GENOTYPE-BY-FLORAL CHARACTERISTICS INTERACTION FOR HYBRID WHEAT (*Triticum aestivum* L.) PRODUCTION IN TEXAS

A Thesis

by

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Submitted to the Office of Graduate and Professional Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE

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August 2019

Major Subject: Plant Breeding

ABSTRACT

The demand for agricultural and natural recourses is rising due to population growth. Hybrid technology is an effective way to increase yield potential and production of wheat (*Triticum aestivum* L.) to meet the demand of 9.7 billion people in 2050. Self-pollinated crops are challenging due to high seed production cost and the need to force them to behave as a cross-pollinated crop. Therefore, a compromise between heterosis and floral suitability often needs to be reached in hybrid wheat production. Recently, the interest in hybrid wheat has been renewed because of higher wheat prices, climate change, new technological developments in next-generation sequencing, and capability of predicting heterosis at the molecular level. In addition, the performance potential of hybrids increased due to more focused studies on wheat flower biology.

It is apparent that the redesign of floral characteristics is a prerequisite for hybrid wheat breeding to achieve high outcrossing ability. Therefore, the purpose of this research was to 1) screen the Uniform Variety Trial (UVT) and Texas Elite (TXE) lines for desirable floral characteristics, and 2) characterize the best male and female candidates for inclusion in the Texas A&M AgriLife hybrid wheat crossing blocks.

The lines were screened for floral characteristics such as days to heading, days to anthesis, anther extrusion, anther score, stigma exsertion, gape, and plant height in College Station and McGregor, TX for two years.

The results of combined environment analyses indicated that genotypic variances were significantly different for all floral characteristics. Non-gender and male traits had high heritability estimates. The heritability of anther extrusion ranged from 0.82 to 0.87. The non-gender and male traits exhibited highly reliable genotypic coefficient of variance (GCV), while female traits had low GCV levels. The correlation between days to heading and anthesis; anther score and anther extrusion; as well as stigma exsertion and gape were positive and significant.

The lines were screened for Rht-B1 and Rht-D1 height reduction genes. Five of the UVT lines had Rht-B1a/ Rht-D1b and only one of the TXE lines had it. The rest of the lines had Rht-B1b/ Rht-D1a genes.

DEDICATION

I dedicate this thesis to my wonderful and supportive parents and sister. They were with me every step of this journey.

ACKNOWLEDGEMENTS

First, I would like to thank my advisor, Dr. Amir M.H. Ibrahim for giving me the opportunity to complete my master's degree at a wonderful University. I appreciate his expertise, help, time, and guidance through the process. Likewise, I would like to thank my committee members, Dr. Jackie Rudd and Dr. Shuyu Liu, for their guidance and support throughout the course of this research.

I would also like to thank the other members of the Texas A&M University Wheat Breeding team and the department faculty and staff for making my time at Texas A&M University easier and meaningful. I would also like to give special thanks to research assistant Dr. Geraldine Opena for her help from day one, and Jorge Valenzuela Antelo for his friendship as well as his help with the courses and every academic aspect.

Thanks also go to my friends for being there with me throughout my journey at Texas A&M, and for making my time at Texas A&M University a great experience.

Very special thanks go to my family for their encouragement and especially for their moral support. The journey was challenging, without them being by my side, I cannot imagine completing this chapter of my life.

At last, I would like to give a sincere thanks to the Turkish Ministry of Education for the scholarship. I am truly grateful for the scholarship and for the opportunity to learn, improve, travel, and study at a top-tier university of higher education.

CONTRIBUTORS AND FUNDING SOURCES

This work was supervised by a dissertation committee consisting of Professors Amir M.H. Ibrahim, Jackie C. Rudd and Shuyu Liu of the Department of Soil and Crop Sciences. All work for the dissertation was completed independently by the student.

Graduate study was supported by a fellowship from the Turkish Ministry of Education.

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1. INTRODUCTION

Studies have shown that the world's population grows constantly and is expected to reach 9 billion by 2050. Food production must be doubled to meet the demands for calories and protein (Godfray et al., 2010). If sharp changes do not occur in people's consumption habits, production must keep up with the demands of the growing population, dietary changes (the increasing demand for calories and protein consumption), and increasing bioenergy use (Foley et al., 2011).

Wheat (*Triticum aestivum* L.) was domesticated 10,000 years ago, and has been one of the major crops all around the world (Dubcovsky and Dvorak, 2007). It now ranks third in terms of global production of food crops behind maize (*Zea mays* L.) and rice (*Oryza sativa* L.) (FAOSTAT, 2017). Twenty percent of the calories humans consume come from wheat-based products, and production exceeded 720 million tons in 2015 (Dubcovsky and Dvorak, 2007; FAO, 2015). Line breeding is the main method used in today's wheat breeding programs. Grain yield improvements are mostly correlated with exploiting heterosis in non-hybrid crops, but today's wheat breeding methodology is not adding enough grain yield to meet the demand (CGIAR, 2016). The Consultative Group on International Agricultural Research (CGIAR) has suggested that wheat annual yield gain should be 1.4% to 1.7% per year in order to fulfill the goal, but the genetic gain is currently below 1% (CGIAR, 2016). Hybrid wheat breeding could be a solution to fill the gap between today's production and future expectations with the promising yield increase.

Interest in hybrid wheat began in the 1960s after cytoplasmic male sterility (CMS) systems were described in wheat (Singh et al., 2010). Studies were mainly very small; therefore, hybrid wheat establishment in the global market could not be achieved (Longin et al., 2012). Currently, the interest in hybrid wheat has been renewed in both the public and private sectors due to increasing problems of abiotic stresses caused by climate change (Boeven et al., 2016) and the needs to increase yield potential shown above. Researchers have indicated that if there is a wider genetic divergence between the parents, heterosis of a hybrid is expected to increase (Whitford et al., 2013). With the new technological developments in next-generation sequencing, molecular markers such as simple sequence repeats (SSRs) and single polymorphic markers (SNP), which measure genetic distance between lines and heterotic groups, have led to faster and cheaper genotyping that reduces the time and cost of selecting parents with good combining ability (Xu et al., 2002; Longin et al., 2012). The main purpose of hybrid wheat programs is to exploit heterosis (Melchinger, 1999). Therefore, interest in hybrid wheat has been renewed, particularly with a focus on arranging floral architecture to be able to facilitate hybrid seed production with these new strategies, technologies, and knowledge (Whitford et al., 2013).

The economic viability of hybrid wheat seed production mostly depends on cost-efficient systems that includes the understanding of fundamental traits that help maximize the seed set of the female parent (Langer et al., 2014; Garst, 2017). Additionally, the number of male parent plants should be reduced to facilitate tillering and lengthen the period of pollen shed (Garst, 2017). Wheat is a self-pollinating crop

with less than 1% outcrossing. As a result, the redesign of floral characteristics is a prerequisite for hybrid wheat breeding studies intended to achieve high outcrossing ability (Langer et al., 2014). The outcrossing ability depends on several traits and their combinations (Boeven et al., 2016). In hybrid wheat seed production, female parent plants must have open florets and extruding stigma (De Vries, 1971). Male parent plants must have viable extruded anthers and shed pollen outside the florets. In addition, parent must have synchronized flowering periods, and the male parents should be taller in order to achieve cross-pollination (Longin et al., 2013). Through new phenotyping techniques for flowering traits and advanced genomic tools, the bottlenecks that are the result of years of domestication could be widened (Dubcovsky and Dvorak, 2007; Longin et al., 2012).

The main objective of this research is to phenotype the floral characteristics of inbred lines for hybrid wheat production in Texas. The specific objectives are 1) to screen the Uniform Variety Trial (UVT) and Texas Elite (TXE) lines for desirable floral characteristics, and 2) to characterize the best male and female candidates for inclusion in the hybrid wheat crossing blocks.

2. LITERATURE REVIEW

2.1 Origin of Modern Wheat

The fundamental aspects of human civilization are the domestication of plants and animals and its adaptation and speciation to the point of an enormous evolutionary experiment of generating incipient species (Peng et al. 2011). As a part of the Neolithic Revolution, which was a conversion from the hunting and collecting of food to settled agriculture, wheat (*Triticum aestivum* L.) was first cultivated approximately 10,000 years ago (Hillman and Davies, 1990; Fuller, 2007). The domestication period lasted several centuries. The earliest cultivated forms of wheat were the diploid einkorn (*Triticum monococcum*) and tetraploid emmer (*T. dicoccum*) species (Shewry, 2009; Charmet, 2011).

A small, specific region called the Fertile Crescent in West Asia is the Center of Origin of wheat as determined by botanical, genetic, and archaeological studies of cultivated crops (Gustafson et al., 2009). More specifically, the origin of modern wheat occurred in a mountain region enclosed by the Tigris and Euphrates rivers (Braidwood et al., 1968). Today this region is in southeastern Turkey and northern Syria (Gustafson et al., 2009).

The wheats (*Triticum spp.)* are in polyploid series based on the seven chromosomes, which are modeled with diploid (2n = 2x =14, AA), tetraploid (2n = 4x = 28, AABB), and hexaploid (2n = 6x = 42, AABBDD) forms (Salamini et al., 2002). Approximately 95% of the world's wheat production is hexaploid bread wheat (*Triticum aestivum)*, while the remaining 5% is tetraploid durum wheat (*T. durum*) (Peng et al.,

2011). Einkorn wheat (*T. monococcum*) is a third species. Even though it has a very small role in modern agricultural production, it is a significant part of wheat domestication history (Feuillet et al., 2008).

Wheat genomes have been researched in order to identify each of their origins. Diploid wheat consists of a group of single genomes with the genome formula AA. The AA is the main genome shared by all polyploid wheat (Lupton 1987). Scientists have conducted studies to determine the origin of the B genome, but there are still some debates about it, so the source remains relatively unknown (Feuillet et al., 2008; Lupton 1987). Wild diploid wheat (*Triticum urartu*) pollinated with one of the closest relatives of goatgrass (*Aegilops speltoides*) – that is, the B genome ancestor – around 500,000 BP (Years Before Present) created wild emmer wheat (*Triticum dicoccoides*) (Huang et al., 2002). Around 10,000 BP, hunter-gatherers domesticated this fertile tetraploid (AABB) (Peng et al., 2011). The selection was made subconsciously and eventually – 10,000 years ago – created cultivated emmer wheat (*Triticum dicoccum*), which is the ancestor of durum wheat (Luo et al., 2007; Charmet, 2011). Macaroni wheat, or *T. durum*, was a result of the selection from progenitor cultivated wheat with a round of modifications to the modern free-threshing, non-fragile forms (Lupton, 1987). The hexaploid (AABBDD) species arose from the second amphiploidy event between tetraploid (AABB) cultivated emmer wheat (*Triticum dicoccu*m) and the wild diploid (DD) species *T. tauschii*. The domesticated form is known as *T. aestivu*m, or bread wheat (Charmet, 2011).

As a result of the domestication of wheat, some traits such as soft glumes, a non-fragile rachis, and free threshing have arisen. Domesticated wheat is separated from its

wild progenitor by two important genetic traits (Nalam et al., 2006). The first trait is the non-shattering spike at maturity level. Even though the brittle rachis character was dominant, through subconscious selection non-brittle rachis eventually became the dominant phenotype (Charmet, 2011). The second trait is naked grain. All these traits were gained by mutation at loci such as brittle rachis (Br), Q, and Tg (Feuillet et al., 2008). The first farmers subconsciously chose the mutant types over their wild relatives because the spikes remain the same without losing seeds until harvest, or because those plants had hulless seeds for easier flour milling (Feuillet et al., 2008).

Central-eastern wild emmer race, more specifically the Southeast Turkey, is believed to be the progenitor of domesticated germplasm (Peng et al., 2011; Salamini et al., 2002). Domesticated naked, free-threshing emmer is believed to have been cultivated in the southern Levant during the period from 9,500 to 9,000 BP (Peng et al., 2011). Domesticated emmer was spread across Asia, Europe, and Africa as a result of agricultural expansion (Dubcovsky and Dvorak, 2007). The northeast expansion of cultivated emmer wheat pollinated with *Aegilops tauschii* and created hexaploid common wheat around the southwestern coastal area of the Caspian Sea (Dubcovsky and Dvorak, 2007). Around 6,000 BC (Before Christ) the first farmers arrived in southeastern Europe, and European farming began in Greece in the late seventh or early sixth century BC. Cultivated wheat spread all over Europe from Greece (Lupton, 1987). This expansion happened via two main routes, namely inland and coastal (Renfrew, 1973). The inland expanded through Hungary, Poland, and Germany and reached the North Sea coast before 4,000 BC. The second route went along the Mediterranean coast

to Spain, went north through the Atlantic coast, and reached the British Isles in 3,500 BC. In comparison, wheat reached China around 3,000 BP when it spread from Iran to central Asia, and to Africa from Egypt (Shewry, 2009). Finally, Spaniards introduced wheat to Mexico in 1529, and it reached Australia in 1788 (Shewry, 2009).

