GENETIC VARIABILITY AND ASSOCIATION AMONG BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES FOR YIELD AND YIELD RELATED CHARACTERS IN SOUTHERN ETHIOPIA

MSC THESIS

MATHEWOS CHUMAMO BUNARO

November, 2019

JIMMA, ETHIOPIA

GENETIC VARIABILITY AND ASSOCIATION AMONG BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES FOR YIELD AND YIELD RELATED CHARACTERS IN SOUTHERN ETHIOPIA

A Thesis

Submitted to Department of Horticulture and Plant Sciences, Jimma University College of Agriculture and Veterinary Medicine, in Partial Fulfillment of a requirement for the Degree of Master of Science in Plant Breeding

By

Mathewos Chumamo Bunaro

Major Advisor: Sentayehu Alamerew (Prof.)

Co-Advisor: Mathewos Ashamo (PhD Candidate)

November, 2019

Jimma, Ethiopia

Jimma University College of Agriculture and Veterinary Medicine

Thesis Submission Request Form (F-08)

Name of student: **Mathewos Chumamo Bunaro** **ID No**: RM 1225/10

Program of study: **Plant Breeding**

Title: Genetic Variability and Association among Bread (*Triticum aestivum* L.) Genotypes for Yield and Yield Related Characters in Southern Ethiopia

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

Mathewos Chumamo Bunaro Signature _____ Date: ___/____/__

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

Major advisor: **Sentayehu Alamerew (Prof.)** Signature _____ Date: __ /___/____

Co-Advisor: **Mathewos Ashamo (PhD Candidate)** Signature _____ Date: ___/____/___

Internal Examiner(If Depends on the Verdict)
Name_____Signanature_____Date:____/___/__

Decision/suggestion of Department Graduate Council (DGC)

_____

_____

_____ _____ ____/____/____

Chairperson, DGC Signature Date

_____ _____ ____/____/____

Chairperson, CGS Signature Date

DEDICATION

I dedicated this manuscript to my beloved family and my best friends who supported and shared unforgettable pain in my life during my MSc study.

STATEMENT OF THE AUTHOR

I hereby declare and confirm that this thesis is my own work and all sources of materials used for this thesis has been acknowledged. I have followed all ethical and technical principles of scholarships in the preparation, data collection, data analysis and completion of this thesis. This thesis has been submitted in partial fulfillment of the requirements for MSc Degree at Jimma University and is deposited at the University Library to be made available to borrowers under the rules of the Library. I declare that this thesis is not submitted to any other institution anywhere for the award of academic degree, diploma or certificate.

Brief quotations from this thesis are allowable without special permission provided that accurate acknowledgement of source is made. Requests for permission for extended quotation from or reproduction of this manuscript in whole or in part may be granted by the head of the major department or the Dean of the School of Graduate Studies when in his or her judgment the proposed use of the material is in the interests of scholarship. In all other instances, however, permission must be obtained from the author of the thesis.

Name: Mathewos Chumamo Bunaro Signature: _____

Place: Jimma University College of Agriculture and Veterinary Medicine

Submission Date: _____

Graduate Studies (Plant Breeding)

School/Department: Horticulture and Plant science Signature: _____

BIOGRAPHICAL SKETCH

The author was born in September, 1990 G.C inDiguna Fango woreda, Wolaita zone of Southern Nations Nationalities and People's Regional State; from his father Ato Chumamo Bunaro and his mother W/ro Meskerem Dogiso. He attended his elementary Schools at Bitana Hamus atDiguna Fangoworeda, secondary and preparatory Schools at Awassa Addis Ketema and Awassa Tabor, respectively. After the completion of his preparatory School, he joined Dilla University in 2010 for his BSc study in plantsciences.Soon after his graduation in November 2012 up to May 2014, he was employed by Diguna Fango Woreda Agricultural office in Crop Extension work process in Wolaita Zone as an expert about one and half years and then after he joined Southern Agricultural Research Institute and served for three years as a junior researcher till 2018. Then after, he joined Jimma University for MScdegree study in plant breeding in 2018.

ACKNOWLEDGEMENTS

First and foremost Admiration and Glory to God, for keeping me healthy and strong enough to successfully undertake both the course and field research works as well as compiling this study.

Secondly, my utmost appreciation goes to Southern Agricultural Research Institute, for granting me this opportunity with the financial support.

I express my special thanks to my major supervisor Prof. Sentayehu Alamerew and Co-supervisor Mr. Mathewos Ashamo for their helpful guidance, wisdom, experience, encouragement, advice and thorough review and constructive criticisms on the manuscript that enables me to shape up in the final thesis.

I gratefully acknowledge the immense contribution made by the Areka Agricultural Research Center during the implementation of the research work, by providing necessary facilities that have made my work smoothly.

I also express special thanks for alltechnicalassistances of cerealcrops improvement case team ofAreka Agricultural Research Centerfor their help in seed and land preparation, recording the field and laboratory data as well as all thetechnical assistances of agronomy, pulse and oil crops ofAreka Agricultural Research Center for helping in planting, harvesting and laboratory data recording. Last, but not least I want to thank the field assistants of Kokate and Hossana research sub stations for their unforgettable support during my field work.

LIST OF ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of variance
ArARC	Areka Agricultural Research Center
ARARI	Amhara Regional Agricultural Research Institute
CFIA	Canadian Food Inspection Agency
CIMMT	Maize and Wheat Improvement Center
EIAR	Ethiopian Institute of Agricultural Research
FAOSTAT	Food and Agriculture Organization of the United Nations
GAIN	Global Agricultural Information Network
IBPGR	International Board for Plant Genetic Resources
ICARDA	International Center for Agricultural Research in Dry Areas
KARC	Kulumsa Agricultural Research Center
OARI	Oromia Agricultural Research Institute
SARI	Southern Agricultural Research Institute
SNNPR	Southern Nations Nationalities and People's Region
TARI	Tigray Agricultural Research Institute
USDA	United States Department of Agriculture

TABLE OF CONTENTS

TABLE OF CONTENTS (*Continued*)

TABLE OF CONTENTS (*Continued*)

LIST OF TABLES

Tables **Page**

LIST OF TABLES IN THE APPENDIX

LIST OF FIGURES IN THE APPENDIX

GENETIC VARIABILITY AND ASSOCIATION AMONG BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES FOR YIELD AND YIELD RELATED CHARACTERS IN SOUTHERN ETHIOPIA

ABSTRACT

Although wheat has a long production history in Ethiopia, the mean national yield of the crop is relatively low in contrast with the world average yield due to limited availability of adaptable and stable varieties. Therefore, this study was conducted to estimate genetic variations among 49 bread wheat genotypes and association among yield and related characters to identify superior genotypes. Field experiment was conducted during 2018 cropping season at Kokate and Hossana, Southern Ethiopia. The experimental design used was simple lattice. Data were collected on 12 quantitative and 6 qualitative characters and all quantitative characsters were subjectd to analysis of variance using SAS statistical analysis while qualitative characters were calculated using Shannon index. Analysis of variance across locations revealed significant variations among location, genotype and genotype x location interactions for most of the quantitative characters considered in the study. Shannon index indicated appreciable diversity for most of the qualitative characters studied. The phenotypic coefficient of variation ranged fron 4.78% for plant height to 26.26% for biological yield while the genotypic coefficient of variation ranged from 3.89% for plant height to 23.69% for biological yield. Heritability ranged from 21.15% for number of kernels per spike to 95.31% for days to heading. Heritability along with genetic advance as percent mean for days to heading, biological yield and harvest index, respectively were (95.31, 20.14), (81.40, 24.1) and (84.90, 38.31),showing presence of additive gene and selection based on these characters would be ideal. The correlation analysis revealed number of kernels per spike, biological yield, thousand seed weight and harvest indixe has positive and significant association($P \leq 0.01$) with grain yield. Path analysis revealed that biological yield exerted positive direct effect on grain yield both at genotypic and phenotypic levels. Cluster analysis grouped 49 genotypes into five clusters and two solitary groups. The highest inter cluster distance occurred between clusters four and five while the lowest was between clusters two and five. Principal component analysis revealed that five principal components had accounted for 77.6% of the total variation. Generally, the study showed existence of significant genetic variability among tested genotypes. Therefore, simple selection of promising genotypes and crossing of highly divergent group to produce best heterotic offspring could be recommended from the present study . For future breeding programs that employ hybridization, parental material selection should be carried out between clusters rather than within clusters.

Key words: Bread wheat, Correlation, Genetic variability, Grain yield, Heritability

1. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a hexaploid (2n = 6x = 42), annual and self-pollinated cereal which is belongs to the family: *Poaceae*, Tribe: "*Triticeae*" and Subfamily: *pooideae* (Sleper and Poehlman, 2006). It is a monoecious plant with perfect flowers, reproducing sexually as an autogamous crop although limited (3%) cross pollination is possible with adventitious root system which arise from the lower nodes of the shoot and shoot system (Mergoum *et al*., 2009). The vegetative state of the plant is characterized by tillers bearing axillary leafy culms. Each spikelet is a condensed reproductive shoot consisting of two subtending sterile bracts or glumes (CFIA, 2014).

It is the most important food security and cash generating crops in many parts of the world and its grain is valued for the preparation of traditional fermented thin bread ("injera"), regular bread ("dabo"), and local beer ("tella") (Tsegaye and Berg, 2007). Wheat accounts for 20% of nutritional sources of the people around the world and provides nearly 55% of carbohydrates, 20% of the daily protein and 21% calories for about 40% of the global population (Khan and Naqvi, 2011; Khabiri *et al*., 2012).

Wheat is produced under a wide range of climatic conditions and geographical areas, and due to its high adaptability to diverse climactic and other environmental conditions, its distribution range is more than any other plant species. It is grown from temperate, irrigated to dry and high-rain-fall areas and from warm, humid to dry cold environments (Kamali, 2008). In Ethiopia, wheat is grown at altitudes ranging from 1500 to 3000 meters above sea level. However, the most appropriate agro-ecological zones fall between 1900 and 2700 m.a.s.l (Abu, 2012).

Globally, in 2019/20,the area covered by wheat was218.78 million hectares whith total production of 768.07 million metric tons (Mmt) and average yield of 3.51 t/ha (USDA, 2019).However, Africa produced more than 25 million tons (MT) on 10 million hectares (Mha) of land. Sub-Sahara Africa (SSA) produced a total of 7.5 million tons (MT) on a total area of 2.9 million hectares (Mha) accounting for 40 and 1.4 per cent of the wheat production in Africa and at global levels, respectively (FAO, 2017).

In Ethiopia, wheat has increasing trends in production and productivity over the last decade. A total of 1,696,907.05 ha of land were covered by wheat (CSA, 2018) and itranks 3rd in yield per ha^{-1} as well as area coverage among cereal crops grown in the country. In the year 2017/18 the national average productivity of wheat was 2.74 t/ha (CSA, 2017), which is relatively low in contrast with yield potential of the crop from 3.5 up to 5.0 t/ha under experimental stations (MoANR,2016), which can be achieved through improved production technologies.

Currently, bread wheat is one of the focus subsectors supported by governmental and nongovernmental organizations in all wheat growing regions of the country due to the increasing number of populations as well as increasing in demand at global level.It is projected that demand for wheat in developing countries will increase by 60 per cent in the year2050 (RosegrantandAgcaoili, 2010). Hence, the global wheat production must increase 2% annually to meet the growing world populations (around 9-10 billion) (RosegrantandAgcaoili, 2010)

The major production constraints that have been responsible for low productivity of the crop at national level in general and Southern Nations Nationalities and People's Region in particular includes: narrow genetic base, shortage of stable and adaptable bread wheat varieties, low productivity potential of the released varieties in the production, biotic factors such as wheat leaf rusts, stem rusts, stripe or yellow rust and abiotic factors such as drought, soil acidity, salinity, water logging, frost (Hailu *et al*., 1991; Yirga *et al.*, 2013;Netsanet *et al*., 2016,Tadesse *et al*. 2018).

According to the survey report (2016) unpublished in Southern Agricultural Research Institute (SARI-Ethiopia), confirmed that limited availability of adaptable and stable bread wheat varieties in the region was major cause for yield reduction of the crop. Moreover, Messay *et al.* (2012) and Mathewos and Yasin (2017) reported limited availability of improved bread wheat varieties as the production constraints in wheat producing Zones of the region.

In the absence of sufficient genetic variability in the existing genetic materials selection for desirable attributes cannot be realized. Hence, generation of the variability and assessment of naturally existing genetic variability is a very important step in crop improvement programs (Rahman *et al*, 2016). Precise knowledge about germplasm variability and

genetic relationships among breeding materials is a pre requisite for crop improvement programs (Rauf *et al*, 2012).

Most researchin the study area have been focused on adaptation and performance evaluation. Hence, limited variety was developed by the region and some of the adapted varieties become exposed to diseases. Some years backsomenationally released varieties viz, HAR-604, Tay, Digelu and Merero were tested, but performed poor in selected areas of the region (Mathewos *et al*., 2012; Mathewos and Yasin, 2017).Some researchers conductedvariability study on bread wheat to evaluate better performing genotypes for further selection and improvement. Kifle *et al*. (2016) conducted a study on 25 bread wheat genotypes in SNNPRof Gurage Zone of Ethiopia and reported highly significant difference among the tested genotypes for days to heading, days to maturity, days to grain filling periods, 1000-kernel weight, above ground biomass, number of spikelets per spike, and spike length.

However, genetic variability studies on bread wheat genotypes are not much in the region and looking for optional varieties. Currently, many bread wheat genotypes were introduced into the country by Kulumsa Agricultural Research Centre,Therefore, currently proposed study includes introduced bread wheat genotypes which were not studied their genetic variability in the past and designed to achieve the following objectives.

General objective:

- ✓ To assess the genetic variability and association of characters in bread wheat genotypes for yield and yield related characters

Specific objectives:

- ✓ To determine variability, heritability and genetic advance of grain yield and associated characters of bread wheat genotypes.
- ✓ To estimate the extent of association between grain yield and yield related characters
- ✓ To cluster the genotypes according to their genetic similarities based on the major phenotypic characters
- ✓ To identify best performing genotypes for further breeding activities

2. LITERATURE REVIEW

2.1. Origin and Production of Bread Wheat

Like many crops of the old world, wheat was one of the first domesticated food crops which was evolved in the Fertile Crescent of the Middle East and has become a basic staple food of the present day human population (Mergoum *et al*., 2009). These earliest cultivated forms were diploid (genome AA) (*einkorn*) and tetraploid (genome AABB) (*emmer*) wheat and their genetic associations show that they originated from the south eastern part of Turkey (Dubcovsky and Dvorak, 2007).

Cultivation spread to the Near East by about 9000 years ago when hexaploid bread wheat made its first appearance (Feldman, 2001). The early domesticated forms of wheat (*einkorn* and *emmer*) are developed from the domestication of natural populations whereas the modern day bread wheat has only existed in cultivation, having arisen by hybridization of cultivated *emmer* with the unrelated wild grass *Triticum tauschii* (also called *Aegilops tauschii* and *Aegilops squarosa*) (Shewry, 2009). The current binomial name, *Triticum aestivum*, refers to hexaploid bread wheat (with genomes A, B, and D), distinguishing it from tetraploid and diploid form of wheat (Dvorak, 1998).

China, India, Russia, USA and Canada arethe major wheat producing countries in the world andthese five countries together contribute more than half of the global wheat production (FAO, 2017). Furthermore, the major wheat producing areas in Ethiopia are situated in Oromia (Arsi, Bale, Shewa, Ilubabor), Southern Nations Nationalities and People's Region (SNNPR) (Hadiya, Sidamo, Kambata Tambaro), Tigray and Amhara (Northern Gondar and Gojam Zones) (CSA, 2017).

2.2. Bread Wheat Research in Ethiopia and the Achievements

Prior to 1930, wheat research dealt mainly with scientific expeditions, germplasm collection, identification and characterization. Koernicke and Werner (1885) made the first description of some Ethiopian wheat and identified five species and nine varieties. Likewise, Percival (1927)

and Ciferri and Giglioli (1939a, 1939b) under took expeditions and reported on Ethiopian wheat germplasm.

During the periods between 1930-1952 collection and evaluation of indigenous wheat and the introduction of exotic germplasm were done for testing under local conditions. A formal wheat improvement program started in 1949 at the Paradiso Government Station near Asmara for with the testing large number of indigenous and exotic varieties. Consequently, some promising local variety selections, including A10, R18, P20 and H23, and three bread wheat varieties of Kenyan origin, viz., Kenya 1, 5 and 6, were released during the early 1950s (Hailu *et al* ., 1991).

Between the periods 1953-1966, wheat research continued at Paradiso, Debre Zeit, Alemaya and Kulumsa. Simultaneously, the station initiated hybridization program among local and exotic bread wheat genotypes. The main objective of these crosses was to incorporate stem and leaf rust resistance genes to the high quality bread wheat cultivars which were susceptible to disease (Nastasi, 1964). The major research activities included germplasm screening, variety testing and crop management studies and seed increase. This effort resulted in the release of six bread wheat varieties and multiplication and distribution of seed of the varieties Kenya 1 and Kenya 5 in the Shewa and Arsi highlands (Tesfaye and Jamal, 1982).

During the periods between 1967-1990, the establishment of the Institute of Agricultural Research (IAR) in 1966 was followed by establishmentof several other research and development institutions, resulting in an effectively organized national wheat research program. The priorities given by the IAR for wheat research emphasized increased wheat production by concentrating on improved varieties with a package of cultural practices.

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

Till 1974, the Debre Zeit Agricultural research center was responsible for coordinating the national wheat program. Since 1975, the coordination of the national wheat research program

was revised and organized into bread wheat and durum wheat components. The Holetta research center was made responsible for the coordination of bread wheat research while the durum wheat program was assigned to Debre Zeit research center. Currently, the government assigned research head quarters at Kulumsa for bread wheat (Hailu *et al*., 1991). To-date, more than 100 bread wheat varieties were released in Ethiopia (MOA, 2017).

Table 1. Some improved varieties of bread wheat released by different regional and national research centers from 2010 to 2016

Variety name	Year of release	Altitude (m.a.s.l)	Rain fall (mm)	Yield (qt/ha)	Maintainer/released
Kakaba	2010	1500-2200	500- 800	33-52	KARC/EIAR
Danda'a	2010	2000-2600	> 600	35-55	KARC/EIAR
Gambo	2011	650-2400	irrigation	37-55	KARC/EIAR
MeKelle-02	2011	-	-	-	Mekelle ARC/TARI
MeKelle-01	2012	-	-	-	KARC/EIAR
Tsehay	2011	-	-	-	Debre Birhan ARC/ARARI/
Hoggana	2011	2200-2900	800-1200	46-60	KARC/ EIAR
Shorima	2011	1900-2600	600-900	44-63	KARC/ EIAR
Mekelle- 03	2012	-	-	-	Mekele and Alamata (TARI)
Hidase	2012	2200-2600	500-800	45-70	KARC/ EIAR
Ogolcho	2012	1600-2100	400-500	33-50	KARC/ EIAR
Hulluka	2012	2200-2600	500-800	44-70	KARC/ EIAR
Jefferson	2012	1200-1900	500	20-30	OARI
Mekel-4	2013	-	-	-	Mekelle and Alamata /TARI
Sorra	2013	-	-	-	Sirinka ARC /ARARI
Sekota-1	2013	-	-	-	SDARC/ARARI
AD EL-6	2013	-	-	-	WARC/EIAR
Lucy	2013	-	-	-	WARC/EIAR

Table 1. Some improved varieties of bread wheat released by different regional and national research centers from 2010 to 2016 (***continued***)

Variety name	Year of release	Altitude (m.a.s.l)	Rain fall (mm)	Yield (qt/ha)	Maintainer/released
Honqolo	2014	2200 - 2850	750 - 1200	35 - 63	KARC/EIAR
Sanate	2014	2300 - 2600	750 -1500	34 - 67	Sinana ARC/ OA RI/
Mandoyu	2014	2200 - 2006	750 -1500	50 - 59	Sinana ARC/ OARI
Biqa	2014	1600 - 1950	450 - 800	32 - 54	KARC/EIAR
Liben	2015	-	-	-	Bako ARC / OARI/
Bulluq	2015	-	-	-	Bako ARC/OARI/
Fentale	2015	-	-	-	Werer ARC/EIAR
Amibera	2015	-	-	-	Werer ARC/EIAR
Dambal	2015	-	-	-	Sinana ARC /OARI/
Obora	2015	-	-	-	Sinana ARC/OARI/
Kingbird	2015	-	-	-	KARC/ EIAR
Lemu	2016	>2200	800 -1100	55 - 65	KARC/ EIAR
Wane	2016	21 00 - 27 00	700 -1000	5 0 - 60	KARC/EIAR/

Source:(MoANR, 2016)

2.3. Genetic Variability and Character Associationin Bread Wheat

2.3.1. Variability

Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1960). If the character expression of two individuals could be measured in an environment identical for both, differences in expression would result from genetic control and hence such variation is called genetic variation (Falconer and Mackay, 1996). Information on the natur e of genetic variability present in a crop species is important for developing effective crop improvement program (Dabholkar, 1999).

Genetic variability, which is due to the genetic differences among individuals within a population, is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations (Sharma, 1998).Genetic variability in a population can be partitioned into heritable and non-heritable variation with the aid of genetic parameters such as variance, genotypic coefficient of variation, heritability and genetic advance, which serve as a basis for selection of some outstanding genotypes from existing ones. According to the study conductedby Kamal*etal*. (2016), statistical parameters like mean, variance, phenotypic, genotypic and environmental coefficients of variation, heritability and genetic advance is helpful to evaluate the performance of any particular genotype and service in determining the success of selection for a particular trait in that genotype.

Genetic variability among traits is important for breeding and in selecting desirable types. Arya *et al*. (2017)reported highly significant differences among the bread wheat genotypes for all the characters under study,suggesting the presence of sufficient variability among the genotypes and provides opportunities for further bread wheatimprovement. Tanzeen *et al. (*2009) also reported presence of high variability that couldbe due to diverse sources of breeding materials collected as well as environmental effects on phenotypes.Similarly, Sabit *et al.* (2017) reported significant differences among bread wheatgenotypes for number of tillers per plant, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, grain yield per plant implyingpresence of sufficient variabilityamong the bread wheat genotypes that would helpto make successful selection.

Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of wheat. Plant breeders commonly select wheat germplasmfor yield components which indirectly increase grainyield. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm (Idris *et al*., 2012).

