a mean value of 2.6 alleles per locus. All the microsatellites employed in this study revealed polymorphism and enabled unambiguous discrimination among the durum wheat genotypes. The genetic diversity in the microsatellites ranged from 0.22 to 0.60 with a mean value of 0.44 similar to the work of (Nefzaoui *et al*., 2014) who worked on the same crop.

SSR markers have a high level of PIC in comparison with other types of molecular markers (Gupta *et al*., 2008). In the previous studies (Henkrar *et al*., 2016) it was reported that PIC values in wheat ranged between 0.07 to 0.84 with an average genetic diversity of 0.48 in Moroccan wheat genotypes. Mattar *et al*. (2009) employed eleven microsatellites generating 44 alleles with an average of 4 alleles per locus comparable to the value of 1.89 alleles per locus as reported in this study.

In the present study, ninety-six Ethiopian bread wheat genotypes (45 released and 51 pipeline) were amplified using 15 SSR markers, of which seven were checked for medium to high polymorphism before embarking on further analysis and selected for being successful in amplifying all the accessions. These SSR markers revealed a total of 65 alleles.

The number of alleles (Na) per locus ranged from 1.2 (xgwn_285) to 2.6 (WMC_24), with an average of 1.89 alleles per locus (Table 18). Ali Reza, *et al*., (2013) in a similar work found a total of 80 alleles, average 3.2 and ranging from 1 to 5 alleles per locus. Liu *et al*., (2007) also reported a total 115 alleles, with 4.6 average and ranging from 2 to 9 alleles per locus. A total of 93 alleles and the number of alleles per primer ranged from 2 to 6, with an average of 3.72 were detected by Sud *et al*., (2005). Number of alleles in each genome was 3.33 (A genome), 3 (B genome) and 3.3 (D genome). That was compared with the other authors (Salem *et al*., 2008). The number of alleles per marker depends on the relative distance of the locus from the centromere (high genetic variation occurs in the non-centromeric regions compared to the centromeric regions of chromosomes.) and also it was related to the motif and repeat number of the allele frequencies (Huang *et al*., 2009).

The values for major allele frequency ranged from 0.47 (WMC_24) to 0.91 (xgwm_285), with an average of 0.67 per marker (Table 18). It coincides with the previous finding of (Liu *et al*., 2007) that the frequency of the allele (allele with the highest frequency of the allele in the one locus) with an average of 0.56, were varied from 0.33 (Xgwm129) to 0.75 (Xgwm540).

Table 18: Genetic diversity indices across the seven SSR loci used in the 96 Bread Wheat genotypes

Locus	MAF	NG	NA	Na	Ne	I	Ho	He	GD	PIC	Fst	Nm	F
WMC_216	0.71	3.00	3.00	2.20	1.82	0.65	0.00	0.44	0.49	0.34	0.05	5.09	1.00
XGWM_3	0.53	2.00	2.00	1.80	1.77	0.55	0.00	0.39	0.41	0.37	0.20	1.02	1.00
XgwM_129	0.59	2.00	2.00	1.80	1.66	0.51	0.00	0.36	0.37	0.37	0.15	1.45	1.00
Xgwm_165	0.74	2.00	2.00	1.80	1.55	0.46	0.00	0.31	0.33	0.31	0.37	0.44	1.00
WMC_44	0.73	2.00	2.00	1.80	1.55	0.46	0.00	0.32	0.33	0.32	0.15	1.42	1.00
Xgwm_285	0.91	2.00	2.00	1.20	1.09	0.10	0.00	0.06	0.07	0.15	0.17	1.25	1.00
WMC_24	0.47	3.00	3.00	2.60	2.22	0.78	0.00	0.48	0.49	0.55	0.27	0.67	1.00
Mean	**0.67**	**2.29**	**2.29**	**1.89**	**1.67**	**0.50**	**0.00**	**0.34**	**0.36**	**0.34**	**0.19**	**1.62**	**1.00**

MAF = major allele frequency; NG = number of genotypes; NA = number of alleles; Na = number of different alleles; Ne = Number of effective alleles; I = Shannon information index; Ho = observed heterozygosity; He = expected heterozygosity; GD = Neis gene diversity; PIC = polymorphic information content.

In this study, the highest PIC value of 0.55 was observed in WMC_24 while lowest value of 0.15 was observed in xgwm_285 with an overall average of 0.34 (Table 19) similar to the previous work of Liu *et al*., (2007) and Sud *et al*., (2005) in their work on genetic diversity or polymorphism information content (PIC) value per locus in across the tested loci. Polymorphic index is as an estimate of discriminatory power every microsatellite with respect to number and relative frequency of each allele. So, although some of the microsatellites have similar alleles, however due to the different frequency of same alleles, suggest a different polymorphic index. From this observation, PIC values increased commensurate with increasing heterozygosity at a locus. Since, scarce alleles have less effect on PIC values than common alleles; this trend was not consistent (Hokanson *et al*., 1998). These primers, being informative, can be recommended to study genetic diversity and group structures in

bread wheat. As Botstein *et al*. (1980) reported that PIC value > 0.5 is considered as being highly informative marker while 0.5 > PIC > 0.25 is just informative marker, while PIC ≤ 0.25 is a slightly informative marker. In previous studies, Landjeva1 *et al*. (2006), reported the PIC values in Bulgarian winter wheat ranged between 0.10-0.81. Bryan *et al*. (1997) found that PIC value with an average of 0.51 from 49 SSR primer pairs was isolated from hexaploid wheat genome. Our work was in conformity with the previous work of genetic differentiation of 60 wheat genotypes selected for adaptation and end-use from Hungary, Austria, and German using 42 microsatellites showed an average PIC value of 0.57 (Stachel *et al*., 2000). Polymorphism among individual genotypes is observed due to variation in DNA sequences present in their chromosomes. Higher polymorphic bands of primers indicate their efficiency to study genetic diversity and discrimination of genotypes (Pradhan *et al*., 2004). Simple sequence repeats or microsatellites are used in a lot of research because of their locus specificity, ease of use, codominance, and high polymorphism (Roder *et al*., 1998; Landjeva *et al*., 2007; Laido *et al*., 2013). Microsatellite markers are useful for marker-assisted selection, identifying quantitative trait loci, genetic diversity, and labeling of stress-tolerant genes in wheat or wild relations (Landjeva *et al*., 2007; Ijaz and Khan, 2009).

A maximum of two alleles are expected per individual plant at single copy microsatellite locus in diploid species. In the present study, the observed heterozygosity (Ho) was found to be zero for all the loci, and the expected heterozygosity (He) values ranged from 0.06 (xgwm_285) to 0.48 (WMC_24), with an average of 0.34 (Table 18).

Table 19: Allele frequency distribution across the five groups

Marker	WMC_216			XGWM_3		XgwM_129		Xgwm_165		WMC_44		Xgwm_285		WMC_24		
Allele	125	135	140	35	50	110	120	200	210	210	280	200	230	130	135	150
Freq,	0.71	0.28	0.01	0.47	0.53	0.41	0.59	0.26	0.74	0.73	0.27	0.91	0.09	0.36	0.47	0.17

Average allelic richness across the five groups revealed that WMC_24 (2.46), WMC_216 (2.06), and XGWM_3 and XGWM_129 (each 1.80) scored the highest frequency in that order (Table 20).

Table 20: Allelic richness across the five groups and seven loci used in the study

Pop	WMC_216	XGWM_3	XgwM_129	Xgwm_165	WMC_44	Xgwm_285	WMC_24	Aver. Loci
Comm_V	2.28	2.00	2.00	1.85	2.00	1.97	2.31	**2.06**
BWPVT-I-2013	2.00	2.00	2.00	2.00	2.00	1.00	3.00	**2.00**
BWPVT-II-2013	2.00	2.00	2.00	2.00	2.00	1.00	3.00	**2.00**
BWNVT-II-13-14	2.00	2.00	2.00	2.00	1.95	1.00	2.98	**1.99**
New_V	2.00	1.00	1.00	1.00	1.00	1.00	1.00	**1.14**
Aver. Pop	**2.06**	**1.80**	**1.80**	**1.77**	**1.79**	**1.19**	**2.46**	

Evaluation of groups allelic richness (allelic diversity) and private allelic richness (private allelic diversity) is an alternative criterion to detect the extent of genetic diversity particularly in groups with different size and hence, their long-run evolutionary potential that especially targets conservation and management programs (Petit *et al*., 1998; Simianer, 2005; Foulley and Ollivier, 2006) since the effects of selection is limited to the initial allelic composition than allelic frequencies (levels of heterozygosity) (Hill and Rasbash, 2009). In addition, measure of allelic richness is useful for inferring the evolutionary histories of groups (Castric and Bernatchez, 2003) and to test reductions in groupsize (Cornuet and Luikart, 1996) as it is more sensitive to the presence of rare alleles (Leberg, 1992) which is prominent in this study, and groupbottlenecks (the current status of the crop) compared to expected heterozygosity. In our study across five groups, average allelic richness was with highest

frequency in order by WMC_24 (2.46), WMC_216 (2.06), and XGWM_3 and XGWM_129 (each 1.80). Similarly, two loci XGWM_285 (0.19) and WMC_216 (0.07) revealed a considerable private allele both for Commercial Verities. All the alleles except one (rare) are common alleles (frequency > 5%). In this regard, all the studied groups showed highest allelic richness, and hence are more interesting in terms of genetic and evolutionary studies on this crop. Moreover, the groupcontaining commercial genotypes showed a relatively high proportion of private alleles which may indicate certain level of independent evolution of their gene pools that allowed maintenance of private alleles at a grouplevel (Slatkin, 1985).

4.4.2. Genetic Variation Within and Among Groups

Genetic diversity in cultivated crops is essential for successful breeding and creation of new genotypes. Estimating the genetic diversity of wheat germplasm can help in identifying diverse parental combinations and creating segregating progeny with high genetic variability for selection (Goyal *et al*., 2015). A narrowed genetic pool increases the development of risk factors. An increase in yield and disease resistance could be provided by expanding the genetic diversity of bread wheat (Nielsen *et al*., 2014).

In the present study, genetic diversity within and among groups, five of the groups considered, the ranges of Ne, He, GD and I were very narrow. In this regard, BWPVT-II-2013 group scored a relatively higher Ne, He, and I while BWPVT-I-2013 group scored a higher GD. However, New Genotypes revealed a minimum (below average) Ne, I, He, GD, and PPL. All the five groups scored a nearly zero Ho. Regardless of the low Ho, all the studied groups had high allelic richness across the entire loci (the least being 1.14 recorded for New Genotype). Private allelic richness was recorded only for Commercial variety at two loci (XGWM_285 and WMC_216) (Table 21). In general, all the

groups except New Genotype showed the highest (average of 74.29%) percentage of polymorphic loci (PPL) (Table 20), which is by far greater than the level reported in accordance with the results of the previous studies (Mondini *et al*., 2012; Abuzied *et al*., 2012) whereby they detected among and within variation, respectively as a low level of variations was observed among groups (19%), while high levels of variation were revealed within group(81%). The relatively higher with-in group variation may be attributed to the presence of genotypes collected from diverse' geographic locations of 14 zones that can be grouped in to three major durum wheat producer regions (Tigray, Amhara and Oromia). Such high percent polymorphism together with the PIC values obtained, which provides an estimate of the discriminatory power of a locus (Marulanda *et al*., 2014), and the allelic diversity suggest great potential of the markers for use in future genetic studies. However, the value of number of effective alleles, expected heterozygosity, genetic diversity and Shannon information index in all groups except BWPVT-II-2013 group that scored a relatively higher Ne, He, and I; and BWPVT-I-2013 group that scored a higher (GD) showed very narrow range. Hence, there is a need to develop more highly informative SSRs or other type of DNA markers such as SNPs that are suitable to characterize Ethiopian bread wheat genetic regroups for efficient conservation and breeding.

The studied loci revealed differences between Ho and He in which half of them showed excess heterozygosity that led to a significant departure from HWE across groups. Such excess heterozygosity is expected in historically outcrossing species that maintain their heterozygosity through reproduction, or if other factors such as natural and artificial selection pressure favor heterozygosity, or minor genotyping errors like null alleles we detected might have contributed (Morin *et al*., 2009). Similar results have been reported (Zawedde *et al*, 2014; Gao *et al*., 2011). In addition, Fisher's exact test, assuming HWE and collapsing less frequent alleles revealed a significant

($p<0.05$) and higher (51%) pairwise genotypic linkage disequilibrium compared to other cereal crops like maize (*Zea mays* L.) (9.7%), (Remington *et al*. 2001). If the loci are not linked, the observed higher LD could be an effect of currently declining groupsize, a low recombination rate or natural selection (Gupta *et al.*, 2005) or genetic isolation between groups because of the usually practiced reproductive methods unlike outcrossing groups that are assumed to have relatively low LD (Jin *et al*., 2010). Hence, SSR markers in general and the developed loci in particular are powerful in detecting the breeding nature of wheat which is the key for further breeding programs and conservation measure.

In general, the current markers detected a wide range of genetic variation among the entire groups. Moreover, the polymorphic information contents of the loci across groups look wider (0.15–0.55). However, despite the range, considerable number of loci are in the range of slightly informative. Thus, a thorough screening procedure should be applied or tried other markers such as SNPs to identify highly variable polymorphic loci that are suitable to group the crop genetic regroups into certain classes for efficient preservation and breeding.

Table 21: Summary of different group diversity indices averaged over the seven loci

Population	Na	Ne	I	Ho	He	GD	F	PPL
Commercial-V.	2.29	1.71	0.60	0.00	0.40	0.40	1.00	100.00
BWPVT-I-2013	2.00	1.79	0.59	0.00	0.40	0.44	1.00	85.71
BWPVT-II-2013	2.00	1.86	0.61	0.00	0.41	0.43	1.00	85.71
BWNVT-II-13-14	2.00	1.82	0.59	0.00	0.40	0.41	1.00	85.71
New-Genotype	1.14	1.14	0.10	0.00	0.07	0.10	1.00	14.29
Mean	**1.89**	**1.67**	**0.50**	**0.00**	**0.34**	**0.36**	**1.00**	**74.29**

4.4.3. Group Genetic Differentiation and Analysis of Molecular Variance (AMOVA)

In our study, the analysis of molecular variance was conducted by grouping the groups according to their source. Accordingly, the result showed 100% allelic diversity attributed to individual accessions within groups. Almost no significant variation for molecular diversity among groups based on groups of collection depicting shared alleles among them (Table 22).

Table 22: Analysis of molecular variance (AMOVA) in Ethiopian Bread wheat groups

Source	df	SS	MS	Est. Var.	%	Value	P-value	Fst
Among groups	4.00	17.56	4.39	0.01	0%			
Among individuals	91.00	377.80	4.15	2.08	100%	1.00	0.001	
Within individuals	96.00	0.00	0.00	0.00	0%			
Total	**191.00**	**395.35**		**2.08**	**100%**			**0.003**

Similarly, Nei's heterozygosity (Nei, 1978) revealed a weak group sub-structuring where the overall Fst (0.003) value was very small (Table 23). However, pairwise group differentiation test (0.01 – 0.35) values looks wider (Table 23). Moreover, maximum overall within group (Fis = 1.00) and total (Fit = 1.00) genetic differentiation values have also been evidenced as revealing fixation of the alleles within the groups. Considerable overall gene flow (Nm = 1.62) was also evident (Table 21).

Table 23: Group pairwise Fst value

Pop	Com_V	BWPVT-I-2013	BWPVT-II-2013	BWNVT-II-13-14	New_V
Com_V	0.00				
BWPVT-I-2013	0.07	0.00			
BWPVT-II-2013	0.04	0.04	0.00		
BWNVT-II-13-14	0.05	0.05	0.01	0.00	
New_V	0.35	0.25	0.30	0.25	0.00

Frequency based Nei's (Nei, 1972) standard genetic distance between all pair-wise combinations among the five bread wheat groups were calculated and the result ranged from 0.01 (BWNVT-II-13-

14 *vs.* BWPVT-II-2013) to 0.51. The highest pairwise genetic distance (0.51) was observed between Commercial Genotype and New Genotype followed by New Genotype and BWPVT-II-2013, New Genotype and BWNVT-II-13-14, and New-V and BWPVT-I-2013 in that order (Table 24).

Table 24: Nei's group pairwise genetic distance

Pop	Com_V	BWPVT-I-2013	BWPVT-II-2013	BWNVT-II-13-14	New_V
Com-Genotype	0.00				
BWPVT-I-2013	0.12	0.00			
BWPVT-II-2013	0.05	0.06	0.00		
BWNVT-II-13-14	0.05	0.07	0.01	0.00	
New Genotype	0.51	0.21	0.32	0.24	0.00

In the present study, Fst averaged across all loci (Fst = 0.003) and pairwise F_{ST} for all pairs of groups (highest value = 0.35) was generally low to moderate on the bases of Wright (1943) and Hartl and Clark (1997) suggestions, that group the levels of differentiation in to low (0.00-0.05), moderate (0.05-0.15) and high (>0.15). Wright (1943) indicated that genetic differentiation among groups can be considered high if the value of F_{ST} is greater than 0.25. This could be partly attained if gene flow, which is a powerful force to decrease differentiation among groups, is low (Nm<1) (Slatkin, 1987) or if genetic drift removes rare or scarce alleles and hence, increase private alleles within groups (Papetti *et al.,* 2012). Hence, the present study showed that Ethiopian bread wheat genotypes have very little group sub-structuring.

A pair-wise groupgenetic differentiation analysis resulted in many more variation in F_{ST} value among pairs of groups (ranging from 0.01 to 0.51). BWPVT-I-2013 groupshowed the highest (0.51) pairwise Nei's standard genetic distance with BWPVT-I-2013 and New Genotype groups and is the most genetically distinct groupwith a mean Nei's standard genetic distance of 0.51. This can be partly explained by the fact that BWPVT-II-2013 and Com Genotype groups were collected from a

relatively different groups and are separated from the other groups with a relatively wider distance that probably restricted recent seed exchange. Hence, these groups may serve as potential groups of new genetic variation of important traits that can be used in breeding programs and as potential parental groups. Genotypes from Commercial Variety groups showed the highest average number of pairwise differences (Pix) within groupthat might be attributed the larger number of groups and the result implies a large amount of genetic diversity of the crop in this groupto be preserved.

In terms of the loci, some of them were represented by excess heterozygosity (negative Fis), indicating that the crop is not suitable for inbreeding because of its seed dispersal nature that preserves heterozygosity and thus keeps the original allele diversity in the groupintact or nearly as high as it was. The other possible reason is selection favoring heterozygosity as it provides the best adaptive fitness. The positive indices in the remaining loci refers to the existence of selection against heterozygosity for certain traits (Kof *et al.*, 2008). Such disparity in fixation indices within a genome provides important insights into the reproductive biology, genome regions under evolutionary processes (or selection) and demographic history of a group(Holsinger and Weir, 2009). The value for Fst and Gst showed a slight variation for several of the loci which might be attributed to the difference in algorithms while considering mutation effect and hence, more markers could be applied to minimize the biasness introduced by any one locus (Frankham *et al.*, 2002).

4.4.4. Group Genetic Relationships

UPGMA based dendrogram analysis generated revealed a complex accession distribution pattern with no clear grouping based on geographic origin. In general, the UPGMA dendrogram resulted in the formation of three clusters comprised of 8 to 76 accessions (Figure 13). The largest cluster, cluster III constituted 76 accessions where accessions from all groups (groups) were lumped together.

The second largest cluster is cluster I that harbored 12 accessions from all the collection areas. The third and last cluster (II) contained 8 accessions.

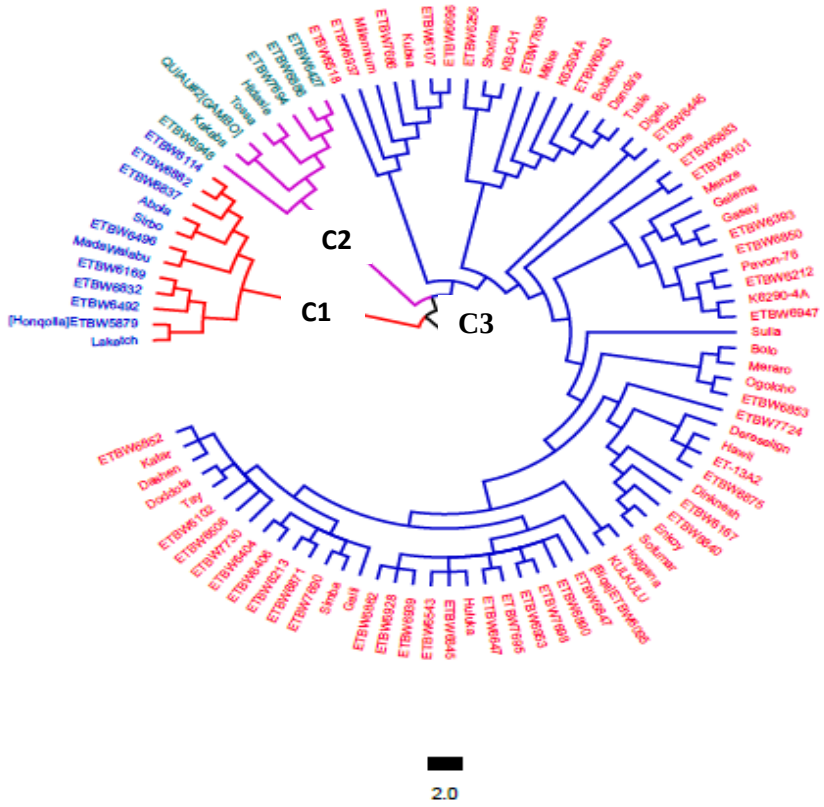


Figure 13: UPGMA dendrogram for the 96 bread wheat genotypes

In the present study, cluster analysis at the genotype level on the basis of SSRs analysis 96 genotypes divided into 3 clusters each containing 76, 12, and 8 genotypes on the basis of UPGMA based dendrogram analysis generated using genetic distance matrix which inferred the relatedness among genotypes (Figure 13). Based on previous literature, these studies have been reported for diversity analysis and determination of genetic variability (Tilahun *et al*., 2016).

The genetic relationships among the genotypes were investigated using cluster analysis dendrogram based on UPGMA that revealed three clusters; cluster I consists of 12 genotypes, cluster II with 8 genotypes and cluster III containing 76 genotypes with a complex accession distribution pattern in each cluster. Each cluster was composed of both released and pipe line genotypes almost with similar distribution, i.e., out of 96 studied genotypes the first cluster composed of 5 released and 7 pipe line genotypes at a total of 12. The second cluster consisting of 4 released and 4 pipe line genotypes at a total of 8 and the third cluster consisting of 36 released and 40 pipe line genotypes at a total of 76 genotypes under study. This result indicated that at least equal proportion of the released and pipeline genotypes were distributed at every cluster without being differentiated by their being released or pipeline consortium.

According to the results of UPGMA cluster analysis (Figure 14), showed that the genotypes with more similar microsatellite loci placed (presence of mixed pipeline and released genotypes) were expected to exist in the same cluster but were distributed throughout the three clusters almost with similar proportions. Hence this finding is contradictory with the previous finding of Reza, *et al*., (2013) whose results showed that the cluster analysis (UPGMA) showed that the genotypes with more similar microsatellite loci (closely related genotypes) placed in same cluster and in addition the cluster analysis showed that some of the genotypes by having higher similarity of microsatellite loci were placed in a group. Grouping of the genotypes in a given cluster is a means of representing similarity in the pedigree of microsatellite loci and uniformity will help the researcher as an indication of the relative genetic similarity of the genotypes. It appears that the type of growth cannot be a factor in the difference between the genotypes in one cluster because the region that controls

type of growth is a small part of the whole genome and genotypes with different growth type can be placed in one group.

Nevertheless, the dendrogram did not indicate any clear divisions among the bread wheat genotypes based on their origin. Distribution of accessions of similar origin into different clusters might indicate the existence of accession diversity within the groups of origin. The distribution of released and pipeline genotypes almost with similar proportions in each cluster. This might indicate that accessions from their origin are more diverse than others. This distribution and pattern of the genotypes, over all the clusters different from their origins, would suggest future collections of the genotypes out of their regions. This result is consistently in agreement with the agronomic and phonologic characterization work of Raman *et al*. (2014) who showed that Ethiopian genotypes formed a very distinct and separate grouping/gene pool than others.

UPGMA analysis using the five groups also revealed two major clusters in which the new verities constituted a separate cluster while the commercial genotypes and other pipeline verities were grouped together (Figure 14).

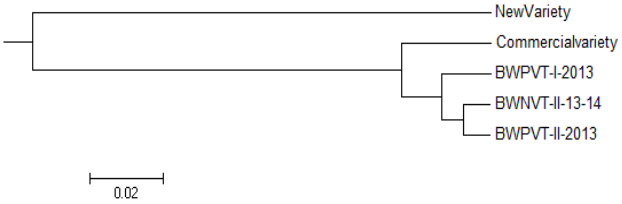


Figure 14: Dendrogram generated for wheat genotypes using UPGMA cluster analysis based on Jacquard Similarity Coefficient using SSR markers

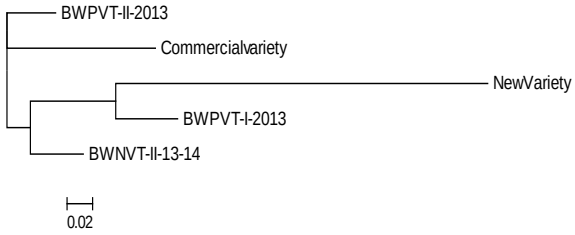


Figure 15: Neighbor joining tree by the shared allele method based on the group of the genotypes

Similarly, group differentiation among groups of UPGMA analysis based on Jacquards similarity coefficient of the markers on the five groups (Figure 14) revealed two major clusters in which the New verity constituted a separate cluster while the commercial genotypes and other pipeline verities were grouped together. According to the history of the genotypes, the new variety groups are those with released genotypes coming recently, while the commercial varieties are those released before the new variety groups. All other genotypes that were included in the sub group level together were the genotypes to be studied further (pipeline genotypes). By the structure analysis, these two major groups were resolved but with no significant admixtures. The cluster analysis also provided an evidence of not having gene flow between these groups. Generally, there was good correspondence between the group pattern observed in the dendrogram and the group structure identified using structure.

Group neighbor joining analysis revealed that New variety group had along evolutionary distance relative to the Commercial and pipeline verities (Figure 15).

NB. It could not be as a result of or genetic difference rather it is due to sample size difference where New variety group are by far smaller than Commercial variety group.

4.4.5. Group Structure Analysis

A total of seven SSR markers were used to analyze the group structure in the panel of 96 Ethiopian bread wheat accessions using a model-based approach in Structure. The results were then permuted for each K value and the results were collected through structure harvester (Earl and von Holdt, 2012). The LnP(D) value for each given K increased with the increase in K, but as there was no clear change in the LnP(D) value, the probable K value could not be inferred. However, on applying

the second-order statistics (ΔK) developed by Evanno *et al.* (2005), a sharp peak in ΔK at K = 2 was observed, suggesting the presence of two major groups (Figure 16A). The analysis of K = 2 groups showed individual accessions from the five collection groups distributed between the two groups (Figure 16B). Pattern of the model-based grouping revealed a significant admixture among the five groups which was somehow congruent with UPGMA dendrogram.

Similar to the genetic relationship in the groups, structural analysis revealed a close relationship (weak sub-division) among the samples from the five groups studied, and in general, five inferred groups (K=2) with no potential admixtures have been observed. It is interesting to indicate that all individual plants have alleles originated from the five clusters, which supports the presence of no gene flow that led to good groupdifferentiation.