As a consequence of selection, diversity among wheat reduced, and this created a genetic bottleneck (Charmet, 2011; Peng et al., 2011). The frequency of selection of the most desirable traits increased, so more diversity was lost (Charmet, 2011). Despite the diversity lost, wheat is one of the most frequently grown crops in the world, and it meets a high percentage of food demands (Singh et al., 2015).

2.2 History and Present Status of Hybrid Wheat

Although allogamous crops such as maize have had significant success with hybrids, autogamous crops except for rice could not yet create market potential. There has been a decrease in the yield gain in wheat in the past few years (Langer et al., 2014). Increasing the grain yield and yield stability is the main goal, and hybrid wheat breeding is a promising method (Boeven et al., 2016). Another goal is to optimize the heterosis (Whitford et al., 2013) with the genetic variation between its parents (Melchinger, 1999).

Hybrid wheat programs began to operate in the 1960s, but hybrids had minor production area (Whitford et al., 2013). The discovery of male sterility and restoration systems was the first step, and it increased the interest in hybrid wheat in both the public and private sectors (Adugna et al., 2004). In 1974, the first commercial CMS hybrid wheat was released in the United States of America (USA), and Monsanto initiated a hybrid wheat program based on chemical hybridizing agent (CHA) Genesis ® in the

USA and Europe in 1982. Cargill, Monsanto, and Dupont stopped their hybrid wheat-based programs in 1990, 2000, and 2002, respectively (Singh et al., 2010). Recently, the growing world population, climate change, and the struggling level of grain yield in wheat line breeding have led to new interest in hybrid wheat (Godfray et al., 2010; Foley et al., 2011; Ray et al., 2013).

The absence of effective fertility-restoration genes made it difficult to use cytoplasmic male sterility. While cytoplasmic male sterility mostly failed because of fertility restoration problems, toxicity and selectivity were the reasons for CHA failure (Whitford et al., 2013). Scientists claimed that increasing yield in wheat depends on the combination of dispersed dominant alleles. Therefore, they believed that line breeding could give similar yield increase as compared to hybrid wheat production (Whitford et al., 2013). These were the reasons that many companies have ended their hybrid wheat programs in spite of interest (Longin et al., 2012).

Even though there are some drawbacks, in the past decade the public and private sectors have initiated new hybrid wheat programs (Longin et al., 2012). Both sectors have realized that there is an increasing demand for agricultural production for an increasing population with problems of abiotic stresses caused by climate change (Longin et al., 2012). In addition, there has been a reduction of investment in seed companies due to farm-saved seed use, and this situation has led to the initiation of hybrid wheat programs (Rajaram, 2001). Moreover, diverse hybrid production mechanisms has been suggested since the last attempt for hybrid wheat production, and there are several proposed or under development for wheat (Kempe and Gils, 2011).

Thus, hybrid wheat has been reassessed in terms of floral characteristics in order to create hybrid seed production with new strategies, technologies, and knowledge (Whitford et al., 2013).

In conclusion, male and female traits are directly related with hybridization system even though studies conducted over the last 50 years have only been moderately successful (Longin et al., 2012). Therefore, new studies on male traits such as pollen amount, spread, and viability and female traits such as glume separation and stigma exsertion should be focused on better understanding and manipulating the genetic characteristics of floral traits (Longin et al., 2012). When advanced high-density genomic tools are combined with new phenotyping techniques for floral traits, they provide strong possibilities for broadening the bottleneck (Longin et al., 2012).

2.3 The Wheat Flower Morphology, Pollination System, and Floral Traits

Wheat is an autogamous crop with 99% self-pollination (Singh et al., 2015). Winter wheat needs two to eight weeks of vernalization, which is a period of cold treatment (0–10 °C) for the initiation of the flowering process (Gregory and Purvis, 1938). During this period, there are some metabolic alterations before morphological changes begin in the shoot apex (Yong et al., 2003). Tiller shoots originate from buds in the axils of plant leaves. Tillers have a major role in wheat production; they develop during autumn and continue to grow during spring in winter wheat. Higher seed production can be related to the plant's tillering ability, especially in winter wheat (Thiry et al., 2002).

The growing point is the part where all wheat stem and tillers are formed. In the early growing stage leaves grow, and then the spikes and their parts arise (Bonnett, 1936). The development of a wheat inflorescence (spike, ear, or head) begins at the tip of the stem and creates the spikelets. There are two opposite rows of spikelets along the main axis or rachis, and their numbers are determined by genotype and environmental conditions. The spikelets are arranged in a spikelet axis (rachilla) alternately on opposite sides and include two small bract leaves called glumes (De Vries, 1971). There are two bract-like structures in each floret: the lemma (the lowermost of the two chaff-like bracts) and the palea (the uppermost of the two chaff-like bracts) (Lersten, 1987). The spikes can have a long, medium, or short awn, which grows from the tip of the lemma, or it can be awnless. The reproductive organs are located in between the lemma and palea (De Vries, 1971). During the anthesis, the lodicule, a small organ at the base of the floret, swells quickly, and the floret opens. This stage is called chasmogamy, and the anthers and pistil are exposed for pollination. Pollen begins to shed when flowers are about to open (Whitford et al., 2013).

The reproductive organs are located inside the same floret. There is a pistil including two styles with feathery stigma branches and three stamens with large anthers in each floret. Also, each floret carries two ovate lodicules, which are interpreted as highly modified perianth structures. Wheat has one ovule and two plumose styles with stigma branches (Lersten, 1987). As a result of the swelling of the lodicules, the floret in the anthers is opened (Lersten, 1987). Anthers are exposed very quickly due to rapid elongation of stamen filaments, which means that they extend their length to three times

the original length in approximately three minutes (Lersten, 1987). Pollen is generally viable for up to 15 to 20 minutes, or 30 minutes in the best conditions, while stigmas are sensitive for pollen for 4 to 13 days (De Vries, 1971). When pollen enters the embryo sac, it germinates in 30 to 60 minutes; otherwise, it dries quickly and loses its functions (Lersten, 1987).

Flowering begins with the first spikelet, which is located in the middle third of the spike near the upper part and continues rapidly upwards, but the downwards flowering process is a little slower. Anthesis begins in the middle of the spikes and progresses up and down (De Vries, 1971). The lowest few spikelets are generally sterile, and sometimes the tip is as well, so the central spikelets are the most representative part of the spike (Lupton, 1987). Maturity begins in the central spikelets of the spikes and continues until all spikes become mature (De Vries, 1971) .

Likely as a result of domestication, cleistogamy evolved in wheat and became a desirable trait for today's line breeding (Boeven et al., 2016). Closed flowering provides high homogeneity, which is necessary for variety registration and seed production (Boeven et al., 2016). On the other hand, cross-pollination is the most important male floral trait for hybrid seed production. Hybrid wheat breeding programs are in a bottleneck in terms of good male lines, because identifying those lines demands a lot of time and effort (Boeven et al., 2016). Anther extrusion and the length of anthers and their filaments are some of the traits that determine the release of pollen outside of the wheat floret, for instance (De Vries, 1971). In addition, environmental conditions of the season have great impact on out-crossing, and wheat has relatively heavy and low viable

pollen (D'SouzA, 1970; De Vries, 1971; Waines and Hegde, 2003). Most importantly, commercial hybrid seed production must have male-sterile female lines to avoid self-pollination and ensure cross-fertilization necessary for heterosis (Whitford et al., 2013).

2.4 Male Sterility Systems for Hybrid Wheat

Wheat is an autogamous self-pollinated crop; therefore, hybrid seed production is a major problem and limits hybrid wheat production (Adugna et al., 2004). As a result of domestication period, wheat flower is cleistogamous which is desirable for line breeding; to get high homogeneity for variety registration (Harlan and Zohary, 1966; D'SouzA, 1970; Boeven et al., 2016). On the other hand, hybrid breeding requires a strict system to control self-pollination (Kempe and Gils, 2011; Boeven et al., 2016). The most desirable floral trait for cross-pollination in hybrid wheat production systems is the open florets for both male and female parents (Whitford et al., 2013). The basic way to achieve cross-pollination is the mechanical removal of the anthers (Koemel et al., 2004). Emasculation is the most common mechanical removal method in small crossing blocks for line development but is impractical for hybrid seed production. Wheat florets are cut with scissors and the anthers are removed with a pair of tweezers before anthesis is reached. Because of the flower structure, emasculation requires intense labor and is time-consuming for wide-ranging breeding programs (Singh et al., 2015).

Hybrid wheat breeding programs require heterosis. Many studies have proved that F_1 hybrids are superior to more yielding parents (Kihara, 1967). Establishing hybrid wheat programs requires male sterility systems. Non-functional anthers, pollen, or male gametes imply male plant sterility (Kempe and Gils, 2011). In wheat, there are several

hybridization systems based on both genetic and chemical male sterility (Adugna et al., 2004). The most practicable ones for autogamous crops are sterility by CHA or cytoplasmic male sterility (CMS), photo or thermo male sterility, and genetically modified hybridization systems (Longin et al., 2012). CHA and CMS systems have the most common use. These two systems have been developed in two different periods. CMS has been used since the 1960s and 1970s, while CHA was first used in the 1980s and continued in the 1990s (Adugna et al., 2004).

A CMS system is one of the ways to achieve cross-pollination for hybrid wheat production (Chen, 2003). The first CMS line was discovered by Kihara (1951); the male sterility came from *Aegilops*-by*Triticum* crosses (Adugna et al., 2004). This discovery, along with the development of fertility restoration systems in common wheat, has initiated a new interest in F_1 hybrids (Murai and Tsunewaki, 1993; Adugna et al., 2004). Since then, several male sterility systems have been proposed, and today approximately 70 different male sterile cytoplasms exist (Murai and Tsunewaki, 1993; Chen, 2003). *T. timopheevii*, *Aegilops kotschyi*, and *Ae. ventricosa* cytoplasms can be used, but most of the hybrid wheat research programs use a single male sterility system derived from *T. timopheevi* (Maan and Lucken, 1972). T-CMS, K-CMS, and V-CMS are some of the CMS types based on the cytoplasm type (Singh et al., 2015). Among all the types, the *T. timopheevi* has been the most widely used since 1962 (Wilson and Ross, 1962; Singh et al., 2015).

A three-line system (male sterile, maintainer, and restorer lines) is used for hybrid wheat production (Guo et al., 2006). The A-line is the male sterile line, which is

commonly derived from *Triticum timopheevi*. i.e., has a *Triticum aestivum* nuclear genes and a *Triticum timopheevi* cytoplasm (Maan and Lucken, 1972). The sterile A-line contributes to male sterility in both genes and the cytoplasm. The B-line is the maintainer line, which carries the same genes as the A-line but has fertile cytoplasm (Prakash et al., 2012). Thus, it has the cytoplasm and nuclear genes from *Triticum aestivum*. Restorer genes were discovered in 1962 (Johnson et al., 1967), and a restorer line contains fertility restoration (Rf) genes. A x R crosses produce fertile hybrid seed (Prakash et al., 2012) that are sold to the producer as F_1 seed. The three-line system is also necessary to produce the next round of hybrid seed production (Guo et al., 2006).

As an alternative to CMS, CHAs are a form of induced male sterility that prohibits active pollen development (Rowell and Miller, 1971; Kempe and Gils, 2011). Chemical hybridizing agents or gametocides is a term used to describe a group of chemicals that cause male sterility in plants (Kempe and Gils, 2011; Whitford et al., 2013). The United States Environmental Protection Agency registered Genesis® (Monsanto) in 1997, which was used as a sterilizing agent for wheat until 2007. Croisor®100 was developed by Saaten Union in France, and today it is the only gametocide for commercial hybrid wheat production (Kempe and Gils, 2011; Whitford et al., 2013).

There are advantages and disadvantages of both hybridization systems. Male sterility is heritable in most of the angiosperm species because CMS is specified by the mitochondrial genome (Kempe and Gils, 2011). In addition, CMS does not cause any intellectual property problems. The discovery of CMS in wheat hybrids opened a new

door to exploit heterosis for grain yield in F_1 (Imrie, 1966). However, cytoplasm-based male sterility has some limitations (Adugna et al., 2004). The restoration system is complex: while A-line has some effects on agronomic traits, maintaining the three-line system does not favor the economic benefits of hybrid production (Chen, 2003; Singh et al., 2015). In addition, the availability of restoring genes and unstable male sterility are other problems associated with CMS systems (Murai and Tsunewaki, 1993).