Phenotypic variability is the total variability which is observable. Phenotypic variation of an individual is made up of genotypic value and environmental deviation. The phenotypic variability in a given environment can be measured easily, but it reflects non genetic as well as

genetic influence on the phenotypic expression (*Bello et al*., 2009). Variation of phenotypic value is therefore determined by variance attributable to genotypic values and environmental deviation (Falconer, 1990; Welsh, 1990; Singh and Ceccarelli, 1996). According to Welsh (1990), environment is the sum total of all factors to which the organism is exposed.

The various factors of environment are called biotic or abiotic depending up on their biological and /or non-biological nature (Welsh, 1990; Singh, 1993). Thus environmental deviations such as differences in fertility level of the soil, moisture content of the soil, and seasonal fluctuations contribute to the component of variation. It is very difficult to determine the presence, amount or types of genetic variability if phenotypic expressions are strongly influenced by the environment (Welsh, 1990).

Although some environmental variation can be reduced by proper experimentation, its total elimination is impossible because it includesthe non-genetic variance that cannot be captured through experimentation (Gomez and Gomez, 1984).In attempting to develop improved varieties, plant breeder bases his/her observation often on the measurement of the phenotype.For plant breeding to be effective there must be phenotypic variation of the desired trait and some of the variation must be heritable from generation to generation (Stoskopf *et al*., 1999).

Variability present in breeding populations can be assessed in the following three ways, (1) by using simple measures of variability, such as range, mean, variance, standard deviation, coefficient of variability and standard error (2) by estimating the various components of variance like GCV (Genetic Coefficient of Variance) and PCV (Phenotypic Coefficient of Variance) (Berhanu, 2004).

Genetic coefficient of variation (GCV) and Phenotypic Coefficient of variation (PCV) values are categorized as low (0-10%), moderate (10-20%) and high (20% and above) values as indicated by Burton and De vane (1953). The high and medium PCV and GCV indicate that selection may be successful based on these traits. Moderate PCV and GCV were recorded in bread wheat for 1000 kernel weight, grain yield, harvest index, number of grains spike^{-1} and number of productive tiller (Gezahegn *et al*., 2015).

The PCV values were generally higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. In most cases, the two values differsslightly indicating less influence of environmental factors (Ali *et al*., 2008).The genotypic variance took somewhat greater proportion of the total variances in bread wheat for days to heading, days to maturity, grain filling period, spike length, number of fertile tillers per plant, number of kernels per spike, thousand kernel weight, biomass yield, grain yield and harvest index. Therefore, genetic components of these traits are essential and selection based on these traits is efficient (Adhiena *et al*., 2016). As described by Dargicho *et al*. (2015a), mean squares of plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and grain yield per plant showed highly significant differences between bread wheatgenotypes.

According to the study conducted by Arya *et al*. (2017), the magnitude of phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied in bread wheat genotypes indicating vital role of environmental interaction in the expression of the characters. Several authors reported highest GCV and PCV and the least difference between PCV and GCV for grain yield per plant, plant height, 1000-grain weight, number of spikelets per spike and number of grains per spike.However, harvest index and gluten content revealed high difference between GCV and PCV in their study comparison to other characters, suggesting that environmental effect was prominent for harvest index and gluten contentand the least difference between PCV and GCV indicating these characters are less influenced by environment (Kumar *et al.*, 2010; Babita*et al*., 2011; Koul and Singh, 2011; Kumar *et al.,* 2013; Yadav *et al*., 2014).

The ultimate goal of any breeding program is to increase grain yield per unit area. However, yield is a quantitative trait controlled by many genes and is greatly influenced by the environment (Ahmed, 2018). Variation in yield from year to year due to unpredictable weather and biotic stresses could result in major economic impact. Improved genetic yield potential of wheat varieties have impact in both favorable and unfavorable agro-ecosystems (Savin*et al*., 1999b; Reynolds and Borlaug, 2006).

To make an effective selection for grain yield, understandig the genetic variability, heritability and genetic advance as percent of mean as well as the association of grain yield with yield

contributing characters is important. In addition, to evolve superior genotype for further hybridization and selection it is important to get precise information on the nature and degree of genetic diversity present in wheat collections from principal areas of cultivation (Ahmed, 2018).

Yield attributes of cereal crops consists of number of panicles per unit area, number of spikelets (florets) per panicle, number of tillers, number of kernels, biomass, 1000 grain weight (Girma, 2018). Several studies indicated that there were significant differences among bread wheat varieties for the yield components (seed number per spike, grain weight per spike, 1000 grain yield, biomass, and harvest index (Shankarrao *et al*., 2010; Mollasadeghi *et al*., 2012; Asaye *et al*., 2013; Kumar *et al*., 2013). Such variability in yield components among varieties indicated that the presence of genetic distance among varieties under investigation that would be preferred for the success of breeding activities (Zecevic *et al*., 2010).

2.3.2. Heritability and genetic advance

The extent of total variation caused by genotype is called heritability, the rangeto which the variability of a trait is passed to the offspring (Allard, 1999). Heritability and genetic advance are two important selection parameters. The breeders are interested in selection of superior genotype based on phenotypic expression. The major function of heritability estimate is to provide information on their phenotypic expression and on the transmission of character from the parent to progeny. Yield and yieldcomponent traits are controlled by poly genes, whose expression is greatly affected by environment.

If a character or trait is controlled by non-additive gene action it gives high heritability but low genetic advance while the character ruled by additive gene action give both high heritability and genetic advance values (Ahmad *et al.,* 2007). Akinwale *et al.* (2011) reported that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program. Knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009; Ullah *etal*., 2011).

There are two types of heritability: broad sense and narrow sense. Broad sense heritability is ratio of the total genetic variance (additive and non-additive variance) to the phenotypic variance

of individuals and expressed in percentage (Allard, 1960). The importance of broad sense heritability in plant breeding is limited because it does not give a clear estimate of the fixable genetic variance for selection (Sleeper and Poehlman, 2006).Heritability combinedwith genetic advance is a more reliable index for selections of traits (Anshuman *et al*., 2013).

Narrow sense heritability is a ratio of additive genetic variance to the total phenotypic variance and it gives the best estimate of heritable variance, which can be fixed by selection (Sleeper and Poehlman, 2006). The highvaluefor heritability in broad sense indicates that the character is least influenced by environmental effects.Moderate heritability with low genetic progress indicated slight chances of improvement of this trait in subsequent generations (Kalimullah *et al*., 2012). Robinson *et al.* (1955) classified heritability values as high (> 60%), moderate (30 to 60%) and low (0 to 30%). Therefore, availability of good knowledge of heritability and genetic progress existing in different yield parameters is a prerequisite for effective plant improvement program.

Several investigators in their findings have reported the presence of high heritability and genetic progress in different yield related characters in wheat (Ansari *et al*., 2004; Ali *et al*., 2008; Yadawad *et al*., 2015; Adhiena *et al*., 2016; Berhanu *et al*., 2017). More variable environmental conditions reduce the magnitude of heritability, while more uniform conditions increase it. The most important function of heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Al-Tabbal and Al-Fraihat, 2012).

In order to have information on how much of the heritable characteristic is achieved in selection, it is important to know the progress attained from selection and this is measured as genetic advance. Genetic progress estimated from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at given selection intensity (Singh, 2001). Since high heritability does not always specify high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate consequence for selecting superior varieties (Ali *et al*., 2002). Genetic advance gives obvious picture and exact view of segregating generations for possible selection. Higher estimates of heritability coupled with better genetic advance confirms the scope

of selection in developing new genotypes with desirable characteristics (Singh *et al*., 2001; Ajmal *et al.*, 2009).

Johanson *et al.* (1955) reported that a character showing high heritability may not be inevitable impart high genetic advance. It can be find out with greater degree of accuracy when heritability coupled with genetic advance is studied (Dudley and Moll, 1969). Therefore, estimation of heritability along with genetic advance is more useful to understand the type of gene action involved in the expression of various polygenic characters. Nagireddy and Jyothula (2009) and Khokhar *et al*. (2011) found high heritability coupled with high genetic advance as percent mean for days to 50% flowering, plant height, number of spikelets per spike, number of grains per spike, 1000 grain weight, biological yield per plant and grain yield per plant in wheat.This indicates substantial contribution of additive gene action in the expression of the characters. Hence, direct selection for such characters would be more effective.

Various authors reported association of high heritability estimates with high genetic advance for number of grains per spike, biological yield per plant and grain yield per plant reflected the involvement of additive gene action in wheat (Atta *et al.*, 2008; Bhoite *et al*., 2008; Ajmal *et al.,*2009; Bharat *et al*., 2013; Kumar *et al*., 2013). As proposed by kumar *et al*. (2013), such estimates of genetic advance in bread wheat genotypes indicated that moderate gains could be achieved with strengthening the selection. This result is contrary to the findings ofEid (2009) in bread wheat who reported low heritability coupled with low genetic advance for plant height and number of grains per spike in the study.

2.3.3. Correlation

Correlation coefficient is the measure of the level for linear association between two characters (Gomez and Gomez, 1984). Correlation coefficient measures the relationship between two variables (Dabholkar, 1992). It measures mutual association without regard to causation (Dewey and Lu, 1959). Generally, there are three types of correlations discussed in quantitative genetics and these are phenotypic, genotypic and environmental correlations.

Phenotypic and genetic correlations are commonly used in plant breeding. Phenotypic correlations involve both genetic and environmental effects (Halluer and Miranda, 1988).

Genetic correlation is the association of breeding values (additive genetic variance) of the two characters (Falconer, 1989). Both measure the extent to which the same genes or closely linked genes cause co-variation in two different characters (Halluer and Miranda, 1988). Genotypic and phenotypic correlation coefficients tell us the association between and among two or more characters. The correlation of environmental deviations together with non-additive genetic deviations (i.e. dominance and epistatic genetic deviations) is referred to as environmental correlations (Falconer and Mackay, 1996; Sharma, 1998).

Correlation among different traits is generally due to the presence of linkage and pleotropic effect of different genes. Environment plays an important role in the development of phenotypic correlation (Ali *et al*., 2009). Phenotypic correlation is the net result of genetic and environmental correlation. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation (Anwar *et al*., 2009). 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 (Amsal, 2001).

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. While selecting the appropriate plant type, correlation studies would offer reliable information in nature, extent and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality characters. A positive value of correlation shows that the changes of two variables are in the same direction, specifically high value of one variable are associated with high values of other and vice-versa. When correlation is negative the movements are in opposite directions, that is, high values of one variable are associated with low values of other (Yadav *et al*., 2011).

Depending on the sign of genetic correlations between two traits 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).

Grain yield is the result of many characters that are interdependent. Grain yield, which is the major economic character in wheat, depends on several component traits, which are mutually related. Breeders always look for characters are related with the important characters like yield. Correlation coefficients, although very useful in quantifying the size and direction of trait associations can be genetic variation among traits to select desirable types. Some of these characters are highly associated among themselves and with grain yield. The analysis of the relationship among these characters and their association with grain yield is essential to establish selection criteria (Singh *et al.,* 1990).

The relationship between wheat yield and yield component traits has been studied widely at phenotypic level. As reported by Moghaddam *et al*. (1997), grain yield, 1000-grain weight, and number of grain per spike were positively correlated whereas spike length only correlated significant and positively with grain yield and finally, grain yieldwas positivelycorrelated with plant height, spike length, number of spike and 1000-grain weight. Most of the previous studiesreported positive correlationsbetween grain yield and otherrelated characters such as, number of spikes, spike length, number of grains per spike and 1000-grain weight (Sharma and Rao, 1989; Singh and Sharma, 1994; Subhani and Khaliq, 1994; Sharma *et al*., 1995; Siahbidi *et al*., 2013).

More recently,Sabit*et al*. (2017)reported positive and significant correlations between grain yield with biological yield, main spike weight and spikelets per spike at genotypic level in their study using 19 bread wheat genotypes. The same authors reported positive significant association between grain yield and biological yield per plant at both genotypic and phenotypic levels. Other researchers such as Mollasadeghi and Shahryari (2011) reported a negative correlation between harvest index and plant height in bread wheat.

2.3.4. Path analysis

Correlation coupled with path analysis would offer a better insight into cause and effect relationship between different pairs of characters (Jayasudha and Sharma, 2010).Mere change in

any one of the component would ultimately disturb the traits. Hence, these interrelated characters have to be analyzed for their action namely direct effect of component traits and the indirect effects *via* other component traits on grain yield. Therefore, the total correlations should be partitioned in to direct and indirect effects (Nagaraju *et al.*, 2013).

Path coefficient analysis a statistical tool developed by Wright (1921) and Dewey and Lu (1959) intended the method for path analysis for the purpose of clarification of a system of correlation coefficients in terms of path causation. Path coefficients differ from correlation coefficients in that they may exceed by +1 or -1 in absolute value as there is no restriction on the relative amounts of the differences of an effect and a cause. To improve grain yield via selection of its components path coefficient analysis is a convenient tool for thoughtful grain yield formation and provides valuable extra information about the characters (Del Moral*et al*., 2003).

Unlike correlation coefficient which measures the extent of relationship, path coefficient measures, the magnitude of direct and indirect contribution of component character to complex character and it has been defined as a standardized partial regression coefficient which splits the correlation coefficient into the measure of direct and indirect effects. Aycicek and Yildirim (2006) recommended that study of direct and indirect effects of yield components to increase the yield provides the basis for its successful breeding program and hence the problem of yield decrease can be more effectively tackled on the basis of performance of yield components and selection for closely related characters.

Path analysis procedure was used by a number of researchers in wheat and can provide useful information about affectability form of traits to each other and relationships between them(Mollasadeghi *et al*., 2011). The same author also reported that number of grain per spike, grain weight, 1000 kernel weight and biological yield had the most direct and positive effect on grain yield. Another researchers (Kashif and Khaliq , 2004) conducted research on wheat and reported high magnitude and maximum positive direct effects between grain yield with days to heading followed by grain filling period, number of grains per spike, tillers per plant and spikelets per spike. As a result, these traits could be considered as essential for selection in wheatbreeding programstargetedfor higher grain yields.

Sabit *et al*. (2017) reported positive direct effect of some traits such asplant height, peduncle length, days to 50% flowering, grain filling periods, biological yield, harvest index, flag leaf length and spike length on grain yield and suggested use of these traits as direct selection criteria for improvement of grain yield. However, the same authors reported negative direct effect of some other characters such as number of productive tiller per plant, spikelets per spike, days to 50% heading, days to 50% maturity and flag leaf width with grain yield. Several otherresearchers also reported negative but non-significant direct effects on grain yield per plant withstraw yield, number of spikes per plant, number of grain per spike and thousand kernel weights (Singh and Diwivedi, 2002; Leilah and Al-Khateeb, 2005; Ali, 2012). On the other hand highest positive indirect effects on grain yield were observed for straw yield, number of spikes per plant, and thousand kernel weight via biological yield and these traits caused increasing of grain yield indirectly (Abinasa *et al*., 2011; Abderrahmane *et al*.,2013).

2.3.5. Cluster analysis

Cluster analysis is a process assemblage of multivariate method, whose main intention is to group individuals based on measured variables in to a number of different groups such that similar individualsare placed in the same group. Accordingly, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart as suggested by (Hair *et al.,* 1995).

Additionally, key aspect in cluster analysis is determining the optimal number of clusters or number of acceptable clusters. In essence, this involves deciding where to "cut" a dendrogram to find the true or natural groups. Cubic clustering criterion (CCC), pseudo F (PSF), and pseudo t^2 (PST^2) statistics were used in determining the number of clusters in the data. That is, local peaks of the CCC and pseudo F statistic combined with a small value of the pseudo t^2 statistic and a larger pseudo t^2 for the next cluster fusion (Mohammadi and Prasanna, 2003).

Dargicho *et al*. (2015b) clustered sixty eight bread wheat germplasm into six groups by considering the most important yield contributing characters viz.,days to 50% heading, days to 75% maturity, grain filling period, plant height, spike length, number of spikelet's per spike, number of kernels per spike, thousand kernels weight, grain yield, biomass yield and harvest index. The authors clustered the germplasms in such a way that 46 germplasm (67.6%) were

grouped into cluster I, 9 germplasm (13.23%) into cluster II, 6 germplasm (8.82%) into cluster III, 2 germplasm (2.94%) into clusters IV, 1 germplasm (1.47%) into cluster V and 4 germplasm (5.88%) into cluster VI, respectively. Finally, the authors suggested that the crossing between superior germplasm of above diverse cluster pair's might provide desirable recombinants for developing high yielding bread wheat varieties. Ahmed *et al.* (2017) also clustered 49 bread wheat genotypes which are released varieties and elite materials obtained from Sinana and Kulumsa Agricultural Research Centers and sorted the genotypes into six clusters by using Cubic clustering criterion (CCC), pseudo F and pseudo t^2 statistics for determining the number of cluster and obtained wider variations among the clusters.

2.3.6. Genetic divergence analysis

Genetic divergence analysis quantifies the genetic distance among the selected germplasm and reflects the relative contribution of specific traits towards the total divergence. Divergence analysis is a technique used to categorize germplasm that are as similar as possible into one group and others into a different. The amount of diversity present between germplasm determines the extent of improvement gained through selection and hybridization. The more divergent the two germplasm are the more will be the probability of improving through selection and hybridization (Dargicho *et al*., 2015b). D-square statistics developed by Mahalanobis (1936) has been used to classify the divergent genotypes in to different groups.

Genetic distances are measures of the average genetic divergence between cultivars or populations and genetic similarity is the converse of genetic distance and it refers to the extent of genetic similarities among cultivars (Smith, 1984). Diversity analysis can be carried out using morphological, cytological, biochemical and molecular characterization methods. Morphological markers were used for diversity analysis and are still in use. It involves morphological characterization of different entries grown in the field and morphological characteristics are the strongest determinant of agronomic value and taxonomic classification of plant (Cholastova and Knotova, 2012). Genetic distance is important for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregates (Akotkar *et al*., 2010). Shujaat *et al*.(2014) suggested that genetic variations is an important feature to get together the diversified goals of plant breeding including higher and quality yield, resistance to diseases, and wider

adaptations. In any breeding program, therefore, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981).

Various researchers grouped their materials under study into distinct groups. Arega *et al.* (2007) reported based on D^2 value estimates of genetic divergence, the 64 durum wheat genotypes were grouped into ten distinct clusters. Ajmal *et al.* (2013) grouped 50 genotypes of bread wheat into 5 clusters based on Ward's method, Salman *et al.* (2014) also reported based on Euclidean dissimilarity distance using Ward's method divided the accessions into six clusters.

2.3.7. Principal component analysis

Principal component analysis (PCA) is one of the multivariate statistical techniques which are a powerful tool for investigating and summarizing fundamental trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components. The first principal component accounts for maximum variability in the data with respect to succeeding components (Leilah and Al-Khateeb, 2005). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis of differentiation. The eigen values greater than unity are often used to determine how many factors to retain (Kaiser 1960).

Ahmad *et al.* (2014) reported, three principal components showed more than one Eigen value and showed about 73.94% of variability in which PC-I showed 39. 17%, PC-II 21.89% and PC-III exhibited 12.89% variability among different traits under experimental genotypes. Singh *et al*. (2014)reported in his study traits such as spike length with element value 0.546,days to heading with element value 0.721 and effective tillers with element value 0.704, contributed maximum to the total divergence of differentiation . Ajmal *et al*. (2013) reportedthe first three PCs with eigen values >1 contributed 70.59% of the variability amongst genotypes and characters contributing more positively with PC1 were number of spikelets per spike, spike length and grain yield.

3. MATERIALS AND METHODS

3.1. Description of Experimental Area

The experiment was conducted at Kokate and Hossana which are located in Wolaita and Hadya Zones, SNNPR of Ethiopia, respectively. The locations were assumed to represent the major and potential bread wheat production areas of Ethiopia. The sub-stations, Kokate and Hossana are located at 378 Km and 232 Km from Addis Ababa, respectively and both sub-stations are two of the research sites administered by ArARC. The experiment was carried out under rain fed conditions in 2018/2019 cropping season. Agro-climatic conditions of study locations are presented in Table 2.

Table 2. Agro-climatic conditions of study locations

Locations	Soil type	pH	Alt. (m.a.s.l)	Lati. (N)	Long. (E)	Rain fall (mm)	Temperature	
							min.	Max.
Kokate	Clay-loam	5.5	2150	6° 53’	37° 48’	800-1200	18°c	28°c
Hossana	Sandy-loam	5.72	2290	07°34’	37° 50’	900-1400	12°c	26°c

Source:(ArARC, 2018)

3.2. Experimental Materials

In this study, a total of 49 bread wheat genotypesof which 48 ICARDA origins which are selected randomly and one recently released variety, allreceived from KARCwereincluded. Thegenotypes werepure lines developed at ICARDA for optimum/potential areasto be further tested in mid- to highlands of Ethiopia for high yield potential, resistance to disease and insect pests.

