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Breeding Bread Wheat (*Triticum aestivum* L.) for Drought-Tolerance in Ethiopia

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By

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Thesis Abstract

Wheat (*Triticum aestivum* L.; 2n=6x=42; AABBDD) is one of the major staple cereal crops in the world. The demand for wheat has rapidly increased in sub-Saharan Africa including Ethiopia because of the growing population, changing food preferences and socio-economic change associated with urbanization. However, production and productivity of wheat in the region is affected by various biotic, abiotic and socio-economic factors. Drought is one of the major abiotic constraints limiting wheat productivity in Ethiopia. Adoption of new improved varieties by farmers is relatively low in marginal, drought-prone areas of the country because of a lack of improved varieties with desirable agronomic and drought-adaptive traits. Developing wheat cultivars, which are drought-tolerant, high and stable yielding with farmers' preferred traits, is a sustainable strategy to ensure food security and to improve livelihoods of farmers in marginal areas. Therefore, the objectives of this study were: i) to assess farmers' production practices, perceived production constraints and preferred traits of bread wheat varieties as a guide to variety development and deployment in drought-prone areas of Ethiopia; ii) to screen bread wheat genotypes for drought-tolerance using phenotypic analysis to select promising lines for use in breeding for drought-tolerance; iii) to estimate the genetic parameters and association of yield and yield components and thus determine the selection criteria to increase genetic gains under drought-stress conditions; iv) to assess the genetic diversity and relationships among the selected wheat genotypes using simple sequence repeat (SSR) markers in order to complement the phenotypic data in identifying complementary parents for further breeding for drought-tolerance; and v) to determine combining ability effects of the selected wheat genotypes, thereby deducing gene action controlling traits of interest and identifying promising families for drought-stress conditions, and to advance these families through the single seed descent selection method. Separate but complementary research activities were conducted to attain the aforementioned objectives.

A participatory rural appraisal (PRA) study was conducted involving 170 randomly selected wheat-producing farmers in selected districts of Arsi zone in the Oromia Regional State of Ethiopia during 2018. Moisture-stress, disease (wheat rusts) and the high cost of fertilizers were the first, second and third ranked production constraints in the study areas. Varietal attributes such as early maturity ($p<0.01$) and tall plant height ($p<0.05$) had positive and significant effects on the adoption of new, improved varieties, while poor adaptation and poor baking quality had negative and significant ($p<0.05$) influences. High grain yield was the most preferred trait as perceived by the farmers in the study areas, followed by stress adaptation (drought and heat stresses-tolerance), disease-resistance and early maturity.

In the second part of the study, 120 genotypes were evaluated at five test sites in the 2018/19 cropping season using a 10 x 12 alpha lattice design with two replicates. The level of drought-stress was imposed

using different sowing dates (early planting resulted in non-stressed plants, while late planting created drought-stressed conditions) following the onset of the main seasonal rain at each site. Grain yield and yield components were recorded, and drought indices were calculated for each genotype. Genotypes such as 'YS-39', 'YS-119' and 'YS-109' were the earliest to mature and can be used in drought-tolerance breeding. Among the drought-tolerance indices, Geometric Mean Productivity (GMP), Mean Productivity (MP), Harmonic Mean (HM), Stress Tolerance Index (STI) and Yield Index (YI) were found to be the most suitable for predicting drought-tolerance because they had significant and positive correlations with yield under drought-stressed and non-stressed conditions. Genotypes 'YS-41', 'YS-92', 'YS-115', 'YS-34' and 'YS-93' were found to be drought-tolerant, and exhibited dynamic stability, with relatively high yield under both drought-stressed and non-stressed conditions. 'YS-90', 'YS-106', 'YS-96', 'YS-102' and 'YS-101' were susceptible to drought-stress, while 'YS-32', 'YS-29', 'YS-14', 'YS-53' and 'YS-11' were relatively drought-tolerant, but exhibited static stability under non-stressed conditions.

In the third part of the study, the extent of the genetic parameters and associations of yield and yield components were determined among the aforementioned 120 genotypes in order to design appropriate breeding strategies for yield improvement in wheat. The highest estimates for genetic variance were obtained for days to heading (DH; 54.0%), followed by Spike length (SL; 38.3%). The high heritability estimated for DH (94.4%), SL (90.2%) and spikeletes per spike (SS; 85.2%), coupled with a high rate of genetic advance, suggest that direct selection for these traits would be effective. Grain yield (GY) exhibited low genetic advancement (9%) and heritability (41.5%) estimates, which were concomitant with its polygenic and complex inheritance pattern. Correlation and path analyses revealed that plant height (PH) and 1000-kernel weight (TKW) were the most important contributing traits for improving grain yield under drought-stress conditions.

In the fourth part of the study, 52 selected bread wheat genotypes were assessed using 20 SSR markers. SSR analysis identified a total of 181 alleles, with a mean of 10.1 alleles per locus. Population structure analysis grouped the test genotypes into three main populations. Analysis of molecular variance revealed that 85% of the variance emanated from intra-population differences. Cluster analysis also grouped the test genotypes into three major groups.

In the fifth part of the study, eight parental lines and 28 crosses obtained from a half-diallel mating design were evaluated at two sites representing drought-stressed and non-stressed conditions. The genotypic effects were significant for all traits studied except grain-filling period (GFP) across the test environments. The parental line 'YS-32' was the best general combiner for DH, days to maturity (DM), GFP and TKW, enabling direct selection for improved grain yield under drought-stress conditions. Parent 'YS-85' can also be used for improving grain yield under drought-stress conditions due to its positive and significant GCA effect on GY. The highest specific combining ability (SCA) effects under

drought-stressed for improving GY were obtained in families 'YS-32' x 'YS-85', 'YS-102' x 'YS-82' and 'YS-102' x 'YS-92'.

Overall, the present study revealed drought-stress was the major bread wheat production constraint in drought-prone agro-ecologies of Ethiopia. And, farmers had varying varietal preferences for adopting newly improved varieties. The tested genotypes proved to be valuable genetic resources to enhancing drought-tolerance and improving farmers' preferred traits. In future, these genetic resources will be used either for developing mapping populations for quantitative trait loci (QTL) analysis underlying traits of interest under drought-stress conditions to serve as long-term breeding materials or release directly as cultivars incorporating farmers' preferred traits.

Declaration

I, Yared Semahegn Belete, declare that:

1. The research reported in this thesis, except where otherwise indicated, is my original research.

2. This thesis has not been submitted for any degree or examination at any other University.

3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.

4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

   a. Their words have been re-written but the general information attributed to them has been referenced.

   b. Where their exact words have been used, then their writing has been placed in italics and inside quotation marks, and referenced.

5. This thesis does not contain text, graphics or tables copied and pasted from the internet, unless specifically acknowledged, and the source being detailed in the thesis and in the references sections.

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Yared Semahegn Belete

As the candidate's supervisor, I agree to the submission of this dissertation:

....

Prof. Hussein Shimelis (Supervisor)

....

Prof. Mark Laing (Co-supervisor)

Acknowledgments

Dedication

This study is dedicated to my wife. *Mestawot Demissie*,

my daughter. *Elyana Yared,*

and my sons, *Eyubel Yared* and *Amanuel Yared*

Table of Contents

Publications Pertaining to this Thesis

Chapter 2

Semahegn, Y., H. Shimelis, M. Laing, and I. Mathew. 2021. Farmers' preferred traits and perceived production constraints of bread wheat under drought prone agro-ecologies of Ethiopia. Journal of Agriculture and Food Security https://doi.org/10.1186/s40066-021-00290-0

Chapter 3

Semahegn, Y., H. Shimelis, M. Laing, and I. Mathew. 2020. Evaluation of bread wheat (*Triticum aestivum* L.) genotypes for yield and related traits under drought-stressed conditions. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science 70(6): 474-484.

Chapter 4

Semahegn, Y., H. Shimelis, M. Laing, and I. Mathew. Genetic variability and association of yield and yield components among bread wheat genotypes grown under drought-stressed conditions. Australian Journal of Crop Science (Accepted)

Chapter 5

Belete, Y., H. Shimelis, M. Laing, and I. Mathew. 2020. Genetic diversity and population structure of bread wheat genotypes determined via phenotypic and SSR marker analyses under drought-stressed conditions. Journal of Crop Improvement https://doi.org/10.1080/15427528.2020.1818342

Chapter 6

Semahegn, Y., H. Shimelis, M. Laing, and I. Mathew. Combining ability of bread wheat (*Triticum aestivum* L.) genotypes for yield and yield-related traits under drought-stressed and non-stressed conditions. South African Journal of Plant and Soil (Accepted)

Thesis Introduction

Background

Wheat (*Triticum aestivum* L.; 2n=6x=42; AABBDD) is the third most important cereal crop in the world next to maize (*Zea mays* L.) and rice (*Oryza sativa* L.) in terms of total production. Globally, China is the largest producer of wheat followed by India, USA, Russian Federation, France, Canada, Germany, Australia, Pakistan and Turkey (FAO, 2019). Ethiopia is the largest wheat producer in sub-Saharan Africa. Wheat is best adapted to temperate agro-ecologies. However, it is also the major cereal crop grown in arid and semi-arid regions of the world (Trethowan and Reynolds, 2007).

In Ethiopia, the major wheat producing areas are mainly found in the mid altitude (1900 to 2300 m above sea level) and high altitude (2300 to 2700 m above sea level) regions that are regarded as high potential crop production environments due to their high and reliable rainfall. Wheat is mainly planted in the summer, before the *meher* (main) season rains in June-September, and then harvested in October-November. Most of the wheat is grown in the Oromia region (58.4%), followed by the Amhara region (28.2%), the two regions accounting for 86.6% of domestic production, with the remaining 13.4% being produced in the other regions of the country (CSA, 2016). Wheat provides 9-20% of the calorie needs of low-income and rural households in Ethiopia (Bergh et al., 2012). It is also a source of cash for smallholder farmers (Bregh et al., 2012). Production and productivity of wheat has shown an increasing trend for the last ten years (Figure 0.1). However, the demand for wheat surpasses domestic supply due to population growth, the emergence of agro-processors, urbanization, and increased household income (Shiferaw et al., 2014; Adhikari et al., 2015; Gebreselassie et al., 2017). For instance, in 2013, 0.86 million tons of wheat was imported, at a cost of USD 438.5 million to meet the domestic demand (Rashid and Lemma, 2014).
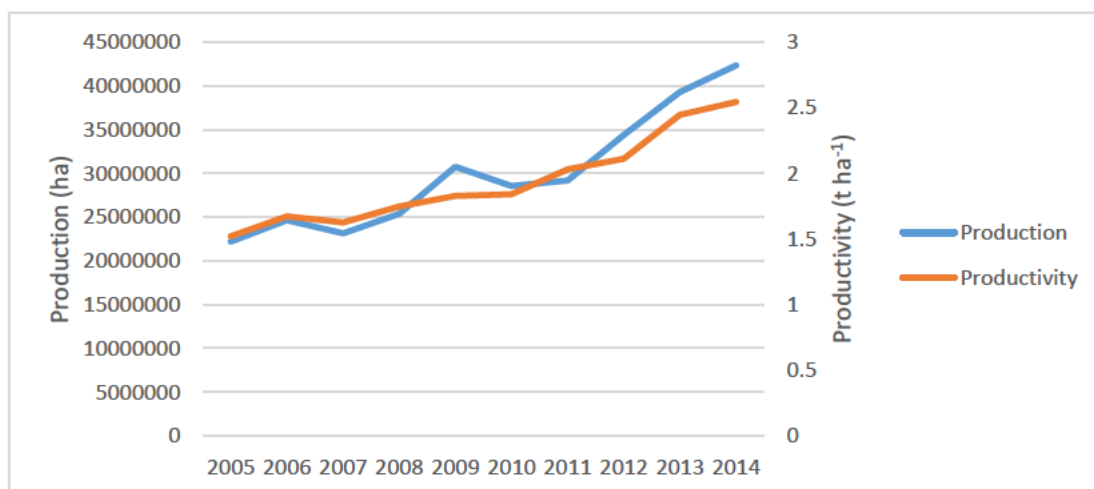
Figure 0.1 Production and productivity of wheat in Ethiopia during the last ten years (2005-2014) (CSA, 2005/06-2014/15).

In spite of the importance of wheat and the efforts made so far to generate improved production technologies, the national average yield is 2.4 t ha^{-1}, which is much lower than world average of 3.4 t ha^{-1} (FAO, 2019) because of several biotic, abiotic and socio-economic constraints (Adhikari et al., 2015; Tadesse et al., 2016). Drought is one of the major abiotic constraints limiting wheat yields and stability globally (Ribaut et al., 2009; Adhikari et al., 2015). In SSA, including Ethiopia, wheat is mainly cultivated under rainfed condition and subject to recurrent drought and heat-stresses associated with climate change (Farshadfar et al., 2012; Adhikari et al., 2015; Tadesse et al., 2016; Gupta et al., 2017). In Eastern Africa up to 72% of wheat yield is expected to decline attributed to climate change (Adhikari et al., 2015). Increasing the productivity of wheat in dryland production areas, where drought-stress is more common, is the most economic and environmentally friendly option to meet the growing demand for wheat (White et al., 2001; Mwadzingeni et al., 2016). Development and adoption of drought-tolerant varieties along with suitable production technologies would enhance productivity of wheat under the changing climate scenario (Negassa et al., 2013; Adhikari et al., 2015).

Most wheat varieties developed for high production environments were not successful in marginal environments despite their high yield potential under optimal conditions (Morris and Bellon, 2004). Only few varieties have been adopted by farmers in marginal environments. Studies showed that a lack of systematic breeding that incorporates farmers' preferred traits, resulted in the poor performance and low adoption rates of new varieties by farmers under marginal conditions (Morris and Bellon, 2004; Asrat et al., 2009; Tadesse et al., 2019).

Rationale of the study

Wheat is one of the major grain crops in Ethiopia. It is the second most important staple food in the country next to maize, and its consumption is rapidly increasing because of the growing population, changing food preferences and socioeconomic change associated with urbanization. It is a source of cash for smallholder farmers. The government spends much of its scarce foreign currency on wheat imports annually to fill the gap between the demand and supply in the country. Associated with the changing climate, different biotic and abiotic, and socio-economic factors result in low yields and quality in wheat. Adoption of improved varieties is low especially in marginal areas due to a lack of improved varieties with desirable agronomic and drought-adaptive traits. Drought is the most yield limiting abiotic factor in wheat production, causing yield losses to reach 60%, or even complete crop failure under severe conditions. Breeding for drought-tolerance is thus one of the overriding considerations identified in the national wheat breeding program.

In Ethiopia, wheat is largely cultivated in the highlands by small-scale farmers under rainfed condition. Substantial amount of wheat is also produced in the mid- and low-land areas of the country. However, the lowlands are dry or warm environments with low and erratic rainfall, which are often constrained

by water-deficits and warm temperatures. The crop performance in diverse environments depends on suitability of the cultivars used to match the agro-ecology of the production areas. Hence, to improve yield and stability of bread wheat in these agro-ecologies, there is a need for a dedicated breeding program that contribute to developing productive bread wheat cultivars across a range of soil moisture conditions. Considerable improvements have been made in adaptation of wheat to drought-prone environments, which has been largely achieved through field-based, empirical selection for drought-tolerance. Breeding crop varieties for drought-tolerance and adaptation to a changing environment would ensure high yields and stable crop productivity. Improving wheat yields through developing drought-tolerant, high-yielding and stable varieties is a continuous process that utilizes the existing genetic resources. Given the release of several drought-tolerant varieties by the national program, farmers' adoption of these varieties is low, and becoming the overriding problem for the production of bread wheat in marginal environments. Therefore, this PhD study answers the research questions: 1) Why farmers' adoption of improved wheat technologies/improved varieties is low in marginal environments; 2) What factors determine adoption of improved varieties; and 3) What breeding strategies should be followed in order to address the above two major questions. Breeding for drought-tolerance was thus proposed with the aforementioned premises.

Overall aim

The overall aim of the study was to contribute to increasing production and productivity through the development of drought-tolerant, high yielding and stable bread wheat cultivars that incorporate traits preferred by farmers in drought-prone agro-ecologies of Ethiopia.

Specific objectives

i. To assess farmers' production practices, perceived constraints and preferred traits of bread wheat varieties as a guide to variety development and deployment in drought-prone areas of Ethiopia;

ii. To screen bread wheat genotypes for drought-tolerance using phenotypic analysis to select promising lines for use in breeding for drought-tolerance;

iii. To estimate the genetic parameters and association of yield and yield components, and thus determine the selection criteria to increase genetic gains under drought-stress conditions;

iv. To assess the genetic diversity and relationships among the selected wheat genotypes using SSR molecular markers in order to complement the phenotypic data in identifying complementary parents for further breeding for drought-tolerance;

v. To determine combining ability effects of the selected wheat genotypes, thereby deducing gene action controlling traits of interest and identifying promising families for drought-

stress conditions, and advance these families through the single seed descent selection method.

Research hypotheses

    i.   There are different farmers' practices, production constraints, and cultivar preferences that influence bread wheat production in drought-prone areas;

    ii.   There is variation among the bread wheat genotypes for drought-tolerance and related phenotypic traits;

    iii.   SSR markers will reveal extensive genotypic variability that complement phenotypic diversity among the bread wheat genotypes;

    iv.   Selected bread wheat genotypes and their crosses show good combining ability effects for drought- tolerance and related phenotypic traits;

    v.   Single seed descent selection method is an effective breeding method to advance the selected families for drought-tolerance and related phenotypic traits under drought-stress conditions

Thesis outline

This thesis consists of six chapters, developed according to the specific objectives set above. Chapter 1 is written as a separate review paper, while Chapters 2 to 6 are written as discrete research papers, each following the format of a stand-alone research paper, followed by a general overview of the research and its implications. The literature review and five experimental chapters of the study made the thesis chapters that were condensed into discrete but inter-dependant papers according to the University of KwaZulu-Natal's dominant thesis format. The Crop Science Journal referencing system was used in all chapters of this thesis.

The outline of the thesis is therefore as follows:

1. Thesis Introduction
2. Chapter One: Review of the Literature
3. Chapter Two: Farmers' production practices, perceived constraints, and preferred traits of bread wheat varieties under drought-prone agro-ecologies of Ethiopia
4. Chapter Three: Evaluation of bread wheat (*Triticum aestivum* L.) genotypes for yield and related traits under drought-stressed and non-stressed conditions
5. Chapter Four: Genetic variability and association of yield and yield components among bread wheat genotypes under drought-stressed and non-stressed conditions

6. Chapter Five: Genetic diversity and population structure of bread wheat genotypes determined via SSR marker analysis

7. Chapter Six: Combining ability of bread wheat (*Triticum aestivum* L.) genotypes for yield and yield-related traits under drought-stressed and non-stressed conditions

8. General overview and implications of the study

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Chapter 1. Review of the Literature

Abstract

Common wheat (*Triticum aestivum* L.; 2n=6x=42; AABBDD) is one of the major food staples worldwide. The market demand for wheat products has rapidly increased in sub-Saharan Africa (SSA), including Ethiopia, due to population pressure, food preferences and socio-economic change associated with urbanization. Conversely, the productivity of wheat is too low in SSA to satisfy local demands, due to various biotic, abiotic, and socio-economic factors. Drought is the most important abiotic constraint limiting wheat production and productivity. Adoption of improved varieties by farmers is relatively low in marginal, drought-prone areas because of a lack of improved varieties with desirable agronomic and drought-adaptive traits. Systematic wheat breeding for drought-prone areas incorporating farmers' preferred traits would boost productivity and increase adoption rates of new wheat varieties. This review provides the theoretical basis on drought-tolerance breeding on wheat. It highlights the following key issues affecting drought-tolerance: the mechanisms of drought responses in wheat, screening techniques, the genetic basis, sources of genetic variation and breeding methodologies. It presents the role of participatory plant breeding and identification of farmers' preferences in wheat varieties to guide future breeding of wheat that includes farmers-preferred traits for production in marginal wheat production areas in Ethiopia or similar agro-ecologies.

Keywords: agro-ecology, drought-tolerance, genetic variation, participatory breeding, wheat improvement

1.1 Introduction

Common wheat (*Triticum aestivum* L.; 2n=6x=42; AABBDD) is a major food crop globally. The market demand for wheat products is rapidly increasing in sub-Saharan Africa (SSA), including Ethiopia, due to population pressure, food preferences and socio-economic change associated with urbanization (Tadesse et al., 2019). In Africa, 61% of wheat demand is met through imports (Negassa et al., 2013). World wheat production is about 7.3 million tons per annum, from an estimated area of about 2.1 million hectares. The mean global productivity of wheat is 3.4 t ha^{-1}, while a mean yield level of 2.6 t ha^{-1} is reported in Africa (FAO, 2019). In SSA, Ethiopia and South Africa are the leading wheat producers. The mean wheat yield in Ethiopia is 2.4 t ha^{-1}, which is far below the global average (FAO, 2019). The low productivity is attributable to various biotic stresses (pests, diseases and weeds), abiotic stresses (heat and drought-stresses, salinity, water logging, low soil fertility and acidity), and socio-economic factors.

Drought is one of the most important abiotic constraints limiting wheat productivity globally (Adhikari et al., 2015). It causes yield losses of up to 60% in SSA (Barnabás et al., 2008). Several improved wheat varieties with high yield potential and quality have been released by various international and national breeding programs. In the past most of the released or introduced wheat varieties were relatively well adopted under favourable growing conditions. However, adoption of improved varieties has been relatively poor in marginal, drought-prone areas because of a lack of improved varieties with agronomic and drought-adaptive traits preferred by farmers. Breeding for drought-tolerance is an economic and sustainable approach to improving yields in marginal areas. Drought-tolerance is, however, a complex polygenic trait and subject to genotype by environment interactions that affect the identification of superior genotypes. Furthermore, the unpredictable nature of drought manifestation and the many different mechanisms adopted by plants to cope with drought-stress complicate the breeding and selection of superior genotypes under variable moisture conditions. Improving crop yields is a continuous process that enables the exploitation of its potential for various purposes that fulfil farmers' preferences. Understanding and broadening the genetic bases of phenotypic traits that contribute to improved yields under drought-stress is crucial for the improvement of wheat productivity.

The first Green Revolution enabled increased production and productivity of wheat under optimal growing conditions. However, the improved varieties have not been adopted in marginal production environments where they are poorly adapted (Morris and Bellon, 2004). This resulted from a lack of systematic breeding for target drought and heat-stressed environments, and the integration of farmers' preferred traits for quality and agronomic performance (Morris and Bellon, 2004; Asrat et al., 2009; Tadesse et al., 2019). Several factors influence the adoption or non-adoption of improved varieties (Kalinda et al., 2014; Solomon et al., 2014; Chilot et al., 2015). Nevertheless, most adoption studies have concentrated on high potential environments, with few adoption studies conducted with farmers

in marginal, low potential environments (Zegeye et al., 2001; Tura et al., 2010; Wondale et al., 2016). It is thus important to gain insight into farmers' preferences for varietal attributes and the challenges pertinent to their production, focusing on drought- and heat-stressed environments (Morris and Bellon, 2004; Beshir and Wegary, 2014; Drabo et al., 2019). This will enable breeders to developing locally adapted and improved varieties with farmers' preferred traits (Asrat et al., 2009; Kalinda et al., 2014), and thereby ensure food security of smallholder farmers in drought-prone areas (Beshir and Wegary, 2014). Therefore, the objectives of this review were to provide the theoretical basis for breeding wheat with drought-tolerance. It highlights key issues affecting drought-tolerance such as the mechanisms of drought responses, screening techniques, the genetic basis, sources of genetic variation and breeding methodologies. It also discusses participatory wheat breeding and the need to discover farmers' trait preferences in wheat varieties to guide future breeding for marginal wheat production areas in Ethiopia or similar agro-ecologies.

1.2 Drought-stress and its effect on wheat production

The lack of adequate soil moisture to support normal crop growth at any phase of crop growth is defined as drought-stress, and it has a negative impact on grain yield and quality (Sehgal et al., 2018). Drought affects wheat development at all growth stages but especially affects the flowering and grain-filling stages. Drought may reduce yields by 58-92% during the post-anthesis stages (Pradhan et al., 2012; Farooq et al., 2014). The impact of drought-stress on crop varieties depends on the genotype, environment (drought intensity, duration, time of onset), crop management practices and their interaction. The occurrence of prolonged drought-stress during vegetative growth stages can be detrimental on plant growth, development and reproduction, leading to poor yields and crop loss. Climate change has resulted in irregular and unpredictable rainfall, and increased mean temperatures in many areas, which has increased the intensity and frequencies of drought-stress globally (Gupta et al., 2017; Senapati et al., 2019).

1.3 Mechanisms of drought response

Understanding the adaptation mechanisms of drought response in crops is fundamental to improving drought-tolerance. There are several mechanisms of drought response in plant species, broadly categorized as drought-escape, avoidance, and tolerance (Senapati et al., 2019). These mechanisms of drought response can be expressed at phenological, morphological, physiological, or biochemical levels.

1.3.1 Drought-escape

Drought-escape is the most widely used mechanism of drought response. Numerous investigations have been conducted to understand and exploit this mechanism for improving drought-tolerance in wheat. Genotypes that utilize the drought-escape mechanism manage to complete their life cycle before the onset of significant drought-stress (Dolferus, 2014). Drought-escape is also often associated with an early plant vigour, i.e., an acceleration of plant development (Kosova et al., 2014). Early flowering and maturity allow crops to avoid terminal water-stress while maintaining potential yields (Shavrukov et al., 2017; Senapati et al., 2019). Genotypes that exhibit early flowering and maturity are characterised by shorter vegetative periods, high metabolic rates and high water use efficiency (Chantereau et al., 2001; Shavrukov et al., 2017). However, under favourable conditions, early flowering and maturity may result in yield penalty due to a shortened lifecycle (Shavrukov et al., 2017). Given the frequent terminal drought-stress events in SSA, breeding for early maturity has been prioritised. It is imperative to identify adequate genetic variation for early flowering and maturity in crops such as wheat to develop early maturing cultivars with a minimum yield penalty. However, flowering and maturity are complex traits that also respond to a defined photoperiod. Selection for early flowering and maturity genotypes is confounded by the interaction effects of genotype and environment. Breeding progress or genetic gains accrued in yield as a result of reduction in flowering and maturity days is a promising strategy of drought-escape (Shavrukov et al., 2017).

1.3.2 Drought-avoidance

Drought-avoidance is a mechanism that enables the plant to endure dry spells, while maintaining the tissue water potential. It is based on minimizing the tissue dehydration, i.e., maintenance of high water potential in plant cells under limited water supply. Plants strive to maximize water uptake by roots and to minimize water release by leaves (Kosova et al., 2014). Different morphological and physiological traits are involved in this mechanism, such as leaf rolling (Bogale et al., 2011), leaf glaucousness (Bennett et al., 2011), shoot vigour (El-Hafid et al., 1998), transpirational cooling (Reynolds and Rebetzke, 2011), stomatal conductance (Akinci and Lösel, 2012), membrane stability (Ciuca and Petcu, 2009), stay green (Gupta et al., 2017), and root architecture (Miyazawa et al., 2011). The responses may either minimize water loss through leaf rolling, stomatal closure, etc. or maximize water uptake through increased root biomass and distribution (Chaves et al., 2003). This mechanism reduces water loss from plants through stomatal control of transpiration. The stomatal closure depends on the status of leaf water potential, light intensity and CO_2 concentration. Leaf rolling can reduce leaf area, which in turn reduces radiation interception, which results in reduced transpiration during water-stress. Increased grain yield, kernel numbers per spike and water use efficiency have been observed in genotypes that showed leaf rolling under water-deficit condition (Bogale et al., 2011). Glaucousness or waxy bloom on leaves helps

with maintenance of high levels of tissue water potential (Ludlow and Muchow, 1990). Glaucousness increases water-use efficiency and provides a cooling effect, which results in a lower rate of leaf senescence (Richrads et al., 1986). High levels of water loss result in cell membrane damage (Kocheva et al., 2004). Biological membranes are sensitive to many abiotic stresses, including drought. The maintenance of the integrity and stability of membranes under water-stress is thus a major component of drought-tolerance in plants (Premachandra et al., 1991; Bajji et al., 2002). High levels of photosynthetic activity can be maintained through delayed senescence during drought-stress condition (Rivero et al., 2009). The green leaf area in the post-anthesis period sustains carbon assimilation and contributes to grain filling due to its association with photosynthetic capacity and mobilization of stem reserves to grains (Gupta et al., 2017). Drought-avoidance in some plants depends on enhanced water uptake through an extensive and prolific root system. Root biomass, length, density and depth are the main drought-avoidance traits that contribute to final yield under terminal drought-stress (Turner et al., 2001). Deep and prolific root systems are able to extract water from considerable depths (Kavar et al., 2007).

1.3.3   Drought-tolerance

Drought-tolerance represents an adaptation of plant physiological functions to a limited water supply and a decreased plant cell water potential in order to reach a sustainable balance between water uptake by roots and water release by shoots (Kosova et al., 2014). Drought-tolerant genotypes achieve better yield levels in particular water-limited environments than drought-sensitive genotypes (Jones, 1993). Physiological responses such as osmotic adjustments (Taiz and Zeiger, 2006), photosynthetic rate (Al-Khatib and Paulsen, 1990), chlorophyll content (Farooq et al., 2009), abscisic acid (ABA) accumulation (Gupta et al., 2017), osmoprotection (Morgan and Tan, 1996; Abebe et al., 2003), water soluble carbohydrates (Rebetzke et al., 2008; Rosa et al., 2009), and the status of the antioxidation and scavenging defence systems against reactive oxygen species (ROS) (Gill and Tuteja, 2010) are the most important physiological responses leading to drought-tolerance.

Osmotic adjustment maintains the cell water balance with the active accumulation of solutes in the cytoplasm, which increases the osmotic pressure of the cytoplasm, thereby minimizing water losses, and reducing the harmful effects of drought (Morgan, 1990). It is an important trait in delaying dehydration damage in water-limited environments by continued maintenance of cell turgor and physiological processes (Taiz and Zeiger, 2006). It also facilitates a better translocation of pre-anthesis carbohydrate partitioning during grain filling (Subbarao et al., 2000), while high turgor maintenance leads to higher photosynthetic rates and plant growth. The osmotic pressure of the elongating regions of wheat leaves are adjusted by the accumulation of sugars, mainly glucose in less severe stress (Kameli and Losel, 1995). Blum et al. (1999) reported a positive effect of osmotic adjustment on final yield of wheat. However, despite the accumulation of ions and organic solutes, allowing osmotic adjustment in

the meristematic and expanding regions, growth of the shoot may be inhibited by drought-stress, either because the levels of osmotic adjustment may not be sufficiently rapid to compensate for growth or due to a stress-induced fall in turgor (Akinci and Lösel, 2012). Osmotic adjustment is usually not permanent and plants often respond rapidly to increased availability of water (Akinci and Lösel, 2012).

Osmoprotectants such as proline, trehalose, fructan, mannitol and glycine betaine are involved in signalling and regulating plant responses to multiple stresses, including reduced growth, which may be part of a plant's adaptation against stress. Osmoprotectants play adaptive roles in mediating osmotic adjustment and protecting subcellular structures in drought-stressed plants. Accumulation of free proline contributes to the cell membrane stability (Zarei et al., 2007), which is a measure of resistance induced in plants that are exposed to drought. Although water-stress may inhibit protein synthesis, some specific proteins (e.g., proline) increase in water-stressed plants (Akinci and Lösel, 2012; Mwadzingeni et al., 2016b). Soluble sugars that accumulate in leaves during water-stress contribute to osmoregulation under stress condition (Akinci and Lösel, 2012). The antioxidant defence system in the plant cell has both enzymatic and non-enzymatic components. Enzymatic components include superoxide dismutase, catalase, peroxidase, ascorbate peroxidase and glutathione reductase. Non-enzymatic components consists of cysteine, reduced glutathione and ascorbic acid (Gong et al., 2005). Plant growth regulators, when applied externally, and phytohormones, when produced internally, are substances that influence the physiological processes of plants at very low concentrations. Drought decreases phytohormones such as auxins, gibberellins and cytokinin and increases abscisic acid and ethylene. Abscisic acid inhibits the growth of the plant under drought-stress condition. Increased levels of abscisic acid, which regulates several physiological processes and contributes to the regulations of gene expression in plants under deficiency, and the induction of many quantitative trait loci (QTL) for the accumulation of abscisic acid, have been reported in wheat grown under drought-stress (Gupta et al., 2017). Osmolytes that affect drought responses are soluble and nontoxic, including soluble sugars, proline, organic acids, glycine betaine, potassium and calcium. These solutes protect plants against drought-stress through osmotic adjustment, detoxification of reactive oxygen species and membrane stabilization. Potassium contributes to osmotic adjustment as one of the primary osmotic substances in many plant species.

1.4 Screening techniques for drought-tolerance

Breeding for drought-tolerance and enhanced yield depends on sources of genetic variation, knowledge on the target environment, timing and severity of the drought-stress. This helps breeders to design a crop ideotype and to establish the optimum breeding strategy for maximizing drought-tolerance and yield response (Kosova et al., 2014; Senapati et al., 2019). Characterization of genotypes for their phenotypic characteristics, including yield, yield components, drought-adaptation and constitutive morpho-physiological characteristics, is a pre-requisite for successful drought-tolerance breeding.

Genotypes that combine yield-contributing agronomic traits under drought-stress conditions are ideal candidates for breeding (Tardieu, 2012; Senapati et al., 2019).

Developing cultivars tolerant to drought is an essential approach for wheat production in drier or warmer environments (White et al., 2001; Adhikari et al., 2015). These areas are characterized by the unpredictable amount and distribution of rainfall. Hence, breeding should focus on cultivars that perform well under a wide range of moisture conditions (Byrne et al., 1995). In order to develop cultivars adapted to drought-stress conditions, various selection environments have been employed such as: i) selection in favourable environments; ii) selection in stress environments; and iii) selection in both stress and non-stress environments. Panthuwan et al. (2002) and Kirigwi et al. (2004) reported that both adaptability and high yield potential could be achieved through screening genotypes in favourable environments. The effectiveness of genotype selection in the absence of drought to improve yield in dry areas has also been reported (Zarei et al., 2007). However, Sio-Se Mardeh et al. (2006) and Mohammadi and Abdulahi (2017) have argued that high yield potential under optimum environments does not necessarily result in improved yield under stress environments. Blum (1996) reported that genotypes with high yield potential may not be stress-resistant, so increasing the yield in these genotypes may be solely due to their yield potential, and not due to stress-resistance mechanisms. Similarly, selection of genotypes with high yield potential in drought-stress environments will lose the best genotypes for yield in non-stress environments (Ceccarelli et al., 1992). Hence, genotype screening in both stress and non-stress environments enhances selection responses for yield potential and drought-tolerance (Clarke et al., 1992; NasirUd-Din et al., 1992; Fernandez, 1992; Simane, 1993; Rajaram and Van Ginkle, 2001). Relative yield response of test genotypes under drought-stress and optimum conditions has been successful for identification of desirable genotypes (Mohammadi et al., 2010). Also, selection in both drought-stress and non-stress environments has led to marked progress in the development of wheat adapted to dryland agro-ecologies (Trethowan et al., 2002). Grain yield response *per se* has been the most crucial trait for assessing drought-tolerance. Fernandez (1992) classified wheat genotypes into four groups based on their productivity under non-stress and stress conditions. The four groups included: genotypes with high productivity under both non-stress and stress conditions (Group A), genotypes with high productivity only under non-stress conditions (Group B), genotypes with high productivity only under stress conditions (Group C) and genotypes with low productivity under both conditions (Group D).

A lack of fast and reproducible screening techniques, as well as defined and repeatable drought-stress conditions, have resulted in slow breeding progress for drought-tolerance (Ramirez and Kelly, 1998). Plant breeders have been successful in increasing the genetic gain for yield under optimal growing conditions. However, it has been a challenge to improve yield under drought-stress conditions (Richards et al., 2002). Screening for drought-tolerant genotypes has been achieved using drought-based grain

yield indices under drought conditions in comparison to non-stress conditions. The most common selection indices used for screening drought-tolerant genotypes are summarised below.

1) Tolerance (TOL) index has been defined as the differences in grain yield under non-stressed and stressed conditions (Hossain et al., 1990).

2) Mean Productivity (MP) index is the average yield of genotypes under non-stressed and stressed conditions (Rosielle and Hamblin, 1981).

3) Stress Susceptibility Index (SSI) measures yield stability based on the changes in both potential and actual grain yields in variable environments (Fischer and Maurer, 1978; Nouri et al., 2011).

4) Stress Tolerance Index (STI) is the ratio of the square root of yield under stressed and non-stressed conditions, and mean yield under non-stressed conditions. It is a useful tool to identify genotypes that produce high yields under both stressed and non-stressed conditions (Fernandez, 1992).

5) Geometric Mean Productivity (GMP) (Fernandez, 1992) is the square root of the product of yield under stressed and non-stressed conditions. It is the most frequently used index to validate relative performance of test genotypes.

6) Yield Index (YI) is the ratio of yield response of a genotype and mean yield under stressed conditions (Gavuzzi et al., 1997).

7) Yield Stability Index (YSI) (Bouslama and Schapaugh, 1984) measures genotype performance under stressed conditions relative to non-stressed conditions. Genotypes with a high YSI are expected to have relatively high grain yields under stressed conditions, but relatively low grain yields under non-stressed conditions (Mohammadi et al., 2010).

Various agronomic and crop management techniques have been used to evaluate drought-tolerance by creating different water regime conditions to mimic natural drought-stressed environments (Mwadzingeni et al., 2016a). A variety of imaging techniques have also been used to develop different platforms for high-throughput automated and integrated field phenotyping of large populations with high resolution and precisions. The imaging techniques include fluorescence, thermal infrared, visible light, spectroscopy, and multispectral methods, among others (Gupta et al., 2017). However, these techniques are not easily accessible and are costly. Furthermore, genotypes that are evaluated under controlled environments that are not similar to farmers' conditions may later affect the performances and adoption rate of the genotypes under real field conditions. Hence, the ultimate goal is evaluating test genotypes under natural field conditions with natural drought-stress (Asfaw and Blair, 2014).

1.5 Genetics of drought-tolerance

Drought-tolerance is a complex trait due to its polygenic inheritance, and its expression is influenced by various environmental factors. The genetic basis of drought-responsive traits is central in cultivar development for drought-stress conditions (Farshadfar et al., 2013). The nature and magnitude of gene actions involved in the inheritance of drought-related traits affects the selection of the most suitable parents, the breeding strategies to be used, and the most promising progeny that are from the segregating breeding populations. Farshadfar et al. (2013) reported that peduncle length, days to flowering and relative water content were controlled by additive and non-additive gene actions while plant height, 1000-kernel weight and stomatal conductance were governed by additive genes. Non-additive gene action was reported to be predominant in controlling grain yield response in wheat (Yao et al., 2011; Zahid et al., 2011). Khiabani et al. (2015) reported that grain yield and plant height in bread wheat were predominantly controlled by additive gene action when genotypes were evaluated under irrigated and water-stressed conditions. For traits controlled by additive gene action, early generation selection would be effective (Joshi et al., 2004; Farshadfar et al., 2013; Khiabani et al., 2015), while for traits governed by non-additive gene action, pure line selection at later generation would be effective (Yao et al., 2011; Zahid et al., 2011). The role of both additive and dominance gene effects have been reported in yield and yield components of wheat under water-stressed conditions (Jatoi et al., 2012). In breeding program, exploiting the additive gene effects is more effective and less costly (Fasahat et al., 2016).

1.6 Breeding for drought-tolerance

Drought-tolerance mechanisms of a crop affects various morphological and physiological traits associated with the crop growth and final yield. These traits are assessed to determine drought-tolerance and for genetic analysis (Kosova et al., 2014). The primary objective in most wheat-breeding programs is to enhancing grain yield. However, breeding for enhanced yield and drought-tolerance is challenging, given the complex nature of the genes involved and the variable environmental conditions. Yield and drought-tolerance responses are complex traits controlled by many genes with lower heritability than their complementary traits. Grain yield and drought-tolerance exhibit variable heritability in different test environments. Hence, direct selection for yield and drought-tolerance may provide limited genetic advances (Barakat et al., 2012). However, selection may be conducted using a number of traits with positive correlations with grain yield under drought-stressed conditions to enhance genetic gain for drought-tolerance (Dodig et al., 2012; Asfaw and Blair, 2014; Lopes et al., 2015; Abraha et al., 2017; Mathew et al., 2018).

Ideal genotypes adapted under moisture-stress conditions should combine a reasonably high yield potential and favourable traits, which could buffer yield against severe moisture-stress (Blum, 1983;

Senapati et al., 2019). Days to flowering and heading, number of productive tillers, plant height, number of kernel per spike, and 1000-kernel weight are some of the important drought and yield-related traits (Kosova et al., 2014). Recent developments in genomics and phenomics technologies are offering unprecedented opportunities for dissecting quantitative traits into their single genetic determinants, referred to as quantitative trait loci (QTL). A large number of QTLs have been identified for morphological and physiological traits related to drought-tolerance in wheat (Nezhad et al., 2012). Genomic markers have been identified associated with agronomic traits such as kernel number, grain yield, biomass, harvest index, plant height, 1000-kernel weight, heading/anthesis, and maturity along with other physiological traits such as water-soluble carbohydrate, stem reserve mobilization, chlorophyll content and accumulation of abscisic acid. These are proven useful for marker-assisted selection for drought-tolerance breeding in wheat (Gupta et al., 2017).