CHAs have some advantages over CMS, but they also have some systemic issues. CHA systems are fast, flexible, and do not require maintainer or restorer lines for hybrid production (Rowell and Miller, 1971; Kempe and Gils, 2011). This system allows large-scale production and reduces the time for hybrid production significantly compared to the CMS system (Kempe and Gils, 2011). Environmental effects such as wind, rain, and heat may decrease the efficiency of the chemicals (Whitford et al., 2013). Male and female parents should be planted separately so as not to effect the male parent's fertility while applying the chemical to the female parent (Singh et al., 2015). Most importantly, CHAs can effect F_1 seed quality and hybrid vigor (Whitford et al., 2013).

Genetic male sterility (GMS) is the male sterility system that uses the nuclear-encoded genes for mutations. GMS could take place spontaneously or be induced (Whitford et al., 2013). While it widely occurs in plants, there are eleven genes in wheat that can induce GMS. GMS system can be used during recurrent selection because it keeps the genetic variation at the same level while favorable alleles frequency increase

in the breeding population. On the other hand, it cannot be identified phenotypically so the system requires significant effort to identify the plant sterility (Singh et al., 2015).

Besides the CMS, CHA, and GMS, there are photo, thermo, and thermo-photo male sterile systems that do not require maintainer lines (Singh et al., 2015). These systems are the results of the interaction of genetic factors and environment. Most of these systems require extreme day length or temperature (Guo et al., 2006).

2.5 Justification for and Benefits of Hybrid Wheat Production

The demand for agricultural and natural recourses is rising due to population growth. Studies have indicated that over a billion people around the world are chronically malnourished (Foley et al., 2011). According to United Nations (UN) population projections, a world population increase of 2.25 billion is expected by 2050, at which point the world population would be 9 billion (Alexandratos and Bruinsma, 2012). Food production should continue to increase steadily to meet future demands caused by climate change and losing agricultural land (Foley et al., 2011). During the last 50 years there was only a 9% increase in agricultural lands, while grain production has almost doubled (Pretty et al., 2005). Recently, a lot of agricultural land has been lost to urbanization, salinization, and soil erosion (Godfray et al., 2010). Therefore, researchers have focused on increasing grain yield in order to be able to create greater yield from less area.

Since wheat was domesticated approximately 10,000 years ago, it has become a major crop all around the world (Dubcovsky and Dvorak, 2007). According to one study conducted by the Food and Agriculture Organization of the United Nations (FAO) and

Organization for Economic Co-operation and Development (OECD), cereals consumption is expected to increase over 390 million tons between 2014 and 2024 (FAO, 2016). If the linear rise remains the same, cereals consumption would have hit 4.8 tons/ha in a year, but it is expected to be around 3.8 in 2050 (Alexandratos and Bruinsma, 2012). Line breeding is the major breeding method used in today's wheat production. In wheat, line breeding is not adding enough yield gain per year to meet future demands (CGIAR, 2016). Therefore, there is new interest in hybrid wheat breeding due to its great potential to increase grain yield and stability (Boeven et al., 2016).

The first period of hybrid wheat production was not a success despite studies that reported heterosis for multiple traits in wheat. There were several reasons for this, including the fact that the studies were too small, which resulted in overestimating heterosis (Barbosa-Neto et al., 1996). On the other hand, hybrids were very promising due to other high-performing hybrid crops in the market (Longin et al., 2014). For instance, yield increase of maize hybrids has continued (FAOSTAT, 2013). The differences between maize and wheat during the first attempts were the amounts of investment and effort put into hybrid corn breeding by the public sector and especially the private sector. Such high investments meant that genetic engineering had been adopted in corn breeding programs at very early stages (Whitford et al., 2013).

Hybrid breeding has several advantages over line breeding (Longin et al., 2014), namely the exploitation of heterosis to increase the value of important traits, as well as yield stability, particularly in low-yielding environments (Tester and Langridge, 2012;

Longin et al., 2014). Genetic diversity between parents is known to be an increasing factor of heterosis (Melchinger, 1999). Briggle (1963), Livers and Heyne (1968), Uddin et al. (1992), Jordaan et al. (1999), and Koemel et al. (2004) have reported heterosis for grain yield in wheat hybrids. Wheat hybrids were shown to have greater genetic gain than the pure lines (Koemel et al., 2004), and the heterosis estimate range is between 3.5% and 15% (Longin et al., 2012). The current prediction about hybrid yields is that hybrids will outperform the line varieties by approximately 10% (Longin et al., 2014). Also, hybrids outperform line varieties in terms of drought tolerance and nutrient use efficiency (Singh et al., 2010).

The long-term achievement of hybrid wheat production relies on several variables (Longin et al., 2014), the most important of which is justifying the cost of hybrid wheat seed production for farmers. Twenty percent heterosis is required to cover the expenses and make a profit (Singh et al., 2010). Breeding companies could increase their profit by using hybrids instead of lines due to the sharp reduction of farm-saved seed. As a result, greater investment in research and development (R&D) could be made. Additionally, it seems impossible to maintain the current R&D budget for line breeding based on the percentage of farm-saved seed (Longin et al., 2014). At some point hybrid breeding programs should be separated from line breeding programs because both have different breeding goals (Boeven et al., 2016). Line breeding still has the advantage of having larger research programs; however, with new developments in hybrid seed production and more detailed screening and selection with the high general combining

ability (GCA), there is a great potential to increase the efficiency of hybrid breeding (Longin et al., 2014).

2.6 High-Parent, Mid-Parent, and Commercial-Heterosis

Heterosis is defined as the attainment of better performance in a progeny compared to its superior parent (Cox and Murphy, 1990). It is also referred to as hybrid vigor and leads to superior progenies that have a higher yield, better quality, or higher resistance to biotic and abiotic stress (Singh et al., 2015).

Heterosis can be estimated in different ways, such as high-parent heterosis, mid-parent heterosis, and commercial heterosis. High parent heterosis is the better performance of the progeny than the superior parent (Packer and Rooney, 2014). Hybrid performance can be estimated according to its genetic potential with high parent heterosis (Boland and Walcott, 1985). If a progeny has better performance than the average of the two parents, it is called mid-parent heterosis (Barbosa-Neto et al., 1996). Finally, commercial heterosis refers to hybrids that outperform the best commercial line and is the most important one in regard to hybrid breeding (Longin et al., 2012), especially in a particular environment (Boland and Walcott, 1985).

Hybrids have several advantages over line breeding, and the main one is the exploitation of heterosis (Longin et al., 2014). Heterosis is exploited successfully by cross-pollinated crops, such as maize (Krystkowiak et al., 2009). After heterosis was reported in autogamous crops in the 1920s (Briggle, 1963), hybrid studies on self-pollinated crops also have been initiated, including wheat (Krystkowiak et al., 2009; Jaiswal et al., 2010). During the first period of hybrid wheat breeding, different levels of

heterosis were observed in the studies; this was because of small plots with a limited environment as well as limited seed production due to hand emasculation and crossing (Boland and Walcott, 1985). In these studies, heterosis for grain yield ranged from 5% to over 10% (Kindred and Gooding, 2005). According to more recent experiments, heterosis for grain yield in hybrids overcame the pure lines by about 5–15% (Singh et al., 2010). On the other hand, due to commercial acceptance for wheat hybrid, the level of heterosis should be more than 20% compared to the best commercial variety for the target area (Singh et al., 2010).

The dominance of the genetic effect is the foundation of heterosis (Barbosa-Neto et al., 1996). It is suggested that if the genetic diversity between parents is enhanced, hybrid heterosis should be increased as well (Barbosa-Neto et al., 1996). Therefore, the aim of the hybrid programs is to create genetically divergent heterotic pools to increase heterozygosity for the hybrids (Whitford et al., 2013). It is not expected to see a genetically divergent heterotic pool in wheat elite germplasm because they are well adapted to a specific area. Therefore, creating a diverse heterotic pool by using pure lines from different environments has been proposed, but this method needs some pre-requirements such as vernalization, photoperiod, and quality (Whitford et al., 2013). Another approach is creating hybrids between different classes of wheat, such as adapted and non-adapted lines (Longin et al., 2012); with this method hybrids yield reached 30% heterosis level compare to their parents (Singh et al., 2010). Nevertheless, commercial hybrids have to obtain the quality, yet hybrids that produced from hard red winter wheat crossed with soft red winter wheat cannot maintain that quality (Singh et al., 2010).

Thus, a more reliable method must be developed to create diverse heterotic pools with high combining ability and high end-use quality (Whitford et al., 2013).

Research on heterosis is also a helpful tool for learning about the combining ability of parents (Singh et al., 2004). It is important to identify the parental genotypes with good general combining ability (GCA) and high specific combining ability (SCA) in hybrid wheat production (Krystkowiak et al., 2009).

2.7 Heritability and Repeatability for Floral Traits in Wheat

Heritability and repeatability are the two aspects of genetic and phenotypic variances that are necessary for designing a sufficient breeding program (Roman et al., 2000). Repeatability is a measurement that compares the proportion of total variance differences of a trait among the individuals (Wolak et al., 2012). It presents a measurement to understand how an individual shows a consistent performance over the years (Dohm, 2002). It also helps to identify which of the traits could be improved by selection (Roman et al., 2000). While low repeatability can be an indicator of measurement problems (Dohm, 2002), a high repeatability estimate could interpret the breeding value of the individuals with a few consecutive measurements (Laviola et al., 2013). Most researchers indicated that repeatability sets an approximate upper limit to the heritability estimate for the specific trait improvement (Wolak et al., 2012), because heritability estimate presents only genetic differences, while repeatability represents both genetic and environmental variation among individuals (Dohm, 2002).

Heritability has an important role in plant breeding. It sets a parameter for a development model of a population and uses the reliability of phenotype to identify

breeding value (Mohsin et al., 2009). Heritability estimate is defined as the ability to distinguish a response for a selected trait from generation to generation. The ratio of the genotypic variance (σ_g^2) to the phenotypic variance (σ_p^2) gives the heritability (H^2) (Fehr, 1991). The genotypic variance includes additive, dominance and epistatic genetic variances, and genetic differences among individuals cause this variation. Phenotypic variance is referred to as the total variation among phenotypes (Dudley and Moll, 1969). The mean of the genotype across *m* trials represents target environments, and *r* replicates for each trial gives the phenotype (Piepho and Möhring, 2007). Multiple locations and years are required to calculate heritability estimates (Holland et al., 2003).

Broad-sense and narrow-sense heritability are ways of explaining heritability (Fehr, 1991). Broad-sense heritability is identified as the ratio of total genetic variance—which includes additive, dominance and epistatic variance—to phenotypic variance (Piepho and Möhring, 2007). Narrow-sense heritability is the proportion of additive genetic variance to phenotypic variance (Dudley and Moll, 1969). Regarding calculating these heritability estimates of a trait, there are several methods. One of them is the variance component method, which provides flexibility to differentiate between the effectiveness of selection procedures based on variance components (Fehr, 1991).

2.8 Semi-dwarfing Genes in Wheat

There are several important requirements of hybrid wheat breeding: synchronizing the flowering time between parents, adequate floral traits such as anther extrusion, and plant height are some of the important requirements (Boeven et al., 2016). Introduction of dwarfing or reduced height (Rht) genes in wheat have led to the Green

Revolution (Buerstmayr and Buerstmayr, 2016). Following the Green Revolution, significant grain yield increase has been observed due to shorter and stiffer plant stems that reduce lodging (Guedira et al., 2010). The most common mutant dwarfing alleles in wheat among a series of homeologous Rht-1 alleles are the Rht-B1b (formerly Rht1) and Rht-D1b (formerly Rht2) (Allan, 1989; Buerstmayr and Buerstmayr, 2016). Today about 90% of U.S. wheat cultivars contain at least one of the two genes shown above (Buerstmayr and Buerstmayr, 2016).

Norman Borlaug successfully imported Rht-B1b and Rht-D1b genes, which were derived from the Japanese genotype "Norin 10" into wheat cultivars (Buerstmayr and Buerstmayr, 2016). These genes are located on chromosomes 4BS and 4DS, respectively (Guedira et al., 2010), and encode DELLA proteins (Boeven et al., 2016). DELLA proteins are a restrained gibberellic acid (GA) that allow responsive growth in the wild types (Rht-B1a and Rht- D1a) while promoting mutant dwarf genes for reduced height (Pearce et al., 2011).

Although the effectiveness of semi-dwarfing alleles was equal in terms of reducing plant height (Buerstmayr and Buerstmayr, 2016), Rht-B1b had a less negative effect on grain size (Allan, 1989). Rht-B1b gene are also correlated to slightly taller plant height than Rht-D1b (Allan, 1989). Studies indicated that semi-dwarf cultivars had a restriction on good male traits, such as pollen mass and pollen that shed outside of the floret (Boeven et al., 2016), meaning that there is a positive correlation between plant height and pollen mass (Langer et al., 2014).