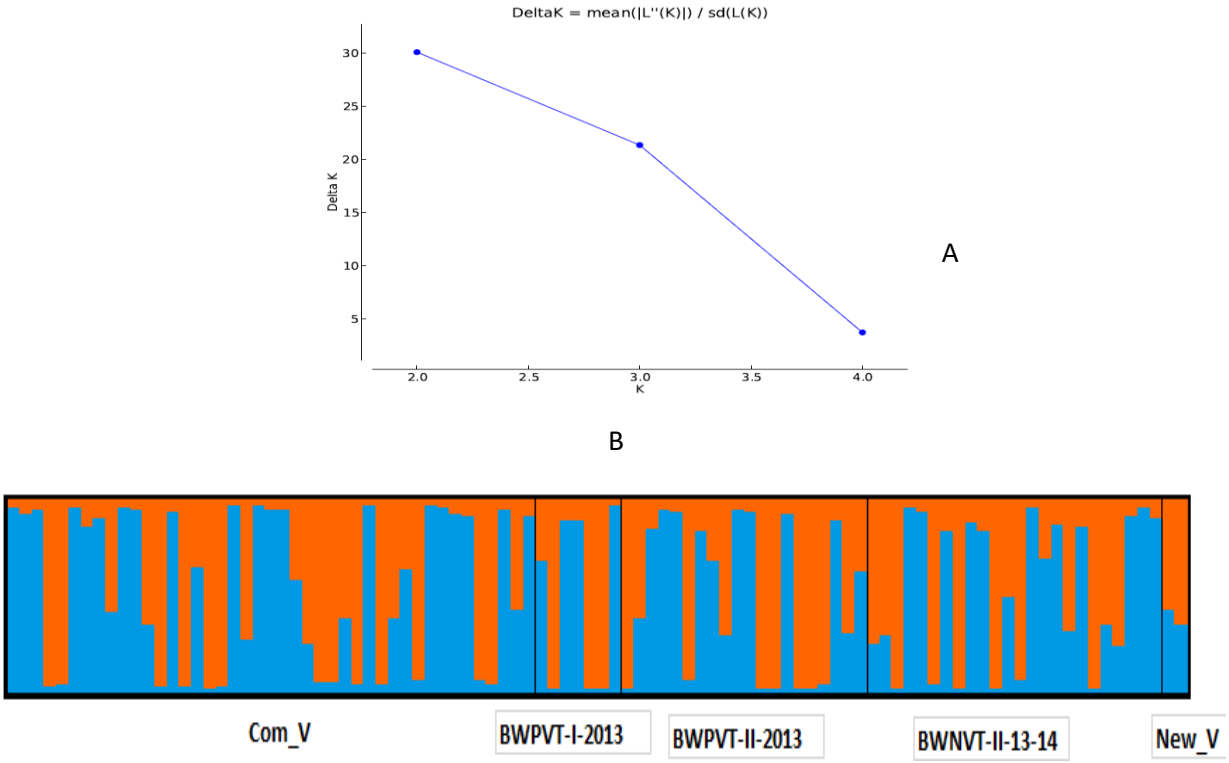


Figure 16 a & b: Group structure of 96 Ethiopian bread wheat genotypes based on 7 SSR panels as obtained from Structure 2.3.4 software

5. CONCLUSION AND RECOMMENDATIONS

5.1. Conclusion

One hundred twenty-one bread wheat genotypes were grown at Adet, Debre Tabor and Kulumsa to determine genetic variability, association among grain yield and yield components, and association of characters to estimate phenotypic diversity of the genotypes.

Generally, the present study revealed the existence of significant genetic variability among the tested genotypes for different traits helpful for direct and indirect selection. Attention should be given for traits which have moderate to high heritability and genetic advance in order to bring an effective response of grain yield improvement. Genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program. Therefore, thousand kernel weights, above ground biomass, harvest index, hectoliter weight and plant height showed positive phenotypic and genotypic correlation with the grain yield. The character harvest index and above ground biomass had highly significant direct effect at both genotypic and phenotypic level to grain yield indicating more attention should be given to those character to improve the grain yield of bread wheat. Due to the presence of variability among the genotypes, heritability and relationships in the tested traits of the genotypes confirmed possibility to increase wheat productivity in target area. Hence, selection and hybridization on those genotypes based on the trait with high GCV, heritability, genetic advance, and positive correlation coefficient and direct effect on grain yield can be recommended for farther yield improvement of bread wheat at respective location.

One hundred twenty-one bread wheat genotypes were used to study genetic diversity of bread wheat genotypes based on the physico-chemical (grain) quality traits and fifty bread wheat genotypes to study the flour quality of the genotypes that were grown at three locations Adet, Debre Tabor and Kulumsa.

During grain quality study, most of the traits used like TGW, HLW, protein content, wet gluten content and SDS showed significant differences among the genotypes, however, there was no any environmental difference among the performance of the genotypes for the traits studied. Hence, selection & further breeding of the varieties is suggested based on the performance of genetic potential, and also it is possible to preserve the genetic potential of the varieties in any environment. However, further multilocation study is important for validation.

Similarly, in the flour quality study, the composition of gliadin, glutenin, and HMW and LMW-GS in the genotypes were independent of environmental fluctuations, though there was significant difference among the genotypes for these factors. So, there was wide range of potential genotypes for the study of genetic diversity in bread wheat genotypes.

Wheat improvement activities for wheat-based cropping systems and to study genetic behavior on the basis of protein profiles can be used for development of high baking quality wheat genotypes, developing and releasing superior-quality wheat genotypes.

Likewise, merging of grain quality and flour quality parameters through analyses by their respective measurements has been revealed as a very promising strategy to select good baking quality in early generations of bread wheat genotypes and for breeding.

Fifty bread wheat Ethiopian bread wheat genotypes assessed based on genetic variability and relationships measurements have been found effective to differentiate the selected genotypes. Highest major allele frequency (MAF) value in the genotypes was found at Adet followed by Kulumsa and last by Debre Tabor for all gliadin, glutenin and HMW and LMW GS composition with little difference in numbers. It is to mean that there was highest variability within the studied genotypes. However, there was no variation in the environments. Similarly, the polymorphic information content (PIC) value found at the informative range (0.5>PIC>0.25) of polymorphism or heterogeneity or variation in the studied genotypes at all locations with the highest value at Debre Tabor followed by Kulumsa and last by Adet being the reverse order is the value of MAF to PIC value for the composition of gliadin, glutenin and HMW- and LMW-GS. So, this situation could be used as baseline information for further study targeting breeding and crossing the crop (hybridization) with other closely related species and/or for mapping its genes on their respective seed storage protein.

Genetic relationship based on the dendrogram and cluster analyses in the genotypes for their composition of gliadin, glutenin and HMW- and LMW-GS have been found effective to differentiate the selected bread wheat genotypes. 6% of the genotypes were common to all locations, 16% common to the locations Adet and Debre Tabor, 12% common to Adet and Kulumsa and 4% common to Debre Tabor and Kulumsa for gliadin composition out of 50 genotypes this indicates that about 58%, i.e., more than half of the genotypes were found to be distributed throughout different clusters, there is much more dissimilarity than similarity among the genotypes. Similarly, from a total of 17 genotypes (34%), 0% genotypes common to all locations, 6% common to Adet and Debre Tabor, 12% common to Adet and Kulumsa, 16% of the genotypes were common with

glutenin composition of the genotypes indicating highest variability for the composition of glutenin than gliadin storage protein was recorded (66% of the genotypes) were distributed throughout different clusters consisting of highest heterozygosity or variability in the studied genotypes. And from a total of 14 genotypes (28%), 0% genotypes common to all locations, 22% common to Adet and Debre Tabor, 4% common to Adet and Kulumsa, 2% of the genotypes were common with HMW GS composition of the genotypes indicating the second highest variability for the composition of HMW GS than glutenin and gliadin storage protein was recorded (72% of the genotypes) were distributed throughout different clusters consisting of the second highest heterozygosity or variability in the studied genotypes next to LMW GS. From a total of 13 genotypes (26%), 0% genotypes common to all locations, 16% common to Adet and Debre Tabor, 6% common to Adet and Kulumsa, 4% of the genotypes were common with LMW GS composition of the genotypes indicating the highest variability for the composition of LMW GS than gliadin, glutenin and HMW GS storage protein recorded (74% of the genotypes) were distributed throughout different clusters consisting of the second highest heterozygosity or variability in the studied genotypes.

However, protein profiling was not as effective as molecular marker but it can be very useful for demonstrating quantitative changes at protein level under different conditions and unique proteins are potentially useful in ultimately understanding the cellular events that are occurring at that time (Ghafoor *et al*., 2002) Similarly, a comparison of protein profiles from different genotypes could lead to the identification of proteins associated directly or indirectly with the genetic variability responses. This could be easily explained that protein/biochemical markers are have environment interaction, therefore protein/enzymes exclusively found in certain genotypes could able to express in certain environmental conditions. The detected variation could be used to provide useful information on individual enzymes or transporters, activity as well as modification of structural protein, protein-protein interactions and

genetic variation of the genotypes dependent protein movement and can be used to classify adapted genotypes to improve the efficiency of bread wheat breeding programs. Nevertheless, it could be concluded that seed storage protein components could be useful markers in cultivar identification, pedigree analysis, registration of new genotypes, and in the characterization of genetic diversity and classification of adapted genotypes, thereby improving the efficiency of wheat breeding programs in cultivar development.

In the present investigation, SSR markers showed a high level of polymorphism and considered to be highly informative marker in hexaploid wheat. The genetic diversity levels observed in bread wheat that are cultivated in Ethiopia would be useful indicators if such an approach is planned for the wheat genome. This makes genomic diversity estimates a potentially valuable predicting source for selecting diverse parent genotypes for favorable heterotic combinations in wheat improvement program.

For many breeding programs, understanding of genetic diversity among genetic materials is important to make genetic group with high level of genetic diversity and it can also help to run a breeding program well. One of the best methods to evaluate genetic diversity is to use molecular markers. It has been confirmed that the molecular markers can discriminate close genotypes. In this study, relationship among different bread wheat genotypes has been characterized by using SSR markers. This result will be useful for breeding programs of bread wheat.

5.2. Recommendations

Immediate actions that targets conservation of the existing gene pool of the crop: collaborative research involving all stakeholders, intensive germplasm collection and preservation, and improvement of farmers' awareness needs to be carried out involving relevant stakeholders.

In addition, it is necessary to further assess the extents of genetic diversity of seed storage protein, and bread making quality of the crop in a more diverse locations and years. Finally, it is important to make national wheat breeding effort more efficient and use marker technology to target specific traits.

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7. APPENDICES

Appendix 1. List of 121 genotypes used for the agro-phenotypic and grain quality study at three locations.

S. N	Genotype	Pedigree	Origin	Source/group	Nature
1	ETBW7686	KIRITATI//ATTILA*2/PASTOR/3/AKURI		BWPVT-I-2013	Pipe line
2	ETBW7688	FRANCOLIN #1/MESIA//MUNAL #1	-	BWPVT-I-2013	Pipe line
3	ETBW7689	FRANCOLIN #1/MESIA//MUNAL #1	-	BWPVT-I-2013	Pipe line
4	ETBW7690	FRET2*2/BRAMBLING/3/FRET2/WBLL1//TACUPETOF2001/4/WBLL1*2/BRAMBLING	-	BWPVT-I-2013	Pipe line
5	ETBW7692	ALTAR84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/KACHU/6/KIRITATI//PBW65/2*SERI.1B	-	BWPVT-I-2013	Pipe line
6	ETBW7693	FRNCLN*2/TECUE #1	-	BWPVT-I-2013	Pipe line
7	ETBW7694	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/4/KINGBIRD #1	-	BWPVT-I-2013	Pipe line
8	ETBW7695	KACHU/KINDE	-	BWPVT-I-2013	Pipe line
9	ETBW7696	KACHU/KINDE	-	BWPVT-I-2013	Pipe line
10	ETBW7698	FRNCLN/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1	-	BWPVT-I-2013	Pipe line
11	ETBW7717	MUU/3/KIRITATI//ATTILA*2/PASTOR/4/MUU	-	BWPVT-I-2013	Pipe line
12	ETBW7723	KIRITATI//ATTILA*2/PASTOR/3/AKURI	-	BWPVT-I-2013	Pipe line
13	ETBW7724	KIRITATI//PRL/2*PASTOR/3/FRANCOLIN #1	-	BWPVT-I-2013	Pipe line
14	ETBW 6911	REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/5/PVN	-	BWPVT-II-2013	Pipe line
15	ETBW 6928	KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES	-	BWPVT-II-2013	Pipe line
16	ETBW 6861	WAXWING*2/HEILO	-	BWPVT-II-2013	Pipe line
17	ETBW 6948	REBWAH-12/ZEMAMRA-8	-	BWPVT-II-2013	Pipe line
18	ETBW 6841	PBW343*2/KUKUNA*2//FRTL/PIFED	-	BWPVT-II-2013	Pipe line
19	ETBW 6947	WON-D 82/3/NS732/HER//KAUZ'S'=(FIDIYA-26)	-	BWPVT-II-2013	Pipe line
20	ETBW 6943	SKAUZ/BAV92/3/CROC-1/AE.SQUARROSA (224)//OPATA	-	BWPVT-II-2013	Pipe line
21	ETBW 6921	ALTAR84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/ 4/WBLL1*2/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES	-	BWPVT-II-2013	Pipe line
22	ETBW 6886	KAUZ/PASTOR//PBW343/3/HAR311/5/OASIS/SKAUZ//4*BCN/3/PASTOR/4/KAUZ*2/YACO//KAUZ	-	BWPVT-II-2013	Pipe line
23	ETBW 6890	ATTILA*2/PBW65*2//MURGA	-	BWPVT-II-2013	Pipe line
24	ETBW 6953	CROW'S'/BOW'S' -3-1994/95//TEVEE'S'/TADINIA	-	BWPVT-II-2013	Pipe line
25	ETBW 6853	BECARD/5/PGO//CROC_1/AE.SQUARROSA (224)/3/2*BORL95/4/CIRCUS	-	BWPVT-II-2013	Pipe line
26	ETBW 6869	MURGA//WAXWING/KIRITATI	-	BWPVT-II-2013	Pipe line
27	ETBW 6852	ROLF07/MUU	-	BWPVT-II-2013	Pipe line
28	ETBW 6939	UTIQUE 96/FLAG-1	-	BWPVT-II-2013	Pipe line
29	ETBW 6876	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311	-	BWPVT-II-2013	Pipe line
30	ETBW 6845	ATTILA*2/PBW65*2//MURGA	-	BWPVT-II-2013	Pipe line
31	ETBW 6875	WAXWING/KIRITATI*2//YANAC	-	BWPVT-II-2013	Pipe line
32	ETBW 6850	FRNCLN/ROLF07	-	BWPVT-II-2013	Pipe line
33	ETBW 6937	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7	-	BWPVT-II-2013	Pipe line
34	ETBW 6871	ROLF07*2/4/CROC_1/AE.SQUARROSA (205) //BORL95/3/2*MILAN	-	BWPVT-II-2013	Pipe line
35	ETBW 6862	KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES	-	BWPVT-II-2013	Pipe line
36	ETBW 6866	KLDR/PEWIT1//MILAN/DUCULA	-	BWPVT-II-2013	Pipe line
37	ETBW 6840	PRL/2*PASTOR*2//FH6-1-7	-	BWPVT-II-2013	Pipe line
38	ETBW 6883	FINSI/METSO//FH6-1-7/3/FINSI/METSO	-	BWPVT-II-2013	Pipe line
39	ETBW 6847	ROLF07*2/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES	-	BWPVT-II-2013	Pipe line
40	ETBW 6848	ROLF07*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC	-	BWPVT-II-2013	Pipe line
41	ETBW 6882	PRL/2*PASTOR*2//FH6-1-7	-	BWPVT-II-2013	Pipe line
42	ETBW 6932	SKAUZ/BAV92//2*WBLL1*2/KKTS	-	BWPVT-II-2013	Pipe line
43	ETBW 6832	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311	-	BWPVT-II-2013	Pipe line

Appendix 1. Continued…

44	ETBW 6837	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7	-	BWPVT-II-2013	Pipe line
45	ETBW 6839	PASTOR/7/YANAC/8/CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/PASTOR	-	BWPVT-II-2013	Pipe line
46	ETBW 6445	SAAR*2/3/C80.1/3*BATAVIA//2*WBLL1	-	BWNVT-II-13-14	Pipe line
47	ETBW 6393	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
48	ETBW 6373	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
49	ETBW 6647	MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2	-	BWNVT-II-13-14	Pipe line
50	ETBW 6398	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
51	ETBW 6404	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
52	ETBW 6543	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07	-	BWNVT-II-13-14	Pipe line
53	ETBW 6506	PFAU/WEAVER//KIRITATI	-	BWNVT-II-13-14	Pipe line
54	ETBW 6496	CROC_1/AE.SQUARROSA (205) //FCT/3/PASTOR	-	BWNVT-II-13-14	Pipe line
55	ETBW 6406	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
56	ETBW 6529	CROC_1/AE.SQUARROSA (205) //BORL95/3/2*MILAN/4/LERKE	-	BWNVT-II-13-14	Pipe line
57	ETBW 6109	SOKOLL/EXCALIBUR	-	BWNVT-II-13-14	Pipe line
58	ETBW 6101	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	-	BWNVT-II-13-14	Pipe line
59	ETBW 6102	NS-732/HER/3/PRL/SARA//TSI/VEE#5/4/FRET2	-	BWNVT-II-13-14	Pipe line
60	ETBW 6518	KINDE	-	BWNVT-II-13-14	Pipe line
61	ETBW 6492	WHEAR/VIVITSI//WHEAR	-	BWNVT-II-13-14	Pipe line
62	ETBW 6130	SOKOLL/EXCALIBUR	-	BWNVT-II-13-14	Pipe line
63	ETBW 6256	BOW#1/FENGKANG 15//MASSIRA	-	BWNVT-II-13-14	Pipe line
64	ETBW7730	ONIX/KBIRD	-	BWNVT-II-13-14	Pipe line
65	ETBW 6696	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KPASTOR	-	BWNVT-II-13-14	Pipe line
66	ETBW 6169	KLDR/PEWIT1//MILAN/DUCULA	-	BWNVT-II-13-14	Pipe line
67	ETBW 6107	KLDR/PEWIT1//MILAN/DUCULA	-	BWNVT-II-13-14	Pipe line
68	ETBW 6174	CROC_1/AE.SQUARROSA (205) //KAUZ/3/LANG	-	BWNVT-II-13-14	Pipe line
69	ETBW 6315	GIRWILL-13/2*PASTOR-2	-	BWNVT-II-13-14	Pipe line
70	ETBW 6167	CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/ AE. SQUARROSA (213)//PGO	-	BWNVT-II-13-14	Pipe line
71	ETBW 6314	GIRWILL-13/2*PASTOR-2	-	BWNVT-II-13-14	Pipe line
72	ETBW 6212	QAFZAH-23/SOMAMA-3	-	BWNVT-II-13-14	Pipe line
73	ETBW 6427	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
74	ETBW 6688	PBW343*2KUKUNA//PARUS/3/PBW343*2/KUKUNA	-	BWNVT-II-13-14	Pipe line
75	ETBW 6114	SOKOLL//SUNCO/2*PASTOR	-	BWNVT-II-13-14	Pipe line
76	ETBW 6439	MELON//FILIN/MILAN/3/FILIN	-	BWNVT-II-13-14	Pipe line
77	ETBW 6095	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	KARC/EIAR	New Genotype	Released
78	ETBW 5879	NJORO SD-7	KARC/EIAR	New Genotype	Released
79	Menze	HAR-3008	DBARC/SARI	Commercial	Released
80	Dinknesh	HAR-3919	SRARC/ARARI	Commercial	Released
81	Tossa	HAR 3123	SRARC/ARARI	Commercial	Released
82	Ogolcho	ETBW 5520	KARC/EIAR	Commercial	Released
83	Galil	Galil	Hazera Genetics	Commercial	Released
84	Meraro	11-6-24	KARC/EIAR	Commercial	Released
85	Millennium	ETBW-4921	KARC/EIAR	Commercial	Released
86	KULKULU	ETBW 4621	HU	Commercial	Released
87	KBG-01	FH-1-7A or Line 8.3.8	KARC/EIAR	Commercial	Released
88	Bolo	HAR-3816	DBARC/ARARI	Commercial	Released
89	Sulla	710/RBC	AwARC/SARI	Commercial	Released
90	Gasay	HAR-3730	ADARC/ARARI	Commercial	Released

Appendix 1. Continued…

91	Kakaba	Picaflor # 1	KARC/EIAR	Commercial	Released
92	Shorima	ETBW 5483	KARC/EIAR	Commercial	Released
93	Laketch	-	ADARC/ARARI	Commercial	Released
94	Hoggana	ETBW 5780	KARC/EIAR	Commercial	Released
95	Huluka	ETBW 5496	KARC/EIAR	Commercial	Released
96	Abola	HAR-1522	KARC/EIAR	Commercial	Released
97	Tusie	HAR-1407	KARC/EIAR	Commercial	Released
98	Hidasie	ETBW5795	KARC/EIAR	Commercial	Released
99	Dure	HAR-1008	SARC/OARI	Commercial	Released
100	Pavon-76	VCMIICN017C/3/KALIBB	KARC/EIAR	Commercial	Released
101	Dashen	-	KARC/EIAR	Commercial	Released
102	Kubsa	HAR-1685	KARC/EIAR	Commercial	Released
103	Katar	HAR-1899	KARC/EIAR	Commercial	Released
104	Simba	HAR-2536	KARC/EIAR	Commercial	Released
105	Sofumar	HAR-1889	SARC/ORI	Commercial	Released
106	Sirbo	HAR-2192	KARC/EIAR	Commercial	Released
107	Bobitcho	HAR-2419	KARC/EIAR	Commercial	Released
108	Tay	ET-12 D4/HAR 604 (1)	ADARC/ARARI	Commercial	Released
109	Hawii	HAR-2501	KARC/EIAR	Commercial	Released
110	Dereselign	-	KARC/EIAR	Commercial	Released
111	Danda'a	Danphe#1	KARC/EIAR	Commercial	Released
112	Mada-Walabu	HAR-1480	SARC/OARI	Commercial	Released
113	Digelu	SHA 7/KAUZ or HAR 3116	KARC/EIAR	Commercial	Released
114	GAMBO	QUIAU#2	KARC/EIAR	Commercial	Released
115	Doddota	HAR-2508	KARC/EIAR	Commercial	Released
116	K 6290-4A	-	KARC/EIAR	Commercial	Released
117	Enkoy	-	KARC/EIAR	Commercial	Released
118	ET-13A2	-	KARC/EIAR	Commercial	Released
119	Galema	HAR-604	KARC/EIAR	Commercial	Released
120	Mitike	HAR-1709	KARC/EIAR	Commercial	Released
121	K 6290-Bulk	-	KARC/EIAR	Commercial	Released

Appendix 2: List of ninety-six bread wheat genotypes used for the investigation of SSR marker analyses along with their pedigree and origin

S.N.	Genotype	Pedigree	Origin	Source/Group	Nature
1	**K 6290-bulk**	-	KARC/EIAR	Commercial genotype	Released
2	**Hawii**	HAR-2501	KARC/EIAR	Commercial genotype	Released
3	**Hoggana**	ETBW 5780	KARC/EIAR	Commercial genotype	Released
4	**Tay**	ET-12 D4/HAR 604 (1)	KARC/EIAR	Commercial genotype	Released
5	**Kakaba**	Picaflor # 1	KARC/EIAR	Commercial genotype	Released
6	**Menze**	HAR-3008	DBARC/SARI	Commercial genotype	Released
7	**Dereselign**	-	KARC/EIAR	Commercial genotype	Released
8	**GAMBO**	**QUIA#2**	KARC/EIAR	Commercial genotype	Released
9	**Bobitcho**	HAR-2419	KARC/EIAR	Commercial genotype	Released
10	**Bolo**	HAR-3816	DBARC/ARARI	Commercial genotype	Released
11	**Ogolcho**	ETBW 5520	KARC/EIAR	Commercial genotype	Released
12	**Simba**	HAR-2536	KARC/EIAR	Commercial genotype	Released
13	**Kulkulu**	ETBW 4621	HU	Commercial genotype	Released
14	**Mitike**	HAR-1709	KARC/EIAR	Commercial genotype	Released
15	**Danda'a**	Danphe#1	KARC/EIAR	Commercial genotype	Released
16	**Sulla**	710/RBC	AwARC/SARI	Commercial genotype	Released
17	**Shorima**	ETBW 5483	KARC/EIAR	Commercial genotype	Released
18	**(Biqa)ETBW 6095**	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	KARC/EIAR	New Genotype	Released
19	**K 6290-4A**	-	KARC/EIAR	Commercial genotype	Released
20	**Enkoy**	-	KARC/EIAR	Commercial genotype	Released
21	**Katar**	HAR-1899	KARC/EIAR	Commercial genotype	Released
22	**ET-13A2**	-	KARC/EIAR	Commercial genotype	Released
23	**Sirbo**	HAR-2192	KARC/EIAR	Commercial genotype	Released
24	**Abola**	HAR-1522	KARC/EIAR	Commercial genotype	Released
25	**Dinknesh**	HAR-3919	SRARC/ARARI	Commercial genotype	Released

Appendix 2. Continued…

26	**Gasay**	HAR-3730	ADARC/ARARI	Commercial genotype	Released
27	**ETBW5879**	**NJORO SD-7**	KARC/EIAR	New Genotype	Released
28	**Dashen**	-	KARC/EIAR	Commercial genotype	Released
29	**Mada Walabu**	HAR-1480	SARC/OARI	Commercial genotype	Released
30	**Meraro**	11-6-24	KARC/EIAR	Commercial genotype	Released
31	**KBG-01**	FH-1-7A or Line 8.3.8	KARC/EIAR	Commercial genotype	Released
32	**Galema**	HAR-604	KARC/EIAR	Commercial genotype	Released
33	**Laketch**	-	ADARC/ARARI	Commercial genotype	Released
34	**Sofumar**	HAR-1889	SARC/ORI	Commercial genotype	Released
35	**Pavon-76**	VCMIICN017C/3/KALIBB	KARC/EIAR	Commercial genotype	Released
36	**Doddota**	HAR-2508	KARC/EIAR	Commercial genotype	Released
37	**Digelu**	SHA 7/KAUZ or HAR 3116	KARC/EIAR	Commercial genotype	Released
38	**Galil**	Galil	Hazera Genetics	Commercial genotype	Released
39	**Hidasie**	ETBW5795	KARC/EIAR	Commercial genotype	Released
40	**Kubsa**	HAR-1685	KARC/EIAR	Commercial genotype	Released
41	**Dure**	HAR-1008	SARC/OARI	Commercial genotype	Released
42	**Tossa**	HAR 3123	SRARC/ARARI	Commercial genotype	Released
43	**Huluka**	ETBW 5496	KARC/EIAR	Commercial genotype	Released
44	**ETBW6406**	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
45	**ETBW 6953**	CROW'S'/BOW'S'-3 1994/95//TEVEE'S'/TADINIA	-	BWPVT-II-2013	Pipe line
46	**ETBW 6114**	SOKOLL//SUNCO/2*PASTOR	-	BWNVT-II-13-14	Pipe line
47	**Millennium**	ETBW-4921	KARC/EIAR	Commercial genotype	Released
48	**ETBW 6107**	KLDR/PEWIT1//MILAN/DUCULA	-	BWNVT-II-13-14	Pipe line
49	**ETBW 6212**	QAFZAH-23/SOMAMA-3	-	BWNVT-II-13-14	Pipe line
50	**Tusie**	HAR-1407	KARC/EIAR	Commercial genotype	Released
51	**ETBW7690**	FRET2*2/BRAMBLING/3/FRET2/WBLL1//TACUPETO F2001/4/WBLL1*2/BRAMBLING	-	BWPVT-I-2013	Pipe line