1.7 Sources of genetic variation for drought-tolerance

Genetic variation for drought-tolerance, yield and yield components is crucial for successful breeding. Artificial selection, repeated use of limited genetic resources and breeding schemes that do not favour wide genetic variation have resulted in a loss of genetic diversity in wheat (Laido et al., 2013; Kosova et al., 2014). Wheat has a large and diverse gene pool, including landraces adapted to various environments, and alien species that are known reservoirs of novel genes/traits for biotic and abiotic stresses breeding (Gupta et al., 2017). At least 23 species of *Triticum* are known, with various ploidy levels (Morris and Sears, 1967). Three gene pools are recognised in wheat, including the primary, secondary and tertiary pools (Chaudhary et al., 2013). The primary gene pool includes types that cross readily with one another, including *T. spelta, T. turgidum, T. monococcum* and *T. tauschii*. The secondary gene pool includes *Aegilops speltoides, T. timopheevii* and *T. zhukovskyi*. A tertiary gene pool includes *Secale cereale, Thinopyrum elongatum, Elymus* spp. and *Th. intermedium*. Gene transfer is possible among members of the first and second pools, and even from the tertiary gene pool, using wide hybridization and genetic transformation (Chaudhary et al., 2013). The tertiary gene pool is useful to create substantial genetic variation (Tiwari et al., 2015). Landraces and wild accessions of wheat can be explored as a source of variability for drought-tolerance (Laido et al., 2013). Wild relatives of wheat with the genomes A and B, and *Aegilops tauschii* with the genome D, were employed to construct synthetic hexaploid wheat by International Maize and Wheat Improvement Centre (CIMMYT) (Reynolds et al., 2007). Synthetic wheat genotypes have the potential for expanding the genetic diversity of cultivated wheat for tolerance to several stresses such as drought, heat, salinity and pathogens (Kosova et al., 2014). Landraces grown in harsh environments can be a valuable resource from which to select the most promising genotypes (Araus et al., 2007). Elite breeding lines developed by CIMMYT are valuable genetic resources as source of genetic variation for breeding programs (Laido

et al., 2013; Mwadzingeni et al., 2016a). These lines can be used in local hybridization programs to create genetic variability for adaptive and constitutive-traits for selection (Mwadzingeni et al., 2016b).

1.8 Breeding methods for drought-tolerance

Developing cultivars tolerant to drought ensures increased wheat production and productivity in marginal growing and drought-affected environments (White et al., 2001). A number of breeding methods have been used in wheat improvement programs. These included the pedigree, modified pedigree, pure line, single seed descent, back cross, and bulk breeding methods (Bos and Caligari, 2008). These methods help to advance segregating material, to accumulate additive genes (Murthy, 1979), and to increase the mean performance of the selected progenies (Kanbar et al., 2011). The choice of the selection method depends on the goal of the breeding program, as well as on a set of other conditions, such as extent of the genetic variability and available resources (facilities, personnel etc.) (Miladinović et al., 2015). Srivastava et al. (1989) noted that single plant selection, single seed descent, bulk population and mechanical mass selection procedures can be used to make selections at the F2, F3 and F4 generations in wheat. However, they determined that F4 progenies derived from F3 SSD population were significantly superior for grain yield. Single seed descent has been more effective than the other methods of selection in other self-pollinating crops such as soybean (Miladinović et al., 2000).

1.9 Participatory plant breeding and farmers' variety preferences

Participatory plant breeding (PPB) is an approach where by smallholder farmers and plant breeders interact to share their knowledge and skills to set objectives, take decisions, share responsibility for decision making and implementation, and generate new crop varieties that meet the farmers' needs (Morris and Bellon, 2004). PPB leads to the joint development of better adapted crop varieties that are closely tailored to small-scale farmers' needs and preferences (Thro and Spilane, 2000). It leads to early adoption of new varieties with limited breeding costs (Witcombe et al., 2003). Farmers in marginal agro-ecologies face several yield-limiting factors, given the heterogeneous production environments. Hence, the farmers require specific ideotypes according to their production conditions and cultural practices.

The PPB is amenable to breeding for marginal environments through selection of desirable parents and segregating populations in environments similar to farmers' conditions. Breeding for specific adaptation is a more sustainable strategy than breeding cultivars that can only express their superiority with higher production inputs (Simane, 1993; Ceccarelli, 1996). This approach aims to empower farmers to increase their freedom to choose varieties, and allows rural communities to maintain genetic resources that they value, and enables them to participate in the development of new varieties that suit their needs. Thus, this method can empower groups that traditionally have been left out of the development process

(McGuire et al., 1999). Plant breeders, often working in relative isolation from farmers, have frequently been unaware of the multitude of preferences of their target farmers. Without knowing the farmers' practices and cultivar preferences, breeders are unable to imagine or anticipate their needs. The identification of farmers' preferences in crop cultivars is a form of market research. It allows cultivars to be selected for testing that are likely to match their requirements, and avoids the release of cultivars that will be unacceptable to the farmers. To identify these requirements, various methods can be used, separately or in combination. Participatory rural appraisal (PRA) is a multi-disciplinary research tool that involves several stakeholders in a value chain (Tongoona et al., 2017). PRA is a preliminary step of identifying farmers' needs and requirements, and those of the marketplace.

1.10   Summary

Drought is the most important abiotic constraint limiting wheat production and productivity globally. Systematic wheat breeding for drought-prone areas incorporating farmers' and market preferred traits would boost productivity and ensure high adoption rates of the new wheat varieties by farmers. This review highlighted key issues on drought-tolerance including the mechanisms of drought response, screening techniques, genetic basis, sources of genetic variation and breeding methodologies and participatory wheat breeding. Information presented in this review may serve as a basis for designing the breeding of drought-tolerant wheat varieties with farmers' preferred traits under marginal wheat production areas in Ethiopia or similar agro-ecologies.

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23

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Chapter 2. Farmers' production practices, perceived constraints, and preferred traits of bread wheat varieties under drought-prone agro-ecologies of Ethiopia

Abstract

A significant proportion of wheat (*Triticum aestivum* L.) is produced under drought-affected and low potential agro-ecologies in sub-Saharan Africa, including Ethiopia. The productivity of wheat in these agro-ecologies is relatively low due to a lack of drought-tolerant varieties and suitable production technologies compared with high rainfall and high input production environments. The objective of this part of the study was to determine farmers' production practices, perceived constraints and preferred traits of bread wheat varieties under drought-prone agro-ecologies of Ethiopia to guide variety development and deployment. A participatory rural appraisal (PRA) study was conducted among 170 randomly selected wheat-producing farmers in the drier areas of Arsi Zone of the Oromia Regional State in Ethiopia. Data were collected through interviews using a semi-structured questionnaire. The survey revealed that wheat followed by tef (*Eragrostis tef* Zucc.) and barley (*Hordeum vulgare*) were the most widely grown crops although there were various biotic, abiotic and socio-economic factors limiting wheat production and productivity in the study areas. Drought-stress, disease (wheat rusts), and the high cost of fertilizers were among the major constraints of wheat production identified by the farmers. On average, between 63.1 and 73.8% reduction in yield was experienced due to drought-stress in the studied areas. Socio-demographic factors such as gender, education level and access to extension officers influenced variety adoption by the farmers. Early maturity, plant height, baking quality and stress adaptation were the major varietal characteristics contributing towards adoption of new improved bread wheat varieties. Farmers had varying variety-specific traits preferences. Grain yield, rust-resistance, adaptation to drought and heat-stresses and early maturity were the most preferred varietal traits in the study areas. Therefore, future wheat breeding for drought-stressed environments in Ethiopia should target improving farmers' preferred traits and drought-tolerance under low input agriculture systems for sustainable wheat production and productivity.

Key words: drought-stress, Ethiopia, farmers' preferred traits, PRA**,** production constraints of wheat

2.1 Introduction

There is need to gain insight into farmers' preferences and the challenges pertinent to their production systems (Morris and Bellon, 2004; Beshir and Wegary, 2014; Drabo et al., 2019). Engaging farmers in a participatory rural appraisal (PRA) provides a means to gather relevant information for decision-making. PRA is a multi-disciplinary research tool that involves several stakeholders in a value chain (Tongoona et al., 2017). In this case, the inclusion of smallholder farmers in the PRA will allow for analysis and interpretation of their production constraints and formulation of possible intervention strategies. These will guide participatory plant breeding (PPB).

The PPB will help breeders to understand better the challenges faced by the farmers and their variety selection criteria and formulate breeding projects accordingly (Halewood et al., 2007). This approach is value-chain-oriented and has been termed demand-led breeding, which is a deviation from the traditional approach of breeding according to breeder objectives. Engaging the farmers through a PPB to identify their challenges and needs will assist developing cultivars that meet farmers' expectations and adapted to their production environments (Ceccarelli et al., 2007; Halewood et al., 2007; Li et al., 2013). Developing cultivars that are relevant to the farmers will improve variety adoption rates (Vernooy and Stanley, 2003; Witcombe et al., 2005; Joshi et al., 2006; Ceccarelli et al., 2009; Tongoona et al., 2017), and thereby increase household income and improve food security of smallholder farmers (Asfaw et al., 2012; Shiferaw et al., 2014). Information on farmers' production practices, perceived constraints, and preferred traits of bread wheat varieties especially under drought-prone agro-ecologies of Ethiopia is lacking. Hence, the objective of this part of the study was to conduct a PRA among smallholder farmers in drought-prone areas of the Arsi Zone in the Oromia Regional State of Ethiopia to assess their production practices, perceived constraints and preferred traits of wheat varieties as a guide to variety development and deployment.

2.2 Materials and methods

2.2.1   Description of the study areas

The study was conducted in Arsi zone in the Oromia Regional State of Ethiopia during 2018 (Figure 2.1). Oromia region accounts for more than 50% of the national wheat production area, while the Arsi zone contributes above 25% of the national wheat production (CSA, 2016). The zone is regarded as one of the wheat belts of the country (Warner et al., 2015). There are about 24 districts in this zone with various agro-ecologies. For the purpose of this study, three wheat-producing districts, namely Sire, Dodota and Hetosa, were selected as these were prone to drought-stress (Piguet, 2003; Warner et al., 2015; Zeleke, 2017). Sire District lies between 1000 and 2500 m above sea level and at a latitude of 7°20'0" North and a longitude of 39°26'0" East. It has monomodal rainfall with a mean annual rainfall

of 500 mm and average maximum and minimum monthly temperature of 30°C and 15°C, respectively. Dodota District is located within an altitude range from 1400 to 2500 m above sea level and latitude 8°14'60" North and 39°19'60" East. It has bimodal rainfall with a mean annual rainfall of 1000 mm and average maximum and minimum monthly temperatures of 25°C and 20°C, respectively. Hetosa District is between 1500 and 4170 m above sea level and latitude 8°04'60" North and 39°14'60'' East. It has monomodal rainfall with a mean annual rainfall of 1000 mm and average maximum and minimum monthly temperatures of 27°C and 14°C, respectively.
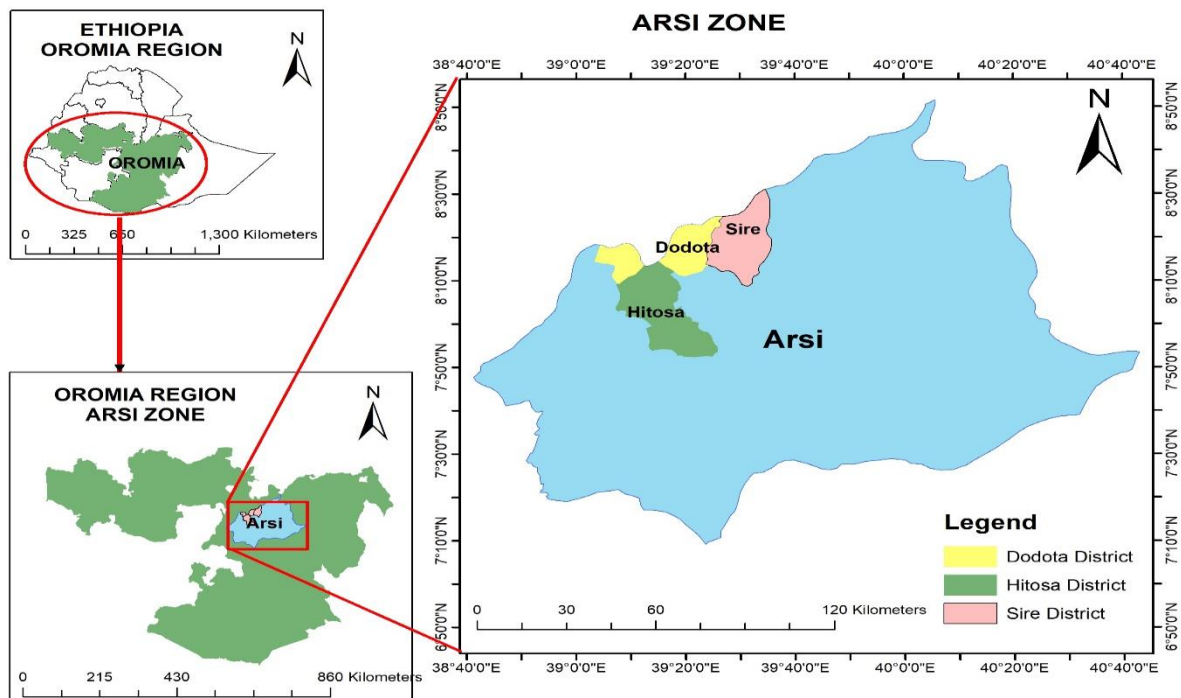
Figure 2.1 Map of the study areas in Ethiopia

2.2.2   Sampling and data collection procedure

A multistage random sampling was employed to arrive at household level. The first stage of selection was based on literature and national central statistical data sources. The zone was identified as one of the wheat-producing regions (CSA, 2016). In this region wheat-producing districts which were prone to drought were selected with the help of Bureau of Agriculture and Natural Resources (BOANR) offices of the respective districts. Secondly, two villages (locally referred to as "Kebeles") from each district, making a total of six villages were selected. Only accessible villages practicing wheat production under dryland system were selected. At the third stage of sampling, 23-31 households from each village were selected following a random sampling procedure, making a total of 170 household respondents (Table 2.1).

27

Table 2.1. Districts, villages and number of farmers sampled for the study

| Districts | Villages | Number of farmers | | |
		Male	Female	Total
Sire	Koloba Bele	31	-	31
	Ebseta Eduga	19	4	23
Dodota	Dodota Alem	26	1	27
	Amigna Dabesa	24	7	31
Hetosa	Anole Salan	25	5	30
	Deyea Debeso	22	6	28
Total		147	23	170

Source: Farm household survey, 2018

Data were collected based on primary and secondary sources. Primary data were collected through a formal survey in which household heads were interviewed using a semi-structured questionnaire. The responses from the sampled farmers were based on their previous farming experiences in the preceding 2017 cropping season. The questionnaire was pre-tested on five farmers and amended accordingly. Enumerators were trained to improve efficiency and accuracy in data collection and clarity in elaborating questions to respondents. Through the questionnaire primary data were collected on demographic and socio-economic characteristics of the households, sources of income, major crops grown and management practices, relative importance of wheat and cultivars grown, production constraints, drought-stress and its impacts, and farmers' coping mechanisms against drought-stress and farmers' preferred traits. Interviews were conducted using the local languages (Oromiffa and Amharic) translated with the help of local people and agricultural extension staff stationed in the respective areas. Secondary data were obtained on cropping system, cropping calendar and the sensitivity of drought in the farming community using a designed checklist, involving key informants comprising districts agricultural office leaders and agricultural extension officers, village agricultural extension officers and village leaders. In addition, personal observations were made by the research team using a transect walk across the villages to visually appreciate the cropping system and weather condition of the areas. Quantitative data further describing the areas regarding altitude, geographic position, rainfall pattern, annual rainfall and temperature were obtained from the respective districts' BOANR offices.

2.2.3   Data analysis

Statistical analyses such as frequency, percentages, chi-square, Kruskal-Wallis H test, Kendall's coefficient of concordance (W), rank based quotient and binary logistic regression model were employed using the Statistical Package for Social Sciences (SPSS) version 24 (SPSS, 2016). Relationships were examined through frequency, percentages, chi-square and Kruskal-Wallis H test values within and between districts for variables considered. Twelve production constraints were pre-defined, and farmers were asked to state if the severity of each was high, medium, or low based on their perception, designated by ranking as first, second or third, respectively. The responses were analysed

using Rank Based Quotient (RBQ) to identify the most important production constraints as perceived by the farmers in the study areas.

RBQ was calculated by using the following formula:

$$RBQ = \sum f_i \, (n + 1 - i)x100/Nxn$$

Where fi=frequency of respondents perceiving a particular constraint under i^{th} rank; N= total number of respondents; n= number of constraints identified; i=rank of the perceived constraint.

To draw inferences on farmers' preferences, analysis was conducted to identify key variables affecting farmer's decision with a dichotomous outcome (Y) depending on socio-demographic characteristics and the specific perceived attributes of the improved bread wheat varieties. Farmer's decision refers to the use of new improved varieties (three new improved varieties were identified out of which a farmer that used at least one was considered as adopter (early adopter) represented by 'Y=1' otherwise non-adopter represented by 'Y=0'. Socio-demographic factors such as gender, age, education, family size, extension contact, farmers' associations and land size were expected to affect farmers' adoption of new improved varieties. Likewise, varietal attributes such as grain yield, early maturity, tillering, plant height, grain weight, disease-resistance, adaptation (drought and heat-stresses) and baking quality were expected to affect farmers' choice of new improved varieties in the study areas. Data were tested using various models, but binary logistic regression model was found to be the best for the present study (Beshir and Wegary, 2014). To examine farmers' preferences for varietal traits, each farmer were asked what specific variety of bread wheat he/she cultivated in 2017 cropping season, and what was his/her perception for certain attributes of the variety. The specific attribute of the variety considered 'good' was assigned a number '1' and otherwise a '2', and Kendall's coefficient of concordance (W) analysis was used to identify the varietal attributes that are most preferred by the farmers (Asante et al., 2013). Attributes that were regarded as neutral (neither good nor bad) were excluded from the analysis.

2.3 Results

2.3.1 Demographic characteristics of the households in the study areas

Household demographic characteristics may affect the decision behaviours of smallholder farmers. Districts significantly varied regarding demographic characteristics such as age (X^2= 22.615; p=0.004), education level (X^2= 23.305; p=0.010), and family size (X^2=20.115; p=0.003) (Table 2.2). In Sire District, 92.6% of the households were male headed. Similarly, 86.2 and 81% of the households in Dodota and Hetosa districts, respectively, were male-headed.

The ages of the respondent farmers varied from 18 to over 60 years. More than 34% of the interviewed farmers in the Dodota and Hetosa districts were between 36 and 45 years of age. However, in Sire

District, farmers in the 26 to 35 years category accounted for the largest proportion (38.9%), while those between 36 and 45 years of age made up 29.6% of the respondents. The Hetosa District had significantly more farmers in advanced age (above 60 years) accounting for 20.7%, compared to less than 8% for the Sire and Dodota regions. There were more youths in Hetosa (5.2%) than Sire (1.9%) and Dodota (1.7%).

The majority (76.4%) of the respondents had attained at least elementary level (Grades 1-4) education and could read and write proficiently, while the remainder was either illiterate or could only read and write with a limited comprehension. At the individual district level, the highest proportion (33.3%) of the respondent farmers in Sire had attended elementary school (Grades 1-4). In comparison, only 15.5 and 13.8% in Dodota and Hetosa, respectively, who attained elementary education. However, more respondents in Dodota (41.4%) and Hetosa (32.8%) had attained Grades 5-8 education than in Sire (27.8%). There were more respondents who attained secondary (25.9%) and higher education (5.2%) in Dodota than Hetosa and Sire districts. None of the respondents in Sire had more than secondary education.

There were significant differences between Hetosa and the other two districts in terms of family size of more than eight family members. 31% of the respondents in Hetosa District had a family of more than eight members, compared to 10.3% in Dodota and 5.6% in Sire districts. There were also significant differences among the districts regarding the smaller family units. Family units with 3 to 5 members accounted for 53.7% of the respondents in Sire compared to 44.8% in Dodota and 24.1% in Hetosa districts. The extent of medium sized families and families with three or less members was not significantly different among the districts. About 40% of the households in all the districts had a family size of between six and eight members, while less than 4% of all respondents had a family size of three or below.

Table 2.2. Demographic characteristics of the households in the study areas

Descriptions	Districts			Degrees of freedom	X^2-value	P-value
	Sire	Dodota	Hetosa			
Sex						
Male	50 (92.6)	50 (86.2)	47 (81)	2	3.198	0.202
Female	4 (7.4)	8 (13.8)	11 (19)			
Age (years)						
18-25	1 (1.9)	1 (1.7)	3 (5.2)			
26-35	21 (38.9)	12 (20.7)	4 (6.9)			
36-45	16 (29.6)	22 (37.9)	20 (34.5)	8	22.615	0.004
46-60	12 (22.2)	19 (32.8)	19 (32.8)			
>60	4 (7.4)	4 (6.9)	12 (20.7)			
Educational level						
Illiterate	9 (16.7)	5 (8.6)	14 (24.1)			
Read and write	2 (3.7)	2 (3.4)	8 (13.8)			
Elementary (Grades 1-4)	18 (33.3)	9 (15.5)	8 (13.8)	10	23.305	0.010
Elementary (5-8)	15 (27.8)	24 (41.4)	19 (32.8)			
Secondary (9-10)	10 (18.5)	15 (25.9)	7 (12.1)			
Higher education	-	3 (5.2)	2 (3.4)			
Family size (number per household)						
< 3	1 (1.8)	1 (1.7)	2 (3.4)			
3-5	29 (53.7)	26 (44.8)	14 (24.1)	6	20.115	0.003
6-8	21 (38.9)	25 (43.1)	24 (41.4)			
>8	3 (5.6)	6 (10.3)	18 (31.0)			

(-) indicates no response. Values outside and inside the bracket indicate the frequency and proportion in percent, respectively.

2.3.2 Institutional characteristics of the households in the study areas

Small-scale farmers' decisions can be affected by their instiitutional characteristics. The farms size ranged between less than 1 ha to more than 3 ha (Table 2.3). The sizes of the farms owned varied significantly across the districts (X^2=18.905; p=0.001). The Sire District was dominated by farmers who owned less than 1 ha (50%), while 56.9 and 65.5% of the farmers in Dodota and Hetosa, respectively, owned between 1 and 3 ha of land. In Dodota, there was a significantly higher proportion (20.7%) of farmers who owned more than 3 ha of land compared to 3.6% in Hetosa and 5.6% in Dodota. The sources of improved seed were also significantly different among the districts (X^2= 34.51; p=0.001). Most of the respondent farmers in Sire (46.3%) and Dodota (44.8%) districts accessed improved seed from their respective BOANR offices, while farmers in Hetosa (34.5%) predominantly sourced their seed from their respective cooperatives. The farmers in all the different surveyed districts obtained information through different channels (X^2= 13.784; p=0.032) (Table 2.3). Agriculture extension services were the major source of information for the farmers in all the districts. More than 53% of all respondents in Sire confirmed that agricultural extension officers were their primary source of information, while the proportions were 67.2 and 72.4% in Hetosa and Dodota, respectively.

The majority (more than 51%) of the respondents in each district confirmed membership to one or multiple farmer organizations. There was also a considerable proportion (up to 48%) who were not members of farmer organization. Most of the farmers (57.4% in Sire, 56.9% in Dodota, and 69% in Hetosa) were members of a farmer organization for less than five years and only 24% respondents in Dodota exceeded 10 years of membership.

Table 2.3. Some institutional characteristics of the households in the study areas

Descriptions	Districts			Degrees of freedom	X^2-value	P-value
	Sire	Dodota	Hetosa			
Farm size owned						
< 1 ha	27 (50.0)	13 (22.4)	18 (31.0)			
1-3 ha	24 (44.4)	33 (56.9)	38 (65.5)	4	18.905	0.001
> 3 ha	3 (5.6)	12 (20.7)	2 (3.4)			
Improved seed source						
Farmers' cooperative	10 (18.5)	7 (12.1)	20 (34.5)			
Research centre	3 (5.6)	3 (5.2)	3 (5.2)			
Seed enterprise	3 (5.6)	2 (3.4)	3 (5.2)			
Farm saved	1 (1.9)	1 (1.7)	9 (15.5)	12	34.51	0.001
Neighbouring farmers	9 (16.7)	18 (31.0)	14 (24.1)			
NGO	3 (5.6)	1 (1.7)	-			
BOANR	25 (46.3)	26 (44.8)	9 (15.5)			
Source of extension information						
Agricultural Extension Staff (DAs)	29 (53.7)	42 (72.4)	39 (67.2)			
Radio	22 (40.7)	13 (22.4)	13 (22.4)	6	13.784	0.032
Television	2 (3.7)	-	-			
Other	1 (1.9)	3 (5.2)	6 (10.3)			
Membership to farmers' organization						
Yes	32 (59.3)	30 (51.7)	33 (56.9)	2	0.681	0.712
No	22 (40.7)	28 (48.3)	25 (43.1)			
Years of membership to farmers' organization						
< 5	31 (57.4)	33 (56.9)	40 (69.0)			
5-10	11 (20.4)	11 (19.0)	7 (12.1)	4	2.556	0.635
> 10	12 (22.2)	14 (24.1)	11 (19.0)			

(-) indicates no response. Values outside and inside the bracket indicate the frequency and proportion in percentage, respectively.

2.3.3 Source of income

The wealth status of smallholder farmers can be a determining factor in adopting improved agricultural technologies including improved cultivars. The Chi-square analysis showed that sources of income significantly differed (X^2= 28.185; p=0.013) between the studied districts (Table 2.4). Trading of field crops was the major source of income for all the respondents in the study areas, with bread wheat being

the predominant field crop and a major income earner. The respondent farmers explained that the income generated from trading wheat is used for various purposes such as to pay school fees, to purchase fertilizers, and buy other foodstuffs, among others (data not shown). The sale of vegetable produce was also an important source of income, although practiced on a relatively small scale compared to field crops, which could explain its lower contribution to household income. The farmers in the study areas also practiced animal husbandry, rearing smaller livestock such as goat, sheep and chickens to complement their income derived from field crops. Larger livestock such as cattle and donkeys were reared for other purposes such as ploughing of fields, transport to the market and fetching of water. The majority of the farmers cited the prevalence of diseases as a major constraint to cattle rearing in the area. During drought years and crop failure, the farmers are usually forced to sell off the larger livestock, even the oxen that provide draught power, in order to survive (data not presented). This implies that the livelihood of the farmers in the areas primarily depends on rainfed crop production. Smallholder shops that sell day-to-day wares, water fetching and labour hire were the other sources of income for the farmers in the study areas (Table 2.4).

Table 2.4. Sources of income of the households in the study areas

Descriptions	Districts			Degrees of freedom	X^2-value	P-value
	Sire	Dodota	Hetosa			
Sources of income						
Field crops	54 (100)	58 (100)	58 (100)			
Vegetables	19 (35.2)	58 (100)	-			
Fruits	3 (5.6)	-	-			
Livestock	39 (72.2)	56 (96.6)	23 (39.7)			
Mini-shop	2 (3.7)	-	2 (3.4)	14	28.185	0.013
Water fetching	-	5 (8.6)	2 (3.4)			
Labour hire	-	1 (1.7)	4 (6.9)			
Others	3 (5.6)	2 (3.4)	6 (10.3)			

(-) indicates no response. Values outside and inside the bracket indicate the frequency and proportion in percentage, respectively; the proportion of respondent farmers in each district could be more than 100% due to having more than one sources of income.

2.3.4 Major crops grown and management practices

The most important crop in all the study areas was wheat, followed by tef, barley, maize, garlic, onion and haricot bean (Table 2.5). Wheat production was the lowest in Sire District compared to the Hetosa and Dodota districts, with average area under cultivation of 0.5, 1.1 and 1.5 ha, respectively. Tef was

cultivated more extensively in Sire District, with a mean of 1.2 ha compared to 0.5 ha for wheat. Wheat productivity in all the districts was similar, with an average of 2.4 t ha^{-1} (Table 2.5).

The time of planting was mostly in the month of July in all the districts, although there were some significant differences among farmers across different districts (X^2= 25.099; p=0.005) (Table 2.6). The majority of respondent farmers in Sire (72.2%) and Hetosa (56.9%) planted wheat at the beginning of July. In Dodota, a similar proportion of farmers planted in early July (46.6%) or late June to early July (43.1%). The farmers in the different districts exhibited significant differences in planting (X^2= 34.658; p=0.000) and weeding (X^2= 25.326; p=0.000) methods. The majority, over 80%, of farmers in Dodota and Hetosa districts planted their wheat using the broadcast method, while both broadcasting (46.3%) and row planting (37%) were used extensively in the Sire District. The majority (more than 70%) of farmers in each of the districts described their soil fertility status as medium and that they applied mostly inorganic fertilizers. About 40% of farmers in the Dodota District used both inorganic and organic fertilizers compared to 34.5 and 24.1% in Hetosa and Sire districts, respectively. Almost all of the respondents (more than 95%) followed a wheat/tef or barley rotation system. A combination of chemical and manual weeding was practiced widely by more than 77% in each district.

Table 2.5. Major crops grown and their productivity in studied regions

Crops		Cultivated area (ha)					Productivity (t ha^{-1})				
		Districts			DF	F-value	Districts			DF	F-value
		Sire	Dodota	Hetosa			Sire	Dodota	Hetosa		
Wheat											
	Mean	0.446	1.448	1.112			2.576	2.323	2.417		
	SD	0.31	1.082	0.752	2	22.423**	1.459	1.03	0.892	2	0.689^{ns}
	SE	0.042	0.142	0.099			0.2	0.135	0.117		
Tef											
	Mean	1.243	0.487	0.278			1.443	0.857	0.918		
	SD	0.947	0.826	0.324	2	12.294**	0.598	0.512	0.423	2	17.921**
	SE	0.129	0.108	0.043			0.081	0.08	0.07		
Maize											
	Mean	0.12	0.231	0.083			3.924	3.068	1.729		
	SD	0.149	0.265	0.113	2	7.641**	2.967	3.468	1.237	2	3.907*
	SE	0.02	0.035	0.015			0.542	0.563	0.253		
Barley											
	Mean	0.064	0.519	0.364			2.9	2.334	2.304		
	SD	0.161	0.372	0.268	2	7.991**	2.165	0.902	1.011	2	1.525^{ns}
	SE	0.022	0.049	0.035			0.579	0.126	0.146		
Garlic and onion											
	Mean	0.039	0.125	0.041			27.467	10.45	8.209		
	SD	0.093	0.232	0.089	2	1.196^{ns}	19.025	7.021	4.159	2	12.475**
	SE	0.013	0.03	0.012			5.492	1.351	1.254		
Haricot bean											
	Mean	0.049	0.052	0.033			2.454	1.067	1.868		
	SD	0.104	0.102	0.079	2	0.245^{ns}	2.325	0.751	1.649	2	2.449^{ns}
	SE	0.014	0.013	0.01			0.645	0.194	0.497		

DF, degree of freedom; SD, standard deviation; SE, standard error; *, $p < 0.01$; **, $p < 0.05$, ns, non-significant.

Table 2.6. Crop management practices followed by the respondent farmers in the study areas

Descriptions	Districts			Degrees of freedom	X^2-value	P-value
	Sire	Dodota	Hetosa			
Planting time						
Mid-June	1 (1.9)	-	1 (1.7)			
Late June	-	6 (10.3)	9 (15.5)			
Early July	39 (72.2)	27 (46.6)	33 (56.9)	10	25.099	0.005
Late June to early July	10 (18.5)	25 (43.1)	14 (24.1)			
Late June to mid-July	2 (3.7)	-	-			
Early July to mid-July	2 (3.7)	-	1 (1.7)			
Planting Method						
Row planting	9 (16.7)	-	1 (1.7)			
Hand broadcasting	25 (46.3)	47 (81.0)	52 (89.7)	4	34.658	0.000
Both row and hand broadcasting	20 (37.0)	11 (19.0)	5 (8.6)			
Fertility status of the land						
High	6 (11.1)	5 (8.6)	3 (5.2)			
Medium	42 (77.8)	41 (70.7)	45 (77.6)	4	3.051	0.549
Low	6 (11.1)	12 (20.7)	10 (17.2)			
Fertilizer type used						
Inorganic	41 (75.9)	34 (58.6)	37 (63.8)			
Organic	-	-	1 (1.7)	4	5.782	0.216
Both inorganic and organic	13 (24.1)	24 (41.4)	20 (34.5)			
Crop rotation						
Yes	54 (100)	57 (98.3)	56 (96.6)	2	1.919	0.383
No	-	1 (1.7)	2 (3.4)			
Weeding						
Hand weeding	8 (14.8)	1 (1.7)	-			
Chemical	1 (1.9)	12 (20.7)	4 (6.9)	4	25.326	0.000
Both hand and chemical weeding	45 (83.3)	45 (77.6)	54 (93.1)			

(-) indicates no response. Values outside and inside the bracket indicate the frequency and proportion in percentage, respectively.

2.3.5 Relative importance of bread wheat and varieties grown in the study areas

All the farmers in Sire and 96.6% of the farmers in Dodota and Hetosa districts considered wheat production as their most important source of income (Table 2.7). In the Sire and Hetosa districts, adaptability of wheat was the next important characteristic according to more than 91% of the respondents, whereas 96.6% of the respondents in the Dodota District considered the quality of straw for animal feed to be more important than adaptability. Adaptation and high yield were considered to be more important than disease-tolerance, early maturity and water logging-tolerance in all the districts.

Wheat varieties such as Ogolcho, Kubsa, Kekeba, Batu, Hidase, Pavon-76, Kingbird, Hawi and Bafane were dominant in the studied areas (Table 2.8). Batu and Kekeba were the most adopted varieties in Sire, grown by 44.4 and 31.5% of the respondents, respectively. In Dodota, variety Ogolcho was grown by 56.9% of the respondents, three times more than the next best adopted variety, Batu with 19%. Variety Kubsa was grown by 46.6% of the respondents in Hetosa, while the varieties Ogolcho and Hidase were also grown with respective adoption rates of 29.3 and 25.9%.

Table 2.7. Relative importance of bread wheat in the study areas

Importances	Districts									Kruskal-Wallis test
	Sire			Dodota			Hetosa			
	High (%)	Medium (%)	Low (%)	High (%)	Medium (%)	Low (%)	High (%)	Medium (%)	Low (%)	
Food	90.7	9.3	-	75.9	20.7	3.4	89.7	8.6	1.7	0.042*
Feed	90.7	9.3	-	96.6	3.4	-	84.5	10.3	5.2	0.019*
Income generation	100	-	-	96.6	3.4	-	96.6	3.4	-	0.388ns
Water logging-tolerance	50	20.4	29.6	32.8	3.4	63.8	24.1	3.4	72.4	0.000**
Pest-tolerance	55.6	25.9	18.5	27.6	15.5	56.9	36.2	17.2	46.6	0.000**
Disease-tolerance	57.4	24.1	18.5	32.8	15.5	51.7	50	15.5	34.5	0.003**
Early maturity	68.5	14.8	16.7	53.4	17.2	29.3	58.6	20.7	20.7	0.217ns
Yield	68.5	25.9	5.6	56.9	29.3	13.8	74.1	17.2	8.6	0.128ns
Adaptation (drought and heat-stresses)	92.6	7.4	-	84.5	15.5	-	91.4	8.6	-	0.318ns
Crop rotation	63	37	-	62.1	37.9	-	75.9	22.4	1.7	0.249ns

*, $p < 0.05$; **, $p < 0.01$; ns, non-significant; (-), no response.

Table 2.8. Wheat cultivars grown, year of release and proportion of farmers growing these in the study areas

Varieties[a]	Year of release/registration[b]	Districts		
		Sire	Dodota	Hetosa
Ogolcho	2012	9 (16.7)	33 (56.9)	17 (29.3)
Hidase	2012	-	-	15 (25.9)
Kekeba	2010	17 (31.5)	1 (1.7)	1 (1.7)
Kingbird	2007	-	1 (1.7)	-
Hawi	2000	-	1 (1.7)	1 (1.7)
Kubsa	1995	3 (5.6)	5 (8.6)	27 (46.6)
Batu	1984	24 (44.4)	11 (19.0)	-
Pavon-76	1982	2 (3.7)	5 (8.6)	-
Bafane	-	-	2 (3.5)	-

[a]Some farmers grow more than one variety, which makes the proportion above 100 percent.
[b]Released/registered by Kulumsa Agricultural Research Centre. (-) indicates not available/no response.
Values outside and inside the bracket indicate the frequency and proportion in percentage, respectively.

2.3.6 Farmers' perceptions of the primary constraints to bread wheat production

The primary production constraints of bread wheat perceived by the farmers in the study areas are presented in Table 2.9. The RBQ result indicated that moisture-stress, disease (rust) and the high cost of fertilizers were the first, second and third ranked production constraints, in that order. Other perceived constraints, such as heat-stress, insect pests, soil erosion and seed shortage, were also considered to be important in the study areas.

Table 2.9. Farmers' perceptions of the primary constraints to bread wheat production in the study areas

Constraints	No of farmers	Ranking			RBQ	Rank
		1	2	3		
Low soil fertility	170	38.2	56.5	5.3	55.5	9
Low yield	170	48.8	51.2	–	56.3	8
Seed shortage	170	54.1	44.1	1.8	56.5	7
Low price	170	24.7	50.6	24.7	53.9	12
High cost of fertilizer	170	72.9	26.5	0.6	57.5	3
Moisture-stress	170	92.9	7.1	–	58.5	1
Heat-stress	170	70.6	29.4	–	57.4	4
Insect pests	170	68.8	25.3	5.9	57.0	5
Disease (rust)	170	85.3	14.1	0.6	58.1	2
Weeds	170	31.2	41.2	27.6	54.1	11
Lack of access to credit	170	40.6	32.4	27.1	54.6	10
Land degradation/soil erosion	170	64.7	31.8	3.5	56.9	6

Source: Farm household survey, 2018. RBQ, rank based quotient.

2.3.7 Effect of drought /moisture-stress on wheat

The respondents indicated that moisture-stress occurred mostly during emergence and grain-filling stages of the wheat (Table 2.10). The occurrence of drought-stress at the seedling emergence stage commonly coincided with the late onset of rain in the areas as indicated by respondents. Moisture-stress reduced yields ranging between 63.1 – 73.8% within the studied regions. Compared to optimum condition, yield was the lowest in Dodota with a mean of 0.8 t ha^{-1}, followed by Sire (0.9 t ha^{-1}) and Hetosa (1.2 t ha^{-1}) under drought-stressed condition (Table 2.11).

Table 2.10. Moisture-stress prevailing at different growing stages indicated by respondent farmers in the study areas

Descriptions	Districts			Degrees of freedom	X^2 value	P-value
	Sire	Dodota	Hetosa			
Stages						
Emergence	17 (31.5)	26 (44.8)	21 (36.2)			
Tillering	2 (3.7)	2 (3.4)	1 (1.7)			
Heading	10 (18.5)	6 (10.3)	5 (8.6)	8	9.044	0.339
Grain filling	23 (42.6)	21 (36.2)	23 (39.7)			
Any stage	2 (3.7)	3 (5.2)	8 (13.8)			

Values outside and inside the bracket indicate the frequency and proportion in percentage, respectively.

Table 2.11. Impact of drought on yield (t ha^{-1}) of bread wheat in the study areas

Conditions		Districts			Degrees of freedom	F-value
		Sire	Dodota	Hetosa		
Optimum						
	Mean	2.889	3.172	3.359		
	SD	1.029	1.231	0.988	2	2.627^{ns}
	SE	0.14	0.162	0.13		
Drought-stress						
	Mean	0.848	0.826	1.241		
	SD	0.468	0.523	0.619	2	10.678**
	SE	0.064	0.069	0.081		

SD, standard deviation; SE, standard error; **, $p < 0.01$; ns, non-significant.

2.3.8 Farmers' coping mechanisms against moisture-stress

The chi-square analysis showed that respondents among districts used significantly different ($X^2 = 25.3$; $p = 0.000$) coping mechanisms to cope moisture-stress (Table 2.12). The lack of options and dependence on government food aid during drought years were significantly high in Sire and Dodota, with 51.9 and 58.6% of the respondents confirming that they lacked coping strategies to reduce the impact of drought-stress. However, the use of early maturing varieties was the most widely used coping strategy by 35.2, 32.8 and 29.3% of respondents in Sire, Hetosa and Dodota districts, respectively. The dependence on government food aid was significantly lower in Hetosa, with only 25.9% of the respondents confirming receipt of the aid. The farmers in Hetosa also used other methods such as soil and water conservation and replacing wheat with other drought-tolerant crops.

Table 2.12. Farmers' coping mechanisms against drought-stress

Descriptions	Districts			Degrees of freedom	X^2-value	P-value
	Sire	Dodota	Hetosa			
Coping mechanisms						
Growing early maturing bread wheat varieties	19 (35.2)	17 (29.3)	19 (32.8)			
Replacing wheat with other drought-tolerant crops	6 (11.1)	2 (3.4)	11 (19)	6	25.3	0.000
Soil and water conservation	1 (1.9)	5 (8.6)	13 (22.4)			
No option except government food aid	28 (51.9)	34 (58.6)	15 (25.9)			

Values outside and inside the bracket indicate the frequency and proportion in percentage, respectively.