Table 3. List of genotypes used in the study

G*	Genotype (Pedigree)	Seed source
G1	WBLL4//OAX93.24.35/WBLL1/4/SHUHA-1/3/MON'S'/ALD'S'//ALDAN'S'/IAS58	ICARDA
G2	KAUZ/STAR/3/MUNIA/ALTAR 84//MILAN/4/LEITH-1	ICARDA
G3	FARIS-22/4/BOW/PRL//BUC/3/WH576/5/NING MAI 9558//CHIL/CHUM18	ICARDA
G4	FILIN/3/CROC-1/AE.SQUARROSA (205)//KAUZ/4/FILIN/5/VEE/MJI//2*TUI/3/PASTOR/6/ASEEL-4	ICARDA
G5	WBLL1*2/BRAMBLING//ZAFIR-3	ICARDA
G6	WEAVER/TSC//WEAVER/3/WEAVER/4/WAXWING/5/DURRA-8	ICARDA
G7	CHAMRAN/4/OPATA/BOW//BAU/3/OPATA/BOW/5/SAMIRA-9	ICARDA
G8	KOUKAB-1//PFAU/MILAN/3/SOSSI-3	ICARDA
G9	VEE/NAC//MILAN/PASTOR/5/HUITES/4/CS/TH.SC//3*PVN/3/MIRLO/BUC	ICARDA
G10	SERI.1B//KAUZ/HEVO/3/AMAD/4/ESWYT99#18/ARRIHANE/5/SKAUZ/BAV92	ICARDA
G11	OPATA/RAYON//KAUZ/3/ETBW 4922/4/MILAN/PASTOR	ICARDA
G12	SHIHAB-19/KHIDER-1/5/YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE.SQUARROSA (224)//OPATA	ICARDA
G13	HUITES/4/CSTH.SC//3*PVN/3/MIRLO/BUC/5/ETBW 4922/6/QADANFER-4	ICARDA
G14	KINGBIRD/IZAZ-11	ICARDA
G15	KIRITATI/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/SHUHA-4/CHAM-8	ICARDA
G16	KRICHAUFF/2*PASTOR//SHUHA-8/DUCULA	ICARDA

Table 2. List of genotypes used in the study(***Continued***)

G*	Genotype (Pedigree)	Seed source
G17	P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN-a	ICARDA
G18	P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN-b	ICARDA
G19	ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA 86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'-a	ICARDA
G20	ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA 86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'-b	ICARDA
G21	PFAU/MILAN//ABIER-2/3/SHUHA-3//TURACO/CHIL	ICARDA
G22	TEVEE-1/STAR'S'//ETBW 4920/3/TEPOCA+LR34/2*BORL95	ICARDA
G23	KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR	ICARDA
G24	CHAM-10/3/PASTOR//MUNIA/ALTAR 84/4/PFAU/MILAN	ICARDA
G25	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-a	ICARDA
G26	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-b	ICARDA
G27	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-c	ICARDA
G28	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-d	ICARDA
G29	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-e	ICARDA
G30	THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B-a	ICARDA
G31	THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B-b	ICARDA
G32	CHAM-8/ETBW 4919//PFAU/MILAN	ICARDA
G33	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/GHALI-1	ICARDA

Table 2. List of genotypes used in the study(***Continued***)

G*	Genotype (Pedigree)	Seed source
G34	KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR	ICARDA
G35	FARIS-17//PFAU/MILAN/3/SOSSI-3	ICARDA
G36	ZERBA-6/FLAG-6/3/TAM200/PASTOR//TOBA97	ICARDA
G37	BABAX/LR42//BABAX*2/3/VIVITSI/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ	ICARDA
G38	TEMPORALERA M 87*2/TUKURU//FAYEQ-2	ICARDA
G39	NESMA*2/14-2//2*SAFI-3/4/PASTOR//HXL7573/2*BAU/3/WBLL1	ICARDA
G40	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/NESMA*2/14-2//2*SAFI-3	ICARDA
G41	FAYEQ-2/3/NESMA*2/14-2//2*SAFI-3	ICARDA
G42	QT6581/4/PASTOR//SITE/MO/3/CHEN/AEGILOPSSQUARROSA (TAUS)//BCN/5/PAVON 76/JADIDA-2	ICARDA
G43	WAXWING*2/VIVITSI//SHUHA-8/DUCULA	ICARDA
G44	WBLL1//TEVEE/KAUZ/3/MILAN/SHA7//POTAM*3KS811261-5	ICARDA
G45	KINGBIRD/3/NESMA*2/14-2//2*SAFI-3a	ICARDA
G46	KINGBIRD/3/NESMA*2/14-2//2*SAFI-3b	ICARDA
G47	KAUZ/STAR//ETBW 4920/3/QAMAR-2	ICARDA
G48	ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA 86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'	ICARDA
G49	WANE(ETBW6130)	KARC

G* = Genotypes used in the study

3.3. Experimental Designand Trial Management

Field experiment was laid out in 7x7 simple lattice designs in each location. The plot size was 2.5m long and 1.2 m wide ($3m^2$) with 6 rows. The space between replications, plots and rows was 2m, 0.5 m and 0.2m, respectively.

The experiment was conducted in 2018/2019 cropping season. As per the recommendation of the study area, a seed rate of 150Kg/ha (45g per plot) was used. Fertilizer, Urea 150Kg/ha and NPS also 100 Kg/ha or 45 and 30 g/plot were applied, respectively. All the NPS (100 kg/ha) was applied at sowing. Urea was applied in two split: one third at sowing, and the remaining two third just after 35-40 days of sowing (ATA and EIAR, 2007). Hand weeding was used for weed control and all other agronomic practices were undertaken uniformly.

3.4. DataCollection

Quantitative and qualitative data were recorded according to theInternational Board for Plant Genetic Resources (IBPGR, 1985)revised descriptor lists for wheat.Data were collected both on plot and plant bases. The four central rows were used for data collection on plot basis; whereas five randomly taken plants from the four central rows of each plot were used for data collection on plant basis. Mean data of the five sample plants were used for data analyses.

3.4.1. Data for quantitative characters

- **Data collected on plot basis**

Days to 50% heading (HD): The number of days from the date of sowing to the stage where 50% of the plants have fully emerged spikes.

Days to 90 % physiological maturity (MD): Recorded by estimating number of days from the date of planting to the date when 90 % of the crop stand stems, leaves, and floral bracts in a plot change to light yellow color.

Grain filling period (GFP): The number of days from heading to maturity obtained by subtracting the number of days to heading from the number of days to maturity.

Thousand seed weight (TSW) (g): The weight of one thousand randomly taken kernels from each experimental plot and adjusted to 12.5% moisture content.

Grain yield plot^{-1} (GY) (g plot^{-1}): Grain yield in grams obtained from the central four rows of each plot, and adjusted to 12.5% moisture content. Grain yield obtained from each plot was used to calculate grain yield in tons per hectare.

Biomass yields(BY) (kg plot^{-1}): The plants in the four central rows were harvested at the point of attachment to the ground, collected, sun-dried and weighed to obtain the biological yield.

Harvest index (HI) (%): Calculated on a plot basis, as the ratio of dried grain weight adjusted to 12.5% moisture content to the dried total above ground biomass weight and multiplied by 100.

Harvest index (HI) $= \frac{Drygrainyield}{Totaldryweght} * \mathbf{100}$ (Baydar, 2005 and Zhang, *et al*., 2008)

- **Data collected on plant basis**

Plant height (PH) (cm): The height of five randomly taken plants was measured at maturity stage from the ground level to the tip of the tallest spike in centimeter.

Spike length (SL) (cm): Actual measurement in centimeters were taken from spike base to tip of the tallest spike excluding awns and expressed as an average of five plants per plot.

Number of kernels per spike (KPS): The numbers of kernels per spike were measured by taking five random plants from each central four rows and counting the seeds in each spike.

Number of spikelets per spike (SPS): Numbers of spikelets per spike were measured by taking five random plants from each central four rows and counting the spikelets in each spike

Productive tillers per m^2 (PT): The ears bearing tillers or spikes were counted from per m^2.

3.4.2. Data for qualitative characters

All data collected for qualitative traits were measured according to the International Board for Plant Genetic Resources(IPGR,1985) revised descriptor lists for wheat**.**Data for the following qualitative parameters were recorded**:**

Spike density (SD): A visual measure of the density of a spike was measured on 1-9 scale. As 1= Verylax, 3 = Lax, 5 = Intermediate, 7 = Dense, 9 = Very dense, respectively.

Seed size (SS): The seed size was measured as 3, 5, and 7 for seeds classified under small, intermediate and large by visual observation, respectively.

Seed color (SC): Colour of the seed was also observed as red, white, brown and purple.

Degree of seed shriveling (DSS): Appearance of dry seed after harvest were recorded as 3= plump**,** 5 = Intermediate, and 7 = Shriveled, respectively.

Kernel Texture (KT):Code representing the relative hardness of a kernel expressed from 1 to 9 with 1= very soft or floury, 9 = very hard or vitreous checked by grinding the seed.

Awnedness (A): Observation on presence or absence of awns were measured as 0 = Awnless, 3 = Awnletted (short awns), and 7= Awned (conspicuous awns), respectively.

3.5. Statistical Analysis

3.5.1. Analysis of variance

The efficiency of simple lattice design over RCBD was checked and found to be efficient for most of the studied characters than RCBD. Thus, ANOVA was computed based on simple lattice design. Prior to performing statistical analysis for individual location, data were checked for the normalityand all data met the normality assumption.The quantitative data for each locations was subjected to analysis of variance (ANOVA) and done using Proc lattice and Proc GLM procedures of SAS version 9.3 (SAS, 2012), according to simple lattice design. Before computing the combined analysis, homogeneity test for the error variance of two locations was done using Hartley`s test (1950) and checked by using F-test (ratio of the largest mean square error to the smallest mean square error in the set) according to Gomez

and Gomez (1984) and they were homogeneous. Hence, combined analysis was computed. Mean comparisons among treatment means was conducted by the least significant difference (LSD) test at 5% levels of significance.

The individual locations data generated using the following model:

$$\mathbf{Pijk = \mu + gi + bk(j) + rj + eijk}$$

Where, Pijk = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j,

μ = grand mean,

gi = the effect of i^{th} genotype,

bk (j) = the effect of incomplete block k within replication j,

rj = the effect of replication j, and

eijk = the residual or effect of random error associated to the observation.

Table 4. Analysis of variance skeleton for individual location in simple lattice design.

Source of variation	DF	SS	MS	F-Value
Replication	R-1	SS_R	MS_R	MS_R/MSE
Block (adjusted)	R(k-1)	SS_B	MS_B	MS_B/MSE
Genotype (adjusted)	G^2-1	SS_{GAdj}	MS_G	MS_G/MSE
Genotype (Unadjusted)	G^2-1	SS_{GU}	MS_{GU}	MS_{GU}/MSE
Intra-block (error)	(k-1)(Rk-k-1)	SS_E	MS_E	
Total	(R)(k^2)-1	SS_T		

NB: R = number of replication, G = number of genotypes, DF = degree of freedom, k = block, SS = Sum of squares, MS = mean squares, SSR and MS_R are sums of squares and mean of replication, respectively. SS_G and MS_G are sums of squares and mean of genotypes, respectively.SS_B and MS_B are sums of squares and mean of blocks within replication, respectively. SS_E and MS_E are sums of squares and mean of intra-block error, respectively and SST is sum of squares of the total.

The combined analysis of variance over two locations was carried out according to the following model:

$$\mathbf{Pijkl = \mu + gi + bk(j)(l) + rj(l) + Ll + (gl)il + eijkl}$$

Where, P_{ijkl} = phenotypic value of i^{th} genotype under j^{th} replication at l^{th} location and k^{th} incomplete block within replication j and location l,

μ= grand mean,

gi= the effect of i^{th}genotype,

bk (j) (l) = the effect of incomplete blocks within replication j and location l,

rj(l) = the effect of replication j within location l,

Ll = the effect of location l,

(gl)il = the interaction effects between genotype and location, and

eijkl = the residual.

Table 5. Analysis of variance skeleton for combined analysis over location in simple lattice design (Kokate and Hossana), SNNPR

Source of variation	DF	SS	MS	F-value
Location(L)	L-1	SS_L	MS_L	
Replication with in location(r)	L(r-1)	SS_r	MS_r	
Blocks with in replication(b)	r(k-1)	SS_b	MS_b	MSb/MSe
Genotypes(adj)	k^2-1	SS_g	MS_g	MSg/MSe
Genotypes x Location	(g-1)(L-1)	SSg_L	MS_{gxL}	
Intra-block error (e)	Lg (r-1)-(rk- 1)	Sse	MS_e	
Total	Lrk2 -1	SS_t		

Key: L = number of location, r = number of replication, g = number of genotypes, DF = degree of freedom, b = block, SSr and MSr are sums of squares and mean of replication, respectively. SSg and MSg are sums of squares and mean of genotypes, respectively. SSb and MSb are sum of squares and mean of blocks within replication respectively. SSE and MSE are sums of squares and mean of intra block error, respectively and SST is sum of squares of the total.

3.6. Estimation of Genetic Parameters

3.6.1. Phenotypic and genotypic variances and coefficients of variation

Estimates of variance components were computed using the formula suggested by Burton and De Vane (1953) as follows:

1) Phenotypic variance($\sigma^2 p$) = $\sigma^2 g + \sigma^2 gl/L + \sigma^2 e/LR = MSG/RL$

Where,$\sigma^2 p$ = Phenotypic variance,

$\sigma^2 g$ = Genotypic variance,

$\sigma^2 gl$ = genotype by location variance,

$\sigma^2 e$ = Environmental variance,

R = number of replication,

L = number of location and

MSG = mean square of genotype

2) Genotypic variance($\sigma^2 g$) = ($MSG - MSGXL/RL$)

Where,$\sigma^2 g$ = genotypic variance,

MSG = mean square of genotype,

MSGxL = mean square of genotype by location,

R = number of replication and

L = number of location.

3) Genotype x location interaction variance($\sigma^2 gl$) = ($MSGXL - MSE)/R$

Where,$\sigma^2 gl$ = genotype by environmental interaction variance,

MSGxL = mean square of genotype by location interaction,

MSE = mean square of error and R = number of replication.

4) Environmental variance (mean square error)($\sigma^2 e$) =MSE

Phenotypic and genotypic coefficient of variation was estimated by using the methods suggested by Singh and Chaudhury (1985) as follows:

Phenotypic coefficients of variation $(\mathbf{PCV}) = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \mathbf{x100}$

Genotypic coefficients of variation $(\mathbf{GCV}) = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \mathbf{x100}$

Where, $\sigma^2 p$ = Phenotypic variance,

$\sigma^2 g$ = Genotypic variance and

$\bar{x}$ = Grand mean of the traits under consideration.

Sivasubramaniam and Menon (1973) and Deshmukh *et al.* (1986) classified 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:

3.6.2.Broad sense heritability ($h^2 b$)

Broad sense heritability values were estimated using the formula adopted from Falconer and Mackay (1996).

$$\mathbf{Heritability}(h^2 b) = \frac{\sigma^2 g}{\sigma^2 p} \mathbf{x\ 100}$$

Where, $h^2 b$ = heritability in broad sense,

$\sigma^2 p$ = Phenotypic variance and

$\sigma^2 g$ = Genotypic variance

The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al*. (1955) as 0 - 30% = low, 30 – 60% = moderate and > 60% = high, respectively.

3.6.3. Estimation of genetic advance

Genetic advance (GA) and percent of the mean (GAM) were calculated by assuming selection of superior 5% of the genotypes estimated in accordance with the methods illustrated by Johnson *et al.(1995) as:*

$$\mathbf{GA = k * \sigma p * h^2 b}$$

Where, GA = expected genetic advance,

K = constant (selection differential where K = 2.06 at 5% selection intensity), σp = phenotypic standard deviation on mean basis and

h^2b = heritability in broad sense.

Genetic advance as percent of mean (GAM) was calculated by using the subsequent formula Johnson *et al*. (1955) and classified as low (<10%), moderate (10-20%) and high (>20%):

$$\mathbf{GAM = \frac{GA}{\bar{x}} X\ 100}$$

Where, GAM = genetic advance as percent of mean, GA = genetic advance under selection, and $\bar{x}$= mean of the population in which selection is effective.

3.7. Association of Characters

3.7.1. Estimation of correlation coefficients

Phenotypic and genotypic association between all possible pair of quantitative character was performed using SAS software version 9.3 (SAS, 2012).

3.7.2. Path coefficients analys

The direct and indirect effect of yield related traits on yield was computed through Path coefficient analysis.The analysis was conducted following the method suggested by Dewey and Lu, (1959) using the phenotypic as well as genotypic correlation coefficients to govern the direct and indirect effects of yield components on grain yield based on the following relationship:

$$\mathbf{rij = Pij + \Sigma rikpkj}$$

Where,

rij = mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient,

Pij = Component of direct effects of the independent trait (i) on the dependent variable (j) measured by the path coefficient,Σrikpkj = Summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) by all other independent traits (k) and the contribution of the remaining unknown characters measured residual effect estimated by the formula as follows:

Residual effect = $\sqrt{\mathbf{1} - \boldsymbol{R^2}}$ Where: - $R^2 = \Sigma p_{ij} r_{ij,}$ R^2 is the residual factor, Pij is the direct effect of yield by i^{th} characters and rij isthe correlation of yield with the i^{th} characters.

3.7.3. Cluster analysis

Clustering of genotypes were done into groups using the average linkage method by PROC clustering strategy of SAS Version 9.3 (SAS, 2012) and appropriate numbers of clusters were determined from the values of Pseudo F and Pseudo T^2 statistics (SAS, 2012). The dendrogram constructed based on the average linkage and Euclidean distance used as a measure of dissimilarity.

3.7.4. Genetic divergence analysis

A measure of a group distance based on multiple traits was given by generalized Mahalanobis D^2 statistics (Mahalanobis, 1936) for quantitative characters. The distance between any two groups was estimated from the following relationship:

$$\boldsymbol{D^2 P = (X_i - X_j)\, S^{-1}\, (X_i - X_j)}$$

Where, D^2p = the squared distance between any two genotypes i and j;

X_i and X_j = the p mean vectors of genotypes i and j, respectively.

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

The significance of the squared distance values attained for a pair of clusters was taken as the calculated value of x^2 (chi-square) and was tested against the tabulated x^2 values at p-1 degree of freedom at 1% and 5% probability level, where p = number of traits used for clustering genotypes (Singh and Chaudhury, 1985).

3.7.5. Principal component analysis

Principal component analysis was computed using SAS soft ware version 9.3(SAS Institute, 2012). Principal component analysis reflects the importance of the traits with largest contributor to the total variation at each axis for differentiation (Sharma, 1998).Principal components (PCs) with eigen value greater than 1.0 had been used as criteria to determine the number of PCs (Kaiser, 1960).

3.8. Analysis of Qualitative Characters

The percentage frequency distribution of phenotypic classes of each qualitative character was computed using excel computer program (Microsoft excel, 2010). The Shannon-Weaver index (H') is one of several diversity indices used to measure diversity in categorical data. Itwas estimated on the phenotypic frequency data and calculated as described by Hutcheson (1970), i.e.

$$H' = -\sum_{i=1}^{s} pi \, ln \, pi$$

Where,H'= Shannon-Weaver diversity index, Pi = is the proportion of the total number of individuals genotypes in the i^{th} class,lnis the natural logarithm, s is the number of phenotypic classes for a given character, and **Σ** is the sum of the calculations.

H was standardized by converting to the relative index (H'), where each value of H were divided by its maximum value as follows, in order to keep the value between zero and one. $H^{'}$ = H/Hmax, where Hmax = ln (n) and n is number of phenotypic classes.Test of independence among the phenotypic classes was also conducted using chi-square (X^2) test.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance (ANOVA)

Mean squares of the characters from analysis of variance (ANOVA) at individual locations (Kokate and Hossana) and combined over the two locations were presented in (Appendix Tables 1 and 2) and (Table 6), respectively.

Table 6. Mean squares of combined analysis of variance for 11 quantitative traits of 49 bread wheat genotypes evaluated in 2018/2019 cropping season at Kokate and Hossana, SNNPR

Traits	MSL (df =1)	MSG (df = 48)	MSGxL(df = 48)	MSE (df = 84)	Cv (%)
HD	374.70**	170.63**	8.00**	2.44	2.39
GFP	105.80**	150.80**	40.98*	22.67	9.48
MD	82.29^{ns}	143.85**	47.00**	23.84	4.31
PH	5620.72**	64.08**	23.12*	11.65	4.54
SL	5.76**	1.11**	0.32^{ns}	0.23	5.61
KPS	7583.92**	72.09**	56.85*	35.37	12.39
SPS	13.80**	3.57**	1.33^{ns}	1.87	7.22
PT	108852.86**	1033.10^{ns}	1020.29^{ns}	1079.48	19.99
BY	66.91**	1.259**	0.23**	0.14	15.69
GY	10.25**	1.774**	0.47**	0.20	13.14
TSW	3173.55**	75.85**	26.14**	14.69	10.58
HI	8091.77**	220.17**	33.25*	25.98	13.57

NB : HD = days to 50% heading, GFP = days to grain filling period, MD = days to 90% physiological maturity, PH = plant height (cm), SL = spike length (cm), KPS = number of kernels per spike, SPS = number of spikelets per spike, BY = biological yield (kg/ha), GY = grain yield (tone/ha), TSW = one thousand seed weight (gm), HI = harvest index (%), MSL = mean square of location, MSG = mean square of genotype, MSGxL = mean square of genotype by location interaction, MSE = mean square of error, CV = coefficient of variation, df = degree of freedom, * = significant at ($p \leq 0.05$), and ** = highly significant at ($p \leq 0.01$)

At individual location and over locations, the analysis result showed highly significant differences (P<0.01) among the tested characters fordays to 50% heading, grain filling periods, days to 90% physiologicalmaturity, plant height, spike length, number of kernels per spike,and 1000- seed weight,indicating the presence of adequate variability which can be exploited through selection.

The pooled analysis showed significant (P < 0.01) location effects except for days to 90% physiological maturity indicating that the phenotypic expression of this trait is similar at both locations. Genotypes effects were highly significant (P < 0.01) for all characters studied across locations except for number of productive tillers per meter square area, indicating that the presence of considerable variation in the genetic materials.

The mean squares due to genotype x location interactioneffects revealed significant (p < 0.05) for grain filling periods, plant height, kernels per spike and harvest index to highly significant (P < 0.01) differences fordays to 50% heading, days to 90% physiological maturity, biological yield,grain yield and 1000-seed weight whereasspike length,spikelet per spike and productive tillers exhibitednon-significant differences among the tested bread wheat genotypes. The significant interaction effects indicate the differential performances of genotypes in the different test locations and that of none significant interaction effects exhibits the traits were similarly performed in both locations. Supportive results were reported by (Kifle *et al*, 2016; Endashaw, 2018;Girma 2018).

4.2. Range and Mean Performance of the Genotypes

4.2.1. Mean and range of yield and major yield related characters

Based on the combined data over the two test locations, wide ranges between the minimum and maximal values were observed for the 11 quantitative characters evaluated in Table 7.