Appendix 2. Continued…

52	**ETBW 6939**	UTIQUE 96/FLAG-1	-	BWPVT-II-2013	Pipe line
53	**ETBW 6875**	WAXWING/KIRITATI*2//YANAC	-	BWPVT-II-2013	Pipe line
54	**ETBW7730**	ONIX/KBIRD	-	BWNVT-II-13-14	Pipe line
55	**ETBW 6837**	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7	-	BWPVT-II-2013	Pipe line
56	**ETBW 6647**	MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2	-	BWNVT-II-13-14	Pipe line
57	**ETBW 6256**	BOW#1/FENGKANG 15//MASSIRA	-	BWNVT-II-13-14	Pipe line
58	**ETBW 6506**	PFAU/WEAVER//KIRITATI	-	BWNVT-II-13-14	Pipe line
59	**ETBW 6840**	PRL/2*PASTOR*2//FH6-1-7	-	BWPVT-II-2013	Pipe line
60	**ETBW 6871**	ROLF07*2/4/CROC_1/AE.SQUARROSA (205) //BORL95/3/2*MILAN	-	BWPVT-II-2013	Pipe line
61	**ETBW 6928**	KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES	-	BWPVT-II-2013	Pipe line
62	**ETBW 6393**	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
63	**ETBW7695**	KACHU/KINDE	-	BWPVT-I-2013	Pipe line
64	**ETBW 6862**	KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES	-	BWPVT-II-2013	Pipe line
65	**ETBW 6496**	CROC_1/AE.SQUARROSA (205) //FCT/3/PASTOR	-	BWNVT-II-13-14	Pipe line
66	**ETBW 6948**	REBWAH-12/ZEMAMRA-8	-	BWPVT-II-2013	Pipe line
67	**ETBW 6445**	SAAR*2/3/C80.1/3*BATAVIA//2*WBLL1	-	BWNVT-II-13-14	Pipe line
68	**ETBW7724**	KIRITATI//PRL/2*PASTOR/3/FRANCOLIN #1	-	BWPVT-I-2013	Pipe line
69	**ETBW 6882**	PRL/2*PASTOR*2//FH6-1-7	-	BWPVT-II-2013	Pipe line
70	**ETBW 6937**	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7	-	BWPVT-II-2013	Pipe line
71	**ETBW 6167**	CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/ AE. SQUARROSA (213)//PGO	-	BWNVT-II-13-14	Pipe line
72	**ETBW 6696**	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KPASTOR	-	BWNVT-II-13-14	Pipe line
73	**ETBW7686**	KIRITATI//ATTILA*2/PASTOR/3/AKURI	-	BWPVT-I-2013	Pipe line
74	**ETBW 6492**	WHEAR/VIVITSI//WHEAR	-	BWNVT-II-13-14	Pipe line
75	**ETBW 6169**	KLDR/PEWIT1//MILAN/DUCULA	-	BWNVT-II-13-14	Pipe line
76	**ETBW 6832**	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311	-	BWPVT-II-2013	Pipe line
77	**ETBW 6947**	WON-D 82/3/NS732/HER//KAUZ'S'=(FIDIYA-26)	-	BWPVT-II-2013	Pipe line

Appendix 2. Continued…

78	**ETBW7696**	KACHU/KINDE	-	BWPVT-I-2013	Pipe line
79	**ETBW 6943**	SKAUZ/BAV92/3/CROC-1/AE.SQUARROSA (224)//OPATA	-	BWPVT-II-2013	Pipe line
80	**ETBW 6845**	ATTILA*2/PBW65*2//MURGA	-	BWPVT-II-2013	Pipe line
81	**ETBW 6404**	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
82	**ETBW 6543**	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07	-	BWNVT-II-13-14	Pipe line
83	**ETBW 6853**	BECARD/5/PGO//CROC_1/AE.SQUARROSA (224)/3/2* BORL95/4/CIRCUS	-	BWPVT-II-2013	Pipe line
84	**ETBW 6847**	ROLF07*2/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES	-	BWPVT-II-2013	Pipe line
85	**ETBW7698**	KACHU/KINDE	-	BWPVT-I-2013	Pipe line
86	**ETBW 6890**	ATTILA*2/PBW65*2//MURGA	-	BWPVT-II-2013	Pipe line
87	**ETBW 6852**	ROLF07/MUU	-	BWPVT-II-2013	Pipe line
88	**ETBW 6518**	KINDE	-	BWNVT-II-13-14	Pipe line
89	**ETBW 6886**	KAUZ/PASTOR//PBW343/3/HAR311/5/OASIS/SKAUZ//4*BCN/3/ PASTOR/4/KAUZ*2/YACO//KAUZ	-	BWPVT-II-2013	Pipe line
90	**ETBW 6102**	NS-732/HER/3/PRL/SARA//TSI/VEE#5/4/FRET2	-	BWNVT-II-13-14	Pipe line
91	**ETBW 6101**	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	-	BWNVT-II-13-14	Pipe line
92	**ETBW 6883**	FINSI/METSO//FH6-1-7/3/FINSI/METSO	-	BWPVT-II-2013	Pipe line
93	**ETBW 6212**	QAFZAH-23/SOMAMA-3	-	BWNVT-II-13-14	Pipe line
94	**ETBW 6850**	FRNCLN/ROLF07	-	BWPVT-II-2013	Pipe line
95	**ETBW 6427**	HUBARA-16/2*SOMAMA-3	-	BWNVT-II-13-14	Pipe line
96	**ETBW7694**	SERI.1B*2/3/KAUZ*2/BOW//KAUZ*2/4/KINGBIRD #1	-	BWPVT-I-2013	Pipe line

Appendix 3: Comparison of some of the major phenotypic and grain quality traits among 121 genotypes at 3 locations

		Adet							Debre Tabor							Kulumsa						
		Phenotypic traits				Grain quality traits			Phenotypic traits				Grain quality traits			Phenotypic traits				Grain quality traits		
S.N	Genotypes	DM	PH	BY	GY	TGW	Prot.	Zele.	DM	PH	BY	GY	TGW	Prot	Zele	DM	PH	BY	GY	TGW	Prot.	Zele.
1	ETBW6921	106.5	76.39	158.75	59.15	38.2	13.15	35.75	104.54	79.75	233.29	86.15	30.55	10.82	28.62	102	76.36	175.23	86.96	28.10	11.85	29.47
2	EBW7686	110	80.8	212.5	70.48	33.4	13.1	33.6	96.02	84.4	184.5	71.66	27.35	10.30	29.60	106.5	84.77	219.76	88.42	22.55	11.85	25.64
3	Galil	107	75.45	181.25	50.68	29.1	12.9	33.4	93.46	70.2	229.65	72.10	25.25	10.05	25.95	103	76	208.73	83.04	25.25	12.23	29.18
4	ETBW6876	108.5	74.56	143.75	46.64	37.8	14.35	33.65	94.08	79.6	166.84	56.46	26.85	11.23	33.03	105	89.58	174.22	63.24	24.01	12	32.47
5	Dereselign	105**	98.5	218.75	61.77	30.3	13.75	34.55	102.04	90.8	230	71.65	26.4	11.95	33.16	99	92.97	235.93	93.75	22.35	12.05	29.62
6	Sirbo	125	78.72	175	45.96	25.15	12.55	36.2	108.08	75.4	213.53	66.21	21.85	10.00	26.30	120.5	79	192.89	74.19	20.25	12.08	29.37
7	Ogolcho	109	79.9	159.38	68.21	34.3	12.3	29.15	96.16	81.9	199.63	93.37	30.95	9.54	24.11	105.5	87.02	171.26	87.17	28.04	12	26.44
8	ETBW7717	109	82.5	193.75	69.21	34.25	13.25	33.85	97.40	88.9	230.34	85.47	28.7	9.62	22.59	106	91.02	214.21	82.58	23.22	12.18	25.34
9	ETBW6543	107	86.2	168.75	55.14	36.2	12.45	33.3	96.08	81.5	219.17	85.55	34.25	9.80	24.66	104	84.55	184.85	75.12	25	12.15	26.58
10	ETBW7724	110.5	77.7	193.75	60.11	27.95	13	37.5	98.54	80.6	208.42	69.88	23.7	9.38	23.31	107	81.11	207.37	83.85	19.74	12.18	19.89
11	ETBW6932	107	85	193.5	83.13	37.6	12.45	31.8	93.58	78.4	206.33	92.36	33.05	11.21	27.59	103	87.49	194.55	87.51	23.50	11.98	28.34
12	ETBW6875	108.5	80.2	212.5	79.03	35.55	12.75	35.45	92.44	78.8	233.13	95.56	28	10.88	28.54	104	84.98	215.55	86.94	25.71	12.1	25.19
13	ETBW6839	105**	74.95	150	56.29	34.85	12.7	33.9	94.86	81.3	204.44	90.69	31	11.49	26.79	102	85.17	170.86	83.57	27.68	9.45	19.29
14	Hawii	107	80.1	213.38	82.16	35.8	12.85	33.85	83.48	79	226.3	95.40	31.55	11.65	28.75	101	88.22	231.59	93.86	26	12.03	29.35
15	ETBW6373	107	71.74	175	61.51	34	12.25	33.25	84.48	71.6	183.41	68.25	24	10.75	27.43	102	82.47	177.95	64.76	16.71	12.05	28.11
16	ETBW6939	105	74.95	150	56.29	34.85	12.7	33.9	86.48	71.9	171.27	69.44	33.15	11.38	29.77	101	76.15	166.59	65.4	27.55	11.83	30.10
17	ETBW6102	107	83.6	206.25	77.62	35.55	13.4	35.4	93.42	78.4	218.32	87.67	32.05	11.15	29.19	104	82.94	205.03	78.04	26.73	12.45	24.01
18	Tusie	110.5	85.63	231.25	79.07	29.55	11.75	30	96.94	82.2	257.83	99.50	24.45	9.85	24.79	106.5	90.94	238.37	90.99	24.57	11.95	27.49
19	ETBW6492	107.5	83.66	212.5	69.20	34.5	10.15	23.55	93.06	89.3	253.4	85.44	27.05	10.78	30.34	103	91.40	230.88	93.12	24.45	12.33	28.58
20	ETBW6130	107	78.75	183.25	71.52	32.85	12.25	30.25	89.29	79.5	227.49	96.33	27.3	10.97	27.93	103	83.49	202.66	95.29	21.53	12.03	29.21
21	Hidasie	105**	81.05	213.38	83.81	38.6	12.45	28.85	94.98	78.1	194.66	85.43	33.3	10.35	26.07	102	88.46	209.47	88.3	25.34	11.85	23.47
22	ETBW6398	108	80.14	182	59.44	34.85	13.4	37.3	96.94	87.8	220.74	78.47	28.05	11.02	29.26	105	92.79	174.79	69.65	24.37	12.39	22.14
23	ETBW7689	109	77.7	187.5	56.14	32.7	12.95	34.5	94.06	84.4	181.5	70.02	26.7	10.24	27.97	105	84.54	187.92	78.61	25.26	12.1	27.85
24	Dure	105**	91.3	169.25	57.99	34	13.45	36.65	89.48	84.9	208.45	74.57	27	11.25	30.32	101	89.93	171.05	66.27	19.35	11.95	25.73
25	ETBW6315	110.5	90.93	186.5	57.65	34.95	12.2	30.00	98.92	89	205.54	79.18	29.4	8.93	17.36	106.5	90.45	196.55	84.92	21.86	11.98	22.73
26	ETBW6840	107	83.4	175	62.69	36.85	13	35.5	95.60	74.8	199.02	80.35	31.1	10.91	29.56	102	78.93	177	76.82	23.85	12.18	26.33
27	ETBW6174	112.5	85.2	202.5	86.25	31.7	11.8	32.55	96.04	83	226.73	85.14	28.5	9.56	25.57	110	83.00	260.92	96.95	21.55	11.9	27.31
28	ETBW6647	105**	82.49	181.75	67.88	39.05	12.35	32.8	88.06	80.5	213.72	86.56	32.9	11.21	29.62	100	79.90	185.79	81.19	26.97	11.98	27.79
29	Bolo	124.5	97.74	261.15	78.79	28.9	10.2	23.7	108.56	103	200.63	82.85	25.75	8.93	18.23	115	101.95	248.9	64.13	20.81	12.28	23.83
30	ETBW6439	105**	77.2	268.75	71.95	36.5	12.45	27.3	98.18	76.1	241.49	82.87	27.95	10.09	25.69	103	79.46	275.9	92.56	24.74	11.98	28.14
31	ETBW6953	104.5	75.65	218.5	69.50	26.45	13.2	36.55	88.10	69.2	221.14	88.56	21.25	10.91	31.15	100	82.42	205.89	53.73	17.37	11.78	29.52
32	KULKULU	123	73.55	178.13	65.77	26.6	14.75	33.55	102.10	81.8	206.54	92.05	26.35	10.64	24.99	117	87.51	187.9	94.72	27.04	11.95	24.11
33	ETBW6406	107	68.6	181	76.97	38.2	14.6	39.15	87.60	75.2	190.5	73.33	32.4	11.01	29.52	103	77.48	187.36	68.36	24.36	12.2	29.76
34	ETBW6314	117	86.6	256.25	84.90	34.2	11.95	32.85	100.50	81.8	206.33	98.16	30.45	8.645	18.29	113	94.98	253.42	93.89	25.89	12.43	19.96
35	Laketch	108.5	72.8	175	59.43	27	12.85	38.05	77.98	68.4	201.82	73.60	24.7	11.66	27.03	100	88.93	169.21	43.23	17.74	12.2	24.89
36	Kubsa	107	82.5	250	96.16	32.45	11.35	31.95	82.54	73.8	255.18	93.50	26.9	10.32	21.68	100	88.46	247.98	91	20.17	11.9	26.27
37	Sofumar	107	90.9	256.25	89.65	33.5	12.4	29.95	93.00	82.1	219.48	90.35	28.7	9.68	23.45	103	96.98	249.31	89	21.31	12.2	25.04
38	ETBW6852	108.5	74.3	200	74.49	34.3	11.3	29.6	93.42	74.2	203.35	86.51	27.75	10.51	28.18	104	84.36	205.27	83	19.81	11.83	25.11
39	Hoggana	125	78.1	175	43.22	22.5	12.15	30.05	110.00	87.2	190.19	63.26	26.45	9.36	18.19	120	94.33	172.22	88.34	27.98	11.93	19.62
40	ETBW6496	111	85.9	231.25	76.93	33.75	12.1	31.95	97.62	90.8	253.49	95.34	29.7	10.70	26.69	107	90.59	243.46	93	21.36	12.15	32.30
41	Millennium	109	83.5	231.38	79.64	30.65	12.6	32.6	93.04	88.3	240.35	94.63	30.2	9.96	21.54	104.5	92.51	226.26	90.7	25.84	11.93	23.98
42	Kakaba	105**	86.6	193.75	71.83	34.65	13.4	38.6	89.54	81	188.18	76.55	30.85	10.14	26.01	101	85.44	205.4	81.44	20.50	12.05	28.82
43	Tay	108.5	94.15	237.75	81.55	32.2	12.7	29.85	98.86	93.9	253.73	95.34	26	9.53	22.97	105	96.98	240.39	90.3	27.10	11.83	26.64
44	ETBW6832	105**	79.75	193.75	73.40	37.45	13.25	38.2	91.04	75.5	209.79	91.85	26.45	10.62	30.72	102	85.46	178.01	46.33	19.88	12.05	32.65
45	ETBW6506	107.5	80.95	268.75	82.66	39.8	13.85	35.3	90.96	79.5	220.62	92.68	31.75	10.83	30.62	103	77.46	187.36	68.36	24.36	12.20	29.76
46	ETBW7694	113	88.05	237.5	87.83	33.55	11.5	26.95	99.98	87.3	255.93	94.78	26.05	9.10	21.28	109	89.50	223.89	88.31	18.98	11.85	23.73
47	ETBW6871	110.5	78.5	156.25	53.71	35.25	12.5	35.75	100.02	79.1	212.29	84.04	31.15	11.81	32.84	107	79.96	165.92	79.54	23.91	8.85	20.55
48	ETBW7723	108.5	81.4	206.75	78.42	33.65	12.2	36.25	96.52	81.9	197.23	83.78	30.25	10.13	26.81	108	83.48	199.59	96.88	23.72	12.18	24.99

Appendix 3: continued…

49	**Pavon76**	107	81.59	243.75	87.36	30.2	12	34.75	91.40	79.5	224.74	92.80	25.2	10.73	30.82	103	83.98	201.5	82.5	22.16	12.15	29.97
50	**ETBW6169**	107	77.45	199.44	75.01	33.05	12.85	34.75	95.48	71.3	203.39	91.21	30.8	11.26	32.42	104	79	193.01	97.5	27.36	12.15	26.81
51	**ETBW6114**	109	75.24	243.75	83.04	32.85	12.65	32.25	96.60	74.2	237.77	97.50	28.2	10.82	30.57	105	75.91	252.93	99.89	24.48	11.8	26.75
52	**ETBW6837**	105**	79.18	162.5	56.04	33.8	11.65	32.55	86.98	71.9	203.17	71.85	26.2	12.53	39.62	100.5	78.95	163.29	59.92	19.52	11.88	30.38
53	**ETBW6948**	115	79.7	218.75	70.54	32.9	13.05	36.25	102.52	84.9	210.26	75.53	27.35	10.28	27.87	112	84.93	214.64	83.17	20.61	12.08	26.27
54	**ETBW6911**	122.5	88.3	200	64.56	35.3	12.45	31.7	105.34	97.5	241.77	85.81	26.6	9.45	20.96	117	97.00	202.2	77.2	19.19	12.13	22.49
55	**ETBW6890**	107.5	78.7	200	70.93	36.05	13.65	40.2	91.02	71	219.53	93.94	32.4	11.69	34.00	103	78.48	181.9	93.25	25.35	11.78	31.20
56	**ETBW6095**	106	76.2	187.5	59.69	32.45	12.6	35.25	94.58	82.8	168.2	60.90	31.55	10.85	31.71	102	85.56	226.8	88	22.74	11.93	27.22
57	**ETBW6847**	105**	74.7	125	45.05	29.85	12	33.2	90.14	77.9	191.2	76.12	29.6	10.90	31.32	101	82.79	136.07	59.86	24.09	12.05	27.91
58	**Dashen**	125.5	80.19	169.16	57.13	26.85	12.25	26.85	109.64	86.85	169.14	59.79	27	11.93	24.04	114	79.07	194.08	71.57	27.18	11.75	26.08
59	**Mitike**	106	97.2	218.75	67.34	30.55	11.8	32.95	97.46	94.4	194.39	55.43	22	10.57	30.05	104	99.61	237.65	60.78	21.68	11.75	27.12
60	**ETBW6943**	106.5	85.4	200	44.90	32.65	12.75	32.65	95.23	84.4	204.51	71.30	29.9	10.64	29.72	103	86.31	217.11	88	26.96	12.13	29.39
61	**Meraro**	124.5	73.5	175	50.44	25.55	12.95	33.3	106.10	73.2	204.52	65.03	23.15	11.30	32.22	119	83.56	187.19	74.22	22.58	11.93	28.97
62	**ETBW6866**	107	79.8	175	64.68	34.1	14.15	37.2	91.60	73.6	203.34	87.30	30.55	10.62	27.73	103	79.60	175.8	85.67	26.04	12.2	27.1
63	**Galema**	110.5	86.45	187.5	53.62	39.15	11.05	29.1	96.52	86.4	234.94	80.46	24.6	11.30	28.46	106	89.29	214.55	85.9	20.53	12.3	29.07
64	**KBG01**	105.5**	76.6	168.75	61.40	24.95	13.5	37.5	95.10	73.2	182.17	72.22	20.8	12.68	38.47	103	76.10	176.37	68.19	13.47	12.13	24.52
65	**Dinknesh**	108.5	85.85	206.25	75.76	37.55	14.85	31.65	103.14	80.8	198.7	82.72	32.75	10.81	24.30	103.5	85.58	199.11	93.3	23.49	12.05	26.44
66	**ETBW6101**	106	86.39	218.75	85.08	32.55	11.75	37.2	90.64	81	206.29	92.43	26.9	10.35	29.21	102	85.59	226.8	88	22.74	11.93	27.22
67	**ETBW6850**	104.5**	75.1	137.5	48.26	33.55	12.5	38	87.86	67	164	63.87	30.9	11.19	32.04	100	75.02	161.23	78.35	23.97	11.83	35.30
68	**ETBW7688**	109.5	82.6	218.75	76.96	34.2	13.6	34.4	92.94	78.2	230.44	90.13	27.6	9.96	26.15	104	83.03	224.81	88.96	25.48	9.05	19.60
69	**Doddota**	107	81.35	189.75	69.01	32.7	12.6	28.75	98.48	79.85	200.5	78.86	24.5	10.80	27.23	102	81.02	208.29	79.33	20.17	12.45	26.34
70	**ETBW6212**	109	76.5	168.75	68.48	34.2	14.05	32.55	98.48	81.45	237.25	86.08	30.5	10.73	25.51	106	81.50	199.58	99.64	21.63	12.2	26.65
71	**ETBW7692**	107	85	156.25	49.59	39.3	12.5	35.85	95.94	79.6	181.39	56.63	29.8	10.49	30.59	104	84.49	175.09	69.6	24.04	11.78	31.24
72	**ETBW6404**	110.5	79.2	168.75	53.24	30.35	12.3	32.43	99.92	76.6	205.58	72.27	28.35	10.29	27.44	108	78.50	180.43	80.8	21.93	11.83	26.96
73	**K6290Bulk**	106	105.95	237.5	74.31	28.3	13.3	39	87.94	98.6	159.66	72.73	28.3	11.58	30.50	101	96.03	209.85	88.56	24.65	12.35	39.6
74	**ETBW6882**	106.5	76.8	193.75	45.85	38.65	13.4	36.75	95.79	74.5	225.71	72.02	30.4	10.41	27.38	104	77.04	201.9	89.42	23.34	11.85	30.69
75	**ETBW6445**	125	91.15	225	70.72	36.25	13.05	31.45	105.98	97.3	232.7	78.01	32.15	9.24	21.24	120	97.57	243.3	82.7	20.71	11.75	24.41
76	**Huluka**	125	84.35	225	74.75	29.35	11.75	30.55	108.48	91.1	249.92	82.05	24.8	8.80	20.42	120	92.01	227.36	90.98	26.4	11.9	27.08
77	**ETBW6869**	106.5	81.87	137.5	45.06	35.7	14.1	43.1	89.56	81.1	172.4	68.88	30.65	11.48	33.39	102	85.04	167.84	86.75	23.84	11.75	31.93
78	**ETBW6883**	107	78.2	175	60.96	38.45	13.05	36.6	84.36	75.7	216.57	76.50	28.65	9.89	28.41	101	78.05	185.3	69.26	17.62	12.03	31.35
79	**Menze**	124.5	99.55	287.5	96.90	33.05	12.75	28.1	107.98	95.9	239.98	97.23	26.8	8.57	19.82	119.5	99.00	286.41	97.98	18.14	11.98	21.01
80	**Shorima**	105**	85.3	187.5	58.86	28.85	11.85	32.1	97.12	87.4	209.51	73.18	26.85	9.01	22.72	102.5	87.56	206.86	97.61	23.73	11.83	24.98
81	**Bobitcho**	109	90.29	225	85.24	32.2	12.99	34.69	102.50	85.4	200.85	88.73	25.6	10.80	28.52	106	86.14	227.56	94.26	24.2	12.13	26.19
82	**ETBW7693**	109.5	80.9	218.75	70.69	31.9	12.7	33.55	90.00	87.9	235.19	87.17	27.5	9.79	25.24	104	84.95	213.37	99.15	23.81	8.93	23.08
83	**ETBW6688**	110.5	88.3	218.75	75.29	35.15	12.35	33.6	95.04	85.8	228.58	88.52	28.05	10.93	30.85	106	89.72	208.77	81.11	26.17	12.08	29.28
84	**ETBW6107**	105**	76.6	181.25	60.00	32.1	12.45	33.05	89.92	75.7	232.17	73.18	27.3	10.37	27.77	101	78.33	193.9	79.56	21.7	11.78	28.38
85	**K62904A**	106	105.95	237.5	74.31	28.3	13.3	39	96.04	101.8	256.42	97.98	27.9	10.47	27.41	103	104.53	242.4	94.78	26.74	12.2	23.16
86	**ETBW7730**	105**	86.67	193.75	63.92	26.9	12.95	32.8	95.50	77.2	205.05	73.94	23.3	11.12	31.42	102	84	200.03	75.74	21.62	11.78	29.13
87	**ETBW6167**	108	87.03	175	65.84	35.8	12.95	38.15	95.04	85.5	208.54	85.71	36.55	11.02	34.33	105	88.08	202.64	91.56	26.92	12.1	32.01
88	**ETBW6529**	108	79.86	156.25	48.85	42.35	14.65	47.45	93.04	74.7	232.59	88.56	37.5	11.30	32.55	104	80.61	181.08	88.96	28.76	12	30.55
89	**ETBW6518**	111	82.35	193.75	48.35	36.25	12.55	34.8	99.00	84.05	209.06	70.16	31.95	10.15	28.45	108	84.28	199.58	72.81	20.05	12.4	20.44
90	**ETBW6109**	110	85.94	218.75	71.15	37.6	13	32.25	96.50	81.3	226.32	81.78	29.2	11.91	33.34	106	85.52	205.02	87.76	22.52	11.93	27.78
91	**ETBW6845**	107.5	75.45	218.75	78.33	32.6	13	38.4	86.94	68.2	227.45	99.29	30.8	12.25	35.24	102	74.99	202.13	82.33	25.11	12.08	29.35
92	**QUIAU#2(GAMBO)**	110.5	88.9	262.5	83.81	37.1	11.7	32.15	94.46	89.2	263.54	92.42	27.95	10.44	27.74	105.5	89.33	247.89	93.59	21.25	7.28	25.79
93	**Simba**	109	80.15	243.75	80.15	35.3	13.25	35.8	93.50	79.6	210.79	86.25	30	12.91	32.57	104.5	82.00	216.03	98.76	24.91	8.83	21.67
94	**Mada Walabu**	109	83.45	225	85.31	38	12.95	34.45	95.96	83.7	245.68	90.73	33.4	10.85	28.89	105.5	84.48	214.31	84.96	24.93	8.93	21.83
95	**ETBW7695**	108	82.91	200	68.40	31.1	13.25	35.45	98.00	78.4	229.36	89.12	26.65	10.83	29.67	105	83.50	205.27	91.63	24.67	12.03	29.32
96	**ETBW6862**	119	85.2	206.25	76.71	32.7	12.45	33.55	97.32	80.4	255.37	97.15	25.05	10.07	25.08	114	85.54	200.47	73.73	21.56	12.05	24.75
97	**ETBW6848**	105	78.1	181.75	72.29	30.8	13.15	37.35	91.96	73.7	210.61	92.19	28	10.42	30.76	102	78.03	162.53	75.67	24.11	12.27	22.15
98	**ETBW6853**	105	73.6	200	51.67	33.25	13.75	38.15	92.88	73.6	219.61	71.49	27.4	10.85	30.89	102	75.12	192.92	84.71	21.87	12.08	28.58
99	**Tossa**	107.5	84	206.25	70.68	29.45	12.5	35	94.58	81.7	206.24	78.88	25.6	10.54	29.64	104	84.04	209.03	95.68	25.21	12.2	26.45
100	**ETBW6393**	107	71.5	168.25	62.20	35.85	14.7	44.35	87.98	66.8	226.69	81.07	25.25	11.55	32.00	103	71.03	154.33	55.78	26.52	12.08	29.94
101	**Abola**	108	87.49	285.72	97.78	29.25	12.45	35.84	102.84	84.05	273.5	96.64	25.4	10.837	29.34	106	90.04	232.37	97.63	24.45	11.9	26.93