2.3.9 Binary logistic regression model for farmers' preferences

Descriptions of the variables used in the binary logistic regression model and the results of the pooled regression coefficients for all districts are summarised in Tables 2.13 and 2.14. Before the variables were entered into the model, multi-collinearity analysis was done. No significant correlation was found between the variables. This was inferred from the Variance Inflation Factor (VIF) estimates, which had values less than 2 (data not shown). Test statistics indicated that the model adequately fitted the data (Table 2.14). The binary logistic regression model showed that the level of education had positive and significant ($p<0.01$) effect on adoption of new improved bread wheat varieties, while gender and contact with extension officers affected the adoption negatively and significantly ($p<0.05$). A unit increase in level of education would increase adoption of improved varieties by a factor of 5.56, whereas gender and a lack of extension contact reduced their adoption by factors of 0.21 and 0.37, in that order. Varietal attributes such as early maturity ($p<0.01$) and tall plant height ($p<0.05$) had positive and significant effects on the adoption of new improved varieties, while lack of good baking qualities, and better adaptation had a negative and significant ($p<0.05$) influence on farmers' preferences for improved varieties. A unit increase in early maturity and plant height would increase adoption of improved varieties by factor of 11.61 and 4.48, in that order. Conversely, a unit decrease in baking quality and adaptation will reduce adoption of improved varieties by a factor of 0.27.

Table 2.13. Description of variables used in the binary logistic regression model (n=170)

Variables	Expected sign
Socio-demographic characteristics	
Gender (male=1)	+/-
Age (productive age between 18 and 60 years; yes=1)	+/-
Education (at least basic=1)	+
Household size (continuous)	+
Extension contact (yes=1)	+
Member to farmers associations (yes=1)	+
Own land size (continuous)	+
Varietal attributes	
High yielding (yes=1)	+
Early maturing (yes=1)	+
Tillering ability (good=1)	+
Plant height (tall) (yes=1)	+
Grain weight (good=1)	+
Resistance to disease (rust) (yes=1)	+
Shattering (yes=1)	+
Baking quality (good=1)	+
Adaptation (drought and heat-stresses) (good=1)	+

+, positive impact; −, negative impact.

Table 2.14. Binary logistic regression estimates of the factors influencing farmers' varietal preferences

Variables	Coefficients	Standard error	Degrees of freedom	P-value	Odds ratio
Socio-demographic characteristics					
Gender	−1.563	0.688	1	**0.023**	0.210
Age	−0.629	0.713	1	0.377	0.533
Education	1.716	0.588	1	**0.004**	5.562
Household size	−0.058	0.085	1	0.494	0.944
Extension contact	−1.004	0.436	1	**0.021**	0.367
Farmers associations	−0.358	0.412	1	0.385	0.699
Own land size	−0.070	0.183	1	0.702	0.932
Varietal attributes					
High yielding	0.519	0.408	1	0.203	1.680
Early maturing	2.452	0.602	1	**0.000**	11.612
Low tillering ability	−0.699	0.713	1	0.327	0.497
Tall plant height	1.500	0.708	1	**0.034**	4.480
Less grain weight	−0.621	0.769	1	0.419	0.537
Susceptibility to disease (rust)	−0.377	0.462	1	0.414	0.686
Shattering	−2.100	1.398	1	0.133	0.122
Poor baking quality	−1.296	0.528	1	**0.014**	0.274

Table 2.14. (continued)

Variables	Coefficients	Standard error	Degrees of freedom	P-value	Odds ratio
Poor adaptation (drought and heat-stresses)	–1.304	0.515	1	**0.011**	0.271
Constant	2.104	1.169	1	0.072	8.202
Statistics					
Omnibus tests					
Chi-square	61.03				
p–value	0.000				
Hosmer and Lemeshow test					
Chi-square	6.801				
p–value	0.558				
-2 Log likelihood	172.28				
Cox & Snell R Square	0.302				
Nagelkerke R Square	0.404				

Source: Farm household survey, 2018; Dependent variable= Growing new improved bread wheat variety (1=yes, 0=no)

2.3.10 Farmers' preferred traits of bread wheat varieties grown under drought-stress condition

Some traits of varieties and their ranking are presented in Table 2.15. High grain yield was the most preferred trait as perceived by the farmers in the study areas, while adaptation to drought and heat-stresses and disease-resistance were ranked a joint second, and early maturity was ranked third. However, farmers in Sire ranked early maturity and adaptation as the second and third most preferred traits, in that order after grain yield. In Dodota, disease-resistance and adaptation were ranked second and third, respectively, with grain yield being the first. In Hetosa, good baking quality and disease-resistance were ranked joint second and stress adaptation was ranked third, while grain yield was ranked first. Across the study areas, good baking quality, tall plant height, and high tillering capacity were considered to be the fourth, fifth and sixth ranked preferred traits, respectively. The Kendall's W result indicated that only 16.5% of the respondent farmers agreed on the outcome of the ranking with probability level of <1% across the study areas. However, the highest agreement among the farmers was observed in Dodota (25.0%) followed by Hetosa (18.1%) and Sire (16.0%) (Table 2.15).

Table 2.15. Ranking of some bread wheat variety traits as perceived by the farmers in the study areas

| Traits | Districts | | | | | | | |
| | Sire | | Dodota | | Hetosa | | Across | |
	Mean rank	Rank	Mean rank	Rank	Mean rank	Rank	Mean rank	Rank
High yielding	3.8	1	2.84	1	3.26	1	3.29	1
Early maturing	3.96	2	5.32	5	5.08	5	4.8	3
High tillering capacity	5.44	6	5.47	7	5.55	7	5.49	6
Plant height (tall)	5.68	8	5.4	6	5	4	5.36	5
Grain weight	5.35	5	5.86	8	5.71	8	5.65	7
Resistance to disease (rust)	5.03	4	4.16	2	5.16	6	4.77	2
Non-shattering	5.6	7	6.02	9	5.79	9	5.81	8
Good baking quality	5.44	6	5.24	4	4.53	2	5.06	4
Adaptation (drought and heat-stresses)	4.7	3	4.7	3	4.92	3	4.77	2
Kendall's W (significance)	0.160 (0.000)		0.250 (0.000)		0.181 (0.000)		0.165 (0.000)	

Source: Farm household survey, 2018

2.4 Discussion

This part of the study enabled breeder to gain insight into farmers' bread wheat production practices, their varietal preferences and the challenges pertinent to their production systems especially under drought-stress environments where research and development effort is relatively low. It indicated the need of systematic wheat breeding for drought-tolerance integrating farmer-preferred traits under such low potential production environments in order to enhance adoption of improved varieties. The majority of the farming households (86.5%) were male-headed, which also meant that land was primarily owned by males, in line with traditional land holding tenure practices common in wheat farming in Ethiopia (Mulugeta and Hundie, 2012). Therefore, most of the wheat farming practices were dictated by males according to their level of education and age group. More than 50% of the respondents had attended elementary school (Grades 1-8) and were between the ages of 26 and 45 years, which is important for information acquisition and decision-making in crop production (Doss et al., 2003; Asfaw et al., 2012; Bashir and Wegary, 2014; Gebreselassie and Bekele, 2015; Kebede et al., 2017). Family members provided most of the farm labour, and large families therefore have a significant advantage in labour provision and can manage larger areas of production (Doss et al., 2003; Gebreselassie and Bekele, 2015). Farmers owned farm size ranging between 0.0 (excluding land rented) and 6.0 ha with a mean of 1.9 ha, which confirms that wheat production in the study areas was practiced on a smallholder scale.

Some farmers joined farmers' organizations for support, information sharing and assistance in input procurement (Doss et al., 2003; Kebede et al., 2017). However, the majority of the farmers (65%) reported that agriculture extension services were their main source of information rather than farmer organization. Similarly, in other studies, the extension service was found to be the major source of

information (Bishaw et al., 2010; Mulugeta and Hundie, 2012). Zegeye et al. (2001) found that Bureau of Agriculture was the most important initial source of seed of improved wheat varieties, further confirming the important role of government agencies in provision of improved technology and inputs such as seed and fertilizers. While government agencies can be the core of extension services, farmer organizations such as cooperatives and support groups also have important roles to play in the wheat value chain since more than 20% of the respondents highlighted that they obtained their seeds from neighbouring farmers or their cooperatives. Husman (2014) also noted that farmers' cooperatives were important and actively involved in seed distribution, allowing their member farmers to easily access seeds of improved varieties.

Crop production was the most important source of income among the surveyed districts. Wheat, tef and barley were found to be the main crops cultivated in the study areas, which corroborated with Abakemal et al. (2013) who reported that wheat, barley, teff, maize and sorghum were the major cereal crops grown in the east Arsi zone of Ethiopia. The majority of the farmers planted wheat early July using the broadcasting method, which agrees with Kebede et al. (2017), who reported that 54% of farmers in eastern Ethiopia used the broadcast planting method. However, differences in farming practices between high and low potential environments are common due to differences in production risk, and the adoption of the most appropriate planting method (Abate et al., 2014). Most of the farmers (75.3%) mentioned that their land was of medium fertility and depended on inorganic fertilizer applications, although the application rates were sub-optimal. Gebreselassie et al. (2017) and Kebede et al. (2017) also found that inorganic fertilizers were used sparingly by smallholder farmers, implying that the provision of fertilizers in addition to improved varieties could boost production and productivity of wheat in the study areas.

Wheat production was influenced by its relative importance in income generation, food and feed production and its adaptability to the environment. While the importance of wheat as a source of food for humans is well documented (Minot et al., 2015), the respondents also mentioned the use of wheat straw as feed for livestock. Bekele et al. (2015) reported that crop residues account for up to 90% of the livestock feed. There were nine improved bread wheat varieties (Ogolcho, Kubsa, Kekeba, Batu, Hidase, Pavon-76, King bird, Hawi and Bafane) that were identified by the respondents. The majority of the respondent farmers (34.7%) in the study areas grew the improved variety Ogolcho, while Kubsa and Batu were also widely grown. However, farmers indicated that some varieties such as Batu were relatively old and had been recycled for many years. This implies that there is an urgent need for varietal replacement with high yielding cultivars possessing traits preferred by the farmers to improve productivity from the current levels of 2.4 t ha^{-1}. Bekele et al. (2015) also reported declining performance of improved varieties over long time, while Tadesse et al. (2016) mentioned that the rate of varietal replacement is generally low in most of Ethiopia, and even worse in drought-prone, rainfed areas. The continued cultivation of old varieties like Batu is probably due to its possession of some

traits preferred by farmers, or a lack of access to alternative improved varieties. There were no local landraces found in the study areas, which corroborate with the result found by Hei et al. (2017).

Respondent farmers ranked drought (moisture-stress) as the most important production constraint, followed by disease (rust), the high cost of fertilizer and heat-stress, showing that the farmers in the study areas face a myriad of challenges that often occur simultaneously. Drought-stress accounted for up to 74% yield losses all the regions. This stress is the leading challenge among smallholder farmers in dryland farming (Adhikari et al., 2015; Tadesse et al., 2019). In other studies, fungal diseases, the high cost of fertilizers, shortage of improved seeds and high seed prices were reported among the major production constraints in rust prone, high potential agro-ecologies of Ethiopia (Hei et al., 2017). Abakemal et al. (2013) found that access to inputs and inadequate rainfall were the major production constraints for maize production in the highlands of Ethiopia. A study conducted in the Bale Highlands and Chilalo Awraja identified the high price of improved seed as an impediment to adoption of improved cultivars (Doss et al., 2003). Zeleke (2017) reported that drought, flood, crop pest/disease and hailstorm were the major climate change related risk factors that influenced farmers' choice of adaptation measures in the Arsi zone of the Oromia region.

The majority of the respondent farmers had no coping strategies against drought-stress except government food aid, implying that there is an urgent need to develop holistic and multi-faceted approaches, including development and adoption of improved varieties and agricultural practices, and adoption of alternative cropping systems for income generation. Among the improved agronomic practices, the growing of early maturing varieties, and soil and water conservation activities were already being practiced by some of the farmers, observations similar to those of Abraha et al. (2016) in the Tigray region of Ethiopia. The combination of drought-tolerant varieties with early or late planting, and active soil and water conservation practices is the most sustainable approach to counter the effects of drought-stress (Zeleke, 2017).

Various factors such as the demographic, socio-economic and variety specific attributes influence farmers' preferences (Joshi and Bauer, 2006; Kotu et al., 2000). Gender, level of education and extension contact were the major factors that influenced adoption of new improved varieties in the study areas. Gender had negative and significant effect on adoption of new improved varieties. Solomon et al. (2014) reported that the gender of the household head had a positive effect on the adoption of improved varieties but a negative effect on the extent to which the improved varieties of wheat were used in the Robe and Digelu Tijo districts of the Arsi Zone. Women are usually deprived of access to external inputs and information (Doss, 2001), which decreases their likelihood of growing improved varieties. The adoption of new improved varieties was positively and significantly affected by the farmer's level of education. Farmers with higher level of literacy were more likely to adopt improved cultivars due to increased access to information, while farmers with lower levels of literacy were likely

to be more averse to new technologies. Similarly, the education level of the household head was found to positively and significantly affect the adoption of improved varieties as reported by different researchers (Beshir and Wegary, 2014; Thomson et al., 2014; Chilot et al., 2015; Gebreselassie and Bekele, 2015). However, in another study no systematic association was found between the farmers' level of education and adoption of improved varieties (Zegeye et al., 2001). The main source of agricultural information for the majority of the sample households (65%) was found to be agricultural extension officers. However, its effect on adoption of new improved varieties was significantly negative, corroborating the result found by Beshir and Wegary (2014), who reported that visits by extension officers were negatively associated with the adoption of hybrid maize in the drought-prone central rift valley of Ethiopia. This implies that extension services were in favour of the previous traditional varieties that had already been cultivated by the farmers, which is a surprising outcome. On the other hand, the provision of extension services has been associated with technology adoption, and infrastructure and market access (Doss et al., 2003; Beshir and Wegary, 2014; Gebreselassie and Bekele, 2015).

Variety specific traits such as early maturity, plant height, adaptation and baking quality were the major contributing traits required for adoption of improved bread wheat varieties. Grain yield showed a positive but non-significant effect on the adoption of new improved varieties. Early maturity and plant height had positive and significant effects on the adoption of new improved varieties. This indicates that an improvement in these attributes would enhance the adoption of new improved varieties, and should increase the overall production and productivity of bread wheat in drought-prone areas. However, poor baking quality and environmental adaptation negatively and significantly affected the adoption of improved varieties, which indicates these attributes were present only in traditional varieties. Kotu et al. (2000) also reported the negative effect of poor baking quality on the adoption of improved wheat varieties in Adaba and Dodola woredas of the Bale Highlands of Ethiopia.

Farmers' varietal preferences vary from season to season, from location to location and from farmer to farmer (Morris and Bellon, 2004), and their perception of varietal attributes affects their adoption of improved varieties (Kalinda et al., 2014). Less than 50% of the farmers concurred in their preferences for varietal traits in each district and across the study areas, calling for efficient breeding aimed at developing cultivars that integrate farmers' preferred traits (Morris and Bellon, 2004). Grain yield was the most preferred trait of bread wheat varieties across the study areas, followed by disease-resistance, adaptation and early maturity. Similarly, Abakemal et al. (2013) reported that grain yield was the most preferred trait in maize in the highlands of Ethiopia. The farmers mentioned that they would prefer varieties with disease-resistance because they do not afford chemical pesticides and have limited information on the suitable chemicals. Smallholder farmers lack options for disease control due to a lack of knowledge, and access to fungicides, among other factors (Kotu et al., 2000). As the study areas were characterized as lowlands that commonly experience moisture-stress during the beginning and

post flowering stages of the crop, farmers preferred an early maturing and well adapted or drought-tolerant variety. Tall varieties with a high tillering capacity and good baking quality were also preferred by the farmers. Baking quality is an important trait because it increases consumers' demand and market value. However, the baking quality of the new improved varieties was recognized as being inferior to that of the traditional varieties. Preference for tall height is usually driven by the need for straw for use as livestock feed. However, the tall varieties should have resistance to lodging that could otherwise have adverse effect on yield and result in low adoption (Kotu et al., 2000).

2.5 Conclusions and implications for wheat breeding

This part of the study proved the hypothesis that there were different farmers' practices, production constraints, and cultivar preferences that influence bread wheat production in drought-prone areas. Drought-stress, disease (especially rust), and the high cost of fertilizers were among the major constraints of wheat production that were identified by the farmers. Drought-stress accounted for up to 74% yield losses all the regions. Socio-demographic factors such as gender, education level and access to extension service influenced variety adoption by the farmers. Early maturity, tall plant height, good baking quality and stress adaptation were the major varietal characteristics contributing towards adoption of new improved bread wheat varieties. Farmers expressed a wide range of variety-specific trait preferences. Grain yield, rust-resistance, adaptation to drought and heat-stresses and early maturity were the most farmer-preferred traits. Therefore, future wheat breeding for drought-stressed environments in Ethiopia should target improving farmers' preferred traits and drought-tolerance under low input agriculture systems for sustainable wheat production and productivity. In addition, farmer training, provision of seed and inputs, and dissemination of information can be provided through government agencies, as they are the single most important source of information.

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Chapter 3. Evaluation of bread wheat (*Triticum aestivum* L.) genotypes for yield and related traits under drought-stressed and non-stressed conditions

Abstract

Drought is a major factor threatening crop production worldwide. Recurrent drought events limit wheat production and productivity in rainfed agrosystems in Ethiopia. Developing wheat varieties that are adapted to drought-prone environments is a sustainable strategy to improve wheat production and productivity. The aim of this part of the study was to evaluate and select bread wheat genotypes for yield and yield components, and for stability under drought-stressed and non-stressed conditions. One hundred and twenty genotypes were evaluated at five test sites in the 2018/19 cropping season using a 10 x 12 alpha lattice design with two replicates. The level of drought-stress was imposed using different sowing dates (early planting representing non-stressed, while late planting as drought-stressed conditions) following the onset of the main seasonal rain at each site. Grain yield and yield components were recorded, and drought indices were calculated for each genotype. The combined analysis of variance showed the existence of considerable genetic variability among the genotypes for all the investigated traits. Genotypes such as 'YS-39', 'YS-119' and 'YS-109' were the earliest to mature and can be used in drought-tolerance breeding. Among the drought-tolerance indices, Geometric Mean Productivity (GMP), Mean Productivity (MP), Harmonic Mean (HM), Stress Tolerance Index (STI) and Yield Index (YI) were found to be the most suitable for predicting drought-tolerance because they had significant and positive correlations with yield under drought-stressed and non-stressed conditions. Genotypes 'YS-41', 'YS-92', 'YS-115', 'YS-34' and 'YS-93' were found to be drought-tolerant, and exhibited dynamic stability, with relatively high yield under both drought-stressed and non-stressed conditions. 'YS-90', 'YS-106', 'YS-96', 'YS-102' and 'YS-101' were susceptible to drought-stress, while 'YS-32', 'YS-29', 'YS-14', 'YS-53' and 'YS-11' were relatively drought-tolerant, but exhibited static stability under non-stressed conditions. The selected promising genotypes could be used in future crossing program for the development of drought-tolerant cultivars incorporating farmers' preferred traits.

Key words: grain yield, drought, drought-tolerance indices, drought-tolerance

3.1 Introduction

Improving production and productivity in the low altitude, drought-prone areas of Ethiopia would have a positive impact on national wheat production. Borlaug and Dowswell (2005) posited that wheat production can only be increased through either increasing yield per unit land, or by expanding the cultivated area. The latter is not a realistic option because land is a finite resource, and expansion of croplands would create conflict with other land uses such as livestock grazing or human settlement. Breeding for drought-tolerance is a sustainable approach to improving yields in marginal areas. Developing wheat varieties and technologies suitable for such areas have been prioritized as mitigation strategies (Negassa et al., 2013; Tadesse et al., 2019).

Although breeding for drought-tolerance is recognised globally as an important strategy, there are still relatively few varieties with stable drought-tolerance expressed under diverse environmental conditions. Drought-tolerance is a complex polygenic trait confounded by environmental factors that affect its expression, and the identification of superior genotypes. Furthermore, the unpredictable nature of drought manifestation and the different mechanisms adopted by plants to cope with drought-stress complicate the identification of superior genotypes under variable moisture conditions. Field-based empirical selection for drought-tolerance is still commonly used (Mwadzingeni et al., 2016). However, the occurrence of drought-stress at various stages of plant growth and development have differential effects on yield and yield components, and there is no consensus on the best time to impose drought-stress in controlled experiments. The objective of this part of the study was to screen bread wheat genotypes for drought-tolerance and yield stability across different test conditions, using yield and yield components, and drought-tolerance indices to select for promising genotypes as parental material that will be useful in breeding for drought-tolerant, high yielding and stable wheat cultivars suitable for moisture-stress areas in Ethiopia.

3.2 Materials and methods

3.2.1 Study sites

The study was conducted at five test sites, namely Alem Tena, Debre Zeit, Dera, Kulumsa and Melkasa. Alem Tena has an altitude of 1611 m above sea level and is situated at a latitude of 8.3°18'North and a longitude of 38.4°57'East. It has a mean annual rainfall of 1054.5 mm and average maximum and minimum monthly temperatures of 26.1°C and 10.4°C, respectively. Debre Zeit is located at an altitude of 1920 m above sea level, and latitude 8.7°44'North and 39.0°58'East. It has a mean annual rainfall of 931.4 mm and average maximum and minimum monthly temperatures of 27.5°C and 11.4°C, respectively. Dera is located at an altitude of 1500 m above sea level and latitude 8.3°20'North and 39.3°19'East and receives a mean annual rainfall of 816.1 mm and average maximum and minimum

monthly temperatures of 29.4°C and 13.7°C, respectively. The Kulumsa site is located at an altitude of 2200 m above sea level and latitude 8.0°02'North and 39.2°10'East with a mean annual rainfall of 946 mm and average maximum and minimum monthly temperatures of 23.1°C and 9.9°C, respectively. Melkasa is situated at an altitude of 1500 m above sea level and latitude 8.4°24'North and 39.3°21'East and receives a mean annual rainfall of 807.3 mm and average maximum and minimum monthly temperatures of 29.9°C and 14.1°C, respectively. The texture of the soil varies from clay to clay loam, with the pH ranging between 6.8 and 7.8 across the test sites (Table 3.1).

Table 3.1. Physico-chemical soil properties of the experimental sites

Soil characteristics	Sites				
	Alem Tena	Debre Zeit	Dera	Kulumsa	Melkasa
Texture	Clay loam	Clay	Clay	Clay	Clay loam
Clay (%)	36.3	58.8	41.3	61.3	35
Organic C (%)	0.7	0.8	0.9	1	1
P (ppm)	17.3	30.4	14.1	13.5	21.9
K (Meq/100g)	3.9	1.6	4.1	2.8	4.1
N (%)	0.7	0.1	0.1	0.1	0.1
P^H	7	7.5	7.8	6.8	7.2
CEC (Meq/100g)	20.6	39.7	24.8	32.8	30.2
EC (**μs**)	100.5	34.1	81	36.7	74.2

C, carbon; P, phosphorus; K, potassium; N, nitrogen; CEC, cation exchange capacity; EC, exchange capacity.

3.2.2 Experimental treatments and design

The genotypes were planted under two different levels of moisture by manipulating the sowing dates (early planting representing non-stressed, while late planting as drought-stressed conditions) following the onset of the main seasonal rain at each site. At Alem Tena the non-stress trial was planted on the 14th July and the drought-stress trial on the 13th August. At Debre Zeit the non-stress trial was planted on the 20th July and the drought-stress trial on the 20th August. At Dera the non-stress trial was planted on the 5th July and the drought-stress trial on the 3rd August. At Kulumsa the non-stress trial was planted on the 4th July, and the drought-stress trial was planted on the 2nd August. At Melkasa the non-stress trial was planted on the 16th July and the drought-stress trial on the 15th August. The total amounts of rainfall received by the non-stress trials compared to drought-stress trials were 527 and 330.9 mm at Alem Tena, 452 and 242 mm at Debre Zeit, 239.1 and 126.7 mm at Dera, 406.9 and 316 mm at Kulumsa, and 421.6 and 275.3 mm at Melkasa, respectively (Figure 3.1). The experiment was laid out in a 10 x 12 alpha lattice design with two replicates. One hundred and twenty bread wheat genotypes were provided by Kulumsa Agricultural Research Centre. The panel included 115 genotypes that were being

developed for drought-stress areas that were originally from the International Maize and Wheat Improvement Centre (CIMMYT) plus five standard checks that were released as drought-tolerant cultivars (Appendix 3.1). The genotypes were developed through various breeding procedures as described in their pedigree in Appendix 3.1. These genotypes were assumed to be in similar maturity groups as they were developed for the similar growing condition. Planting is usually done early to mid-July, depending on the onset of rainfall in all the study areas. Each genotype was hand planted in 2 m long rows, spaced at 0.2 m apart. A plot for each genotype consisted of four rows. The seed rate was 150 kg ha^{-1}. NPS and urea fertilisers were applied at 121 kg ha^{-1} and 150 kg ha^{-1}, respectively. Other cultural practices were carried out as per standard recommendation for wheat in the areas.
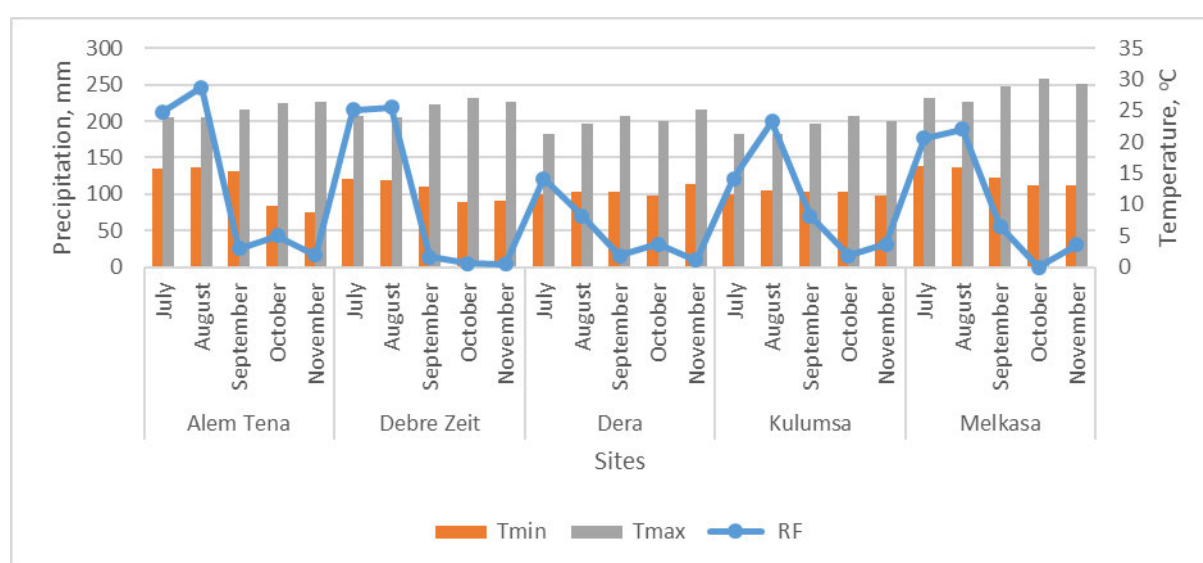
Figure 3.1 Rainfall and temperature conditions of the five experimental sites during 2018 crop-growing season

3.2.3 Data collection

Data on yield and yield components were collected at various stages of the crop cycle. The days to heading (DH) were recorded from the date of sowing to the date when 50% of heads had fully emerged from flag leaf. The days to maturity (DM) were recorded as the number of days from the date of sowing to a stage when 90% of plants reached harvest maturity. Plant height (PH) was measured in centimetres from the soil surface to tip of spike for five randomly sampled plants. The spike length (SL) was measured in centimetres from the base to the tip of a fully developed spike. The number of spikelets per spike (SS) were counted per spike and recorded as a mean of five spikes from five randomly sampled plants. The number of kernels per spike (KS) was recorded as a proportion of kernels to the total number of spikes from five randomly sampled plants. One thousand kernels randomly selected from each plot were weighed on a laboratory precision scale to estimate the 1000-kernel weight (TKW) in grams for

each genotype. Finally, grain yield (GY) was measured by harvesting the grain from the two central rows in each plot, sun drying it, measuring it in grams, and then converting it into tons ha^{-1}, based on the plot size.

A number of drought-tolerance/susceptibility indices were calculated, based on the yield, under both drought-stressed and non-stressed conditions, using the following formulae:

Stress susceptibility index (SSI) $= \dfrac{1-(Ys/Yp)}{1-(Ys/\bar{Y}p)}$ (Fischer and Maurer, 1978).

Geometric mean productivity (GMP) $= \sqrt{Yp \; x \; Ys}$ (Ramirez and Kelly, 1998).

Mean productivity (MP) $= \dfrac{Yp+Ys}{2}$ (Rosielle and Hamblin, 1981).

Harmonic mean (HM) $= \dfrac{2(Y_p \; X \; Y_s)}{Y_p + Y_s}$ (Jafari et al., 2009).

Tolerance (TOL) $= Yp - Ys$ (Rosielle and Hamblin, 1981).

Stress tolerance index (STI) $= \dfrac{Yp \; X \; Ys}{(\bar{Y}p)^2}$ (Fernandez, 1992).

Yield index (YI) $= \dfrac{Y_s}{\bar{Y}_s}$ (Gavuzzi et al., 1997).

Yield stability index (YSI) $= \dfrac{Ys}{Yp}$ (Bouslama and Schapaugh, 1984).

Where Ys is yield under drought-stressed conditions, Yp is yield under non-stressed conditions, $\bar{Y}$s is the mean yield of genotypes under drought-stressed conditions and $\bar{Y}$p is the mean yield of genotypes under non-stressed conditions.

3.2.4 Data analysis

Combined analysis of variance was carried out, after testing for homogeneity of variance, using a general linear model (GLM) in SAS, version 9.3 (SAS Institute, 2012). In addition, the means of genotypes and the different water regimes were separated using Fisher's protected least significant difference (LSD) at a 5% significance level to quantify the effects of genotype, environment and water regime. The bivariate correlations among drought-tolerance/susceptible indices and grain yield were analysed using the Pearson's correlation procedure, using Statistical Software for Social Science (SPSS, 2016). Multivariate associations were analysed using the principal component and biplot analyses in GenStat® version 18.2.0, VSN, International (Payne and Roger, 2015).

3.3 Results

3.3.1 Effects of genotypes, sites, stress conditions and their interactions on agronomic traits

The analysis of variance (ANOVA) revealed that the three-way interaction between genotype, water regimes and site had significant ($p<0.01$) effects on days to heading (DH), days to maturity (DM), 1000-kernel weight (TKW) and spike length (SL), showing non-significant effects on plant height (PH) spikelet per spike (SS), kernel per spike (KS) and grain yield (GY). Traits such as DH, DM and SL were significantly ($p<0.01$) affected by the genotype by water regime interaction, while the genotype by site interaction effect was significant ($p<0.05$) for DH, DM, PH, TKW, GY and SS. All the traits were significantly ($p<0.01$) affected by the water regime by site interaction, which had a significant impact on all the measured traits. Genotype, water regimes and site had significant ($p<0.01$) effects on all the measured traits (Table 3.2), indicating genotypes were significantly different for all traits measured under two different water regimes across sites.

Table 3.2. Combined analysis of variance with mean squares of 8 agronomic traits of 120 wheat genotypes evaluated over the five test sites and two water regimes

Source of variation	DF	DH	DM	PH	SL	SS	KS	TKW	GY
Site	4	10136.7**	46284.5**	79858.5**	222.416**	837.436**	54672.6**	5300.01**	2928.323**
Replication (Site)	5	19.6525**	33.2525**	1050.09**	1.33412**	12.638**	60.2995^{ns}	35.5627*	16.438**
Block (Replication)(Site)	90	10.048**	15.1414**	57.5056**	0.52419^{ns}	5.67292**	45.0358^{ns}	16.5236*	3.008**
Genotype	119	169.689**	74.7564**	157.791**	4.4326**	15.5627**	153.71**	52.3911**	3.564**
Water regime	1	941.985**	1989.85**	47047**	14.4329**	669.309**	18413.3**	739.896**	2017.522**
Genotype x Water regime	119	11.722**	13.3393**	35.2608^{ns}	0.60113**	2.89206^{ns}	50.8146^{ns}	14.3339^{ns}	1.518^{ns}
Genotype x Site	476	8.66807**	12.1653**	41.5134**	0.46035^{ns}	3.02736*	45.217^{ns}	19.6522**	2.418**
Site x Water regime	4	736.527**	3416.88**	6904.42**	90.4918**	548.266**	9039.31**	2105.12**	365.812**
Genotype x Site x Water regime	301	13.8691**	10.5422**	32.0755^{ns}	0.51529*	2.73672^{ns}	47.1907^{ns}	16.065**	1.961^{ns}
Residual	747	6.47	7.52	30.78	0.43	2.56	42.53	11.77	1.725
CV (%)		4.4	2.8	9.1	8.1	9.7	15.4	12.1	28.8

DF, degree of freedom; DH, days to heading; DM, days to maturity; PH, plant height (cm); SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); CV, coefficient of variation; *, p< 0.05; **, p<0.01; ns, non-significant.

3.3.2 Genotypic response of agronomic traits to drought-stress

Table 3.3 shows the mean agronomic performances of the top twenty and the bottom ten genotypes grown under non-stressed and drought-stressed conditions. There was significant variation in genotypic performance in the agronomic traits under non-stressed and drought-stressed conditions (Appendix 3.2). The mean days to heading was 57.1 days under non-stressed compared to 60.4 days under drought-stressed conditions. Genotypes such as 'YS-119', 'YS-109' and 'YS-113' were early flowering under non-stressed conditions, with mean DH values of 47.2, 47.5 and 49.5 days, respectively, while 'YS-67', 'YS-86' and 'YS-70' with DH values of 69.4, 69.1 and 67.2 days to flower, respectively, were late flowering genotypes under the same conditions. Under drought-stressed conditions, the earliest flowering genotypes were 'YS-119', 'YS-109' and 'YS-39' with mean DH values of 51.4, 52.3 and 52.7 days, respectively, compared to late flowering 'YS-86', 'YS-67', 'YS-29' and 'YS-70' genotypes which took 71.3, 70.3 , 70 and 70 days to flower, respectively. 'YS-119' and 'YS-109' also exhibited early maturity, with mean DM values of 93 and 94.1 under non-stressed conditions. The mean DM of the earliest maturing genotypes under drought-stressed were 87.3 and 90.3 days by 'YS-119' and 'YS-88'. Under drought-stressed conditions, genotypes such as 'YS-119', 'YS-88' and 'YS-39' with values of 87.3, 90.8 and 91 days, were early maturing while genotypes 'YS-29', 'YS-70' and 'YS-86', with values of 114, 112 and 112 days, were the most late maturing genotypes. Plant height varied significantly from 56.1 cm, recorded for genotype 'YS-62', to 75.9 cm recorded for genotype 'YS-119', which was for a check cultivar, grown under non-stressed conditions. Plant height under drought ranged between 38 cm recorded for genotype 'YS-1' and 66.4 cm recorded for genotype 'YS-71', showing a wide variation for increasing genetic gain from selection.

There was also a significant differential response to drought among the genotypes with respect to grain yield (Appendix 3.2). Yield under drought-stressed ranged between 4.8 t ha^{-1} and 0.9 t ha^{-1}, with a mean of 2.9 t ha^{-1}, while it ranged from 7.4 t ha^{-1} to 2.9 t ha^{-1}, with a mean of 5.6 t ha^{-1} under non-stressed conditions. 'YS-32' was ranked the highest yielding (4.8 t ha^{-1}) genotype under drought-stressed conditions, followed by 'YS-41' (4.4 t ha^{-1}), 'YS-26' (4.4 t ha^{-1}) and 'YS-29' (4.3 t ha^{-1}), while 'YS-66' (0.9 t ha^{-1}) was the lowest yielding followed by 'YS-84' (1.0 t ha^{-1}), 'YS-67' (1.5 t ha^{-1}) and 'YS-60' (1.7 t ha^{-1}). Under non-stressed conditions, genotype 'YS-90' had the highest yield (7.4 t ha^{-1}) followed by genotype 'YS-106' (7.2 t ha^{-1}) and genotype 'YS-96' (6.8 t ha^{-1}), while genotypes 'YS-60' (3.7 t ha^{-1}), 'YS-84' (3.4 t ha^{-1}) and 'YS-66' (2.9 t ha^{-1}) had the lowest grain production. In general, under non-stressed conditions, 74.8% of the genotypes outperformed the overall mean grain yield performance of the standard checks. Under the drought-stressed conditions, 81% of the genotypes attained better grain yield than the standard checks (Appendix 3.2), which indicated that the yield potential of the majority of the genotypes was stable under both drought-stressed and non-stressed conditions.

Table 3.3. Means for 8 agronomic traits of 120 genotypes showing the top 20 and bottom 10 ranked genotypes evaluated under drought-stressed and non-stressed conditions across the test sites, ranked according to their performance under drought-stressed conditions

Genotype code	DH		DM		PH		SL		SS		KS		TKW		GY	
	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS
Top twenty genotypes																
YS-32	62.3	68	99.9	108	65.8	60.5	8.1	8.3	16.4	15.8	41.7	39.7	27.6	27.6	5.2	4.8
YS-41	57.8	61.2	99.5	105.4	68.3	56.2	8.7	8.9	17	14.8	42.6	35.2	33.2	32.5	6.5	4.4
YS-26	58.3	62	96.3	100.2	65.8	61.6	7.4	7.9	15.4	15.4	39	36.5	29.8	32.7	6.0	4.4
YS-29	63.1	70	100.9	114.3	64	65.9	8.6	8.9	18.8	17.3	49.9	59.7	26.9	30.5	5.1	4.3
-YS-92	51.6	59	96.2	97.6	64.2	57.6	8.1	8.4	16.4	15.2	43.1	39.1	29.5	27.5	6.4	4.3
YS-14	58	63.8	99	107.5	67.6	60.3	7.8	8.4	16.5	16.3	42.4	39.7	29.7	26.8	4.3	4.2
YS-93	57.2	61.6	98.2	98	62.8	53.1	8.7	9	18	15.8	46.8	44.4	27	26.2	6.2	4.2
YS-53	58.1	62.5	97.7	103.3	64.1	55.4	8.7	8.3	17.6	15.3	44.1	46.5	29.2	33.6	5.2	4.2
YS-115	58.2	61	99.4	100.3	69.6	60.3	8.3	8.3	19.2	16.7	49.9	42.4	29.1	27.9	6.6	4.1
YS-31	54.9	59.8	95.7	92	72.6	59.8	7.5	7.7	15.4	15.7	41.4	32.2	30.9	31.8	5.9	4.1
YS-13	55.1	61.2	96.6	99.5	60.7	53.5	7.8	7.6	15.1	13.9	37	31.9	31.4	30.5	5.5	4.0
YS-95	51.6	59.5	94.8	95.7	65	55.2	7.5	7.8	15.6	14.7	41.7	35.6	30.1	30	6.1	4.0
YS-56	58.1	62.8	98.4	104.8	68.3	60.1	7.5	7.8	18.5	16.5	48.4	48.8	28.8	26.2	6.0	3.9
YS-50	51.7	59.3	95.7	98.5	67.7	63.5	9.3	9.5	17.1	16.9	48.8	40.2	32	34.2	6.0	3.8
YS-83	51.9	58.2	95.9	93.7	65.1	57.3	8.1	8.7	15.2	15	41.3	36	31.8	30.7	5.8	3.8
YS-89	55.6	62.2	96.1	98.8	68.4	59.5	7.6	7.6	16.3	14.8	46.6	41.2	32.3	33	6.1	3.7
YS-34	51.4	55.4	94.9	98.2	68.8	61.8	8.3	8.3	16.5	15.2	45.2	38	30.2	29.7	6.6	3.7
YS-11	56.7	61.5	97.5	105.8	64.3	59.8	8	8.5	16.6	16.6	42.6	43.8	27.6	27.7	4.1	3.7
YS-112	55.1	60.6	95.7	99.6	65.6	59.4	8.2	8.8	16.1	17	40.1	37.9	30.3	29	5.9	3.7
YS-15	55.2	59.5	96.3	98.7	67.2	60.1	9.2	8.9	17.5	15.6	44.4	39.5	29.5	30.6	5.3	3.7
Bottom ten genotypes																
YS-86	69.1	71.3	102.4	111.7	66	52.3	7.7	8.3	16.1	16.7	34.1	35.2	27.6	29.5	5.3	2.0
YS-57	63.6	66.2	103.3	105.5	61.1	51.6	8.8	8.3	17.2	16	42.4	38.3	23	21.1	4.2	1.9
YS-118	59.1	61.9	98.6	100.5	72.1	56.1	8.9	9	18	16.1	44.5	36.2	26	26.8	4.7	1.9
YS-119	47.2	52.3	93	87.3	75.9	63.2	7.6	7.5	13.8	13.1	31.8	28.6	27.9	24.1	4.4	1.8
YS-42	59.8	62.3	101.3	100.4	72.2	50.9	8.9	8.3	19.9	17.3	46.7	38.4	29	26.6	5.8	1.8
YS-78	52	57.8	95.6	94.2	68.1	52.1	7	7.2	17.1	15.9	49	43.1	29	23.4	4.9	1.7
YS-60	54.6	60.2	97.6	97.2	61.1	48.1	6.5	6.7	17.1	14.9	46.3	39.7	25.6	22.4	3.7	1.7
YS-67	69.4	70.3	104.6	111	62.3	53	7.9	7.8	16.7	16.9	41.1	52.8	27.1	29.1	4.6	1.5
YS-84	59.8	58	96.1	91.5	62.1	55.5	8.5	8.1	17.4	17	29.1	39.7	28.5	31.1	3.4	1.0
YS-66	66.9	68.5	100.9	107	60.3	51.5	7.8	8	17.3	19.4	35.2	43.4	21.6	24.4	2.9	0.9
LSD (0.05)	2.4	2.5	2.2	3.7	5.3	6.5	0.5	1.1	1.6	1.7	5.7	7.6	3	4.3	1.3	1.1

DH, days to heading; DM, days to maturity; PH, plant height (cm); SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); NS, non-stressed conditions; DS, drought-stressed conditions; LSD, list significant difference.