3. MATERIALS AND METHODS

Texas A&M University's "College Station Center of Excellence" wheat breeding pipeline is explained in Table 1 with selection years and period span. The "Amarillo Center of Excellence" has a similar pipeline where the Amarillo Advanced, Amarillo Preliminary and Amarillo observations are similar to the South Texas Advanced (STA), South Texas Preliminary (STP) and South Texas Observations (SOBS), respectively. The Uniform Variety (UVT) and Texas Elite (TXE) Trials were used for this research. The measurements were taken for two years. During the 2016–2017 growing season the lines were planted as plots with two replications, and the lines were planted in a meter row with three replications in the 2017–2018 growing season. A randomized complete block design (RCBD) was used for this research. In November 2016, 34 UVT lines and 37 TXE lines were planted in College Station (CS) and McGregor (MCG), Texas (TX). The TXE lines were the same in both locations. On the other hand, 31 UVT lines were the same in both locations, but there were three different lines in CS and MCG. 'Billings', 'Jackpot', and 'SY Razor' were planted in CS, while 'Underwood', 'WB 4269', and 'Zenda' were planted in MCG. In November 2017, 37 of the same UVT lines and 37 of the same TXE lines were planted in both locations.

In both locations, beginning from the initial floral observations, notes were taken as frequently as possible in order to record the floral traits as accurately as possible.

Table 1. The Texas A&M AgriLife hard red winter wheat breeding pipeline.

Year	Trial Name	Generation
1	GH Crossing Block	
2	GH Rows	F_1
3-5	Field Plots	F_2-F_4
6	Head-rows	$F_{4:5}$
7	Observation Nurseries (SOBS)	$F_{4:6}$
8	Preliminary Yield Trials (STP)	$F_{4:7}$
9	Advanced Yield Trials (STA)	Advanced
10	TXE	
11	TXE, SRPN, Increase	
12	TXE, UVT, SRPN, Increase	
13	Release	

GH = Greenhouse; SOBS = South Texas Observations; STP = South Texas Preliminary; STA= South Texas Advanced; TXE= Texas Elite; UVT= Uniform Variety Trials; SRPN = Southern Regional Performance Nursery.
Source: Dr. Amir Ibrahim, Texas A&M University- College Station. This pipeline shows operations for the College Station Center of Excellence that develops and releases wheat cultivars for south, central and northeast Texas.

3.1 Non-Gender-Specific Categories

3.1.1 Heading Date

Heading date was the initial observation taken on both the UVT and TXE in both growing seasons. It was noted when at least 50% of the spikes in the plots or rows were completely out of the boot. Days to heading was noted according to Julian Calendar.

3.1.2 Anthesis Date

The anthesis date was noted when at least 50% of the spikes in the plots or rows were showing yellow pollen, either outside or inside of the florets. The anthers were sometimes trapped inside of the floret. To observe the pollen inside of the floret, it was necessary to carefully pull the palea and lemma apart and look at the inside of the floret to observe anthesis. It was important not to damage the florets, because this could have

affected the later observations for anther extrusion. Days to anthesis was noted according to Julian Calendar.

3.1.3 Plant Height

Plant height was measured at the end of the growing season when the plants were all senesced. Representative plants in the center of the plots or rows were measured in centimeters with a yardstick from the soil surface to the tip of the spike excluding the awns.

3.2. Gender-Specific Categories

3.2.1 Male Traits

3.2.1.1 Anther Extrusion

Anther extrusion is an important feature in hybrid breeding programs. If a genotype shows a high percentage of anther dispersal (Figure 1), it would be a great male parent for hybrid wheat production. A few spikelets become viable at a time, and the whole period lasts for one to three days. Therefore, three days after the anthesis date, five plants from each plot or row were selected randomly, counted for pollen dispersal, and divided into a number of spikelets. The top and bottom two spikelets were not included in the counting. Anther extrusion is listed in the tables as a percentage.

Figure 1. Anther extrusion in a wheat spike.

3.2.1.2 Anther Score

The anther score is a visual scoring for anther extrusion that includes anther size and how many anthers extruded out of one floret (Figure 2). The scoring system is based on a scale of 1 – 9, where 1 is the lowest extrusion and 9 is the maximum attained extrusion.

Figure 2. Visual estimation of anther extrusion rates. The scoring system is based on a scale of 1 – 9, where 1 is the lowest extrusion and 9 is the maximum attained extrusion.

3.2.2 Female Traits

During the 2016 – 2017 season, there were no separate plots for measuring female traits. Therefore, two plants from each plot were entirely emasculated. Notes were only taken at CS for the female traits, but at both CS and MCG for the male traits.

There were some issues with collecting female traits notes; for example, sometimes secondary tillers were used, or the emasculated spikes received pollen from outside. Such issues made these types of observations difficult; therefore, during the 2017–2018 growing season, separate head-rows were planted to allow for applying Croisor CHA agent to obtain sterile females in both locations with two replications. Due to weather conditions, Croisor application occurred a bit late. March 20, 2018 was the date for CS, and March 24, 2018 for MCG for the CHA application. As a result of the late application, there were a lot of missing data. Table 2 modified from A. PH. De Vries (De Vries, 1971), and use for visual assessment of gape and stigma exsertion.

Figure 3. Open florets. Figure is showing clear separation between the lemma and palea that are important for producing F_1 hybrid seed.

3.2.2.1 Angle of Glume Separation During Viability (Gape)

The angle of glume separation during viability, or gape, is a visual measurement for glume separation (Figure 3). The gape observation was taken after anthesis was reached

when the palea and lemma separated due to the swelling of the lodicule. This may happen to allow anthers to be extruded outside of the floret but also for the female florets to receive viable pollens. The scoring system is based on a scale of 1 – 5, where 1 and 5 are the lowest and highest glume speration values, respectively.

3.2.2.2 Stigma Exsertion

With the glume separation, it is possible for the feathery stigma branches to extrude outside of the floret during the viability period. Stigma exsertion is a visual measurement that determines how much stigma extrudes from the floret. The scoring system is based on a scale of 1 – 5, where 1 and 5 are lowest and highest exsertion values, respectively.

Table 2. Guidelines for measuring female floral characteristics in common wheat.

Floral Characteristics	Scoring Scale				
	1	2	3	4	5
Gape	0–5^{o}	6–10^{o}	11–15^{o}	16–20^{o}	≥ 21^{o}
Stigma Exsertion	No movement	Reaching toward top	Tips breach glume	Branches visible outside of glume	Branches highly visible outside of glume

Modified from A. PH. De Vries (1971) (De Vries, 1971).

3.3 Statistical Analyses

The analysis of variance (ANOVA), means, LSD and Pearson's correlation coefficients analyses were performed using SAS software version 9.4. Traits total means for each genotype over environments were used to preform Pearson's correlation coefficients analyses.

Repeatability sets the upper limit for heritability. Repeatability results were calculated based on the ANOVA of individual years and locations, while the ANOVA of the combined environments were used for estimating broad-sense heritability values. Repeatability results were estimated from variance components with the equation $R = \sigma_g^2 / \sigma_p^2$, where σ_g^2 is the genetic variance and σ_p^2 is the phenotypic variance in individual environments. Heritability coefficients were estimated from variance components with the equation $H^2 = \sigma_g^2 / [(\sigma_e^2/rt) + (\sigma_{ge}^2/t) + \sigma_g^2]$, where σ_g^2 is the genetic variance, σ_e^2 is the experimental error, σ_{g*e}^2 is the genotype-by-environment interaction, r is the number of replications, and t is the number of test environments.

The coefficient of variation, which is the ratio of the standard deviation to the mean, is a measure of dispersion used to express precision and variation. In this study, environmental coefficient of variation (ECV) and genotypic coefficient of variation (GCV) were calculated. ECV values were calculated using SAS. The formula of ECV is $[(\sqrt{\sigma_e^2})/ \bar{x}] *100$, where σ_e^2 is the experimental error variance, and $\bar{x}$ is the total mean. The GCV equation is $[(\sqrt{\sigma_g^2})/ \bar{x}] *100$, where σ_g^2 is the genetic variance, and $\bar{x}$ is the total mean.

3.4 Molecular Analyses

All of the genotypes were planted in trays, and then DNA was isolated from young leaves according to the protocol of CTAB DNA extraction (Liu et al., 2013). SNP markers associated with the height reduction genes Rht1-B1 and Rht1-D1 were used for genotyping the UVT and TXE lines. SNP genotyping was performed using the LGC platform (formerly KBiosiences) (Semagn et al., 2014).

4. RESULTS AND DISCUSSION

Floral characteristic observations were collected from 37 UVT and 37 TXE lines over two years and two locations. First, all of the floral traits were analyzed for normality (Ghasemi and Zahediasl, 2012), and results showed a normal distribution, which means the assumptions of ANOVA were met. Therefore, ANOVA was performed using SAS for individual years and locations as well as the combined environments. UVT and TXE lines were found to be significantly different ($P < 0.05$) for non-gender and male traits according to ANOVA tables for individual year and location (Tables 3, 4, 5 and 6); the exception was the plant height of UVT lines in 2017 in MCG (Tables 3). In 2017, female traits were evaluated only in CS and lines were found to be significantly different (Tables 3 and 4). On the other hand, UVT lines in MCG trials were significantly different ($P < 0.05$) as well as TXE lines in CS for stigma exsertion ($P < 0.05$) and gape ($P < 0.01$) in 2018 (Table 5 and 6). The combined environments analyses showed significant variability among genotypes ($P < 0.05$) for all floral characteristics except gape in TXE (Table 7). In addition, the genotype-by-environment interactions were significant ($P < 0.05$) for all traits, indicating the environmental effects for these traits (Table 7). The significant genotype-by-environment interaction is comparable to previous findings reported by Langer et al. (2014) and Boeven et al. (2016).

There are several factors that affect floral measurements, including emasculation, labor intensity, time constraints, and weather conditions. During 2016–2017 growing season, emasculation was done in the field in order to observe female floral traits. However, emasculation is a very labor-intensive process and time constraints created

some measurement problems. In addition, because of limited time, CS was the only location where notes were collected for stigma exsertion and gape in 2017. After plants headed, observations needed to be taken daily, but sometimes it was not possible to do so because of weather conditions. Genotype-by-environment interactions were observed in both UVT and TXE trials. Genotype-by-environment interaction refers to the phenomenon that genotypes show different performance from one environment to another, and weather conditions could be one of the reasons for this. When the days to heading trait was compared between the growing seasons, it was 15 days earlier for UVT lines (Table 13) and 21 days for TXE lines in CS in 2017 (Table 14). The gap was similar for the genotypes in McGregor. In mid-March and mid-April of 2017 at CS, the lowest and highest maximum temperatures observed were 20 °C and 34 °C, while it was 13 °C and 27 °C in 2018. Also, more sunny days were experienced in 2017 compared to 2018. Weather data were taken from www.wunderground.com for the peak observation period for floral traits.

Days to heading and days to anthesis showed high repeatability with ranged from 0.82 to 0.99 for each year and location (Table 8, 9, 10, and 11). The heritability estimates for these traits were approximately 0.90 and 0.88 for the UVT and TXE, respectively (Table 12). The high heritability estimate of days to heading is supported by previous studies published by Langer et al. (2014) and Boeven et al. (2016). Female traits had low repeatability values in 2017 for CS as well as in 2018 for both locations (Tables 8, 9, 10, and 11). Even though female traits had very low heritability estimates due to problems during the collection of data, we believe there are some promising lines

that can have suitable characteristics of hybrids as female parents. There is a lack of detailed research focusing on female traits in general. Improved and standardized methods on studying female traits would increase the reliability of studies, and this could increase both repeatability and heritability estimates. According to studies conducted by Langer et al. (2014), Boeven et al. (2016) and Muqaddasi et al. (2016), anther extrusion is a highly heritable trait which supports findings reported in this study. The heritability of anther extrusion ranged from 0.82 to 0.87 for TXE and UVT lines (Table 12), respectively. Anther score had similar heritability results as anther extrusion, ranging from 0.81 to 0.84 for TXE and UVT lines (Table 12), respectively. The repeatability of male traits supports the heritability estimates of anther extrusion and anther score (Tables 8, 9, 10, 11, and 12). This indicates that male traits could be enhanced by selection and plant breeding.