Appendix 3: continued…

102	**Danda'a**	124.5	93.9	237.72	71.23	37.8	13.24	33.45	106.52	91.9	229.8	89.50	32.50	9.373	22.73	119.5	93.51	203.04	75.68	27.9	12.2	27.97
103	**ETBW7696**	116	72.15	181.25	53.55	32.45	12.25	31.15	99.90	73.9	257.97	85.56	27.45	10.812	25.90	113	77.62	178.84	74.32	25	12.28	26.1
104	**ETBW6696**	111	89.4	243.75	93.59	33.95	11.7	31.1	98.02	83	268.83	99.00	30.15	10.066	26.35	108	91.07	222.83	93.62	23.88	11.93	22.32
105	**Katar**	109	92.75	221.5	81.79	34.1	12.3	36.55	92.52	84.9	237.14	87.99	25.75	10.419	28.54	105	92.02	223.5	82.85	22.78	12.03	26.23
106	**ETBW6947**	108.5	83.58	231.25	76.90	33.6	12.5	32.7	98.98	77.8	242.49	92.83	28.9	10.417	30.20	106	82.98	216.75	93	20.65	12.05	28.41
107	**ETBW5879**	109	80.25	218.75	79.91	35.25	11.75	32	96.96	76.1	254.8	94.66	31.95	9.315	23.40	107	81.49	200.73	75.21	21.26	11.93	25.23
108	**ETBW6928**	122	84.7	187.5	62.75	32.55	12.25	32.35	99.02	81.4	274	93.59	26.15	10.798	29.77	116	86.50	201.27	78.4	20.78	11.8	29.56
109	**Gasay**	105.5**	88	206	64.65	30	11.05	28.6	99.10	86.6	255.61	93.07	27.8	8.854	20.10	111	89.04	207.93	87.5	20.10	12.05	24.93
110	**ET13A2**	110	102	231.25	66.75	31.65	13.35	38.75	102.98	101	247.52	88.34	30.1	9.537	24.01	108	104.53	198.93	87.32	25.78	12.1	28.23
111	**ETBW6256**	108	83.1	206.25	61.47	36.7	13.65	38.6	94.82	80.6	241.38	90.02	32.4	10.098	25.60	105	83.47	209.15	87.9	29.03	11.95	28.05
112	**ETBW6937**	105**	88.05	193.75	65.57	31.3	12.6	37.4	96.96	83.1	211.41	88.08	30.9	11.298	28.73	103	80.96	180.53	93.5	27.16	12.08	28.24
113	**ETBW7698**	109	89.1	231.25	85.00	35.5	12.85	35.55	97.50	78.4	213.06	87.09	32.6	11.359	30.49	106	88.93	239.99	98.22	27.01	11.95	29.77
114	**Sulla**	105**	84.96	225	80.27	34	12.6	35.3	84.96	83.9	240.68	97.35	28.4	10.328	10.46	100.5	87.71	224.71	95.75	26.37	8.58	28.19
115	**Digelu**	124	104.7	231.25	82.25	34.1	12.15	27.9	108.94	102	202.85	79.05	27.8	8.176	17.01	119.5	103.92	223.01	98.55	22.83	12.18	21.52
116	**ETBW7690**	108.5	86.1	218.75	75.80	33.75	12.4	32.45	96.00	83.2	242.83	92.20	30.75	9.527	22.02	105	86	216.64	87.6	24.21	12.35	25.31
117	**ETBW6886**	115	87.2	206.25	68.87	32.15	11.5	29.75	97.58	82	256.84	93.59	26.35	9.215	21.31	110	87.47	219.69	95.13	21.28	12	24.04
118	**ETBW6841**	100**	81.95	225	83.15	36	12.35	35.3	90.50	83.9	234.58	96.67	28.45	10.834	42.14	97	84.54	208.85	85.48	22.14	12.23	36.83
119	**ETBW6861**	109	89.19	193.38	71.58	32.25	13.9	29.85	98.88	87.8	194.02	77.10	28.6	9.773	22.46	106	90.25	198.43	96.51	27.21	12.03	28.61
120	**Enkoy**	105**	93.7	237.5	73.10	29.65	14.45	44.75	95.50	88.7	221.08	93.75	28.95	10.630	26.35	103	93.45	292.64	95.86	24.41	11.9	28.02
121	**ETBW6427**	108.5	93.5	250	80.99	32.95	11.15	28.2	106.46	86.6	239.87	85.68	25.95	7.810	12.26	108	92.96	244.33	63.93	16.11	12.1	15.85

Appendix 4: Analysis of variance for twelve phenotypic characters of bread wheat genotypes tested at Adet analyzed as Simple-Lattice Design

	Groups						
	Replication	**Block (Replication)**	**Genotype**	**Error**	**Mean**	**CV (%)**	**Efficiency**
Characters	**DF = 1**	**DF =20**	**DF = 120**	**DF =100**			
DH	0.4132	0.2723	70.2722	0.2414	58.07438	0.846035	100.24
DM	0.5950	0.3678	65.4948	0.3605	109.6942	0.547352	100.01
SDO	4.9813	0.4447	22.6366	0.3285	79.14041	0.724194	101.48
ST	0.000093	0.7411	51.0693	0.2350	87.97054	0.551079	122.00
PH	0.03920	0.9066	107.33	0.7375	83.35967	1.030195	100.69
BY	13.0096	2.9268	2062.45	2.7349	203.3962	0.813073	100.08
NT	0.1599	0.1524	0.3971	0.06552	2.389091	10.71430	111.51
SL	0.1687	0.1824	1.2237	0.09781	7.336405	4.263016	106.21
NSPS	0.1209	0.3407	3.3490	0.2295	15.44112	3.102369	102.50
NSS	0.09560	0.4722	50.3334	0.3895	39.66103	1.573681	100.60
GY	12.1569	0.2979	322.87	0.2848	69.15066	0.771683	100.03
HI	0.000041	0.000017	0.003027	0.000028	0.340744	1.556818	93.5389

*Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively.CV= coefficient of variations and DF= degree freedom, DH=* Days to heading, *DM*= Days to maturity, SDO= Septoria disease occurrence, ST= Stand percent, PH= Plant height, BY= Biological yield, NT= Number of tillers, SL= Spike length, NSPS= Number of spike-lets per spike, NSS= Number of seeds per spike, GY= grain yield, and HI= Harvest index.

Appendix 5: Analysis of variance for twelve phenotypic characters of bread wheat genotypes tested at Debre Tabor analyzed as Simple-Lattice Design

	Groups						
	Replication	**Block (Replication)**	**Genotype**	**Error**	**Mean**	**CV (%)**	**Efficiency**
Characters	DF = 1	DF =20	DF = 120	DF = 100			
DH	0.03719	0.2417	71.3423	0.2563	50.76446	0.997237	99.0541
DM	0.3347	0.4165	75.3324	0.2283	95.78099	0.498906	105.77
SDO	1.0579	0.4260	20.2904	0.2942	80.52479	0.673601	102.20
ST	0.6983	0.5347	40.0980	0.4111	83.88430	0.764328	101.12
PH	0.9547	0.5478	113.79	0.4270	81.82397	0.798601	101.00
BY	26.1759	27.3068	1254.38	25.9304	219.0881	2.324264	100.04
NT	0.1741	0.1135	0.3128	0.05395	2.557893	9.080653	108.87
SL	0.01166	0.09621	0.5976	0.08387	8.054876	3.595457	100.31
NSPS	0.2202	0.1985	3.1862	0.1017	16.40455	1.944411	107.15
NSS	0.2202	0.6128	43.9777	0.5515	38.37727	1.935074	100.18
GY	0.2745	1.9405	230.65	1.7805	83.54930	1.597102	100.12
HI	0.000149	0.000012	0.002963	0.000014	0.382438	0.965287	97.8876

*Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively.CV= coefficient of variations and DF= degree freedom*

Appendix 6: Analysis of variance for twelve phenotypic characters of bread wheat genotypes tested at Kulumsa analyzed as Simple-Lattice Design

	Groups						
	Replication	**Block (Replication)**	**Genotype**	**Error**	**Mean**	**CV (%)**	**Efficiency**
Characters	**DF = 1**	**DF =20**	**DF = 120**	**DF = 100**			
DH	0.5000	0.1227	65.1029	0.1555	54.41736	0.724543	96.4912
DM	0.06612	0.04339	55.2753	0.07066	105.7686	0.251324	93.5673
SDO	0.03719	0.07355	17.1428	0.08992	79.18595	0.378681	96.9669
ST	0.1033	0.1124	32.7819	0.1015	84.28512	0.377968	100.17
PH	0.01058	0.1415	90.3874	0.07810	85.88182	0.325398	105.64
BY	0.8820	0.03994	1528.61	0.03570	206.2667	0.091608	100.21
NT	0.01058	0.07208	0.3746	0.04498	2.379339	8.913459	103.55
SL	0.04231	0.07340	0.5859	0.05890	7.067769	3.433682	100.79
NSPS	0.3498	0.03748	2.9555	0.06491	16.21901	1.570797	92.9572
NSS	0.004132	0.04495	70.8181	0.02727	38.34545	0.430643	103.99
GY	0.004384	0.004365	280.52	0.004376	83.47665	0.079243	99.9584
HI	6.612E-6	1.612E-6	0.006179	1.612E-6	0.408017	0.311134	100.00

*Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively.CV= coefficient of variations and DF= degree freedom*

Appendix 7: Phenotypic mean performance of one hundred twenty-one bread wheat genotypes tested at Adet

S.N.	Treatment	DH	DM	SD	ST	PH	BY	NT	SL	NSLP	NSS	GY	HI
1	**ETBW6921**	49.5	106.5	76.50	84.91	76.39	158.75	2.29	7.80	15.60	37.20	59.15	0.3750
2	**EBW7686**	60	110	71.50	87.52	80.8	212.5	2.32	6.60	14.80	35.20	70.48	0.3300
3	**Galil**	59	107	81.00	92.41	75.45	181.25	1.83	6.96	15.35	36.00	50.68	0.2800
4	**ETBW6876**	53	108.5	76.50	80.15	74.56	143.75	1.74	7.93	14.10	36.50	46.64	0.3250
5	**Dereselign**	61	105	77.45	87.62	98.5	218.75	2.45	6.90	14.10	35.90	61.77	0.2850
6	**Sirbo**	66.5	125	82.00	92.47	78.72	175	2.04	5.82	15.20	39.00	45.96	0.2600
7	**Ogolcho**	58.5	109	76.00	87.50	79.9	159.38	2.57	7.77	15.20	45.80	68.21	0.4300
8	**ETBW7717**	59.5	109	81.50	90.00	82.5	193.75	2.76	7.97	14.90	36.10	69.21	0.3600
9	**ETBW6543**	57.5	107	82.00	82.59	86.2	168.75	2.02	7.67	14.90	38.00	55.14	0.3300
10	**ETBW7724**	69	110.5	76.50	89.78	77.7	193.75	1.68	7.45	15.60	38.60	60.11	0.3100
11	**ETBW6932**	55	107	81.00	97.21	85	193.5	2.98	8.04	16.30	45.60	83.13	0.4300
12	**ETBW6875**	55	108.5	81.00	89.62	80.2	212.5	2.71	7.69	15.50	38.20	79.03	0.3700
13	**ETBW6839**	48	105	81.50	79.75	74.95	150	3.06	7.19	14.70	31.80	56.29	0.3750
14	**Hawii**	53	107	82.00	87.44	80.1	213.38	2.35	7.25	14.40	36.90	82.16	0.3850
15	**ETBW6373**	49	107	82.50	84.81	71.74	175	2.08	6.03	13.60	30.40	61.51	0.3500
16	**ETBW6939**	48	105	81.50	79.99	74.95	150	2.97	7.14	14.70	31.80	56.29	0.3750
17	**ETBW6102**	50	107	81.50	82.37	83.6	206.25	2.86	8.01	14.90	41.35	77.62	0.3800
18	**Tusie**	58.5	110.5	77.00	92.47	85.63	231.25	2.39	6.16	15.50	40.60	79.07	0.3400
19	**ETBW6492**	58	107.5	76.50	92.34	83.66	212.5	2.10	7.74	15.40	40.60	69.20	0.3250
20	**ETBW6130**	55	107	81.50	82.34	78.75	183.25	2.00	5.85	13.70	43.00	71.52	0.3900
21	**Hidasie**	55	105	81.00	92.05	81.05	213.38	2.01	6.39	13.90	36.00	83.81	0.3900
22	**ETBW6398**	58.5	108	72.00	92.25	80.14	182	2.23	7.26	16.05	39.00	59.44	0.3250
23	**ETBW7689**	59.5	109	81.50	84.78	77.7	187.5	2.82	7.14	15.80	39.20	56.14	0.3000
24	**Dure**	50	105	81.00	82.41	91.3	169.25	2.32	6.41	14.50	35.75	57.99	0.3450
25	**ETBW6315**	62.5	110.5	76.50	82.50	90.93	186.5	2.01	7.42	15.20	40.10	57.65	0.3100
26	**ETBW6840**	54.5	107	81.00	79.97	83.4	175	2.89	7.86	15.00	40.70	62.69	0.3600
27	**ETBW6174**	58.5	112.5	76.50	85.02	85.2	202.5	1.87	8.27	16.80	49.80	86.25	0.4300
28	**ETBW6647**	59	105	77.00	90.12	82.49	181.75	2.50	7.93	15.70	39.70	67.88	0.3700
29	**Bolo**	69.5	124.5	81.00	94.91	97.74	261.15	1.99	5.22	15.25	44.00	78.79	0.3000
30	**ETBW6439**	55	105	81.50	85.00	77.2	268.75	2.51	6.07	12.55	35.00	71.95	0.2700
31	**ETBW6953**	55	104.5	81.00	89.71	75.65	218.5	1.93	6.53	15.80	36.15	69.50	0.3200
32	**KULKULU**	69.5	123	71.50	87.65	73.55	178.13	3.08	7.76	16.35	42.60	65.77	0.3700
33	**ETBW6406**	50	107	81.00	80.09	68.6	181	2.26	6.54	13.70	32.90	76.97	0.4300
34	**ETBW6314**	64	117	76.50	94.75	86.6	256.25	2.30	7.60	15.40	41.00	84.90	0.3300
35	**Laketch**	55	108.5	81.50	79.99	72.8	175	3.25	6.91	13.70	38.40	59.43	0.3400
36	**Kubsa**	58	107	81.50	94.94	82.5	250	2.27	6.66	14.10	36.20	96.16	0.3800
37	**Sofumar**	58.5	107	71.50	94.88	90.9	256.25	2.12	7.67	15.25	35.75	89.65	0.3500
38	**ETBW6852**	55	108.5	82.50	92.38	74.3	200	2.85	7.70	16.00	42.20	74.49	0.3750
39	**Hoggana**	73.5	125	76.00	92.59	78.1	175	2.38	6.89	15.90	38.20	43.22	0.2450
40	**ETBW6496**	61	111	81.00	92.47	85.9	231.25	2.49	6.92	15.40	41.55	76.93	0.3300
41	**Millennium**	60	109	81.00	92.56	83.5	231.38	2.44	6.60	14.40	35.50	79.64	0.3450
42	**Kakaba**	55	105	82.00	80.11	86.6	193.75	2.86	7.12	14.40	40.70	71.83	0.3750
43	**Tay**	62.5	108.5	81.50	89.97	94.15	237.75	2.78	8.13	17.60	47.40	81.55	0.3400
44	**ETBW6832**	51.5	105	82.00	84.68	79.75	193.75	3.00	8.08	14.20	42.70	73.40	0.3800
45	**ETBW6506**	55	107.5	76.00	85.21	80.95	268.75	2.16	8.50	14.20	41.00	82.66	0.3100
46	**ETBW7694**	66.5	113	81.50	87.59	88.05	237.5	2.33	7.25	15.90	47.20	87.83	0.3700

47	**ETBW6871**	61	110.5	81.00	77.83	78.5	156.25	2.27	8.93	16.30	48.40	53.71	0.3450
48	**ETBW7723**	57	108.5	81.00	87.66	81.4	206.75	2.38	7.26	14.30	36.00	78.42	0.3800
49	**Pavon76**	56	107	82.00	92.59	81.59	243.75	2.46	6.86	14.00	35.10	87.36	0.3600
50	**ETBW6169**	55	107	82.25	89.97	77.45	199.44	2.21	6.93	14.30	35.55	75.01	0.3800
51	**ETBW6114**	62	109	77.50	90.19	75.24	243.75	2.90	6.94	16.85	39.20	83.04	0.3400
52	**ETBW6837**	53	105	81.00	80.31	79.175	162.5	2.19	7.57	15.20	39.40	56.04	0.3450
53	**ETBW6948**	62.5	115	82.00	87.78	79.7	218.75	1.85	8.26	17.25	40.70	70.54	0.3200
54	**ETBW6911**	65	122.5	81.50	87.69	88.3	200	1.89	7.30	17.20	44.20	64.56	0.3200
55	**ETBW6890**	55	107.5	76.00	87.39	78.7	200	1.91	7.87	15.60	41.70	70.93	0.3550
56	**ETBW6095**	56	106	71.50	92.41	76.2	187.5	2.11	7.29	14.40	33.00	59.69	0.3200
57	**ETBW6847**	51.5	105	82.00	77.48	74.7	125	2.40	7.88	16.40	54.00	45.05	0.3600
58	**Dashen**	71.5	125.5	81.50	90.74	80.185	169.16	2.22	6.02	18.10	43.22	57.13	0.3350
59	**Mitike**	52.5	106	71.50	84.89	97.2	218.75	2.45	7.29	15.80	37.30	67.34	0.3100
60	**ETBW6943**	55	106.5	77.00	84.89	85.4	200	2.35	8.28	15.80	38.80	44.90	0.2250
61	**Meraro**	69	124.5	76.00	92.51	73.5	175	2.04	6.64	15.30	39.60	50.44	0.2900
62	**ETBW6866**	53	107	76.50	87.29	79.8	175	2.98	6.91	14.30	39.70	64.68	0.3700
63	**Galema**	71.5	110.5	76.00	94.79	86.45	187.5	2.31	6.79	13.10	26.50	53.62	0.2900
64	**KBG01**	50	105.5	81.50	92.17	76.6	168.75	2.16	6.50	14.90	39.70	61.40	0.3650
65	**Dinknesh**	50	108.5	82.00	92.09	85.85	206.25	2.47	6.16	15.60	36.90	75.76	0.3650
66	**ETBW6101**	57	106	76.00	92.35	86.39	218.75	2.43	7.45	14.90	35.50	85.08	0.3900
67	**ETBW6850**	50	104.5	81.00	87.56	75.1	137.5	2.35	7.72	13.90	36.30	48.26	0.3500
68	**ETBW7688**	59	109.5	81.00	92.56	82.6	218.75	1.82	7.29	15.40	36.90	76.96	0.3500
69	**Doddota**	57.5	107	71.50	87.62	81.35	189.75	1.37	6.90	14.10	31.40	69.01	0.3650
70	**ETBW6212**	58.5	109	76.50	87.80	76.5	168.75	2.26	8.28	15.40	34.50	68.48	0.4050
71	**ETBW7692**	61	107	82.50	90.28	85	156.25	2.28	7.73	16.30	39.70	49.59	0.3200
72	**ETBW6404**	50	110.5	76.50	85.68	79.2	168.75	1.65	6.89	15.20	36.30	53.24	0.3150
73	**K6290Bulk**	55	106	82.50	92.43	105.95	237.5	2.20	6.98	13.55	39.70	74.31	0.3100
74	**ETBW6882**	53	106.5	71.50	80.16	76.8	193.75	2.18	8.18	15.80	43.50	45.85	0.2400
75	**ETBW6445**	67.5	125	81.00	90.25	91.15	225	2.24	7.89	17.30	42.30	70.72	0.3150
76	**Huluka**	73.5	125	76.50	92.36	84.35	225	1.90	8.30	16.20	45.70	74.75	0.3300
77	**ETBW6869**	55	106.5	76.00	90.16	81.87	137.5	2.29	8.38	16.70	29.40	45.06	0.3250
78	**ETBW6883**	55	107	81.50	82.69	78.2	175	2.65	7.83	16.30	38.70	60.96	0.3500
79	**Menze**	69	124.5	82.50	92.71	99.55	287.5	2.01	5.26	15.80	42.30	96.90	0.3400
80	**Shorima**	56	105	81.00	87.69	85.3	187.5	2.45	7.29	15.30	36.00	58.86	0.3150
81	**Bobitcho**	58.5	109	81.45	94.41	90.29	225	1.96	7.94	16.00	46.54	85.24	0.3800
82	**ETBW7693**	59	109.5	81.00	82.60	80.9	218.75	2.18	7.66	13.80	40.80	70.69	0.3200
83	**ETBW6688**	61	110.5	81.00	84.90	88.3	218.75	2.17	7.65	18.60	49.10	75.29	0.3450
84	**ETBW6107**	55	105	82.00	90.10	76.6	181.25	3.11	6.84	14.90	36.10	60.00	0.3300
85	**K62904A**	55	106	82.50	92.66	105.95	237.5	2.23	6.99	13.55	39.70	74.31	0.3100
86	**ETBW7730**	59	105	76.50	85.31	86.67	193.75	2.64	7.57	17.70	49.70	63.92	0.3300
87	**ETBW6167**	55.5	108	82.00	83.78	87.03	175	2.70	8.70	15.40	42.00	65.84	0.3750
88	**ETBW6529**	55	108	71.50	65.33	79.86	156.25	3.32	8.41	16.10	35.60	48.85	0.3100
89	**ETBW6518**	62.5	111	82.00	92.62	82.35	193.75	2.27	7.79	16.95	44.10	48.35	0.2500
90	**ETBW6109**	61	110	81.50	87.50	85.94	218.75	2.00	6.40	14.50	37.05	71.15	0.3250
91	**ETBW6845**	54.5	107.5	81.85	82.55	75.45	218.75	2.28	7.41	14.90	37.80	78.33	0.3600
92	**QUIAU#2(GAMBO)**	62	110.5	81.50	92.31	88.9	262.5	2.83	7.82	15.00	40.80	83.81	0.3200
93	**Simba**	55	109	82.00	92.24	80.15	243.75	2.64	7.50	15.40	30.90	80.15	0.3300
94	**Mada Walabu**	55	109	81.00	90.16	83.45	225	2.81	8.01	15.90	35.90	85.31	0.3800
95	**ETBW7695**	66.5	108	76.50	82.68	82.91	200	1.99	8.34	18.50	50.40	68.40	0.3400
96	**ETBW6862**	57.5	119	77.00	82.53	85.2	206.25	2.32	7.82	19.20	51.30	76.71	0.3700
97	**ETBW6848**	48	105	71.50	79.94	78.1	181.75	3.05	7.47	13.40	39.10	72.29	0.4000
98	**ETBW6853**	52.5	105	82.00	87.44	73.6	200	2.08	6.73	15.20	42.00	51.67	0.2600
99	**Tossa**	56	107.5	82.00	92.53	84	206.25	2.62	6.47	14.60	33.10	70.68	0.3400
100	**ETBW6393**	49.5	107	76.00	82.32	71.5	168.25	2.04	6.38	14.80	30.50	62.20	0.3700
101	**Abola**	55	108	81.50	89.54	87.49	285.72	2.42	7.23	15.20	41.49	97.78	0.3400
102	**Danda'a**	65	124.5	81.50	93.03	93.9	237.72	2.87	7.54	16.40	42.20	71.23	0.3000
103	**ETBW7696**	66.5	116	81.50	92.45	72.15	181.25	2.29	7.57	18.00	40.80	53.55	0.2950
104	**ETBW6696**	58.5	111	81.50	92.64	89.4	243.75	1.78	7.04	16.70	42.50	93.59	0.3850
105	**Katar**	55	109	76.50	92.51	92.75	221.5	1.81	7.24	14.30	42.60	81.79	0.3700
106	**ETBW6947**	63	108.5	76.00	90.17	83.58	231.25	2.32	6.84	15.10	37.70	76.90	0.3300
107	**ETBW5879**	60	109	83.00	90.07	80.25	218.75	2.64	7.13	14.70	38.30	79.91	0.3650
108	**ETBW6928**	62.5	122	76.00	82.69	84.7	187.5	4.60	9.22	20.50	54.10	62.75	0.3350
109	**Gasay**	60	105.5	76.00	92.54	88	206	2.93	7.26	15.20	38.10	64.65	0.3150
110	**ET13A2**	60	110	81.00	89.95	102	231.25	2.56	6.94	16.60	38.80	66.75	0.2900
111	**ETBW6256**	58	108	76.50	87.54	83.1	206.25	2.64	6.88	15.20	34.10	61.47	0.3000
112	**ETBW6937**	55	105	72.00	87.45	88.05	193.75	2.07	8.01	16.25	40.60	65.57	0.3400
113	**ETBW7698**	62	109	76.00	92.69	89.1	231.25	2.91	9.11	17.50	45.80	85.00	0.3650
114	**Sulla**	50	105	76.00	82.66	84.96	225	1.83	7.54	14.50	36.90	80.27	0.3600
115	**Digelu**	70	124	77.00	85.06	104.7	231.25	2.60	5.11	16.10	45.00	82.25	0.3550
116	**ETBW7690**	55	108.5	82.00	90.13	86.1	218.75	2.29	8.63	16.20	42.90	75.80	0.3500
117	**ETBW6886**	68	115	81.50	92.54	87.2	206.25	1.94	7.91	15.88	42.20	68.87	0.3300
118	**ETBW6841**	55	100	82.00	92.25	81.95	225	3.16	6.86	15.10	38.60	83.15	0.3700
119	**ETBW6861**	55	109	81.50	89.95	89.19	193.38	2.90	8.75	16.50	45.30	71.58	0.3700
120	**Enkoy**	50	105	81.00	90.01	93.7	237.5	2.12	6.33	13.30	35.70	73.10	0.3100
121	**ETBW6427**	66.5	108.5	82.00	89.82	93.5	250	2.75	7.79	16.40	48.40	80.99	0.3200
	CV	**0.846**	**0.55**	**0.72**	**0.55**	**1.03**	**0.81**	**10.71**	**4.26**	**3.10**	**1.57**	**0.77**	**1.5600**
	LSD at (0.01)	**1.286**	**1.57**	**1.50**	**1.3435**	**2.25**	**4.33**	**0.703**	**0.852**	**1.25**	**1.63**	**1.40**	**0.0139**
	at (0.05)	**0.9728**	**1.19**	**1.13**	**1.0151**	**1.70**	**3.27**	**0.531**	**0.644**	**0.95**	**1.24**	**1.06**	**0.0105**

DH: days to heading, DM: days to maturity, GFP: grain filling period, GY: grain yield, TKW: 1000 kernel weight, AGB: aboveground biomass (kgha-1), HI: harvest index, HW: hectoliter weight, TPP: tillers per plant, PH: plant height (cm), SPS: spike lets per spike, KPS: kernels per spike, SL: spike length, SPP, spikes per plant. LSD= list significant difference, CV= coefficient of variations

Appendix 8: Phenotypic mean performance of one hundred twenty-one bread wheat genotypes tested at Debre Tabor