3.3.3 Comparison and selection of genotypes based on tolerance indices and yield

The different tolerance indices varied in magnitude, which reflected their differences in identifying tolerant or susceptible genotypes (Table 3.4). However, the Geometric Mean Productivity (GMP), the Harmonic Mean (HM) and the Mean Productivity (MP) indices were similar in categorising the genotypes 'YS-41', 'YS-92' and 'YS-115' as the most drought-tolerant. According to the Drought Stress Susceptibility (SSI) and Tolerance (TOL) indices, 'YS-11', 'YS-14' and 'YS-32' were the most drought-tolerant genotypes, although these indices ranked the genotypes differently. The Drought Stress Tolerance Index (STI) indicated that genotypes 'YS-41', 'YS-92' and 'YS-115' were the most drought-tolerant. Likewise, the Yield Index (YI) revealed genotypes 'YS-26', 'YS-32' and 'YS-41' as the most drought-tolerant, while the Yield Stability Index (YSI) identified genotypes 'YS-11', 'YS-14' and 'YS-32' as the most drought-tolerant. All the other indices, except TOL, were consistent in identifying the genotypes 'YS-84' and 'YS-66' among the most drought-sensitive. For instance, these genotypes had the highest SSI value of 1.5 and the lowest STI value of 0.1. However, there were variations in the ranking of the genotypes by the different indices. For instance, TOL identified genotypes 'YS-106', 'YS-90' and 'YS-44' as the most susceptible, while the other indices differed in one of the top three susceptible genotypes. Due to the lack of consistency by the indices in their ability to identify tolerant /susceptible genotypes, the rank mean was calculated, and this ranked genotypes between 21.8 and 105. According to the rank mean, genotypes 'YS-115', 'YS-41', 'YS-92', 'YS-34', 'YS-85' and 'YS-93'were identified as the most drought-tolerant genotypes, while 'YS-66', 'YS-60' and 'YS-84' were identified as the genotypes most sensitive to drought (Appendix 3.3).

Table 3.4. Mean grain yield and drought selection indices of the top 20 and 10 bottom performing genotypes out of the 120 genotypes evaluated across the five test sites under drought-stressed and non-stressed conditions, ranked according to their performance under drought-stressed conditions

Genotype code	Yp	R	Ys	R	SSI	R	GMP	R	MP	R	HM	R	TOL	R	STI	R	YI	R	YSI	R	R⁻
Top twenty genotypes																						
YS-32	5.2	76	4.8	1	0.2	119	5	6	5	11	5	6	0.4	118	0.8	6	1.6	1	0.9	2	34.6
YS-41	6.5	8	4.4	2	0.7	102	5.3	1	5.4	1	5.2	1	2.1	85	1	1	1.5	2	0.7	19	22.2
YS-26	6	29	4.4	3	0.6	110	5.1	4	5.2	4	5.1	3	1.6	104	0.9	4	1.5	3	0.7	11	27.5
YS-29	5.1	81	4.3	4	0.3	117	4.7	17	4.7	25	4.7	12	0.8	117	0.7	17	1.5	4	0.9	4	39.8
YS-92	6.4	10	4.3	5	0.7	100	5.2	2	5.4	2	5.1	2	2.1	80	0.9	2	1.5	5	0.7	21	22.9
YS-14	4.3	112	4.2	6	0	120	4.2	37	4.2	54	4.2	27	0.1	120	0.6	37	1.4	6	1	1	52
YS-93	6.2	19	4.2	7	0.7	101	5.1	5	5.2	5	5	5	2	90	0.9	5	1.4	7	0.7	20	26.4
YS-53	5.2	74	4.2	8	0.5	116	4.7	18	4.7	24	4.6	13	1.1	113	0.7	18	1.4	8	0.8	5	39.7
YS-115	6.6	6	4.1	9	0.8	90	5.2	3	5.3	3	5.1	4	2.5	60	0.9	3	1.4	9	0.6	31	21.8
YS-31	5.9	37	4.1	10	0.7	103	4.9	9	5	10	4.8	8	1.9	95	0.8	9	1.4	10	0.7	18	30.9
YS-13	5.5	59	4	11	0.6	111	4.7	14	4.8	20	4.7	11	1.5	107	0.8	14	1.4	11	0.7	10	36.8
YS-95	6.1	25	4	12	0.7	99	4.9	8	5	9	4.8	7	2	86	0.8	8	1.4	12	0.7	22	28.8
YS-56	6	30	3.9	13	0.8	94	4.8	10	4.9	13	4.7	10	2.1	82	0.8	10	1.3	13	0.7	27	30.2
YS-50	6	33	3.8	14	0.8	92	4.7	13	4.9	16	4.6	15	2.2	77	0.8	13	1.3	14	0.6	29	31.6
YS-83	5.8	50	3.8	15	0.8	96	4.7	20	4.8	21	4.6	16	2	87	0.7	20	1.3	15	0.7	25	36.5
YS-89	6.1	22	3.7	16	0.9	82	4.8	12	4.9	14	4.6	14	2.4	62	0.8	12	1.3	16	0.6	39	28.9
YS-34	6.6	5	3.7	17	0.9	67	4.9	7	5.1	6	4.8	9	2.8	41	0.8	7	1.3	17	0.6	54	23
YS-11	4.1	117	3.7	18	0.2	118	3.9	69	3.9	89	3.9	55	0.4	119	0.5	69	1.3	18	0.9	3	67.5
YS-112	5.9	34	3.7	19	0.8	84	4.7	19	4.8	19	4.5	19	2.3	67	0.7	19	1.2	19	0.6	37	33.6
YS-15	5.3	70	3.7	20	0.7	104	4.4	28	4.5	36	4.3	22	1.7	101	0.7	28	1.2	20	0.7	17	44.6
Bottom ten genotypes																						
YS-86	5.3	65	2	111	1.4	10	3.2	109	3.7	105	2.9	110	3.4	20	0.4	109	0.7	111	0.4	111	86.1
YS-57	4.2	114	1.9	112	1.2	32	2.8	115	3.1	116	2.6	114	2.3	66	0.3	115	0.7	112	0.5	89	98.5
YS-118	4.7	100	1.9	113	1.3	22	3	112	3.3	113	2.7	113	2.8	42	0.3	112	0.6	113	0.4	99	93.9
YS-119	4.4	110	1.8	114	1.3	28	2.8	116	3.1	115	2.6	115	2.5	53	0.3	116	0.6	114	0.4	93	97.4
YS-42	5.8	45	1.8	115	1.5	4	3.2	108	3.8	94	2.8	112	4	6	0.4	108	0.6	115	0.3	117	82.4
YS-78	4.9	92	1.7	116	1.4	8	2.9	114	3.3	112	2.6	116	3.1	32	0.3	114	0.6	116	0.4	113	93.3
YS-60	3.7	118	1.7	117	1.2	31	2.5	118	2.7	118	2.3	117	2	88	0.2	118	0.6	117	0.5	90	103.2
YS-67	4.6	102	1.5	118	1.5	5	2.6	117	3	117	2.2	118	3.1	29	0.2	117	0.5	118	0.3	116	95.7
YS-84	3.4	119	1	119	1.5	2	1.9	119	2.2	119	1.6	119	2.4	63	0.1	119	0.4	119	0.3	119	101.7
YS-66	2.9	120	0.9	120	1.5	3	1.6	120	1.9	120	1.3	120	2	89	0.1	120	0.3	120	0.3	118	105

Yp, yield under non-stressed conditions; Ys, yield under drought-stressed conditions; R, rank; SSI, stress susceptibility index; GMP, geometric mean productivity; MP, mean productivity; HM, harmonic mean; TOL, tolerance index; STI, stress tolerance index; YI, yield index; YSI, yield stability index; R⁻, rank mean.

3.3.4 Association of grain yield and tolerance indices

Grain yield under non-stressed conditions (Yp) was positively correlated with grain yield under drought-stressed conditions (Ys) (r=0.300; p<0.01) and all the selection indices except YSI, which exhibited negative association with Yp (r=–0.240; p<0.01) (Table 3.5). Likewise, yield under drought-stressed conditions (Ys) was positively associated with most of the tolerance indices, except SSI (r=–0.840; p<0.01) and TOL (r=–0.548; p<0.01). Regarding drought indices, GMP, MP, HM, STI and YI were positively and significantly correlated, indicating the value of these indices for selection of high yielding genotypes under drought-stressed conditions.

Table 3.5. Pearson's correlation coefficients (r) between grain yield and drought selection indices for 120 wheat genotypes evaluated over five test sites under drought-stressed and non-stressed conditions

	Yp	Ys	SSI	GMP	MP	HM	TOL	STI	YI
Yp	1.000								
Ys	0.300**	1.000							
SSI	0.240**	–0.840**	1.000						
GMP	0.681**	0.901**	–0.530**	1.000					
MP	0.823**	0.789**	–0.346**	0.975**	1.000				
HM	0.549**	0.957**	–0.654**	0.986**	0.924**	1.000			
TOL	0.634**	–0.548**	0.891**	–0.133ⁿˢ	0.081ⁿˢ	–0.295**	1.000		
STI	0.659**	0.901**	–0.523**	0.989**	0.961**	0.977**	–0.153*	1.000	
YI	0.300**	1.000**	–0.840**	0.901**	0.789**	0.957**	–0.548*	0.901**	1.000
YSI	–0.240**	0.840**	–1.000**	0.530**	0.346**	0.654**	–0.891**	0.523**	0.840**

Yp, yield under non-stressed conditions; Ys, yield under drought-stressed conditions; SSI, stress susceptibility index; GMP, geometric mean productivity; MP, mean productivity; HM, harmonic mean; TOL, tolerance index; STI, drought stress tolerance index; YI, yield index; YSI, yield stability index; *, p< 0.05; **, p<0.01; ns, non-significant.

3.3.5 Principal component analysis (PCA)

The first two principal components with eigenvalues greater than 1.0 explained 99.3% of the total variation (Table 3.6). The first principal component (PC1) accounted for 70.2%, while the second principal component (PC2) accounted for 29.2% of the total variation. The yield under drought-stressed conditions (Ys), GMP, MP, HM and YSI made large (more than 30% each) and positive contributions to the total variation explained by PC1. Thus, PC1 can be regarded as an axis for high yield and drought-tolerance under drought-stressed conditions. On the other hand, Yp and TOL (with more than 50% contribution each), and SSI and MP (more than 30% each) had positive loadings, and substantially contributed to PC2. This component could be regarded as a component associated with high yield under non-stressed conditions, and high drought-susceptibility exhibited by the negative (–36%) variation contributed by YSI.

Table 3.6. Principal component analysis of grain yield and drought selection indices for 120 wheat genotypes evaluated over five test sites under drought-stressed and non-stressed conditions

Traits	PC1	PC2
Yp	0.15313	0.53296
Ys	0.37501	−0.06537
SSI	−0.29358	0.36277
GMP	0.35629	0.19229
MP	0.32207	0.30432
HM	0.37088	0.09928
TOL	−0.16989	0.52029
STI	0.35471	0.18457
YI	0.37501	−0.06537
YSI	0.29358	−0.36277
Eigen value	7.02	2.92
Proportion of total variance (%)	70.17	29.18
Cumulative variance (%)	70.17	99.34

Yp, yield under non-stressed conditions; Ys, yield under drought-stressed conditions; SSI, stress susceptibility index; GMP, geometric mean productivity; MP, mean productivity; HM, harmonic mean; TOL, tolerance index; STI, drought stress tolerance index; YI, yield index; YSI, yield stability index; PC1, the first principal component; PC2, the second principal component.

3.3.6 Principal component biplot analysis

The principal component biplot analysis revealed that most of the genotypes were grouped around the centre of the biplot axes. However, some genotypes could be identified as drought-tolerant and high yielding under both drought-stressed and non-stressed conditions, including 'YS-41', 'YS-92', 'YS-115', 'YS-34' and 'YS-93' (Figure 3.2). Genotypes such as 'YS-106', 'YS-96', 'YS-102' and 'YS-101' were susceptible to drought-stress and performed well only under non-stressed conditions, while genotypes 'YS-32', 'YS-29', 'YS-14', 'YS-53' and 'YS-11' were found to be high yielding genotypes under drought-stressed conditions only. Genotypes 'YS-66', 'YS-84' and 'YS-60' were identified as being the most susceptible to drought and were low yielding genotypes under both drought-stressed and non-stressed conditions.
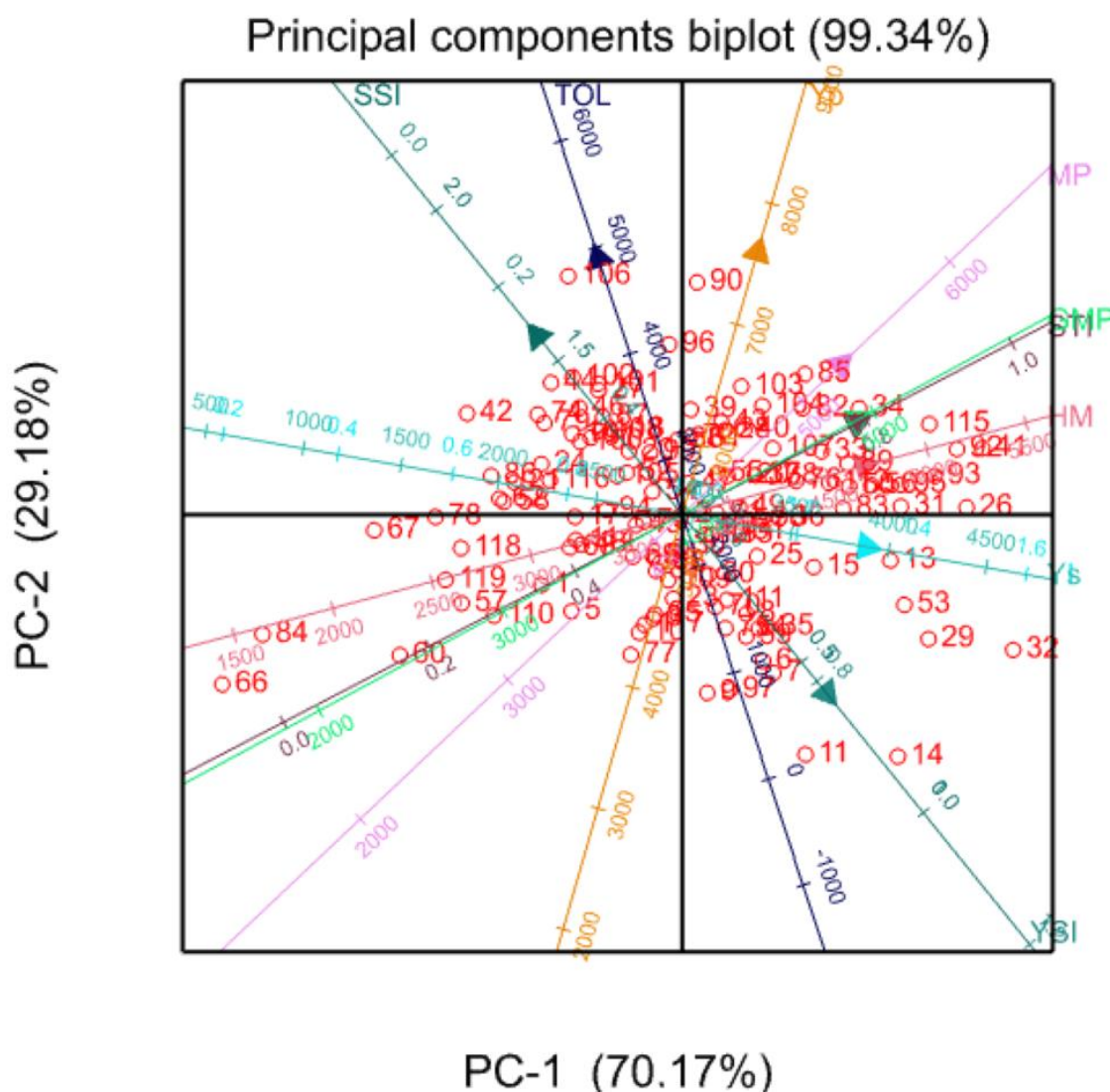
Figure 3.2 Biplot based on the first two principal component axes for 120 wheat genotypes evaluated under non-stressed and drought-stressed conditions across the five test sites.

3.4 Discussion

3.4.1 Effects of genotypes, sites, stress conditions and their interactions on agronomic traits

Analysis of variance (Table 3.2) showed that significant differences existed among the wheat genotypes for all the traits studied, which indicated the presence of considerable genetic variation that could be exploited to improve yield and drought-tolerance. The presence of genetic variability among the test genotypes for traits related to stress-tolerance is of paramount importance for successful breeding aimed to develop cultivars adapted to a range of stress environments (Asfaw and Blair, 2014; Sharma et al., 2014; Mwadzingeni et al., 2017; Mathew et al., 2018). There existed crossover ranking in agronomic traits of the test genotypes under drought-stressed and non-stressed conditions suggesting differential

genetic responses to changes in water availability. Crossover ranking has been reported previously and may confound the identification of superior genotypes, while on the other hand, it helps to identify genotypes adapted to specific or broad environments (Badu-Apraku et al., 2017; Mafouasson et al., 2018).

3.4.2 Genotypic response for agronomic traits under drought-stress

Differences in agronomic performance are indicative of genetic variation, which is the basis for crop improvement (Seher et al., 2015; Ayalew et al., 2016). Early maturing genotypes such as 'YS-39', 'YS-119' and 'YS-109' would be preferred in dry environments because they may be able to escape terminal drought-stress, and could fit in multiple cropping cycles due to their relatively short growing cycles. However, early maturity is often associated with an undesirable yield penalty, as evidenced in genotype 'YS-119'. Yield penalties have been reported by others in some early maturing genotypes of wheat (Mwadzingeni et al., 2016). Early maturity, combined with short plant height, may be preferred for drought-escape because early and tall genotypes might not have enough time to accumulate and translocate sufficient photo-assimilate reserves from the stem to the head, resulting in low grain yields. The mean grain yield reduction by 47.4% from 5.6 t ha^{-1} to 2.9 t ha^{-1} due to drought-stress was in agreement with other authors who reported that drought caused a 35.0-40.6% reduction in bread wheat (Mwadzingeni et al., 2016; Mathew et al., 2019) and 63.0% in durum wheat (Mohammadi, 2012).

3.4.3 Comparison and selection of genotypes based on tolerance indices and yield response

Drought-tolerance indices are important criteria in identifying genotypes tolerant to drought (Ballesta et al., 2019). Three drought-tolerance indices, GMP, MP and HM were equally effective at identifying drought-tolerant and high yielding genotypes, showing that they could be used interchangeably. Selection indices, SSI, TOL and YSI, favoured genotypes with high yields under drought-stressed conditions and low yield under non-stressed conditions, which agrees with the results reported elsewhere (Golabadi et al., 2006; Mohammadi et al., 2010). According to the rank mean, genotypes 'YS-115', 'YS-41', 'YS-92', 'YS-34', 'YS-85' and 'YS-93'were identified as the most drought-tolerant genotypes, while 'YS-66', 'YS-60' and 'YS-84' were identified as the genotypes most sensitive to drought.

3.4.4 Association of grain yield and tolerance indices

The presence of positive and significant correlations for grain yield of some genotypes under drought-stressed and non-stressed conditions agreed with Mursalova et al. (2015). The positive and significant correlation of yield under both sets of conditions identified high potential genotypes that performed

well under both drought-stressed and non-stressed conditions. Drought indices such as GMP, MP, HM, STI and YI had positive and significant associations with grain yield under both drought-stressed and non-stressed conditions, making these indices the most suitable criteria to select for drought-tolerance (Ballesta et al., 2019). Mohammadi et al. (2010), Farshadfar et al. (2012), Mursalova et al. (2015) and Ayalew et al. (2016) asserted that these indices were the best for identifying superior genotypes across various water availability conditions. The SSI had a positive and significant association with grain yield under non-stressed conditions, which implies that selection for certain traits that favour yield potential may result in genotypes with increased susceptibility to drought-stress (Akçura et al., 2011), and vice versa (Bayoumi et al., 2008).

3.4.5   Principal component analysis (PCA)

The first two principal components explained 99.3% of the total variation. PCA confirmed the correlation result that revealed positive correlation between grain yield under drought-stressed conditions and drought indices such as GMP, MP, HM, STI, YI and YSI, which indicates the similarity of these indices in identifying genotypes tolerant to drought-stress. Farshadfar et al. (2012) also reported that STI, GMP and YI were positively associated and similar in identifying genotypes tolerant to drought-stress. However, the intensity of drought-stress may have an effect on the determination of appropriate selection indices (Sio-Se Mardeh et al., 2006). Akçura et al. (2011) reported that SSI is a valuable selection criterion in wheat breeding when the drought-stress applied is severe, whereas GMP, MP, HM, TOL and STI are important when the drought-stress is less severe.

3.4.6   Principal component biplot analysis

The biplot analysis did not clearly separate the genotypes based on their yield response under drought-stressed and non-stressed conditions. It showed that the majority of the genotypes were clustered around the centre of the biplot, implying these genotypes were moderately tolerant or susceptible. However, Genotypes 'YS-41', 'YS-92', 'YS-115', 'YS-34' and 'YS-93' were drought-tolerant and had the ability to increase yield in response to improved conditions in the target environments. Genotypes that exhibit dynamic stability are ideal because they are able to use water efficiently under moisture-limited conditions but possess the capacity to improve their yield potential with improvement in environmental conditions (Rajaram, 2005). Genotypes with dynamic stability can be selected for multiple environments or mega-environments because they show wide adaptation. Genotypes 'YS-106', 'YS-96', 'YS-102' and 'YS-101' showed low drought-tolerance, while genotypes 'YS-32', 'YS-29', 'YS-14', 'YS-53' and 'YS-11' exhibited static stability; under drought-stressed condition, they performed adequately, however, they did not improve their performance when moisture became more available.

Genotypes with static stability can be selected for specific environments to which they are highly adapted (Mafouasson et al., 2018).

3.5 Conclusions

This study shows the existence of considerable genetic variability among the genotypes of wheat for yield and yield related traits, which can further be exploited to improve wheat productivity in Ethiopia. The yield potential of the majority of tested genotypes were stable and better than the checks across a wide range of environments. Genotypes such as 'YS-39', 'YS-119' and 'YS-109' were the earliest to mature and may be used in drought-tolerance breeding to exploit their drought-escape mechanism. Genotypes such as 'YS-1', 'YS-62' and 'YS-54' had short plant heights, whereas 'YS-71', 'YS-29' and 'YS-120' were tall genotypes. The above complementary genotypes could be used for developing high yielding wheat varieties with medium to tall plant height and adapted to drought-stress. Drought selection indices varied in their ability to identify tolerant genotypes but GMP, MP, HM, STI and YI were better selection criteria for drought-tolerance than TOL, SSI and YSI. Genotypes 'YS-41', 'YS-92', 'YS-115', 'YS-34' and 'YS-93' were found to be drought-tolerant, and exhibited dynamic stability, with relatively high yield under both drought-stressed and non-stressed conditions. 'YS-90', 'YS-106', 'YS-96', 'YS-102' and 'YS-101' were susceptible to drought-stress, while 'YS-32', 'YS-29', 'YS-14', 'YS-53' and 'YS-11' were relatively drought-tolerant, but exhibited static stability under non-stressed conditions. These selected genotypes could be utilized in further breeding for enhancing drought-tolerance and farmers' preferred traits in bread wheat.

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Appendix 3.1. List of genotypes considered in the study

Genotype Code	Name	Pedigree	Genotype code	Name	Pedigree
YS-1	ETW17-268	Meraro/HA304	YS-61	ETW17-351	FRANCOLIN #1
YS-2	ETW17-269	KAUZ//MON/CROW/4/SERI.1B//KAUZ/HEVO/3/AMAD	YS-62	ETW17-352	FRANCOLIN #1/3/PBW343*2/KUKUNA*2//YANAC
YS-3	ETW17-270	KAUZ//MON/CROW/4/SERI.1B//KAUZ/HEVO/3/AMAD	YS-63	ETW17-353	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/BOW/URES//2*WEAVER/3/CROC_1/AE.SQUARROSA (213)//PGO/6/WAXWING/PARUS//WAXWING/KIRITATI/7/FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
YS-4	ETW17-271	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/TEVEE'S/BOBWHITE #1	YS-64	ETW17-354	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/KITE/6/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI/7/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/TNMU/6/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
YS-5	ETW17-272	DEBEIRA/4/KAUZ//ALTAR 84/AOS/3/KAUZ	YS-65	ETW17-355	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/6/WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI
YS-6	ETW17-273	ATTILA 50Y//ATTILA/BCN/3/PFAU/MILAN	YS-66	ETW17-356	FRET2/KUKUNA//FRET2/3/WHEAR/4/FRET2*2/KUKUNA/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
YS-7	ETW17-274	OPATA/RAYON//KAUZ/3/2*MILAN/DUCULA	YS-67	ETW17-357	GLADIUS/5/2*W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
YS-8	ETW17-275	QADANFER-11/REBWAH-11	YS-68	ETW17-358	GW322/6/FRET2/KUKUNA//FRET2/3/TNMU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/7/KINGBIRD #1//INQALAB 91*2/TUKURU
YS-9	ETW17-276	JAWAHIR-1/GIRWILL-5	YS-69	ETW17-359	HW2045/3/WAXWING/SRTU//WAXWING/KIRITATI/4/KINGBIRD #1//INQALAB 91*2/TUKURU
YS-10	ETW17-277	JAWAHIR-1/GIRWILL-5	YS-70	ETW17-361	KACHU/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/6/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI/7/TACUPETO F2001/BRAMBLING*2//KACHU
YS-11	ETW17-279	ATTILA/3*BCN//FLAG-2	YS-71	ETW17-362	KACHU/SAUAL*2//KINGBIRD #1
YS-12	ETW17-280	NJORO SD-7//VEE/NAC	YS-72	ETW17-363	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI/6/KACHU/SAUAL
YS-13	ETW17-281	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	YS-73	ETW17-364	KRONSTAD F2004/3/TRCH/SRTU//KACHU/4/TRCH/SRTU//KACHU
YS-14	ETW17-282	CROC-1/AE.SQUARROSA (224)//OPATA/3/FLAG-7	YS-74	ETW17-365	LIVINGSTON/5/2*W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
YS-15	ETW17-283	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	YS-75	ETW17-366	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN*2/4/SUNCO/2*PASTOR//EXCALIBUR
YS-16	ETW17-284	KAUZ/PASTOR//FLAG-4	YS-76	ETW17-367	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI
YS-17	ETW17-285	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	YS-77	ETW17-368	MP4010/3/TRCH/SRTU//KACHU/4/KINGBIRD #1//INQALAB 91*2/TUKURU
YS-18	ETW17-286	ENKOY/FLAG-5	YS-78	ETW17-369	MUNAL #1/3/KINGBIRD #1//INQALAB 91*2/TUKURU
YS-19	ETW17-287	ICARDA-SRRL-9/JAWAHIR-22	YS-79	ETW17-370	MUTUS/DANPHE #1/4/C80.1/3*BATAVIA//2*WBLL1/3/C80.1/3*QT4522//2*PASTOR
YS-20	ETW17-288	KBG-01/FLAG-7	YS-80	ETW17-372	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/OR 9437534/SOKOLL//SOKOLL
YS-21	ETW17-290	FLAG-3/ICARDA-SRRL-5	YS-81	ETW17-373	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/T.TAU.83.2.36//SUNCO/2*PASTOR/5/W15 92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
YS-22	ETW17-291	CROC1/AE.SQUARROSSA(205)//KAUZ/3/ATTILA/4/FLAG-1	YS-82	ETW17-374	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/5/CROC_1/AE.SQUARROSA (213)//PGO/3/CMH81.38/2*KAUZ/4/BERKUT/6/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
YS-23	ETW17-292	CROC-1/AE.SQUARROSA (224)//OPATA/3/FLAG-7	YS-83	ETW17-375	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/7/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1

Appendix 3.1. (continued)

Genotype Code	Name	Pedigree	Genotype code	Name	Pedigree
YS-24	ETW17-293	P1.861/RDWG/4/KAUZ//ALTAR 84/AOS/3/KAUZ	YS-84	ETW17-376	PASTOR//HXL7573/2*BAU/3/WBLL1/4/SOKOLL/3/PASTOR//HXL7573/2*BAU
YS-25	ETW17-294	KAUZ//MON/CROW?S?/3/VEE/PJN//2*KAUZ	YS-85	ETW17-377	PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR/4/MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2
YS-26	ETW17-295	KAUZ//MON/CROW?S?/4/SERI.1B//KAUZ/HEVO/3/AMAD	YS-86	ETW17-378	PBW343*2/KUKUNA*2//FRTL/PIFED/3/BECARD/KACHU
YS-27	ETW17-296	KAUZ//MON/CROW?S?/4/SERI.1B//KAUZ/HEVO/3/AMAD	YS-87	ETW17-379	PBW343*2/KUKUNA*2//KITE/3/ATTILA*2/PBW65*2//YANAC/4/SAUAL/YANAC//SAUAL
YS-28	ETW17-297	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/TEVEE'S'/BOBWHITE #1	YS-88	ETW17-380	PRL/2*PASTOR*2/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2
YS-29	ETW17-298	DEBEIRA/4/KAUZ//ALTAR 84/AOS/3/KAUZ	YS-89	ETW17-381	PRL/2*PASTOR*2/7/TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ
YS-30	ETW17-299	SERI.1B//KAUZ/HEVO/3/AMAD/4/PFAU/MILAN	YS-90	ETW17-383	ROLF07*2/KIRITATI*2/10/PFAU/WEAVER*2//BRAMBLING/9/RABE/6/WRM/4/FN/3*TH//K58/2*N/3/AUS-6869/5/PELOTAS-ARTHUR/7/2*RABE/8/IRENA
YS-31	ETW17-301	HUBARA-5/ANGI-1	YS-91	ETW17-384	ROLF07/4/WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI/5/SAUAL/MUTUS
YS-32	ETW17-302	SERI.1B//KAUZ/HEVO/3/AMAD/4/KAUZ/FLORKWA-1	YS-92	ETW17-385	ROLF07/SAUAL*2/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
YS-33	ETW17-303	SERI.1B//KAUZ/HEVO/3/AMAD/4/PFAU/MILAN	YS-93	ETW17-386	ROLF07/SAUAL/4/SHA7/VEE#5//ARIV92/3/PBW343*2/KUKUNA/5/ROLF07/SAUAL
YS-34	ETW17-304	SOMAMA-9/NEJMAH-18	YS-94	ETW17-387	SAAR//PBW343*2/KUKUNA/3/ROLF07/YANAC//TACUPETO F2001/BRAMBLING/6/CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7
YS-35	ETW17-305	QAFZAH-35/AMIR-2	YS-95	ETW17-388	SAUAL/3/KAUZ/PASTOR//PBW343/4/KINGBIRD #1/5/SAUAL/KRONSTAD F2004
YS-36	ETW17-306	KAUZ//ALTAR 84/AOS/3/MILAN/DUCULA	YS-96	ETW17-389	SAUAL/3/KAUZ/PASTOR//PBW343/4/TRCH/SRTU//KACHU/5/SAUAL/PI 610750/ATTILA/3/SAUAL
YS-37	ETW17-307	ESDA/SHWA//BCN/3/MILAN/PASTOR	YS-97	ETW17-390	SAUAL/3/SW89.3064//CMH82.17/SERI/4/SAUAL/5/MUU #1/SAUAL//MUU
YS-38	ETW17-308	PFAU/MILAN	YS-98	ETW17-391	SAUAL/MUTUS*2//PICAFLOR #1
YS-39	ETW17-309	KAUZ//ALTAR 84/AOS 3/KAUZ/3/ATTILA 50Y//ATTILA/BCN/4/PASTOR-6	YS-99	ETW17-392	SAUAL/MUTUS/3/TACUPETO F2001/BRAMBLING//KIRITATI
YS-40	ETW17-310	SAMIRA-9	YS-100	ETW17-394	SOKOLL/WBLL1/4/2*SOKOLL/3/PASTOR//HXL7573/2*BAU
YS-41	ETW17-312	SHUHA-4//NS732/HER/3/ANGI-1	YS-101	ETW17-395	SUP152/3/TRCH/SRTU//KACHU
YS-42	ETW17-313	CROC-1/AE.SQUARROSA (224)//OPATA/3/FLAG-7	YS-102	ETW17-396	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/TRCH/SRTU//KACHU
YS-43	ETW17-314	KBG-01/FLAG-7	YS-103	ETW17-397	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/WAXWING/SRTU//WAXWING/KIRITATI
YS-44	ETW17-315	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	YS-104	ETW17-398	TC870344/GUI//TEMPORALERA M 87/AGR/3/2*WBLL1/5/ONIX/4/MILAN/KAUZ//PRINIA/3/BAV92
YS-45	ETW17-316	KAUZ/PASTOR//FLAG-4	YS-105	ETW17-399	TILHI/SOKOLL/8/2*ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR
YS-46	ETW17-317	ENKOY/FLAG-5	YS-106	ETW17-400	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1*2/8/ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR
YS-47	ETW17-318	SOMAMA-9/ICARDA-SRRL-2	YS-107	ETW17-401	TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ*2/7/PVN
YS-48	ETW17-319	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PFAU/MILAN	YS-108	ETW17-402	TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/7/CIRNOC 2008/8/SAUAL/KRONSTAD F2004

Appendix 3.1. (continued)

Genotype Code	Name	Pedigree	Genotype code	Name	Pedigree
YS-49	ETW17-320	HUBARA-1/5/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR	YS-109	ETW17-403	TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/7/SERI.1 B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI/8/ATTILA*2/PBW65*2//W485/HD29
YS-50	ETW17-321	SERI.1B//KAUZ/HEVO/3/AMAD/4/SHUHA-7//SERI 82/SHUHA'S'	YS-110	ETW17-404	TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/7/TRCH/SRTU//KACHU
YS-51	ETW17-339	BAJ #1*2/CIRNO C 2008	YS-111	ETW17-405	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1*2/5/SOKOLL//SUNCO/2*PASTOR
YS-52	ETW17-340	BAVIS #1/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	YS-112	ETW17-406	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5/SOKOLL/3/PASTOR//HXL7573/2*BAU
YS-53	ETW17-341	BAVIS #1/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	YS-113	ETW17-407	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92
YS-54	ETW17-342	BAVIS*2/4/PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1	YS-114	ETW17-408	WAXWING//INQALAB 91*2/KUKUNA/3/WBLL1*2/TUKURU/8/2*NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/KUKUNA
YS-55	ETW17-343	BAVIS/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	YS-115	ETW17-409	WAXWING/7/TNMU/6/CEP80111/CEP81165/5/IAC5/4/YKT406/3/AG/ASN//ATR/8/ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE#5//ARIV92
YS-56	ETW17-344	BECARD #1/3/PBW343*2/KUKUNA//PBW343*2/KUKUNA	YS-116	Kekeba	Standard check
YS-57	ETW17-345	BECARD/KACHU/3/UP2338*2/KKTS*2//YANAC	YS-117	King bird	Standard check
YS-58	ETW17-346	C80.1/3*BATAVIA//2*WBLL1/3/PBW343*2/KUKUNA*2/8/SHA7//PRL/VEE#6/3/FASAN/4/HAAS8446/2*FASAN/5/CBRD/KAUZ/6/MILAN/AMSEL/7/FRET2*2/KUKUNA	YS-118	Ogolcho	Standard check
YS-59	ETW17-348	CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC/5/PFAU/WEAVER/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	YS-119	Dereselegn	Standard check
YS-60	ETW17-350	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/4/PARUS/PASTOR	YS-120	Bikan	Standard check

Appendix 3.2. Means for 8 agronomic traits of 120 genotypes evaluated under drought-stressed and non-stressed conditions across five test sites

Genotype	DH		DM		PH		SL		SS		KS		TKW		GY	
Code	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS
YS-1	51.8	59	95.2	92.3	60.6	38	7.5	5.1	15.4	10.7	46.5	32	28.8	18.1	4.6	2.3
YS-2	59.7	59.8	98.7	97.3	63.7	57.5	8	7.6	17.3	15.6	47.1	38.6	27.8	25.5	5.4	2.9
YS-3	61.5	63	98.6	99.5	64.2	53.6	8.8	9	17.8	17.6	43.4	42.8	28	29.3	4.6	2.9
YS-4	53.9	54.3	97	94.6	68.6	56.5	9.6	9.7	16.9	16.5	50.8	42.3	32	28.7	4.8	3.4
YS-5	60.3	62	98	98.6	65.4	50.3	7.7	7.9	15.9	15	38.3	37.5	25.5	25.3	4.4	2.5
YS-6	55.3	59.8	96.7	100	67.9	60.1	7.9	8.4	15.4	15.8	39.2	40.8	32.6	31.5	4.6	3.5
YS-7	58.5	62.6	100.2	106	66	55	7.9	8.3	16	15.9	41.6	33.8	28.7	27	4.5	3.5
YS-8	53.4	56.3	94.7	95	64.9	54.3	7.9	7.9	16.1	14.7	43.6	37.7	31.3	27.2	4.8	3.3
YS-9	57.3	60.1	97.4	96	69.5	56.1	7.8	7.9	15.9	14.5	41.9	34.9	31.4	26.1	4.2	3.2
YS-10	57.8	61.5	98.9	99.2	64.8	51.5	8.5	8.3	16.3	14.2	36.6	38.9	30.3	30	4.5	2.8
YS-11	56.7	61.5	97.5	105.8	64.3	59.8	8	8.5	16.6	16.6	42.6	43.8	27.6	27.7	4.1	3.7
YS-12	53	57.4	97.8	98.4	62.6	48.6	7.4	7.1	16.2	14.7	43.6	38.4	31.1	26.9	5.3	3.1
YS-13	55.1	61.2	96.6	99.5	60.7	53.5	7.8	7.6	15.1	13.9	37	31.9	31.4	30.5	5.5	4.0
YS-14	58	63.8	99	107.5	67.6	60.3	7.8	8.4	16.5	16.3	42.4	39.7	29.7	26.8	4.3	4.2
YS-15	55.2	59.5	96.3	98.7	67.2	60.1	9.2	8.9	17.5	15.6	44.4	39.5	29.5	30.6	5.3	3.7
YS-16	61	61.8	101.3	103.7	65.1	53.9	8.6	8.3	18.2	16.1	39.1	41.2	30.8	27.8	5.8	2.3
YS-17	56.8	59.6	97.4	98.6	66.9	55.2	8.3	7.8	16.7	15	42.8	37.9	31	28	5.2	2.4
YS-18	61.3	62.5	99.8	100	70.5	55.5	8.5	8.5	17.6	16.3	46.1	40.8	26.8	25.3	6.0	2.5
YS-19	57.9	58.4	100.2	99.8	62.2	57.2	8.2	8.2	16.4	15.6	40.2	40.6	30.8	28.5	5.3	3.1
YS-20	56.9	57.2	97.6	99.6	62.8	54.7	7.9	8.5	15.3	15.3	41.5	39.2	32.2	30.1	5.8	2.6
YS-21	61.8	63.2	99.9	100.2	64.4	51.4	8.4	7.8	18.9	16.7	49.4	41.5	26	24.8	5.3	2.1
YS-22	62.4	65	100.1	104.6	66	54.6	8.6	8.8	19.5	18	53.5	53.7	28.9	26.8	5.4	3.2
YS-23	56.4	59	96.5	98.4	59.2	55.5	8.7	8.8	17	15.9	42	45.2	29.8	27.7	4.8	3.0
YS-24	59.7	65.4	99.8	106.4	62	57.3	8	8.4	17.9	16.9	47.6	47.4	30.6	28.9	5.5	2.2
YS-25	62.2	66	98.2	107	65.7	54.3	9.2	9.3	18.3	17.4	44.6	43	29.2	29.7	5.3	3.4
YS-26	58.3	62	96.3	100.2	65.8	61.6	7.4	7.9	15.4	15.4	39	36.5	29.8	32.7	6.0	4.4
YS-27	59.6	61.1	97.8	96.6	66.7	54.9	8.5	8.4	17.7	16.2	45.7	32.3	30.1	25.2	6.3	2.4
YS-28	53.4	57.9	95.3	93.8	66.5	57.1	8	7.9	16.5	15.2	40.1	36.7	30.3	27.8	6.2	3.1
YS-29	63.1	70	100.9	114.3	64	65.9	8.6	8.9	18.8	17.3	49.9	59.7	26.9	30.5	5.1	4.3
YS-30	53.2	59.9	95.3	93.4	62.3	51.6	7.8	8.3	16	14.5	42.9	35.8	29.7	28.4	5.2	3.0
YS-31	54.9	59.8	95.7	92	72.6	59.8	7.5	7.7	15.4	15.7	41.4	32.2	30.9	31.8	5.9	4.1
YS-32	62.3	68	99.9	108	65.8	60.5	8.1	8.3	16.4	15.8	41.7	39.7	27.6	27.6	5.2	4.8
YS-33	60.2	65.8	96.7	107.3	64	58.4	8.6	9.3	18.2	17.4	43.7	50.5	30.3	31.3	6.2	3.6
YS-34	51.4	55.4	94.9	98.2	68.8	61.8	8.3	8.3	16.5	15.2	45.2	38	30.2	29.7	6.6	3.7
YS-35	61.9	65.3	99.7	105.8	65.3	61.2	8.9	8.8	19	17.2	45.5	46.4	26.1	26.9	4.8	3.5
YS-36	60.1	59.3	97.3	96.2	65.7	56.8	8.9	8.5	15.9	14.9	41	38.9	27.2	28	5.6	3.4
YS-37	59.3	64.3	99.2	105.3	65.7	59	8.6	8.9	18.4	17.7	49.6	47	27.6	26.9	5.9	3.3
YS-38	52.5	56.9	94.7	92.6	62.1	54.3	7	7.2	14.4	13.9	40.9	29.9	31.3	27.1	5.9	3.4
YS-39	50.1	51.4	95	91	62.3	52.8	8.2	8.1	14.3	13.1	37.8	31.1	35.3	29.4	6.3	2.9
YS-40	60.3	63.2	98.4	97.8	61.8	53.5	7.2	8.1	15.5	16.3	40.6	40.4	29.6	29.7	6.2	3.2
YS-41	57.8	61.2	99.5	105.4	68.3	56.2	8.7	8.9	17	14.8	42.6	35.2	33.2	32.5	6.5	4.4
YS-42	59.8	62.3	101.3	100.4	72.2	50.9	8.9	8.3	19.9	17.3	46.7	38.4	29	26.6	5.8	1.8
YS-43	54.6	59.3	97.2	93.5	64.2	55.1	8	8.1	17.2	15.8	43.3	33.7	31.5	28.7	6.2	3.0
YS-44	60.5	64.8	99.3	102	61.2	55.3	9.3	8.7	18.6	16.5	45.1	39.6	31.3	29.2	6.2	2.2
YS-45	60.2	62.8	99.1	102.2	61.9	50.3	7.8	7.4	16.7	14.8	44.1	37.8	30.1	28.2	5.2	2.7
YS-46	61.9	64.2	100.7	103.2	62.6	47.2	8.2	7.8	17.7	15	51.7	44.8	28.1	22.7	6.1	2.3
YS-47	51.9	58.4	95.7	96.6	63.8	52.7	8.1	8.4	17	16.5	47	40.5	30.5	26	5.7	2.9
YS-48	57.9	60.2	97.1	100.7	64.6	52.1	8.8	8.8	17.5	16.8	45.3	41.1	28.6	27.2	5.0	2.5
YS-49	55.4	60.5	95.7	100.8	64.3	53	8.8	8.9	16.7	15.6	43.9	42.4	28.9	30.6	5.6	3.2
YS-50	51.7	59.3	95.7	98.5	67.7	63.5	9.3	9.5	17.1	16.9	48.8	40.2	32	34.2	6.0	3.8
YS-51	63.3	66.6	98.8	106.4	62.1	53	7.9	8	18.6	17	45.2	37.9	26.9	25.4	5.4	3.2
YS-52	56.9	62	94.9	99.4	62.4	54.2	7.1	7.8	15.5	15.7	44.5	42.4	27.2	27.9	5.6	2.6
YS-53	58.1	62.5	97.7	103.3	64.1	55.4	8.7	8.3	17.6	15.3	44.1	46.5	29.2	33.6	5.2	4.2
YS-54	52.7	55.6	94.9	91.3	60.1	45	7.3	7.8	16.5	15.4	44.6	39.2	26.6	26.4	5.5	2.8
YS-55	62.6	64.8	97.9	103.7	67.9	53.2	8.2	7.9	18.8	17.6	45.2	45.6	25.5	26.1	5.8	3.1
YS-56	58.1	62.8	98.4	104.8	68.3	60.1	7.5	7.8	18.5	16.5	48.4	48.8	28.8	26.2	6.0	3.9
YS-57	63.6	66.2	103.3	105.5	61.1	51.6	8.8	8.3	17.2	16	42.4	38.3	23	21.1	4.2	1.9
YS-58	53.2	60.9	97.5	99.4	67	54.8	7.3	7.5	16.5	15.2	40.6	37.5	28.4	28.3	5.1	2.1
YS-59	59	65.8	99.7	104	58.5	50.3	8	8.2	18.3	16.6	46.3	53	24.6	28	4.7	3.4
YS-60	54.6	60.2	97.6	97.2	61.1	48.1	6.5	6.7	17.1	14.9	46.3	39.7	25.6	22.4	3.7	1.7