The environmental coefficient of variation (ECV) and genotypic coefficient of variation (GCV) are common tools for explaining variation. High ECV values point to a higher degree of error associated with variability among lines treated alike in the trials. High ECV reflects either high variation due to environmental effects or problems during the data collection. On the other hand, high GCV indicates that there is a minor environmental effect and points to good variability among lines to warrant selection. The non-gender floral traits exhibited low ECV values for each growing season for both locations as well as in the combined analyses, which render them highly reliable (Tables 13 and 14). In addition, days to heading and days to anthesis had higher GCV, compare to ECV, ranged from 5.37% to 5.50% for both trials in both years based on combined

environments analyses. (Tables 13 and 14). This indicates that there is a variation among the Texas A&M AgriLife wheat pipeline in terms of reaching the maturity that can help for matching ideal parents for hybrid studies in the future. On the other hand, plant height higher ECV results compare to GCV values for both trials based on combined environments analyses, that means there is not enough variation amongst to lines in terms of plant height. Male floral traits showed higher GCV for both trials ranged from 27.28% to 58.56 based on individual years and location analyses (Tables 15 and 16). The results assure that male traits did not affected by the environments over years and there is a good variability among lines in terms of anther extrusion and anther score. Female floral characteristics, stigma exsertion and gape had the lowest GCV levels among the gender floral traits and lower than the ECV values (Tables 15 and 16). UVT lines had a 12.43% GCV for stigma exsertion (Table 15), while it was 16.07% for TXE lines (Table 16). Gape had 14.76% and 8.89% GCV values in the UVT and TXE, respectively (Tables 15 and 16). This indicates that the variability of female traits was significantly affected by environmental factors compared to the rest of the traits. In addition, the variability of floral traits was low among the Texas A&M AgriLife wheat pipeline.

UVT lines included either commercially released varieties or the promising advanced lines from the TXE lines. Lines entered into the UVT represent release candidates for the Southern Great Plains submitted by public and private breeding programs, including the Texas A&M AgriLife breeding programs in Amarillo and College Station, TX. The TXE is comprised of only Texas advanced lines in addition to commercial check cultivars. The TXE advanced lines are typically tested for two years

prior to their advancement into the UVT or exclusion from further testing. The best lines tested in the first year TXE are also tested in the Southern Regional Performance Nursery (SRPN) in more than forty environments in the U.S. In both growing seasons, TXE lines had better repeatability results compared to the UVT lines for male and female traits in both locations (Table 8, 9, 10, and 11). We can assume that because TXE lines are more adapted the Texas adaptation zones, they exhibited higher repeatability results during the growing seasons. On the other hand, the mean and ranges of all investigated traits were higher for UVT lines, which can be attributed to larger genetic diversity (Table 15 and 16). However, the differences were not significant based on LSD values at 0.05 level of significance. The male traits GCV values of the TXE were generally higher across most environments, whereas the UVT had higher GCV values across most environments for female parents (Table 15 and 16).

The mean of the floral traits was calculated in order to determine best and poor performing lines. Pollen viability is an important factor for hybrid wheat to synchronize male and female parents; hence, days to heading and days to anthesis notes were taken (Table 13 and 14). Males must reach anthesis after females because they have a shorter window for pollen viability than female parents' stigma receptivity. Also, male candidates must be taller than female parents to maximize cross-pollination (Table 13 and 14). The selection criteria did not set for the non-gender traits at this point, but the mean of this results can be used in the future studies for hybrid breeding to match the parents.

Male parent candidates must have good anther extrusion and should not be trapped inside the florets (Longin et al., 2012). The percentage of anther extrusion directly affects cross-pollination ratio in wheat. Tables 15 and 16 include the anther extrusion and anther score means for each genotype. For UVT lines, the lines that had more than 50% of anther extrusion were chosen (Table 17). Even though the mean of anther extrusion is 33% for TXE lines (Table 16), the minimum was set as 41% of anther extrusion for male parent candidates. When UVT and TXE lines were compared, UVT lines had better anther score and anther extrusion (Table 15 and 16). The lines were selected to have at least a score of 5 and 4 for anther score for UVT and TXE, respectively (Table 17).

In hybrid wheat production, female parents must have open florets and extrude stigmas to increase the chance of cross-pollination. Therefore, stigma exsertion and gape notes were collected during the growing seasons (Table 15 and 16). Problems during the data collection process have resulted in significant missing data for the female traits. For this reason, as mentioned previously, the female traits have low GCV levels. The lowest score should be set at 2 for stigma exsertion and 2.5 for gape for both UVT and TXE lines. Based on these criteria, UVT and TXE lines were selected as candidates for the hybrid-breeding program (Table 17). Some of the lines could be used as both male and female parents, as they showed good performance in terms of male and female traits.

Pearson's correlation coefficients were calculated to identify whether there is any correlation between the floral traits. Days to heading and days to anthesis were positively and significantly correlated in both UVT and TXE lines ($r=0.99$; $P<0.001$) for

combined environment analyses (Table 18) and individual years and location analyses (Table 19). Stigma exsertion was positively and significantly correlated to gape. The correlation was more significant for UVT lines ($r = 0.77$; $P < 0.001$) compared to TXE genotypes ($r = 0.53$; $P < 0.001$). The range, based on individual years and locations correlation analyses, was between 0.58 to 0.86 ($P < 0.001$; Table 19). The positive correlation between female traits was expected. The results suggested that if the angle of glume separation increased, more stigma feathers could extrude outside of the floret. There was a positive and significant correlation between anther extrusion and visual anther extrusion, which is called anther score in this study (Table 18). The correlation between these two male traits was approximately 0.97 for both UVT and TXE lines ($P<0.001$; Table 18). In addition, the correlation results between male traits based on each years and locations were ranged from 0.92 to 0.96 ($P < 0.001$; Table 19). In previous research, Langer et al. (2014) and Boeven et al. (2016) found positive and significant correlation between anther extrusion and anther score as well. In terms of these finding, anther extrusion assessment can be made visually instead of using the time-consuming and labor-intensive method of anther counting in the field. This way, notes could be taken faster and could reduce the effect of weather, such as wind and rain, on anther extrusion. Finally, the floral traits did not show significant correlation between each other except the ones previously mentioned (Table 18).

The semi-dwarfing phenotypes are mainly controlled by two genes, Rht1 and Rht2. Rht-B1a and Rht-D1a are the wild alleles, while Rht-B1b and Rht-D1b are the dwarf alleles. Thus, lines were tested for these alleles to identify how many of them have

semi-dwarfing genes. UVT and TXE lines belong to the Texas A&M hard red winter wheat breeding pipeline, which means they were likely selected against their plant height in earlier generations. The semi-dwarfing phenotype is an important part of wheat line breeding in U.S. hard red winter, especially in Texas. The results indicating that only two lines had the wild alleles (Rht-B1a/Rht-D1a) (Table 20). None of the genotypes had double dwarfing alleles (Rht-B1b/ Rht-D1b). Five of the UVT genotypes had Rht2 gene and only one of the TXE line had it (Table 20). In addition, according to Guedira et al. (2010), the hard winter cultivars developed between 1808–2008 had Rht-B1b allele at 77% and Rht-D1b at 8% frequency. Mean values showed that the lines with the wild alleles were taller than the ones with semi-dwarfing genes (Table 21). Also, Rht2 genes were expressed as slightly shorter than Rht1 (Table 21); this result is comparable to the previous study by Pearce et al. (2011). Langer et al. (2014) and Boeven et al. (2016) proposed that dwarfing genes might have negative effects on male traits such as pollen mass and anther extrusion. The wild type had an anther score mean of around 5.4, while it was 4.4 for the lines with Rht1 and 3.9 for the lines with Rht2 for UVT trials (Table 21). In addition, anther extrusion showed similar results as anther score. The lines with Rht2 genes might be used as female parents due to their shorter plant height and higher reducing effect on male traits. However, the conclusions from the height reduction study in terms of comparing plant height between Rht1 and Rht2 genes and the effects of semi-dwarfing genes on male traits are not very strong; because the majority of the lines had Rht1 genes and there are only 6 lines with Rht2 genes.

4.1 Conclusions

The good variability of male floral characteristics showed that Texas A&M AgriLife wheat germplasm have some lines that can be used as male parents in hybrid wheat programs. The high heritability estimates indicate that male traits could be improved by selection and breeding. Also, the significant and positive correlation between anther extrusion and anther score gives the reassurance that visual assessment of anther extrusion could be used alone for selecting parent candidates for hybrid wheat production. Methods of assessing female traits need to be improved and standardized. There are several factors that affect hybrid breeding, and most of them have been studied; however, the most important one is having lines with good anther extrusion. Consequently, selection of lines that have good anther extrusion is important for producing economical hybrid wheat seed.

Table 3. Analysis of variance of the Uniform Variety trial (UVT) in College Station (CS) and McGregor (MCG), TX in 2017 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion	Gape
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	CS
Rep	4.25	1.2	5.9	0	353.3	18.02	2.88	0.14	304.9	33.88	0.06	0.015
Genotype	166.3**	105.2**	167.2**	107.7**	709**	659**	6.78**	7.11**	80**	55.2^{ns}	0.96*	1.08*
Error	2.07	1.04	2.4	0.82	164.8	133.23	1.25	0.62	27.2	38.2	0.50	0.50

* Significant at the 0.05 probability level. ** Significant at the 0.01 probability level. ns not significant at any probability level.

Table 4. Analysis of variance of the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2017 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion	Gape
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	CS
Rep	4.88	3.04	8.45	3.04	31.14	0.49	0.01	0.34	16.55	60.66	0.01	0.05
Genotype	216.80**	75.66**	214.3**	82.14**	630.6**	513.2**	6.88**	4.46**	71.4**	68.3**	0.25**	0.23**
Error	1.49	1.32	2.56	2.18	98.0	72.8	0.74	0.56	17.67	19.4	0.07	0.08

* Significant at the 0.05 probability level. ** Significant at the 0.01 probability level. ns not significant at any probability level.

Table 5. Analysis of variance of the Uniform Variety Trial (UVT) in College Station (CS) and McGregor (MCG), TX in 2018 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion		Gape	
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG
Rep	7.90	1.62	3.53	4.93	718.8	754.7	3.01	4.69	9.82	60.73	0.94	0.69	0.02	3.25
Genotype	55.96**	46.33**	52.81**	45.26**	992.3**	723.7**	7.54**	5.81**	42.11**	43.44**	1.05^{ns}	1.30*	1.27^{ns}	1.60*
Error	2.06	2.14	1.86	2.50	105.2	116.4	0.81	0.88	14.12	8.02	0.74	0.53	1.14	0.70

* Significant at the 0.05 probability level. ** Significant at the 0.01 probability level. ns not significant at any probability level.

Table 6. Analysis of variance of the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2018 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion		Gape	
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG
Rep	3.60	4.45	4.47	3.73	38.20	249.4	0.51	0.40	9.44	148.3	1.27	0.06	1.27	2.88
Genotype	56.90**	30.60**	49.70**	30.70**	838.5**	689**	7.29**	4.65**	40.0**	50.00**	1.11*	0.80^{ns}	1.31**	1.69^{ns}
Error	1.45	2.12	1.24	2.13	89.2	76.2	0.53	0.45	11.0	14.84	0.56	0.51	0.56	1.16

* Significant at the 0.05 probability level. ** Significant at the 0.01 probability level. ns not significant at any probability level.

Table 7. Analysis of variance of the combined environments of the Uniform Variety Trial (UVT) and the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2017 and 2018 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion		Gape	
	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE
Env.	1225**	1240**	1626**	1599**	9609**	10928**	119**	89**	729**	1607**	5.94**	22.18**	47.5**	62.94**
Rep (Env.)	4.08^{ns}	4.00*	3.80^{ns}	4.65*	548**	101^{ns}	3.07**	0.4^{ns}	80.0**	65.4**	0.57^{ns}	0.45^{ns}	1.10^{ns}	1.40^{ns}
Genotypes	289**	292**	284**	289**	2032**	1618**	17.1**	14.0**	92.1**	112**	0.96*	0.86**	1.70**	0.85^{ns}
Geno*Env.	30.0**	40.1**	32.0**	41.0**	292**	332**	3.04**	3.1**	42.2**	39.0**	1.17**	0.66**	1.15*	1.20**
Error	1.93	1.65	2.00	1.91	123	83.6	0.87	0.54	18.1	15.0	0.59	0.37	0.76	0.60

* Significant at the 0.05 probability level. ** Significant at the 0.01 probability level. ns not significant at any probability level.

Table 8. Repeatability results of the Uniform Variety Trial (UVT) in College Station (CS) and McGregor (MCG), TX in 2017 for the traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion	Gape
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	CS
σ^2_g	82.12	52.08	82.40	53.44	272	263	2.77	3.245	26.40	8.5	0.23	0.29
σ^2_p	84.19	53.12	84.80	54.26	437	396.2	4.02	3.865	53.60	46.7	0.73	0.79
R	0.98	0.98	0.97	0.98	0.62	0.66	0.70	0.84	0.49	0.18	0.32	0.37

σ^2_g = genetic variance; σ^2_p = phenotypic variance; R = repeatability.