S. N	Treatment	DH	DM	SD	ST	PH	BY	NT	SL	NSLP	NSS	GY	HI
1	ETBW6921	49.5	104.54	80.5	86.5	79.75	233.29	2.57	7.74	17.11	39.6	86.15	0.3700
2	EBW7686	53.5	96.02	74	90	84.4	184.5	2.52	8	15.75	38.3	71.66	0.3900
3	Galil	51	93.46	82	85	70.2	229.65	1.97	7.4	15.59	38.1	72.10	0.3100
4	ETBW6876	46.5	94.08	77.5	87.5	79.6	166.84	1.97	8.3	14.45	36.9	56.46	0.3400
5	Dereselign	46.5	102.04	79.5	86.5	90.8	230	2.73	8.2	14.39	33.7	71.65	0.3100
6	Sirbo	58.5	108.08	83	82.5	75.4	213.53	2.26	6.9	15.59	29	66.21	0.3100
7	Ogolcho	53	96.16	77.5	80	81.9	199.63	2.70	7.7	16.68	42.3	93.37	0.4700
8	ETBW7717	54.5	97.40	83.5	85	88.9	230.34	2.94	8.7	16.43	44.8	85.47	0.3700
9	ETBW6543	52	96.08	83	75	81.5	219.17	2.16	8	15.09	41.6	85.55	0.3900
10	ETBW7724	63	98.54	77.5	92.5	80.6	208.42	1.85	8.2	16.10	41.9	69.88	0.3350
11	ETBW6932	48.5	93.58	82	80	78.4	206.33	3.17	8.8	17.13	40.4	92.36	0.4500
12	ETBW6875	47	92.44	82.5	80	78.8	233.13	2.90	8.2	16.04	39.1	95.56	0.4100
13	ETBW6839	54	94.86	83	82.5	81.3	204.44	2.81	7.9	17.32	39	90.69	0.4400
14	Hawii	41.5	83.48	83	87.5	79	226.3	2.40	8	14.98	30.2	95.40	0.4200
15	ETBW6373	38.5	84.48	84	90	71.6	183.41	2.30	7.7	15.83	37.8	68.25	0.3750
16	ETBW6939	39.5	86.48	82.5	77.5	71.9	171.27	3.21	7.6	14.74	29.6	69.44	0.4100
17	ETBW6102	43.5	93.42	82.5	80	78.4	218.32	3.07	8.2	15.78	34.1	87.67	0.4000
18	Tusie	52	96.94	78.5	82.5	82.2	257.83	2.58	7.3	16.03	38.3	99.50	0.3900
19	ETBW6492	50.5	93.06	77.5	82.5	89.3	253.4	2.25	8.8	15.82	41.1	85.44	0.3400
20	ETBW6130	46	89.29	82.5	82.5	79.5	227.49	2.19	7.4	15.86	43.1	96.33	0.4200
21	Hidasie	50	94.98	82	85	78.1	194.66	2.21	8.2	15.56	46.2	85.43	0.4400
22	ETBW6398	53	96.94	72	87.5	87.8	220.74	2.41	8	18.45	35.5	78.47	0.3550
23	ETBW7689	51.5	94.06	83	92.5	84.4	181.5	3.00	7.9	17.40	39.3	70.02	0.3850
24	Dure	42.5	89.48	82	82.5	84.9	208.45	2.62	7.6	16.18	37.8	74.57	0.3600
25	ETBW6315	56	98.92	78	80	89	205.54	2.19	8.6	18.52	40.3	79.18	0.3850
26	ETBW6840	48.5	95.60	82	80	74.8	199.02	3.11	8.2	15.99	38.9	80.35	0.4000
27	ETBW6174	48.5	96.04	78	85	83	226.73	2.07	8.1	17.04	42.5	85.14	0.3750
28	ETBW6647	49	88.06	78.5	80	80.5	213.72	2.68	8	15.49	33.7	86.56	0.4050
29	Bolo	59	108.56	82	90	103	200.63	1.92	6.3	16.91	44.4	82.85	0.4100
30	ETBW6439	52	98.18	82.5	82.5	76.1	241.49	2.65	7.7	13.98	36	82.87	0.3400
31	ETBW6953	47	88.10	82	92.5	69.2	221.14	2.12	7.4	16.72	36.9	88.56	0.4000
32	KULKULU	58	102.10	74	92.5	81.8	206.54	3.27	7.6	17.45	35.3	92.05	0.4500
33	ETBW6406	41	87.60	82	85	75.2	190.5	2.41	7.3	16.34	38.7	73.33	0.3800
34	ETBW6314	55	100.50	78	80	81.8	206.33	2.55	7.2	15.32	34.7	98.16	0.4800
35	Laketch	40	77.98	82.5	85	68.4	201.82	3.62	7.1	16.07	31.4	73.60	0.3650
36	Kubsa	44.5	82.54	83	90	73.8	255.18	2.55	7.6	15.31	35	93.50	0.3700
37	Sofumar	51	93.00	73.5	85	82.1	219.48	2.37	7.4	16.43	35.3	90.35	0.4100
38	ETBW6852	47.5	93.42	83.5	82.5	74.2	203.35	3.06	8.2	16.41	41.7	86.51	0.4250
39	Hoggana	64.5	110.00	77.5	90	87.2	190.19	2.63	8.2	17.31	35.2	63.26	0.3300
40	ETBW6496	53.5	97.62	82	82.5	90.8	253.49	2.70	7.2	16.70	41.8	95.34	0.3800
41	Millennium	51	93.04	82	87.5	88.3	240.35	2.65	7.3	15.66	30	94.63	0.3900
42	Kakaba	47	89.54	83	87.5	81	188.18	3.16	7.7	14.87	38.6	76.55	0.4100
43	Tay	57	98.86	82.5	90	93.9	253.73	3.04	8.3	18.15	42.3	95.34	0.3800
44	ETBW6832	45	91.04	83	77.5	75.5	209.79	3.27	8.3	15.75	33.7	91.85	0.4400
45	ETBW6506	46.5	90.96	77.5	80	79.5	220.62	2.37	8.5	16.92	46.9	92.68	0.4200
46	ETBW7694	59	99.98	82.5	85	87.3	255.93	2.52	8.2	17.98	53.3	94.78	0.3700
47	ETBW6871	55.5	100.02	82	77.5	79.1	212.29	2.52	9.5	16.82	44.7	84.04	0.4000
48	ETBW7723	51	96.52	82	85	81.9	197.23	2.60	7.7	15.26	39.4	83.78	0.4250
49	Pavon76	48	91.40	83	90	79.5	224.74	2.61	7.8	15.36	35.3	92.80	0.4100
50	ETBW6169	49	95.48	83.5	75	71.3	203.39	2.40	7.4	15.38	41.3	91.21	0.4500
51	ETBW6114	54.5	96.60	79	85	74.2	237.77	3.05	7.9	16.95	40	97.50	0.4100
52	ETBW6837	44	86.98	82	77.5	71.9	203.17	2.38	8	15.06	39.4	71.85	0.3500
53	ETBW6948	55.5	102.52	83	82.5	84.9	210.26	1.90	9.1	20.81	42.4	75.53	0.3600
54	ETBW6911	56	105.34	82.5	90	97.5	241.77	2.09	7.9	17.70	39	85.81	0.3500
55	ETBW6890	47	91.02	77.5	85	71	219.53	2.12	8.4	16.30	36.5	93.94	0.4300
56	ETBW6095	50	94.58	73.5	82.5	82.8	168.2	2.34	8.5	15.37	34.4	60.90	0.3600
57	ETBW6847	44	90.14	83	85	77.9	191.2	2.57	8.5	17.66	49.9	76.12	0.4000
58	Dashen	56.5	109.64	82.5	87.5	86.85	169.14	2.48	8.6	18.48	38.5	59.79	0.3550
59	Mitike	48.5	97.46	73.5	87.5	94.4	194.39	2.66	8.9	18.25	39	55.43	0.2850
60	ETBW6943	49	95.23	78.5	80	84.4	204.51	2.52	8.5	16.60	40.5	71.30	0.3500
61	Meraro	59	106.10	77.5	90	73.2	204.52	2.25	8.3	19.31	44.6	65.03	0.3200
62	ETBW6866	45.5	91.60	78	77.5	73.6	203.34	3.19	8.1	16.43	32.2	87.30	0.4300
63	Galema	66	96.52	77.5	90	86.4	234.94	2.48	8	16.26	25.6	80.46	0.3400
64	KBG01	45	95.10	83	80	73.2	182.17	2.37	8.5	16.03	48.2	72.22	0.4000
65	Dinknesh	45	103.14	83	79.5	80.8	198.7	2.69	7.8	17.90	41.8	82.72	0.4150
66	ETBW6101	48.5	90.64	78	82.5	81	206.29	2.67	8.3	17.62	47.8	92.43	0.4500
67	ETBW6850	42	87.86	82	82.5	67	164	2.54	7.9	14.58	35.1	63.87	0.3900
68	ETBW7688	50	92.94	82	87.5	78.2	230.44	2.04	7.5	17.30	34.6	90.13	0.3900
69	Doddota	47.5	98.48	74	82.5	79.85	200.5	1.63	7.9	14.68	35.5	78.86	0.3900
70	ETBW6212	53	98.48	77.5	85	81.45	237.25	2.54	8	16.74	35	86.08	0.3600
71	ETBW7692	50	95.94	83.5	85	79.6	181.39	2.50	8.6	18.08	40.1	56.63	0.3100
72	ETBW6404	45.5	99.92	78.5	87.5	76.6	205.58	1.90	7.9	17.44	41.3	72.27	0.3500
73	K6290Bulk	46	87.94	84	85	98.6	159.66	1.92	7.9	16.70	37.5	72.73	0.4600
74	ETBW6882	48	95.79	73.5	80	74.5	225.71	2.41	8.1	15.82	37.3	72.02	0.3200
75	ETBW6445	57	105.98	82	82.5	97.3	232.7	2.43	8.5	18.63	46.4	78.01	0.3400

76	**Huluka**	64	108.48	78	87.5	91.1	249.92	2.14	8.3	17.32	43.3	82.05	0.3300
77	**ETBW6869**	46.5	89.56	77.5	82.5	81.1	172.4	2.48	9.1	16.67	30.9	68.88	0.4000
78	**ETBW6883**	43.5	84.36	82.5	77.5	75.7	216.57	2.82	7.5	15.65	37.6	76.50	0.3500
79	**Menze**	60	107.98	83.5	97.5	95.9	239.98	2.20	6.5	16.47	40.2	97.23	0.4050
80	**Shorima**	51.5	97.12	82	85	87.4	209.51	2.58	8.5	16.00	34.4	73.18	0.3500
81	**Bobitcho**	55.5	102.50	82.5	94.5	85.4	200.85	2.13	8.2	16.88	46.5	88.73	0.4450
82	**ETBW7693**	49	90.00	82	85	87.9	235.19	2.35	8.2	15.24	37.5	87.17	0.3700
83	**ETBW6688**	53	95.04	82	80	85.8	228.58	2.35	8.5	18.25	43.1	88.52	0.3900
84	**ETBW6107**	47.5	89.92	83	82.5	75.7	232.17	3.10	8.2	16.11	41.6	73.18	0.3150
85	**K62904A**	50	96.04	84	82.5	101.8	256.42	2.43	7.9	14.62	40.3	97.98	0.3800
86	**ETBW7730**	53.5	95.50	78	80	77.2	205.05	2.81	7.8	15.62	40.7	73.94	0.3600
87	**ETBW6167**	49	95.04	83	80	85.5	208.54	2.83	8.9	15.27	41	85.71	0.4100
88	**ETBW6529**	47	93.04	73.5	77.5	74.7	232.59	3.34	8.5	14.68	32	88.56	0.3800
89	**ETBW6518**	56	99.00	83	80	84.05	209.06	2.46	8.4	18.77	37.8	70.16	0.3400
90	**ETBW6109**	53.5	96.50	83	75	81.3	226.32	2.26	7.6	15.32	37.9	81.78	0.3600
91	**ETBW6845**	43.5	86.94	83	87.5	68.2	227.45	2.52	8.4	16.48	33.6	99.29	0.4400
92	**QUIAU#2(GAMBO)**	53	94.46	83	85	89.2	263.54	3.05	8.2	16.83	36.5	92.42	0.3500
93	**Simba**	47	93.50	83	87.5	79.6	210.79	2.87	8.7	17.26	32.1	86.25	0.4100
94	**MadaWalabu**	48.5	95.96	82	85	83.7	245.68	3.03	8.3	14.12	37.5	90.73	0.3700
95	**ETBW7695**	60.5	98.00	78	82.5	78.4	229.36	2.27	8.5	17.08	39.7	89.12	0.3900
96	**ETBW6862**	47	97.32	78.5	80	80.4	255.37	2.54	8.4	17.96	38.9	97.15	0.3800
97	**ETBW6848**	42	91.96	73.5	77.5	73.7	210.61	3.27	8.7	14.04	35.4	92.19	0.4400
98	**ETBW6853**	46	92.88	83	82.5	73.6	219.61	2.27	8.2	15.52	39.9	71.49	0.3250
99	**Tossa**	49.5	94.58	83	87.5	81.7	206.24	2.80	7.9	14.71	32.2	78.88	0.3800
100	**ETBW6393**	40.5	87.98	77.5	80	66.8	226.69	2.19	7.6	14.86	35.4	81.07	0.3600
101	**Abola**	53	102.84	82.5	90	84.05	273.5	2.58	7.8	16.69	39.3	96.64	0.3500
102	**Danda'a**	56	106.52	82.5	85.5	91.9	229.8	2.61	8.3	16.59	43.25	89.50	0.3900
103	**ETBW7696**	67.5	99.90	82.5	85	73.9	257.97	2.41	8.1	17.55	40.6	85.56	0.3300
104	**ETBW6696**	51.5	98.02	82.5	85	83	268.83	1.90	7.6	14.80	33.7	99.00	0.3700
105	**Katar**	46.5	92.52	88	75	84.9	237.14	2.00	8	15.95	37.3	87.99	0.3700
106	**ETBW6947**	58	98.98	77.5	77.5	77.8	242.49	2.47	7.6	15.25	30.9	92.83	0.3800
107	**ETBW5879**	53.5	96.96	84	82.5	76.1	254.8	2.76	7.2	16.01	34.2	94.66	0.3700
108	**ETBW6928**	51	99.02	77.5	80	81.4	274	2.81	8.6	18.21	40.2	93.59	0.3400
109	**Gasay**	51.5	99.10	77.5	85	86.6	255.61	3.04	8	16.74	36	93.07	0.3600
110	**ET13A2**	56.5	102.98	82	85	101	247.52	2.71	7.4	16.47	33.8	88.34	0.3600
111	**ETBW6256**	51	94.82	78	85	80.6	241.38	2.86	8.6	17.92	34.9	90.02	0.3700
112	**ETBW6937**	50.5	96.96	73.5	82.5	83.1	211.41	2.29	8.7	17.00	40.6	88.08	0.4200
113	**ETBW7698**	55.5	97.50	77	77.5	78.4	213.06	3.18	8.6	17.24	32.4	87.09	0.4100
114	**Sulla**	41	84.96	77	80	83.9	240.68	2.05	9.3	15.88	34.1	97.35	0.4050
115	**Digelu**	61.5	108.94	78.5	90	102	202.85	2.84	6.8	18.24	46.5	79.05	0.3900
116	**ETBW7690**	48.5	96.00	83	85	83.2	242.83	2.47	9.1	17.93	43.8	92.20	0.3800
117	**ETBW6886**	58	97.58	82.5	80	82	256.84	2.12	8.4	17.57	37.6	93.59	0.3600
118	**ETBW6841**	50	90.50	83	82.5	83.9	234.58	3.39	8.1	16.02	39.5	96.67	0.4100
119	**ETBW6861**	50	98.88	82.5	87.5	87.8	194.02	3.08	8.2	15.08	31.5	77.10	0.3950
120	**Enkoy**	45.5	95.50	82.5	87.5	88.7	221.08	2.37	7.7	13.98	38.1	93.75	0.4200
121	**ETBW6427**	66	106.46	83.5	80	86.6	239.87	2.97	8.4	16.99	41.8	85.68	0.3600
	CV	**0.997**	**0.4989**	**0.6736**	**0.764**	**0.798**	**2.3242**	**9.080**	**3.5954**	**1.9444**	**1.9351**	**1.5971**	**0.9652**
	LSD at (0.01)	**1.325**	**1.30**	**1.4197**	**1.678**	**1.710**	**13.328**	**0.64**	**0.758**	**0.8709**	**1.9438**	**3.4926**	**0.0096**
	at (0.05)	**1.002**	**0.98**	**1.0739**	**1.269**	**1.294**	**10.082**	**0.48**	**0.5734**	**0.658**	**1.4704**	**2.642**	**0.0073**

DH: days to heading, DM: days to maturity, GFP: grain filling period, GY: grain yield, TKW: 1000 kernel weight, AGB: above ground biomass (kgha-1), HI: harvest index, HW: hectoliter weight, TPP: tillers per plant, PH: plant height (cm), SPS: spikelets per spike, KPS: kernels per spike, SL: spike length, SPP, spikes per plant. LSD= list significant difference, CV= coefficient of variations

Appendix 9: Phenotypic mean performance of one hundred twenty-one bread wheat genotypes tested at kulumsa

S.N.	Treatment	DH	DM	SD	ST	PH	BY	NT	SL	NSLP	NSS	GY	HI
1	**ETBW6921**	46	102	76.5	84	76.3622	175.23	2.55	8.2	16.6	39.1	86.96	0.5
2	**EBW7686**	57.5	106.5	73	90.5	84.7695	219.76	2.55	7	15.4	38.2	88.42	0.4
3	**Galil**	55	103	80.5	86	75.998	208.73	1.9	6.4	15.45	37.9	83.04	0.4
4	**ETBW6876**	50	105	76.5	88	89.5776	174.22	1.9	7.3	14.1	36.7	63.24	0.36
5	**Dereselign**	55	99	77	90	92.9654	235.93	2.7	7.2	14.1	33.7	93.75	0.4
6	**Sirbo**	63	120.5	81.5	83	78.998	192.89	2.1	6.2	15.4	28.9	74.19	0.38
7	**Ogolcho**	56	105.5	76	81.5	87.0224	171.26	2.5	6.7	16.4	42.1	87.17	0.51
8	**ETBW7717**	57	106	81	85	91.0183	214.21	2.6	7.7	16.1	44.8	82.58	0.39
9	**ETBW6543**	55	104	81.5	77	84.5489	184.85	2	7	14.7	41.5	75.12	0.41
10	**ETBW7724**	66	107	76.5	92.5	81.1102	207.37	1.7	7.2	16	41.7	83.85	0.4
11	**ETBW6932**	52	103	80.5	80.5	87.4898	194.55	3	7.8	16.9	40.3	87.51	0.45
12	**ETBW6875**	51	104	80.5	75.5	84.9837	215.55	2.5	7.2	16	39.1	86.94	0.4
13	**ETBW6839**	58	102	82	83.5	85.1715	170.86	2.5	6.9	17.2	38.9	83.57	0.49
14	**Hawii**	47.5	101	81.5	87.5	88.2224	231.59	2.25	7	15.2	30.1	93.86	0.41
15	**ETBW6373**	44	102	77	90.5	82.4715	177.95	2	6.7	15.7	37.7	64.76	0.36
16	**ETBW6939**	44	101	81	79	76.1511	166.59	2.9	6.6	14.6	29.6	65.4	0.39
17	**ETBW6102**	47	104	81	80.5	82.943	205.03	2.9	7.2	15.6	33.9	78.04	0.38
18	**Tusie**	55.5	106.5	77	84.5	90.9389	238.37	2.5	6.3	15.8	38.2	90.99	0.38
19	**ETBW6492**	54	103	76.5	83.5	91.3959	230.88	2.2	7.3	15.6	40.9	93.12	0.4

20	**ETBW6130**	51	103	81	73	83.4919	202.66	1.8	6.4	15.9	43.1	95.285	0.47
21	**Hidasie**	53	102	80.5	86	88.4633	209.47	2	7.2	15.3	46.1	88.3	0.42
22	**ETBW6398**	56	105	72	87.5	92.7857	174.79	2.2	7	18.3	35.4	69.65	0.4
23	**ETBW7689**	56	105	81	92.5	84.543	187.92	2.8	6.9	17	39.2	78.61	0.42
24	**Dure**	46.5	101	80.5	83.5	89.9308	171.05	2.25	6.6	16	37.45	66.27	0.39
25	**ETBW6315**	59	106.5	76.5	80.5	90.4511	196.55	1.9	7.6	17.6	40.1	84.92	0.43
26	**ETBW6840**	51	102	80.5	85.5	78.9308	177	2.8	7.2	15.7	38.8	76.82	0.43
27	**ETBW6174**	53	110	76.5	85.5	83.0022	260.92	1.8	7.1	16.7	42.3	96.95	0.37
28	**ETBW6647**	54	100	77	80.5	79.8982	185.79	2.4	7	15.7	33.5	81.19	0.44
29	**Bolo**	61	115	80.5	90	101.95	248.9	1.9	5.6	17.2	44.3	64.13	0.26
30	**ETBW6439**	54	103	81	83.5	79.4552	275.9	2.4	6.7	13.6	36	92.56	0.34
31	**ETBW6953**	51	100	80.5	92.5	82.4226	205.89	1.9	6.4	16.2	36.5	53.73	0.26
32	**KULKULU**	64	117	72	92.5	87.5104	187.9	2.65	6.65	17.2	35.1	94.72	0.5
33	**ETBW6406**	45.5	103	81	85	77.4817	187.36	2.2	6.3	16.1	38.5	68.36	0.365
34	**ETBW6314**	59.5	113	76.5	80.5	94.9756	253.42	2.3	6.2	15.1	34.7	93.89	0.37
35	**Laketch**	47.5	100	81	85	88.9348	169.21	3.2	6.1	15.8	31.3	43.23	0.26
36	**Kubsa**	51.5	100	81	90	88.4633	247.98	2.2	6.6	15.1	35	91	0.37
37	**Sofumar**	55	103	73	85	96.9776	249.31	2.2	6.4	16.2	35.6	89	0.36
38	**ETBW6852**	51.5	104	82	83.5	84.3633	205.27	2.7	7.2	16.3	41.5	83	0.4
39	**Hoggana**	69	120	76	90	94.3308	172.22	2.4	7.2	17.1	35	88.34	0.51
40	**ETBW6496**	57.5	107	80.5	83.5	90.5878	243.46	2.5	6.2	16.2	41.6	93	0.38
41	**Millennium**	55.5	104.5	80.5	87.5	92.5143	226.26	2.5	6.3	15.3	29.9	90.7	0.4
42	**Kakaba**	51	101	81.5	78.5	85.443	205.4	2.9	6.7	14.6	38.4	81.44	0.4
43	**Tay**	60	105	81	90.5	96.9837	240.39	2.7	7.3	18	42.2	90.3	0.38
44	**ETBW6832**	48.5	102	81.5	80	85.4552	178.01	3.1	7.3	15.6	33.5	46.33	0.26
45	**ETBW6506**	45.5	103	81	85	77.4552	187.36	2.2	6.3	16.1	38.5	68.36	0.365
46	**ETBW7694**	63	109	80.5	85.5	89.498	223.89	2.3	7.2	17.8	53.1	88.31	0.39
47	**ETBW6871**	58.5	107	80.5	79	79.9633	165.92	2.6	8.55	16.6	44.5	79.54	0.48
48	**ETBW7723**	54	108	80.5	85	83.4837	199.59	2.3	6.7	15.1	39.2	96.88	0.49
49	**Pavon76**	52	103	81.5	90	83.9837	201.5	2.6	6.8	15.2	35.1	82.5	0.41
50	**ETBW6169**	52	104	81.5	77.5	78.9959	193.01	2.2	6.4	15.2	41.1	97.5	0.51
51	**ETBW6114**	58	105	77.5	85	75.9081	252.93	2.9	6.9	16.7	40	99.89	0.395
52	**ETBW6837**	49	100.5	80.5	79	78.9511	163.29	2.3	7	15.1	39.2	59.92	0.37
53	**ETBW6948**	59	112	81.5	83	84.9346	214.64	1.9	8.1	20.3	42.3	83.17	0.39
54	**ETBW6911**	61	117	81	90	97.0041	202.2	1.9	6.9	17.3	38.9	77.2	0.38
55	**ETBW6890**	51	103	76.5	85	78.4756	181.9	2	7.4	16.1	36.4	93.25	0.51
56	**ETBW6095**	53	102	76.5	83.5	85.5591	226.8	2.4	7.3	17.6	47.1	88	0.39
57	**ETBW6847**	47.5	101	82.5	85	82.7885	136.07	2.4	7.5	17.4	49.7	59.86	0.44
58	**Dashen**	60.5	114	82	73.5	79.0672	194.08	2.3	7.6	18.3	27.1	71.57	0.37
59	**Mitike**	50.5	104	72.5	87.5	99.6079	237.65	2.4	7.9	17.7	38.8	60.78	0.26
60	**ETBW6943**	52	103	77.5	81.5	86.312	217.11	2.3	7.5	16.2	40.5	88	0.41
61	**Meraro**	64	119	76.5	90	83.555	187.19	2.1	7.3	19.2	44.4	74.22	0.4
62	**ETBW6866**	49	103	77	80	79.6018	175.8	3	7.1	16.3	32	85.67	0.49
63	**Galema**	67.5	106	76.5	90	89.2876	214.55	2.3	7	16.5	15.5	85.9	0.4
64	**KBG01**	47.5	103	81.5	82	76.0998	176.37	2.1	7.5	16.1	45	68.19	0.39
65	**Dinknesh**	45.5	103.5	82	79	85.5794	199.11	2.5	6.8	17.5	41.7	93.3	0.47
66	**ETBW6101**	53	102	76.5	83.5	85.5876	226.8	2.4	7.3	17.6	47.1	88	0.39
67	**ETBW6850**	46	100	81	83.5	75.0204	161.23	2.4	6.9	14.6	35	78.35	0.49
68	**ETBW7688**	54.5	104	81	88	83.0346	224.81	1.9	6.5	17.1	34.4	88.96	0.4
69	**Doddota**	53	102	72.5	83.5	81.0204	208.29	1.4	6.9	14.6	35.4	79.33	0.38
70	**ETBW6212**	56	106	77	85	81.5	199.58	2.4	7	16.6	34.8	99.64	0.5
71	**ETBW7692**	58	104	82.5	86	84.4878	175.09	2.4	7.6	17.9	39.9	69.6	0.4
72	**ETBW6404**	48	108	77	87.5	78.4919	180.43	1.7	6.9	17.3	41.2	80.8	0.45
73	**K6290Bulk**	51	101	82	86	96.0326	209.85	1.7	6.9	16.6	37.4	88.56	0.42
74	**ETBW6882**	51	104	72.5	80.5	77.0407	201.9	2.2	7.1	15.7	37.2	89.42	0.44
75	**ETBW6445**	62	120	81.5	83.5	97.5713	243.3	2.3	7.5	18.6	46.2	82.7	0.34
76	**Huluka**	69	120	77	88.5	92.0122	227.36	2	7.3	17.2	43.2	90.98	0.4
77	**ETBW6869**	51	102	76.5	83	85.0448	167.84	2.3	8.1	16.5	25.8	86.75	0.52
78	**ETBW6883**	49	101	81.5	79	78.0529	185.3	2.6	6.5	15.1	47.5	69.26	0.37
79	**Menze**	64.5	119.5	82.5	88	99.0041	286.41	2	5.5	16.15	40	97.98	0.34
80	**Shorima**	54	102.5	81	86	87.557	206.86	2.4	7.5	15.8	34.3	97.61	0.47
81	**Bobitcho**	55	106	77	90	86.1448	227.56	1.9	7.2	16	39.2	94.26	0.41
82	**ETBW7693**	54	104	81	85	84.9468	213.37	2.2	7.2	15.2	37.4	99.15	0.46
83	**ETBW6688**	57	106	81	81.5	89.7244	208.77	2.2	7.5	18.1	42.9	81.11	0.39
84	**ETBW6107**	51.5	101	82	83.5	78.3326	193.9	3.1	7.25	16	41.4	79.56	0.41
85	**K62904A**	53	103	82.5	83	104.53	242.4	2.2	6.9	14.6	40.2	94.78	0.39
86	**ETBW7730**	56.5	102	77	81.5	84	200.03	2.7	6.8	15.4	40.5	75.74	0.38
87	**ETBW6167**	52	105	82	80.5	88.0835	202.64	2.7	7.9	15.2	41	91.56	0.45
88	**ETBW6529**	51	104	73	79	80.6122	181.08	3.4	7.5	14.4	31.9	88.96	0.49
89	**ETBW6518**	59.5	108	82	82	84.2672	199.58	2.3	7.4	18.5	37.7	72.81	0.36
90	**ETBW6109**	57.5	106	81.5	77.5	85.5163	205.02	2	6.9	15.1	37.8	87.76	0.43
91	**ETBW6845**	49	102	82	88	74.9878	202.13	2.3	7.4	16.3	33.5	82.33	0.41
92	**QUIAU#2(GAMBO)**	57.5	105.5	81.5	85	89.3285	247.89	2.8	7.2	16.6	36.4	93.59	0.38
93	**Simba**	51	104.5	82	87.5	82.0081	216.03	2.7	7.7	17	32	98.76	0.46
94	**MadaWalabu**	52	105.5	81	85.5	84.4837	214.31	2.9	7.3	14.1	67.4	84.96	0.4
95	**ETBW7695**	64	105	77	85.5	83.4959	205.27	2.1	7.5	16.9	39.55	91.63	0.45
96	**ETBW6862**	52.5	114	77.5	81.5	85.5367	200.47	2.3	7.4	17.5	38.8	73.73	0.37
97	**ETBW6848**	45	102	73	80	78.0305	162.53	3.1	7.7	14	35.3	75.67	0.465
98	**ETBW6853**	50	102	82	83	75.1163	192.92	2.1	7.2	15.4	39.8	84.71	0.44
99	**Tossa**	53	104	82	87.5	84.0407	209.03	2.6	6.9	14.5	32	95.68	0.46
100	**ETBW6393**	45	103	76.5	80.5	71.0285	154.33	1.9	6.6	14.6	35.3	55.78	0.36