Appendix 3.2. (continued)

Genotype	DH		DM		PH		SL		SS		KS		TKW		GY	
Code	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS
YS-61	53.6	56.5	95.3	94.3	59	49.7	7.3	7	15.6	14	42.3	36.7	31.2	31.7	6.0	2.9
YS-62	60.4	62.6	97	97.4	56.1	42	7.9	7.6	17.4	15.3	49.3	44.4	24.6	22.5	5.2	2.0
YS-63	59	59.3	96.4	97.3	61.1	49.2	7.7	8	15.9	15.6	42.9	40.5	27.2	25.1	5.0	2.9
YS-64	51.9	59.1	95.5	95	59.1	49.7	7.5	7.9	15.8	16	40.7	35.9	28.3	26.5	5.0	2.8
YS-65	58.8	61.8	100.2	102.2	63.1	52.5	7.4	7.9	16.2	16.4	42.4	43.5	28.2	28.4	4.6	2.9
YS-66	66.9	68.5	100.9	107	60.3	51.5	7.8	8	17.3	19.4	35.2	43.4	21.6	24.4	2.9	0.9
YS-67	69.4	70.3	104.6	111	62.3	53	7.9	7.8	16.7	16.9	41.1	52.8	27.1	29.1	4.6	1.5
YS-68	62	65	98.5	104.3	58	47.7	7.6	8.3	17	16.9	42	47.3	26	26.4	4.9	2.4
YS-69	52.9	57.9	95.9	92.6	57.3	45.7	5.9	6	13.5	13.2	32.7	32.7	27.9	24.8	5.0	2.7
YS-70	67.2	70	101.7	111.7	65.2	58.3	8.4	8.4	17.5	16.5	35	38.1	25.2	29.6	4.8	3.2
YS-71	60.7	63.4	99	105.4	70.9	66.4	7.9	8.2	17.5	17	44.4	45	27.2	27.7	5.5	3.1
YS-72	59	60.6	96.2	94.5	61.5	49.5	7.2	7.3	16.8	16.2	44.1	44.3	26.7	27	6.0	2.9
YS-73	56	60	97.2	96	63.1	53.1	8.8	9.5	17.9	17.7	45.1	46.2	27.6	23.9	5.3	2.8
YS-74	63.3	66.2	99.7	99.8	63.6	51.1	7.8	8	18.8	17.8	47.1	45.3	28.5	26.5	5.9	2.1
YS-75	62.1	66.8	97.3	101	62.8	58.6	7.8	9	18.1	19.4	46.4	54.1	26.6	28.4	4.7	3.2
YS-76	55.1	58.3	96.4	95.2	61.8	53.5	7.9	8.4	18.3	17.2	48.1	49.5	29.7	26.7	5.9	3.5
YS-77	63.3	64	98.9	102.8	60.3	51	8.4	8.6	17.6	17.2	44.7	43.6	22.9	23	4.3	2.8
YS-78	52	57.8	95.6	94.2	68.1	52.1	7	7.2	17.1	15.9	49	43.1	29	23.4	4.9	1.7
YS-79	54.4	58.2	94.9	93.5	61.3	53.9	6.4	6.6	18.7	16.6	49.4	46	25.2	20	5.9	2.2
YS-80	60.3	65	97	101.3	59.6	56.5	7	8	15.8	16.6	45.5	55.6	26.7	28.2	5.0	3.1
YS-81	60.1	62.7	96.5	98	59	51.6	7.4	14	17.4	16.8	51.6	51.9	25.8	23.6	4.9	2.9
YS-82	54.6	57.8	95.7	93.8	64.4	55.8	8	8	15.7	15.2	42.6	43.1	30.7	29.9	6.5	3.4
YS-83	51.9	58.2	95.9	93.7	65.1	57.3	8.1	8.7	15.2	15	41.3	36	31.8	30.7	5.8	3.8
YS-84	59.8	58	96.1	91.5	62.1	55.5	8.5	8.1	17.4	17	29.1	39.7	28.5	31.1	3.4	1.0
YS-85	57.4	58.8	98	96.3	66.4	55.7	8	8.2	18.3	16.7	52.6	39.3	27.4	25.7	6.7	3.4
YS-86	69.1	71.3	102.4	111.7	66	52.3	7.7	8.3	16.1	16.7	34.1	35.2	27.6	29.5	5.3	2.0
YS-87	56.5	60.6	97.4	96.7	67.5	53.8	8.7	8.5	17.2	15.4	41.1	37.8	32.9	29.9	6.0	2.5
YS-88	50	55.1	95.2	90.8	71.1	54.5	7.7	7.8	15.1	14.6	46.1	32.3	31.7	29.6	6.0	2.8
YS-89	55.6	62.2	96.1	98.8	68.4	59.5	7.6	7.6	16.3	14.8	46.6	41.2	32.3	33	6.1	3.7
YS-90	52.6	57.4	96.3	94.9	68.7	54.8	7.7	7.6	17.7	15.7	46.4	41.4	32.9	28.7	7.4	3.4
YS-91	61.9	62.6	100.8	101.3	68.1	54.7	9.2	8.8	20.8	17.7	48.6	43.1	27.4	26.2	5.8	2.4
YS-92	51.6	59	96.2	97.6	64.2	57.6	8.1	8.4	16.4	15.2	43.1	39.1	29.5	27.5	6.4	4.3
YS-93	57.2	61.6	98.2	98	62.8	53.1	8.7	9	18	15.8	46.8	44.4	27	26.2	6.2	4.2
YS-94	60.1	61	97.2	98.1	67.9	56.4	8.6	8.7	17.7	17.2	45.3	41.7	29.2	27.5	5.3	2.6
YS-95	51.6	59.5	94.8	95.7	65	55.2	7.5	7.8	15.6	14.7	41.7	35.6	30.1	30	6.1	4.0
YS-96	54.1	58.8	98.2	95.1	64.8	53.5	8.8	8	17.9	15.3	48.4	32.2	31.1	30.7	6.8	2.7
YS-97	63.1	67.3	99.2	105.5	63.6	61.3	8.5	9.1	18.9	19.6	43.5	50.9	27.1	33.5	4.3	3.3
YS-98	58	62.9	97.1	102.3	71.7	62.5	9	9.1	17.8	16.3	47.2	38.8	31.5	29.7	5.5	3.3
YS-99	52.2	57.3	97.1	94.9	64.1	54.5	8.7	8.5	16.4	14.5	40.4	33.8	27.3	25.3	5.8	2.7
YS-100	56.2	60.6	97.1	97	68.2	54.7	8.4	8.6	16.8	14.3	48.3	38.5	29.4	27.4	5.8	2.4
YS-101	61.4	63	98.8	101.4	70.3	53	8.9	8.8	17.8	15.4	43.6	33.9	29.1	27.3	6.3	2.4
YS-102	50.3	53.3	95.1	92	63.9	48.8	7.6	7.5	15.4	13.5	42.7	32.9	28.6	26.3	6.3	2.3
YS-103	51.8	56.6	95.2	94.2	71.3	55.9	8.2	7.8	15.9	13.9	41.9	31	28.2	25.8	6.5	3.1
YS-104	51.3	58.6	97	93.4	69.7	56.6	8.3	8.1	17.2	15.6	47.2	32.2	30.2	26.3	6.4	3.2
YS-105	63.3	65	98.4	102.8	67.9	59.9	9.2	8.9	18.7	16.9	44.7	32.4	28.1	30	5.6	2.6
YS-106	57	59.8	99	94.2	66.7	52.2	8.4	8.2	16.9	15.2	41.6	31.6	32.3	28.2	7.2	2.1
YS-107	51.1	55.5	94.8	94.8	62.5	57.4	7.7	8	16	15.4	42.5	43.8	29.4	24.2	6.1	3.3
YS-108	55.1	59	96.5	93.9	63.6	50.4	8.6	8.4	17.4	16.6	44.5	39.5	29.5	26.1	5.9	2.5
YS-109	47.5	52.7	94.1	91.3	61	58.6	6.8	7.4	13.3	13.5	41.5	37.8	32.6	28.7	4.9	2.9
YS-110	57.7	60.4	97.5	95.7	59.9	47.9	7.3	7.7	17	16.2	43.2	34.8	24.8	25	4.2	2.1
YS-111	56.1	60.7	96.3	98	64.4	57.2	8	8.6	15.6	16.6	42.7	34.6	27.4	30.4	4.9	3.2
YS-112	55.1	60.6	95.7	99.6	65.6	59.4	8.2	8.8	16.1	17	40.1	37.9	30.3	29	5.9	3.7
YS-113	49.2	57.4	95.9	97.1	67.7	55.6	8.5	7.9	16.7	14.9	49.8	42.4	30	26.2	5.3	3.1
YS-114	51.7	55.4	98.1	98	67.5	55.7	9.1	9	17.6	15.8	49.6	39	27.2	26.6	5.0	2.4
YS-115	58.2	61	99.4	100.3	69.6	60.3	8.3	8.3	19.2	16.7	49.9	42.4	29.1	27.9	6.6	4.1
YS-116	51.3	56.6	99.3	97.8	69.3	58.8	7.7	8.3	16	16	41.6	46.2	26.8	23.6	5.4	2.3
YS-117	55.3	59.4	97.1	95.5	65	53	7.4	7.4	16.2	14.8	47.3	40.1	25.7	27	4.5	2.8
YS-118	59.1	61.9	98.6	100.5	72.1	56.1	8.9	9	18	16.1	44.5	36.2	26	26.8	4.7	1.9
YS-119	47.2	52.3	93	87.3	75.9	63.2	7.6	7.5	13.8	13.1	31.8	28.6	27.9	24.1	4.4	1.8
YS-120	51.9	56.5	95.4	99.7	67.7	64.4	8.9	8.5	16.7	15.7	43.6	42.1	27.3	25.8	5.8	3.1
Mean	57.1	60.4	97.6	98.3	64.8	54.6	8.1	8.2	16.9	15.8	43.9	39.6	28.8	27.5	5.6	2.9

DH, days to heading; DM, days to maturity; PH, plant height (cm); SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); NS, non-stressed conditions; DS, drought-stressed conditions

Appendix 3.3. Mean seed yield and drought selection indices among 120 wheat genotypes evaluated under drought-stressed and non-stressed conditions across five test sites

Genotype code	Yp	R	Ys	R	SSI	R	GMP	R	MP	R	HM	R	TOL	R	STI	R	YI	R	YSI	R	R
YS-1	4.6	104	2.3	99	1.1	50	3.2	111	3.4	111	3.1	106	2.3	68	0.4	111	0.8	99	0.5	71	93
YS-2	5.4	62	2.9	61	1	60	4.0	55	4.2	62	3.8	62	2.5	59	0.5	55	1	61	0.5	61	59.8
YS-3	4.6	103	2.9	66	0.8	89	3.6	93	3.7	98	3.5	80	1.7	98	0.5	93	1	66	0.6	32	81.8
YS-4	4.8	97	3.4	28	0.6	107	4.0	52	4.1	67	4.0	42	1.4	109	0.6	52	1 2	28	0.7	14	59.6
YS-5	4.4	109	2.5	88	1	63	3.3	106	3.4	110	3.2	103	2.0	91	0.4	106	0.8	88	0.6	58	92.2
YS-6	4.6	105	3.5	25	0.5	113	4.0	58	4.0	80	3.9	48	1.1	112	0.5	58	1 2	25	0.8	8	63.2
YS-7	4.5	107	3.5	22	0.5	115	4.0	56	4.0	79	3.9	46	1.0	116	0.5	56	1 2	22	0.8	6	62.5
YS-8	4.8	93	3.3	33	0.7	105	4.0	53	4.1	68	4.0	45	1.5	106	0.6	53	1 1	33	0.7	16	60.5
YS-9	4.2	115	3.2	44	0.5	112	3.7	91	3.7	102	3.6	70	1.0	114	0.5	91	1 1	44	0.8	9	79.2
YS-10	4.5	108	2.8	72	0.8	91	3.5	97	3.6	106	3.4	88	1.6	102	0.4	97	1	72	0.6	30	86.3
YS-11	4.1	117	3.7	18	0.2	118	3.9	69	3.9	89	3.9	55	0.4	119	0.5	69	1 3	18	0.9	3	67.5
YS-12	5.3	69	3.1	55	0.9	73	4.0	51	4.2	60	3.9	53	2.2	71	0.6	51	1	55	0.6	48	58.6
YS-13	5.5	59	4.0	11	0.6	111	4.7	14	4.8	20	4.7	11	1.5	107	0.8	14	1.4	11	0.7	10	36.8
YS-14	4.3	112	4.2	6	0	120	4.2	37	4.2	54	4.2	27	0.1	120	0.6	37	1.4	6	1	1	52
YS-15	5.3	70	3.7	20	0.7	104	4.4	28	4.5	36	4.3	22	1.7	101	0.7	28	1 2	20	0.7	17	44.6
YS-16	5.8	43	2.3	98	1.3	18	3.7	88	4.1	69	3.3	94	3.5	13	0.5	88	0.8	98	0.4	103	71.2
YS-17	5.2	78	2.4	92	1.2	35	3.5	98	3.8	96	3.3	97	2.8	45	0.4	98	0.8	92	0.5	86	81.7
YS-18	6.0	32	2.5	85	1.3	29	3.9	66	4.3	52	3.6	77	3.4	18	0.5	66	0 9	85	0.4	92	60.2
YS-19	5.3	66	3.1	52	0.9	75	4.1	50	4.2	56	3.9	51	2.2	72	0.6	50	1 1	52	0.6	46	57.05
YS-20	5.8	46	2.6	82	1.2	30	3.9	67	4.2	57	3.6	74	3.2	24	0.5	67	0 9	82	0.5	91	62
YS-21	5.3	68	2.1	107	1.3	16	3.3	105	3.7	101	3.0	107	3.2	23	0.4	105	0.7	107	0.4	105	84.4
YS-22	5.4	61	3.2	43	0.9	77	4.2	44	4.3	47	4.0	41	2.2	70	0.6	44	1 1	43	0.6	44	51.4
YS-23	4.8	96	3.0	57	0.8	85	3.8	84	3.9	91	3.7	68	1.8	96	0.5	84	1	57	0.6	36	75.4
YS-24	5.5	58	2.2	102	1.3	19	3.5	101	3.9	90	3.2	104	3.3	22	0.4	101	0.8	102	0.4	102	80.1
YS-25	5.3	73	3.4	31	0.8	93	4.2	41	4.3	46	4.1	33	1.9	93	0.6	41	1 1	31	0.6	28	51
YS-26	6.0	29	4.4	3	0.6	110	5.1	4	5.2	4	5.1	3	1.6	104	0.9	4	1 5	3	0.7	11	27.5
YS-27	6.3	14	2.4	93	1.3	15	3.9	70	4.3	44	3.5	83	3.9	8	0.5	70	0.8	93	0.4	106	59.6
YS-28	6.2	21	3.1	54	1.1	48	4.3	32	4.6	31	4.1	32	3.1	35	0.6	32	1	54	0.5	73	41.2
YS-29	5.1	81	4.3	4	0.3	117	4.7	17	4.7	25	4.7	12	0.8	117	0.7	17	1 5	4	0.9	4	39.8
YS-30	5.2	77	3.0	58	0.9	69	3.9	64	4.1	73	3.8	63	2.2	73	0.5	64	1	58	0.6	52	65.1
YS-31	5.9	37	4.1	10	0.7	103	4.9	9	5.0	10	4.8	8	1.9	95	0.8	9	1.4	10	0.7	18	30.9
YS-32	5.2	76	4.8	1	0.2	119	5.0	6	5.0	11	5.0	6	0.4	118	0.8	6	1.6	1	0.9	2	34.6
YS-33	6.2	20	3.6	21	0.9	74	4.7	16	4.9	15	4.5	17	2.6	51	0.8	16	1 2	21	0.6	47	29.8
YS-34	6.6	5	3.7	17	0.9	67	4.9	7	5.1	6	4.8	9	2.8	41	0.8	7	1 3	17	0.6	54	23
YS-35	4.8	95	3.5	24	0.6	109	4.1	48	4.1	65	4.0	40	1.3	110	0.6	48	1 2	24	0.7	12	57.5
YS-36	5.6	53	3.4	27	0.8	83	4.4	29	4.5	34	4.3	26	2.2	79	0.7	29	1 2	27	0.6	38	42.5
YS-37	5.9	41	3.3	37	1	64	4.4	30	4.6	33	4.2	29	2.6	50	0.7	30	1 1	37	0.6	57	40.8
YS-38	5.9	39	3.4	30	0.9	68	4.4	26	4.6	30	4.3	25	2.5	55	0.7	26	1 1	30	0.6	53	38.2
YS-39	6.3	15	2.9	64	1.2	33	4.2	36	4.6	32	3.9	47	3.4	19	0.6	36	1	64	0.5	88	43.4
YS-40	6.2	18	3.2	46	1.1	53	4.4	27	4.7	28	4.2	30	3.0	37	0.7	27	1 1	46	0.5	68	38
YS-41	6.5	8	4.4	2	0.7	102	5.3	1	5.4	1	5.2	1	2.1	85	1	1	1 5	2	0.7	19	22.2
YS-42	5.8	45	1.8	115	1.5	4	3.2	108	3.8	94	2.8	112	4.0	6	0.4	108	0.6	115	0.3	117	82.4
YS-43	6.2	17	3.0	56	1.1	45	4.4	31	4.6	29	4.1	34	3.2	26	0.6	31	1	56	0.5	76	40.1

Genotype code	Yp	R	Ys	R	SSI	R	GMP	R	MP	R	HM	R	TOL	R	STI	R	YI	R	YSI	R	R
YS-44	6.2	16	2 2	104	1.4	6	3.7	89	4.2	58	3.2	100	4.1	3	0 5	89	0.7	104	0.4	115	68.4
YS-45	5.2	75	2.7	79	1.1	54	3.8	79	4.0	82	3.6	76	2.5	56	0 5	79	0.9	79	0 5	67	72.6
YS-46	6.1	24	2 3	97	1.3	14	3.8	81	4.2	59	3.4	90	3.7	10	0 5	81	0.8	97	0.4	107	66
YS-47	5.7	51	2 9	59	1.1	55	4.1	47	4.3	48	3.9	56	2.7	47	0.6	47	1	59	0 5	66	53.5
YS-48	5.0	87	2 5	86	1.1	47	3.5	99	3.7	99	3.3	96	2.5	58	0.4	99	0.8	86	0 5	74	83.1
YS-49	5.6	54	3 2	42	0.9	71	4.2	38	4.4	42	4.1	35	2.4	65	0.6	38	1.1	42	0.6	50	47.7
YS-50	6.0	33	3.8	14	0.8	92	4.7	13	4.9	16	4.6	15	2.2	77	0.8	13	1.3	14	0.6	29	31.6
YS-51	5.4	64	3 2	38	0.9	80	4.2	43	4.3	45	4.1	37	2.2	78	0.6	43	1.1	38	0.6	41	50.7
YS-52	5.6	52	2.6	81	1.2	37	3.8	72	4.1	66	3.6	75	3.0	39	0 5	72	0.9	81	0 5	84	65.9
YS-53	5.2	74	4 2	8	0.5	116	4.7	18	4.7	24	4.6	13	1.1	113	0.7	18	1.4	8	0.8	5	39.7
YS-54	5.5	57	2.8	74	1.1	49	3.9	62	4.1	63	3.7	66	2.8	44	0 5	62	0.9	74	0 5	72	62.3
YS-55	5.8	48	3 1	53	1	57	4.2	39	4.4	40	4.0	38	2.7	48	0.6	39	1.1	53	0 5	64	47.9
YS-56	6.0	30	3 9	13	0.8	94	4.8	10	4.9	13	4.7	10	2.1	82	0.8	10	1.3	13	0.7	27	30.2
YS-57	4.2	114	1 9	112	1.2	32	2.8	115	3.1	116	2.6	114	2.3	66	0 3	115	0.7	112	0 5	89	98.5
YS-58	5.1	80	2 1	109	1.3	21	3.2	107	3.6	107	2.9	108	3.1	36	0.4	107	0.7	109	0.4	100	88.4
YS-59	4.7	99	3.4	32	0.6	108	4.0	59	4.0	77	3.9	52	1.3	111	0 5	59	1.1	32	0.7	13	64.2
YS-60	3.7	118	1.7	117	1.2	31	2.5	118	2.7	118	2.3	117	2.0	88	0 2	118	0.6	117	0 5	90	103.2
YS-61	6.0	28	2 9	60	1.1	42	4.2	40	4.5	35	4.0	44	3.1	34	0.6	40	1	60	0 5	79	46.2
YS-62	5.2	79	2.0	110	1.3	17	3.2	110	3.6	108	2.9	109	3.1	31	0.4	110	0.7	110	0.4	104	88.8
YS-63	5.0	84	2 9	67	0.9	70	3.8	77	3.9	84	3.6	69	2.1	81	0 5	77	1	67	0.6	51	72.7
YS-64	5.0	82	2.8	71	1	65	3.8	80	3.9	85	3.6	71	2.2	76	0 5	80	1	71	0.6	56	73.7
YS-65	4.6	101	2 9	65	0.8	87	3.6	92	3.7	97	3.5	78	1.7	97	0 5	92	1	65	0.6	34	80.8
YS-66	2.9	120	0 9	120	1.5	3	1.6	120	1.9	120	1.3	120	2.0	89	0 1	120	0.3	120	0 3	118	105
YS-67	4.6	102	1 5	118	1.5	5	2.6	117	3.0	117	2.2	118	3.1	29	0 2	117	0.5	118	0 3	116	95.7
YS-68	4.9	89	2.4	94	1.1	44	3.4	104	3.7	104	3.2	99	2.5	57	0.4	104	0.8	94	0 5	77	86.6
YS-69	5.0	85	2.7	77	1	62	3.7	87	3.9	92	3.5	81	2.3	69	0 5	87	0.9	77	0.6	59	77.6
YS-70	4.8	94	3 2	45	0.7	97	3.9	63	4.0	81	3.8	61	1.6	103	0 5	63	1.1	45	0.7	24	67.6
YS-71	5.5	60	3 1	49	1	66	4.1	45	4.3	49	4.0	43	2.4	64	0.6	45	1.1	49	0.6	55	52.5
YS-72	6.0	27	2 9	63	1.1	40	4.2	42	4.5	37	3.9	50	3.1	30	0.6	42	1	63	0 5	81	47.5
YS-73	5.3	72	2.8	76	1	56	3.8	74	4.0	78	3.6	72	2.5	54	0 5	74	0.9	76	0 5	65	69.7
YS-74	5.9	35	2 1	105	1.4	9	3.6	96	4.0	75	3.1	105	3.8	9	0.4	96	0.7	105	0.4	112	74.7
YS-75	4.7	98	3 2	39	0.7	106	3.9	65	4.0	83	3.8	60	1.4	108	0 5	65	1.1	39	0.7	15	67.8
YS-76	5.9	38	3 5	23	0.9	78	4.5	22	4.7	26	4.4	21	2.4	61	0.7	22	1.2	23	0.6	43	35.7
YS-77	4.3	113	2.8	73	0.8	95	3.4	103	3.5	109	3.4	91	1.5	105	0.4	103	0.9	73	0.7	26	89.1
YS-78	4.9	92	1.7	116	1.4	8	2.9	114	3.3	112	2.6	116	3.1	32	0 3	114	0.6	116	0.4	113	93.3
YS-79	5.9	40	2 2	103	1.4	11	3.6	94	4.0	76	3.2	102	3.7	11	0.4	94	0.7	103	0.4	110	74.4
YS-80	5.0	83	3 1	48	0.8	86	4.0	60	4.1	72	3.9	59	1.9	94	0 5	60	1.1	48	0.6	35	64.5
YS-81	4.9	88	2 9	68	0.9	72	3.8	85	3.9	88	3.6	73	2.1	84	0 5	85	1	68	0.6	49	76
YS-82	6.5	9	3.4	26	1	58	4.7	15	5.0	12	4.5	20	3.0	38	0.8	15	1.2	26	0 5	63	28.2
YS-83	5.8	50	3.8	15	0.8	96	4.7	20	4.8	21	4.6	16	2.0	87	0.7	20	1.3	15	0.7	25	36.5
YS-84	3.4	119	1.0	119	1.5	2	1.9	119	2.2	119	1.6	119	2.4	63	0 1	119	0.4	119	0 3	119	101.7
YS-85	6.7	4	3.4	29	1.1	52	4.8	11	5.1	7	4.5	18	3.3	21	0.8	11	1.2	29	0 5	69	25.1
YS-86	5.3	65	2.0	111	1.4	10	3.2	109	3.7	105	2.9	110	3.4	20	0.4	109	0.7	111	0.4	111	86.1
YS-87	6.0	26	2 5	87	1.3	23	3.9	71	4.2	53	3.5	82	3.6	12	0 5	71	0.8	87	0.4	98	61
YS-88	6.0	31	2.8	69	1.2	38	4.1	46	4.4	41	3.9	58	3.1	28	0.6	46	1	69	0 5	83	50.9

Appendix 3.3. (continued)

Genotype code	Yp	R	Ys	R	SSI	R	GMP	R	MP	R	HM	R	TOL	R	STI	R	YI	R	YSI	R	R⁻
YS-89	6.1	22	3.7	16	0.9	82	4.8	12	4.9	14	4.6	14	2.4	62	0.8	12	1.3	16	0.6	39	28.9
YS-90	7.4	1	2.8	75	1.4	12	4.5	23	5.1	8	4.0	39	4.6	2	0.7	23	0.9	75	0.4	109	36.7
YS-91	5.8	42	2.4	91	1.3	25	3.8	82	4.1	64	3.4	89	3.4	16	0.5	82	0.8	91	0.4	96	67.8
YS-92	6.4	10	4.3	5	0.7	100	5.2	2	5.4	2	5.1	2	2.1	80	0.9	2	1.5	5	0.7	21	22.9
YS-93	6.2	19	4.2	7	0.7	101	5.1	5	5.2	5	5.0	5	2.0	90	0.9	5	1.4	7	0.7	20	26.4
YS-94	5.3	71	2.6	84	1.1	41	3.7	90	3.9	86	3.4	87	2.7	46	0.5	90	0.9	84	0.5	80	75.9
YS-95	6.1	25	4.0	12	0.7	99	4.9	8	5.0	9	4.8	7	2.0	86	0.8	8	1.4	12	0.7	22	28.8
YS-96	6.8	3	2.7	80	1.3	20	4.3	34	4.7	22	3.9	57	4.1	4	0.6	34	0.9	80	0.4	101	43.5
YS-97	4.3	111	3.3	36	0.5	114	3.8	83	3.8	95	3.7	64	1.0	115	0.5	83	1.1	36	0.8	7	74.4
YS-98	5.5	56	3.3	34	0.9	81	4.3	33	4.4	39	4.2	31	2.2	75	0.6	33	1.1	34	0.6	40	45.6
YS-99	5.8	44	2.7	78	1.2	36	4.0	54	4.3	51	3.7	65	3.1	33	0.5	54	0.9	78	0.5	85	57.8
YS-100	5.8	49	2.4	96	1.3	24	3.7	86	4.1	71	3.4	92	3.4	17	0.5	86	0.8	96	0.4	97	71.4
YS-101	6.3	13	2.4	95	1.4	13	3.9	68	4.4	43	3.5	85	3.9	7	0.5	68	0.8	95	0.4	108	59.5
YS-102	6.3	12	2.3	100	1.4	7	3.8	76	4.3	50	3.3	93	4.1	5	0.5	76	0.8	100	0.4	114	63.3
YS-103	6.5	7	3.1	51	1.1	39	4.5	25	4.8	18	4.2	28	3.4	15	0.7	25	1.1	51	0.5	82	34.1
YS-104	6.4	11	3.2	40	1.1	51	4.6	21	4.8	17	4.3	24	3.2	25	0.7	21	1.1	40	0.5	70	32
YS-105	5.6	55	2.6	83	1.2	34	3.8	75	4.1	70	3.5	79	3.0	40	0.5	75	0.9	83	0.5	87	68.1
YS-106	7.2	2	2.1	106	1.5	1	3.9	61	4.7	27	3.3	95	5.1	1	0.5	61	0.7	106	0.3	120	58
YS-107	6.1	23	3.3	35	1	61	4.5	24	4.7	23	4.3	23	2.8	43	0.7	24	1.1	35	0.6	60	35.1
YS-108	5.9	36	2.5	89	1.3	26	3.8	73	4.2	61	3.5	86	3.5	14	0.5	73	0.8	89	0.4	95	64.2
YS-109	4.9	90	2.9	62	0.9	79	3.8	78	3.9	87	3.7	67	2.0	92	0.5	78	1	62	0.6	42	73.7
YS-110	4.2	116	2.1	108	1.1	46	3.0	113	3.1	114	2.8	111	2.1	83	0.3	113	0.7	108	0.5	75	98.7
YS-111	4.9	91	3.2	41	0.7	98	4.0	57	4.1	74	3.9	54	1.7	100	0.5	57	1.1	41	0.7	23	63.6
YS-112	5.9	34	3.7	19	0.8	84	4.7	19	4.8	19	4.5	19	2.3	67	0.7	19	1.2	19	0.6	37	33.6
YS-113	5.3	66.5	3.1	50	0.9	76	4.1	49	4.2	55	3.9	49	2.2	74	0.6	49	1.1	50	0.6	45	56.35
YS-114	5.0	86	2.4	90	1.1	43	3.5	102	3.7	100	3.3	98	2.6	52	0.4	102	0.8	90	0.5	78	84.1
YS-115	6.6	6	4.1	9	0.8	90	5.2	3	5.3	3	5.1	4	2.5	60	0.9	3	1.4	9	0.6	31	21.8
YS-116	5.4	63	2.3	101	1.3	27	3.5	100	3.8	93	3.2	101	3.2	27	0.4	100	0.8	101	0.4	94	80.7
YS-117	4.5	106	2.8	70	0.8	88	3.6	95	3.7	103	3.5	84	1.7	99	0.4	95	1	70	0.6	33	84.3
YS-118	4.7	100	1.9	113	1.3	22	3.0	112	3.3	113	2.7	113	2.8	42	0.3	112	0.6	113	0.4	99	93.9
YS-119	4.4	110	1.8	114	1.3	28	2.8	116	3.1	115	2.6	115	2.5	53	0.3	116	0.6	114	0.4	93	97.4
YS-120	5.8	47	3.1	47	1	59	4.3	35	4.5	38	4.1	36	2.7	49	0.6	35	1.1	47	0.5	62	45.5

Yp, yield under non-stressed conditions; Ys, yield under drought-stressed conditions; R, rank; SSI, stress susceptibility index; GMP, geometric mean productivity; MP, mean productivity; HM, harmonic mean; TOL, tolerance index; STI, stress tolerance index; YI, yield index; YSI, yield stability index, R⁻.

Chapter 4. Genetic variability and association of yield and yield components among bread wheat genotypes under drought-stressed and non-stressed conditions

Abstract

Drought is one of the major constraints to wheat production and productivity globally. Developing drought-adapted wheat cultivars is paramount to increase wheat productivity under variable rainfall conditions. Understanding the genetic parameters and trait association is key to the development of improved wheat cultivars. The objective of this part of the study was to determine the extent of the genetic parameters and associations of yield and yield components, present in wheat genotypes, in order to design appropriate breeding strategies for yield improvement in wheat. The highest estimates for genetic variance were obtained for DH (54.0%), followed by SL (38.3%). The high heritability estimated for DH (94.4%), SL (90.2%) and SS (85.2%), coupled with a high rate of genetic advance, suggest that direct selection for these traits would be effective. GY exhibited low genetic advance (9%) and heritability (41.5%) estimates, which were concomitant with its polygenic and complex inheritance pattern. Correlation and path analyses revealed that PH and TKW were the most important contributing traits for improving grain yield under drought-stress condition.

Key words: correlation, drought-stress, genetic advance, heritability, path analysis, yield and yield components

4.1 Introduction

Developing drought-tolerant cultivars that can withstand terminal drought, which is prevalent in low-lying areas of Ethiopia, is key to improving wheat productivity. The success of any attempts to improve drought-tolerance in wheat will depend on the amount of genetic variation available. Semahegn et al. (2020) reported the presence of significant genetic variation for yield and related traits in bread wheat genotypes evaluated under drought-stressed and non-stressed conditions, which would provide important genetic resources for a drought-tolerance breeding program. However, there is a need to investigate the genetic basis and association among yield and yield components to design suitable breeding strategies for yield and drought-tolerance improvement. Furthermore, partitioning of variation into its components simplifies selection for agronomic traits contributing to grain yield under different environments, and enables the calculation of heritability estimates to predict genetic gains.

Heritability estimates help to predict the performance of progenies and to forecast potential genetic gains from selection (Ali et al., 2010). Traits with high heritability estimates accompanied with rapid genetic advances can be selected more effectively via direct selection (Ali et al., 2009b; Ali et al., 2010; Farshadfar et al., 2014; Okechukwu et al., 2015; Abraha et al., 2017). Yield components have been reported to have higher heritability estimates than grain yield *per se*, which facilitates indirect selection for grain yield under variable environments (Mathew et al., 2018). High genetic variance, heritability and genetic advance estimates could also be used to indicate a trait that is controlled by fewer genes and is most probably under the influence of additive genes. Such traits are improved effectively by crossing parents with desirable performance of economic traits.

In contrast, improving grain yield and drought-tolerance, which is a primary objective in most wheat-breeding programs, is more difficult because yield and drought-tolerance are complex traits controlled by many genes and therefore they exhibit lower heritability than their complementary agronomic traits. Also, grain yield and drought-tolerance exhibit variable heritability and genetic variance under variable environments, which make direct selection for yield and drought-tolerance unlikely to achieve significant genetic advance. Hence, selection of agronomic traits with favourable correlations with grain yield is used to indirectly improve grain yield and drought-tolerance in most crops, including wheat (Dodig et al., 2012; Asfaw and Blair, 2014; Lopes et al., 2015; Abraha et al., 2017; Mathew et al., 2018). Mwadzingeni et al. (2017) and Mathew et al. (2018) evaluated variance components in wheat and found that grain yield had the least genetic variance, heritability and genetic gain estimates, and recommended indirect selection using highly heritable and yield-influencing agronomic traits. However, other reports cite different estimates for the variance components, showing that variance components evaluated in different populations may only serve as a guide, and that evaluating each population individually is needed for practical breeding purposes.

The amount of genetic gain observed in grain yield after indirect selection via yield components is influenced by the association between the trait and grain yield. Thus, evaluating correlations among grain yield and its components would be helpful in selecting the target traits for simultaneous selection for high yield and drought-tolerance (Ali et al., 2009a; Kandic et al., 2009; Ali et al., 2011; Baranwal et al., 2012; Seher et al., 2015). Simple correlations may be inadequate in quantifying the importance of each yield component where there are several components directly and indirectly contributing to the final yield (Bizeti et al., 2004; Sreckov et al., 2011). Therefore, there is a need for a more in-depth analysis such as the path coefficient analysis, which partitions the observed correlation into direct and indirect contributory effects (Garcia del Moral et al., 2003; Ali et al., 2009a; Kandic et al., 2009; Baranwal et al., 2012). The variations in path coefficients of yield components in relation to grain yield have been reported by several studies (Subhani and Chowdhry, 2000; Khaliq et al., 2004; Anwar et al., 2009; Khan et al., 2010; Baranwal et al., 2012). These show that correlations and path coefficients are specific to a population under investigation and the prevailing environmental conditions. Therefore, there is a need to deduce the associations among yield and yield components for each population and environment to serve as a guide during the designing of a breeding program. Given the above background, the present investigation was undertaken with the aim to estimate genetic parameters, and the associations between yield and yield components of bread wheat genotypes evaluated under drought-stressed and non-stressed conditions to determine selection criteria as a guide for drought-tolerance breeding for enhanced yield gains in moisture-stressed areas of Ethiopia.

4.2 Materials and Methods

4.2.1 Plant materials and trial conditions

One hundred and twenty bread wheat genotypes comprising of 115 breeding lines that were being developed for drought-stress areas that were originally sourced from CIMMYT, and five standard checks that were released as drought-tolerant cultivars, were tested in five sites. Details of the genotypes along with their pedigree is described in Section 3.2.2. The test sites were Alem Tena, Debre Zeit, Dera, Kulumsa and Melkasa, and two contrasting moisture regimes were imposed using two different sowing dates as described in Section 3.2.2.

4.2.2 Data collection and analysis

Data were recorded on days to heading (DH), days to maturity (DM), plant height (PH), spike length (SL), number of spikelets per spike (SS), number of kernels per spike (KS), 1000-kernel weight (TKW), and grain yield (GY) as described in Section 3.2.3. Variance components for each trait were estimated using expected mean squares from the respective ANOVA results obtained using the GLM procedure in SAS version 9.3 (SAS Institute, 2012). Site and water regime were considered to be fixed factors, while genotype was considered as having a random effect. Negative variance estimates were considered as zero (Robinson et al., 1955; Annicchiarico, 1997). Expected mean squares were calculated following Shimelis and Shiringani (2010), as presented in Table 4.1. The broad sense heritability values were calculated following Allard (1996). Genetic advance (GA) was calculated according to Johnson et al. (1955). Pearson's correlation coefficients were estimated using the Statistical Software for Social Science version 24 (SPSS, 2016). Path coefficient analysis was conducted following Dewey and Lu (1959).