Table 9. Repeatability results of the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2017 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion	Gape
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	CS
σ^2_g	107.66	37.17	105.87	39.98	266.30	220.20	3.07	1.95	26.87	24.45	0.09	0.08
σ^2_p	109.15	38.49	108.43	42.16	364.30	293.00	3.81	2.51	44.54	43.85	0.16	0.16
R	0.99	0.97	0.98	0.95	0.73	0.75	0.81	0.78	0.60	0.56	0.56	0.48

σ^2_g = genetic variance; σ^2_p = phenotypic variance; R = repeatability.

Table 10. Repeatability results of the Uniform Variety Trial (UVT) in College Station (CS) and McGregor (MCG), TX in 2018 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion		Gape	
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG
σ^2_g	17.97	14.73	17.00	14.25	295.7	202.4	2.24	1.64	9.33	11.81	0.155	0.385	0.065	0.45
σ^2_p	20.03	16.87	78.86	16.75	400.9	318.8	3.05	2.52	23.45	19.83	0.895	0.915	1.205	1.15
R	0.90	0.87	0.90	0.85	0.74	0.63	0.73	0.65	0.40	0.60	0.17	0.42	0.05	0.40

σ^2_g = genetic variance; σ^2_p = phenotypic variance; R = repeatability.

Table 11. Repeatability results of the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2018 for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion		Gape	
	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG	CS	MCG
σ^2_g	18.48	9.49	16.15	9.52	249.7	204.2	2.25	1.40	9.67	11.72	0.28	0.15	0.38	0.27
σ^2_p	19.93	11.61	17.39	11.65	338.9	280.4	2.78	1.85	20.67	26.56	0.84	0.66	0.94	1.43
R	0.93	0.82	0.93	0.82	0.74	0.73	0.81	0.76	0.47	0.44	0.33	0.22	0.40	0.19

σ^2_g = genetic variance; σ^2_p = phenotypic variance; R = repeatability.

Table 12. Heritability estimates on entry-mean basis of the Uniform Variety Trial (UVT) and the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX based on combined environments ANOVA for the floral traits.

Source	Days to Heading		Days to Anthesis		Anther Extrusion		Anther Score		Plant Height		Stigma Exsertion		Gape	
	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE	UVT	TXE
σ^2_g	23.92	24.20	23.50	23.92	159.08	127.87	1.35	1.12	6.17	8.08	0.06	0.08	0.16	0.04
σ^2_e	1.93	1.65	2.00	1.91	123.00	83.60	0.87	0.54	18.10	15.00	0.59	0.37	0.76	0.60
σ^2_{ge}	9.36	12.82	10.00	13.03	56.33	82.80	0.72	0.85	8.03	8.00	0.29	0.15	0.20	0.30
H^2	0.91	0.88	0.90	0.88	0.87	0.82	0.84	0.81	0.64	0.71	0.24	0.43	0.45	0.17

σ^2_g = genetic variance; σ^2_e = experimental error; σ^2_{ge} = genotype x environment interaction; H^2 = broad sense heritability.

Table 13. Mean, coefficient of variation (CV%), range, and LSD for floral characteristics of non-gender traits of the Uniform Variety Trial (UVT) in College Station (CS) and McGregor (MCG), TX in 2017 and 2018.

Name	Days to Heading				Days to Anthesis				Plant Height			
	CS		MCG		CS		MCG		CS		MCG	
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
AP11T2222	71.00	84.00	77.50	89.67	72.00	86.00	79.00	92.00	81.50	79.33	72.00	70.67
BENTLEY	74.00	87.00	80.00	92.00	74.50	88.33	82.00	94.00	82.50	84.00	69.00	84.00
Billings	73.00	83.33	.	87.33	74.00	85.67	.	89.67	86.00	80.33	.	75.00
CPLN 69-16	97.00	.	105.50	.	98.00	.	106.50	.	70.00	.	76.50	.
Doans	84.50	86.00	87.00	90.00	84.50	87.33	87.00	91.67	85.00	76.33	78.50	83.00
Duster	83.50	87.67	87.00	91.33	84.00	88.67	87.00	93.00	84.00	82.67	76.00	79.67
Fannin	79.00	84.33	78.00	88.00	79.50	86.00	79.00	90.33	81.00	82.33	84.00	80.00
Gallagher	82.50	85.67	86.50	92.00	83.50	86.67	87.00	93.67	86.50	81.67	71.50	75.67
GREER	75.00	87.00	83.00	94.67	75.50	88.00	84.00	96.00	79.00	79.33	70.50	81.33
Iba	92.00	89.33	89.00	92.33	92.50	90.67	89.00	93.67	76.00	82.33	77.50	77.67
Jackpot	93.50	92.00	.	95.33	93.50	94.00	.	96.33	79.00	88.33	.	86.00
LCS Mint	86.00	92.00	90.00	98.00	86.50	92.33	90.50	100.00	82.00	85.00	74.50	82.00
LCS PISTOL	98.50	93.00	94.00	99.33	99.50	93.67	94.00	101.33	76.50	81.33	72.50	79.33
Progeny PGX 16-21	99.50	91.33	100.50	92.00	100.00	91.67	102.00	93.67	70.50	83.17	77.00	75.33
SY Drifter	84.00	89.33	90.00	93.33	84.00	90.00	90.50	94.00	76.50	85.00	63.00	78.67
SY Flint	85.50	87.00	87.00	90.67	85.50	88.00	87.00	92.33	81.00	80.33	66.00	78.33
SY Grit	83.00	86.67	84.00	90.67	83.50	88.33	84.00	92.67	84.00	82.33	73.00	81.33
SY Llano	80.50	83.67	82.50	89.33	81.00	85.67	83.50	91.33	76.50	78.33	73.00	73.33
SY RAZOR	78.00	85.67	.	89.33	78.00	86.67	.	91.00	92.50	88.17	.	86.67
SY Southwind	85.00	87.33	89.00	91.00	85.00	88.00	89.00	93.00	83.00	78.00	73.00	75.33
T158	96.00	92.00	94.00	93.33	96.50	92.67	94.00	94.00	79.00	81.67	80.00	80.00
TAM 114	95.50	94.00	100.50	98.00	96.00	94.00	102.00	100.00	80.50	88.33	76.00	84.67
TAM 204	78.00	89.67	84.00	95.00	78.00	91.00	84.50	96.00	82.00	71.67	78.00	81.67
TAM 304	79.00	84.67	82.50	90.33	80.00	86.00	83.00	92.33	80.00	77.00	68.50	72.33
TAM 305	85.00	89.67	89.00	93.33	85.00	91.67	89.50	94.00	73.00	80.67	72.00	81.00
TAM 401	70.50	86.00	83.00	92.33	70.50	87.00	83.50	94.00	87.50	81.69	72.00	85.00
TAM W-101	95.00	98.67	100.50	100.67	95.50	100.33	102.00	102.67	84.50	79.67	63.50	79.00
TX11A001295	94.50	93.33	94.00	97.67	95.00	94.33	94.00	100.00	72.50	84.00	74.50	82.33

Table 13. Continued.

Name	Days to Heading				Days to Anthesis				Plant Height			
	CS		MCG		CS		MCG		CS		MCG	
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
TX12M4068	78.00	84.67	81.00	88.00	78.50	86.33	82.50	90.33	101.00	85.33	86.50	82.33
Underwood	.	86.67	84.00	92.67	.	87.67	84.00	93.67	.	75.67	71.50	77.67
WB 4269	.	87.00	84.00	95.67	.	87.67	84.00	96.67	.	77.67	72.50	75.67
WB 4303	68.50	83.33	76.00	89.67	69.00	84.67	76.00	91.67	86.50	72.67	73.00	81.00
WB 4458	72.50	84.67	78.00	91.33	73.00	86.00	77.50	93.00	90.50	79.00	75.50	79.00
WB 4515	89.00	94.67	92.50	101.33	89.50	95.00	92.50	103.33	79.50	81.00	76.50	79.33
WB Cedar	95.00	84.67	87.50	88.33	95.50	86.00	89.00	91.00	74.00	81.69	67.00	75.33
WB Grainfield	95.00	101.33	95.00	102.33	95.50	103.00	95.00	104.33	80.50	87.00	83.00	80.00
Zenda	.	86.33	82.50	93.33	.	87.00	83.00	94.00	.	80.67	77.50	82.00
Mean	84.60	88.44	87.60	93.05	85.06	89.61	88.15	94.74	81.3	81.21	74.00	79.49
Range	68.50-99.50	83.33-101.33	76.00-105.50	87.33-102.33	69.00-100.00	85.67-103.00	76.00-106.50	89.67-104.33	70.00-101.00	71.67-88.33	63.00-86.50	71.67-88.33
σ^2_e	2.07	2.06	1.04	2.14	2.40	1.86	0.82	2.50	27.20	14.12	38.20	8.02
σ^2_g	82.12	17.97	52.08	14.73	82.40	17.00	53.44	14.25	26.40	9.33	8.50	11.81
ECV%	1.70	1.62	1.16	1.57	1.82	1.52	1.03	1.67	6.40	4.63	8.35	3.56
GCV%	10.71	4.79	8.24	4.12	10.67	4.60	8.29	3.98	6.32	3.76	3.94	4.32
LSD (0.05)	2.93	2.34	2.08	2.39	3.15	2.22	1.84	2.57	10.61	6.34	12.57	4.61
Combine results of non-gender traits for four environments.												
Mean	88.95				90.02				79.27			
Range	68.50 - 105.50				69.00 - 106.50				63.00 - 101.00			
σ^2_e	1.93				2.00				18.10			
σ^2_g	23.92				23.50				6.17			
ECV%	1.56				1.57				5.36			
GCV%	5.50				5.39				3.13			
LSD (0.05)	1.12				1.14				3.41			

"." indicate missing data.

Table 14. Mean, coefficient of variation (CV%), range, and LSD for floral characteristics of non-gender traits of the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2017 and 2018.

Name	Days to Heading				Days to Anthesis				Plant Height			
	CS		MCG		CS		MCG		CS		MCG	
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
CT199	97.00	93.67	93.50	95.00	98.00	94.00	94.50	96.67	75.50	88.67	79.50	75.00
TAM 112	90.00	88.33	89.00	91.00	90.00	90.00	89.00	93.00	69.50	86.00	68.50	72.67
TAM 113	96.00	98.33	97.00	101.33	96.50	99.00	98.50	103.00	73.50	86.00	74.00	73.67
TAM 304	79.00	85.67	80.00	90.00	79.50	87.33	82.00	92.33	77.50	78.00	71.00	70.33
TAM W-101	97.50	99.00	99.50	99.67	98.50	99.33	101.50	101.67	79.00	86.00	69.00	75.33
TX09V7446-AZ258	95.00	97.00	98.50	97.33	95.50	97.67	100.50	99.33	74.50	87.67	71.50	76.00
TX11A001295-AZ33	96.00	94.67	94.00	96.67	96.00	95.00	94.50	98.00	70.00	90.33	77.50	81.00
TX11A001295-AZ34	94.50	94.00	94.00	100.67	94.50	94.33	94.50	102.00	78.50	88.33	78.00	78.67
TX12A001041	94.50	92.67	93.50	94.20	94.50	94.00	94.50	94.19	80.50	84.67	80.00	81.55
TX12A001106	94.00	92.67	94.00	96.00	95.00	94.00	94.50	97.67	75.00	83.33	74.00	74.67
TX12A001621	90.50	93.67	93.50	93.67	90.50	94.00	94.00	94.00	78.00	86.33	69.00	79.00
TX12A001638	64.00	85.33	83.00	92.00	65.00	86.33	84.00	93.33	80.00	86.00	67.50	77.67
TX12V7220	62.50	85.33	87.50	92.33	63.50	87.00	88.00	94.00	81.50	82.67	66.50	71.33
TX12V7229	88.00	92.00	87.00	94.00	88.00	94.00	87.00	94.00	78.00	83.67	74.50	74.33
TX12V7415	87.50	87.00	87.00	92.00	87.50	88.67	87.00	93.67	80.00	82.33	71.00	72.00
TX12V7606	89.00	99.00	91.50	99.67	89.50	99.33	92.00	101.67	79.50	89.00	91.50	76.00
TX13A001069	82.00	88.33	87.00	93.00	82.00	90.00	84.50	94.00	79.00	77.67	69.00	72.00
TX13A001169	62.50	85.00	82.00	92.33	63.00	86.00	83.00	94.00	89.00	86.67	83.50	82.33
TX13A001561	77.50	89.67	83.00	93.00	78.00	91.00	83.50	94.00	83.00	84.33	71.00	72.67
TX13M5580	79.50	85.33	77.00	89.33	80.00	86.33	77.00	92.00	84.50	83.33	77.00	73.00
TX13M5625	79.00	87.67	82.50	93.33	80.50	89.33	83.00	94.67	85.00	82.67	77.50	76.00
TX13V7725	92.00	94.33	91.50	98.00	92.50	95.00	92.00	100.00	79.50	87.67	81.00	76.33
TX13V7913	65.00	86.33	77.00	90.67	65.00	87.00	77.00	92.33	68.50	.	76.00	70.33
TX14A001035	73.50	84.00	75.50	90.33	74.00	86.00	77.00	92.67	80.00	81.67	71.50	71.67
TX14A001112	87.00	90.67	86.50	93.33	87.50	92.33	87.00	94.00	71.50	82.00	75.00	70.67
TX14A001113	85.50	88.33	86.50	91.00	86.00	90.00	87.00	92.33	75.00	79.33	76.00	73.00
TX14A001154	87.00	91.67	89.00	94.67	87.50	93.67	90.00	95.00	77.50	85.00	72.00	77.67
TX14A001185	89.00	87.33	87.50	91.67	85.00	88.67	88.00	93.33	80.00	77.67	79.00	71.00

Table 14. Continued.