Table 7. Estimates of ranges, mean, standard deviation (SD) and Variance components for 11 quantitative characters combined over the two locations, Kokate and Hossana, SNNPR, 2018

Traits	Range	Mean±SD	$\sigma^2 e$	$\sigma^2 p$	$\sigma^2 g$	PCV %	GCV %	$h^2 b$ %	GA	GAM %
HD	54.25 -73.50	63.69±1.56	2.44	42.66	40.66	10.26	10.01	95.31	12.82	20.14
GFP	39.50- 67.50	52.12±4.76	22.67	37.70	27.45	11.78	10.05	72.82	9.21	17.67
MD	103.25 -130.75	115.81±4.88	23.84	35.96	24.21	5.18	4.25	67.33	8.31	7.18
PH	74.500- 91.15	82.27±3.41	11.65	16.02	10.24	4.87	3.89	63.92	5.27	6.41
SL	7.25 - 9.85	8.44±0.48	0.23	0.28	0.20	6.24	5.26	71.10	0.77	9.14
KPS	37.50 -57.40	48.00±5.95	35.37	18.02	3.81	8.85	4.07	21.15	1.85	3.85
SPS	14.90 - 18.90	16.96±1.37	1.87	0.89	0.561	5.57	4.42	62.81	1.22	7.21
BY	1.58 - 2.90	2.14±0.37	0.14	0.32	0.26	26.26	23.69	81.40	0.53	24.71
GY	2.34 - 4.41	3.38±0.45	0.20	0.44	0.25	19.74	14.87	56.78	0.52	15.37
TSW	25.84 - 42.39	34.98±3.83	14.69	18.96	12.43	12.45	10.08	65.54	5.88	16.81
HI	22.32 - 42.30	33.87±5.01	25.98	55.04	46.73	21.90	20.19	84.90	12.98	38.31

NB: HD = days to 50 heading, GFP = grain filling period, MD = days to 90% physiological maturity, PH = plant height (cm), SL = spike length (cm), KPS = number of kernels per spike, SPS = number of spikelets per spike, BY= biological yield (kg/plot), GY = grain yield (tone/ha), TSW = thousand seed weight (gm/plot) and HI = harvest index (%)

Grain yield ranged from2.34to 4.41 with the grandmean performance of 3.38. The highest yield was recorded for genotype 22 (G22) and the lowest was recorded for genotype 13 (G13)and genotype 44 (G44). Depending on the mean performance, only one genotype (G22) hadthe highest yield (4.41) performance than the standard check variety (Wane).Generally, the range of variation was wide for all the studied characters. Various investigators reported wide range of variation among the tested bread wheatgenotypes. Berhanu *et al*. (2017) conducted genetic variability among 49 bread wheat genotypes at Axum, Northern, Ethiopia and reported a wide range of grain yield from 2.37 to 5.44 t ha^{-1} with grandmean of 3.95 t ha^{-1}. Similar ranges realised for 1000-seed weight in the present study was also reported by many authors (Rizwana*et al*., 2010; Obsa, 2014; Gezahegn *et al*., 2015).

In the present study ondays to 50% heading, genotype 48 (G48) was foundthe earliest (54.25 days) while genotype 9 (G9) showed the latest heading (73.50 days) with a grand mean of 63.69. Days to grain filling periods ranged from 39.50 to 67.50 days for the genotype 19(G19) and genotype 48(G48), respectively, with the grand mean of 52.12 while days to maturity ranged from 103.25to130.75 day for the genotype 19 (G19) and genotype 9 (G9) with the mean of 115.81, respectively. Among the tested genotypes 26.5% had early days to heading than the standard check G49 (Wane) while 6.12% of the genotypes had early grain filling period and days to maturity than the standard check.

Comparative trends of variability in phenology were also reported in bread wheat i.e., 47 to 74 days to flowering, 36 to 60 days to grain filling period and 86 to 120 for days to maturity (James *et al.,* 2017). Furthermore, differences in days to heading, grain filling period and maturity in different genotypes reported by Endashaw (2018), who observed 53 to 80 days for 50% heading, 126 to 143 days to maturity and 58 to 78 days for grain filling period, The result indicates that genotypes that is early heading do not necessarily mature early because some genotypes take more time for reproductive stage while other genotypes need longer time for days to maturity and take less time for the vegetative stage . This variation among genotypes might be due to the genetic factors carried by the genotypes for each character as well as the differences of growth seasons and environments under which the materials are evaluated.

Plant height ranged from 74.50 to 91.15cm with the grand mean of 82.27cm with maximum number of plant height was observed for genotype 42 (G42) while minimum number was recorded for genotype 2(G2). The shortestbread wheat genotypes are resistant to lodging problems in areas where continuous rain fall exist as of the area where the present study was conducted while the reverse is true for the longest genotypes. Among the tested bread wheat genotypes 83.63% have shorter plant height than the standard check this provides better opportunity to select lodging resistant genotypes for high rain fall areas for further genetic improvement. Several investigators reported wide range of variation in plant height among the tested bread wheat genotypes. Obsa (2014) observed wide variation among the tested bread wheat genotypes ranged from 80.28 to 112.59 cm with the grand mean value of 93.34 cm. Furthermore, Kotal *et al*. (2010) and Khan (2013) obtained wide variation on bread wheat genotypes for the traits under consideration.

Traits like, number of kernels per spike is an important plant attribute that depends upon spike length, spikelets per spike and spike density. Accordingly, wide genotypes variation for spike length, spikelets per spike, number of kernels per spike and 1000- seed weight ranged from 7.25 to 9.85cm,14.90 to 18.90,and 37.50 to 57.40 and 25.84 to 42.39 with an average value of 8.44cm,16.96,47.99 and 34.98, respectivelyTable 7. The mean performances of genotypes for biomass yield and harvest index were ranged from 1.58 to 2.90 and 22.32 to 42.30 with the grand mean of 2.14 and 33.87, respectively. This wide ranges of mean values of these characters depicted that bread wheat genotypes possess good amount of genetic variability.

Among the tested bread wheat genotypes all genotypes showed longer spike length than standard check (Wane) with the longest spike length was recorded for genotype 30(G30) and the shortest for genotype 49(Wane) or the standard check.High number of kernels per spike was recorded for genotype 1(G1) and the lower number of kernels per spike were recorded for genotype 44 (G44). Among the tested genotypes seven genotypes (G1, G47, G10, G28, G38, G32, and G3) have higher number of kernels per spike (57.40,56.45,54.15,53.65,52.75,52.75 and 52.50), respectively than that of the standard check (Wane) with the mean performance of 52.25 i.e., 14.28% of the tested bread wheat genotypes have mean performance greater than the standard check while all genotypes performed higher spikelet per spike than the standard check (Wane) where as only two genotypes G14(KING BIRD/IZAZ-11) and G15 superior for

1000-seed weight with the grand mean performance of 42.39,41.38, respectively than the check variety (Wane).

4.3. Estimation of Variability Components

4.3.1. Phenotypic and genotypic coefficient of variation, heritability and genetic advance of combined analysis

The estimated PCV and GCV values from combined analysis over the two test locations were presented in Table 7. The PCV value ranged from 4.87 % for plant height to 26.26% for biological yield and the GCV value also ranged from 3.89 % for plant height to 23.69% for biological yield, which indicated a wide range of estimates for all the characters.

Sivasubramaniam and Menon (1973) and Deshmukh *et al*. (1986) classified PCV and GCV values greater than 20% as high, values between 10% and 20% to be moderate where as less than 10% are considered to be low. Based on this categorization, high PCV and GCV values were observed for biological yield and harvest index; 26.26% and 23.69% and 21.91% and 20.19%, respectively, where as moderate phenotypic and genotypic coefficients of variation were observed for days to 50 % heading (10.26%, 10.01%), grain filling period (11.78%, 10.05%), grain yield (19.74%, 14.87%) and thousand seed weight (12.43%, 10.08%), respectively these might imply selection based on these characters could be effective .

Though the PCV values were higher than the GCV values for all characters studied in the present study (Table 7), the magnitude of the difference was small for all characters. This indicates that the variability among genotypes for such a character could be due to genetic effects than that of environmental effects. Therefore, selection for these characters based on phenotypic appearance would likely result in improvement of other correlated character. Similar results to the current findings depicting closer values of the PCV to the GCV estimates for most characters there by showing little environmental effect on the expression of the characters were also reported (Ali *et al*., 2012; Dawit *et al*., 2012; Dargicho *et al*., 2015b and Adhiena *et al*., 2016).

4.3.2. Estimates of broad sense heritability (h^2b)

In this study, broad sense heritability values ranged from 21.15% for number of kernels per spike to 95.31% for days to 50% heading Table 7. Robinson *et al*. (1955) suggested heritability as low, moderate and high for the values 0 to 30%, 30 to 60% and above 60%, respectively.

In the present study,all the tested characters had moderate to high heritability values except number of kernels per spike with heritabilityvalue 21.15%. High heritability values were recorded for days to 50% heading (95.31%), harvest index (84.90%), biological yield (81.40%), grain filling period (72.82%), spike length (71.10%), days to 90% physiological maturity (67.33%), thousand seed weight (65.54%), plant height (63.92%) and number of spikelet per spike (62.81%). High heritability values for these characters might indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. Results from the present studywere in agreement with results reported byDargicho *et al.* (2015a), and Abebe and Desta (2015).

Moderate heritability value wasrecorded for grain yield (56.78 %). The present findings were in agreement with the result of Obsa (2014) and Berhanu *et al*. (2017) in bread wheat, who reported moderate values of 43.57% and 52.83% for grain yield, respectively. In the present study,low heritability (21.15%)was recorded for number of kernels per spike showing that the character washighly influenced by environmental effect and genetic improvement through selection couldbe difficult.Similarly, Endashaw (2018) in bread wheat also reported low heritability value of 29.62 % for number of kernels per spike.

4.3.3. Estimates of genetic advance (GA) and genetic advance as percent of mean (GAM)

According to Johnson (1955) heritability alone does not provide information on the genetic progress for an effective selection of the best individual but heritability in conjunction with genetic advance would give a more reliable index of selection. The range of genetic advance and genetic advance as percent of mean is classified as low if it is less than 10%, moderate between 10 and 20% and high if more than 20% (Johnson,1955). Accordingly, low GA was recorded for grain filling period, days to maturity,plant height, spike length, number of

kernels per spike, spikelets per spike, biological yield, gain yield and thousand seed weight where as moderate GA was recorded for days to 50% heading and harvest index Table 7.

Genetic advance as percent of mean (GAM) values ranged between 3.85% for number of kernels per spike and 38.31% for harvest index and low GAM was recorded for number of kernels per spike, days to maturity, plant height, spike length, and number of spikelet per spikeand moderate GAM was recorded for grain filling periods, grain yield and thousand seed weight whereas high GAM was recorded for days to 50% heading, biological yield and harvest index Table 7.

In the present study high heritability along with high genetic advance as percent of the mean was exhibited by days to 50% heading, biological yield and harvest index indicating these are inherited characters that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these characters. More recently, comparative findings were reported by Rathwa *et al.* (2018) in wheat. The authors reported high heritability coupled with high genetic advance as percent of mean for days to 50% heading, biological yield and harvest index.

High heritability with moderate GAM was exhibited by grain filling period and thousand seed weight. Similar results were reported by Obsa *et al*. (2014), Gezahegn *et al.* (2015) and Berhanu *et al.* (2017). Moderate heritability with moderate GAM was obtained for grain yield. This is in accordance with James *et al*. (2017) and Kifle *et al*. (2016) in bread wheat genotypes. but contradicted the findings of Endashaw (2018) who obtained low heritability along with low genetic advance as percent of the mean. The dissimilarity in findings may be due to various reasons including the genetic material used and environmental conditions in which the experiments were conducted.

High heritability with low GAM was observed for days to maturity, plant height, spike length and number of spikelet per spike, implyingless influence of environment but prevalence of non-additive gene action in which selection would be less effective. Hence, heterosis breeding or hybridization followed by repeated selection (recurrent selection) would be recommended for the improvement of such characters (Mohammed, 2019). The present results go in linewith those previously reported by Kashif and Khaliq (2004) and Neru *et al.* (2017) in bread wheat

genotypes. Low heritability with low genetic advance as percent the mean was observed by number of kernels per spike; reflecting that these characters are governed by non additive gene actions and highly influenced by the environment. For these characters breeder may not benefits from selection as well as hybridization because high involvement of environment. Hence, it is better to create variation by genetic engineering or mutation rather than selection.

4.4. Correlation Coefficient Analysis

4.4.1. Phenotypic andgenotypiccorrelation coefficients of grain yield with other characters

In the present study, grain yield showed varying trends of association with yieldcomponents at both genotypic and phenotypic levelsTable 8.

Table 8. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients

Traits	HD	GFP	MD	PH	SL	KPS	SPS	BY	TSW	HI	GY
HD		-0.116^{ns}	0.633**	0.041^{ns}	0.339*	0.273^{ns}	0.520**	0.479**	0.065^{ns}	0.537**	-0.045^{ns}
GFP	-0.104^{ns}		0.696**	0.013^{ns}	0.269^{ns}	-0.060^{ns}	0.145^{ns}	0.142^{ns}	0.220^{ns}	-0.006^{ns}	0.041^{ns}
MD	0.604**	0.730**		0.040^{ns}	0.455**	0.150^{ns}	0.489**	0.457**	0.125^{ns}	-0.393**	-0.001^{ns}
PH	0.045^{ns}	0.015^{ns}	0.043^{ns}		0.148^{ns}	0.030^{ns}	-0.061^{ns}	0.127^{ns}	0.285*	-0.080^{ns}	0.121^{ns}
SL	0.310**	0.255*	0.417**	0.117^{ns}		0.235^{ns}	0.631**	0.305*	0.311*	-0.303*	0.029^{ns}
KPS	0.219*	0.048^{ns}	0.112^{ns}	0.041^{ns}	0.208*		0.368**	0.299*	0.023^{ns}	0.013^{ns}	0.303*
SPS	0.396**	0.041^{ns}	0.305**	-0.064^{ns}	0.365**	0.220*		0.373**	-0.063^{ns}	-0.316*	0.062^{ns}
BY	0.422**	0.108^{ns}	0.377**	0.142^{ns}	0.290**	0.262**	0.228*		0.141^{ns}	-0.432**	0.561**
TSW	-0.051^{ns}	0.164^{ns}	0.097^{ns}	0.277**	0.245*	-0.024^{ns}	-0.020^{ns}	0.135^{ns}		0.195^{ns}	0.317*
HI	-0.458**	-0.021^{ns}	-0.332**	-0.108^{ns}	-0.235*	-0.001^{ns}	-0.174^{ns}	-0.466**	0.133^{ns}		0.446**
GY	-0.038^{ns}	0.011^{ns}	-0.017^{ns}	0.106^{ns}	0.050^{ns}	0.261**	0.089^{ns}	0.531**	0.274**	0.416**	

NB: HD = days to 50% heading, GFP = grain filling period, MD = days to 90% physiological maturity, PH = plant height (cm), SL = spike length (cm), KPS = number of kernels per spike, SPS = number of spikelets per spike, BY= biological yield (kg/plot),GY= grain yield (tone/ha), TSW = thousand seed weight (gm/plot) and HI = harvest index (%).

The range of genotypic correlation was from -0.001 for days to maturity to 0.561 for biological yield where as phenotypic correlation from 0.011 for grain filling period to 0.531 for biological yield. The analysis revealed that grain yield had positive and significant association with number of kernels per spike (rg = 0.303, rp = 0.261), biological yield (rg = 0.561, rp = 0.531), thousand seed weight (rg = 0.317, rp = 0.274) and harvest index (rg = 0.446, rp = 0.416). This signified that the improvement of one character will simultaneously improve the other.

Results from the present study go in line with the results reported by Kashif and Khaliq (2004), Obsa (2014), Kifle *et al.* (2016), and Kumar *et al*. (2016). These authors reported significant and positive correlation of grain yield with biological yield, harvest index and thousand seed weight in bread wheat genotypes.

4.4.2. Genotypic and phenotypic correlations among yield related characters

In this study, days to 50% heading was correlated positively and significantly with days to maturity, spike length, number of spikelets per spike and biological yield both at genotypic and phenotypic levels Table 8. These results implythat early heading genotypes had a probability to mature early with significant number of spikelet per spike that contributes better spike length andbiological yield. Similar results were reportedby Kumar *et al.* (2013) and Girma (2018). These authors reported highly significant association of days to heading with days to maturity and spikelet per spike.

In the present study, days to 50% heading exhibited positive and significant correlation with number of kernels per spike at phenotypic level. It showed positive and highly significant correlation with harvest index at genotypic level whereas negative and highly significant correlation was exhibited at phenotypic level with harvest index. Similar to the present study, Endashaw (2018) reported positive and significant association among days to heading with number of kernels at phenotypic level.

Positive and highly significant correlation of grain filling period was realizedwith days to maturity both at genotypic and phenotypic levels; positive and significant correlation of grain filling period was observed with spike length at phenotypic level (Table 8), indicating

genotypes that reached grain filling period early had better chance to mature early, and also at phenotypic level late maturing genotypes had higher spike length. Therefore, early maturity is animportant character for a breederas early maturinggenotypes canescape unfavorable environmental conditions during growth stages.

The study revealed that days to maturity had positive and significant correlation with spike length, number of spikelet per spike and biological yield both at genotypic and phenotypic levels (Table 8), showing genotypes that have early grain filling period had resulted in early maturity and genotypes that mature lately had higher spike length and number of spikelet per spike which in turn resulted in higher biological yield. However, there was highly significant and negative correlation existed among days to maturity and harvest index at genotypic and phenotypic levels.

James *et al.* (2017) also reportedhighly significant and positive correlation between days to maturity with number of spikelet per spike and spike length as well as significant and negative association of days to maturity with harvest index. Similarly,Sabit *et al*. (2017)reported highly significant and negative correlation among days to maturity and harvest in bread wheat.

Plant height showed positive and significant correlation with thousand seed weight at genotypic and phenotypic levels but positively and none significantly correlated with spike length, number of kernels per spike and biological yield at genotypic and phenotypic levels where as negative and non significant correlation with harvest index at genotypic and phenotypic levels Table 8. Supportive finding was reported by Kashif and Khaliq (2004) who reported positive and significant relation of plant height with thousand seed weight; positive and non significant correlation of spike length but positive and significant correlation with spikelet per spike both at genotypic and phenotypic levels. Furthermore, Eid (2009) reportedpositive relationship of plant height with spike length, number of spikes, and number of grains per spike and 1000-grain weightin bread wheat. Similarly, Girma (2018) also reported negative and non significant correlation of plant height with harvest index.

The study indicated that spike length had positive and significant correlation with number of spikelets per spike, biological yield and thousand seed weight at phenotypic and genotypic levels indicating genotypes with larger spike length had high number of spikelet per spike and

biological yield but positively and non significantly correlated with number of kernels per spike at genotypic level while negatively and significantly correlated with harvest index both at genotypic and phenotypic levels. The same findings were reported in bread wheatby Kashif and Khaliq (2004), Alemu and Desta (2017), James *et al.* (2017) and Obsa *et al.* (2017).

Kernels per spike foundpositively and significantly correlated with spikelet per spike and biological yield butnegatively and none significantly related with thousand seed weight and harvest index. Spikelet per spike had showed positive and significant relation with biological yield at both levels while negatively and none significantly correlated with thousand seed weight and harvest index at phenotypic level but had negative and highly significant relation with harvest index at genotypic level Table 8.This finding is go in linewith Dogan and Senyigit (2016) who reportedpositive and significant correlation with kernels per spike and spikelet per spike in hexaploid triticale.Biological yield exhibited negative and highly significant correlation with harvest index at genotypic and phenotypic levels. Similarly, Sohail *et al*. (2018) had found negative and highly significant correlation between biological yield and harvest index in bread wheat genotypes.

4.5. Path Coefficient Analysis

In current study, traits that showed significant correlation with grain yield were advanced to path coefficient analysis both at genotypic and phenotypic levels. The results of path analysis for direct and indirect effects of the characters studied both at genotypic and phenotypic levels are illustrated in Tables 8 and 9, respectively.

4.5.1. Genotypic path coefficient analysis

The results of path coefficient analysis at genotypic level is presented in Table 9

Table 9. Genotypic path coefficient analysis direct (diagonal) and indirect (off diagonal) effect of the characters

Variables	KPS	BY	TSW	HI	rg
KPS	**0.018**	0.273	0.001	0.011	0.303*
BY	0.005	**0.913**	0.004	-0.361	0.561**
TSW	0.000	0.129	**0.026**	0.162	0.317*
HI	0.000	-0.394	0.005	**0.835**	0.446**

NB: Residual = 0.32, * = significant at $p \leq 0.05$, ** = highly significant at $p \leq 0.01$, KPS = number of kernels per spike, BY = biological yield (kg/plot), TSW = thousand seed weight (gm), HI = harvest index (%), rg = genotypic correlation of the character with grain yield.

The results revealed that biological yield exhibited the highest positive direct effect (0.913)on grain yield followed by harvest index (0.835), indicated that the positive and significant correlation of biomass yield and harvest index with grain yield at genotypic level was due to the direct effect of these characters on grain yield. Similar results were reported in bread wheatgenotypes by James *et al.* (2017), who obtained maximum positive direct of biological yield followed by harvest index. Some other authors (Obsa, 2014; Dargicho *et al*., 2015a) were also reported similar results.

The lowest positive direct effect was exhibitedby kernels per spike (0.018), indicatingthat the positive association of kernels per spike with grain yield was due to the indirect effect of this character on yield through other characters such as biomass yield and harvest index.This shows the importance of considering harvest index and biomass yield when selection of wheat genotypes for higher grain yield is desired. Similarly, Endashaw (2018) reported the lowest positive direct of kernels per spike on grain yieldin bread wheat genotypes.Conversely, Obsa (2014) reported maximum negative direct effect of kernels per spike on grain yield followed by days to heading and grain filling period.

The direct genotypic effect of kernels per spike was positive (0.018).The maximum positive indirect effect of kernels per spike was scored via biological yield (0.273) where as the lowest was scored through thousand seed weight (0.001) followed by harvest index (0.011). The

present study go in line with Kifle *et al*. (2016), who reported positive direct effect of kernels per spike on grain yield and they reportedmaximum positive indirect effect of kernels per spike via biological yield. Onthe contrary, Abderrahmane*et al.* (2013) realizednegative direct effect of kernels per spike on grain yield and the maximumindirect effect was observed through harvest index followed by straw yield, thousand seed weight, and spike number per plant. The same authors reported negative indirect effect on grain yield with biological yield in bread wheat genotypes under semi arid conditions.

As indicated in Table 9, the direct effect of biological yield on grain yield was positive (0.913) indicating that considering biological yield during genotype selection could result significant improvement in grain yield. In other words, biological yield had positive effect on grain yield via kernels per spike and thousand seed weight with respective values of 0.005and 0.004. However, its indirect effect on grain yield via harvest index was recorded negative with the value -0.361. Similar results werereported by Abderrahmane *et al.* (2013) in wheat genotypes and reported the positive direct effect of biological yield on grain yield and the positive indirect effectof biological yield through number of grains per spike and thousand seed weight. Similarly, its indirect effect on grain yield via harvest was reported as negative.

Furthermore, James *et al.* (2017) reportedpositive direct effect of biological yield on grain yield and also reported indirectly biological yield had positive effect on grain yield through thousand seed weight. Similar to the present findings, the same author also reported the indirect effect of biological yield on grain yield through harvest index was recorded as negative value.