Table 4.1. Partial computation of expected mean squares for the wheat genotypes evaluated on five sites and two water regimes

Source of variation	Degree of freedom	Expected mean squares
Genotype (g)	g–1	$\sigma^2_e + r\sigma^2_{gsw} + rw\sigma^2_{gs} + rs\sigma^2_{gw} + \sigma^2_g$
Site (s)	s–1	–
Water regime (w)	w–1	–
g × s	(g–1)(s–1)	$\sigma^2_e + r\sigma^2_{gsw} + rs\sigma^2_{gw} + rw\sigma^2_{gs}$
g × w	(g–1)(w–1)	$\sigma^2_e + r\sigma^2_{gsw} + rs\sigma^2_{gw}$
g × s × w	(g–1)(s–1)(w–1)	$\sigma^2_e + r\sigma^2_{gsw}$
Residual	sw(g–1)(r–1)	σ^2_e

σ^2_e, environmental variance; σ^2_g, genotypic variance; σ^2_{gs}, genotype by site interaction variance; σ^2_{gw}, genotype by water regime interaction variance; σ^2_{gsw}, genotype by site by water regime interaction; r, replication.

4.3 Results

4.3.1 Variance components, heritability and genetic advance

The results from the separate and combined variance component analyses indicated that phenotypic variances were higher than genotypic variances for all the measured traits (Table 4.2). Under non-stressed conditions, the highest genotypic variance was recorded for DH (68.1%), followed by SL (55.3%) and SS (31.3%). Similarly, DH recorded the highest genetic variance of 62.3% under drought-stressed conditions followed by DM (35.9%) and SL (27.7%). Genetic variance decreased under drought-stressed conditions compared to non-stressed conditions for traits such as DH, SL, SS and KS.

The genetic variance for grain yield was 4.4% under non-stressed conditions as compared to 8.9% under drought-stressed conditions. A combined analysis of variance across all test environments was conducted to test the consistency of genetic and environmental effects on traits performances. Overall, the highest genotypic variance was recorded for DH (54.0%) followed by SL (38.6%), while GY (4.5%) had the lowest. Broad sense heritability values ranged from 28.1 to 94.2% under non-stressed conditions while a range of 44.6 to 91.5% was observed under drought-stressed conditions. Across the test environments, broad sense heritability values ranged between 41.5 and 94.4%. DH, SL and SS had high heritability estimates (above 79%) under both drought-stressed and non-stressed conditions. GY had the lowest heritability (<45%) under both conditions. The maximum genetic advance was recorded for SL (15.1%) followed by DH (14.6%), SS (12.7%) and KS (11.8%) under non-stressed conditions while GY (14.9%) showed the greatest genetic advance followed by SL (11.9%), TKW (10.9%) and SS (10.7%) under drought-stressed conditions. Across test environments, the greatest genetic advance was observed in SL (13.4%) followed by DH (12.2%), KS (12.2%) and SS (11.6%). Concomitant with high genetic variance and heritability estimates, the greatest genetic advance (>12%) was achieved in DH and SL under both non-stressed and drought-stressed conditions.

Table 4.2. Variance components, broad sense heritability and genetic advance for eight agronomic traits of 120 wheat genotypes evaluated across five sites under non-stressed and drought-stressed conditions

Component	DH		DM		PH		SL		SS		KS		TKW		GY	
	Var	%	Var	%	var	%	var	%	var	%	var	%	var	%	var	%
Non-stressed conditions																
Genotype (g)	17.52	68.1	2.51	28.0	8.29	19.0	0.39	55.3	1.34	31.3	9.92	17.3	2.71	15.0	0.12	4.4
g × s	2.67	10.4	1.06	11.8	6.27	14.4	0.06	9.0	0.31	7.2	7.93	13.8	4.68	25.8	0.47	17.9
Residual	5.53	21.5	5.39	60.2	29.13	66.7	0.25	35.7	2.64	61.5	39.62	68.9	10.73	59.2	2.04	77.6
Total variance	25.71		8.96		43.70		0.70		4.29		57.47		18.12		2.63	
$\delta^2 p$	18.60		3.27		12.46		0.42		1.67		15.45		4.72		0.42	
Heritability (%)	94.2		77.0		66.6		91.2		80.5		64.1		57.5		28.1	
GAM (%)	14.6		2.9		7.4		15.1		12.7		11.8		8.9		6.7	
Drought-stressed conditions																
Genotype (g)	9.44	62.3	8.00	35.9	9.28	24.8	0.28	27.7	0.86	29.2	6.20	12.3	3.30	17.9	0.10	8.9
g × s	3.04	20.0	5.06	22.7	4.41	11.8	0	0	0.28	9.4	2.60	5.2	3.31	18.0	0.22	19.1
Residual	2.68	17.7	9.25	41.4	23.65	63.3	0.73	72.3	1.81	61.6	41.42	82.5	11.79	64.1	0.82	72.1
Total variance	15.17		22.32		37.34		1.01		2.94		50.22		18.40		1.13	
$\delta^2 p$	10.32		9.94		12.52		0.35		1.1		10.86		5.14		0.23	
Heritability (%)	91.5		80.5		74.1		79.2		78.4		57.1		64.2		44.6	
GAM (%)	10.0		5.3		9.9		11.9		10.7		9.8		10.9		14.9	
Combined																
Genotype (g)	12.69	54.0	4.85	31.8	9.19	20.5	0.31	38.6	1.00	26.4	8.36	15.4	2.69	14.6	0.1	4.5
g × w	0	0	0.48	3.2	0.55	1.2	0.01	1.8	0.03	0.7	0.63	1.2	0	0	0	0
g × s	0	0	0.65	4.2	3.59	8.0	0	0	0.11	2.9	0	0	1.41	7.7	0.18	8.2
g × w × s	4.34	18.5	1.77	11.6	0.76	1.7	0.05	6.2	0.10	2.7	2.74	5.0	2.52	13.7	0.14	6.5
Residual	6.47	27.5	7.52	49.2	30.78	68.6	0.43	53.1	2.56	67.2	42.53	78.4	11.77	64.0	1.73	80.8
Total variance	23.51		15.28		44.87		0.81		3.81		54.25		18.39		2.14	
$\delta^2 p$	13.45		5.78		11.80		0.34		1.18		11.07		3.81		0.23	
Heritability (%)	94.4		84.0		77.9		90.2		85.2		75.5		70.6		41.5	
GAM (%)	12.2		4.3		9.0		13.4		11.6		12.2		10.0		9.0	

s, site; w, water regime; DH, days to heading; DM, days to maturity; PH, plant height (cm); SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); var, variance; GAM, genetic advance as percent of mean; $\delta^2 p$, phenotypic variance.

4.3.2 Correlation of yield and yield components

GY exhibited the strongest association with TKW under both drought-stressed and non-stressed conditions (Table 4.3). Under drought-stressed conditions, the coefficient of correlation between GY and TKW was 0.49 (Table 4.3, above diagonal) compared to 0.45 under non-stressed conditions (Table 4.3, below diagonal). GY also exhibited stronger associations with PH ($r=0.49$; $p<0.01$) and SL ($r=0.24$; $p<0.01$) under drought-stressed conditions. Likewise, there were significant correlations between GY with PH ($r=0.26$; $p<0.01$) and KS ($r=0.28$; $p<0.01$). GY exhibited negative correlations with DH ($r= -0.27$; $p<0.01$) and DM ($r= -0.19$; $p<0.05$) under non-stressed conditions while these traits showed non-significant association with GY under drought-stressed conditions. DH and DM showed strong positive correlations with each other ($r\geq0.80$; $p<0.01$) under both drought-stressed and non-stressed conditions, indicating selection for early maturing genotypes based on either of the two would be effective.

Table 4.3. Pearson's correlation coefficients (r) for eight agronomic traits of 120 wheat genotypes evaluated under drought-stressed and non-stressed conditions in five test sites

| | Drought-stressed conditions | | | | | | | |
	DH	DM	PH	SL	SS	KS	TKW	GY
DH	1	0.86**	0.06^{ns}	0.27**	0.61**	0.48**	0.09^{ns}	-0.01^{ns}
DM	0.80**	1	0.26**	0.37**	0.56**	0.50**	0.17^{ns}	0.15^{ns}
PH	-0.15^{ns}	0.00^{ns}	1	0.45**	0.27**	0.14^{ns}	0.48**	0.49**
SL	0.24**	0.31**	0.37**	1	0.58**	0.33**	0.35**	0.24**
SS	0.54**	0.53**	0.12^{ns}	0.53**	1	0.63**	0.10^{ns}	-0.04^{ns}
KS	0.01^{ns}	0.07^{ns}	0.08^{ns}	0.21*	0.57**	1	-0.02^{ns}	0.09^{ns}
TKW	$-0.48**$	$-0.35**$	0.28**	0.11^{ns}	$-0.31**$	-0.08^{ns}	1	0.49**
GY	$-0.27**$	$-0.19*$	0.26**	0.13^{ns}	0.08^{ns}	0.28**	0.45**	1
	Non-stressed conditions							

DH, days to heading; DM, days to maturity; PH, plant height (cm); SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); *, p<0.05; **, p<0.01; ns, non-significant.

4.3.3 Path coefficient analysis

Under non-stressed conditions, TKW, SS and KS recorded strong and positive direct effects, with values of 0.51, 0.23 and 0.20 on GY (Table 4.4, boldfaced text). In comparison, PH (0.37), TKW (0.26) and KS (0.23) exhibited strong positive direct effects on GY under drought-stressed conditions. SS (–0.44) showed the highest but negative direct effect on GY under drought-stressed conditions. The highest positive indirect effects on GY were 0.14 and 0.13, under non-stressed and drought-stressed conditions, respectively, exhibited by PH through TKW. Similarly, the high but negative indirect effects on GY under non-stressed conditions were exhibited through TKW by DH (–0.24) and DM (–0.18).

Under the drought-stressed conditions, DH (–0.27), DM (–0.25), SL (–0.26) and KS (–0.28) had substantial indirect reducing effects on GY through SS.

Table 4.4. The direct (bold faced values) and indirect effects of seven agronomic traits on grain yield of 120 wheat genotypes evaluated in drought-stressed and non-stressed conditions across the five test sites

		DH	DM	PH	SL	SS	KS	TKW	rGY
DH	NS	**–0.04**	–0.08	–0.02	–0.02	0.13	0.00	–0.24	–0.27**
	DS	**0.00**	0.07	0.02	0.03	–0.27	0.11	0.02	–0.01[ns]
DM	NS	–0.03	**–0.10**	0.00	–0.03	0.12	0.02	–0.18	–0.19*
	DS	0.00	**0.08**	0.10	0.05	–0.25	0.12	0.04	0.15[ns]
PH	NS	0.01	0.00	**0.11**	–0.03	0.03	0.02	0.14	0.26**
	DS	0.00	0.02	**0.37**	0.06	–0.12	0.03	0.13	0.49**
SL	NS	–0.01	–0.03	0.04	**–0.09**	0.12	0.04	0.05	0.13[ns]
	DS	0.00	0.03	0.17	**0.13**	–0.26	0.08	0.09	0.24**
SS	NS	–0.02	–0.05	0.01	–0.05	**0.23**	0.12	–0.16	0.08[ns]
	DS	0.00	0.05	0.10	0.07	**–0.44**	0.15	0.03	–0.04[ns]
KS	NS	0.00	–0.01	0.01	–0.02	0.13	**0.20**	–0.04	0.28**
	DS	0.00	0.04	0.05	0.04	–0.28	**0.23**	0.00	0.09[ns]
TKW	NS	0.02	0.03	0.03	–0.01	–0.07	–0.02	**0.51**	0.49**
	DS	0.00	0.01	0.18	0.04	–0.04	0.00	**0.26**	0.45**

NS, non-stressed conditions; DS, drought-stressed conditions; DH, days to heading; DM, days to maturity; PH, plant height (cm); SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); rGY, correlation with grain yield; *, $p<0.05$; **, $p<0.01$; ns, non-significant.

4.4 Discussion

4.4.1 Variance, heritability and genetic advance

The higher estimates for phenotypic variance compared to genotypic variance showed that the environment had greater effects on conditioning phenotypic traits than the genetic constitution of the test genotypes. The high environmental variance was expected since quantitative traits such as grain yield are known to be significantly affected by changes in environmental conditions such as water availability (Mwadzingeni et al., 2017; Mathew et al., 2018). This condition varied between the drought-stressed and non-stressed conditions, and from one site to another. The differential performance of the genotypes necessitates the need to separate the genetic from environmental variance components, and quantify the contribution of each component in order to devise efficient breeding strategies for target environments (Farshadfar et al., 2014). The genetic component is the most important for breeding purposes because it affects the portion of variation that is passed to offspring during the breeding process. The high genetic variance estimates for traits such as DH and SL, implied that these traits were

less influenced by environmental factors and can be effectively and directly selected based on their phenotypic expression (Shimelis and Shiringani, 2010). Similarly, Mathew et al. (2018) found high genetic variance estimates, above 75%, for DH under drought-stressed and non-stressed conditions and concluded that water availability had less impact on flowering compared to grain yield, which had lower genetic variance. The overall genetic variance for GY of 4.5% found in this study was also comparable to 3.9% reported by Mathew et al. (2018). Traits with low genetic variance, such as GY will be difficult to improve by direct selection under various environments since their selection would be confounded by large variation across the different test environments.

The heritability estimates ranged from moderate (41.5%, GY) to high (94.4%, DH), which is concomitant with variation in genetic control of different traits. Variation in heritability estimates imply that the different traits cannot be improved through the same breeding strategy. Similar ranges of heritability estimates (between 30 and 95%) for agronomic traits in wheat have been reported (Okechukwu et al., 2015; Mwadzingeni et al., 2016; Mathew et al., 2018). Baranwal et al. (2012) also reported high broad sense heritability estimates for DH, PH and KS. Similarly, Kandic et al. (2009) reported high broad sense heritability for DH. The heritability estimates for GY were moderate, which is attributable to the polygenic nature and complexity of GY. The heritability estimates for GY were comparable to 22.1, 38.9 and 39.0% reported by Ali et al. (2010), Mwadzingeni et al. (2016) and Okechukwu et al. (2015), respectively. However, heritability estimates as high as 74% have also been reported previously (Kandic et al., 2009; Farshadfar et al., 2014). High heritability estimates along with high genetic advance were calculated for DH, SL and SS, suggesting that these traits were under the influence of additive genes, which favours their improvement via direct selection, even under drought-stressed conditions (Ali et al., 2009a; Farshadfar et al., 2014). Several other studies have reported high heritability and genetic advance for traits such as DH, PH, SL and TKW (Ali et al., 2010; Gashaw et al., 2010; Riaz-ud-din et al., 2010). The high heritability and genetic advance of these traits would increase their importance in the improvement of drought-tolerance and GY.

4.4.2   Trait associations

Traits with poor genetic advance values and low heritability estimates are difficult to select directly and should be indirectly selected via related traits. Indirect selection for positively associated traits with high heritability and genetic advance values will enhance genotypic response to selection under various environmental conditions (Okechukwu et al., 2015; Mwadzingeni et al., 2017). The yield-related traits exhibited various levels of associations with GY in line with their genetic relationship and environmental impact. The associations showed variation between the different environments showing that the level of association between traits is influenced by prevailing conditions such as water availability. Therefore, selection strategies must account for these changes in trait association. TKW and PH exhibited the strongest positive direct associations with GY, which corroborated previous

studies (Kandic et al., 2009; Lopes et al., 2015; Okechukwu et al., 2015). Thus, selecting for taller plants with heavier seed weight would potentially improve GY. However, increased PH is often associated with lodging under particular circumstances (Tadesse et al., 2010; Okechukwu et al., 2015). Baranwal et al. (2012) reported significant and negative correlation between GY and PH, which would allow for simultaneous GY improvement and reduction in susceptibility to lodging. Early flowering and maturity were associated with higher GY under non-stressed conditions, which might be attributed to shorter vegetative period (Shavrukov et al., 2017) and an extended grain-filling period (Dodig et al., 2012).

4.5 Conclusions

PH and TKW had strong positive direct effect on GY under both drought-stressed and non-stressed conditions, which provides a basis for selection and improvement of GY under a wide range of environments. These traits, however, had moderate heritability that could be improved through selection at later generation, thereby enhancing drought-tolerance and grain yield. Further genotyping the materials with selected molecular markers such as SSR or SNPs will complement the present data set to select complementary genotypes for drought-tolerance breeding that integrate farmers' preferred traits.

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Chapter 5. Genetic diversity and population structure of bread wheat genotypes determined via SSR marker analysis

Abstract

Genetic diversity is fundamental for conducting successful crop improvement programs. The objectives of this study were to assess the genetic diversity and to deduce the population structure among bread wheat (*Triticum aestivum* L.) genotypes using simple sequence repeat (SSR) markers to identify divergent and complementary parental genotypes for drought-tolerance breeding. The selected 52 test genotypes were assessed using 20 SSR markers. SSR analysis identified a total of 181 alleles, with a mean of 10.1 alleles per locus. Population structure analysis grouped the test genotypes into three main populations. Analysis of molecular variance revealed that 85% of the variance was attributable to intra-population differences. Cluster analysis also grouped the test genotypes into three major groups. Overall, the SSR markers were useful and provided complementary data for selecting agronomically suitable parental lines for drought-tolerance breeding.

Keywords: bread wheat, cluster analysis, molecular variance, polymorphism, *Triticum aestivum*

5.1 Introduction

The development of improved cultivars is dependent on the availability of genetic diversity in the genetic pool for economic traits. Genetic diversity provides opportunities to identify suitable genotypes for use as parental lines in designed crosses to create superior progenies for selection. Understanding the extent and patterns of genetic diversity and relationships among the genetic resources are essential in devising appropriate strategies to attain maximum achievable genetic gains from selection. However, the development of superior cultivars has been curtailed by bottlenecks, such as limited genetic variation and progressive loss of the genetic diversity among crop species. Genetic diversity can be lost across time from selective breeding, and environmental and climate changes (Govindaraj et al., 2015; Henkrar et al., 2015). Selection of a few elite parental genotypes for use in modern breeding programs has significantly narrowed the genetic base, which predisposes crops to biotic and abiotic stresses (Van de Wouw et al., 2010; Keneni et al., 2012). Continuous assessment of genetic diversity to identify sources of new genetic variation is vital to developing high-performing cultivars that have the capacity to adapt to the ever-changing environment (Arora et al., 2014; Verma et al., 2019). According to Gill et al. (2014), functioning native agroecosystems as well as sources of new genetic diversity are needed to combat climate change.

Genetic variation and divergence among wheat genetic resources have been assessed using phenotypic and molecular methods, independently or in combination (Fufa et al., 2005; Dodig et al., 2010; Ayed et al., 2010; Laido et al., 2013; Arora et al., 2014). The advent of molecular markers has complemented phenotypic characterization (Fufa et al., 2005). Semahegn et al. (2020) reported substantial genotypic differences among sets of bread wheat genotypes for key agronomic traits under drought-stressed and non-stressed conditions. Phenotypic characteristics are key for ideotype breeding. However, germplasm characterization using phenotypic traits is subject to genotype by environment interaction effects that reduce the correlation between genotype and phenotype. The significant impact of environmental conditions makes phenotypic markers less accurate than DNA-based markers in evaluating genetic diversity for quantitative traits that are controlled by polygenes and influenced by environmental factors (Mulualem et al., 2018). Thus, phenotypic evaluation can over- or under-estimate the actual genetic diversity within genetic resources, depending on the prevailing environmental conditions. In some instances, phenotypic characterization can detect traits controlled by dominant genes in both the homozygous and heterozygote states, while traits controlled by recessive genes can only be expressed phenotypically when they occur in the homozygous state (Holland, 2007; Sackton and Hartl, 2016). The skewed observation towards dominant phenotypes distorts the identification of the total genetic diversity for breeding purposes. Molecular markers provide a direct measure of genetic diversity and circumvents the environmental influences, providing complementary data through an efficient assessment of genetic diversity in crop genetic resources (Verma et al., 2019).

Several types of molecular markers, including random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), single nucleotide polymorphism (SNP) and simple sequence repeat (SSR) or microsatellite markers, have been used in the genetic analysis of bread wheat (Mandoulakani et al., 2010; Cifci and Yagdi, 2012; Malik et al., 2013; Haile et al., 2013; Kumar et al., 2019). SSR markers are widely used in genetic studies because they are multi-allelic, chromosome-specific, contain highly polymorphic information and are ubiquitous across the genome (Haile et al., 2013; Khaled et al., 2015; Sönmezoğlu and Terzi, 2018). Several studies have successfully assessed genetic variation in wheat using SSR markers. For instance, 20 wheat genotypes were genotyped using 16 SSR markers by Poudel et al. (2019), revealing that the genotypes were significantly divergent and should be useful in developing breeding populations. Asmamaw et al. (2019) evaluated 160 genotypes of durum wheat (*Triticum turgidum* L.) and found significant genetic variation based on 12 SSR markers, while Chen et al. (2012) delineated the population structure and linkage disequilibrium among 90 genotypes of wheat using SSR markers. Therefore, the objectives of this part of the study were to assess the genetic diversity and to deduce the population structure among bread wheat genotypes using simple sequence repeat (SSR) markers. This should identify genetically divergent and complementary parental genotypes for use in future drought-tolerance breeding.

5.2 Materials and methods

5.2.1 Plant materials

The study used 52 bread wheat lines selected from a previous investigation in Section 3.2.2. that involved the screening of 120 genotypes. The test lines were selected for their desirable agronomic traits (earliness, plant height, spike length, spikelets per spike, kernel per spike, 1000-kernel weight and grain yield) and drought-tolerance. The details of the test materials, including their Stress Tolerance Index (STI) values, are presented in Table 5.1. Based on STI, the selected genotypes were classified into three categories, i.e., high drought-tolerance (HDT), medium drought-tolerance (MDT) and low drought-tolerance (LDT) (Table 5.1).

Table 5.1. Descriptions of the 52 bread wheat genotypes used in the study

N<u>o</u>	Genotype code	Pedigree	STI	Drought -tolerance level
1	YS-4	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/TEVEE'S'/BOBWHITE #1	0.6	MDT
2	YS-6	ATTILA 50Y//ATTILA/BCN/3/PFAU/MILAN	0.5	MDT
3	YS-7	OPATA/RAYON//KAUZ/3/2*MILAN/DUCULA	0.5	MDT
4	YS-8	QADANFER-11/REBWAH-11	0.6	MDT
5	YS-11	ATTILA/3*BCN//FLAG-2	0.5	MDT
6	YS-13	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	0.8	MDT
7	YS-14	CROC-1/AE.SQUARROSA (224)//OPATA/3/FLAG-7	0.6	MDT
8	YS-15	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	0.7	MDT
9	YS-25	KAUZ//MON/CROW?S?/3/VEE/PJN//2*KAUZ	0.6	MDT
10	YS-26	KAUZ//MON/CROW?S?/4/SERI.1B//KAUZ/HEVO/3/AMAD	0.9	HDT
11	YS-27	KAUZ//MON/CROW?S?/4/SERI.1B//KAUZ/HEVO/3/AMAD	0.5	MDT
12	YS-29	DEBEIRA/4/KAUZ//ALTAR 84/AOS/3/KAUZ	0.7	MDT
13	YS-31	HUBARA-5/ANGI-1	0.8	HDT
14	YS-32	SERI.1B//KAUZ/HEVO/3/AMAD/4/KAUZ/FLORKWA-1	0.8	HDT
15	YS-33	SERI.1B//KAUZ/HEVO/3/AMAD/4/PFAU/MILAN	0.8	MDT
16	YS-34	SOMAMA-9/NEJMAH-18	0.8	HDT
17	YS-35	QAFZAH-35/AMIR-2	0.6	MDT
18	YS-36	KAUZ//ALTAR 84/AOS/3/MILAN/DUCULA	0.7	MDT
19	YS-37	ESDA/SHWA//BCN/3/MILAN/PASTOR	0.7	MDT
20	YS-38	PFAU/MILAN	0.7	MDT
21	YS-39	KAUZ//ALTAR 84/AOS 3/KAUZ/3/ATTILA 50Y//ATTILA/BCN/4/PASTOR-6	0.6	MDT
22	YS-40	SAMIRA-9	0.7	MDT
23	YS-41	SHUHA-4//NS732/HER/3/ANGI-1	1.0	HDT
24	YS-43	KBG-01/FLAG-7	0.6	MDT
25	YS-44	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2	0.5	LDT
26	YS-50	SERI.1B//KAUZ/HEVO/3/AMAD/4/SHUHA-7//SERI 82/SHUHA'S'	0.8	MDT
27	YS-51	BAJ #1*2/CIRNO C 2008	0.6	MDT

Table 5.1. (continued)

No	Genotype code	Pedigree	STI	Drought-tolerance level
28	YS-53	BAVIS #1/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	0.7	MDT
29	YS-56	BECARD #1/3/PBW343*2/KUKUNA//PBW343*2/KUKUNA	0.8	MDT
30	YS-59	CHIR3/4/SIREN//ALTAR 84/AE.SQUARROSA (205)/3/3*BUC/5/PFAU/WEAVER/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	0.5	MDT
31	YS-76	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI	0.7	MDT
32	YS-82	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/5/CROC_1/AE.SQUARROSA (213)//PGO/3/CMH81.38/2*KAUZ/4/BERKUT/6/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	0.8	MDT
33	YS-83	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/7/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	0.7	MDT
34	YS-85	PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR/4/MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2	0.8	MDT
35	YS-89	PRL/2*PASTOR*2/7/TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ	0.8	MDT
36	YS-90	ROLF07*2/KIRITATI*2/10/PFAU/WEAVER*2//BRAMBLING/9/RABE/6/WRM/4/FN/3*TH//K58/2*N/3/AUS-6869/5/PELOTAS-ARTHUR/7/2*RABE/8/IRENA	0.7	MDT
37	YS-92	ROLF07/SAUAL*2/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI	0.9	HDT
38	YS-93	ROLF07/SAUAL/4/SHA7/VEE#5//ARIV92/3/PBW343*2/KUKUNA/5/ROLF07/SAUAL	0.9	HDT
39	YS-95	SAUAL/3/KAUZ/PASTOR//PBW343/4/KINGBIRD #1/5/SAUAL/KRONSTAD F2004	0.8	HDT
40	YS-96	SAUAL/3/KAUZ/PASTOR//PBW343/4/TRCH/SRTU//KACHU/5/SAUAL//PI 610750/ATTILA/3/SAUAL	0.6	MDT
41	YS-97	SAUAL/3/SW89.3064//CMH82.17/SERI/4/SAUAL/5/MUU #1/SAUAL//MUU	0.5	LDT
42	YS-98	SAUAL/MUTUS*2//PICAFLOR #1	0.6	MDT
43	YS-101	SUP152/3/TRCH/SRTU//KACHU	0.5	MDT
44	YS-102	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/TRCH/SRTU//KACHU	0.5	LDT
45	YS-103	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/WAXWING/SRTU//WAXWING/KIRITATI	0.7	MDT
46	YS-104	TC870344/GUI//TEMPORALERA M 87/AGR/3/2*WBLL1/5/ONIX/4/MILAN/KAUZ//PRINIA/3/BAV92	0.7	MDT
47	YS-106	TRAP#1/BOW/3/VEE/PJN/2*TUI/4/BAV92/RAYON/5/KACHU #1*2/8/ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR	0.5	MDT
48	YS-107	TUKURU//BAV92/RAYON/6/NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ*2/7/PVN	0.7	MDT
49	YS-112	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5/SOKOLL/3/PASTOR//HXL7573/2*BAU	0.7	MDT
50	YS-115	WAXWING/7/TNMU/6/CEP80111/CEP81165/5/IAC5/4/YKT406/3/AG/ASN//ATR/8/ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE#5//ARIV92	0.9	HDT
51	YS-24	P1.861/RDWG/4/KAUZ//ALTAR 84/AOS/3/KAUZ	0.4	LDT
52	YS-74	LIVINGSTON/5/2*W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	0.4	LDT

STI, stress tolerance index; HDT, high drought-tolerance; MDT, medium drought-tolerance; LDT, low drought-tolerance.

5.2.2 Genotyping

5.2.2.1 DNA sampling, SSR markers and polymerase chain reaction (PCR) amplification

The 52 bread wheat lines selected from a previous investigation in Section 3.2.2. that involved the screening of 120 genotypes, were planted in a glasshouse at the University of KwaZulu-Natal, South Africa. Fifteen seeds of each genotype were sown in a plastic pot and the seedlings were raised to the 4-leaf stage. Young, fresh leaves were collected from each genotype for DNA extraction. The fresh leaf samples were immediately sent to the SciCorp Laboratory in South Africa (SciCorp [Pty] Ltd) for DNA extraction and analysis. The DNA was extracted following the cetyl-trimethyl ammonium bromide (CTAB) method (Doyle and Doyle, 1990).

Twenty selected SSR markers were used in this study (Table 5.2). The SSR markers were selected because they were highly polymorphic and provided good genome coverage (Gupta et al., 2002). The primer sequences used for PCR amplification were according to Gupta et al. (2002). The PCR amplification was performed according to Röder et al. (1998). The SSR data were provided by SciCorp Laboratory using Excel sheet.

Table 5.2. Descriptions of the 20 microsatellite markers and their chromosome location used in genotyping 52 bread wheat lines

No	Markers	Primer sequences		Chromosome location
		Forward	Reverse	
1	WMC24	GTGAGCAATTTTGATTATACTG	TACCCTGATGCTGTAATATGTG	2A
2	WMC25	TCTGGCCAGGATCAATATTACT	TAAGATACATAGATCCAACACC	2AS,2BS,2DS
3	WMC44	GGTCTTCTGGGCTTTGATCCTG	TGTTGCTAGGGACCCGTAGTGG	1B
4	WMC47	GAAACAGGGTTAACCATGCCAA	ATGGTGCTGCAACAACATACA	7A
5	WMC104	TCTCCCTCATTAGAGTTGTCCA	ATGCAAGTTTAGAGCAACACCA	6BS
6	WMC149	ACAGACTTGGTTGGTGCCGAGC	ATGGGCGGGGGTGTAGAGTTTG	2B
7	WMC167	AGTGGTAATGAGGTGAAAGAAG	TCGGTCGTATATGCATGTAAAG	2D
8	WMC169	TACCCGAATCTGGAAAATCAAT	TGGAAGCTTGCTAACTTTGGAG	3A
9	WMC216	ACGTATCCAGACACTGTGGTAA	TAATGGTGGATCCATGATAGCC	7B
10	WMC232	GAGATTTGTTCATTTCATCTTCGCA	TATATTAAAGGTTAGAGGTAGTCAG	4AL
11	WMC233	GACGTCAAGAATCTTCGTCGGA	ATCTGCTGAGCAGATCGTGGTT	5DS
12	WMC243	CGTCATTTCCTCAAACACACCT	ACCGGCAGATGTTGACAATAGT	2BL
13	WMC245	GCTCAGATCATCCACCAACTTC	AGATGCTCTGGGAGAGTCCTTA	2AS,2BS,2DS
14	WMC254	AGTAATCTGGTCCTCTCTTCTTCT	AGGTAATCTCCGAGGTGCACTTCAT	1A
15	WMC256	CCAAATCTTCGAACAAGAACCC	ACCGATCGATGGTGTATACTGA	6A,6D
16	WMC257	GGCTACACATGCATACCTCT	CGTAGTGGGTGAATTTCGGA	2B
17	WMC261	GATGTGCATGTGAATCTCAAAAGTA	AAAGAGGGTCACAGAATAACCTAAA	2A
18	WMC262	GCTTTAACAAAGATCCAAGTGGCAT	GTAAACATCCAAAGTCGAACG	4A,5B
19	WMC264	CTCCATCTATTGAGCGAAGGTT	CAAGATGAAGCTCATGCAAGTG	3A
20	WMC265	GTGGATAACATCATGGTCAAC	TACTTCGCACTAGATGAGCCT	2B

5.2.2.2 SSR data analysis

Genetic parameters for individual markers were computed using the GenAlEx program version 6.5 (Peakall and Smouse, 2012). The genetic parameters included the number of alleles (Na), number of effective alleles (Ne), number of rare (unique) alleles (Nu), Shannon's information index (I), observed heterozygosity (Ho), expected heterozygosity (He) and polymorphic information content (PIC). The PIC values were calculated according to Anderson et al. (1993) as follows:

$$PIC = 1 - \sum P_i{}^2$$

where P_i is the frequency of the ith allele.

The population structure analysis was done using the Bayesian clustering method in STRUCTURE software version 2.3.4 (Pritchard et al., 2000). The parameters for the clustering method were set at 10,000 for the burn-in period and Markov Chain Monte Carlo (MCMC), and 10,000 iterations (Evanno et al., 2005). To obtain an accurate estimation of the number of populations, 20 runs were performed for each K-value (assumed number of subpopulations). The K values were assumed to be between 2 and 10. Further, delta K values were calculated and an appropriate K value was estimated using Evanno et al. (2005) method with the STRUCTURE Harvester program (Earl and von Holdt, 2012). No significant variation was found within and between drought-tolerance groups (data not shown). Analysis of molecular variance (AMOVA) was, therefore, carried out to partition the genetic variation into between and within population variance components of the populations identified by the structure analysis. The SSR data were subjected to dissimilarity coefficient analysis using standardized Euclidean distance to obtain a dissimilarity matrix in DARwin program version 6.01.21 (Perrier and Jacquemoud, 2006). The dissimilarity matrix was then used to construct a dendrogram via the Neighbour-Joining algorithm, based on 1000 bootstraps. This dissimilarity matrix was also used to conduct factorial analysis to visualize the genetic relationships among the genotypes in a two-dimensional plot using DARwin program version 6.01.21 (Perrier and Jacquemoud, 2006).

5.3 Results

5.3.1 Marker and genotype characterisation

Out of the 20 SSR markers selected, only 18 were used for analysis (Table 5.3). One of the markers, WMC 254, did not amplify during the PCR, while another marker, WMC 104, was monomorphic. Hence, these two markers were excluded from subsequent analysis. The sizes of the amplified fragments varied from 98 to 349bp. The marker WMC 261 had the smallest fragment while WMC 265 had the largest. In total, 181 alleles were identified with a mean of 10.06 alleles per locus among the genotypes. Among the identified alleles, 125 were effective and 30 were rare or unique alleles. The effective number of alleles identified per marker varied from 3.18 (for marker WMC 233) to 11.80 (WMC 25),

with a mean of 6.90 alleles per locus. Marker WMC 262 had eight rare alleles followed by WMC 25 and WMC 149, which had five and four rare alleles, respectively. The Shannon information index (I) ranged from 0.10 (exhibited by marker WMC 233) to 1.53 (WMC 25) with a mean value of 0.85. The maximum heterozygosity estimate was 0.74 recorded for Marker WMC 25 followed by 0.71 for Marker WMC 149 and 0.66 for Marker WMC 265. The mean heterozygosity estimate was 0.48. The maximum polymorphic information content was 0.74. The trend for PIC values among the markers was similar to the heterozygosity values exhibited by the markers. Thirteen markers had a PIC value greater than 0.5, while the mean PIC value was 0.48.

Table 5.3. Genetic parameters computed in 18 polymorphic SSR markers used to evaluate 52 bread wheat genotypes

Markers	Fragment size (bp)	Na	Ne	Nu	I	Ho	He	PIC
WMC 25	153-242	19.00	11.83	5.00	1.53	0.98	0.74	0.74
WMC 44	227-284	7.00	3.57	2.00	0.27	0.10	0.14	0.14
WMC 47	155-161	4.00	3.44	0.00	0.16	0.07	0.10	0.10
WMC 167	206-208	5.00	3.24	0.00	0.14	0.01	0.07	0.07
WMC 169	142-181	12.00	8.10	1.00	1.12	0.99	0.63	0.63
WMC 216	111-171	11.00	8.22	0.00	1.10	0.97	0.63	0.63
WMC 232	115-161	10.00	7.42	0.00	0.95	0.65	0.58	0.58
WMC 233	275-280	4.00	3.18	1.00	0.10	0.00	0.05	0.05
WMC 245	142-170	8.00	6.75	2.00	0.84	1.00	0.55	0.55
WMC 256	130-152	11.00	7.86	2.00	1.06	1.00	0.62	0.62
WMC 257	342-349	9.00	7.07	1.00	0.82	0.00	0.45	0.45
WMC 261	98-145	7.00	6.46	1.00	0.79	1.00	0.53	0.53
WMC 262	132-237	16.00	6.44	8.00	1.02	0.12	0.52	0.52
WMC 264	136-157	10.00	6.81	0.00	0.92	0.20	0.55	0.55
WMC 243	151-192	9.00	7.60	0.00	0.99	1.00	0.60	0.60
WMC 149	176-299	16.00	10.93	4.00	1.35	0.63	0.71	0.71
WMC 265	279-315	14.00	8.99	1.00	1.22	0.99	0.66	0.66
WMC 24	145-173	9.00	6.95	2.00	0.86	0.08	0.53	0.53
Total		181.00	124.86	30.00	–	–	–	–
Mean		10.06	6.94	1.70	0.85	0.54	0.48	0.48
SE		0.99	0.57	0.50	0.10	0.11	0.05	0.05

Na, number of alleles; Ne, number of effective alleles; Nu, number of unique alleles; I, Shannon's information index; Ho, observed heterozygosity; He, expected heterozygosity or gene diversity; PIC, polymorphic information content; SE, standard error.

5.3.2 Population structure of the 52 bread wheat genotypes

Population structure analysis grouped the 52 bread wheat genotypes into three major populations (Figure 5.1A and 5.1B). The first (I) and second (II) populations each comprised 38.5% of the total genotypes, while the third (III) population consisted of 23% of the genotypes. The populations consisted

of genotypes from different drought-tolerance groups. For instance, 44, 33 and 22% of the HDT genotypes were allocated into the first, second and third populations, respectively (data not shown).

Analysis of molecular variance showed that significant ($p<0.01$) variation was observed among individual genotypes within population, which accounted for 85% of the total variation (Table 5.4). The differences among the populations were also significant ($p<0.01$), although they explained only 15% of the total variation in the test germplasm (Table 5.4). Factor analysis showed that the first two principal axes accounted for 23.9 and 18.3% of the total variation among the genotypes, in that order (Figure 5.2).
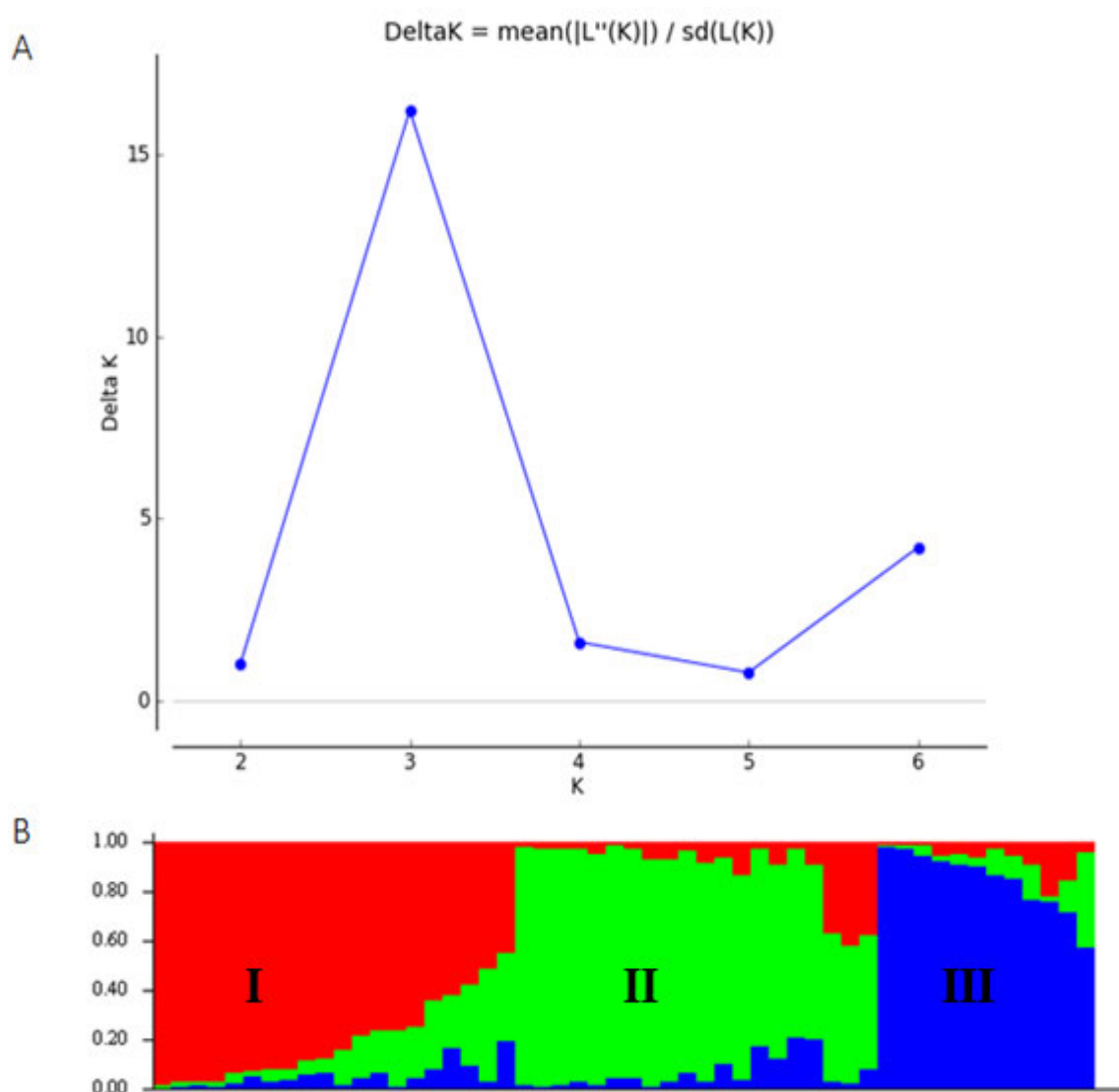
Figure 5.1 Population structure analysis of 52 bread wheat genotypes; (A) Delta K showing the number of populations, (B) Bar plot of populations sorted by kinship matrix.