101	**Abola**	52.5	106	81.5	87.5	90.0367	232.37	2.3	7.3	17	36.7	97.63	0.42
102	**Danda'a**	60.5	119.5	81.5	86	93.5081	203.04	2.4	7.3	16.3	40.2	75.68	0.37
103	**ETBW7696**	62	113	81.5	85	77.6163	178.84	2.2	7.15	17.3	40.6	74.32	0.42
104	**ETBW6696**	55	108	81.5	86	91.0672	222.83	1.7	6.6	14.6	33.6	93.62	0.42
105	**Katar**	51	105	77	77	92.0163	223.5	1.7	7.3	15.8	37.2	82.85	0.37
106	**ETBW6947**	61	106	76.5	79	82.9837	216.75	2.3	6.6	15.1	30.8	93	0.43
107	**ETBW5879**	57.5	107	83	83	81.4878	200.73	2.55	6.2	15.7	34	75.21	0.37
108	**ETBW6928**	57	116	76.5	82	86.4959	201.27	4.6	7.6	17.8	40.1	78.4	0.39
109	**Gasay**	56	111	76.5	86	89.0407	207.93	2.8	7	16.5	35.8	87.5	0.42
110	**ET13A2**	58	108	81	86	104.53	198.93	2.5	6.4	16.3	33.6	87.32	0.44
111	**ETBW6256**	54.5	105	77	86	83.4674	209.15	2.6	7.6	17.7	34.8	87.9	0.42
112	**ETBW6937**	53	103	73	83.5	80.9613	180.53	2.1	7.7	16.9	40.4	93.5	0.52
113	**ETBW7698**	59	106	76.5	79.5	88.9267	239.99	3	7.6	17.1	32.3	98.22	0.41
114	**Sulla**	45.5	100.5	76.5	82.5	87.7145	224.71	1.9	8.3	15.8	33.9	95.75	0.43
115	**Digelu**	66	119.5	77.5	90	103.92	223.01	2.6	5.8	18	56.5	98.55	0.44
116	**ETBW7690**	52	105	82	85	85.998	216.64	2.3	8.1	17.7	43.6	87.6	0.4
117	**ETBW6886**	63	110	81.5	82	87.4715	219.69	1.9	7.4	17.3	37.4	95.13	0.43
118	**ETBW6841**	53	97	82	86.5	84.5389	208.85	3.2	7.1	15.9	39.3	85.48	0.41
119	**ETBW6861**	53	106	81.5	87.5	90.2471	198.43	2.9	7.2	15	31.5	96.51	0.49
120	**Enkoy**	48	103	81	87.5	93.4471	292.64	2.1	6.8	14	37.9	95.86	0.33
121	**ETBW6427**	66	108	82	81.5	92.9593	244.33	2.7	7.4	17	41.7	63.93	0.26
	CV	**0.724**	**0.2513**	**0.3787**	**0.378**	**0.32539**	**0.09160**	**8.9135**	**3.4337**	**1.5708**	**0.4306**	**0.0792**	**0.3111**
	LSD at (0.01)	**1.032**	**0.6958**	**0.7849**	**0.8338**	**0.7607**	**0.4946**	**0.5551**	**0.6352**	**0.6668**	**0.4322**	**0.173**	**0.00332**
	at (0.05)	**0.780**	**0.5263**	**0.5937**	**0.6307**	**0.5748**	**0.3741**	**0.4199**	**0.4805**	**0.5044**	**0.3269**	**0.131**	**0.00251**

DH: days to heading, DM: days to maturity, GFP: grain filling period, GY: grain yield, TKW: 1000 kernel weight, AGB: above ground biomass (kgha-1), HI: harvest index, HW: hectoliter weight, TPP: tillers per plant, PH: plant height (cm), SPS: spikelets per spike, KPS: kernels per spike, SL: spike length, SPP, spikes per plant. LSD= list significant difference, CV= coefficient of variations

Appendix 10: Phenotypic mean performance of one hundred twenty-one bread wheat genotypes tested across locations

S. N	Treatment	DH	DM	SD	ST	PH	BY	NT	NSLP	NSS	GY	HI
1	**ETBW6921**	48.33	104.33	77.8333	85.1667	77.4967	189.088	2.4833	16.4333	38.6333	77.42	0.415
2	**EBW7686**	57	104.1667	72.8333	89.3333	83.3333	205.587	2.45	15.3	37.2333	76.8517	0.373333
3	**Galil**	55	101.1667	81.1667	87.8333	73.8833	206.543	1.9	15.4667	37.3333	68.6067	0.33
4	**ETBW6876**	49.83	102.5	76.8333	85.1667	81.2533	161.603	1.9	14.2	36.7	55.445	0.341667
5	**Dereselign**	54.167	102	77.9817	88	94.1	228.227	2.6667	14.2	34.4333	75.7233	0.331667
6	**Sirbo**	62.667	117.8333	82.1667	86	77.7067	193.805	2.1	15.4	32.3	62.1183	0.316667
7	**Ogolcho**	55.833	103.5	76.5	83	82.9333	176.757	2.5667	16.0667	43.4	82.9133	0.47
8	**ETBW7717**	57	104.1667	82	86.6667	87.4667	212.767	2.7333	15.8333	41.9	79.085	0.373333
9	**ETBW6543**	54.833	102.3333	82.1667	78.1667	84.0667	190.922	2.0667	14.8833	40.3667	71.9333	0.376667
10	**ETBW7724**	66	105.3333	76.8333	91.6667	79.8	203.178	1.7	15.9	40.7333	71.2783	0.348333
11	**ETBW6932**	51.833	101.1667	81.1667	86	83.6333	198.127	3.0667	16.7667	42.1	87.665	0.443333
12	**ETBW6875**	51	101.6667	81.3333	81.8333	81.3333	220.393	2.6333	15.8667	38.8	87.1733	0.393333
13	**ETBW6839**	53.333	100.6667	82.1667	82	80.4833	175.1	2.7667	16.4333	36.5667	76.8467	0.435
14	**Hawii**	47.333	97.1667	82.1667	87.5	82.4333	223.755	2.3167	14.8667	32.4	90.4717	0.405
15	**ETBW6373**	44	97.8333	81.1667	88.5	75.28	178.785	2.0667	15.0667	35.3	64.8383	0.361667
16	**ETBW6939**	43.833	97.5	81.6667	78.8333	74.35	162.62	3.0333	14.6833	30.3333	63.7083	0.391667
17	**ETBW6102**	46.833	101.5	81.6667	81	81.6667	209.867	2.9	15.4333	36.45	81.11	0.386667
18	**Tusie**	55.333	104.6667	77.5	86.5	86.2767	242.483	2.5	15.8	39.0333	89.8533	0.37
19	**ETBW6492**	54.167	101.1667	76.8333	86.1667	88.12	232.26	2.1333	15.6	40.8667	82.585	0.355
20	**ETBW6130**	50.667	99.8333	81.6667	79.3333	80.5833	204.465	1.9333	15.2	43.0667	87.71	0.426667
21	**Hidasie**	52.667	100.6667	81.1667	87.8333	82.55	205.835	2.0667	14.9333	42.7667	85.8467	0.416667
22	**ETBW6398**	55.833	103.3333	72	89.1667	86.9133	192.508	2.2667	17.6167	36.6333	69.1867	0.36
23	**ETBW7689**	55.667	102.6667	81.8333	90	82.2333	185.64	2.8	16.7333	39.2333	68.255	0.368333
24	**Dure**	46.333	98.5	81.1667	82.8333	88.7333	182.917	2.3667	15.5667	37	66.2767	0.365
25	**ETBW6315**	59.167	105.3333	77	81	90.1433	196.195	1.9667	17.1333	40.1667	73.9133	0.375
26	**ETBW6840**	51.333	101.5	81.1667	81.8333	79.0667	183.673	2.8667	15.5667	39.4667	73.2833	0.396667
27	**ETBW6174**	53.333	106.1667	77	85.1667	83.7667	230.048	1.8667	16.8333	44.8667	89.445	0.391667
28	**ETBW6647**	54	97.6667	77.5	83.5	80.9967	193.753	2.5333	15.6333	35.6333	78.54	0.405
29	**Bolo**	63.167	116	81.1667	91.6667	100.913	236.893	1.9167	16.45	44.2333	75.2533	0.323333
30	**ETBW6439**	53.667	102	81.6667	83.6667	77.6	262.047	2.4667	13.35	35.6667	82.4567	0.316667
31	**ETBW6953**	51	97.5	81.1667	91.6667	75.7833	215.177	1.9667	16.2333	36.5167	70.595	0.326667
32	**KULKULU**	63.833	114	72.5	90.8333	80.9833	190.857	3	16.9833	37.6667	84.18	0.44
33	**ETBW6406**	45.5	99.1667	81.3333	83.3333	73.7667	186.287	2.2667	15.3667	36.7	72.885	0.391667
34	**ETBW6314**	59.5	110.1667	77	85.1667	87.8	238.667	2.3667	15.2667	36.8	92.315	0.393333
35	**Laketch**	47.5	95.5	81.6667	83.3333	76.7333	182.008	3.3667	15.1667	33.7	58.7533	0.321667
36	**Kubsa**	51.333	96.5	81.8333	91.6667	81.6	251.053	2.3333	14.8333	35.4	93.5533	0.373333
37	**Sofumar**	54.833	101	72.6667	88.3333	90	241.68	2.2667	15.95	35.55	89.665	0.373333
38	**ETBW6852**	51.333	102	82.6667	86.1667	77.6211	202.872	2.9	16.2333	41.8	81.33	0.4
39	**Hoggana**	69	118.3333	76.5	90.8333	86.5667	179.137	2.5333	16.7667	36.1333	64.9383	0.361667
40	**ETBW6496**	57.333	105.1667	81.1667	86.1667	89.1	242.733	2.5667	16.0667	41.65	88.42	0.363333
41	**Millennium**	55.5	102.1667	81.1667	89.1667	88.1	232.662	2.5667	15.1	31.8	88.3217	0.378333
42	**Kakaba**	51	98.5	82.1667	82	84.3667	195.775	3.0333	14.6	39.2333	76.6067	0.395
43	**Tay**	59.833	104.1667	81.6667	90.1667	95.0167	243.955	2.8333	17.9333	43.9667	89.0633	0.366667
44	**ETBW6832**	48.333	99.3333	82.1667	80.8333	80.25	193.85	3.1667	15.1667	36.6333	70.525	0.36
45	**ETBW6506**	49	100.5	78.1667	83.3333	79.3167	225.577	2.2667	15.7333	42.1333	81.23	0.365
46	**ETBW7694**	62.833	107.3333	81.5	86	88.2833	239.105	2.4333	17.2333	51.2	90.3067	0.376667

47	**ETBW6871**	58.333	105.8333	81.1667	78	79.2	178.153	2.5333	16.5667	45.8667	72.4267	0.408333
48	**ETBW7723**	54	104.3333	81.1667	85.8333	82.2667	201.19	2.4333	14.9	38.2	86.3567	0.431667
49	**Pavon76**	52	100.5	82.1667	90.8333	81.6967	223.328	2.6	14.8667	35.1667	87.5533	0.393333
50	**ETBW6169**	52	102.1667	82.4167	80.8333	75.9167	198.61	2.2667	14.9667	39.315	87.9067	0.446667
51	**ETBW6114**	58.167	103.5	78	86.6667	75.1133	244.815	2.9667	16.8167	39.7333	93.475	0.381667
52	**ETBW6837**	48.667	97.5	81.1667	78.8333	76.6917	176.32	2.3667	15.1333	39.3333	62.6033	0.355
53	**ETBW6948**	59	109.8333	82.1667	84.3333	83.1667	214.55	1.9333	19.45	41.8	76.4133	0.356667
54	**ETBW6911**	60.667	115	81.6667	89.1667	94.2667	214.655	1.9667	17.4333	40.7	75.8567	0.35
55	**ETBW6890**	51	100.5	76.6667	85.8333	76.0667	200.475	2.0667	16	38.2	86.04	0.431667
56	**ETBW6095**	53	100.8333	72.8333	86.1667	81.5	194.167	2.2667	15.8	38.1667	69.5283	0.356667
57	**ETBW6847**	47.667	98.6667	82.5	82.5	78.4167	150.755	2.4667	17.1667	51.2	60.3433	0.4
58	**Dashen**	62.833	116.3333	82	83.9033	82.0117	177.458	2.3667	18.3	36.2717	62.83	0.353333
59	**Mitike**	50.5	102.5	72.5	86.6667	97.0333	216.93	2.4667	17.3	38.3667	61.18	0.285
60	**ETBW6943**	52	101.5	77.6667	82.1667	85.3333	207.205	2.3667	16.2	39.9333	68.065	0.328333
61	**Meraro**	64	116.5	76.6667	90.8333	76.7333	188.902	2.1667	17.9667	42.8667	63.2283	0.336667
62	**ETBW6866**	49.167	100.5	77.1667	81.6667	77.6333	184.713	3.0667	15.7	34.6333	79.2167	0.43
63	**Galema**	68.333	104.3333	76.6667	91.6667	87.35	212.328	2.3667	15.3167	22.5333	73.3267	0.343333
64	**KBG01**	47.5	101.1667	82	84.8333	75.2667	175.762	2.1667	15.7	44.3	67.2667	0.385
65	**Dinknesh**	46.833	105	82.3333	83.6667	84.05	201.353	2.5667	17.0167	40.1333	83.925	0.416667
66	**ETBW6101**	52.833	99.5	76.8333	86.1667	84.2967	217.28	2.4667	16.7333	43.4667	88.5033	0.41
67	**ETBW6850**	46	97.5	81.3333	84.5	72.3667	154.242	2.4667	14.4	35.4667	63.4933	0.41
68	**ETBW7688**	54.5	102.1667	81.3333	89.3333	81.2667	224.667	1.9667	16.6333	35.3	85.3483	0.38
69	**Doddota**	52.667	102.5	72.6667	84.5	80.7333	199.513	1.4667	14.5	34.1	75.73	0.378333
70	**ETBW6212**	55.833	104.5	77	85.8333	79.8167	201.86	2.4667	16.2667	34.7667	84.73	0.421667
71	**ETBW7692**	56.333	102.3333	82.8333	87	83.0333	170.91	2.4667	17.4667	39.9	58.6067	0.343333
72	**ETBW6404**	47.833	106.1667	77.3333	86.8333	78.1	184.92	1.7667	16.6667	39.6	68.7667	0.371667
73	**K6290Bulk**	50.667	98.3333	82.8333	87.8333	100.183	202.335	1.9333	15.65	38.2	78.5317	0.396667
74	**ETBW6882**	50.667	102.1667	72.5	80.1667	76.1	207.118	2.2667	15.8333	39.3333	69.095	0.333333
75	**ETBW6445**	62.167	117	81.5	85.3333	95.3167	233.665	2.3667	18.2	44.9667	77.1433	0.331667
76	**Huluka**	68.833	117.8333	77.1667	89.5	89.15	234.092	2.0667	16.9333	44.0667	82.5933	0.353333
77	**ETBW6869**	50.833	99.3333	76.6667	85.1667	82.6567	159.247	2.3667	16.6333	28.7	66.895	0.415
78	**ETBW6883**	49.167	97.5	81.8333	79.6667	77.3	192.29	2.6667	15.7	41.2667	68.9033	0.356667
79	**Menze**	64.5	117.3333	82.8333	92.6667	98.15	271.295	2.0667	16.1167	40.8333	97.3683	0.361667
80	**Shorima**	53.833	101.5	81.3333	86.1667	86.7333	201.288	2.4667	15.6667	34.9	76.55	0.378333
81	**Bobitcho**	56.333	105.8333	80.315	92.9817	87.2633	217.803	1.9667	16.2833	44.0783	89.4067	0.411667
82	**ETBW7693**	54	101.1667	81.3333	84.1667	84.5667	222.437	2.2667	14.7333	38.5667	85.6683	0.383333
83	**ETBW6688**	57	103.8333	81.3333	82.1667	87.9333	218.698	2.2667	18.3	45.0333	81.6383	0.375
84	**ETBW6107**	51.333	98.6667	82.3333	85.3333	76.8667	202.44	3.1183	15.6667	39.7	70.9117	0.351667
85	**K62904A**	52.667	101.6667	83	86	104.083	245.438	2.2667	14.25	40.0667	89.02	0.36
86	**ETBW7730**	56.333	100.8333	77.1667	82.1667	82.6233	199.61	2.7667	16.2333	43.6333	71.2	0.356667
87	**ETBW6167**	52.167	102.6667	82.3333	81.3333	86.8433	195.392	2.7667	15.2667	41.3333	81.0367	0.411667
88	**ETBW6529**	51	101.6667	72.6667	73.8333	78.3867	189.972	3.4	15.0333	33.1667	75.455	0.393333
89	**ETBW6518**	59.333	106	82.3333	84.8333	83.5333	200.797	2.3667	18.05	39.8667	63.7733	0.316667
90	**ETBW6109**	57.333	104.1667	82	80	84.2467	216.695	2.0667	14.9667	37.5833	80.2267	0.371667
91	**ETBW6845**	49	98.8333	82.2833	86	72.8833	216.108	2.3667	15.8667	34.9667	86.6483	0.403333
92	**QUIAU#2(GAMBO)**	57.5	103.5	82	87.5	89.1333	257.977	2.8667	16.1333	37.9	89.9383	0.35
93	**Simba**	51	102.3333	82.3333	89.1667	80.5833	223.523	2.7667	16.5333	31.6667	88.385	0.4
94	**MadaWalabu**	51.833	103.5	81.3333	86.8333	83.8833	228.33	2.9667	14.7	49.3333	86.9983	0.383333
95	**ETBW7695**	63.667	103.6667	77.1667	83.5	81.6033	211.543	2.1667	17.4667	43.2167	83.0483	0.393333
96	**ETBW6862**	52.333	110.1667	77.6667	81.3333	83.7	220.695	2.3667	18.2333	43	82.53	0.373333
97	**ETBW6848**	45	99.6667	72.6667	79.1667	76.6	184.962	3.1667	13.8	36.6	80.0483	0.435
98	**ETBW6853**	49.5	100	82.3333	84.3333	74.1	204.177	2.1667	15.3667	40.5667	69.2883	0.341667
99	**Tossa**	52.833	102	82.3333	89.1667	83.2333	207.173	2.6667	14.5667	32.4333	81.7467	0.393333
100	**ETBW6393**	45	99.3333	76.6667	81	69.7667	183.09	1.9667	14.7333	33.7333	66.35	0.363333
101	**Abola**	53.5	105.6667	81.8333	89	87.18	263.862	2.3667	16.3	39.1633	97.35	0.37
102	**Danda'a**	60.5	116.8333	81.8333	88.26	93.1	223.518	2.61	16.4	41.8833	78.8017	0.353333
103	**ETBW7696**	65.333	109.6667	81.8333	87.5	74.55	206.018	2.2667	17.6	40.6667	71.14	0.348333
104	**ETBW6696**	55	105.6667	81.8333	87.8333	87.8	245.135	1.7667	15.3333	36.6	95.4033	0.391667
105	**Katar**	50.833	102.1667	80.5	81.5	89.8833	227.378	1.7667	15.3333	39.0333	84.21	0.37
106	**ETBW6947**	60.667	104.5	76.6667	82.1667	81.46	230.163	2.3667	15.1333	33.1333	87.5767	0.38
107	**ETBW5879**	57	104.3333	83.3333	85.1667	79.2833	224.76	2.6	15.4333	35.5	83.26	0.368333
108	**ETBW6928**	56.833	112.3333	76.6667	81.5	84.2	220.922	4	18.8	44.8	78.2467	0.355
109	**Gasay**	55.833	105.1667	76.6667	87.8333	87.8667	223.18	2.8667	16.1	36.6333	81.7383	0.365
110	**ET13A2**	58.167	107	81.3333	87	102.5	225.898	2.5667	16.4333	35.4	80.8017	0.363333
111	**ETBW6256**	54.5	102.6667	77.1667	86.1667	82.4	218.925	2.6667	16.9667	34.6	79.795	0.363333
112	**ETBW6937**	52.833	101.6667	72.8333	84.5	84.05	195.23	2.1667	16.7167	40.5333	82.3817	0.426667
113	**ETBW7698**	58.833	104.1667	76.5	83.1667	85.5	228.1	3.0667	17.2667	36.8333	90.1	0.395
114	**Sulla**	45.5	96.8333	76.5	81.6667	85.5533	230.128	1.9667	15.4	34.9667	91.1233	0.398333
115	**Digelu**	65.833	117.5	77.6667	88.3333	103.567	219.035	2.6667	17.4333	49.3333	86.6133	0.395
116	**ETBW7690**	51.833	103.1667	82.3333	86.6667	85.1	226.072	2.3667	17.2667	43.4333	85.1967	0.376667
117	**ETBW6886**	63	107.5	81.8333	84.8333	85.5667	227.592	1.9667	16.8917	39.0667	85.8617	0.373333
118	**ETBW6841**	52.667	95.8333	82.3333	87.1667	83.4833	222.81	3.2667	15.6667	39.1333	88.4317	0.396667
119	**ETBW6861**	52.667	104.6667	81.8333	88.3333	89.0967	195.273	2.9667	15.5333	36.1	81.7267	0.418333
120	**Enkoy**	47.833	101.1667	81.5	88.3333	91.9667	250.405	2.1667	13.7667	37.2333	87.5683	0.353333
121	**ETBW6427**	66.167	107.6667	82.5	83.8333	91.0333	244.733	2.7667	16.8	43.9667	76.8633	0.313333
	CV	**0.8435**	**0.458435**	**0.60722**	**0.60576**	**0.77251**	**1.47634**	**9.3263**	**2.30508**	**1.46794**	**1.05232**	**1.000008**
	LSD at (0.05)	**1.1752**	**1.2177**	**1.2378**	**1.3242**	**1.6552**	**7.922**	**0.5831**	**0.9455**	**1.458**	**2.1211**	**0.0097**

DH: days to heading, DM: days to maturity, GFP: grain filling period, GY: grain yield, TKW: 1000 kernel weight, AGB: above ground biomass (kgha-1), HI: harvest index, HW: hectoliter weight, TPP: tillers per plant, PH: plant height (cm), SPS: spike-lets per spike, KPS: kernels per spike, SL: spike length, SPP, spikes per plant. LSD= list significant difference, CV= coefficient of variations

Appendix 11: Analysis of variance for seven characteristics of bread wheat genotypes for grain quality tested at Adet analyzed as Simple-Lattice Design

	Groups					
	Replication	**Block (Replication)**	**Genotype**	**Error**	**Mean**	**CV (%)**
Characters	**DF = 1**	**DF =20**	**DF = 120**	**DF = 100**		
TGW	0.619081	0.457499	23.194869	0.269557	33.32975	1.557735
HLW	0.0149174	0.4751119	5.7328752	0.2594624	74.21537	0.686346
MOC	0.3800335	2.6953128	2.3296941	0.2948735	13.74616	3.950359
Prot	1.8188446	0.2537028	1.3566567	0.2203610	12.71678	3.691393
Starch	1.0120764	0.3052228	5.3093261	0.3375332	65.41731	0.888107
GLU	1.1538186	0.3520895	6.0850027	0.3786504	26.27996	2.341502
Zele	3.714051	0.289769	27.447791	0.422939	33.95876	1.915080

*Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively.CV= coefficient of variations and DF= degree freedom*

Appendix 11: Analysis of variance for seven characteristics of bread wheat genotypes for grain quality tested at Debre Tabor analyzed as Simple-Lattice Design

	Groups					
	Replication	**Block (Replication)**	**Genotype**	**Error**	**Mean**	**CV (%)**
Characters	**DF = 1**	**DF =20**	**DF = 120**	**DF = 100**		
TGW	0.001438	0.670429	16.431887	0.616920	28.45864	2.759945
HLW	2.771942	0.241033	13.999215	0.200324	68.12273	0.657014
MOC	0.04500000	0.10563636	0.12983333	0.05967273	11.99876	2.035877
Prot	0.3651240	0.2824876	1.4170255	0.0807512	10.49587	2.707424
Starch	0.0874380	0.1869835	7.5759835	0.131729	65.70661	0.552372
GLU	2.923802	0.334165	14.075968	0.176729	21.05372	1.996756
Zele	1.324008	0.301872	42.065592	0.138036	27.37149	1.357366

*Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively.CV= coefficient of variations and DF= degree freedom*

Appendix 12: Analysis of variance for twelve characteristics of bread wheat genotypes for grain quality tested at Kulumsa analyzed as Simple-lattice design

	Groups					
	Replication	**Block (Replication)**	**Genotype**	**Error**	**Mean**	**CV (%)**
Characters	DF = 1	DF =20	DF = 120	DF =100		
TGW	0.00350	0.10389	116.07966	0.08214	57.79364	0.495890
HLW	0.018572	0.134706	16.687760	0.185935	23.41182	1.841813
MOC	0.0125107	0.0606735	1.1932873	0.0616232	10.28017	2.414749
Prot	0.0005355	0.0105537	1.3397219	0.0204319	11.81876	1.209435
Starch	0.000026	0.090835	41.034405	0.082443	64.35074	0.446193
GLU	0.000992	0.061310	9.545163	0.063680	20.52988	1.229174
Zele	0.107479	0.110100	24.352494	0.175247	26.84785	1.559251

Note, ** and * indicates highly significant at (1%) and significant at (5%) probability levels, respectively.CV= coefficient of variations and DF= degree freedom

Appendix 13: Mean performance of one hundred twenty-one bread wheat genotypes for grain quality characteristics tested at Adet