The results of path coefficient analysis also revealed that direct effect of thousand seed weight on grain yield was positive (0.026) which is similarto the finding reported by Endashaw (2018). However, Obsa *et al.* (2017) reported negative direct effect of the character on grain yield. The indirect effect of kernels per spike, biological yield and harvest index were found positive.

The direct effect of harvest index on grain yield was positive (0.835). The indirect effect of kernels per spike and thousand seed weight through harvest index on grain yield were positive where as the indirect effect of biological yield on grain yield via harvest index was scored as

negative. Several authors reported similar results to the present findings (Abderrahmane *et al.*, 2013; Obsa *et al.,* 2017; Sabit *et al.,* 2017).

The residual effect in the present study was 0.32,implyingthat 68 % of the variability in grain yield was contributed by characters considered in the path analysis study whereas the remaining 32% is the contribution of other characters whichare not considered in the path analysis and environmental factors. This further elaborate that the choice of yield attributing characters in the study was quite better, even if other characters are also needed to justify grain yield in bread wheat.

4.5.2. Phenotypic path coefficient analysis

The results of path coefficient analysis at phenotypic level is presented in Table 10

Table 10. Phenotypic path coefficient analysis direct (diagonal) and indirect (off diagonal) effect of the characters

Variables	KPS	BY	TSW	HI	rp
KPS	**0.026**	0.237	-0.001	-0.001	0.261**
BY	0.007	**0.906**	0.006	-0.388	0.531**
TSW	-0.001	0.123	**0.042**	0.110	0.274**
HI	0.000	-0.422	0.006	**0.832**	0.416**

NB: Residual effect = 0.39, ** = highly significant at $p \leq 0.01$, KPS = number of kernels per spike, BY = biological yield (kg/plot), TSW = thousand seed weight (gm), HI = harvest index (%), rp = phenotypic correlation of the character with grain yield.

Phenotypic path coefficient analysis revealed that biological yield (0.906)and harvest index (0.832) exerted high and favorable direct effects on grain yield. This justifies the presence of true relationship between these characters and grain yield as depicted by positive and significant correlations of grain yield with harvest index and biological yield there by direct selection through these characters would result reasonable effect on grain yield. Similar finding wasalso reported by James *et al.* (2017). But, the lowest positive direct effect at phenotypic level was displayed by kernels per spike (0.026).The highest positive indirect

effect at this level was exerted by biological yield **(**0.237) through kernels per spike. In other cases, the highest negative indirect effect on grain yield was also recorded by biological yield (-0.422) via harvest index Table 10. From the presentresult, biological yield had highest positive and highly significant correlation with grain yield (rp = 0.531) with its positive and negative indirect effects through other characters which counter balance each other and result in this high association with grain yield.

The study also revealed that direct effect of kernels per spike on grain yield was positive (0.026).The maximum positive indirect effect of kernels per spike (0.237) on grain yield was recorded through biological yield as descried earlier and the negative indirect effect of kernels per spike (-0.001) were recorded via thousand seed weight and harvest index in similar magnitude.

The phenotypic path coefficient analysis showed that direct effect of biological yield on grain yield was positive (0.906). In directly, biological yield had positive effect on grain yield via kernels per spike (0.007) and thousand seed weight (0.006). But, the negative indirect effect of biological yield on grain yield (-0.388) were scored through harvest index. Thousand seed weight had direct effect of (0.042) and its indirect effect on grain yield were recorded via biological yield, harvest index and kernels per spike with respective value of 0.123,0.110 and -0.001. The direct effect of harvest index on grain yield was 0.832. Its indirect effect on grain yield obtained via thousand seed weight, kernels per spike and biological yield (0.006, 0.000 and -0.422), respectively (Table 10).

The phenotypic path coefficient analysis exhibited the residual value of0.39indicating that 61% of the variability in grain yield was contributed by characters considered in the path analysis study and the remaining 39% was the contribution of other characters whichwerenot considered in the path analysis and environmental factors.

4.6. Cluster Analysis

The D^2 values based on the pooled mean of genotypes resulted in classifying the 49 bread wheat genotypes into five clusters and two solitary groups (Table 10 and Appendix fig 1).

Table 11. Clustering of 49 bread wheat genotypes based on Mahalanobis (D^2) distance evaluated at Kokate and Hossana, SNNPR, 2018 cropping season

Clusters	No. of genotypes	Proportion	Genotypes (G*)
C-I	33	70.21	G17, G43, G8, G23, G5, G6, G34, G35, G18, G46, G20, G41, G4, G40, G14, G47, G22, G39, G21, G 44, G45, G24, G26, G12, G32, G38, G37, G16, G 29, G36, G31, G2, G3
C-II	5	10.64	G33, G42, G7, G15, G30
C-III	4	8.51	G11, G28, G9, G27
C-IV	3	6.38	G1, G49, G10
C-V	2	4.25	G19, G25

G* = Genotypes used in the study

Among the clusters, cluster-I is the largest and contained 33 (70.21%) genotypes followed by Cluster-II and III contained 5 (10.64%) and 4 (8.51%) genotypes, respectively Cluster- IV contained 3 (6.38%) genotypes including the check variety, Wane, followed by cluster-V contained 2(4.25%) genotypes where as genotype 13(G13) and genotype 48(G48) were considered as solitary groups due to their unique characteristics. The unique characteristics that made G13 different from another genotypes were itslowest harvest index, thousand seed weight, grain yield and highest number of spikeletes per spike compared to genotypes in another clusters where as G48 wereits shortest days to 50% heading and longest days to grain filling periods.

Thisdifferent cluster indicated that the crossing between superior genetic divergences of above diverse clusters might provide desirable recombinants for developing high yielding

bread wheat genotypes. This is because the cluster analysis sequestrates genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters (Jaynes *et al*., 2003).

Several authors reported the presence of divergence among bread wheat genotypes indicating grouping in different numbers of distinct clusters. Arya *et al.* (2017) grouped 49 bread wheat genotypes into eight clusters, Dargicho *et al.* (2015a) classified 68 bread wheat germplasms into six clusters, Ahmad *et al*. (2014), classified 19 genotypes into threeclusters on the basis of average linkage, and Salman *et al.* (2014) classified 65 bread wheat genotypes into sixclusters.

4.6.1. Cluster mean analysis

The mean value of the 11 quantitative characters in each cluster is presented in Table 12.

Table 12. Cluster mean on 47 bread wheat genotypes evaluated in 2018 cropping season at Kokate and Hossana, SNNPR

Traits	C-I	C-II	C-III	C-IV	C-V
HD	62.48	69.74**	68.97	60.14*	64.13
GFP	51.43	53.96	58.95**	52.32	38.31*
MD	113.91	123.71	127.92**	112.46	102.43*
PH	81.17	88.63	79.12*	89.45**	79.79
SL	8.33	8.95**	8.75	8.26*	8.31
KPS	47.31	48.19	49.47	55.84**	45.85*
SPS	16.75	17.61	17.89**	16.24*	17.20
BY	2.08	2.42**	2.30	2.35	1.81*
GY	3.32*	3.56	3.38	4.10**	3.34
TSW	34.55	39.66**	32.41*	36.67	34.88
HI	34.23	30.53*	31.85	37.41	37.68**

NB: HD = days to 50% heading, GFP = grain filling period, MD = days to 90% physiological matu rity, PH = plant height (cm), SL = spike length (cm), KPS = number of kernels per spike,SPS = numbe r of spikelet per spike, BY= biological yield (kg/plot),GY= grain yield (tone/ha),TSW = thousand seed weight (gm), HI = harvest index (%), * = lowest cluster mean and ** = highest cluster mean values, respectively.

The genotypes in Cluster-II are characterized by longest spike length, highest biological yield and thousand seed weight whereas genotypes in Cluster-III are characterized by shortest in plant height and high number of spikelet per spike. The genotypes in Cluster-IV are characterized by early days to 50% heading,high number of kernels per spike and grain yield where as genotypes in Cluster-V are characterized by early days to grain filling period and days to maturity as well high number of harvest index.

The results indicates that genotypes in cluster-II could be used for crossing, if the aim is to develop hybrid with long spike length, high number of biological yield and thousand seed weight. Cluster-III could be used for crossing to develophybrid with early grain filling, short statured genotypesfor high rain fall areas where the present study conducted and high number of spikelet per spike. Genotypes in Cluster-IV could be used to develop hybrid for early days to 50% heading, high number of kernels per spike and grain yieldwhereas Cluster-V could be used for crossing if the aim is to develop hybrid with early grain filling period and days to maturity as well as high number of harvest index.

Several investigators havegrouped various bread wheat germplasms into distinct clusters as well as identified and recommended clusters that contain desirable characters for hybridization programs.Salman *et al*. (2014) identified one cluster among six to be used as source of early maturing materials while Desheva and Cholakov (2014) reported acluster which wassuitable for hybridization programs aimed at developing high yielding wheat varieties. Launching sound hybridization program needs the availability of genetically divergent genotypes for quantitative characters that contribute towards yield enhancement(Singh, 1983), and, therefore, in any breeding program, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981).

4.7. Genetic Distance (Genetic Divergence) Analysis

The genetic divergence as measured by Mahalanobis D^2 statistics were presented in Table 13.

Table 13. Average inter cluster divergence (D^2) value among 47 bread wheat genotypes evaluated at Kokate and Hossana,SNNPR, 2018 cropping season

Clusters	I	II	III	IV	V
I	**0**	16.99^{ns}	13.93^{ns}	29.75**	47.20**
II		**0**	21.19*	67.28**	13.58^{ns}
III			**0**	28.73**	30.95**
IV				**0**	104.40**
V					**0**

NB: * = significant, ** = highly significant (at 5% and 1%) probability levels, respectively and X^2 = 18.31 at 5% and 23.21 at 1% probability levels, respectively.

The results showed that there washigh genetic distance and significant variations at $p < 0.01$ and $p < 0.05$ among five clusters except the three clusters, cluster-I and II, I and III, II and V(Table 13). The maximum squared inter cluster distance was found between cluster-IV and V (D^2= 104.40) followed by cluster-II and IV(D^2 = 67.28) and cluster-I and V (D^2 = 47.20).The greater distance between clusters, indicating that the genotypes included in these clusters revealed broad spectrum of genetic diversity and may be used in hybridization programme for wheat improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters might produce desirable transgressive segregants. This would be useful in wheat breeding programs for developing the high yield potential varieties. Similar findings were reportedby (Yadav *et al*., 2006; Chapla *et al.*, 2008 and Singh *et al*., 2010).

The shortest squared distance was found between cluster-II and V (D^2 =13.58) followed by cluster-I and III (D^2 = 13.93) and Cluster-I and II (D^2 = 16.99). The shortest inter-cluster distance indicating that genotypes in these clusters were not genetically enough to diverse or there was little genetic diversity between these clusters. This signifies that crossing of genotypes from these two clusters might not give higher heterotic value in F_1 and narrow range of variability in the segregating F_2 population. Maximum genetic recombination is expected from the parents selected from divergent clusters groups (Mohammed, 2019). Therefore, maximum recombination and segregation of progenies might be expected from

crosses involving parents selected fromCluster-IV and V, followed by Cluster-II and IVand Cluster-I and V, respectively.

4.8. Principal Component Analysis

Principal component analysis (PCA)with Eigenvalues greater one are presented in Table 14 for 11 quantitative characters evaluated in SNNPR

Table 14. Eigen vector and Eigen values of the first five principal components (PCs) for 11 characters of bread wheat genotypes evaluated in Kokate and Hossana, SNNPR, 2018

Characters	PC-1	PC-2	PC-3	PC-4	PC-5
DH	0.741	-0.342	0.200	-0.165	0.098
GFP	0.411	0.205	-0.555	0.518	0.374
MD	0.817	-0.080	-0.280	0.276	0.349
PH	0.126	0.384	-0.424	-0.614	-0.178
SL	0.728	0.158	-0.164	0.009	-0.426
KPS	0.315	0.217	0.666	0.099	-0.218
SPS	0.659	-0.079	0.445	0.295	-0.189
BY	0.640	0.268	0.200	-0.433	0.281
GY	0.105	0.788	0.420	-0.034	0.266
TSW	0.159	0.662	-0.365	-0.048	-0.205
HI	-0.526	0.573	0.162	0.478	-0.010
Eigen Value	3.252	1.850	1.690	1.339	1.182
Variability	0.271	0.154	0.141	0.112	0.099
Cumulative	0.271	0.425	0.566	0.678	0.776

NB: DH = days to 50% heading, GFP = grain filling period, MD = days to 90% maturity, PH = plant height (cm), SL = spike length (cm), KPS = number of kernels per spike, SPS = number of spikelet per spike, BY = biological yield (kg/plot), GY = grain yield (tone/ha), TSW = thousand seed weight (gm), HI = harvest index (%)

Inthis study, the five PCAs extracted had eigen values more than unity (eigen values >1) and the first five principal components (PC_1 to PC_5) explained 77.6% of the total variation among 11 quantitative characters (Table 14).Out of the total principal component analysis, PC_1 had

recorded the highest variation 27.1% followed by second PC which account 15.4%, 14.1%forthird PC, 11.2% for fourth and 9.9% for fifth PC.In each PC indicated maximum variation was found in first PC, therefore, selection for characters under PC_1 may be desirable.

InPC_1 which accounted the highest variability was mostly related with characters days to 90% physiological maturity, days to 50% heading and spike length. In PC2, grain yield, thousand seed weight and harvest index are the most contributed characters for the variation.In PC3, characters like number of kernels per spike, grain filling period and number of spikelet per spike accounted the highest variation among the studied characters. The characters, which contributed more variation to PC_4 includes plant height, grain filling period and harvest index where as spike length, grain filling period and days to 90% physiological maturity contributed the highest variation among the evaluated characters in PC_5.

Therefore, the present study confirmed that bread wheat genotypes included in the current studyhadsignificant variations for the characters studied providing opportunities for genetic improvement through selection. Similar works have beendone by Khodadadi *et al.* (2011), Dawit *et al*. (2012) and Ashraf *et al*. (2012). Singh *et al*. (2014) also reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization.

4.9. Qualitative CharacterAnalysis

Shannon weaver diversity indexes(H') of six qualitative characters are described in Table 15

Table 15. Estimates of Shannon weaver diversity index for six qualitative characters of 49 bread wheat genotypes evaluated in Southern Ethiopia, 2018 cropping season

No.	Traits	Diversity index($H^{'}$)
1	Seed colour	0.90
2	Seed size	0.89
3	Kernel texture	0.69
4	Degree of seed shriveling	0.919
5	Spike density	0.909
6	Awnedness	0.506

The Shannon diversity indexes(H')of six qualitative charactersindicated that the phenotypic diversity available for these characters in the studied bread wheat genotypes (Table 15). The diversity indexes(H') fordegree of seed shriveling after harvest (0.919), spike density (0.909),seed colour (0.90), seed size (0.89), kernel texture (0.69), and awnedness (0.506) indicates the diversity of the genotypes was high. Shannon diversity indexes are categorized as high greater than (0.67), intermediate (0.34 to 0.66) and low (0.01 to 0.33)(Firdissa *et al*, 2005),accordingly, there was moderate to high diversity for the evaluated qualitative characters.

Several authors conducted research on wheat to identify the diversity indexes for the characters under study. Geleta and Grausgruber (2011) reportedmedium to high diversity indexes for seed size, seed shape and seed plumpness in their study using 53 bread wheat accessions.AlKhanjari *et al.* (2008) also realized in their study using Omani wheat that the majority of spikes were intermediate to dense andreported that lax spike types were rare. Bechere *et al.* (1996)and Negassa (1986a) also reported similar results for Ethiopian wheats.

4.9.1.Variation in individual genotypes, the percentage value of spike, awn and seed characters

The variation in individual genotypes and the percentage value of six qualitative charactersof 49 bread wheat genotypes are presented in Table 16

Table 16. Variation in individual genotypesand the percentage value of six qualitative characters of 49 bread wheat genotypes evaluated in Southern Ethiopia

Characters	Phenotypic classes	Code	Frequency (%)	X^2	Probability
Seed colour	Brown	B	53.06	15.500**	<0.01
	White	W	38.78		
	Red	R	8.16		
Seed size	Small	3	28.57	19.640**	<0.01
	Medium	5	61.22		
	Large	7	10.20		
Kernel texture	Soft	1	51.02	0.020^{ns}	0.886
	Hard	9	48.98		
Degree of seed Shriveling	Plump	3	46.94	13.990**	<0.01
	Intermediate	5	44.90		
	Shriveled	7	8.16		
Spike density	Lax	3	14.29	12.305**	<0.01
	Intermediate	5	42.86		
	Dense	7	30.61		
	Very dense	9	12.24		
Awnness	Awnletted	3	79.59	17.163**	<0.01
	Awned	7	20.41		

Seed colour was widely distributed in most of the genotypes. The colour ranged from brown for 26 (53.06%)ofthe tested genotypes to white for19 (38.78%)genotypesfollowed by red for4 (8.16%) genotypeswith brown being dominant. More than half of the present genotypes were brown colored. Many other authors revealed this type of seed colour in their test materials (Bekele, 1984; Bechere *et al*., 1996; Firdissa *et al*., 2005). Alkhanjari (2008) reported white and red as dominating grain colors in their study conducted using wheat land race diversity. Geleta and Grausgruber (2011) also reported higher proportion for white seed colour, as high as 90%, being red seed colour most frequent among accessions assigned in one of the accession groups.

The genotypes showed three seed characters; small (14 genotypes), medium (30 genotypes) and large (5 genotypes) among 49 tested genotypes with the percentage of 28.57%, 61.2% and 10.2 %, respectively, this indicates the presence of high diversity in the studied genotypes. The physical properties of grain have a direct or indirect influence on the milling and baking quality of wheat. Some researchers discovered that grain size had an influence on wheat milling and baking qualities (Marshall *et al*., 1984; Berman *et al*., 1996). Millers can obtain more flour per unit of weight from large, round, uniform and well-filled kernels. Similarly maltsters and brewers can obtain more extracts from large kernels (Dziki and Laskowski, 2005).

Wheat grains of smaller size are considered harder than larger grain and have inferior milling and baking characteristics, whereas larger wheat grains generally have higher weight, which means more endosperm (Gaines *et al*., 1997). Furthermore, Geleta and Grausgruber (2011) reported in his study the dominancy of medium to large seeds within all regions included under study and concluded a strong selection pressure was made towards large seed size by Ethiopian farmers and modern breeders. Large seed size is often associated with increased seedling vigour and hardiness, improved stand establishment and higher productivity (Grieve and Francois, 1992).

Out of 49 bread wheat genotypes studied; 23 genotypes (46.93%) were plump, 22 (44.89 %) were intermediate and 4 genotypes (8.16%) were shriveled, indicating better opportunity for quality seed development. Gaines *et al.* (1997) reported that shriveling greatly reduced test

weight and decreased the amount of flour produced during milling.So seed shriveling should be taken into consideration for milling quality.

Outof 49 tested bread wheat genotypes; 21 genotypes (42.85%) had intermediate, 15 genotypes (30.61%) had dense, seven genotypes (14.28 %) had lax and six genotypes (12.24%) had very dense spike density, respectively Table 16. The inflorescence in wheat is spike and it has a direct bearing on grain yield in the crop.Hence, any improvement of spike characteristics through selection and breeding would help improve the per plant productivity. (Iqbal and Khan, 2006)

The genotypes showed two awn character; awnletted (genotypes which has short awns) and awned (genotypes which has long awns), respectively. Out of the tested genotypes more than 39 (79.59%) genotypes were awnletted,and 10 (20.41%) genotypes were awned. Awn is the long slender extension of lemma in wheat and plays an important role in protection against animals and as a mechanism of seed dispersalas well as an important transpiration and photosynthetic organ in ear.Awn has a dominant role in contributing to large grains and a high grain yield in awned wheat cultivars, particularly during the grain- filling stages(Li and Hong-Gang, 2010).Similar to the current findings,Firdissa *et al*. (2005) reported long awned lines in wheat population containing landraces of Ethiopia tetraploid wheat.

5. SUMMARY AND CONCLUSION

Studying the extent and pattern of genetic variability and association of characters provide valuable information for plant breeders to design further breeding strategy. In order to generate such information, 49 bread wheat genotypes including the check variety were evaluated using 7x7 simple lattice design to estimate the magnitude of genetic variability and association among yield and yield related characters. Data recorded for 12 quantitative characters were subjected to analysis of variance and the analysis of variance revealed the presence of significant differences ($P < 0.01$ or $P < 0.05$) among the tested genotypes for most of the quantitative characters considered, which indicates that there is a considerable genetic variability in the tested bread wheat genotypes.

Similarly, phenotypic diversity based on qualitative characters showed appreciable diversity for seed shriveling, spike density, seed colour and seed size followed by awnedness. The ranges of mean values for most of the characters were large, showing the existence of variations among the tested genotypes.The PCV and GCV values of the studied characters ranged from (26.26, 23.69)for biological yield to (8.85, 4.07) for number of kernels per spike, respectively.Biological yield, harvest index, days to 50% heading, grain filling periods and thousand seed weight had recorded a PCV and GCV values of (26.26, 23.69), (21.91, 20.19) , (10.26, 10.01), (11.78, 10.05) and (10.09, 65.54), respectively implying selection may be effective based on these characters and their phenotypic expression would be good indication of the genetic potential.

Theestimated heritability in broad sense along with genetic advance as percent of the mean recorded for days to 50% heading, grain filling periods, biological yield, grain yield, thousand seed weight, and harvest index were (95.31, 20.14), (72.82, 17.67), (81.40, 24.71), (56.78, 15. 37), (65.54, 16.81), (84.99, 38.31), respectively indicating these are inherited characters that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these characters.

The greater genotypic correlation coefficients values that of the phenotypic correlation coefficients for most of the studied characters demonstrating that, the observed relationships among the various characters were due to genetic. Among the characters, number of kernels

per spike, biological yield, thousand seed weight, and harvest index were positively and significantly correlated with grain yield both at genotypic and phenotypic levels. The significant positive correlations between grain yield and yieldcomponents at genotypic and phenotypic levels indicated that these characters contributed positively towards yield and should be considered when selecting for high grain yield.

The results of path coefficient analysis at bothgenotypic and phenotypic levels revealed that biological yield exhibited the highest positive direct effect on grain yield followed by harvest index, number of kernels per spike and thousand seed weight indicating existence of positive and significant association between these characters with grain yield at bothgenotypic and phenotypic levels. This further elucidates the direct effect of the characters on grain yield.