Name	Days to Heading				Days to Anthesis				Plant Height			
	CS		MCG		CS		MCG		CS		MCG	
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
TX14A001215	94.00	97.00	94.00	98.67	94.00	98.00	95.00	100.67	70.50	85.33	80.50	75.67
TX14A001234	94.50	92.67	88.00	93.00	95.00	93.67	88.00	94.00	81.00	84.00	76.00	75.33
TX14A001249	83.50	86.00	83.50	90.00	84.00	87.00	84.00	92.33	81.00	81.33	79.50	75.33
TX14M7051	77.00	88.00	84.00	92.33	77.00	89.00	84.00	94.00	101.00	84.33	81.00	84.00
TX14M7061	78.50	85.67	84.50	90.33	79.50	87.33	84.50	92.67	82.00	77.89	62.50	65.00
TX14M7088	91.00	93.67	88.50	94.67	92.00	94.33	89.00	95.33	70.00	78.33	75.50	69.33
TX14M7177	71.50	87.33	78.00	92.67	72.00	88.67	78.00	93.67	79.50	87.38	86.50	81.00
TX14V70086	87.50	89.33	90.50	91.67	87.50	90.67	91.00	93.00	78.00	77.00	74.00	76.00
TX14V70088	98.50	91.33	94.00	93.33	99.50	93.67	95.00	94.33	76.50	78.00	70.50	68.33
Mean	85.00	90.50	88.00	94.00	85.50	91.67	88.50	95.30	78.50	83.61	75.1	74.70
Range	62.50-98.50	84.00-99.00	75.50-99.50	89.33-101.33	63.00-99.50	86.00-99.33	77.00-101.50	92.00-103.00	68.50-101.00	77.00-90.33	62.50-91.50	65.00-84.00
σ^2_e	1.49	1.45	1.32	2.12	2.56	1.24	2.18	2.13	17.67	11.00	19.40	14.84
σ^2_g	107.66	18.48	37.17	9.49	105.87	16.15	39.98	9.52	26.87	9.67	24.45	11.72
ECV%	1.43	1.33	1.31	1.55	1.90	1.21	1.67	1.53	5.36	3.97	5.86	5.16
GCV%	12.21	4.75	6.93	3.28	12.03	4.38	7.14	3.24	6.60	3.72	6.58	4.58
LSD (0.05)	2.50	2.00	2.33	2.40	3.24	1.81	3.00	2.40	8.50	5.60	9.00	6.30
Combine results of non-gender traits for four environments.												
Mean	90.00				91.00				78.11			
Range	62.50 - 101.33				63.00 - 103.00				62.50 - 101.00			
σ^2_e	1.65				1.91				15.00			
σ^2_g	24.20				23.92				8.08			
ECV%	1.43				1.52				4.94			
GCV%	5.47				5.37				3.64			
LSD (0.05)	1.03				1.11				3.11			

"."indicate missing data.

Table 15. Mean, coefficient of variation (CV%), range, and LSD for floral characteristics of gender traits of the Uniform Variety Trial (UVT) in College Station (CS) and McGregor (MCG), TX in 2017 and 2018.

Name	Anther Extrusion (%)				Anther Score				Stigma Exsertion			Gape		
	CS		MCG		CS		MCG		CS		MCG	CS		MCG
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2018	2017	2018	2018
AP11T2222	60	16	18	34	6.50	2.33	1.50	3.67	1.50	1.13	1.88	2.00	0.98	2.75
BENTLEY	63	28	22	36	5.50	3.00	2.00	3.00	1.50	1.50	1.12	2.00	2.50	2.25
Billings	72	6	.	13	8.00	1.33	.	1.67	2.00	0.87	2.50	3.00	3.02	3.50
CPLN 69-16	63	.	54	.	6.00	.	5.50	.	1.00	.	.	1.50	.	.
Doans	82	35	58	49	8.00	3.33	5.50	4.67	1.00	2.87	2.00	1.00	4.02	3.00
Duster	68	20	21	9	6.50	2.00	2.00	1.67	1.50	3.50	3.12	1.00	4.00	4.25
Fannin	11	4	11	11	2.00	1.33	1.50	1.33	2.50	1.87	3.12	2.00	2.02	2.25
Gallagher	7	10	23	7	1.00	1.33	2.00	1.33	1.50	2.50	1.12	1.50	3.00	4.25
GREER	64	36	40	36	8.00	3.33	3.50	3.67	3.00	2.50	1.50	3.00	3.00	3.50
Iba	45	25	38	22	6.50	2.33	3.50	2.33	1.00	2.50	1.50	1.00	3.50	2.00
Jackpot	62	32	.	15	6.50	2.67	.	2.00	1.00	3.50	3.00	1.50	4.50	4.00
LCS Mint	40	31	21	22	3.50	3.67	1.50	2.00	1.50	2.50	3.00	2.50	4.00	4.50
LCS PISTOL	49	53	49	33	6.00	6.00	3.50	3.00	1.00	2.50	1.50	1.00	3.00	3.50
Progeny PGX 16-21	45	23	44	27	4.50	2.67	3.50	2.00	1.00	2.00	2.00	1.50	2.50	4.50
SY Drifter	75	60	77	51	8.00	5.67	7.50	4.33	1.00	1.00	2.50	1.00	2.50	3.00
SY Flint	83	46	65	38	7.50	3.67	6.00	3.33	1.00	1.00	2.50	1.00	1.50	3.00
SY Grit	34	58	45	44	3.00	4.33	5.00	4.33	1.00	3.00	1.50	1.00	4.00	3.50
SY Llano	67	52	50	52	7.50	4.67	5.50	5.00	2.00	.	1.12	2.00	.	3.25
SY RAZOR	57	55	.	41	7.50	5.00	.	4.00	2.00	3.87	0.88	2.00	3.02	0.75
SY Southwind	78	44	65	46	7.50	4.00	6.00	5.00	2.00	1.50	1.00	1.00	2.50	2.50
T158	73	45	76	46	6.50	4.33	7.50	3.67	1.00	2.50	4.00	1.50	4.00	4.00
TAM 114	70	34	51	39	7.00	4.00	4.00	3.00	1.00	2.50	2.50	1.00	3.50	3.50
TAM 204	89	64	60	44	8.50	6.00	5.50	4.33	3.00	1.50	1.00	3.00	3.50	2.50
TAM 304	72	23	38	35	7.50	2.33	3.50	2.67	3.00	1.00	1.50	3.00	2.00	3.50
TAM 305	59	26	56	47	5.00	2.33	6.00	4.33	2.00	3.00	2.00	2.00	3.50	3.00
TAM 401	67	58	68	38	6.50	7.00	7.00	3.33	2.00	1.13	2.50	2.50	1.98	5.00
TAM W-101	39	28	43	8	4.00	2.00	4.00	1.00	1.00	2.50	2.00	1.00	4.00	4.00
TX11A001295	54	22	37	16	5.50	2.67	3.50	1.67	1.00	3.00	2.00	1.00	3.50	3.00

Table 15. Continued.

Name	Anther Extrusion (%)				Anther Score				Stigma Exsertion			Gape		
	CS		MCG		CS		MCG		CS		MCG	CS		MCG
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2018	2017	2018	2018
TX12M4068	56	34	45	31	6.50	3.33	4.00	3.00	3.00	2.13	3.12	3.00	4.98	5.25
Underwood	.	63	52	49	.	5.33	5.00	4.67	.	3.00	4.00	.	4.50	5.00
WB 4269	.	69	59	66	.	6.67	5.50	5.67	.	2.50	3.00	.	2.00	4.50
WB 4303	82	74	89	69	8.00	6.67	9.00	7.33	2.00	1.13	3.88	2.00	2.98	4.75
WB 4458	61	16	50	46	7.00	2.33	5.50	4.00	1.00	2.00	1.00	1.00	3.00	2.50
WB 4515	33	48	65	31	3.50	4.33	6.00	3.00	1.00	3.00	2.00	1.00	3.50	2.50
WB Cedar	60	24	59	48	5.50	2.33	5.00	4.67	1.00	2.13	0.88	1.00	2.98	0.75
WB Grainfield	52	42	34	28	5.50	4.00	3.00	3.00	1.00	3.00	1.50	1.00	4.00	3.00
Zenda	.	35	49	33	.	3.00	3.00	2.33	.	2.50	1.50	.	3.00	3.00
Mean	58	37	48	35	6.1	3.65	4.5	3.33	1.56	2.30	2.10	1.66	3.20	3.37
Range	7 - 89	4 - 74	11 - 89	7 - 69	1.00-8.50	1.33-7.00	1.50-9.00	1.00-7.33	1.00-3.00	0.87-3.87	0.88-4.00	1.00-3.00	0.98-4.98	0.75-5.25
σ^2_e	164.8	105.2	133.2	116.4	1.25	0.81	0.62	0.88	0.50	0.74	0.53	0.50	1.14	0.70
σ^2_g	272	295.7	263	202.4	2.77	2.24	3.25	1.64	0.23	0.16	0.39	0.29	0.07	0.45
ECV%	22.0	27.6	24.17	30.7	18.4	24.66	17.52	28.07	45.9	37.54	34.80	43.8	33.39	24.64
GCV%	28.44	46.48	33.79	40.65	27.28	41.00	40.03	38.46	30.74	17.12	29.55	32.44	7.97	19.91
LSD (0.05)	26.12	16.7	23.5	17.6	2.27	1.47	1.6	1.52	1.46	1.98	1.69	1.48	1.59	1.93
Combine results of male and female traits with four and three environments, respectively.														
Mean	43				4.18				1.97			2.71		
Range	4 - 89				1.00 - 9.00				0.87 - 4.00			0.75 - 5.25		
σ^2_e	123				0.87				0.59			0.76		
σ^2_g	159.08				1.35				0.06			0.16		
ECV%	26.01				22.33				39.00			32.24		
GCV%	29.33				27.80				12.43			14.76		
LSD (0.05)	8.90				0.75				0.88			1.00		

"." indicate missing data. There are no measurements for stigma exsertion and gape in McGregor, TX in 2017.

Table 16. Mean, coefficient of variation (CV%), range, and LSD for floral characteristics of gender traits of the Texas Elite (TXE) trial in College Station (CS) and McGregor (MCG), TX in 2017 and 2018.