Table 5.4. Analysis of molecular variance among and within populations in 52 bread wheat genotypes using 18 SSR markers

Source of variation	DF	SS	MS	Est. Var.	%	P-value
Among populations	2	77.127	38.563	1.705	15%	0.001
Within population	49	475.7	9.708	9.708	85%	0.001
Total	51	552.827		11.413	100%	

DF , degree of freedom; SS, sum of squares; MS, mean squares; Est. var., estimate of variance; %, percentage of total variation.
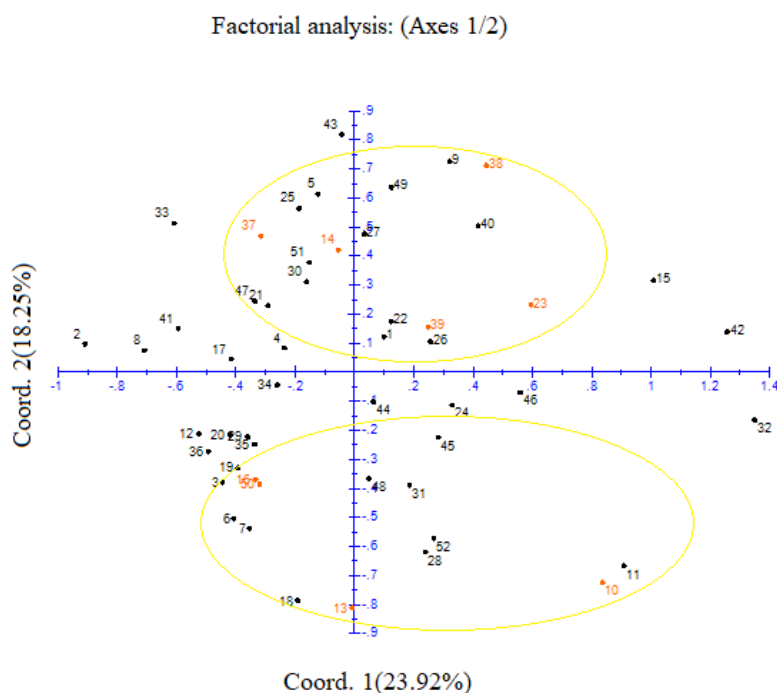
Figure 5.2 The first two principal coordinate axes elucidating the patterns of distribution of the 52 bread wheat genotypes evaluated using 18 SSR markers. Note: genotypes in red colour represented in each circle are highly drought-tolerant (HDT).

5.3.3   Genetic diversity and population patterns of SSR polymorphism

The genetic diversity and parameters of the test genotypes grouped under each population are presented in Table 5.5. The mean number of alleles per locus in genotypes belonging to population I was 3.3 and genotypes in populations II and III had 4.2 and 2.9 alleles per locus, respectively. Similarly, genotypes in population I had 2.3 effective number of alleles per locus while populations II and III had 2.7 and 2.2 effective number of alleles per locus, in that order. Population II contained a significantly higher number of unique alleles per locus, with a mean value of 1.1. The maximum Shannon information index was recorded for population II (1.00), followed by population I (0.88) and population III (0.80). The heterozygosity and PIC values for all the populations were similar (~ 0.50). The genetic distances for each pair of populations are presented in Table 5.6. The greatest genetic distance (0.189) was observed

99

between the first and third populations, while the lowest (0.086) was between the first and second populations.

Table 5.5. SSR- based genetic parameters among 52 bread wheat genotypes of the three populations

SSR marker parameters	I (20)	II (20)	III (12)
Na	3.33	4.17	2.94
Ne	2.33	2.69	2.24
Nu	0.4	1.05	0.71
I	0.88	1	0.8
He	0.51	0.52	0.46
PIC	0.51	0.52	0.46

Na, number of alleles; Ne, number of effective alleles; Nu, number of unique alleles; I, Shannon's information index; Ho, observed heterozygosity; He, expected heterozygosity; PIC, polymorphic information content.

Table 5.6. Pairwise Nei's genetic distance among the three populations of 52 bread wheat genotypes evaluated by 18 SSR markers

Populations	Genetic distance		
	I	II	III
I	0	0.086	0.189
II		0	0.174
III			0

5.3.4 Clustering of bread wheat genotypes based on SSR markers

The 52 genotypes were further clustered using the neighbour-joining algorithm based on SSR data (Figures 5.3). The dendrogram based on SSR markers delineated the genotypes into three major clusters, which was also similar to the Bayesian clustering. Clusters II, I and III comprised of 23, 17 and 12 genotypes in a decreasing order, respectively. HDT genotypes were distributed in all clusters (shown in red colours) in the dendrogram (Figures 5.3).

The genetic distance based on SSR data ranged between 0.5 and 2.39 (data not shown). The SSR analysis, involving HDT genotypes, the maximum genetic distance was observed between genotypes 'YS-26' and 'YS-92', followed by 'YS-31' and 'YS-93', and 'YS-93' and 'YS-115' with dissimilarity coefficients of 1.85, 1.82 and 1.67, respectively.
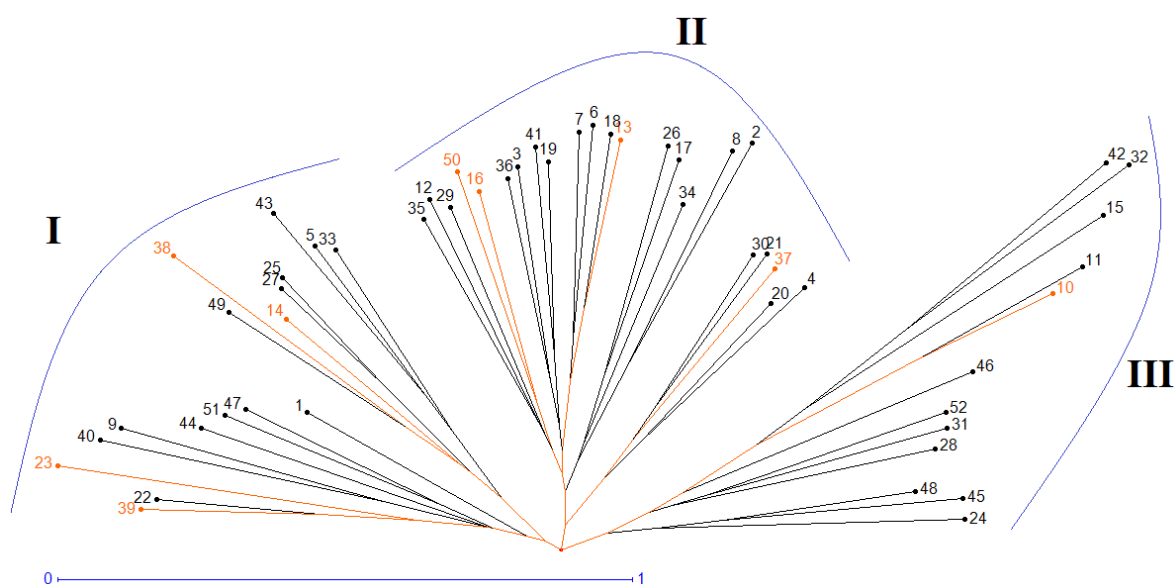
Figure 5.3 Dendrogram showing the genetic relationship among 52 bread wheat genotypes based on SSR data. Note: see genotypes code in Table 5.1.

5.4 Discussion

5.4.1   Marker and genotype characterization

A significant level of genetic variation was detected among the 52 bread wheat genotypes when evaluated using the selected SSR markers (Table 5.3). The mean number of alleles per locus was 10.1 compared with 9.3 reported by Jamalirad et al. (2012), who assessed the genetic diversity among 70 bread wheat genotypes using 40 polymorphic SSR markers. The number of alleles per locus found in this study was significantly higher than the 3.1 alleles per locus reported by Arora et al. (2014), who evaluated 319 Indian wheat varieties using 16 polymorphic primers. Sönmezoğlu and Terzi (2018) reported 5.9 alleles per locus from a study in which they assessed the genetic diversity among 10 cultivars and 9 breeding lines of bread wheat in Turkey using microsatellite markers. Genetic composition influences the allelic diversity in a population, which influences the number of alleles identifiable per locus. In addition, different markers have varied ability to discriminate the genotypes and this is directly linked to the number of alleles that can be potentially identified at different loci. In the current study, the mean number of effective alleles per locus was 6.9, suggesting that the SSR markers were informative and that the test genotypes were genetically divergent.

It is important to assess the allelic diversity of a given set of populations to discern the genetic attributes. Markers WMC 262, WMC 25 and WMC 149 exhibited a considerable number of unique or rare alleles. Unique or rare alleles increase when they were linked to a specific phenotype, such as disease or drought-resistance (Reyes-Valdés et al., 2018) but can be detrimental if they are linked to recessive

101

deleterious genes. It is important to adapt a breeding strategy that increases or preserves the frequency of desirable rare alleles to maintain the allelic diversity in the resultant recombinant inbred lines. The higher mean values for Shannon information index, heterozygosity and PIC recorded in this study (Table 5.3) indicated that the tested germplasm exhibited considerable diversity. The high Shannon index of 0.85 highlights the genetic richness of the test population. Hence, the test populations represented divergent genotypes, which would be useful for widening the genetic base of the breeding population through developing new recombinant lines. Abouzied et al. (2013) reported a Shannon index of 0.45 among 15 bread and 30 durum wheat genotypes assessed by 11 SSR markers and concluded that there was adequate genetic diversity in the test germplasm for use in a breeding program. The level of gene diversity observed in this study was similar to the finding of Henkrar et al. (2015), who reported a mean gene diversity of 0.49 among Moroccan durum wheat cultivars assessed with 13 SSR markers.

The mean PIC value in this study was 0.48, which indicated that the markers were informative and effective. The PIC value estimates the probability of a marker being passed on to the offspring after recombination and can be used to trace markers that are in disequilibrium or describe allelic richness of a population (Meti et al., 2013; Salem and Sallam, 2016). Compared with the present findings, a mean PIC value of 0.48 was recorded among drought-tolerant wheat genotypes evaluated by Faheem et al. (2015). Dodig et al. (2010) and Slim et al. (2019) found higher mean PIC values of 0.61 among bread wheat and 0.57 among durum wheat genotypes. The number of alleles detected by a particular marker is positively associated with its PIC value (Dodig et al., 2010; Tekeu et al., 2017; Sönmezoğlu and Terzi, 2018; Slim et al., 2019). In the present study, the PIC value for WMC 262 marker was 0.52, which was much lower than the PIC value of 0.71 for the marker WMC 149. Both markers expressed 16 alleles per locus. The difference in their PIC values could be attributable to the presence of rare alleles relative to marker WMC162. Rare alleles are known to alter the level of polymorphisms detected by a gene locus (Dodig et al., 2010). Based on the allelic diversity exhibited by the presently used SSR markers, the tested germplasm possessed considerable diversity for further use in drought-tolerance breeding.

5.4.2 Population structure among 52 bread wheat genotypes

The population structure analysis separated the 52 genotypes into three major groups. A significant level of variation (85%) was attributed to the within-population component (Table 5.4), suggesting that intra-population selection should be effective in enhancing genetic gain. Variance among populations accounted for only 15% of the total variation. Thus, selection strategies that exploit between-populations variation would provide only a limited response to selection. Similarly, larger and more significant variation within populations compared to between populations was reported by other investigators, who also used SSR markers (Dodig et al., 2010; Arora et al., 2014; Henkrar et al., 2015). The first two principal axes together explained 42.2% of the total genetic variation, confirming the

outline of the distribution of the HDT genotypes found by the population structure analysis. This finding agrees with Dodig et al. (2010), who reported that associations of spring and winter wheat genotypes existed irrespective of the drought-tolerance of the genotypes. The genetic composition of drought-tolerant genotypes could be different, requiring combining drought-tolerance genes from various sources for selection (Dodig et al., 2010).

5.4.3 Genetic diversity and population patterns of SSR polymorphism

It is important to assess the genetic diversity of the genotypes present among the populations identified to enhance efficiency of selection for traits of interest (Dodig et al., 2010). The PIC and heterozygosity estimates of the populations showed that there was moderate diversity among the populations (Table 5.5). Highest gene diversity and polymorphisms were detected within populations; hence, unique individuals could be selected, maintaining high gene frequency of rare alleles. The largest genetic distance was observed between the first population and the third population (Table 5.6). Selection from these two populations should be prioritized to increase chances of creating the most divergent parents for breeding.

5.4.4 Clustering of bread wheat genotypes based on SSR markers

Genotypes were clustered into different groups based on SSR molecular markers. The allocation of genotypes in related clusters could be attributed to their genetic descent and common ancestry. Most of the test genotypes were sourced from CIMMYT and had been developed for the semi-arid regions, sharing related parentage. For instance, 23 of the genotypes included the parent KAUZ in their pedigree, whereas 15 genotypes had genes introgressed from PASTOR. Thus, there is a need to identify individual members of clusters based on their agronomic attributes, drought-tolerance and SSR profile to facilitate within and between cluster selections. Genetic distance was the highest between genotypes 'YS-26' and 'YS-92', between 'YS-31' and 'YS-93', and between 'YS-93' and 'YS-115'. This suggests that these genotypes were the most divergent, with possible complementary traits and should be exploited for developing breeding populations. Genotype 'YS-26', which was drought-tolerant, high yielding and stable genotype, was particularly genetically distant from several test genotypes, indicating its potential breeding value in future improvement program.

5.5 Conclusions

The SSR markers were useful and provided complementary data for selecting agronomically suitable parental lines for drought-tolerance breeding. The SSR markers used in this study were effective in discriminating among the test genotypes. Markers WMC 25, WMC 149 and WMC 265 were the most informative markers, with PIC values of 0.74, 0.71 and 0.66, respectively. The genotypes were grouped into three distinct populations. Intra-population selection is recommended over inter-population selection for identifying genetically divergent parents that complement phenotypic diversity for further crossing program.

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Chapter 6. Combining ability of bread wheat (*Triticum aestivum* L.) genotypes for yield and yield-related traits under drought-stressed and non-stressed conditions

Abstract

Drought is a major cause of reduced yields in dryland wheat production. Identifying suitable parental lines and deducing gene action in hybrid combinations for yield and component traits is a prerequisite to develop drought-tolerant varieties. The aim of this study was to determine the combining ability effects of selected wheat genotypes, thereby identifying appropriate parents and crosses, and to deduce the mode of gene action controlling the expression of yield and agronomic traits. Eight parental lines were selected and crossed using a half-diallel mating design. The parents and 28 crosses were evaluated at two sites representing drought-stressed and non-stressed conditions using a 6 x 6 simple lattice design. The genotypic effects were significant for all traits studied except grain-filling period (GFP) across the test environments. The parental line 'YS-32' was the best general combiner for days to heading (DH), days to maturity (DM), GFP and 1000-kernel weight (TKW) enabling direct selection for improved grain yield under drought-stressed condition. Parent 'YS-85' could also be used for improving grain yield under drought-stress condition due to its positive and significant GCA effect on grain yield (GY). Families such as 'YS-32' x 'YS-85', 'YS-102' x 'YS-82' and 'YS-102' x 'YS-92' were the best specific combiners for improving GY under drought-stressed condition. Both additive and non-additive gene effects were significant, conditioning the inheritance of DH, DM, spike length (SL), spikelets per spike (SS) and TKW under both drought-stressed and non-stressed conditions. The ratios of additive and non-additive gene effects for most traits, except plant height (PH) and GY, were close to 1.0, showing a preponderance of additive gene effects under drought-stressed condition. The identified parental lines and families with good GCA and SCA effects should be useful for population development and genetic advancement to enhance yield and agronomic traits in wheat under drought-affected agro-ecologies.

Keywords: agronomic traits, combining ability effects, drought-tolerance, gene action, genotypic variation

6.1 Introduction

Successful improvement of yield and drought-tolerance in wheat hinges on identifying genetic variation and selecting suitable parental lines that have high *per se* performance and are able to pass yield-influencing genes onto their progeny. Yield and drought-tolerance are complex polygenic traits that are best selected indirectly via related agronomic traits. Hence, assessing the combining ability effects of parental lines and their progenies, and the type of gene action that control phenotypic expression of agronomic traits in these populations would be helpful in a selection program. This will identify the most suitable parents and families, and identify the most appropriate breeding strategies to improve both yield and drought-tolerance. Appropriate parents and progenies are selected through progeny tests via combining ability evaluations (Singh et al., 2004; Fasahat et al., 2016).

Combining ability parameters indicate the ability of a set of genotypes to transmit desirable genes to their progenies through a defined mating design (Allard, 1960). Assessing the combining ability effects of a set of parental genotypes and their progenies for diverse traits will quantify the nature and magnitude of gene action involved in the inheritance of quantitative traits, as basis for selection. Two combining ability effects are distinguished, the general combining ability (GCA) and the specific combining ability (SCA). General combining ability of parents is the average and relative performance of parental lines, while specific combining ability (SCA) of progenies represents the performance of a particular cross relative to other hybrid combinations (Griffing, 1956). Parental lines that exhibit good GCA effects would be useful in population development or maintenance of pure lines, while crosses with good SCA effects would be useful for hybrid breeding, and in genetic advancement and development of pure line cultivars. The GCA component is indicative of additive gene action, whereas SCA provides an estimation for the non-additive gene action (Falconer, 1981). The preponderance of additive gene action conditioning agronomic traits provides opportunities for early generation selection in wheat (Joshi et al., 2004; Farhsadfar et al., 2013). Conversely, non-additive gene action controlling grain yield has been found to be predominant in early generation of wheat populations (Yao et al., 2011; Zahid et al., 2011). Hence, pure line selection would be effective after continuous selfing and homozygous population development (Bos and Caligari, 2008).

Various mating designs including the diallel (Griffing, 1956), North Carolina (Comstock and Robinson, 1948), and line x tester (Kempthorne, 1957) designs have been used to determine combining ability effects in various crops including wheat (Fasahat et al., 2016). The choice of a mating design depends on the objectives of the study, time, space, cost and other biological considerations. The diallel mating design has been used in genetic analysis of agronomic traits such as earliness to flowering and maturity, plant height and grain yield in wheat (Edwards et al., 1976; Subhani and Chowdhry, 2000; Khahani et al., 2017). Various diallel designs are available enabling the evaluation of the desired combinations of crosses developed from inbred lines or genetically divergent varieties (Awata et al., 2018).

Drought-tolerance is subject to genotype by environmental interaction. Environmental variance is a challenge in most drought-tolerance breeding programs. For instance, genotypes selected under optimal conditions may not perform well under drought-stress conditions. Thus, evaluating combining ability effects under contrasting environments will provide useful information to identify suitable parents and more productive progenies for the target production environments. Previously genetic variation of 120 bread wheat genotypes were evaluated using key agronomic traits and SSR molecular markers (Semahegn et al., 2020; Belete et al., 2020), and promising genotypes were selected with drought-tolerance and desirable agronomic traits. The identified genotypes are useful genetic resources for drought-tolerance breeding but their combining ability effects and the nature of gene action have not been evaluated previously in hybrid combinations. Therefore, the objectives of this part of the study were to determine combining ability effects of the selected wheat genotypes, thereby deducing gene action controlling traits of interest and identifying promising families for drought-stress conditions and to advance these families through the single seed descent selection method.

6.2 Materials and methods

6.2.1   Parental lines and generation of F1 crosses

Eight parental bread wheat genotypes, namely 'YS-53', 'YS-32', 'YS-102', YS-82', 'YS-85', 'YS-92', 'YS-106' and 'YS-115', were selected for promising agronomic traits (earliness, plant height, kernel per spike, spikelets per spike, 1000-kernel weight and grain yield) and drought-tolerance (see Section 3.2.2). Table 6.1 presents the details of the selected parents including their pedigree. The eight parents were crossed using a half-diallel mating design and 28 progenies developed. Crossing blocks were established in a screenhouse under natural conditions at the Kulumsa Agricultural Research Center (Figure 6.1). The parental lines were stagger-planted at two-week intervals to cater for differences in flowering and maturity and to ensure synchronized flowering and a continuous supply of pollen. Three plantings were conducted during the off-season between February to May 2019. Crosses were generated by hand emasculation of florets and subsequent pollination, following standard practices for wheat crossing (Curtis and Croy, 1958). All the 28 first filial generation (F1) crosses were generated successfully for the study (Table 6.2).

Figure 6.1 Crossing block at Kulumsa Agricultural Research Center

Table 6.1. Characteristics and pedigree of parental genotypes used in the study

Parents	Name/design ation	Pedigree	STI	Drought-tolerance level
YS-53	ETW17-341	BAVIS #1/6/MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	0.7	MDT
YS-32	ETW17-302	SERI.1B//KAUZ/HEVO/3/AMAD/4/KAUZ/FLORKWA-1	0.8	HDT
YS-102	ETW17-396	TACUPETO F2001/BRAMBLING/5/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR*2/6/TRCH/SRTU//KACHU	0.5	LDT
YS-82	ETW17-374	SHUHA-4//NS732/HER/3/ANGI-1	0.8	MDT
YS-85	ETW17-377	PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR/4/MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2	0.8	MDT
YS-92	ETW17-385	ROLF07/SAUAL*2/5/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI	0.9	HDT
YS-106	ETW17-400	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1*2/8/ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR	0.5	MDT
YS-115	ETW17-409	WAXWING/7/TNMU/6/CEP80111/CEP81165/5/IAC5/4/YKT406/3/AG/ASN//ATR/8/ATTILA/3*BCN//BAV92/3/TILHI/4/SHA7/VEE#5//ARIV92	0.9	HDT

STI, stress tolerance index; LDT, low drought-tolerant; HDT, high drought-tolerant; MDT, medium drought-tolerant.

Table 6.2. A half-diallel Method II scheme showing the parental lines and crosses used in the study

Parents	YS-53	YS-32	YS-102	YS-82	YS-85	YS-92	YS-106	YS-115
YS-53	X	YS-53 x YS-32	YS-53 x YS-102	YS-53 x YS-82	YS-53 x YS-85	YS-53 x YS-92	YS-53 x YS-106	YS-53 x YS-115
YS-32		X	YS-32 x YS-102	YS-32 x YS-82	YS-32 x YS-85	YS-32 x YS-92	YS-32 x YS-106	YS-32 x YS-115
YS-102			X	YS-102 x YS-82	YS-102 x YS-85	YS-102 x YS-92	YS-102 x YS-106	YS-102 x YS-115
YS-82				X	YS-82 x YS-85	YS-82 x YS-92	YS-82 x YS-106	YS-82 x YS-115
YS-85					X	YS-85 x YS-92	YS-85 x YS-106	YS-85 x YS-115
YS-92						X	YS-92 x YS-106	YS-92 x YS-115
YS-106							X	YS-106 x YS-115
YS-115								X

6.2.2 Study sites, treatments and experimental design

The study was conducted at two sites, namely Dera and Kulumsa, in Ethiopia during the main crop-growing season from July to November in 2019. Dera (39.3°19'E and 8.3°20'N) is representative of the major drought-prone areas of the country. This site is situated in the rift valley of Ethiopia at an altitude of 1500 m above sea level. The average annual rainfall is 811.4 mm with recurrent drought-stress and erratic rainfall distribution. The average monthly temperatures ranges between 13.74 and 29.37°C. The soil texture at Dera is predominantly clay. Kulumsa (39°9'E and 8°1'N) is located at 2200 m above sea level with long term annual precipitation of about 973.5 mm and temperatures ranging between 9.89 and 23.11°C. The soil type at Kulumsa is predominantly clay. Details of the weather conditions during the growing season at the two sites are presented in Figure 6.2. The experiment at Dera was planted on the 18th of July. The total rainfall received at this site was 353 mm, and was considered to be a drought-stressed environment. At the Kulumsa site, the planting occurred on the 10th of July and received a total rainfall of 509 mm, and was regarded as the non-stressed environment. The 36 genotypes, comprising of the 8 parental lines and their 28 F1 crosses, were evaluated at both sites using a 6×6 simple lattice design with two replications. The parents and their crosses each planted on a 2 m single row plot. Inter-row spacing was at 0.2 m. A row on either side of each plot was planted with the released cultivar 'Ogolcho' to provide uniform competition. Other cultural practices were carried out as per standard recommendation for wheat in the areas.
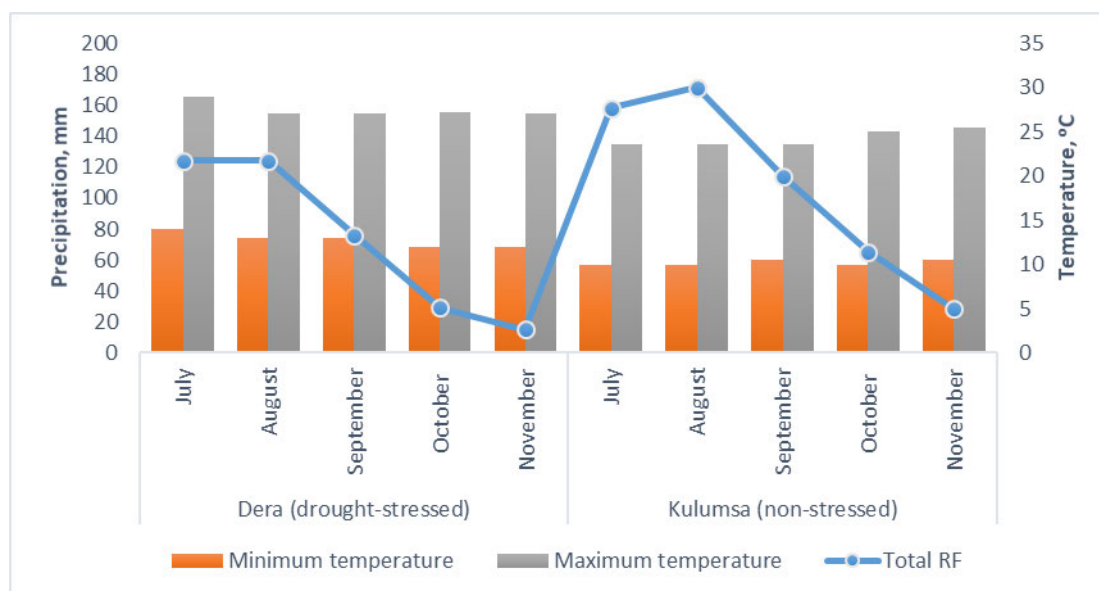

Figure 6.2 Rainfall and temperature conditions at the two experimental sites during the crop-growing season in 2019.

6.2.3 Data collection

Data on yield and yield components were collected at various stages of the crop cycle including days to 50% heading (DH), days to 90% maturity (DM), plant height (PH), spike length (SL), number of spikelets per spike (SS), number of kernels per spike (KS) and 1000-kernel weight (TKW) as described in Section 3.2.3. Grain-filling period (GFP) was recorded as the number of days from date of flowering to the date of maturity. Number of tillers (NT) was recorded as total number of tillers per plant. Finally, grain yield per plot (GY) was recorded and then converted into tons ha^{-1}.

6.2.4 Data analyses

A combined analysis of variance across sites was conducted using the SAS general linear model (GLM) procedure (SAS Institute, 2012) to test genotypic and site effects. Means were separated by the Fischer's protected Least Significant Difference test at a 5% probability level. A combining ability analysis of variance was carried out to compute the GCA and SCA effects using the DIALLEL-SAS05 program developed by Zhang et al. (2005) in SAS software version 9.3 (SAS Institute, 2012). The GCA and SCA effects were determined for each site using the Model I Method II of Griffings (1956) as follows:

$$Y_{ijk} = \mu + r_k + g_i + g_j + s_{ij} + \varepsilon_{ijk}$$

Where, Y_{ijk} = observed trait value for each experimental unit (i and j parents; k replication), μ = population mean, r_k = replication effect, g_i= GCA effect for the ith parent, g_j = GCA effect for jth parent, s_{ij} = SCA effects for the ijth F1 hybrid and ε_{ijk}= residual effect.

The relative contribution of GCA to SCA was estimated using the Baker's ratio (Baker, 1978): When the value close to 1, the additive effect is predominant, while it approaches to 0, non-additive gene effect is more pronounced.

$$\frac{GCA}{SCA} = \frac{2MS_{GCA}}{2MS_{GCA} + MS_{SCA}}$$

Where, MS_{GCA}= mean square of GCA and MS_{SCA}= mean square of SCA.

6.3 Results

6.3.1 Analysis of variance and mean performance of the genotypes

Combined analysis of variance showed that genotype by site interactions effects were significant for DH, DM, GFP and TKW. The genotype effects were significant ($p<0.01$) for all traits measured except GFP (Table 6.3).

The parents and their crosses exhibited differential response under drought-stressed and non-stressed conditions as presented in Tables 6.4a and 6.4b. The parents flowered taking 56 days on average under

drought-stressed condition. Under non-stressed condition, the parents took 68 days on average to flower (Table 6.4a). Similarly, parents showed a mean DM of 101 days under the drought-stressed condition (Table 6.4a). The parents matured in 117 days on average under the non-stressed condition (Table 6.4b). There was about a 42% decline in yield potential from 4.8 t ha^{-1} to 2.8 t ha^{-1} under the drought-stressed condition. Cross 'YS-32' x 'YS-82' had higher yield potential ($\geq$3.0 t ha^{-1}) compared to their respective high yielder parent under the drought-stressed condition. Families such as 'YS-53' x 'YS-82' and 'YS-32' x 'YS-92' yielded better ($\geq$4.8 t ha^{-1}) than their respective high yielder parents under the non-stressed condition. Similarly, crosses 'YS-32' x 'YS-82', 'YS-102' x 'YS-92' and 'YS-85' x 'YS-92' had higher yield level compared to the average performance of their parents under the drought-stressed condition, while crosses 'YS-53' x 'YS-82', 'YS-32' x 'YS-92' and 'YS-102' x 'YS-92' were better than the average performance of their parents under the non-stressed condition. Crosses 'YS-32' x 'YS-82' and 'YS-102' x 'YS-92' had higher grain yields than their parental mean performance under both drought-stressed and non- stressed conditions (Tables 6.4a and 6.4b).

Table 6.3. Mean squares for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under two different growing conditions

Source of variation	DF	Mean squares									
		DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
Site	1	4366.71**	8665.74**	170.60**	729.48**	28.82**	0.43^{ns}	78.02**	2197.32**	290.12**	134.46**
Replication (Site)	2	27.44**	61.33**	30.84^{ns}	131.11**	3.22**	0.40^{ns}	0.07^{ns}	109.44^{ns}	26.69**	0.15*
Block (Replication)(Site)	20	1.96^{ns}	17.29^{ns}	16.62^{ns}	16.72^{ns}	0.20^{ns}	0.27^{ns}	0.69^{ns}	53.76^{ns}	4.54^{ns}	0.03^{ns}
Genotype	35	43.34**	55.05**	50.78**	17.74^{ns}	0.55**	1.77**	7.45**	149.65**	32.1**	0.18**
Genotype × Site	35	3.12*	18.17*	18.29^{ns}	30.21**	0.15^{ns}	0.12^{ns}	0.83^{ns}	40.0^{ns}	9.18**	0.07^{ns}
Residual	50	1.78	9.94	16.7	11.27	0.18	0.15	0.62	47.38	3.55	0.04
CV (%)		2.2	2.9	4.5	7.1	11.1	4.4	4.5	17.1	6.3	5.5

DF, degree of freedom; DH, days to heading; DM, days to maturity; PH, plant height (cm); GFP, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); CV, coefficient of variation; *, p< 0.05; **, p< 0.01; ns, non-significant.

Table 6.4a. Means for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under drought-stressed condition at Dera Research Station

Parents/crosses	DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
Parents										
YS-53	52	99	82	47	4	8.2	17	44	26.1	3.1
YS-32	55	99	94	44	3	8.3	15	30	33.8	2.6
YS-102	59	106	88	47	3	8.7	18	23	30.7	2.9
YS-82	63	105	93	42	5	9.3	20	56	24.0	2.8
YS-85	56	99	84	44	4	9.0	17	40	29.5	2.5
YS-92	55	98	94	43	3	7.4	15	28	32.7	2.6
YS-106	51	99	86	48	4	9.2	17	40	30.5	3.1
YS-115	54	100	95	47	3	9.9	17	31	27.2	2.8
Crosses										
YS-53 x YS-32	55	101	87	42	4	8.3	17	47	28.7	2.7
YS-53 x YS-102	61	103	89	49	4	10.0	19	43	27.1	2.9
YS-53 x YS-82	52	101	96	44	4	11.0	17	45	28.4	2.8
YS-53 x YS-85	58	102	91	45	3	8.3	16	27	24.0	2.7
YS-53 x YS-92	54	99	96	48	3	8.5	15	33	30.6	2.9
YS-53 x YS-106	55	102	89	47	3	8.5	16	31	28.7	2.8
YS-53 x YS-115	52	99	80	44	3	8.3	16	36	31.1	2.5
YS-32 x YS-102	55	99	89	47	3	9.2	15	27	32.7	2.9
YS-32 x YS-82	54	101	86	50	3	8.6	17	38	26.7	3.4
YS-32 x YS-85	52	102	79	48	3	7.6	16	27	27.8	2.9
YS-32 x YS-92	53	101	82	44	3	8.2	14	31	33.1	2.4
YS-32 x YS-106	55	99	91	46	3	8.5	17	34	28.6	2.8
YS-32 x YS-115	54	100	91	50	3	9.4	16	32	25.7	3.1
YS-102 x YS-82	55	105	90	42	3	8.9	18	36	32.5	2.6
YS-102 x YS-85	59	101	93	42	4	8.3	16	41	21.1	2.6
YS-102 x YS-92	53	103	86	50	3	8.6	16	28	30.6	3.2
YS-102 x YS-106	54	100	87	47	3	8.8	15	37	37.3	2.8
YS-102 x YS-115	64	104	94	41	4	8.8	20	45	21.7	2.5
YS-82 x YS-85	54	99	79	45	4	9.1	17	39	24.7	2.8
YS-82 x YS-92	61	103	89	42	4	8.8	18	46	27.8	2.6
YS-82 x YS-106	63	102	88	39	4	10.0	18	38	30.4	2.5
YS-82 x YS-115	55	99	90	44	3	7.2	14	29	32.4	2.7
YS-85 x YS-92	52	99	94	47	3	8.5	16	33	27.5	3.0
YS-85 x YS-106	63	108	92	45	4	8.4	17	45	21.8	3.0
YS-85 x YS-115	51	100	82	49	3	8.4	15	34	30.1	2.9
YS-92 x YS-106	62	103	94	41	3	8.4	16	32	29.6	2.6
YS-92 x YS-115	63	99	90	36	3	9.3	18	37	30.6	2.3
YS-106 x YS-115	62	103	87	41	3	9.0	18	35	24.2	2.6
Mean	56	101	89	45	3	8.7	17	36	28.6	2.8
LSD (0.05)	3	4	-	6	-	0.9	2	-	4.6	0.5

DH, days to heading; DM, days to maturity; PH, plant height (cm); GF, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); LSD, least significant difference.

Table 6.4b. Means for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under non-stressed condition at Kulumsa Research Station

Parents/crosses	DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
Parents										
YS-53	62	119	83	57	5	8.3	18	49	29.0	4.8
YS-32	67	112	97	45	4	7.9	16	36	31.3	4.4
YS-102	71	125	89	54	5	8.9	21	48	35.4	4.9
YS-82	72	126	88	54	6	9.5	21	67	30.7	5.0
YS-85	69	109	92	40	4	9.0	19	41	29.4	4.6
YS-92	67	109	98	42	4	7.7	16	37	32.8	4.3
YS-106	62	108	94	46	4	8.5	17	38	30.0	4.9
YS-115	67	111	96	44	4	10.0	18	45	31.8	5.3
Crosses										
YS-53 x YS-32	68	118	94	51	4	8.6	19	46	28.2	4.7
YS-53 x YS-102	71	125	87	54	5	10.0	20	54	36.7	5.2
YS-53 x YS-82	66	116	99	50	5	10.0	18	50	35.6	5.4
YS-53 x YS-85	68	120	90	52	4	8.5	18	42	25.7	4.7
YS-53 x YS-92	67	116	91	50	4	8.4	17	37	35.7	4.6
YS-53 x YS-106	68	123	88	56	3	7.9	17	26	29.7	4.6
YS-53 x YS-115	65	113	93	48	4	8.5	17	46	30.8	4.7
YS-32 x YS-102	68	114	89	46	4	9.4	19	40	34.5	4.8
YS-32 x YS-82	66	116	85	50	4	8.5	18	41	29.4	4.8
YS-32 x YS-85	62	117	84	56	4	7.8	17	44	30.4	4.9
YS-32 x YS-92	67	113	89	47	4	8.7	17	41	33.2	4.8
YS-32 x YS-106	70	118	95	48	4	8.2	17	39	30.5	4.3
YS-32 x YS-115	66	112	95	46	4	9.4	17	45	32.3	5.0
YS-102 x YS-82	68	122	91	54	4	9.2	19	45	35.8	5.1
YS-102 x YS-85	70	123	86	53	4	8.8	17	43	27.1	4.6
YS-102 x YS-92	65	118	91	53	4	9.3	18	44	31.5	5.2
YS-102 x YS-106	67	120	89	53	4	8.9	17	41	34.0	4.8
YS-102 x YS-115	74	126	90	52	5	9.0	20	51	26.3	4.7
YS-82 x YS-85	66	112	86	46	5	9.8	19	52	30.1	5.1
YS-82 x YS-92	72	125	87	53	5	8.6	21	50	33.7	4.6
YS-82 x YS-106	72	126	88	54	4	10.0	22	44	36.3	5.1
YS-82 x YS-115	67	111	95	45	4	7.5	16	37	31.3	4.3
YS-85 x YS-92	63	107	101	44	5	8.6	18	50	31.3	4.9
YS-85 x YS-106	72	125	90	53	5	9.4	21	60	30.8	5.1
YS-85 x YS-115	65	108	92	43	4	8.2	16	44	32.5	4.7
YS-92 x YS-106	72	122	91	51	4	8.4	18	37	31.2	4.5
YS-92 x YS-115	71	126	88	55	5	9.9	20	51	34.5	4.8
YS-106 x YS-115	71	123	92	52	4	9.5	20	45	28.6	4.9
Mean	68	117	91	50	4	8.9	18	45	31.6	4.8
LSD (0.05)	2	8	5.5	8	1	0.8	2	12	3.0	0.4

DH, days to heading; DM, days to maturity; PH, plant height (cm); GF, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); LSD, least significant difference.

6.3.2 Combining ability effects among parents and crosses

The mean squares for GCA and SCA effects, and the Baker's ratios for yield and yield components under drought-stressed and non-stressed conditions are presented in Tables 6.5a and 6.5b, respectively. Under drought-stressed condition, the GCA effects were significant ($p<0.05$) for DH, DM, GFP, SL, SS and TKW except for GY (Table 6.5a). The SCA effects were also significant ($p<0.05$) for most traits except NT and KS. In comparison, the GCA and SCA effects were significant for all the traits under the non-stressed condition except GFP (Table 6.5b). The Baker's ratios were close to 1.0 for all assessed traits under both drought-stressed and non-stressed conditions except for PH and GY.

Table 6.5a. Fixed model ANOVA for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under drought-stressed condition at Dera Research Station

| Source of variation | DF | Mean squares | | | | | | | | | |
| | | Drought-stressed condition | | | | | | | | | |
		DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
GCA	7	31.23**	13.26**	27.44^{ns}	15.19*	0.46^{ns}	0.97**	5.22**	118.36^{ns}	33.7**	0.07^{ns}
SCA	28	33.67**	9.95**	47.85*	23.28**	0.32^{ns}	1.02**	3.9**	82.71^{ns}	25.23**	0.13**
Residual	35	2.37	4.07	24.73	6.32	0.27	0.21	0.59	68.96	5.38	0.05
Baker's ratio		0.65	0.73	0.53	0.57	0.74	0.66	0.73	0.74	0.73	0.52

DF, degree of freedom; DH, days to heading; DM, days to maturity; PH, plant height (cm); GFP, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); *, p< 0.05; ** , p< 0.01; ns, non-significant.

Table 6.5b. Fixed model ANOVA for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under non-stressed condition at Kulumsa Research Station

| Source of variation | DF | Mean squares | | | | | | | | | |
| | | Non-stressed condition | | | | | | | | | |
		DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
GCA	7	21.51**	114.48**	23.93*	59.59*	0.40**	1.06**	5.6**	115.18**	0.95**	0.12*
SCA	28	20.06**	63.85**	35.39**	29.19^{ns}	0.33**	1.13**	4.36**	94.16**	0.78**	0.16**
Residual	35	1.3	19.95	9.47	19.21	0.1	0.16	0.68	30.02	0.25	0.04
Baker's ratio		0.68	0.78	0.57	0.80	0.71	0.65	0.72	0.71	0.71	0.60

DF, degree of freedom; DH, days to heading; DM, days to maturity; PH, plant height (cm); GFP, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); *, p< 0.05; **, p< 0.01; ns, non-significant.