The maximum squared inter cluster distance was realized between Cluster-IV and Vfollowed by Cluster-II and IVwhile the minimum was found between Cluster-II and V. Therefore, maximum recombination and segregation of progenies is expected from cross involving parents selected fromCluster-IV and V followed by Cluster-II and IV.

Principal component analysis of a character revealed that five principal components PC1 to PC5 with eigen values greater than unity have accounted for 77.6% of the total variation of thebread wheat genotypes evaluated for 11 quantitative characters.PC1 contributed 27.1% of the total variation, and the remaining (PC2, PC3, PC4 and PC5) contributed 15.4%, 14.1%, 11.2% and 9.9 %, respectively of the total variation, as a resultPCindicating that there is genetic variation in the studied genotypes.In each PC indicated maximum variation was found in the first PC, therefore, selection for characters under PC_1 may be desirable.

The present study generally indicated that there was significant genetic variation among the tested genotypes implying better opportunity for further improvement through selection and other breeding approaches. Therefore, it can be concluded that biological yield, harvest index, number of kernels per spike, thousand seed weightand grain yield could be considered as important selection criteria for bread wheat yield improvement. Additionally, crossing of genotypes for selected characters ofCluster-IV and Vas well asCluster-II and IV would result in heterotic progenies.

Therefore, simple selection of promising genotypes and crossing of highly divergent group to produce best heterotic progenies were recommended from the studied bread wheatgenotypes.Accordingly, 21 genotypes (G1, G6, G7, G9, G10, G12, G14, G18, G22, G25, G26, G29, G31,G33, G39, G42, G46, G47, G49, G27, and G37) were selected for the next breeding steps.

However, the experiment should be repeated at more locations with more number of genotypes to effectively predict genotypic performance for the major wheat diseases and insect pests as well as to validate the obtained current results. Moreover, further molecular characterization is needed to supplement agronomic characterization to give strong recommendations.

6. REFERENCES

Abderrahmane, H., El Abidine, F.Z., Hamenna, B. and Ammar, B., 2013. Correlation, path analysis and stepwise regression in durum wheat (*Triticum durum Desf*.) under rainfed conditions. *Journal of Agriculture and Sustainability*, ***3*****(2):**122-131

Abebe, A.A. and Desta, M.T., 2015. Genetic variability and character association of some local wheat varieties (*Triticum* species) using agro morphological traits grown in South Gondar zone, Ethiopia. *African Journal of Biotechnology*, **16(44)**: 2100-2105

Abinasa, M., Ayana, A. and Bultosa, G., 2011.Genetic variability, heritability and associations in durum wheat (*Triticum turgidum L. var. durum*) genotypes. *African Journal of Agricultural Research*, **6 (17):** 3972 – 3979

Abu T., 2012. Grain and feed annual report. Grain report number: ET1201, Addis Ababa, Ethiopia. *Research in Plant Biology*, **3(1):** 33-36

Adhiena M., Wassu, M. and Tadesse, D., 2016.Estimation of Heritability and Genetic Advance of Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum* L.). Genotypes at Ofla District, Northern Ethiopia. *International Journal of Plant Breeding and Genetics*, **10:31**-37

Ahmad, H. M., Awan, S. I., Aziz, O. and Muhammad, A. A., 2014.Multivariative analysis of some metric traits in bread wheat (*Triticum aestivum* L.).*European Journal of Biotechnology and Bioscience*, **1 (4)**: 22-26

Ahmed, A.S.M., 2018. Genetic Variability and Yielding Ability of Selected Bread Wheat (*Triticum aestivum* L.)Genotypes under Winter Conditions, Gezira State, Sudan. A Dissertation presented to the School of Graduate Studies ofGezira University, p.44.

Ahmed, G.,Fisseha, W., Sentayehu,A., 2017. Multivariate Analyses of Phenotypic Diversity of Bread Wheat (*Triticum aestivum* L.) in the Highlands of Northern Ethiopia. *Adv Crop Sci Tech*. **5(5)**

Ahmed, N., Chowdhry, M.A., Khaliq, I. and Maekawa, M., 2007.The inheritance of yield and yield components of five wheat hybrid population under drought conditions. *Indonesian Journal of Agricultural Sciences*, **8 (2)**:53-59

Ajmal, S.U., Minhas, N.M., Hamdani, A., Shakir, A., Zubair, M. and Ahmad, Z., 2013. Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*L.) germplasm. *Pakistan Journal of Botany*, **45(5)**:1643-1648

Akinwale, G., Akinyele, G. F., Nwilene, M.G., Ogunbayo, B.O. and Odiyi, A.C., 2011. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science*, **5**: 207-212

Akotkar, P.K., De, D.K. and Pal, A.K., 2010. Genetic variability and diversity in okra (*Abelmoschus esculentus* L. Moench). *Electron. J. Plant Breed*, **1(4):**393-398

Al- Khanjari, A. A., Filatenko, K., Hammer, A., Buerkert, A., 2008. Morphological spike diversity of Omani wheat. *Genet Resour Crop Evol*.**55**:1185–1195

Ali, I.H., 2012. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. *Mesopotamia Journal of Agriculture*, **40(4):**27-39

Ali, M.A., Nawab, N.N., Abbas, A., Zulkiffal, M. and Sajjad, M., 2009.Evaluation of selection criteria in (*Cicer arietinum* L.) using correlation coefficients and path analysis . *Australian Journal of Crop Science*, ***3*(2):**65-67

Ali, Y., Atta, B.M., Akhter, J., Monneveux, P. and Lateef, Z., 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pak. J. Bot*. **40(5)**:2087-2097

Ali, Z., Khan, A.S. and Asad, M.A., 2002. Salt tolerance in bread wheat: Genetic variation and heritability for growth and ion relation. *Asian J. Plant Sci*, **1(4)**:420-422

Allard, R.W. and Allard, R.W., 1999. Principles of plant breeding. John Wiley & Sons.

Allard, R.W., 1960. Principle of Plant Breeding. John Wiley and sons, New York. p185.

Al-Tabbal, J.A. and Al-Fraihat, A.H., 2012. Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Sciences*, **4(3)**: 52-56

Amsal, 2001.Studies on Genotypic Variability and Inheritance of Water logging Tolerance in Wheat.ADissertation presented to University of the Free State, Bloemfontein, South Africa.P.123.

Ansari, B. A., Ansari, K. A. and Khund, A., 2004. Extent of heterosis and heritability in some quantitative characters of bread wheat.*Indus Journal of Plant Science*, **3:189**-192

Anshuman, V., Dixit, N.N., Sharma, S.K. and Marker, S., 2013. Studies on heritability and genetic advance estimates in maize genotypes. *Bioscience Discovery*, ***4*(2):**165-168

Anwar, J., Ali, M.A., Hussain, M., Sabir, W., Khan, M.A., Zulkiffal, M. and Abdullah, M., 2009. Assessment of yield criteria in bread wheat through correlation and path analysis. *Journal of Animal and Plant Sciences*, **19(4)**:185-188

Arega, G., Mohammed, H. and Singh, H., 2007. Genetic divergence in selected durum wheat *genotypes* of Ethiopian plasm. *African Crop Science Journal*, **15(2)**

Arya, V.K., Singh, J., Kumar, L., Kumar, R., Kumar, P. and Chand, P., 2017. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian Journal of Agricultural Research*, **51(2**):128-134

Asaye, D., Tadesse, D. and Getachew A., 2013. Genetic variation of bread (*Triticum aestivum* L.) genotypes based on number of phonological and morphological traits at Marwold Kebele, Womberma Woreda, West Gojam. *Wudpecker Journal of Agricultural Research*, **2(6**):160-166

Ashraf, A., Abd El, M., Samir, R.., Abo, H. and Taha, M. H., 2012.Genotypic and phenotypic interrelationships among yield and yield components in Egyptian bread wheat

genotypes, Cairo University, Giza, Egypt.*Journal of plant breeding and crop science*,**4(1)**:9-16

ATA and EIAR (Agricultural Transformation Agency and Ethiopian Institute of Agricultural Research), 2007. Cereal Crops production Package Manual. Addis Abeba, Ethiopia. P.60

Aycicek, M. and Yildirim, T., 2006. Heritability of yield and some yield components in bread wheat (*Triticum aestivum* L.) genotypes. *Bangladesh J. Bot*. **35 (1)**:17-22

Ayele, B. and Bekele, H., 2016. Incidence and Challenges of Rusts in Wheat Production. In: Bishaw, Z., Dawit, A., Abebe, A., Abebe, K. (eds.). Containing the Menace of Wheat Rusts: Institutionalized Interventions and Impacts. EIAR, Addis Ababa, pp.41-48.

Babita, G., Yadava, R.K. and Pawan, K., 2011. Assessment of genetic parameters for spike traits and yield attributes in bread wheat genotypes following Line X Tester mating system. *Environment and Ecology*, **29(2A):**752-756

Baydar, H., 2005. Breeding for the improvement of the ideal plant type of sesame. *Plant Breeding*, **124(3)**: 263-267.

Bechere, E., Belay, G., Mitiku, D., Merker, A., 1996. Phenotypic diversity of tetraploid wheat landraces from northern and north-central regions of Ethiopia. *Hereditas*, **124**:165–172

Bekele, E., 1984. Analysis of regional patterns of phenotypic diversity in the Ethiopian tetraploid and hexaploid wheats. *Hereditas*, **100(1):**131-154.

Bello, O.B. and Olaoye, G., 2009. Combining ability for maize grain yield and other agronomic characters in a typical southern guinea savanna ecology of Nigeria. *African Journal of Biotechnology*, ***8*(11)**

Berhanu, M.A., 2004. Genetic variability and character associations in bread wheat (*Triticum aestivum* L.) genotypes developed for semiarid areas. An MSc Thesis Presented to the School of Graduate Studies of Alemaya University, Ethiopia.

Berhanu, M., Wassu, M. and Yemane, T., 2017. Genetic variability, correlation and path analysis of yield and grain quality traits in bread wheat (*Tritium aestivum* L.) genotypes at Axum, Northern Ethiopia. *Journal of Plant Breeding and Crop Science*, **9(10)**:175-185

Berman, M., Bason, M.L., Ellison,R., Peden,G. and Wrigley,C.W., 1996. Image analysis of whole grain to screen for flour milling yield in wheat breeding. Cereal Chemistry.**73**: 323-327

Burton, G.W. and Devane, E.H., 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45(10)**:478-481

CFIA, 2014 (Canadian Food Inspection Agency). The Biology of Wheat (*Triticum aestivum* L.). p.49.

Chapla, J.N., Dobariya, K.L., Khanpara, M.D., Jivani, L.L. and Kachhadia, V.H., 2008. Genetic divergence in bread wheat (*Triticum aestivum* L.).*J. of Plant Improvement*, **10(2)**: 97-102

Chatterjee, B.N. and Maiti, S., 1985. Principles and practice of crops growing. New at various levels and its residual effect on wheat in rice wheat cropping system. *Soil Environment*, **27(1)**:131-137

Cholastova, T. and Knotova, D., 2012. Using morphological and Microsatellites (SSR) markers to assess the genetic diversity in Alfalfa (*Medicago Sativa* L.). *International Journal of Biology*, **6(9)**:78-787

Ciferri, R. and Giglioli,G.R., 1939a, Cereal cultivation in East Africa (Ethiopia). The hard (durum) wheat. Italia Agricola, **76**: 247-257

Ciferri, R. and Giglioli, G.R., 1939b. Cereal cultivation in East Africa (Ethiopia).The wheat pyramidal, turgidum, polonium and dicoccum. L. Italia Agricola, **76**: 379-387

CSA (Central Statistical Agency), 2018. Report on Area and Production of Major Crops (Private Peasant Holdings, Meher Season) for 2017/2018. Statistical Bulletin No.586. Centeral Statistics Authority of Ethiopia, Addis Ababa

Dabholkar, A.R., 1992.Elements of Biometrical Genetics. Concept publishing Company, New Dehli. P.431.

Dabholkar, A.R., 1999. Elements of Biometrical Genetics. Concept Publishing Company, New Delhi. P.209-219.

Dargicho, D., Sentayehu, A., Firdisa, E. and Ermias, A., 2015.Genetic Variability in Bread Wheat(*Triticum aestivum* L.) Germplasm for Yield and Yield Component Traits.*Journal of Biology*, *Agriculture and Health care*, **5**:17

Dargicho, D., Sentayehu, A., Firdisa, E. and Ermias, A., 2015b. Path Coefficient and Correlation Studies of Yield and Yield Associated Traits in Bread Wheat (*Triticum aestivum* L.) Germplasm.*World Applied Sciences Journal*, **33 (11)**: 1732-1739

Dargicho, D., Sentayehu, A., Firdisa, E. and Gezahegn, F., 2015a. Genetic Variability in Bread Wheat (*Triticum aestivum* L.) Germplasm for Yield and Yield Traits. *Journal of Biology, Agriculture and Healthcare*, **5:**13

Dawit, T., Tadesse, D., Yigzaw, D. and Getnet, S., 2012. Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum Desf*). *Wudpecker Research Journals*, **1(4):**107 -112

Del Moral, L.F., Rharrabti, Y., Villegas, D. and Royo, C., 2003. Evaluation of grain yield and its components in durum wheat under Mediterranean conditions. *Agronomy Journal* , ***95*(2):**266-274

Dewey, D.R. and Lu, K., 1959. A correlation and path-coefficient analysis of components of crested wheat grass seed production. *Agronomy journal*,**51(9**):515-518

Dobariya, K.L., Ribadia, K.H., Padhar, P.R. and Ponkia, H.P., 2006. Analysis of genetic divergence in some synthetic lines of bread wheat (*Triticum aestivum* L.). Advances in Plant Sciences, **19(1)**: 221-225

Dogan,R. and Senyigit,E., 2016. Correlation and Path Coefficient Analysis of Yield and Yield Components in Hexaploid Triticale (*XTriticosecale Wittmack*) Genotypes under Mediterranean Conditions.*J. Biol. Environ. Sci*.**10(28)**: 21-27

Dubcovsky, J. and Dvorak, J., 2007. Genome plasticity a key factor in the success of polyploidy wheat under domestication.*Science*,**316**:1862-1866

Dudley, J.W. and Moll, R.H., 1969. Interpretation and uses of estimates of heritability and genetic advance in plant breeding.*Crop Sci*.**9:** 257-262

Dvorak, J., 1998. Genome analysis in the *Triticum-Aegilops alliance*, In: A.E. Slinkard (eds.), Proceedings of the 9th International Wheat Genetics Symposium, Saskatoon, Saskatchewan, Canada, University Extension Press, University of Saskatchewan, Saskatoon, Saskatchewan. **1**:8-11.

Dziki, D. and Laskowski,J., 2005. Wheat kernel physical properties and milling process.*Acta Agrophysica*.**6**: 59-71

Eid,M. H., 2009. Estimation of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought condition.*International Journal of Genetics and Molecular Biology*, **1(7)**: 115-120

Endashaw, G., 2018. Genetic Variability and Gain in Grain Yield and Associated Traits of Ethiopian Bread Wheat (*Triticum aestivium* L.) Varieties.An MSC thesis Presented to the School of Graduate studies, Jimma University College of Agriculture and Veterinary Medicine.P.81.

Falconer, D.S. and T. F. C. Mackay, 1996.An Introduction to Quantitative Genetics. 4th ed. Prentice Hall, London.

Falconer, D.S., 1989.Introduction to Quantitative Genetics. 3rd ed. Longman, New York.P.438.

Falconer, D.S., 1990.Introduction to Quantitative Genetics. 3rd ed. John Wiley and Sons. Inc., New York.

FAO (Food and Agricultural Organization), 2017. Crop Prospects and Food Situation. Quart erly Global Report. March 2018.

Feldman, M., 2001. Origin of cultivated wheat. In: Bonjean AP, Angus WJ, (eds.), The world wheat book: a history of wheat breeding. Paris, France: Lavoisier Publishing.PP.3–56

Firdissa E., Bekele E., Belay G., Borner A., 2005. Phenotypic diversity in tetraploid wheats collected from Bale and Wello regions of Ethiopia. *Plant Genet Resour*, **3**:35–43

Gaines, C.S., Finney,P.L. and Andrew,L.C., 1997. Influence of kernel size and shriveling on soft wheat milling and baking quality. Cereal Chemistry.**74 (6)**: 700-704

Gezahegn, F., Sentayehu, A., Zerihun, T., 2015. Genetic Variability Studies in Bread Wheat (*Triticum aestivum* L.) Genotypes at Kulumsa Agricultural Research Center, South East Ethiopia.*Journal of Biology, Agriculture and Healthcare*, **5(7)**

Girma, D., 2018. Genetic Variability, correlation and path coefficient analysis of Agro Morphological Traits among Bread Wheat (*Triticum aestivum* L.)Genotypes at Raya Valley of Southern Tigray, Ethiopia. An MSc Thesis Submitted to Postgraduate program of Haramaya University.P.98.

Gomez, A.G. and Gomez, A. A., 1984. Statistical procedure for Agricultural research, Jhon Wiley and son Inc., New York

Grieve,C.M. and Francois, L.E., 1992. The importance of initial seed size in wheat plant response to salinity.*Plant and Soil*, **147(2):**197-205

Hailu, G.M., Tanner, D.G. and Mengistu, H., 1991. Wheat Research in Ethiopia A historical perspective. Institute of Agricultural Research, Addis Ababa, Ethiopia. P.9

Hair, J. F., Tatham, R. L.; Anderson,R.E. and Black .W., 1995. Multivariate Data Analysis. (5th ed). Prentice-Hall.New Jersey. USA. P.768

Halluer, A.R. and Miranda, J.B., 1988. Quantitative Genetics in Maize Breeding (2nd ed.). Lowa state University press, Ames, Lowa. P.468.

Hutcheson, K., 1970.A test of comparing diversities based on the Shannon formula.*Journal of theoretical Biology*, **29(1):**151-154

IBPGR(International Board for Plant Genetic Resources), 1985. Revised descriptor list for Wheat (*Triticum* spp.). IBPGR Secretariat, Rome 1985.P.14.

Idris, A.E., Justin, F.J., Dagash, Y.M.I. and Abuali, A.I., 2012. Genetic Variability and Inter Relationship between Yield and Yield Components in Some Rice Genotypes. *American Journal of Experimental Agriculture*, **2(2)**: 233-239

Iqbal, M. and Khan, A.A., 2006.Analysis of combining ability for spike characteristics in wheat (*Triticum aestivum* L.). *Int J Agric Biol*. **8**:684-687

James, G., Dawit, A. and Gidada, A., 2017.A study of genetic variation and grain quality traits in bread wheat (*Tritium aestivum* L.) genotypes. *African Journal of Plant Breeding,***4 (1)**: 172-182

Jayasudha, S. and Deepak, S., 2010.Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. *Electronic Journal of Plant Breeding*, **1(5):**1332-1338

Johnson, H.W., Robinson, H.F. and Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy journal*, **47(7):**314-318

Johnson, R. and Wichern, D., 1992. Applied multivariate statistical methods. Prentice Hall, Englewood Cliffs, NJ.

Kaiser, H. F., 1960. The application of electronic computers to factor analysis. Educational and Psychological Measurement, **20**:141-151

Kalimullah, S., Khan, J., Irfaq, M. and Rahman, H.U., 2012. Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. *J. Anim. Plant Sci*, **22(2***):*330-333

Kamal, H. G., Abdel, A. N. S., Nesma, A. N.A. S., 2016. Genetic parameters for yield and yield components traits of some wheat genotypes grown in newly reclaimed soils. *International Journal of Agronomy and Agricultural Research*, **9 (4)**:1-8

Kamali, J. M., 2008. Review on wheat status in the past, present and future. Key papers for 10th conference on sciences of breeding in Iran: pp.23-45.

Kamboj, R.K., 2003. Genetic Variability, Heritability and Genetic gain in Bread Wheat (*Triticum aestivum* L). Agricultural Science Digest, **23 (4):**309 – 310

Kashif, M. and Khaliq, I., 2004.Heritability, Correlation and Path Coefficient Analysis for Some Metric Traits in Wheat. *Int. J. Agri. Biol*. **6(1):** 138–142

Khabiri, E., Imani, A.A. andShahbazi, H., 2012. Studying the grain yield and yield components in advanced rain fed wheat genotypes. Scholars Research Library. Annals of Biological Research, **3 (12)**:5647-5650

Khan, N. and Naqvi, F.N., 2011. Heritability of Morphological Traits in Bread Wheat Advanced Lines Under Irrigated and Non-Irrigated Conditions.*Asian Journal of Agricultural Sciences,***3(3):** 215-222

Khan, S.A., 2013.Genetic Variability and Heritability Estimates in Genotypes. *International Journal of Agriculture and Crop Sciences*, **5(9):** 983-986

Khodadadi, M., Fotokian, M. H., Miransari, M., 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *African Journal Crops Science*, **5(1):**17-24

Kifle, Z., Firew, M., Tadesse, D., 2016.Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.) Genotypes at Gurage Zone, Ethiopia.*International Journal of Microbiology and Biotechnology*,**1(1):**1-9

Koernicke, F. and Werner, H., 1885. Weed biology and management. Verlag von Paul Parey, Berlin. P.59.