S.N.	Treatment	TGW	HLW	MC	Protein	Starch	Gluten	Zeleny
1	**ETBW6921**	38.2	73.88	13.4	13.15	66.35	25.85	35.75
2	**EBW7686**	33.4	74.46	12.7	13.1	64.8	26.05	33.6
3	**Galil**	29.1	74.81	12.9	12.9	64.65	25	33.4
4	**ETBW6876**	37.8	67.77	12.6	14.35	61.7	25.45	33.65
5	**Dereselign**	30.3	73.30	13.25	13.75	65.2	26.5	34.55
6	**Sirbo**	25.15	74.58	15.15	12.55	66.45	27.3	36.2
7	**Ogolcho**	34.3	75.60	13.05	12.3	64.15	24.6	29.15
8	**ETBW7717**	34.25	74.59	12.55	13.25	63.8	24.5	33.85
9	**ETBW6543**	36.2	74.25	12.2	12.45	64.45	25.85	33.3
10	**ETBW7724**	27.95	73.26	12.7	13	65.45	29.6	37.5
11	**ETBW6932**	37.6	75.53	11.95	12.45	63.6	25.25	31.8
12	**ETBW6875**	35.55	75.54	15.45	12.75	64	24.5	35.45
13	**ETBW6839**	34.85	73.48	14.3	12.7	67.2	27.25	33.9
14	**Hawii**	35.8	73.73	13.95	12.85	64.4	26.2	33.85
15	**ETBW6373**	34	72.56	14.5	12.25	65.25	24.35	33.25
16	**ETBW6939**	34.85	73.44	14.3	12.7	67.2	27.25	33.9
17	**ETBW6102**	35.55	74.93	13.15	13.4	64.1	27.05	35.4
18	**Tusie**	29.55	74.98	14.7	11.75	67.35	23.25	30
19	**ETBW6492**	34.5	74.08	12.45	10.15	68.15	21.95	23.55
20	**ETBW6130**	32.85	73.06	12.3	12.25	65.3	27.25	30.25
21	**Hidasie**	38.6	73.11	13.95	12.45	63.15	26.35	28.85
22	**ETBW6398**	34.85	74.56	14.87	13.4	66.4	27.45	37.3
23	**ETBW7689**	32.7	73.28	12.1	12.95	64	27.15	34.5
24	**Dure**	34	77.63	15.75	13.45	62.1	26.35	36.65
25	**ETBW6315**	34.95	74.41	13.45	12.2	63.4	23.15	29.955
26	**ETBW6840**	36.85	72.30	11.5	13	64.85	27.3	35.5
27	**ETBW6174**	31.7	76.08	12.25	11.8	67.55	24.51	32.55
28	**ETBW6647**	39.05	74.92	13.35	12.35	64.1	27.25	32.8
29	**Bolo**	28.9	73.31	15.515	10.2	70.445	21.825	23.7
30	**ETBW6439**	36.5	73.42	14.4	12.45	65.5	24.05	27.3
31	**ETBW6953**	26.45	75.15	12.8	13.2	64.55	27.2	36.55
32	**KULKULU**	26.6	70.24	12.45	14.75	65.2	28.45	33.55
33	**ETBW6406**	38.2	72.87	13.45	14.6	61.85	28.2	39.15
34	**ETBW6314**	34.2	76.72	15.5	11.95	66.45	24.15	32.85
35	**Laketch**	27	74.82	13.3	12.85	65.6	26.65	38.05
36	**Kubsa**	32.45	72.75	15.5	11.35	69.4	24.15	31.95
37	**Sofumar**	33.5	76.15	13.3	12.4	62.75	25.3	29.95
38	**ETBW6852**	34.3	73.47	14.85	11.3	69.2	24.45	29.6
39	**Hoggana**	22.5	70.37	15.25	12.15	66.35	26.5	30.05
40	**ETBW6496**	33.75	75.87	13.25	12.1	66.6	26.95	31.95
41	**Millennium**	30.65	75.92	12.55	12.6	65.35	26.2	32.6
42	**Kakaba**	34.65	74.63	13.2	13.4	66	27.55	38.6
43	**Tay**	32.2	73.85	13.05	12.7	63.2	23.85	29.85
44	**ETBW6832**	37.45	74.80	12.7	13.25	63.8	26.4	38.2
45	**ETBW6506**	39.8	73.54	15.55	13.85	64.95	29.4	35.3

46	**ETBW7694**	33.55	73.46	13.2	11.5	64.7	26.55	26.95
47	**ETBW6871**	35.25	73.65	13.65	12.5	66.75	31.35	35.75
48	**ETBW7723**	33.65	74.96	14.7	12.2	66.05	28.05	36.25
49	**Pavon76**	30.2	75.29	15.4	12	67.35	27.7	34.75
50	**ETBW6169**	33.05	78.54	15.3	12.85	63.95	25.65	34.75
51	**ETBW6114**	32.85	75.28	13.75	12.65	65	26.25	32.25
52	**ETBW6837**	33.8	74.88	13.3	11.65	67.3	26.25	32.55
53	**ETBW6948**	32.9	76.53	12.25	13.05	63.85	26.9	36.25
54	**ETBW6911**	35.3	71.47	12.95	12.45	64.65	25.8	31.7
55	**ETBW6890**	36.05	77.01	13.65	13.65	65.3	28.8	40.2
56	**ETBW6095**	32.45	73.72	12.2	12.6	65.35	25.95	35.25
57	**ETBW6847**	29.85	72.32	13.8	12	66.35	25.75	33.2
58	**Dashen**	26.85	73.43	14.85	12.25	63.7	25.2	26.85
59	**Mitike**	30.55	75.87	13.1	11.8	66.85	25.4	32.95
60	**ETBW6943**	32.65	74.07	12.1	12.75	63.7	25.6	32.65
61	**Meraro**	25.55	74.37	14.2	12.95	65	27.2	33.3
62	**ETBW6866**	34.1	76.75	14.45	14.15	63.05	26.65	37.2
63	**Galema**	39.15	74.47	13.15	11.05	66.75	23.75	29.1
64	**KBG01**	24.95	74.73	15.8	13.5	63.65	24.35	37.5
65	**Dinknesh**	37.55	74.20	14.95	14.85	63.05	23.35	31.65
66	**ETBW6101**	32.55	74.35	15.5	11.75	67.6	25.1	37.2
67	**ETBW6850**	33.55	74.59	14.85	12.5	67.6	26.7	38
68	**ETBW7688**	34.2	74.97	13.3	13.6	63.2	25.9	34.4
69	**Doddota**	32.7	74.57	19.95	12.6	64.5	26.7	28.75
70	**ETBW6212**	34.2	69.65	14.15	14.05	63.35	24.85	32.55
71	**ETBW7692**	39.3	75.19	13	12.5	65.3	25.8	35.85
72	**ETBW6404**	30.35	71.14	13.05	12.3	65.7	27.39	32.425
73	**K6290Bulk**	28.3	75.55	15	13.3	67.2	29	39
74	**ETBW6882**	38.65	72.62	14.55	13.4	64.8	26.45	36.75
75	**ETBW6445**	36.25	72.94	13.15	13.05	62.9	24.25	31.45
76	**Huluka**	29.35	74.62	12.8	11.75	65.95	23.85	30.55
77	**ETBW6869**	35.7	73.69	12.9	14.1	65.6	30.3	43.1
78	**ETBW6883**	38.45	75.23	13.55	13.05	65.75	27.8	36.6
79	**Menze**	33.05	75.60	15.95	12.75	64.55	26.55	28.1
80	**Shorima**	28.85	74.14	14.15	11.85	67.2	24.75	32.1
81	**Bobitcho**	32.2	73.60	14.4	12.99	66.65	25.8	34.69
82	**ETBW7693**	31.9	68.42	13.8	12.7	65.45	25.95	33.55
83	**ETBW6688**	35.15	74.27	13.3	12.35	66.95	26.5	33.6
84	**ETBW6107**	32.1	77.15	13.05	12.45	65.8	29.15	33.05
85	**K62904A**	28.3	75.22	15	13.3	67.2	29	39
86	**ETBW7730**	26.9	74.24	14.6	12.95	64.6	26.5	32.8
87	**ETBW6167**	35.8	75.99	13.95	12.95	66.4	29.6	38.15
88	**ETBW6529**	42.35	71.91	13.25	14.65	63.2	31.95	47.45
89	**ETBW6518**	36.25	76.09	14.55	12.55	66.9	26.25	34.8
90	**ETBW6109**	37.6	72.32	12.7	13	62.85	24.5	32.25
91	**ETBW6845**	32.6	76.10	12.55	13	68.3	25.2	38.4
92	**QUIAU#2(GAMBO)**	37.1	75.70	13.5	11.7	66.15	24.95	32.15
93	**Simba**	35.3	76.57	13.3	13.25	65.4	28.3	35.8
94	**Mada Walabu**	38	73.14	14.65	12.95	66.75	26.8	34.45
95	**ETBW7695**	31.1	69.61	13.65	13.25	65.45	26.2	35.45
96	**ETBW6862**	32.7	73.03	13.65	12.45	65.9	24.8	33.55
97	**ETBW6848**	30.8	73.72	13.55	13.15	66.1	27.6	37.35
98	**ETBW6853**	33.25	69.75	13	13.75	62.8	27.6	38.15
99	**Tossa**	29.45	76.04	13.35	12.5	65.4	25.75	35
100	**ETBW6393**	35.85	74.26	13.1	14.7	62.65	28.7	44.35
101	**Abola**	29.25	76.19	15.55	12.45	66.2	25.75	35.84
102	**Danda'a**	37.8	72.14	13.25	13.24	65.5	25.55	33.45
103	**ETBW7696**	32.45	74.31	12.8	12.25	65.25	26.7	31.15
104	**ETBW6696**	33.95	74.06	14.15	11.7	66.5	24.8	31.1
105	**Katar**	34.1	75.29	15.05	12.3	68.7	27.4	36.55
106	**ETBW6947**	33.6	76.91	12.85	12.5	65.7	27.3	32.7
107	**ETBW5879**	35.25	75.46	13.65	11.75	66.9	25.2	32
108	**ETBW6928**	32.55	71.77	12.4	12.25	64.95	27.55	32.35
109	**Gasay**	30	74.81	14.35	11.05	67.8	23.4	28.6
110	**ET13A2**	31.65	74.24	13.45	13.35	66.25	30.05	38.75
111	**ETBW6256**	36.7	75.47	12.5	13.65	64.45	28.8	38.6
112	**ETBW6937**	31.3	73.37	14.55	12.6	66	27.75	37.4
113	**ETBW7698**	35.5	74.85	13.15	12.85	65.55	25.5	35.55
114	**Sulla**	34	75.59	14	12.6	66.6	26.75	35.3
115	**Digelu**	34.1	74.34	12.85	12.15	64.85	23.2	27.9
116	**ETBW7690**	33.75	73.94	14	12.4	65.35	25.7	32.45
117	**ETBW6886**	32.15	77.29	13	11.5	66.2	24	29.75
118	**ETBW6841**	36	73.82	14.45	12.35	66.5	25.5	35.3
119	**ETBW6861**	32.25	74.29	12.65	13.9	60.6	25.35	29.85
120	**Enkoy**	29.65	75.77	13.75	14.45	66.45	31.2	44.75
121	**ETBW6427**	32.95	73.14	14	11.15	68.45	23.65	28.2
	CV	**1.56**	**0.686**	**3.95**	**3.69**	**0.888**	**2.342**	**1.915**
	LSD at (0.01)	**1.36**	**1.3872**	**1.42**	**1.229**	**1.521**	**1.611**	**1.702**
	at (0.05)	**1.03**	**1.0481**	**1.075**	**0.29**	**1.15**	**1.218**	**1.288**

TGW: 1000 grain weight, HIW: hectoliter weight, Prot.: Protein content, Starch: Starch content, Glue: Gluten content and Zele: Sedimentation volum content. LSD= list significant difference, CV= coefficient of variations

Appendix 14: Mean performance of one hundred twenty-one bread wheat genotypes for grain quality characteristics tested at Debre Tabor

S.N.	Treatment	TGW	HLW	MC	Protein	Starch	Gluten	Zeleny
1	ETBW6921	30.55	68.75	11.523	10.820	67.15	20.823	28.619
2	EBW7686	27.35	66.85	11.762	10.298	66.55	20.793	29.603
3	Galil	25.25	67.8	12.305	10.045	67.9	18.884	25.953
4	ETBW6876	26.85	66.45	12.236	11.231	67	24.500	33.029
5	Dereselign	26.4	66.85	11.908	11.950	66.1	26.134	33.155
6	Sirbo	21.85	68.3	11.935	10.002	66.1	18.780	26.297
7	Ogolcho	30.95	70.4	11.828	9.537	66.4	17.387	24.105
8	ETBW7717	28.7	64.9	11.936	9.620	65.9	15.697	22.593
9	ETBW6543	34.25	71.65	11.693	9.799	66.2	18.344	24.659
10	ETBW7724	23.7	66.45	12.331	9.383	68	18.154	23.306
11	ETBW6932	33.05	69.2	11.730	11.206	64.25	21.934	27.586
12	ETBW6875	28	65.6	11.962	10.880	65.2	20.094	28.543
13	ETBW6839	31	70.6	11.887	11.493	64.5	23.774	26.790
14	Hawii	31.55	68.85	12.174	11.646	64.2	23.234	28.746
15	ETBW6373	24	65.25	12.066	10.749	65.1	20.820	27.434
16	ETBW6939	33.15	71.25	11.867	11.379	67.25	24.590	29.766
17	ETBW6102	32.05	70.65	12.444	11.145	64.25	22.983	29.190
18	Tusie	24.45	69.2	11.790	9.847	67	17.774	24.792
19	ETBW6492	27.05	64.7	12.410	10.784	65.35	21.877	30.342
20	ETBW6130	27.3	66	12.268	10.968	64.85	21.937	27.930
21	Hidasie	33.3	66.45	11.762	10.353	66.85	19.824	26.073
22	ETBW6398	28.05	65.65	11.805	11.018	65	21.713	29.256
23	ETBW7689	26.7	67.3	12.534	10.239	66.35	20.160	27.969
24	Dure	27	74.15	12.009	11.252	65.35	22.890	30.316
25	ETBW6315	29.4	67.8	11.990	8.927	65.15	15.203	17.356
26	ETBW6840	31.1	63.1	12.088	10.908	65.15	22.536	29.560
27	ETBW6174	28.5	70.95	12.016	9.555	66.55	17.899	25.566
28	ETBW6647	32.9	67.9	11.711	11.207	64.1	23.389	29.618
29	Bolo	25.75	66.75	12.626	8.927	70.05	18.029	18.232
30	ETBW6439	27.95	64.35	12.282	10.094	66.05	19.293	25.668
31	ETBW6953	21.25	69.1	11.834	10.912	64.55	21.740	31.149
32	KULKULU	26.35	67.7	12.039	10.638	65.35	20.606	24.992
33	ETBW6406	32.4	71.15	12.296	11.005	66.35	23.700	29.522
34	ETBW6314	30.45	70.85	12.410	8.645	66.2	14.425	18.286
35	Laketch	24.7	73.5	12.142	11.661	61.45	25.014	27.033
36	Kubsa	26.9	64.55	12.214	10.315	64.95	20.901	21.677
37	Sofumar	28.7	70.45	12.203	9.683	67.15	17.344	23.449
38	ETBW6852	27.75	65	11.735	10.508	66	21.105	28.182
39	Hoggana	26.45	69.2	12.188	9.363	65.95	18.754	18.185
40	ETBW6496	29.7	70.15	12.408	10.700	66.6	22.408	26.685
41	Millennium	30.2	74.3	11.872	9.962	66.75	17.565	21.539
42	Kakaba	30.85	65	11.765	10.144	66.85	18.921	26.009
43	Tay	26	67.7	12.216	9.533	66.95	17.118	22.973
44	ETBW6832	26.45	67.45	12.010	10.619	67.35	22.205	30.715
45	ETBW6506	31.75	66.7	11.784	10.828	66.15	23.494	30.617
46	ETBW7694	26.05	62.85	11.795	9.100	66.75	16.074	21.283
47	ETBW6871	31.15	68	11.507	11.811	64.1	25.451	32.843
48	ETBW7723	30.25	67.25	12.257	10.132	67.4	21.631	26.811
49	Pavon76	25.2	65.95	12.377	10.725	66.15	21.335	30.816
50	ETBW6169	30.8	74.05	12.003	11.262	64.75	24.005	32.420
51	ETBW6114	28.2	68.85	11.850	10.817	64.5	20.988	30.569
52	ETBW6837	26.2	63.65	11.780	12.530	63.7	28.384	39.619
53	ETBW6948	27.35	71.7	11.864	10.279	66.45	20.795	27.873
54	ETBW6911	26.6	60.2	11.858	9.450	65.45	18.048	20.957
55	ETBW6890	32.4	71.25	11.802	11.686	65.25	23.935	33.999
56	ETBW6095	31.55	72.2	11.704	10.847	65.1	22.479	31.714
57	ETBW6847	29.6	70.25	12.084	10.898	65.55	23.480	31.320
58	Dashen	27	68.5	11.827	11.931	60.7	20.686	24.040
59	Mitike	22	67.25	11.778	10.570	67.4	22.133	30.054
60	ETBW6943	29.9	69.6	12.170	10.636	65.85	22.173	29.716
61	Meraro	23.15	69.45	11.949	11.299	64.15	23.419	32.216
62	ETBW6866	30.55	72.15	12.214	10.620	66.35	22.759	27.730
63	Galema	24.6	70.5	12.097	11.295	64.15	21.920	28.464
64	KBG01	20.8	65.35	11.872	12.682	63.95	26.540	38.467
65	Dinknesh	32.75	68	12.272	10.805	49.75	21.320	24.297
66	ETBW6101	26.9	64.5	11.926	10.351	66.15	21.116	29.208
67	ETBW6850	30.9	70.7	11.860	11.190	65.9	24.579	32.037
68	ETBW7688	27.6	67.3	12.178	9.964	66.05	19.117	26.153
69	Doddota	24.5	64.55	12.640	10.796	65.05	22.824	27.231
70	ETBW6212	30.5	67.7	12.391	10.725	67.3	22.394	25.513
71	ETBW7692	29.8	65.35	12.013	10.494	65.8	21.428	30.589
72	ETBW6404	28.35	69.15	11.968	10.292	66.1	20.837	27.437
73	K6290Bulk	28.3	68.35	12.136	11.577	65.35	24.349	30.590
74	ETBW6882	30.4	68.85	11.842	10.414	65.65	20.841	27.377
75	ETBW6445	32.15	66.85	11.698	9.243	65.2	16.839	21.243

76	Huluka	24.8	67.65	12.036	8.800	65.65	15.379	20.420
77	ETBW6869	30.65	71.05	11.634	11.481	65.15	24.732	33.389
78	ETBW6883	28.65	65	11.876	9.892	66.9	20.318	28.410
79	Menze	26.8	68.5	11.952	8.570	69.45	18.214	19.820
80	Shorima	26.85	71.2	11.718	9.009	67.75	16.658	22.722
81	Bobitcho	25.6	66	12.170	10.804	65.85	21.625	28.523
82	ETBW7693	27.5	64.95	11.862	9.792	66.2	19.144	25.236
83	ETBW6688	28.05	65.05	12.120	10.927	65.6	23.105	30.853
84	ETBW6107	27.3	69.5	11.695	10.367	66	23.155	27.769
85	K62904A	27.9	69.25	12.024	10.473	68	22.651	27.414
86	ETBW7730	23.3	66.05	11.798	11.122	63.9	22.854	31.422
87	ETBW6167	36.55	74	12.132	11.020	65.75	24.665	34.326
88	ETBW6529	37.5	70.65	11.875	11.303	65.4	25.021	32.546
89	ETBW6518	31.95	71.15	12.138	10.151	67	21.297	28.448
90	ETBW6109	29.2	66.25	12.130	11.905	63.7	25.182	33.335
91	ETBW6845	30.8	73.25	11.908	12.251	64.8	26.095	35.242
92	QUIAU#2(GAMBO)	27.95	64.9	11.826	10.435	64.7	19.656	27.744
93	Simba	30	69.9	11.476	12.908	60.05	27.986	32.574
94	MadaWalabu	33.4	62.65	11.403	10.853	62.95	23.586	28.893
95	ETBW7695	26.65	65.25	11.681	10.834	64	19.752	29.667
96	ETBW6862	25.05	62.9	12.182	10.073	65.9	19.549	25.081
97	ETBW6848	28	67.8	12.118	10.423	65.35	23.175	30.757
98	ETBW6853	27.4	65.8	12.201	10.848	66.6	23.686	30.891
99	Tossa	25.6	69	12.174	10.540	66.25	21.139	29.643
100	ETBW6393	25.25	68.05	12.126	11.549	64.95	24.433	32.001
101	Abola	25.4	68.1	12.082	10.837	67.3	19.776	29.338
102	Danda'a	32.50	67.15	12.276	9.373	65.15	17.263	22.730
103	ETBW7696	27.45	69.55	12.201	10.812	63.95	21.013	25.897
104	ETBW6696	30.15	70.35	11.888	10.066	65.8	19.423	26.354
105	Katar	25.75	67.45	11.980	10.419	67.25	20.459	28.542
106	ETBW6947	28.9	69.05	11.603	10.417	65.35	19.412	30.200
107	ETBW5879	31.95	70.5	11.708	9.315	66.5	16.772	23.398
108	ETBW6928	26.15	64.3	11.681	10.798	64.45	20.629	29.774
109	Gasay	27.8	69.75	12.374	8.854	67.8	16.766	20.100
110	ET13A2	30.1	70.2	12.018	9.537	68.05	20.751	24.014
111	ETBW6256	32.4	70.3	12.086	10.098	66.75	19.368	25.601
112	ETBW6937	30.9	70.1	11.972	11.298	65.8	23.944	28.727
113	ETBW7698	32.6	71.6	11.735	11.359	63.9	22.721	30.486
114	Sulla	28.4	67.85	10.757	10.328	66.25	20.254	10.462
115	Digelu	27.8	65.25	11.962	8.176	69.6	16.514	17.011
116	ETBW7690	30.75	69.65	12.392	9.527	65.95	16.715	22.017
117	ETBW6886	26.35	70.6	11.878	9.215	67.1	16.008	21.312
118	ETBW6841	28.45	65.35	12.580	10.834	66.75	21.655	42.143
119	ETBW6861	28.6	68.75	12.205	9.773	68.65	19.205	22.460
120	Enkoy	28.95	73.05	12.184	10.630	68.6	23.201	26.354
121	ETBW6427	25.95	61	12.330	7.810	67.25	15.975	12.264
	CV	2.76	0.66	2.0359	2.707	0.553	1.997	1.357
	LSD at (0.01)	2.06	1.17	0.6643	0.7894	0.95	1.1464	1.0188
	at (0.05)	1.56	0.89	0.5019	0.5964	0.7186	0.8662	0.7697

TGW: 1000 grain weight, HlW: hectoliter weight, Prot.: Protein content, Starch: Starch content, Glue: Gluten content and Zele: Sedimentation volum content. LSD= list significant difference, CV= coefficient of variations

Appendix 15: Mean performance of one hundred twenty-one bread wheat genotypes for grain quality characteristics tested at Kulumsa

S.N.	Treatment	HLW	TGW	Protein	MoC	Starch	W. Glue	Zeleny
1	ETBW6921	28.095	61.85	11.85	10.66	66.42	22.495	29.47
2	EBW7686	22.55	64	11.85	10.13	66.645	19.305	25.635
3	Galil	25.245	66.405	12.225	10.67	66.26	21.68	29.18
4	ETBW6876	24.01	48.03	12	11.21	67.24	25.345	32.47
5	Dereselign	22.35	60.73	12.05	10.485	66.13	22.825	29.62
6	Sirbo	20.245	45.47	12.075	10.305	65.52	21.775	29.365
7	Ogolcho	28.035	64.705	12	10.14	66.105	19.545	26.435
8	ETBW7717	23.215	45.38	12.175	9.765	66.885	17.755	25.335
9	ETBW6543	25	64.28	12.15	9.975	66.275	19.245	26.575
10	ETBW7724	19.735	60.82	12.175	8.745	68.73	17.545	19.885
11	ETBW6932	23.495	59.955	11.975	10.76	65.14	21.505	28.335
12	ETBW6875	25.71	63.96	12.1	10.62	61.83	21.585	25.19
13	ETBW6839	27.68	63.035	9.45	8.73	47.295	18.725	19.29
14	Hawii	26	61.675	12.025	11.37	64.275	23.61	29.345
15	ETBW6373	16.705	46.625	12.05	10.55	66.165	20.655	28.105
16	ETBW6939	27.545	63.28	11.825	11.025	66.09	23.85	30.095
17	ETBW6102	26.73	65.375	12.45	9.86	65.21	18.93	24.01
18	Tusie	24.565	64.915	11.95	10.735	66.3	21.315	27.485
19	ETBW6492	24.445	62.525	12.325	10.645	65.75	22.11	28.575
20	ETBW6130	21.525	58.22	12.025	10.56	65.68	21.75	29.205

21	Hidasie	25.34	59.355	11.85	9.46	68.235	19.395	23.47
22	ETBW6398	24.365	59.99	12.39	10.39	48.67	16.205	22.14
23	ETBW7689	25.255	64.275	12.1	10.705	65.12	21.67	27.85
24	Dure	19.35	42.87	11.95	10.14	65.92	19.285	25.725
25	ETBW6315	21.86	60.93	11.975	9.39	65.61	17.395	22.725
26	ETBW6840	23.85	55.17	12.175	10.115	65.235	20.075	26.33
27	ETBW6174	21.55	60.9	11.9	10.03	66.27	19.62	27.31
28	ETBW6647	26.97	61.625	11.975	11.025	65.895	23.34	27.785
29	Bolo	20.81	62.7	12.275	10.5	67.3	21.045	23.825
30	ETBW6439	24.735	62.04	11.975	10.54	65.55	20.55	28.135
31	ETBW6953	17.37	42.97	11.775	10.875	64.445	21.92	29.515
32	KULKULU	27.035	25.16	11.95	10.97	65.025	22.63	24.11
33	ETBW6406	24.355	44.34	12.2	10.9	65.755	23.205	29.76
34	ETBW6314	25.885	64.75	12.425	8.995	66.005	15.465	19.955
35	Laketch	17.735	45.2	12.2	10.985	63.185	23.085	24.885
36	Kubsa	20.165	58.4	11.9	10.415	65.275	20.38	26.265
37	Sofumar	21.305	59.125	12.2	9.795	66.39	18.08	25.035
38	ETBW6852	19.81	53.4	11.825	9.95	65.655	19.605	25.11
39	Hoggana	27.975	63.97	11.925	9.36	65.71	17.905	19.615
40	ETBW6496	21.36	61.41	12.15	11.725	65.245	24.375	32.295
41	Millennium	25.84	67.36	11.925	10.245	66.11	19.48	23.975
42	Kakaba	20.5	56.54	12.05	10.4	66.15	20.77	28.815
43	Tay	27.095	63.92	11.825	9.985	66.635	19.8	26.64
44	ETBW6832	19.88	40.79	12.05	10.73	66.64	23.325	32.65
45	ETBW6506	24.355	44.34	12.2	10.9	65.755	23.205	29.76
46	ETBW7694	18.975	53.415	11.85	9.77	66.54	17.395	23.725
47	ETBW6871	23.905	63.01	8.85	8.44	49.68	15.93	20.545
48	ETBW7723	23.72	56.525	12.175	9.765	67.285	18.82	24.985
49	Pavon76	22.155	60.02	12.15	10.85	65.21	20.555	29.97
50	ETBW6169	27.355	67.24	12.15	10.485	66.575	21.21	26.81
51	ETBW6114	24.475	63.85	11.8	11.14	62.585	21.35	26.745
52	ETBW6837	19.52	54.365	11.875	10.735	64.835	22.115	30.38
53	ETBW6948	20.605	59.985	12.075	10.21	66.195	19.72	26.27
54	ETBW6911	19.19	54.67	12.125	9.4	66.655	18.275	22.49
55	ETBW6890	25.345	63.27	11.775	11.07	65.66	23.465	31.195
56	ETBW6095	22.74	62.01	11.925	10.26	66.46	19.965	27.215
57	ETBW6847	24.09	64.195	12.05	10.265	66.03	20.485	27.91
58	Dashen	27.175	62.47	11.75	10.75	63.89	21.6	26.08
59	Mitike	21.675	45.995	11.75	10.15	66.77	20.11	27.12
60	ETBW6943	26.955	64.08	12.125	10.83	65.66	22.305	29.385
61	Meraro	22.58	49.135	11.925	10.95	65.24	21.99	28.97
62	ETBW6866	26.04	65.77	12.2	10.375	66.53	21.475	27.1
63	Galema	20.525	59.37	12.3	11.06	65.065	21.17	29.065
64	KBG01	13.465	46.825	12.125	10.215	65.51	21.025	24.52
65	Dinknesh	23.49	57.555	12.05	10.36	58.285	21.015	26.44
66	ETBW6101	22.74	62.01	11.925	10.26	66.46	19.965	27.215
67	ETBW6850	23.965	58.35	11.825	11.97	64.88	26.3	35.295
68	ETBW7688	25.475	56.09	9.05	7.74	49.01	15.75	19.6
69	Doddota	20.17	55.385	12.45	10.895	64.405	21.735	26.335
70	ETBW6212	21.625	43.355	12.2	10.715	66.255	21.86	26.65
71	ETBW7692	24.035	61.66	11.775	11.15	65.615	22.96	31.235
72	ETBW6404	21.925	45.27	11.825	10.29	66.535	20.11	26.955
73	K6290Bulk	24.65	61.02	12.35	11.155	66.065	23.155	39.6
74	ETBW6882	23.335	63.305	11.85	11.215	65.995	23.9	30.685
75	ETBW6445	20.71	43.455	11.75	9.89	64.965	18.77	24.41
76	Huluka	26.4	62.895	11.9	10.115	65.68	20.555	27.08
77	ETBW6869	23.835	66.06	11.75	11.525	64.765	23.88	31.93
78	ETBW6883	17.615	40.63	12.025	10.565	67.01	22.81	31.35
79	Menze	18.14	43	11.975	9.635	68.485	20.44	21.005
80	Shorima	23.73	64.62	11.825	9.78	66.935	18.37	24.975
81	Bobitcho	24.2	60.955	12.125	10.165	66.235	19.61	26.19
82	ETBW7693	23.81	61.76	8.925	8.565	48.095	16.435	23.08
83	ETBW6688	26.165	61.525	12.075	10.775	66.95	22.82	29.275
84	ETBW6107	21.7	59.97	11.775	10.725	66.03	22.805	28.38
85	K62904A	26.74	65.06	12.2	9.785	67.915	19.335	23.16
86	ETBW7730	21.62	61.33	11.775	10.88	64.91	21.9	29.13
87	ETBW6167	26.92	51.2	12.1	11.17	65.565	23.565	32.01
88	ETBW6529	28.76	63.82	12	11.46	64.865	24.22	30.55
89	ETBW6518	20.045	60.805	12.4	9.485	68.405	18.62	20.44
90	ETBW6109	22.52	57.715	11.925	10.705	65.05	20.59	27.775
91	ETBW6845	25.105	66.605	12.075	10.965	65.845	21.465	29.345
92	QUIAU#2(GAMBO)	21.25	57.74	7.28	7.87	48.865	14.7	25.79
93	Simba	24.905	65.245	8.825	8.24	48.94	15.365	21.665
94	MadaWalabu	24.925	54.17	8.93	8.08	49.09	16.49	21.825
95	ETBW7695	24.665	63.93	12.025	10.98	64.13	21.78	29.32
96	ETBW6862	21.555	39.995	12.05	9.775	65.83	17.52	24.745
97	ETBW6848	24.11	62.885	12.265	8.91	48.26	15.48	22.145
98	ETBW6853	21.865	60.82	12.075	10.595	66.415	21.63	28.575
99	Tossa	25.205	61.82	12.2	10.695	57.91	21.065	26.445
100	ETBW6393	26.515	48.765	12.075	11.365	65.24	23.99	29.94
101	Abola	24.445	58.675	11.9	10.225	65.85	19.77	26.925