6.3.3 General and specific combining ability effects of parental lines and crosses

The parental lines and the test crosses exhibited variable GCA and SCA effects under both drought-stressed and non-stressed conditions (Tables 6.6a and 6.6b). Under the drought-stressed condition, parental lines 'YS-53' and 'YS-32' exhibited negative and significant GCA effects for DH in a desirable direction. Genotype 'YS-32' had desirable and significant GCA effect for DM, GFP and TKW. Desirable positive GCA effects for NT, SL, SS and KS were recorded in the parental line 'YS-82'. Only the parent 'YS-85' exhibited positive and significant GCA effects for GY (Table 6.6a). Under the non-stressed condition, parental lines 'YS-32' and 'YS-85' exhibited significant negative GCA effects for DH and DM. Parental lines 'YS-102' and 'YS-82' had significant positive GCA effects for SL, SS, KS, TKW and GY (Table 6.6b).

Seven crosses including 'YS-53' x 'YS115', 'YS-102' x 'YS82' and 'YS-102' x 'YS92' exhibited significant and negative SCA effects for DH under both drought-stressed and non-stressed conditions. Significant and positive SCA effects for GY were observed in the families 'YS-32' x 'YS-85', 'YS-102' x 'YS-82' and 'YS-102' x 'YS-92' under the drought-stressed condition (Table 6.6a). Crosses 'YS-53' x 'YS-82' and 'YS-53' x 'YS-115' had significant and negative SCA effects for PH under the non-stressed condition (Table 6.6b). Similarly, significant positive SCA values for GY were recorded for families 'YS-53' x 'YS-102', 'YS-53' x 'YS-82', 'YS-32' x 'YS-115', 'YS-82' x 'YS-106' and 'YS-85' x 'YS-106' under the non-stressed condition. Cross 'YS-102' x 'YS-92' had significant positive SCA for GY under both drought-stressed and non-stressed conditions.

Table 6.6a. General and specific combining ability effects for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under drought-stressed condition at Dera Research Station

Parents/Crosses	DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
	Parents GCA effects estimates									
YS-53	−1.37**	−0.44^{ns}	0.43^{ns}	0.93^{ns}	0.13^{ns}	0.13^{ns}	0 10^{ns}	2.10^{ns}	−0.26^{ns}	0.04^{ns}
YS-32	−2.18**	−1.00*	−1.45^{ns}	1.18*	−0.17^{ns}	−0.23*	−0.84**	−2.76^{ns}	1.10*	0.03^{ns}
YS-102	1.20**	1.44**	0.68^{ns}	0.24^{ns}	−0.06^{ns}	0.20^{ns}	0.50**	−0.91^{ns}	0.66^{ns}	0.01^{ns}
YS-82	0.76*	0.63^{ns}	0.18^{ns}	−0.13^{ns}	0.31*	0.30**	0.73**	4.95*	−0.18^{ns}	0.00^{ns}
YS-85	−0.68^{ns}	0.06^{ns}	−2.01^{ns}	0.74^{ns}	−0.02^{ns}	−0.28**	−0.34^{ns}	−0.28^{ns}	−2.74**	0 11*
YS-92	0.32^{ns}	−0.63^{ns}	1.80^{ns}	−0.95^{ns}	−0.15^{ns}	−0.28**	−0.53**	−0.47^{ns}	1.75**	−0.05^{ns}
YS-106	1.63**	0.69^{ns}	0.62^{ns}	−0.95^{ns}	0.04^{ns}	0.12^{ns}	0 31^{ns}	0.57^{ns}	0.35^{ns}	−0.04^{ns}
YS-115	0.32^{ns}	−0.75^{ns}	−0.26^{ns}	−1.07^{ns}	−0.08^{ns}	0.04^{ns}	0.07^{ns}	−1.20^{ns}	−0.67^{ns}	−0.09^{ns}
	Crosses SCA effects estimates									
YS-53 x YS-32	2.37*	1.50^{ns}	−0.99^{ns}	−0.87^{ns}	0.71*	−0.36^{ns}	0 93^{ns}	11.4*	−0.72^{ns}	−0.04^{ns}
YS-53 x YS-102	4.99**	1.06^{ns}	−1.12^{ns}	−3.93*	0.39^{ns}	1.26**	2.09**	6.21^{ns}	−1.82^{ns}	−0.10^{ns}
YS-53 x YS-82	−3.57**	−0.13^{ns}	6.38*	3.45*	0.13^{ns}	1.31**	−0.35^{ns}	2.15^{ns}	0.29^{ns}	0.13^{ns}
YS-53 x YS-85	3.87**	0.94^{ns}	3.57^{ns}	−2.93^{ns}	−0.65^{ns}	−0.28^{ns}	0.03^{ns}	−10.3^{ns}	−1.59^{ns}	−0.07^{ns}
YS-53 x YS-92	−1.13^{ns}	−1.38^{ns}	4.76^{ns}	−0.24^{ns}	−0.16^{ns}	−0.06^{ns}	−0.98*	−2.63^{ns}	0.52^{ns}	−0.09^{ns}
YS-53 x YS-106	−1.95*	0.81^{ns}	−1.05^{ns}	2.76^{ns}	−0.47^{ns}	−0.46^{ns}	−0.62^{ns}	−7.57^{ns}	0.02^{ns}	0.13^{ns}
YS-53 x YS-115	−3.13**	−0.75ns	−9.18**	2.38^{ns}	−0.07^{ns}	−0.63*	−0.78^{ns}	−1.20^{ns}	3.49*	0.13^{ns}
YS-32 x YS-102	−0.20^{ns}	−2.88*	0.76^{ns}	−2.68^{ns}	−0.31^{ns}	0.50^{ns}	−1.77**	−4.92^{ns}	2.36^{ns}	−0.28*
YS-32 x YS-82	−0.76^{ns}	−0.06^{ns}	−1.24^{ns}	0.70^{ns}	−0.02^{ns}	−0.24^{ns}	0 59^{ns}	−0.29^{ns}	−2.74^{ns}	0.09^{ns}
YS-32 x YS-85	−1.32^{ns}	2.00^{ns}	−6.55*	3.32*	−0.38^{ns}	−0.65*	0 17^{ns}	−6.16^{ns}	0.94^{ns}	0.53**
YS-32 x YS-92	−1.32^{ns}	1.69^{ns}	−7.37*	3.01^{ns}	0.03^{ns}	−0.01^{ns}	−0.85^{ns}	0.53^{ns}	1.73^{ns}	0.14^{ns}
YS-32 x YS-106	−0.63^{ns}	−2.13^{ns}	3.32^{ns}	−1.49^{ns}	−0.01^{ns}	−0.11^{ns}	1.02*	−0.21^{ns}	−1.39^{ns}	−0.37**
YS-32 x YS-115	−0.82^{ns}	0.31^{ns}	3.70^{ns}	1.13^{ns}	−0.01^{ns}	0.82**	−0.25^{ns}	−0.24^{ns}	−3.26*	0.13^{ns}
YS-102 x YS-82	−3.13**	1.50^{ns}	0.63^{ns}	4.63**	−0.28^{ns}	−0.37^{ns}	−0.15^{ns}	−4.44^{ns}	3.45*	0 30*
YS-102 x YS-85	2.30*	−1.44^{ns}	5.32^{ns}	−3.74*	0.37^{ns}	−0.34^{ns}	−0.97*	5.89^{ns}	−5.39**	−0.31*
YS-102 x YS-92	−4.70**	0.75^{ns}	−4.99^{ns}	5.45**	−0.30^{ns}	−0.09^{ns}	−0.68^{ns}	−4.72^{ns}	−0.36^{ns}	0.44**
YS-102 x YS-106	−5.51**	−3.06*	−2.80^{ns}	2.45^{ns}	0.11^{ns}	−0.29^{ns}	−2.02**	1.84^{ns}	7.74**	0.02^{ns}
YS-102 x YS-115	5.80**	2.38^{ns}	4.57^{ns}	−3.43*	0.68*	−0.21^{ns}	3.22**	10.90*	−6.85**	−0.21^{ns}
YS-82 x YS-85	−2.26*	−2.63*	−7.68*	−0.37^{ns}	−0.12^{ns}	0.36^{ns}	−0.11^{ns}	−1.97^{ns}	−0.91^{ns}	−0.12^{ns}
YS-82 x YS-92	3.74**	2.06^{ns}	−1.99^{ns}	−1.68^{ns}	0.50^{ns}	0.06^{ns}	1.28*	8.02^{ns}	−2.33^{ns}	−0.14^{ns}
YS-82 x YS-106	3.93**	−0.75^{ns}	−1.30^{ns}	−4.68**	−0.20^{ns}	0.86**	0 54^{ns}	−3.22^{ns}	1.72^{ns}	−0.24^{ns}
YS-82 x YS-115	−2.76**	−2.31^{ns}	1.07^{ns}	0.45^{ns}	−0.67*	−1.91**	−3.32**	−10.70*	4.70**	−0.01^{ns}
YS-85 x YS-92	−4.32**	−1.88^{ns}	5.20^{ns}	2.45^{ns}	−0.04^{ns}	0.29^{ns}	0.45^{ns}	−0.69^{ns}	−0.11^{ns}	0.20^{ns}
YS-85 x YS-106	5.87**	5.81**	4.88^{ns}	−0.05^{ns}	0.58^{ns}	−0.16^{ns}	0.82^{ns}	9.20^{ns}	−4.33**	0.15^{ns}
YS-85 x YS-115	−4.82**	−0.75^{ns}	−4.24^{ns}	4.07*	−0.01^{ns}	−0.08^{ns}	−1.85**	−0.12^{ns}	5.0**	0.15^{ns}
YS-92 x YS-106	3.87**	1.50^{ns}	3.07^{ns}	−2.37^{ns}	−0.14^{ns}	−0.16^{ns}	−0.40^{ns}	−2.31^{ns}	−1.01^{ns}	−0.10^{ns}
YS-92 x YS-115	5.68**	−1.06^{ns}	−0.55^{ns}	−6.74**	0.30^{ns}	0.77**	1.74**	4.87^{ns}	0.95^{ns}	−0.38**
YS-106 x YS-115	3.37**	1.63^{ns}	−2.37^{ns}	−1.74^{ns}	−0.04^{ns}	0.12^{ns}	1.00*	−0.67^{ns}	−4.01**	−0.02^{ns}

DH, days to heading; DM, days to maturity; PH, plant height (cm); GFP, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); *, $p<0.05$; **, $p<0.01$; ns, non-significant.

Table 6.6b. General and specific combining ability effects for yield and yield-related traits from an 8x8 half-diallel cross of bread wheat evaluated under non-stressed condition at Kulumsa Research Station

Parents/Crosses	DH	DM	PH	GFP	NT	SL	SS	KS	TKW	GY
	Parents GCA effects estimates									
YS-53	-1.16^{**}	0.92^{ns}	-0.12^{ns}	2.09^{*}	-0.06^{ns}	-0.06^{ns}	-0.40^{*}	-0.96^{ns}	-0.22^{ns}	0.00^{ns}
YS-32	-1.29^{**}	-2.89^{**}	0.26^{ns}	-1.60^{ns}	-0.18^{*}	-0.34^{**}	-0.83^{**}	-3.05^{*}	-0.43^{ns}	-0.09^{*}
YS-102	1.40^{**}	3.61^{**}	-1.80^{*}	2.21^{*}	0.08^{ns}	0.32^{**}	0.68^{**}	1.31^{ns}	1.01^{**}	0.11^{*}
YS-82	0.71^{**}	1.36^{ns}	-0.87^{ns}	0.65^{ns}	0.22^{**}	0.32^{**}	0.85^{**}	3.79^{**}	1.21^{**}	0.10^{*}
YS-85	-1.10^{**}	-2.89^{**}	-0.62^{ns}	-1.79^{ns}	0.14^{ns}	-0.14^{ns}	-0.23^{ns}	2.30^{*}	-1.99^{**}	0.03^{ns}
YS-92	-0.04^{ns}	-0.95^{ns}	1.26^{ns}	-0.91^{ns}	-0.07^{ns}	-0.21^{*}	-0.09^{ns}	-1.20^{ns}	1.34^{**}	-0.10^{*}
YS-106	1.21^{**}	2.67^{**}	0.13^{ns}	1.46^{ns}	-0.19^{*}	0.00^{ns}	0.18^{ns}	-3.18^{*}	-0.26^{ns}	-0.03^{ns}
YS-115	0.27^{ns}	-1.83^{ns}	1.76^{*}	-2.10^{*}	0.06^{ns}	$0\ 12^{ns}$	-0.15^{ns}	1.00^{ns}	-0.65^{ns}	-0.02^{ns}
	Crosses SCA effects estimates									
YS-53 x YS-32	2.23^{**}	2.27^{ns}	2.80^{ns}	0.04^{ns}	0.31^{ns}	0.08^{ns}	1.75^{**}	5.35^{ns}	-2.82^{**}	0.0^{ns}
YS-53 x YS-102	2.54^{**}	2.27^{ns}	-1.63^{ns}	-0.27^{ns}	0.52^{*}	1.12^{**}	1.74^{**}	8.79^{*}	4.29^{**}	0.30^{*}
YS-53 x YS-82	-1.27^{ns}	-3.98^{ns}	9.43^{**}	-2.71^{ns}	0.14^{ns}	1.07^{**}	-0.83^{ns}	2.31^{ns}	3.0^{**}	0.45^{**}
YS-53 x YS-85	2.04^{**}	3.77^{ns}	-0.32^{ns}	1.73^{ns}	-0.24^{ns}	-0.22^{ns}	0.05^{ns}	-4.10^{ns}	-3.71^{**}	-0.12^{ns}
YS-53 x YS-92	-0.02^{ns}	-1.67^{ns}	-0.70^{ns}	-1.65^{ns}	-0.34^{ns}	-0.21^{ns}	-0.79^{ns}	-5.70^{ns}	2.95^{ns}	-0.13^{ns}
YS-53 x YS-106	-0.27^{ns}	1.70^{ns}	-2.57^{ns}	1.98^{ns}	-0.84^{**}	-0.91^{**}	-1.31^{*}	-14.32^{**}	-1.5^{ns}	-0.22^{ns}
YS-53 x YS-115	-1.84^{*}	-3.80^{ns}	0.30^{ns}	-1.96^{ns}	0.06^{ns}	-0.49^{ns}	-0.73^{ns}	1.10^{ns}	-0.01^{ns}	-0.08^{ns}
YS-32 x YS-102	0.16^{ns}	-4.42^{ns}	-0.01^{ns}	-4.59^{ns}	-0.15^{ns}	0.55^{*}	0.57^{ns}	-2.62^{ns}	2.24^{*}	0.00^{ns}
YS-32 x YS-82	-1.15^{ns}	-0.67^{ns}	-4.95^{*}	0.48^{ns}	-0.23^{ns}	-0.35^{ns}	-0.70^{ns}	-3.90^{ns}	-3.01^{**}	-0.05^{ns}
YS-32 x YS-85	-3.84^{**}	5.08^{ns}	-6.20^{**}	8.91^{**}	-0.01^{ns}	-0.59^{*}	0.08^{ns}	-0.21^{ns}	1.14^{ns}	0.16^{ns}
YS-32 x YS-92	0.10^{ns}	-0.86^{ns}	-3.07^{ns}	-0.96^{ns}	0.05^{ns}	0.33^{ns}	-0.46^{ns}	0.89^{ns}	0.62^{ns}	0.20^{ns}
YS-32 x YS-106	1.85^{*}	0.02^{ns}	4.05^{ns}	-1.84^{ns}	0.03^{ns}	-0.38^{ns}	-0.83^{ns}	0.56^{ns}	-0.44^{ns}	-0.37^{**}
YS-32 x YS-115	-1.21^{ns}	-1.48^{ns}	1.93^{ns}	-0.27^{ns}	0.16^{ns}	0.69^{**}	-0.20^{ns}	2.79^{ns}	1.7^{ns}	0.32^{**}
YS-102 x YS-82	-1.84^{*}	-0.67^{ns}	2.62^{ns}	1.16^{ns}	-0.24^{ns}	-0.36^{ns}	-1.01^{ns}	-4.16^{ns}	1.9^{ns}	0.08^{ns}
YS-102 x YS-85	1.98^{**}	4.08^{ns}	-2.13^{ns}	2.10^{ns}	-0.31^{ns}	-0.30^{ns}	-1.23^{*}	-5.19^{ns}	-3.6^{**}	-0.31^{*}
YS-102 x YS-92	-4.09^{**}	-2.86^{ns}	0.49^{ns}	1.23^{ns}	-0.05^{ns}	0.26^{ns}	-0.67^{ns}	-0.77^{ns}	-2.48^{*}	0.38^{**}
YS-102 x YS-106	-3.34^{**}	-3.98^{ns}	0.12^{ns}	-0.65^{ns}	-0.08^{ns}	-0.34^{ns}	-2.44^{**}	-1.40^{ns}	1.62^{ns}	-0.1^{ns}
YS-102 x YS-115	4.60^{**}	6.02^{*}	-1.01^{ns}	1.41^{ns}	0.27^{ns}	-0.32^{ns}	1.69^{**}	4.53^{ns}	-5.73^{**}	-0.25^{*}
YS-82 x YS-85	-1.34^{ns}	-4.17^{ns}	-3.07^{ns}	-2.84^{ns}	0.06^{ns}	0.70^{**}	-0.10^{ns}	0.95^{ns}	-0.8^{ns}	0.15^{ns}
YS-82 x YS-92	3.60^{**}	6.89^{*}	-3.95^{ns}	3.29^{ns}	0.14^{ns}	-0.39^{ns}	1.77^{**}	2.45^{ns}	-0.53^{ns}	-0.23^{ns}
YS-82 x YS-106	1.85^{*}	3.77^{ns}	-2.32^{ns}	1.91^{ns}	-0.04^{ns}	1.21^{**}	2.40^{**}	-0.67^{ns}	3.72^{**}	0.24^{*}
YS-82 x YS-115	-2.21^{**}	-6.23^{*}	3.55^{ns}	-4.02^{ns}	-0.71^{**}	-1.82^{**}	-2.47^{**}	-12.05^{**}	-0.92^{ns}	-0.61^{**}
YS-85 x YS-92	-4.09^{**}	-7.36^{*}	9.30^{**}	-3.27^{ns}	0.26^{ns}	0.03^{ns}	-0.16^{ns}	4.34^{ns}	0.32^{ns}	0.14^{ns}
YS-85 x YS-106	4.16^{**}	7.52^{**}	-0.07^{ns}	3.35^{ns}	0.97^{**}	0.67^{*}	2.47^{**}	16.42^{**}	1.38^{ns}	0.32^{**}
YS-85 x YS-115	-2.40^{**}	-5.48^{ns}	-0.20^{ns}	-3.09^{ns}	-0.23^{ns}	-0.66^{*}	-1.90^{**}	-3.86^{ns}	3.51^{**}	-0.12^{ns}
YS-92 x YS-106	2.60^{**}	2.58^{ns}	-1.45^{ns}	-0.02^{ns}	-0.19^{ns}	-0.27^{ns}	-0.06^{ns}	-3.19^{ns}	-1.51^{ns}	-0.16^{ns}
YS-92 x YS-115	3.04^{**}	10.58^{**}	-5.57^{**}	7.54^{**}	0.39^{ns}	1.06^{**}	1.97^{**}	6.64^{ns}	2.13^{*}	0.10^{ns}
YS-106 x YS-115	1.79^{*}	3.95^{ns}	-0.95^{ns}	2.16^{ns}	0.15^{ns}	0.45^{ns}	1.30^{*}	2.61^{ns}	-2.12^{*}	0.14^{ns}

DH, days to heading; DM, days to maturity; PH, plant height (cm); GFP, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); *, p<0 .05; **, p< 0.01; ns, non-significant.

6.3.4   Association of GCA and SCA estimates and per se performances of genotypes

Significant and positive associations between GCA effects and parental *per se* performance were found for NT, SS and KS under both drought-stressed and non-stressed conditions (Table 6.7). The correlations between GCA effects and parental performance were strong ranging from 0.73 to 0.91 for traits NT, SS and KS under both conditions. The correlations between SCA and *per se* performances of the crosses were significant and positive for all traits measured under both drought-stressed and non-stressed conditions with coefficients between 0.44 and 0.91.

Table 6.7. Relationship between GCA, SCA and their respective *per se* performances for 10 traits of bread wheat genotypes evaluated under drought-stressed condition at Dera Research station and non-stressed condition at Kulumsa Research station

Traits	GCA vs parents		SCA vs crosses	
	Drought-stressed condition (Dera)	Non-stressed condition (Kulumsa)	Drought-stressed condition (Dera)	Non-stressed condition (Kulumsa)
DH	0.21^{ns}	0.24^{ns}	0.91^{**}	0.91^{**}
DM	0.74^{*}	0.57^{ns}	0.88^{**}	0.83^{**}
PH	0.11^{ns}	0.66^{ns}	0.95^{**}	0.93^{**}
GFP	-0.20^{ns}	0.82^{*}	0.55^{**}	0.79^{**}
NT	0.91^{**}	0.73^{*}	0.85^{**}	0.88^{**}
SL	0.46^{ns}	0.69^{ns}	0.91^{**}	0.92^{**}
SS	0.91^{**}	0.82^{*}	0.89^{**}	0.89^{**}
KS	0.91^{**}	0.75^{*}	0.86^{**}	0.88^{**}
TKW	0.47^{ns}	0.59^{ns}	0.90^{**}	0.89^{**}
GY	-0.29^{ns}	0.55^{ns}	0.44^{*}	0.92^{**}

DH, days to heading; DM, days to maturity; PH, plant height (cm); GFP, grain-filling period; SL, spike length (cm); SS, spikelet per spike; KS, kernel per spike; TKW, 1000-kernel weight (g); GY, grain yield (t ha^{-1}); *, $p<0.05$; **, $p<0.01$; ns, non-significant.
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6.4 Discussion

The significant differences in genotype performance across the different moisture conditions (Table 6.3) showed that genotype response is subject to genotype by environment interaction effect (Rebetzke et al., 2003). Significant genotype by environment interaction effects on trait expression confounds the correlation between genotype and phenotype values, and this reduces selection response (Bustos-Korts et al., 2016). It will be relatively easier to improve traits such as SL, SS and KS, whose expression was not significantly affected by environmental or genotype by environment interaction (Table 6.3). Overall, the study found the existence of considerable genetic variation among the parental lines and their crosses, which may further be exploited for drought-tolerance and yield improvement purposes. Mwadzingeni et al. (2018) reported the existence of considerable genetic variation among 12 parents of bread wheat and their crosses developed using a similar half-diallel mating design evaluated under drought-stressed and non-stressed conditions.

Parental lines such as 'YS-53' and 'YS-106', which were the earliest to heading and maturity under different growing conditions (Tables 6.4a and 6.4b), would be useful for gene introgression for early heading and maturity for drought-escape breeding. Earliness to heading and maturity are important traits to escape terminal drought-stress, which is prevalent in sub-Saharan Africa. Several studies have exploited earliness to heading and maturity in wheat to indirectly improve drought-tolerance and yield potential (Reynolds, 2002; Shavrukov et al., 2017; Abraha et al., 2018). However, the advantage of early maturity is more significant in environments with short seasons or limited moisture availability, while reduction in yield potential has been reported in early maturing varieties due to their shortened growth cycles (Mwadzingeni et al., 2016). Similarly, the above-mentioned parents exhibited desirable mean performance for other agronomic traits such as PH, GFP, NT, TKW and GY (Tables 6.4a and 6.4b). This makes them ideal candidates for improving yield and drought-tolerance in bread wheat. Selection of parental lines with desirable agronomic performance using multiple traits would result in the simultaneous improvement of the traits if they have favourable correlations and are controlled by additive gene effects.

The higher mean performance by some of the crosses compared to their parents (Tables 6.4a and 6.4b) indicates the possibility of genetic gain in yield potential. The high relative performance in crosses compared to their parents is an indication of dominance gene action and provides a basis for transgressive selection. Cross such as 'YS-32' x 'YS-82' that showed higher yield under drought-stressed condition than their parental average performance can be used for transgressive selection under drought-stressed conditions, while crosses 'YS-53' x 'YS-82', 'YS-32' x 'YS-92' and 'YS-102' x 'YS-92' can be selected under non-stressed conditions to achieve higher genetic gains for grain yield. Crosses such as 'YS-102' x 'YS-92' and 'YS-32' x 'YS-82' should be selected for drought-tolerance and higher

yield potential as they exhibited higher mean value for GY under both drought-stressed and non-stressed conditions.

Traits such as DH, DM, SL, SS and TKW had significant mean squares for both GCA and SCA effects (Tables 6.5a and 6.5b), suggesting that both additive and non-additive gene actions conditioning the inheritance of these traits. Conversely, only SCA effects were significant for PH and GY under the drought- stressed condition (Table 6.5a), indicating that non-additive gene action was important for the expression of these traits. The discrepancy in the GCA effects of traits between drought-stressed and non-stressed conditions suggest that there is a need to select families for specific environmental adaptation (Makumbi et al., 2011). The GCA effects of a particular line for a trait were not consistent under both environments, suggesting that selection efforts should consider the attendant conditions that may affect trait heritability. Hei et al. (2015) reported significant GCA and SCA effects for most of the traits assessed in bread wheat, showing that both additive and non-additive effects were important for trait heritability.

The Baker's ratios showed that additive gene effects were more pronounced than non-additive gene effects for all traits, except for grain yield and plant height, under both drought-stressed and non-stressed conditions (Tables 6.5a and 6.5b). The preponderance of additive gene effects indicates that early generation selection would be effective for trait improvement (Amegbor et al., 2017). Similarly, Farhsadfar et al. (2013) and Joshi et al. (2004) reported that additive gene effects were more predominant than dominance gene effects for key traits in bread wheat. Contrarily, Saeed et al. (2016) reported that non-additive gene effects were more predominant in the inheritance of agronomic traits that were evaluated in wheat. The variation in the relative importance of additive or non-additive gene effects reported by different studies suggests that the nature of germplasm used and environmental conditions are important determinants that should be accounted for during breeding.

The Consultative Group on International Agricultural Research (CGIAR), through the International Maize and Wheat Improvement Center (CIMMYT) and the International Centre for Agricultural Research in Dry Areas (ICARDA), and various national breeding programs are engaged in wheat improvement for the drier regions of the world. Developing wheat cultivars adapted for drier environments is particularly important for regions such as sub-Saharan Africa where wheat is mainly cultivated under dryland condition using residual soil moisture (Haque et al., 2016). Identifying parental lines with good combining ability for drought-adaptive traits is an important preliminary stage to developing drought-tolerant and high yielding cultivars for deployment in marginal environments. Parental genotypes with suitable GCA effects for agronomic traits and grain yield can be used for developing breeding populations (Maich et al., 2000). Parents with desirable GCA effects under specific conditions transfer additive genes to their offspring, although parents that exhibit the desirable GCA effects under diverse conditions will be more useful for breeding (Dholariya et al., 2014). Parental line

'YS-32' was the best general combiner for reducing DH and DM under both drought-stressed and non-stressed conditions (Tables 6.6a and 6.6b). This suggests that it possessed genes for earliness that could be transferred to offspring. Conversely, the parental line 'YS-102' could be used to develop late maturing genotypes suitable for production under long season and optimal environments where early maturity causes yield penalties. Parents 'YS-32', 'YS-85' and 'YS-115' are sources of genes for reducing plant height under drought-stressed conditions, while parent 'YS-102' had favourable GCA for reducing plant height under non-stressed conditions. Genotypes with semi-dwarfing genes *Rht1* and *Rht2* have been reported to be drought-tolerant (Miralles et al., 1997) and thus it would be prudent to target breeding for semi-dwarf genotypes that maximize translocation of assimilates to yield components. Parent 'YS-32' was a good general combiner for GFP under the drought-stressed condition, while parents 'YS-53' and 'YS-102' were good combiners for this trait under the non-stressed condition. No parents had consistently good combining ability for all traits measured. Parent 'YS-82' was a consistently good general combiner for NT, SL, SS and KS under both drought-stressed and non-stressed conditions. TKW is an important yield component affected by drought (Nezhad et al., 2012). Improving this trait could be achieved by using the parent 'YS-92' that had consistently positive and significant GCA effects for this trait under both drought-stressed and non-stressed conditions (Tables 6.6a and 6.6b). Parent 'YS-85' had positive and significant GCA effects for GY under the drought-stressed condition, which implied that this parent possessed favourable alleles for grain yield and would contribute to developing populations with high yield under drought-stressed conditions. Favourable GCA effects exhibited by a parental line indicate possession of favourable alleles that could potentially be transmitted to offspring during crosses and selection (Amegbor et al., 2017). Parental lines with desirable GCA effects for particular traits would be important for selection to maintain pure lines for breeding purposes.

The SCA effects are not very important in the improvement of self-pollinated crops like wheat, except when transgressive segregants can be used for developing more vigorous homozygous lines in advanced generations. Exploitation of heterosis caused by dominant gene effects has not been commercially utilized in self-pollinating crops such as wheat, although it holds the potential to break yield barriers (Singh et al., 2010). The presence of families such as 'YS-32' x 'YS-82', 'YS-102' x 'YS-92' and 'YS-85' x 'YS-92' that had higher mean values for GY than their parental mean performance suggests the existence of polygenes controlling this trait (Rebetzke et al., 2003). Improvement of traits under non-additive gene control can be achieved by selection of transgressive segregants at advanced generations after successive inbreeding generations, followed by pure line selection (Hallauer and Miranda, 1988; Susanto, 2018). Transgressive segregants obtained from parental lines that exhibited poor GCA effects but good SCA effects for a particular trait can be selected to exploit dominant or epistatic gene action (Singh et al., 2012). Cross 'YS-102' x 'YS-92' that exhibited high positive SCA effects for GY under both drought-stressed and non-stressed conditions, was derived from both parents with low GCA effect.

This suggest that there was a dominance × dominance gene action involved in the control of this trait (Wassimi et al., 1986). Crosses 'YS-53' x 'YS-115', 'YS-102' x 'YS-82', 'YS-102' x 'YS-106', 'YS-82' x 'YS-115', 'YS-85' x 'YS-92' and 'YS-85' x 'YS-115' had desirable SCA effects for DH under both drought-stressed and non-stressed conditions (Tables 6.6a and 6.6b). Hence, these families would be selected for population improvement for drought-escape breeding. For reduced plant height, cross 'YS-32' x 'YS-85' is an ideal candidate under the two moisture conditions. Negative SCA effects for PH are more desirable in drought-prone and waterlogged conditions to minimise lodging (Tadesse et al., 2010). A long grain-filling period was maintained by the cross 'YS-32' x 'YS-85' under both drought-stressed and non-stressed conditions, which could positively contribute to improving grain weight and yield of the population in diverse environments. Grain yield under drought-stressed conditions could be improved through selections among crosses such as 'YS-32' x 'YS-85' and 'YS-102' x 'YS-92'. These crosses had high *per se* performance and significant positive SCA effects. These genotypes have the capability to produce transgressive segregants for selection (Singh et al., 2004; Fasahat et al., 2016). Crosses 'YS-53' x 'YS-102', 'YS-53' x 'YS-82', 'YS-32' x 'YS-115', 'YS-102' x 'YS-92', 'YS-82' x 'YS-106' and 'YS-85' x 'YS-106' had positive and significant SCA for GY under the non-stressed condition. This suggests that these crosses could be used to develop hybrids for improving grain yield of bread wheat under well-managed agriculture systems through heterosis and transgressive breeding program.

The correlations between the GCA of parents and *per se* performances of parents and crosses help to predict the performances of hybrids (Ertiro et al., 2013; Amegbor et al., 2017). The relationship between the GCA effects and parental *per se* performances was significantly positive for NT, SS and KS under both drought-stressed and non-stressed conditions (Table 6.7). This implies that selection based on *per se* performances of parents could be effective for these traits. However, the association between parental *per se* performance and GCA effects was not significant for the other traits including grain yield under both drought-stressed and non-stressed conditions. This indicates that high yielding parents do not always result in high yielding hybrids, due to unfavourable gene combinations in the F1 generation (Ertrio et al., 2013). The SCA effects were positively and significantly associated with *per se* performances of the crosses for all traits studied under both drought-stressed and non-stressed conditions (Table 6.7). Akata et al. (2017) reported hybrid *per se* performance was found to be closely correlated to SCA of all traits studied in West African sorghum landraces, which is corroborated by the results of this study. Gramaje et al. (2020) reported that GCA effects were poorly correlated with SCA effects and hybrid performance in cytoplasmic male sterile hybrid rice.

6.5 Conclusions

Substantial genetic variation existed among the parents and their crosses that could be exploited through advancing promising families for yield and related traits under drought-stress conditions. The parental line 'YS-32' was the best general combiner for DH, DM, GFP and TKW, enabling direct selection for improved grain yield under drought-stressed conditions. Parent 'YS-85' could also be used for improving grain yield under drought-stressed conditions due to its positive and significant GCA effect on GY. Likewise, grain yield under drought-stressed conditions may be improved through selection involving crosses such as 'YS-32' x 'YS-85', 'YS-102' x 'YS-82' and 'YS-102' x 'YS-92'. The promising families identified will be utilized for individual plant selection at the F2 to be advanced through single seed descent selection method either for use as a mapping population to further enhance traits of interest under drought-stress conditions or directly use as improved cultivars.

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Overview of the research findings

Introduction and objectives of the study

Ethiopia is the leading wheat producer in sub-Saharan Africa (SSA) followed by South Africa in terms of total annual production. However, the demand for wheat is rapidly increasing in Ethiopia because of several factors, including population pressure, changing food preferences and socio-economic change associated with urbanization. Several improved varieties were released nationally that enabled wheat yields to increase, reaching a mean yield of 2.4 t ha^{-1}. However, the yield level remains well below the world average of 3.4 t ha^{-1}. Furthermore, the adoption rate of the available improved varieties is low, especially by farmers in drought-prone marginal areas in the country. Therefore, there is a need for a systematic breeding program to developing cultivars with farmers' preferred traits and tolerant to drought-stress, which in turn will enhance adoption and increase production and productivity in the country. This study was therefore executed with the following objectives:

i.   To assess farmers' production practices, perceived production constraints, and preferred traits of bread wheat varieties as a guide to variety development and deployment in drought-prone areas of Ethiopia;

ii.   To screen bread wheat genotypes for drought-tolerance using phenotypic analysis to select promising lines for use in breeding for drought-tolerance and related phenotypic traits;

iii. To estimate the genetic parameters and association of yield and yield components and thus to determine the selection criteria to increase genetic gains under drought-stress conditions;

iv.   To assess the genetic diversity and relationships among the selected wheat genotypes using SSR molecular markers in order to complement the phenotypic data in identifying complementary parents for further breeding for drought-tolerance;

v.   To determine combining ability effects of the selected wheat genotypes, thereby deducing gene action controlling traits of interest and identifying promising families for drought-stress conditions and to advance these families through the single seed descent selection method.

Research findings in brief

➢ Importance of drought-stress and farmers' preferred traits determined

➢ Tested genotypes showed considerable phenotypic and genotypic diversity to select promising lines for use in breeding for drought-tolerance

➢ Key selection criteria under drought-stress conditions determined

➢ Promising families were identified that will be advanced through single seed descent selection method

Farmers' production practices, perceived constraints, and preferred traits of bread wheat varieties under drought-prone agro-ecologies of Ethiopia

A participatory rural appraisal (PRA) study was conducted among 170 randomly selected wheat-producing farmers in the drier areas of the Arsi Zone of the Oromia Regional State in Ethiopia. Data were collected through interviews using a semi-structured questionnaire. The main outcomes were as follows:

- Wheat followed by tef (*Eragrostis tef* Zucc.) and barley (*Hordeum vulgare* L.) were the most widely grown crops in the study areas.

- Drought-stress, diseases (rust), and the high cost of fertilizers were among the major constraints of wheat production identified by the farmers.

- On average, between 63.1 and 73.8% reduction in yield was experienced due to drought-stress in the studied areas.

- Socio-demographic factors such as gender, education level and access to extension service influenced variety adoption by the farmers.

- Early maturity, tall plant height, good baking quality and stress adaptation were the major varietal characteristics contributing towards adoption of new improved bread wheat varieties.

- Farmers had varying variety-specific traits preferences; grain yield, rust-resistance, adaptation to drought and heat-stresses and early maturity were the most preferred varietal traits in the study areas.

Evaluation of bread wheat (*Triticum aestivum* L.) genotypes for yield and related traits under drought-stressed and non-stressed conditions

One hundred and twenty genotypes were evaluated at five test sites in the 2018/19 cropping season using a 10 x 12 alpha lattice design with two replications. The level of drought-stress was imposed using different sowing dates (early planting representing non-stressed, while late planting as drought-stressed conditions) following the onset of the main seasonal rain at each site. Grain yield and yield components were recorded, and drought indices were calculated for each genotype. The main findings were as follows:

- Genotypes such as 'YS-39', 'YS-119' and 'YS-109' were the earliest to mature and may be used in drought-tolerance breeding to exploit their drought-escape mechanism.

- Genotypes such as 'YS-1', 'YS-62' and 'YS-54' were selected for their short plant height, whereas 'YS-71', 'YS-29' and 'YS-120' were tall genotypes.

- Among the drought-tolerance indices, Geometric Mean Productivity (GMP), Mean Productivity (MP), Harmonic Mean (HM), Stress Tolerance Index (STI) and Yield Index (YI) were found to be the most suitable for predicting drought-tolerance.

- Genotypes 'YS-41', 'YS-92', 'YS-115', 'YS-34' and 'YS-93' were found to be high yielding under a range of environments

- Genotypes 'YS-90', 'YS-106', 'YS-96', 'YS-102' and 'YS-101' were susceptible to drought-stress, but high yielding under optimum environments

- Genotypes 'YS-32', 'YS-29', 'YS-14', 'YS-53' and 'YS-11' were high yielding only under drought-stress conditions.

Genetic variability and association of yield and yield components among bread wheat genotypes under drought-stressed and non-stressed conditions

Data collected from 120 genotypes were used to estimate variance components, broad sense heritability and genetic advance. Data were recorded on agronomic traits such as days to heading (DH), days to maturity (DM), plant height (PH), spike length (SL), spikelet per spike (SS), kernel per spike (KS), 1000-kernel weight (TKW) and grain yield (GY). The main findings were as follows:

- Traits such as DH, SL and SS exhibited high genetic variance, heritability and genetic advance under both drought-stressed and non-stressed conditions.

- GY exhibited low estimates of genetic advance (9%) and heritability (41.5%).

- PH and TKW had a strong positive direct effect on GY under both drought-stressed and non-stressed conditions.

Genetic diversity and population structure of bread wheat genotypes determined via SSR marker analysis

Fifty-two selected bread wheat genotypes were evaluated using 20 SSR markers. The main findings were as follows:

- SSR analysis identified a total of 181 alleles, with a mean of 10.1 alleles per locus.

- Population structure analysis grouped the test genotypes into three main populations.

- Analysis of molecular variance revealed that 85% of the variance emanated from intra-population differences.

Combining ability of bread wheat (*Triticum aestivum* L.) genotypes for yield and yield-related traits under drought-stressed and non-stressed conditions

Eight parental lines and 28 crosses obtained from a half-diallel mating design were evaluated at two sites representing drought-stressed and non-stressed conditions. The main outcomes were as follows:

- Both GCA and SCA effects were significant for days to heading (DH), days to maturity (DM), spike length (SL), spikelets per spike (SS) and 1000-kernel weight (TKW) under both drought-stressed and non-stressed conditions.

- The parental line 'YS-32' was the best general combiner for DH, DM, grain-filling period (GFP) and TKW.

- Parent 'YS-85' had a positive and significant GCA effect on GY.

- Families 'YS-32' x 'YS-85', 'YS-102' x 'YS-82' and 'YS-102' x 'YS-92' had the highest specific combining ability (SCA) effects on GY under drought-stressed condition.

Implications of findings of this study for breeding for drought-tolerance in bread wheat

- Wheat breeding for drought-prone areas in Ethiopia should integrate farmers' preferred traits and drought-tolerance for sustainable wheat production and productivity.

- The considerable genetic variability among the wheat genotypes for yield and yield-related traits can further be exploited to improve wheat productivity in Ethiopia.

- Traits such as DH, SL and SS exhibited high genetic variance, heritability and genetic advance, and these can be improved through direct selection under drought-stress conditions.

- PH and TKW had a strong positive direct effect on GY, which provide a basis for selection and improvement of GY under drought-stress conditions.

- The SSR markers were useful and provided complementary data for selecting agronomically suitable parental lines for drought-tolerance breeding

- SSR markers WMC 25, WMC 149 and WMC 265 were the most informative markers.

- The parental line 'YS-32' was the best general combiner for DH, DM, GFP and TKW, enabling direct selection for improved grain yield under drought-stress conditions.

- Parent 'YS-85' can also be used for improving grain yield under drought-stress conditions due to its positive and significant GCA effect.

- Grain yield under drought-stress conditions can be improved through selection involving crosses such as 'YS-32' x 'YS-85', 'YS-102' x 'YS-82' and 'YS-102' x 'YS-92'.

- The promising F1 families identified in this study will be utilized for selection of F2 plants that will be advanced through single seed descent selection method to enhancing drought-tolerance, grain yield, and stability with farmers' preferred traits in dryland wheat production areas.
- Overall, the present study revealed drought-stress was the major bread wheat production constraint in drought-prone agro-ecologies of Ethiopia. And, farmers had varying varietal preferences for adopting newly improved varieties. The tested genotypes proved to be valuable genetic resources to enhancing drought-tolerance and improving farmers' preferred traits.

- In future, these genetic resources will be used either for developing mapping populations for quantitative trait loci (QTL) analysis underlying traits of interest under drought-stress conditions to serve as long-term breeding materials or release directly as cultivars.