Kotal, B.D., Das, A. and Choudhury, B.K., 2010.Genetic variability and association of characters in wheat (*Triticum aestivum* L.).*Asian journal of crop science*, **2(3):**155-160

Koul, D.K. and Singh, B., 2011. Evolution for drought Tolerance in elite genotypes of Bread Wheat (*Triticum aestivum*L.). Advances in Plant Sciences, **24 (1)**: 141-144

Kumar, P., Singh, G., Kumar, S., Kumar, A., Ojha, A., 2016.Genetic analysis of grain yield and its contributing traits for their implications in improvement of bread wheat cultivars.*J. Appl. Nat. Sci*.**8(1):**350-357

Kumar, R. and Singh, G., 2017. Genetic Diversity for yield and yield traits in wheat.*Journal of Pharmacognosy and Phytochemistry*, **6(5):** 2062-2066

Kumar, R., Gaurav, S.S., Bhushan, B. and Pal, R., 2013. Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*Triticum aestivum*L.).*J. of Wheat res*.**5 (2):** 39-42

Kumar, S., Singh, D. and Dhivedi, V.K., 2010.Analysis of yield components and their association in wheat for arthitecturing the desirable plant type.*Indian J. Agric. Res*.**44(4):**267-273

Legendre, P.and Legendre,L., 1998. Numerical Ecology. 2nd ed. Amsterdam, Elsevier, p.853

Leilah, A.A. and Al-Khateeb, S.A., 2005.Statistical analysis of wheat yield under drought conditions.*Journal of Arid Environments*, **61(3)**: 483– 496

Li, X.F., Bin, D. and Hong-Gang, W., 2010.Awn anatomy of common wheat (*Triticum aestivum* L.) and its relatives. *Caryologia*, ***63*(4)**:391-397

Mahalanobis, P.C., 1936. The generalized distance in statistics. Proceeding of Indian National Institute of Science, **2**: 49-55

Marshall, D.R., Ellison, E.W. andMares, D.J., 1984. Effects of grain shape and size on milling yield in wheat. Theoretical analysis based on simple geometric models. *Australian Journal of Agricultural Research,***35**: 619-630

Mathewos, A. and Yasin, G., 2017. Varietal and seed replacement as a means to improve crop productivity in GTP I: The case of major cereals in some districts of Southern Ethiopia. Food Science and Quality Management,**60**:70-76

Mathewos, A., Tewodros, M. and Yasin, G., 2012. Participatory On-Farm Evaluation of Improved Bread Wheat Technologies in Some Districts of Southern Ethiopia. *Journal of Biology, Agriculture and Healthcare*, **2(4):**2012

Mergoum, M., Singh, P.k., Anderson, J.A., Peiia, R.J, Singh, R.P., Xu S.S, and Ransom, J.K. 2009. Hand Book of plant breeding partly from Spring Wheat Breeding. North Dakota State University. Fargo ND 58108-6050 USA.

Mesay, Y.G., Fekadu, D., Terfe, F., Sultan, U., 2012. Prospects and challenges of wheat production in Ethiopia: Evidence from major wheat producing regions of the country. https:// www.slideshare.net/ CIMMYT/ Ethiopia

MoANR (Ministry of Agriculture andNatural ResourcesPlant Variety Release, Protection and Seed Qual1ty Control Directorate), Crop Variety Register Issue No.19, June, 2016, Addis Ababa, Ethiopia

MOA (Ministry of Agriculture and Livestock Resource, Plant Variety Release, Protection and Seed Quality Control Directorate), 2017.Crop Variety Register Issue No.20. Addis Ababa, Ethiopia, 28-56

Moghaddam, M., Ehdaie, B. and Waines, J.G., 1997. Genetic variation and interrelationships of agronomic characters in landraces of bread wheat from southern Iran, Euphytica,**95(3)**: 361– 369

Mohammadi, S.A. and Prasanna, B.M., 2003. Analysis of genetic diversity in crop plants salient statistical tools and considerations. *Crop science*, **43(4)**: 1235-1248

Mohammed, H., 2019.Variability study andassociation of character in indigeneous and exotic sesame(*Sesamum indicum*L.) Germplasm for yield and yield componenets at werer, north-estern ethiopia. An MSc Thesis presented to School of Graguate studies,Jimma University,Jimma Ethiopia, P.113.

Mollasadeghi, V., Elyasi, S. and Mirzamasoumzadeh, B., 2012. Genetic variation of 12 bread wheat genotypes based on number of phonological and morphological traits. Annals of Biological Research, **3 (10)**:4734-4740

Mollasadeghi, V., Shahryari, R., 2011.Important morphological markers for improvement of yield in bread wheat. *Advances Environ. Biol*.**5 (3)**: 538 – 542

Nagireddy, A.V. and Jyothula, D.P.B., 2009. Heritability and interrelationship of yield and certain agronomic traits in wheat.*Research on Crops*, **10(1)**: 124-127

Nastasi, V., 1964.Wheat production in Ethiopia. Near East Wheat and Barley Improvement and Production Project, **1 (3):** 13-24

Neeru, I.S. and Singh, P.V., 2017. Genetic Parameters of Variability and Path Analysis in Wheat under Timely and Late Sown Conditions.*International Journal of Current Microbiology and Applied Sciences*, **6 (7)**:1914-1923

Negassa, M., 1986a.Estimates of phenotypic diversity and breeding potential of Ethiopian wheats.*Hereditas*, **104**: 41–48

Netsanet, H., Hussein, A., Shimelisand, M. L., 2016. Appraisal of farmers' wheat production constraints and breeding priorities in rust prone agro-ecologies of Ethiopia.*African Journal of Agricultural Research*, **12(12)**: 944-952

Obsa, C., 2014.Genetic Variability among Bread Wheat (*Triticum Aestivum* L.) Genotypes For Growth Characters, Yield And Yield Components in Bore District, Oromia Regional State. An MSC Thesis Submitted to the Department of Plant Sciences, School of Graduate Studies, Haramaya University, Ethiopia. P.79.

Obsa, C., Wassu, M., Firdissa, E., 2017. Analysis of Genetic Variability among Bread Wheat Genotypes for Growth, Yield and Yield Components in Bore District, Oromia Regional State. *Agriculture, Forestry and Fisheries*, **6(6)**: 188-199

Percival, J., 1927. The Coleoptile Bundles of Indo-Abyssinian Emmer Wheat (*Triticum dicoccum*). Annals of Botany, **41 (161):** 101-105

Pooja, S.S., Dhanda, N.R., Yadav, R.S., Beniwal, A., 2018. Estimation of genetic variability in recombinant inbred lines of bread wheat (*Triticum aestivum* L.) for yield and yield component traits. *International Journal of Chemical Studies*, **6(3)**: 1006-1011

Rahman, M.A., Kabir, M.L., Hasanuzzaman, M., Rumi,R.H., Afrose, M.T., 2016.Study of variability in bread wheat (*Triticum aestivum* L.).*Int. J. Agric. Res*. **8**:66-76

Rathwa, H.K., Pansuriya, A.G., Patel, J.B. and Jalu, R.K., 2018. Genetic Variability, Heritability and Genetic Advance in Durum Wheat (*Triticum durum Desf*.).*International Journal of Current Microbiology and Applied Sciences*, **7(01):**1208-1215

Rauf, S., Tariq, S.A., Hassan, S.W., 2012. Estimation of pedigree based diversity in Pakistani wheat (*Triticum aestivum*L.) germplasm. *Communications in Biometry and Crop Science,* **7 (1)**: 14–22

Reynolds, M.P. and Borlaug, N.E., 2006. Applying innovations and new technologies for international collaborative wheat improvement.*Journal of Agricultural Science*, **144(2)**:95-110

Rizwana, M., Muhammad, S., Ihsan, K., Khan, A.S. and Khan, S.H., 2010. Morphological diversity and traits association in bread wheat (*Triticum aestivum* L.). *American-Eurasian Journal of Agricultural and Environmental Science*, ***8*(2):**216-224

Rosegrant, M.W. and Agcaoili, M., 2010. Global Food Demand, Supply, and Price Prospects, International Food Policy Research Institute, Washington, DC.

Sabesan, T., Suresh, R. and Saravanan, K., 2009.Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu.*Electronic Journal of Plant Breeding*, **1(1):**56-59

Sabit, Z., Yadav, B. and Rai, P.K., 2017. Genetic variability, correlation and path analysis for yield and its components in f5 generation of bread wheat (*Triticum aestivum* L.).*Journal of Pharmacognosy and Phytochemistry*, **6(4)**: 680-687

Salman, S., Shah, J., Khan, J., Rehmat, K., Khan, U. and Khan, I., 2014. Genetic variability studies in bread wheat (*Triticum aestivum* L.) accessions. *Pakistan Journal of Agricultural Research*, ***27*(1)**

SAS, 2012.Statistical analysis System. Version 9.3., SAS Institute Inc. Cary, NC., USA

Savin, R., Calderini, D.F., Slafer, G.A. and Abeledo, L.G., 1999.Final grain weight in wheat as affected by short periods of high temperature during pre-and post-anthesis under field conditions. Functional Plant Biology, ***26*(5)**:453-458

Shankarrao, B.S., Mukherjee, S., Pal, A.K. and De, D.K., 2010. Estimation of variability for yield parameters in Bread Wheat (*Triticum aestivum* L.) grown in Gangetic West Bengal. *Electronic Journal of Plant Breeding*, ***1*(4):**764-768

Sharma, J.R., 1998. Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited Publishers, New Delhi: p.432.

Sharma, S.C. and Rao, S.R.G., 1989.Genetic variability and association among metric traits and path coefficient analysis in Triticale.*Ann Agric Res*., **10 (2)**: 145 – 152

Shewry, P.R., 2009. Wheat. *Journal of Experimental Botany*, **60**: 1537-1553

Shujaat, A., Azhar., H.S., Rehmani, G., Habib, A., Hasnian, N., Sikandar, K.S., 2014. Morpho agronomic characterization of okra [*Abelmoschus esculentus*(L.)Moench]. *World Applied Sciences Journal*, **31(3):**336-340

Siahbidi, M.M.P., Aboughadareh, A.P., Tahmasebi, G.R., Teymoori, M. and Jasemi, M., 2013. Evaluation of genetic diversity and interrelationships of agro-morphological characters in durum wheat (*Triticum durum* Desf.) lines using multivariate analysis. *International Journal of Agriculture*, ***3*****(1):**184-194

Singh, B. D., 1993.Plant Breeding: principles and methods.Kalyani publishers. Ludhiana.

Singh, B.D., 2001. Plant Breeding: Principles and methods.Kalyani Publishers, New Delhi. P.896.

Singh, D. and Singh, K.N., 2010. Variability analysis for yield and yield attributes of bread wheat under salt affected conditions. Wheat / information service.**110**: 35-39

Singh, I. and Sharma, S.K., 1994. Interrelationship of harvest index and other traits in wheat.*Hayrana Agricultural University Journal of Research*, **24(1)**: 33 – 38

Singh, K.B., Bejiga, G. and Malhotra, R.S., 1990. Association of some characters with seed yield in chickpea collections.*Euphytica*, **49**:83-88

Singh, M.P. and Ceccerelli,R.B., 1996. Estimation of heritability of crop traits from variety trial data. Technical Manual No.21, ICARDA, Aleppo.Syria.

Singh, S. P., Singh, A. K., Sharma, M. and Salgotra, S. K., 2014.Genetic divergence study in improved bread wheat varieties (*Triticum aestivum*).*African Journal of Agricultural Research*, **9(4):**507-512

Singh, S.P. and Diwivedi, V.K., 2002. Character association and path analysis in wheat (*Triticum aestivum* L.). .*Agric. Sci. Digest*, **22 (4)**: 255 – 257

Sleper, D.A. and Poehlman, J.M., 2006. Breeding Field Crops.5th edition.Blackwell Publishing, Professional, Ames, Iowa.

Smith, J. L., 1984. Genetic variability with U.S. hybrid maize: Multivariate analysis of isozyme data. *Crop science*, **24**:1041-1046

Sohail, A., Rahman, H., Ullah, F., Shah, S.M., Burni, T. and Ali, S., 2018.Evaluation of F4 bread wheat (*Triticum aestivum* L.) genotypes for genetic variability, heritability, genetic advance and correlation studies. *J. Plant Breed. Genet*. ***6***:1-7

Stoskopf, N. C., Tomes,D. T. and Christie,B.R., 1999. Plant breeding: Theory and practice. Scientific publishes, India.P.435.

Subhani, G.M.,Khaliq, I., 1994. Path coefficient analysis in wheat.*Pakistan J. Scie Indu Res*.**37(11)**: 474– 476

Tadesse, W., Zewdie, B., Solomon, A., 2018. Wheat production and breeding in sub-Saharan Africa: Challenges and opportunities in the face of climate change. *International Journal of Climate Change Strategies and Management*. https://doi.org/10.1108/IJCCSM-02-2018-0015.

Tazeen, M. and Naqvi., F.N., 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat.*J. of Food, Agri. and Environ.***7(3/4)**:278-282

Tesfaye, T. and Jamal, M., 1982.Review of Wheat Breeding in Ethiopia.*Ethiopian Journal of Agricultural Sciences*, **39**: 38–44

Tsegaye, B. and Berg, T., 2007. Utilization of durum wheat landraces in East Shewa, central Ethiopia: Are home uses an incentive for on-farm conservation? Agriculture and Human Values.**24**, 219- 230

Ullah, M.Z., Bashar, M.K., Bhuiyan, M.S.R., Khalequzzaman, M. and Hasan, M.J., 2011. Interrelationship and cause-effect analysis among morpho-physiological traits in biroin rice of Bangladesh. *Int. J. Plant Breed. Genet*. ***5*(3):**246-254

USDA., 2019. United States Department of Agriculture Office of Global Analysis .World Agricultural Production. Available at: https://ipad.fas.usda.gov/ (accessed August 2019). Washington DC, USA. P36.

Welsh, J. R., 1981. Fundamentals of plant genetics and breeding, John willey and Sons, Inc. Newyork. P.290.

Welsh, J., 1990. Fundamentals of Plant Breeding and Genetics. John Wiley & Sons, New York

Yadav, D.K., Pawar, I.S., Sharma, I.S. and Lamba, R.A.S., 2006. Evaluation of variability parameters and path analysis in bread wheat.*J. of PlantImprov*.**8(1)**: 86-89

Yadav, S.K., Singh, A.K., Baghel, S.S., Jarman, M. and Singh, A.K., 2014. Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm.*J.of Wheat Res*.**6 (2):** 154-159

Yadawad, A., Hanchinal,R.R., Nadaf,H. L., Desai,S. A.,Suma, B.V. and Rudra, N., 2015. Genetic variability for yield parameters and rust resistance in f2 population of wheat (*Triticum aestivum* L.) Karnataka, India. *The Bioscan*. **10(2)**: 707-710

Yirga, C., Jaleta, M., Shiferaw, B., Groote de, H., Kassie, M., Mebratu, T., Mohammad, A., 2013.Analysis of Adoption and Diffusion of Improved Wheat Technologies in Ethiopia.Research Report 101.Ethiopian Institute of Agricultural Research (EIAR) and CIMMYT, Addis Ababa, Ethiopia.P.69.

Yongqing, M. A., 2005. Allelopathic studies of common wheat (*Triticum aestivum* L.). Weed Biology and Management, **5**:93-104

Zecevic, V., Boskovic, J., Dimitrijevic, M. and Petrovic, S., 2010. Genetic and phenotypic variability of yield components in wheat (*Triticum aestivum* L.).*Bulgarian Journal of Agricultural Science*, **16 (4)**:422-428

Zhang, X., Chen, S., Sun, H., Pei, D. and Wang, Y., 2008. Dry matter, harvest index, grain yield and water use efficiency as affected by water supply in winter wheat.Irrigation Science, **27(1):**1-10

7. APPENDICES

Appendix Table 1. Analysis of variance summary for 12 quantitative yield and related characters evaluated at Kokate, 2018 cropping season

Characters	Mean square							
	Replication (Df = 1)	Blocks with in rep.(ad) (df = 12)	Trmt. (df = 48)		Error			CV (%)
			unadju.	Adju.	Intra block (df = 36)	RCBD (df = 8)	Rel. E .to RCBD (%)	
HD	0.16	3.15	26.91	24.1**	2.20	2.43	103.07	2.38
GFP	4.94	52.17	50.53	50.52**	29.50	35.17	107.53	10.28
MD	3.31	57.69	71.51	71.50**	29.93	36.87	109.96	4.75
PH	50.57	23.31	51.50	48.57**	14.71	16.86	104.94	4.98
SL	0.34	0.28	0.68	0.58**	0.22	0.24	101.33	5.46
KPS	224.11	49.64	53.39	53.38**	38.67	41.41	101.49	14.80
SPS	102.04	1.48	3.24	3.13^{ns}	2.94	2.57	87.54	10.27
PT	445.72	801.69	946.50	1029.09^{ns}	918.24	889.10	96.83	21.50
BY	0.85	0.03	0.11	0.09^{ns}	0.08	0.07	85.43	18.47
GY	0.54	0.14	0.21	0.19^{ns}	0.19	0.19	92.21	14.38
TSW	2.32	11.38	38.52	29.3**	7.88	8.76	103.17	7.19
HI	164.35	16.64	63.56	59.4^{ns}	37.26	32.11	86.17	15.10

HD = days to 50% heading, GFP = days to grain filling period, MD = days to maturity, PH = height (cm), SL = spike length (cm), KPS = number of kernels per spike, PT = number of productive tillers per meter square area, BY = biological yield (kg/plot), GY = grain yield (tone/ha), TSW = thousand seed weight (gm/plot), and HI = harvest index (%).

Appendix Table 2. Analysis of variance summary for 12 quantitative yield and related characters evaluated at Hossana, 2018 cropping season

Characters	Mean square							CV (%)
	Replication (Df = 1)	Blocks with in rep. (ad) (df = 12)	Trmt. (df = 48)		Error			
			unadju.	Adju.	Intra block (df = 36)	RCBD (df = 48)	Rel.E. to RCBD (%)	
HD	0.26	3.08	63.50	54.49**	1.93	2.21	105.11	2.14
GFP	2.61	8.28	86.36	79.73**	13.11	11.90	90.78	7.04
MD	4.50	5.67	133.23	121.2**	14.58	12.35	84.71	3.27
PH	12.93	21.89	44.63	37.30**	8.45	11.81	121.15	3.31
SL	0.69	0.17	0.98	0.80**	0.25	0.23	91.90	6.01
KPS	202.87	18.78	80.11	66.28*	33.65	29.93	88.95	10.69
SPS	29.32	1.19	1.85	1.83*	0.94	1.01	101.30	5.64
PT	392.00	718.39	1140.61	1064.79^{ns}	1372.31	1208.83	88.09	19.71
BY	0.29	0.14	0.43	0.40*	0.20	0.18	92.24	16.31
GY	1.50	0.28	1.07	0.94**	0.16	0.19	106.39	11.20
TSW	24.59	25.43	55.93	52.11**	18.49	20.23	102.40	13.89
HI (%)	81.28	13.17	44.33	37.31**	15.63	15.02	96.07	14.40

HD = days to 50% heading, GFP = days to grain filling period, MD = days to maturity, PH = plant height (cm), SL = spike length (cm), KPS = number of kernels per spike, PT = number of productive tillers per meter square area, BY = biological yield (kg/plot), GY = grain yield (tone/ha), TSW = thousand seed weight (gm/plot), and HI = harvest index (%)

Appendix Table 3. Mean of Tested Bread wheat genotypes evaluated at Kokate and Hossana, SNNPR , 2018

G*	HD	GFP	MD	PH	SL	KPS	SPS	PT
G1	64.500^{i-o}	53.750^{c-m}	118.250^{d-i}	89.850^{ab}	8.9500^{b-f}	57.400^{a}	16.600^{c-j}	155.00^{a-h}
G2	59.750^{r}	56.750^{b-g}	116.500^{e-k}	74.500^{p}	8.2000^{h-m}	47.200^{c-k}	16.100^{f-j}	143.50^{d-h}
G3	58.750^{rs}	51.000 $^{f-m}$	109.750^{k-q}	76.400^{n-p}	8.8500^{c-h}	52.500^{a-e}	17.900^{a-f}	130.25^{h}
G4	66.500^{e-i}	50.000 $^{h-m}$	116.500^{e-k}	81.100^{h-n}	8.8500^{c-h}	45.850^{c-k}	16.100^{f-j}	149.00^{c-h}
G5	57.000st	51.750^{e-m}	108.750^{l-q}	81.050^{h-n}	8.4500^{e-k}	41.700^{i-l}	16.600^{c-j}	136.25^{gh}
G6	56.500^{tu}	52.750^{d-m}	109.250^{l-q}	79.850^{i-o}	8.3000^{f-l}	39.000^{kl}	15.100^{ij}	189.25^{a-d}
G7	69.750^{bc}	55.000^{b-j}	124.750^{a-d}	87.150^{a-e}	8.8500^{c-h}	52.000^{a-f}	18.100^{a-e}	184.75^{a-e}
G8	64.750^{i-m}	53.750^{c-m}	118.500^{d-g}	83.100^{c-k}	8.7500^{c-i}	44.850^{e-l}	18.000^{a-f}	169.75^{a-h}
G9	73.500^{a}	57.250^{b-f}	130.750^{a}	79.700^{i-o}	9.1500^{b-d}	48.800^{b-j}	17.600^{a-g}	200.00^{a}
G10	56.500^{tu}	54.250^{b-l}	110.750^{j-p}	91.100^{a}	8.4500^{e-k}	54.150^{a-c}	17.300^{a-h}	174.00^{a-h}
G11	65.750^{g-k}	56.500^{b-h}	122.250^{b-e}	86.000^{b-g}	9.3500^{a-c}	49.550^{a-i}	18.200^{a-d}	162.25^{a-h}
G12	54.500^{uv}	53.750^{c-m}	108.250^{m-q}	82.200^{f-k}	8.0000^{j-o}	43.650^{g-l}	16.100^{f-j}	159.00^{a-h}
G13	71.500^{ab}	47.750^{l-n}	119.250^{d-i}	83.100^{c-k}	8.9500^{b-f}	47.000^{c-k}	18.900^{a}	141.75^{e-h}
G14	65.000 $^{i-m}$	48.250^{k-m}	113.250^{h-o}	82.350^{f-k}	8.3000^{f-l}	52.100^{a-f}	17.900^{a-f}	165.50^{a-h}
G15	69.000^{cd}	60.500^{b}	129.500^{a}	83.550^{c-k}	8.9000^{c-g}	48.700^{b-j}	17.500^{a-h}	166.75^{a-h}
G16	63.750^{k-o}	52.500^{d-m}	116.250^{e-k}	86.100^{b-g}	9.6000^{a-b}	46.500^{c-k}	17.600^{a-g}	145.50^{c-h}
G17	59.000^{rs}	50.750^{f-m}	109.750^{k-q}	86.800^{a-f}	8.2500^{g-m}	46.000^{c-k}	15.900^{g-j}	150.75^{b-h}

Appendix Table3. Mean of Tested Bread wheat genotypes evaluated at Kokate and Hossana, SNNPR , 2018 **(*Continued*)**