102	Danda'a	27.9	62.025	12.2	10.69	65.55	20.79	27.965
103	ETBW7696	25	60.465	12.275	10.535	65.62	21.005	26.1
104	ETBW6696	23.88	62.06	11.925	9.48	65.475	17.485	22.315
105	Katar	22.78	62.035	12.025	10.015	67.585	20.485	26.23
106	ETBW6947	20.65	56.445	12.05	10.73	65.335	20.64	28.41
107	ETBW5879	21.255	48.69	11.925	10.6	63.975	20.865	25.225
108	ETBW6928	20.775	56.435	11.8	10.815	64.88	20.78	29.56
109	Gasay	20.095	43.135	12.05	9.82	67.575	19.355	24.925
110	ET13A2	25.78	59.805	12.1	10.73	65.755	22.6	28.225
111	ETBW6256	29.03	65.785	11.95	9.725	66.5	18.345	28.045
112	ETBW6937	27.16	64.88	12.075	10.85	65.84	21.915	28.235
113	ETBW7698	27.01	63.29	11.95	10.99	64.355	22.68	29.765
114	Sulla	26.365	62.95	8.58	8.28	49.57	17.26	28.185
115	Digelu	22.825	63.125	12.175	9.42	68.03	19.445	21.515
116	ETBW7690	24.205	48.28	12.35	10.165	66.095	19.945	25.31
117	ETBW6886	21.28	62.935	12	10.235	65.54	18.45	24.035
118	ETBW6841	22.135	58.945	12.225	10.225	66.43	20.085	36.83
119	ETBW6861	27.205	64.475	12.025	10.65	66.91	21.475	28.61
120	Enkoy	24.405	63.175	11.9	10.675	66.525	21.925	28.02
121	ETBW6427	16.11	45.68	12.1	8.41	67.05	15.535	15.85
	CV	1.841813	0.49589	1.209435	2.414749	0.446193	1.229174	1.559251
	LSD at (0.01)	1.1286	0.7501	0.3741	0.6497	0.7515	0.6605	1.0957
	at (0.05)	0.8537	0.5674	0.283	0.4915	0.5685	0.4996	0.8288

TGW: 1000 grain weight, HlW: hectoliter weight, Prot.: Protein content, Starch: Starch content, Glue: Gluten content and Zele: Sedimentation volume content. LSD= list significant difference, CV= coefficient of variations

Appendix 16: Mean performance of one hundred twenty-one bread wheat genotypes for grain quality characteristics tested across locations

S.N.	Treatment	TGW	HLW	Prot.	MoC	Star.	Glu.	Zele.
1	**ETBW6921**	43.5333	56.8817	11.9	66.64	66.64	23.0317	31.2567
2	**EBW7686**	41.5833	54.6	11.77	66	65.9983	22.085	29.6283
3	**Galil**	40.2517	55.8817	11.71	66.27	66.27	21.8433	29.51
4	**ETBW6876**	37.56	52.6867	12.5	65.31	65.3133	25.0983	33.0233
5	**Dereselign**	39.1433	54.1333	12.58	65.81	65.81	25.175	32.44
6	**Sirbo**	30.8233	54.3483	11.53	66.02	66.0233	22.6083	30.605
7	**Ogolcho**	43.3183	57.945	11.28	65.55	65.5517	20.515	26.5617
8	**ETBW7717**	36.11	54.1717	11.64	65.53	65.5283	19.3017	27.2117
9	**ETBW6543**	44.91	56.95	11.45	65.64	65.6417	21.165	28.1583
10	**ETBW7724**	37.49	53.0617	11.51	67.39	67.3933	21.765	26.8617
11	**ETBW6932**	43.535	56.0317	11.83	64.33	64.33	22.885	29.195
12	**ETBW6875**	42.5033	55.57	11.87	63.68	63.6767	22.0283	29.68
13	**ETBW6839**	42.9617	57.2267	11.17	59.67	59.665	23.2083	26.6467
14	**Hawii**	43.0083	56.2167	12.13	64.29	64.2917	24.3367	30.615
15	**ETBW6373**	34.875	51.5183	11.63	65.51	65.505	21.9017	29.5683
16	**ETBW6939**	43.76	57.3983	11.91	66.85	66.8467	25.2	31.215
17	**ETBW6102**	44.325	57.46	12.32	64.52	64.52	22.9933	29.5367
18	**Tusie**	39.6383	56.255	11.15	66.88	66.8833	20.7717	27.4117
19	**ETBW6492**	41.3583	54.3817	11.06	66.42	66.4167	21.9533	27.475
20	**ETBW6130**	39.4567	53.5083	11.68	65.28	65.2767	23.6	29.0683
21	**Hidasie**	43.7517	54.9633	11.47	66.08	66.0783	21.815	26.0733
22	**ETBW6398**	40.9633	54.8717	12.2	60.02	60.0233	21.735	29.53
23	**ETBW7689**	41.225	55.2517	11.75	65.16	65.1567	22.9733	30.0833
24	**Dure**	34.6233	57.0333	12.2	64.46	64.4567	22.8117	30.9083
25	**ETBW6315**	41.76	54.6867	10.99	64.72	64.72	18.5483	23.31
26	**ETBW6840**	41.04	53.1167	12.01	65.08	65.0783	23.275	30.46
27	**ETBW6174**	40.3667	56.2333	11.1	66.79	66.79	20.6933	28.5033
28	**ETBW6647**	44.525	56.6233	11.84	64.7	64.6983	24.6633	30.0783
29	**Bolo**	39.1167	53.6533	10.43	69.27	69.265	20.2567	21.9083
30	**ETBW6439**	42.1633	54.1617	11.51	65.7	65.7	21.2833	27.045
31	**ETBW6953**	30.2233	53.89	11.91	64.52	64.515	23.59	32.3717
32	**KULKULU**	26.0367	54.995	12.42	65.19	65.1917	23.8767	27.5367
33	**ETBW6406**	38.3133	56.1683	12.58	64.65	64.6517	25.035	32.8033
34	**ETBW6314**	43.1333	57.7783	10.99	66.22	66.2183	17.9883	23.6517
35	**Laketch**	32.3	55.3783	12.25	63.41	63.4117	24.9283	29.995
36	**Kubsa**	39.25	52.505	11.17	66.54	66.5417	21.7767	26.605
37	**Sofumar**	40.4417	55.985	11.38	65.43	65.43	20.1933	26.1117
38	**ETBW6852**	38.4833	52.7367	11.19	66.95	66.9517	21.685	27.62
39	**Hoggana**	37.64	55.8583	11.14	66	66.0033	21.0517	22.605
40	**ETBW6496**	41.62	55.77	11.65	66.15	66.1483	24.5583	30.2983
41	**Millennium**	42.7367	58.7133	11.48	66.07	66.07	21.0767	26.0083
42	**Kakaba**	40.68	53.3667	11.83	66.33	66.3333	22.39	31.105
43	**Tay**	40.7067	56.1983	11.31	65.6	65.595	20.2167	26.43
44	**ETBW6832**	34.8967	54.0433	11.92	65.93	65.93	23.9417	33.8
45	**ETBW6506**	38.63	54.885	12.35	65.62	65.6183	25.4183	31.9367

46	**ETBW7694**	37.6717	51.775	10.82	66	65.9967	19.9983	23.9917
47	**ETBW6871**	43.1367	55.1683	11.07	60.18	60.1767	24.26	29.715
48	**ETBW7723**	40.1417	55.3233	11.53	66.91	66.9117	22.84	29.3617
49	**Pavon76**	38.4733	54.435	11.65	66.24	66.2367	23.2017	31.8733
50	**ETBW6169**	43.6967	59.935	12.12	65.09	65.0917	23.6367	31.32
51	**ETBW6114**	41.6333	56.175	11.8	64.03	64.0283	22.8833	29.8817
52	**ETBW6837**	38.1217	52.69	12.06	65.28	65.2783	25.6217	34.21
53	**ETBW6948**	40.0783	56.3017	11.83	65.5	65.4983	22.5067	30.14
54	**ETBW6911**	38.8567	50.2633	11.34	65.59	65.585	20.7083	25.03
55	**ETBW6890**	43.9067	57.865	12.36	65.4	65.4033	25.405	35.115
56	**ETBW6095**	42.0033	56.2467	11.84	65.64	65.6367	22.855	31.4383
57	**ETBW6847**	41.215	55.58	11.67	65.98	65.9767	23.2783	30.82
58	**Dashen**	38.7733	56.3583	11.98	62.76	62.7633	22.5167	25.66
59	**Mitike**	32.8483	54.9117	11.37	67.01	67.0067	22.5533	30.0233
60	**ETBW6943**	42.21	56.8517	11.88	65.07	65.07	23.385	30.6117
61	**Meraro**	32.6117	55.4767	12.09	64.8	64.7967	24.2467	31.5233
62	**ETBW6866**	43.4733	58.33	12.32	65.31	65.31	23.625	30.6833
63	**Galema**	41.04	55.1417	11.57	65.32	65.3217	22.29	28.905
64	**KBG01**	30.8583	51.1383	12.79	64.37	64.37	23.9917	33.49
65	**Dinknesh**	42.6183	55.23	12.55	57.03	57.0283	21.905	27.4467
66	**ETBW6101**	40.4867	53.88	11.36	66.74	66.7367	22.0717	31.2217
67	**ETBW6850**	40.9333	56.3883	11.88	66.13	66.1267	25.8667	35.1483
68	**ETBW7688**	39.2967	55.925	10.88	59.42	59.42	20.25	26.7333
69	**Doddota**	37.5283	53.1067	11.98	64.65	64.6517	23.7617	27.4617
70	**ETBW6212**	36.0183	52.975	12.35	65.64	65.635	23.0533	28.25
71	**ETBW7692**	43.5867	54.8617	11.64	65.57	65.5717	23.4367	32.595
72	**ETBW6404**	34.6567	54.0917	11.54	66.11	66.1117	22.8333	28.9933
73	**K6290Bulk**	39.2067	56.1333	12.45	66.21	66.205	25.5183	36.4
74	**ETBW6882**	44.1183	54.9117	11.9	65.48	65.4817	23.7333	31.595
75	**ETBW6445**	37.285	53.52	11.38	64.36	64.355	19.99	25.72
76	**Huluka**	39.015	56.2167	10.82	65.76	65.76	19.935	26.01
77	**ETBW6869**	44.1367	56.1617	12.5	65.17	65.1717	26.3267	36.1767
78	**ETBW6883**	35.91	52.6383	11.68	66.55	66.5533	23.6533	32.1167
79	**Menze**	34.2833	54.1467	11.18	67.5	67.495	21.7967	23.035
80	**Shorima**	40.1067	56.3767	10.96	67.3	67.295	19.9567	26.6417
81	**Bobitcho**	39.585	54.6	12.02	66.25	66.245	22.37	29.81
82	**ETBW7693**	40.3867	52.4533	10.49	59.92	59.915	20.5117	27.31
83	**ETBW6688**	41.575	55.205	11.79	66.5	66.5	24.1567	31.2417
84	**ETBW6107**	39.79	56.1333	11.58	65.94	65.9433	25.0517	29.7767
85	**K62904A**	40.42	57.13	12.03	67.71	67.705	23.6783	29.8867
86	**ETBW7730**	37.1767	54.0233	12.01	64.47	64.47	23.8	31.16
87	**ETBW6167**	41.1833	59.04	12.07	65.91	65.905	25.9883	34.8533
88	**ETBW6529**	47.89	57.1367	12.68	64.49	64.4883	27.09	36.8667
89	**ETBW6518**	43.0017	55.7983	11.72	67.44	67.435	22.0733	27.8967
90	**ETBW6109**	41.505	53.7233	12.29	63.87	63.8667	23.4133	31.125
91	**ETBW6845**	43.335	58.185	12.49	66.32	66.315	24.2883	34.365
92	**QUIAU#2(GAMBO)**	40.93	53.9167	9.827	59.91	59.905	19.7667	28.5467
93	**Simba**	43.515	57.135	11.64	58.13	58.13	23.8717	29.9883
94	**Mada Walabu**	41.8567	53.5917	10.94	59.6	59.5967	22.3133	28.4083
95	**ETBW7695**	40.56	53.1717	12.04	64.53	64.5267	22.5767	31.4733
96	**ETBW6862**	32.5817	52.485	11.52	65.88	65.8767	20.6067	27.765
97	**ETBW6848**	40.5617	55.2367	11.94	59.9	59.9033	22.06	30.0817
98	**ETBW6853**	40.49	52.455	12.24	65.27	65.2717	24.2933	32.5583
99	**Tossa**	38.9567	56.735	11.78	63.19	63.1867	22.655	30.3817
100	**ETBW6393**	36.6217	56.255	12.81	64.28	64.28	25.7133	35.4467
101	**Abola**	37.775	56.2483	11.73	66.45	66.45	21.7567	30.705
102	**Danda'a**	44.1067	55.75	11.6	65.4	65.4	21.1967	28.055
103	**ETBW7696**	40.1217	56.2833	11.81	64.94	64.94	22.9017	27.7667
104	**ETBW6696**	42.0533	56.1433	11.26	65.93	65.925	20.595	26.6217
105	**Katar**	40.6283	55.21	11.61	67.85	67.845	22.7783	30.4767
106	**ETBW6947**	39.6483	55.5667	11.7	65.46	65.4617	22.48	30.4867
107	**ETBW5879**	38.63	55.785	11.06	65.79	65.7917	20.9883	26.9417
108	**ETBW6928**	38.3783	52.2917	11.63	64.76	64.76	22.9933	30.5867
109	**Gasay**	33.645	54.8817	10.7	67.73	67.725	19.8517	24.5917
110	**ET13A2**	40.5183	56.7767	11.67	66.69	66.685	24.45	30.3583
111	**ETBW6256**	44.9617	58.2433	11.83	65.9	65.9	22.1317	30.6983
112	**ETBW6937**	42.36	56.8867	11.93	65.88	65.88	24.4883	31.4283
113	**ETBW7698**	43.7967	57.8033	12	64.6	64.6017	23.61	31.905
114	**Sulla**	41.7833	56.605	10.48	60.81	60.8067	21.42	24.645
115	**Digelu**	41.675	54.1583	10.83	67.49	67.4933	19.7317	22.155
116	**ETBW7690**	37.5933	55.9517	11.38	65.8	65.7983	20.7817	26.57
117	**ETBW6886**	40.4783	56.36	10.88	66.28		19.4667	25.0283
118	**ETBW6841**	41.1317	53.7617	11.73	66.56	66.56	22.3783	38.0433
119	**ETBW6861**	41.775	56.7183	11.86	65.39	65.3867	21.975	26.97
120	**Enkoy**	40.5917	57.7517	12.28	67.19	67.1917	25.4083	33.0233
121	**ETBW6427**	34.86	50.0367	10.32	67.58	67.5833	18.3617	18.7333
	CV	1.457126	0.846025			0.659324	2.002793	1.669305
	LSD at (0.05)	1.4871	1.1968	0.8589		1.0999	1.16	1.2562

TGW: 1000 grain weight, HlW: hectoliter weight, Prot.: Protein content, Starch: Starch content, Glue: Gluten content and Zele: Sedimentation volum content. LSD= list significant difference, CV= coefficient of variations

Table 18: Gliadin and Glutenin (HMW- and LMW-GS) composition of fifty bread wheat genotypes collected at three locations

		Molecular weights of Gliadin composition in (KDa)													Molecular weights of Glutenin composition in (KDa)								
															HMW GS					LMW GS			
Protein markers		**54**	**53**	**52**	**51**	**50**	**49**	**48**	**43**	**42**	**41**	**38**	**23**	**21**	**160**	**150**	**145**	**130**	**65**	**55**	**50**	**45**	**35**
1	K 6290-bulk	0	1	1	0	0	1	1	0	0	0	0	1	0	1	0	1	0	0	0	1	1	1
2	Hawii	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	0
3	Hoggana	1	0	0	0	1	1	0	0	0	0	0	1	0	1	1	1	0	1	1	0	1	0
4	Tay	0	0	0	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	0	1	1	0
5	Kakaba	1	0	0	0	0	1	0	0	0	0	1	1	0	0	1	0	1	1	0	1	1	0
6	Menze	1	1	1	0	1	1	0	0	0	0	0	0	1	0	0	1	1	1	1	1	1	0
7	Dereselign	1	0	0	0	0	1	0	0	0	0	0	0	1	1	0	1	0	1	0	0	1	0
8	QUIA#2 (GAMBO)	0	1	1	1	0	1	0	1	0	0	1	1	1	1	0	1	0	0	1	1	1	0
9	Bobitcho	0	1	1	1	0	1	0	1	0	0	1	1	1	1	1	1	0	0	1	1	0	0
10	Bolo	1	0	0	1	0	0	0	0	0	0	1	1	1	0	0	1	1	1	1	1	1	1
11	Ogolcho	1	1	0	1	0	1	0	0	0	0	1	0	1	0	0	0	1	0	1	1	1	0
12	Simba	0	0	0	0	0	1	1	1	0	0	0	1	0	1	0	1	0	1	0	0	0	0
13	Kulkulu	1	1	0	1	1	1	1	1	0	0	0	1	0	1	0	1	0	1	1	1	1	0
14	Mitike	0	1	0	1	0	1	1	0	0	0	1	0	0	1	0	1	0	0	0	1	1	0
15	Sulla	0	1	1	1	0	1	0	1	0	0	0	0	0	1	0	1	0	0	1	1	1	0
16	Shorima	1	1	0	1	1	1	0	0	0	0	0	0	0	1	0	1	0	1	1	0	1	0
17	Danda'a	0	0	1	1	0	1	0	1	0	0	1	1	0	0	1	0	1	0	0	0	0	0
18	ETBW 6095	1	1	1	1	0	1	0	1	0	0	1	1	0	1	0	1	1	1	1	1	0	0
19	K 6290-4A	0	1	1	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0	1	1	0
20	Enkoy	0	1	1	1	0	1	0	1	0	0	1	1	0	1	0	1	0	0	0	1	1	0
21	Katar	0	1	1	1	0	1	0	1	0	0	1	1	0	1	0	0	1	0	1	1	1	0
22	ET-13A2	0	0	1	0	0	1	0	1	0	0	0	1	0	0	0	1	0	0	0	1	1	0
23	Sirbo	1	1	0	1	1	1	1	0	0	0	0	1	0	1	0	1	0	1	1	1	1	0
24	Abola	0	1	1	1	1	0	0	1	0	0	0	1	0	1	0	1	1	0	1	1	1	0

Table 18: Cont,d…

25	Dinknesh	0	0	0	0	0	1	1	0	0	1	0	1	1	1	0	1	0	0	0	0	0	0
26	Gasay	0	1	1	1	0	1	1	0	0	0	1	0	0	1	0	1	1	1	1	0	0	0
27	Honqollo (ETBW5879)	0	1	0	0	0	1	1	0	0	0	1	1	0	1	0	0	1	1	0	0	0	0
28	Dashen	0	0	0	0	0	1	0	0	0	1	1	0	0	1	0	1	0	0	0	0	1	0
29	Mada Walabu	0	1	0	1	1	1	1	0	0	0	0	1	1	1	0	0	1	0	1	1	1	0
30	Meraro	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0	1	0	1	1	1	1	1
31	KBG-01	0	1	0	0	1	0	0	1	0	0	1	0	1	1	0	1	0	0	1	0	0	0
32	Glema	0	1	1	1	1	0	1	0	0	0	0	0	0	1	0	0	1	0	1	1	1	0
33	Laketch	0	1	0	1	0	1	0	0	0	0	1	1	0	1	0	0	1	0	1	1	1	0
34	Sofumar	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	1	0
35	Pavon-76	0	1	1	0	0	1	1	0	0	0	0	0	0	1	0	1	1	0	1	1	1	0
36	Doddota	0	1	1	1	1	1	1	0	0	0	0	0	0	1	0	0	1	0	1	1	1	0
37	Digelu	1	1	0	1	1	1	0	0	0	0	0	1	1	0	0	1	1	1	1	1	1	1
38	Galil	0	0	0	0	0	1	0	1	0	0	0	1	1	1	0	1	1	0	0	1	1	0
39	Hidasie	0	0	1	0	0	1	0	1	0	0	0	1	0	1	0	0	1	0	0	0	1	0
40	Kubsa	0	1	1	0	1	1	0	1	0	0	1	1	0	1	0	1	0	0	0	1	1	0
41	Dure	0	1	1	1	1	1	0	1	0	0	0	1	0	1	0	0	1	0	1	1	1	1
42	Tossa	0	1	1	0	0	1	0	1	0	0	0	0	0	1	0	0	1	0	1	1	1	0
43	Huluka	1	1	0	1	1	1	0	0	0	0	0	1	0	1	0	1	0	1	1	1	1	1
44	ETBW6406	1	1	0	1	0	1	1	0	0	0	0	1	0	0	0	0	1	1	1	1	1	0
45	ETBW 6953	0	1	1	1	0	0	0	1	0	0	0	1	0	1	0	1	1	0	0	1	1	0
46	ETBW 6114	1	1	0	1	0	1	1	0	0	0	1	1	1	0	1	1	1	1	1	1	1	0
47	Millenium	0	0	0	0	0	1	1	0	0	1	1	1	0	0	1	1	1	0	0	1	1	0
48	ETBW 6107	0	1	1	1	1	1	1	0	0	1	0	1	0	0	1	1	0	0	1	1	1	1
49	ETBW 6212	0	1	0	1	0	0	1	1	0	1	0	1	0	0	0	0	1	1	1	1	0	1
50	Tusie	0	0	0	1	0	0	1	0	0	1	1	1	0	1	1	1	0	0	0	0	0	1
No. alleles (bands)		16	34	22	29	18	42	19	20	0	6	19	32	13	36	8	35	25	19	30	38	40	9
Sub total		**270**													**104**					**136**			

Appendix 19: Optimized protocol for protein extraction

Major steps during protein extraction

1. Seven to Eight selected and matured bread wheat seeds were grinded using tissue lyzer for 10 to 20 min at 30 vibrations per second.
2. The powder is put in Eppendorf, adding 400microliter of deionized water and incubated at the interval of vortexing, finally put on ice.
3. Centrifugate for 5min of 12000rpm, 9acceleration, at 9break for 4^{o}C: in the supernatant albumen is expected if needed to study one can continue with this product but we need the residue for the next step.
4. Residue is treated with addition of 200microliter of deionized water, then vertex it for 1min and leave the content for 5min on ice.
5. Centrifuge the content for 5min, the supernatant is added to the above for the albumen analysis.
6. Residue taken is treated with 200microliter deionized water, vortex for 1min and left for 5minon ice
7. Centrifugate for 5min then the supernatant is mixed with the other albumen contents
8. Residue was treated with 400microliter of 0.5M NaCl, then incubated for 30min at 37^{o}C at the interval of 10min vortexing.
9. Centrifugate for 5min, the supernatant is removed for globulin product.
10. Residue was treated with 200microliter of 0.5M NaCl, then vortexed for 1min and left for 5min on ice.
11. Centrifugate for 5min, the supernatant is also collected for further study with the other above globulin product.
12. The residue was treated with 200µl of 0.5M NaCl and vortexed for 1min and left for 5min on ice
13. Centrifugate for 5min and remove the supernatant to collect the globulin with the above two globulin products.
14. The residue was treated with400µl deionized water whose function is to wash the product to remove salt from it. vortex for 1min and left for 5min on ice.
15. Centrifuge for 5min, the supernatant as it is full of salt in it so discard to get pure gliadin.

16. The residue was treated with 400µl of 50%Isopropanol, and incubate for 30minbat 45oC with an interval of 10min vortexing.
17. Centrifuge then the first supernatant to be collected was the gliadin in a new tube
18. The residue was treated with 200µl of 50%Isopropanol, vortexed for 1min and left open on ice for 5min
19. Centrifuge the solution, the supernatant was collected in the tube that contains the gliadin
20. The residue was treated with 200µl 50% isopropanol, the solution was vortexed for 1min and left on ice for 5min.
21. Centrifugation the solution was containing the third gliadin product and was collected with other gliadin in a tube.
22. The residue was treated with 400µl of (50% isopropanol and 0.08M tris mix solution), Incubate at 60oC for 30min of interval vortexing.
23. Centrifugate for 5min, add 350µl of (50% isopropanol plus 0.08M Tris plus 1.4% PVP mix)
24. Incubate for 30minat 60oC with an interval of vortexing
25. Centrifugate, the supernatant was containing the first glutenine to be collected in a new tube.
26. In a residue add 200µl of (50% isopropanol plus 0.08M Tris plus 1.4% PVP mix), vortex for 1min, and left on ice for 5min
27. Centrifugate and collect the second glutenine with the other in in the new tube
28. The residue was treated with 200µl of (50% isopropanol plus 0.08M Tris plus 1.4% PVP mix), vortex for 1min, and left on ice for 5min
29. Centrifuge collected the last supernatant to be collected in the tube containing the other glutenine.
30. Finally the residue was removed, remaining un used.

NB: Storage temperature for the products of both gliadin and glutenin sub unites were stored in the refrigerator of -20^{o}C at freezing temperature until it is run in the gel.

Labeling was done on each extracts of the protein to identify them clearly to avoid confusion of the types of the products.