G*	HD	GFP	MD	PH	SL	KPS	SPS	PT
G18	59.250^{r}	53.250^{d-m}	112.500^{i-o}	83.800^{c-j}	8.3500^{f-l}	48.400^{b-j}	17.500^{a-h}	177.50^{a-g}
G19	63.750^{k-o}	39.500^{o}	103.250^{q}	84.800^{c-h}	8.5500^{d-j}	48.000^{c-j}	16.500^{c-j}	157.75^{a-h}
G20	64.750^{i-m}	49.250^{i-m}	114.000^{g-o}	81.700^{g-l}	7.2500^{p}	49.750^{a-i}	17.000^{a-i}	153.00^{b-h}
G21	60.500^{p-r}	54.500^{b-k}	115.000^{f-m}	77.050^{l-p}	7.7500^{l-p}	42.350^{h-l}	16.200^{e-j}	189.75^{a-c}
G22	63.000^{m-o}	48.250^{k-m}	111.250^{j-o}	81.350^{g-m}	8.0000 $^{j-o}$	45.450^{d-l}	16.300^{d-j}	196.00^{ab}
G23	63.250^{l-o}	53.000^{d-m}	116.250^{e-k}	82.150^{f-k}	8.8000^{c-h}	49.700^{a-i}	18.200^{a-d}	167.25^{a-h}
G24	66.000^{f-j}	50.750^{f-m}	116.750^{e-j}	75.450^{op}	8.3500^{f-l}	48.800^{b-j}	17.000^{a-i}	165.50^{a-h}
G25	64.250^{j-o}	39.750^{n-o}	104.000^{pq}	76.200^{op}	8.2500^{g-m}	46.950^{c-k}	17.200^{a-h}	164.25^{a-h}
G26	66.000^{f-j}	51.000^{f-m}	117.000^{e-j}	75.650^{op}	8.5000^{d-k}	51.250^{a-g}	17.900^{a-f}	163.25^{a-h}
G27	69.750^{b-c}	58.500^{b-d}	128.250^{ab}	79.250^{j-p}	8.2000^{h-m}	46.850^{c-k}	17.100^{a-h}	180.75^{a-g}
G28	67.250^{d-h}	60.000^{b-c}	127.250^{ab}	76.000^{op}	8.7000^{c-i}	53.650^{a-d}	18.100^{a-e}	148.25c-h
G29	68.500 $^{c-e}$	51.000^{f-m}	119.500^{c-h}	75.750^{op}	8.3500^{f-l}	51.300^{a-g}	18.800^{ab}	153.25^{b-h}
G30	72.000^{a}	54.250^{b-l}	126.250^{a-c}	87.700^{a-c}	9.8500^{a}	43.950^{f-l}	18.400^{a-c}	174.75^{a-h}
G31	63.500^{l-o}	55.750^{b-i}	119.250^{d-i}	83.500^{c-k}	8.8500^{c-h}	49.400^{a-i}	17.500^{a-h}	170.50^{a-h}
G32	67.750^{c-g}	48.750^{j-m}	116.500^{e-k}	82.400^{e-k}	7.8500^{k-o}	52.750^{a-e}	16.700^{c-j}	155.50^{a-h}
G33	68.000^{c-f}	52.250^{d-m}	120.250^{c-g}	87.350^{a-d}	8.7000^{c-i}	50.050^{a-h}	16.900^{b-i}	141.00^{e-h}
G34	62.250^{o-q}	52.250^{d-m}	114.500^{g-n}	76.850^{m-p}	9.3000a-c	52.250^{a-f}	17.500^{a-h}	176.75^{a-g}
G35	60.750^{p-r}	54.000^{b-m}	114.750^{g-n}	76.950^{l-p}	9.0500^{b-e}	50.200^{a-h}	16.600^{c-j}	171.00^{a-h}
G36	59.000^{rs}	58.000^{b-e}	117.000^{e-j}	87.550^{a-c}	8.5500^{d-j}	45.800^{d-l}	16.200^{e-j}	146.75^{c-h}
G37	64.250^{j-o}	50.000^{h-m}	114.250^{g-o}	84.350^{c-i}	8.3000^{f-l}	47.150^{c-k}	16.600^{c-j}	159.25^{a-h}

Appendix Table 3. Mean of Tested Bread wheat genotypes evaluated at Kokate and Hossana, SNNPR , 2018(***Continued***)

G*	HD	GFP	MD	PH	SL	KPS	SPS	PT
G38	62.250^{n-p}	53.000^{d-m}	115.500^{e-l}	87.650^{a-c}	8.4500 $^{e-k}$	52.750^{a-e}	16.400^{d-j}	150.25^{b-h}
G39	66.250^{f-j}	41.250^{no}	107.500^{o-q}	82.050^{f-k}	8.1000^{i-n}	49.050^{b-j}	17.000^{a-i}	181.75^{a-g}
G40	65.250^{i-l}	51.250^{f-m}	116.500^{e-k}	83.100^{c-k}	7.4000^{op}	39.100^{kl}	16.400^{d-j}	172.25^{a-h}
G41	67.250^{d-h}	48.250^{k-m}	115.500^{e-l}	82.700^{d-k}	7.9000^{j-p}	50.150^{a-h}	15.700^{g-j}	155.25^{a-h}
G42	69.250^{cd}	50.250^{g-m}	119.500^{c-h}	91.150^{a}	8.7000^{c-i}	44.850^{e-l}	17.200^{a-h}	175.50a-h
G43	60.250^{qr}	48.000^{k-m}	108.250^{m-q}	83.350^{c-k}	8.2500^{g-m}	41.000^{j-l}	15.800^{g-j}	163.00^{a-h}
G44	60.500^{p-r}	53.500^{c-m}	114.000^{g-o}	81.950^{g-k}	7.6000^{m-p}	37.500^{l}	15.600^{h-j}	177.75^{a-g}
G45	60.000^{r}	53.250^{d-m}	113.250^{h-o}	78.900^{k-p}	7.4500^{n-p}	48.550^{b-j}	14.900^{j}	184.00^{a-f}
G46	60.000^{r}	48.750^{j-m}	108.750^{l-q}	81.600^{g-m}	7.6000^{m-p}	47.050^{c-k}	16.400^{d-j}	164.25^{a-h}
G47	65.000^{i-m}	51.250^{f-m}	116.250^{e-k}	79.650^{i-o}	8.9000^{c-g}	56.450^{ab}	17.900^{a-f}	171.00^{a-h}
G48	54.250^{v}	67.500^{a}	121.750^{b-f}	82.450^{e-k}	8.4500^{e-k}	42.250^{h-l}	17.100^{a-h}	138.50h^{gh}
G49	60.500^{p-r}	47.500^{mn}	108.000^{n-q}	87.150^{a-e}	7.2500^{p}	52.250^{a-f}	14.900^{j}	184.50^{a-f}
Mean	63.689	52.122	115.811	82.273	8.443	47.998	16.959	164.352
LSD(at 5%)	2.197	6.696	6.867	4.800	0.672	8.33	1.92	46.200
CV (%)	2.39	9.48	4.31	4.54	5.61	12.39	7.22	19.99

Appendix Table 3. Mean of Tested Bread wheat genotypes evaluated at Kokate and Hossana, SNNPR, 2018**(*Continued*)**

G*	BY	GY	TSW	HI
G1	2.4500^{a-e}	4.0025^{a-c}	39.828^{a-d}	35.120^{b-k}
G2	1.8750^{f-k}	2.9650^{g-j}	37.205^{a-j}	38.443^{a-f}
G3	1.5750^{k}	3.1075^{e-j}	37.868^{a-i}	42.300^{a}
G4	1.8275^{h-k}	2.7750^{i-k}	40.625^{a-c}	30.898^{g-k}
G5	1.9750^{e-k}	3.3250^{d-i}	35.368^{c-l}	34.663^{c-m}
G6	2.1250^{b-i}	3.5725^{b-g}	37.328^{a-j}	34.825^{c-m}
G7	2.5750^{a-c}	3.8475^{a-d}	40.778^{ab}	30.295^{i-n}
G8	2.1750^{b-h}	2.7625^{i-k}	31.36 $^{k-o}$	27.125^{no}
G9	2.9000^{a}	3.6000^{b-f}	36.565^{b-k}	27.088^{no}
G10	2.1775^{b-h}	3.7300^{b-e}	30.455^{l-p}	36.538^{a-j}
G11	2.3250^{b-h}	3.2750^{d-i}	33.123^{g-n}	29.080^{k-o}
G12	2.1000^{c-j}	3.5600^{b-g}	32.895^{i-n}	35.800^{a-k}
G13	2.2500^{b-h}	2.3400^{k}	25.843^{p}	22.323^{o}
G14	2.0550^{d-k}	3.6275^{b-f}	42.393^{a}	37.480^{a-h}
G15	2.5000^{a-d}	3.4300^{c-h}	41.383^{ab}	29.083^{k-o}
G16	2.1000^{c-j}	3.0900^{f-j}	40.838^{ab}	31.813^{f-n}
G17	2.1750^{b-h}	3.4875^{c-g}	34.268^{e-n}	33.598^{c-n}
G18	2.0000^{d-k}	3.5975^{b-f}	36.230^{b-k}	37.455^{a-i}
G19	1.5800^{k}	3.1025^{f-i}	37.255^{a-j}	39.533^{a-d}

Appendix Table 3. Mean of Tested Bread wheat genotypes evaluated at Kokate and Hossana, SNNPR, 2018(***Continued***)

G*	BY	GY	TSW	HI
G20	1.9575^{e-k}	2.7575^{i-k}	29.838^{m-p}	31.785^{f-n}
G21	2.0000^{d-k}	3.0950^{f-i}	31.958^{j-n}	33.413^{c-n}
G22	2.5000^{a-d}	4.4100^{a}	33.060^{h-n}	36.213^{a-k}
G23	2.2000^{b-h}	3.1975^{e-i}	32.308^{j-n}	30.743^{g-n}
G24	2.4500^{a-e}	3.4600^{c-g}	30.173^{l-p}	30.450^{h-n}
G25	2.1250^{b-i}	3.6900^{b-f}	30.553^{l-p}	35.223^{a-l}
G26	2.2250^{b-h}	3.8375^{a-d}	30.133^{l-p}	37.578^{a-h}
G27	1.9750^{e-k}	3.4900^{c-g}	29.453^{n-p}	39.680^{a-d}
G28	2.1750^{b-h}	3.4075^{c-h}	32.100^{j-n}	32.693^{d-n}
G29	2.6250^{ab}	3.8525^{a-d}	30.150^{l-p}	31.858^{f-n}
G30	2.3000^{b-h}	3.4075^{c-h}	38.505^{a-g}	30.145^{j-n}
G31	2.3250^{b-h}	4.1825^{ab}	38.748^{a-f}	39.135^{a-e}
G32	2.1500^{b-h}	2.9675^{g-j}	34.140^{f-n}	27.873^{m-o}
G33	2.4250^{a-e}	3.6250^{b-f}	38.440^{a-h}	31.800^{f-n}
G34	2.1000^{c-j}	3.3300^{d-i}	36.695^{b-k}	31.695^{f-n}
G35	2.3500^{b-g}	3.2500^{d-i}	39.563^{a-e}	30.923^{h-n}
G36	1.8575^{f-k}	3.3750^{d-i}	33.715^{f-n}	38.420^{a-f}
G37	1.9750^{e-k}	3.4800^{c-g}	34.095^{f-n}	42.058^{ab}
G38	2.3250^{b-g}	3.1075e-i	34.625^{d-n}	28.465^{l-o}

Appendix Table 3. Mean of Tested Bread wheat genotypes evaluated at Kokate and Hossana, SNNPR , 2018. ***(Continued)***

G*	BY	GY	TSW	HI
G39	2.2500^{b-h}	3.6675^{b-f}	33.805^{f-n}	34.005^{c-n}
G40	2.2000^{b-h}	3.3100^{d-i}	38.310^{a-h}	32.105^{e-n}
G41	1.6000^{jk}	2.4050^{jk}	26.318^{op}	29.645^{j-n}
G42	2.2500^{b-h}	3.5600^{b-g}	38.825^{a-f}	33.323^{c-n}
G43	1.8500^{g-k}	2.8275^{h-k}	32.073^{j-n}	32.613^{d-n}
G44	1.6250^{i-k}	2.3400^{k}	33.893^{f-n}	32.520^{d-n}
G45	1.8500^{g-k}	3.2650^{d-i}	32.245^{j-n}	38.360^{a-f}
G46	1.9750^{e-k}	3.5425^{c-g}	31.423^{k-o}	37.765^{a-g}
G47	2.1000^{c-j}	3.5850^{b-g}	35.190^{d-m}	35.608^{a-l}
G48	1.8250^{h-k}	3.4925^{c-g}	40.848^{ab}	39.905^{a-c}
G49	2.3750^{b-f}	4.3575^{a}	41.295^{ab}	39.968^{a-c}
Mean	2.136	3.377	34.981	33.866
LSD (at 5%)	0.518	0.624	5.390	7.167
CV (%)	15.69	13.14	10.58	13.57

G* = Genotypes used in the study, LSD = least significant difference, CV = coefficient of variation, HD = days to 50% heading, GFP = days to grain filling period, MD = days to 90% physiological maturity, PH = plant height (cm), SL= spike length (cm), KPS = number of kernels per spike, SPS = number of spikelets per spike, SPS = number of productive tillers per meter square area, BY = biological yield (kg/ha), GY = grain yield (tone/ha), TSW = one thousand seed weight (gm), HI = harvest index (%).

Appendix Table 4. The description of morphological characters of tested bread wheat genotypes

Genotypes	A	SD	SS	SC	KT	DSS
WBLL4//OAX93.24.35/WBLL1/4/SHUHA-1/3/MON'S'/ALD'S'//ALDAN'S'/IAS58	7	3	5	brown	1	3
KAUZ/STAR/3/MUNIA/ALTAR 84//MILAN/4/LEITH-1	3	3	5	brown	1	3
FARIS-22/4/BOW/PRL//BUC/3/WH576/5/NING MAI 9558//CHIL/CHUM18	3	9	5	white	9	3
FILIN/3/CROC-1/AE.SQUARROSA	3	5	5	white	1	5
(205)//KAUZ/4/FILIN/5/VEE/MJI//2*TUI/3/PASTOR/6/ASEEL-4						
WBLL1*2/BRAMBLING//ZAFIR-3	7	3	5	white	9	3
WEAVER/TSC//WEAVER/3/WEAVER/4/WAXWING/5/DURRA-8	3	5	3	brown	9	5
CHAMRAN/4/OPATA/BOW//BAU/3/OPATA/BOW/5/SAMIRA-9	3	9	5	brown	9	3
KOUKAB-1//PFAU/MILAN/3/SOSSI-3	3	5	5	white	9	3
VEE/NAC//MILAN/PASTOR/5/HUITES/4/CS/TH.SC//3*PVN/3/MIRLO/BUC	7	9	5	white	9	3
SERI.1B//KAUZ/HEVO/3/AMAD/4/ESWYT99#18/ARRIHANE/5/SKAUZ/BAV92	7	3	5	brown	9	5
OPATA/RAYON//KAUZ/3/ETBW 4922/4/MILAN/PASTOR	3	5	5	white	1	3
SHIHAB-19/KHIDER-1/5/YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE.SQUARROSA	7	7	5	brown	1	3
(224)//OPATA						
HUITES/4/CS/TH.SC//3*PVN/3/MIRLO/BUC/5/ETBW 4922/6/QADANFER-4	3	7	5	brown	9	5
KINGBIRD/IZAZ-11	3	5	5	brown	1	3
KIRITATI/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/SHUHA-4/CHAM-8	3	5	5	brown	9	3
KRICHAUFF/2*PASTOR//SHUHA-8/DUCULA	3	5	5	Red	1	5

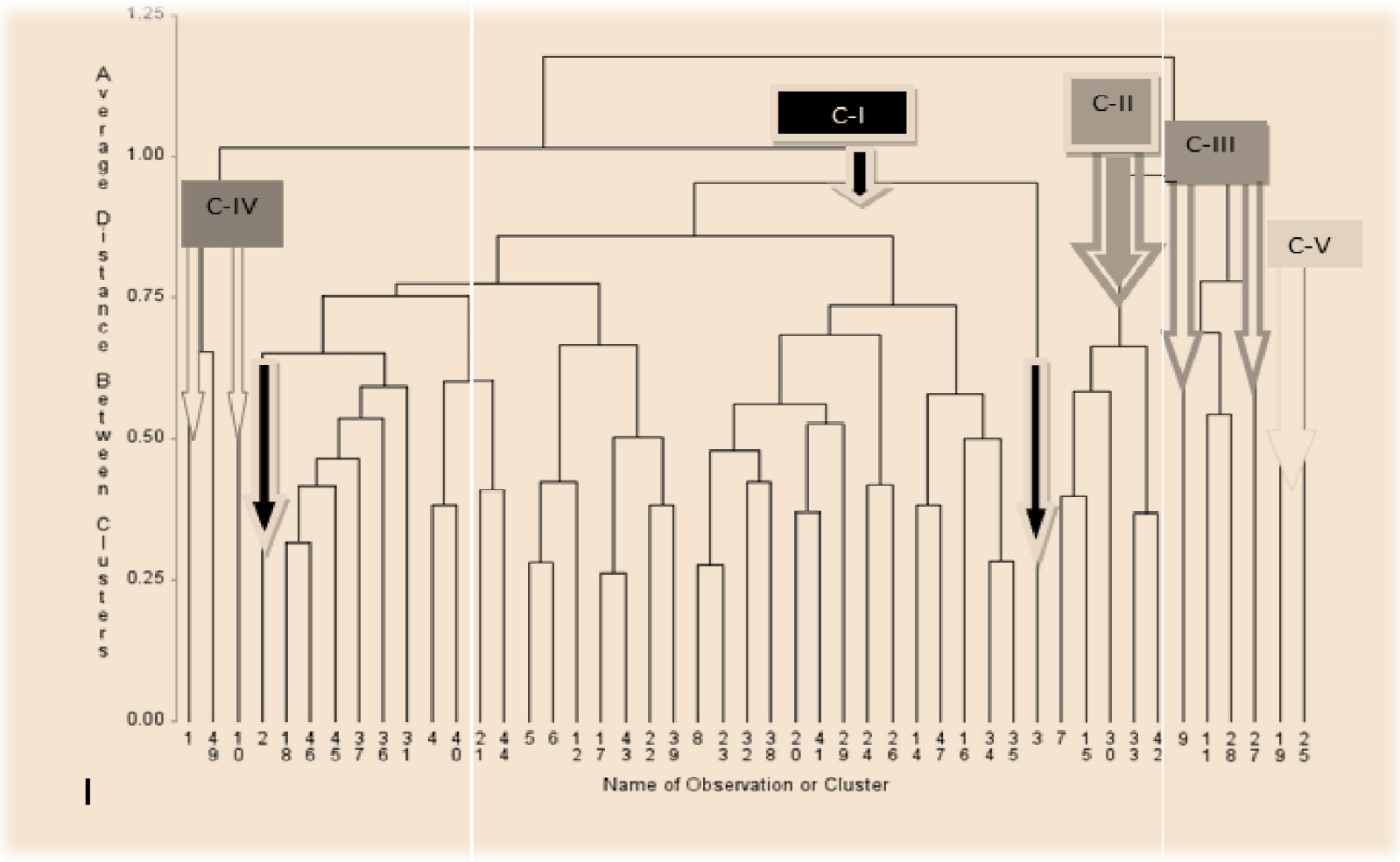
Appendix Table 4. The description of morphological characters of tested bread wheat genotypes(***Continued***)

Genotypes	A	SD	SS	SC	KT	DSS
P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN-a	3	7	3	brown	1	5
P1.861/RDWG//ESWYT99#18/ARRIHANE/3/PFAU/MILAN-b	7	5	5	brown	9	3
ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'-a	7	7	5	brown	9	5
ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S'-b	7	3	7	white	1	5
PFAU/MILAN//ABIER-2/3/SHUHA-3//TURACO/CHIL	3	7	5	white	9	5
TEVEE-1/STAR'S'//ETBW 4920/3/TEPOCA+LR34/2*BORL95	3	7	7	white	1	3
KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR	3	7	5	white	9	5
CHAM-10/3/PASTOR//MUNIA/ALTAR 84/4/PFAU/MILAN	3	5	5	white	9	3
SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-a	3	5	5	red	9	3
SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-b	7	7	7	white	1	3
SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-c	3	7	5	white	1	5
SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-d	3	9	5	brown	9	3
SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5-e	3	5	5	red	9	5
THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B-a	3	5	3	brown	9	5
THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B-b	3	3	5	brown	1	7
CHAM-8/ETBW 4919//PFAU/MILAN	7	5	5	white	1	3

Appendix Table 4. The description of morphological characters of tested bread wheat genotypes (***Continued***)

Genotypes	A	SD	SS	SC	KT	DSS
ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/GHALI-1	3	3	5	Brown	1	7
KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR	7	5	5	White	1	3
FARIS-17//PFAU/MILAN/3/SOSSI-3	3	5	5	White	1	5
ZERBA-6/FLAG-6/3/TAM200/PASTOR//TOBA97	3	3	7	Red	9	5
BABAX/LR42//BABAX*2/3/VIVITSI/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ	3	7	5	Brown	1	5
TEMPORALERA M 87*2/TUKURU//FAYEQ-2	3	7	5	Brown	9	3
NESMA*2/14-2//2*SAFI-3/4/PASTOR//HXL7573/2*BAU/3/WBLL1	3	5	5	White	1	3
MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/NESMA*2/14-2//2*SAFI-3	3	7	3	Brown	1	7
FAYEQ-2/3/NESMA*2/14-2//2*SAFI-3	3	7	3	White	1	5
QT6581/4/PASTOR//SITE/MO/3/CHEN/AEGILOPSSQUARROSA (TAUS)//BCN/5/PAVON 76/JADIDA-2	3	5	3	Brown	9	5
WAXWING*2/VIVITSI//SHUHA-8/DUCULA	3	5	3	Brown	9	5
WBLL1//TEVEE/KAUZ/3/MILAN/SHA7//POTAM*3KS811261-5	3	9	7	Brown	1	3
KINGBIRD/3/NESMA*2/14-2//2*SAFI-3a	3	5	3	Brown	9	5
KINGBIRD/3/NESMA*2/14-2//2*SAFI-3b	3	5	3	Brown	1	5
KAUZ/STAR//ETBW 4920/3/QAMAR-2	3	5	3	Brown	9	7
ATTILA/3*BCN//MILAN/DUCULA/7/BACANORA	3	9	3	White	1	3
86/6/SN64/HN4//REX/3/EDCH/MEX/4/SLS'S'/5/BOW'S' WANE(ETBW6130)	3	7	3	Brown	1	7

A = awnedness, SD = spike density, SS = seed size, SC = seed colour, KT = kernel texture, DSS = degree of seed shriveling



Appendix Figure 1. Dendrogram showing grouping of 47 bread wheat genotypes into 5 clusters based on 11 quantitative characters

Appendix Figure 2. Partial view of bread wheat genotypes used for morpho – agronomic variability

Appendix Figure 2. Partial view of bread wheat genotypes used for morpho – agronomic variability(***Continued***)