Name	Anther Extrusion (%)				Anther Score				Stigma Exsertion			Gape		
	CS		MCG		CS		MCG		CS		MCG	CS		MCG
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2018	2017	2018	2018
CT199	62.50	44.00	38.00	21.67	6.00	5.00	3.50	1.67	1.00	2.50	1.50	1.00	3.50	2.00
TAM 112	36.50	8.67	20.50	12.33	3.50	1.00	2.00	1.33	1.00	2.00	2.50	1.00	2.50	3.00
TAM 113	21.50	10.67	9.50	16.33	2.00	1.00	1.00	1.67	1.00	2.00	1.50	1.00	3.50	2.00
TAM 304	75.50	24.00	44.50	49.00	7.50	2.33	3.50	3.33	1.50	3.00	2.00	1.50	2.00	2.00
TAM W-101	24.00	56.67	38.50	16.00	2.00	4.67	3.00	2.00	1.00	1.50	2.00	1.00	2.50	4.50
TX09V7446-AZ258	22.50	8.00	13.00	8.00	2.50	1.00	1.00	1.00	1.00	2.00	1.50	1.00	3.50	2.00
TX11A001295-AZ33	31.50	15.00	30.00	21.00	2.50	2.00	2.50	2.00	1.00	3.00	1.50	1.00	4.00	1.50
TX11A001295-AZ34	21.50	6.67	23.00	8.33	2.00	1.33	2.00	1.00	1.00	2.00	2.00	1.00	3.50	3.00
TX12A001041	57.00	45.33	31.50	30.97	3.50	5.00	2.50	2.94	1.00	1.00	1.00	1.50	2.50	3.00
TX12A001106	30.50	12.33	25.00	6.33	3.00	2.33	2.00	1.00	1.00	3.00	2.50	1.00	4.00	3.00
TX12A001621	47.50	44.00	64.00	31.33	4.50	5.67	6.50	3.00	1.00	3.50	2.00	1.00	4.00	3.00
TX12A001638	46.00	12.67	9.00	19.33	4.00	1.33	1.50	1.67	1.50	2.00	1.50	1.00	3.00	3.00
TX12V7220	43.50	10.00	15.00	10.33	3.00	1.33	1.00	1.00	1.00	1.00	2.00	1.00	1.50	2.50
TX12V7229	29.50	28.67	16.00	13.67	2.50	3.33	1.50	1.33	1.00	2.00	1.50	1.00	3.00	3.00
TX12V7415	83.00	34.33	48.00	11.67	7.50	2.67	3.50	1.33	1.00	2.00	3.00	1.00	2.50	4.50
TX12V7606	45.50	50.33	40.00	16.67	4.00	4.67	5.00	1.67	1.00	2.00	2.00	1.00	3.00	2.50
TX13A001069	55.50	32.67	43.50	35.67	5.00	2.00	3.50	3.00	1.00	3.00	2.00	1.00	2.50	3.50
TX13A001169	56.00	17.67	20.50	13.67	4.50	1.33	2.00	1.67	2.00	1.50	2.50	2.00	3.00	4.00
TX13A001561	53.50	37.00	17.00	18.00	5.00	3.00	2.00	2.00	1.00	1.00	1.50	1.00	1.00	2.00
TX13M5580	49.00	26.67	60.00	59.67	4.50	2.67	4.50	5.00	1.00	1.00	2.03	1.50	2.50	2.79
TX13M5625	51.00	42.00	38.00	30.67	4.50	3.67	3.00	2.67	2.50	1.00	2.50	2.00	2.00	3.00
TX13V7725	37.00	34.33	41.00	16.67	4.00	3.33	4.50	1.33	1.00	2.50	1.00	1.50	3.00	2.00
TX13V7913	69.00	61.67	71.00	59.67	7.50	5.33	7.00	6.00	1.00	1.00	2.00	1.00	1.00	4.50
TX14A001035	65.50	10.00	43.50	9.67	6.00	1.33	3.00	1.00	1.50	3.50	2.00	2.00	4.50	2.00
TX14A001112	72.50	20.00	24.50	20.67	7.50	2.00	2.00	2.33	1.00	2.86	3.00	1.00	3.86	3.00
TX14A001113	82.00	33.00	28.00	47.33	8.50	2.67	2.50	4.33	1.00	3.86	2.50	1.00	4.86	3.50
TX14A001154	68.50	38.00	46.50	20.33	7.00	4.33	4.50	2.00	1.00	3.00	2.50	1.50	3.00	2.00
TX14A001185	35.50	18.33	15.00	7.33	3.00	1.67	2.00	1.00	1.50	2.86	2.00	1.00	2.86	1.50

Table 16. Continued.

Name	Anther Extrusion (%)				Anther Score				Stigma Exsertion			Gape		
	CS		MCG		CS		MCG		CS		MCG	CS		MCG
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2018	2017	2018	2018
TX14A001215	52.00	73.00	52.50	34.67	5.00	7.00	4.50	2.67	1.00	1.50	2.50	1.00	2.50	4.00
TX14A001234	52.00	27.00	33.50	18.67	5.00	2.33	3.50	2.33	1.00	1.50	1.00	1.00	3.00	1.50
TX14A001249	85.50	49.67	55.50	48.67	8.00	4.67	5.00	4.67	2.00	2.00	3.50	1.00	2.50	3.50
TX14M7051	43.00	23.67	27.00	13.67	4.00	1.67	2.00	2.00	1.00	2.00	2.00	2.00	2.50	1.50
TX14M7061	56.50	13.00	12.50	40.67	5.50	1.33	1.50	3.00	1.00	1.50	.	1.00	2.00	0.00
TX14M7088	53.50	40.67	36.50	37.33	4.00	3.67	3.50	3.33	1.00	2.00	1.50	1.00	2.50	2.00
TX14M7177	53.50	49.33	24.50	46.33	6.50	4.67	2.00	4.33	1.00	2.00	3.50	1.50	2.50	4.50
TX14V70086	74.50	32.00	52.50	19.00	6.50	2.67	5.00	2.00	1.00	2.86	3.03	1.00	2.86	3.79
TX14V70088	42.50	28.67	26.50	12.00	4.00	3.00	2.00	1.67	1.00	2.86	2.50	1.00	1.86	2.50
Mean	51.00	30.30	33.40	24.40	4.70	3.00	3.00	2.33	1.15	2.10	2.07	1.20	2.81	2.81
Range	21.5-85.5	6.7 - 73.0	9.0 - 71.0	6.3 - 59.7	2.00-8.50	1.00-7.00	1.00-7.00	1.00-6.00	1.00-2.50	1.00-3.86	1.00-3.50	1.00-2.00	1.00-4.86	1.50-4.50
σ^2_e	98.0	89.2	72.8	76.2	0.74	0.53	0.56	0.45	0.07	0.56	0.51	0.08	0.56	1.16
σ^2_g	266.3	249.7	220.2	204.2	3.07	2.25	1.95	1.40	0.09	0.28	0.15	0.08	0.38	0.27
ECV%	19.40	31.20	25.60	35.80	18.00	24.80	24.80	28.80	22.90	35.50	34.06	24.10	26.50	38.20
GCV%	32.00	52.15	44.43	58.56	37.28	50.00	46.55	50.78	26.09	25.20	18.71	23.57	21.94	18.49
LSD (0.05)	20.00	15.40	17.30	14.30	1.74	1.20	1.50	1.10	0.53	1.62	1.50	0.58	1.62	2.25
Combine results of male and female traits with four and three environments, respectively.														
Mean	33.30				3.14				1.76			2.25		
Range	6.3 - 85.5				1.00 - 8.50				1.00 - 3.86			1.00 - 4.86		
σ^2_e	83.60				0.54				0.37			0.60		
σ^2_g	127.87				1.12				0.08			0.04		
ECV%	27.47				23.95				34.40			34.00		
GCV%	33.96				33.70				16.07			8.89		
LSD (0.05)	7.34				0.59				0.70			0.89		

"." indicate missing data. There are no measurements for stigma exsertion and gape in McGregor, TX in 2017.

Table 17. Selected genotypes as male and female parents from the Uniform Variety Trial (UVT) and the Texas Elite (TXE) trial measured for the floral traits.

Trial	Genotype	Days to Anthesis	Anther Extrusion	Anther Score	Stigma Exsertion	Gape	Plant Height	Male Parent	Female Parent
UVT	WB 4303	80.34	78.5	7.75	2.34	3.24	78.29	X	X
UVT	SY Drifter	89.63	65.75	6.38			75.79	X	
UVT	WB 4269	89.45	64.67	5.95	2.75	3.25	75.28	X	X
UVT	TAM 204	87.38	64.25	6.08			78.34	X	
UVT	T158	94.29	60	5.5	2.5	3.17	80.17	X	X
UVT	SY Southwind	88.75	58.25	5.63			77.33	X	
UVT	SY Flint	88.21	58	5.13			76.42	X	
UVT	TAM 401	83.75	57.75	5.96			81.55	X	
UVT	Doans	87.63	56	5.38			80.71	X	
UVT	SY Llano	85.38	55.25	5.67			75.29	X	
UVT	Underwood	88.45	54.67	5	3.5	4.75	74.95	X	X
UVT	SY RAZOR	85.22	51	5.5			89.11	X	
UVT	TX12M4068	84.42			2.75	4.41	88.79		X
UVT	Duster	88.17			2.71	3.08	80.59		X
UVT	Jackpot	94.61			2.5	3.33	84.44		X
UVT	GREER	85.88			2.33	3.17	77.54		X
UVT	LCS Mint	92.33			2.33	3.67	80.88		X
UVT	TAM 305	90.04			2.33	2.83	76.67		X
UVT	TAM 114	98			2	2.67	82.38		X
UVT	TX11A001295	95.83			2	2.5	78.33		X
UVT	Zenda	88			2	3	80.06		X
TXE	CT199	95.79	41.54	4.04			79.67	X	
TXE	TX14A001154	91.54	43.33	4.46			78.04	X	
TXE	TX14M7177	83.09	43.42	4.38	2.17	2.83	83.6	X	X
TXE	TX14V70086	90.54	44.5	4.04	2.3	2.55	76.25	X	X
TXE	TX12A001621	93.13	46.71	4.92	2.17	2.67	78.08	X	X
TXE	TX14A001113	88.83	47.58	4.5	2.45	3.12	75.83	X	X
TXE	TAM 304	85.29	48.25	4.17			74.21	X	
TXE	TX13M5580	83.83	48.84	4.17			79.46	X	
TXE	TX14A001215	96.92	53.04	4.79			78	X	
TXE	TX14A001249	86.83	59.84	5.59			79.29	X	
TXE	TX13V7913	80.33	65.34	6.46			71.61	X	
TXE	TX14A001035	82.42			2.33	2.83	76.21		X
TXE	TX14A001112	90.21			2.29	2.62	74.79		X
TXE	TX12A001106	95.29			2.17	2.67	76.75		X
TXE	TX12V7415	89.21			2	2.67	76.33		X
TXE	TX13A001169	81.5			2	3	85.38		X

X = Selected genotype.

Table 18. Pearson's correlation coefficients calculated by using traits total means for each genotype over environments for the Uniform Variety Trial (UVT, right above) and the Texas Elite (TXE, lower left) trial for the floral traits.

Source	Days to Heading	Days to Anthesis	Anther Extrusion	Anther Score	Stigma Exsertion	Gape	Plant Height
HD		**0.99*****	-0.03^{ns}	-0.12^{ns}	-0.11^{ns}	-0.11^{ns}	-0.16^{ns}
AD	**0.99*****		-0.07^{ns}	-0.14^{ns}	-0.12^{ns}	-0.12^{ns}	-0.16^{ns}
AE	-0.27^{ns}	-0.28^{ns}		**0.97*****	-0.01^{ns}	0.003^{ns}	-0.22^{ns}
AS	-0.23^{ns}	-0.23^{ns}	**0.98*****		-0.03^{ns}	-0.03^{ns}	-0.16^{ns}
SE	-0.16^{ns}	-0.14^{ns}	0.20^{ns}	0.23^{ns}		**0.77*****	0.33*
G	0.003^{ns}	0.005^{ns}	0.19^{ns}	0.20^{ns}	**0.53*****		0.24^{ns}
HT	0.05^{ns}	0.04^{ns}	-0.10^{ns}	-0.09^{ns}	-0.05^{ns}	0.27^{ns}	

Correlation coefficients results top and bottom belong to UVT and TXE, respectively. HD = days to heading; AD = days to anthesis; AE = anther extrusion; AS = anther score; SE = stigma exsertion; G = gape; HT = plant height.

*, **, *** Significant at the 0.05, 0.01, or 0.001 probability level, respectively. 'ns' not significant at any probability level.

Table 19. Pearson's correlation coefficients calculated by using traits total means for each genotype for each years and locations for the Uniform Variety Trial (UVT) and the Texas Elite (TXE) trial for the floral traits.

Source	UVT				TXE			
	CS		MCG		CS		MCG	
	2017	2018	2017	2018	2017	2018	2017	2018
HD-AD	0.99***	0.99***	0.99***	0.99***	0.99***	0.99***	0.99***	0.98***
AE-AS	0.92***	0.95***	0.96***	0.95***	0.95***	0.94***	0.94***	0.96***
SE-G	0.86***	0.65***		0.65***	0.51***	0.69***		0.58***

HD = days to heading; AD = days to anthesis; AE = anther extrusion; AS = anther score; SE = stigma exsertion; G = gape; HT = plant height.

*, **, *** Significant at the 0.05, 0.01, or 0.001 probability level, respectively. 'ns' not significant at any probability level.

Table 20. The height reduction (Rht) genotypes of the Uniform Variety Trial (UVT) and the Texas Elite (TXE) trial.

UVT	Rht alleles		TXE	Rht alleles
AP11T2222	B1b / D1a		CT199	B1b / D1a
BENTLEY	B1b / D1a		TAM 112	B1b / D1a
Billings	B1b / D1a		TAM 113	B1b / D1a
CPLN 69-16	B1b / D1a		TAM 304	B1b / D1a
Doans	B1a / D1a		TAM W-101	B1a / D1b
Duster	B1b / D1a		TX09V7446-AZ258	B1b / D1a
Fannin	B1b / D1a		TX11A001295-AZ333	B1b / D1a
Gallagher	B1b / D1a		TX11A001295-AZ348	B1b / D1a
GREER	B1b / D1a		TX12A001041	B1b / D1a
Iba	B1b / D1a		TX12A001106	B1b / D1a
Jackpot	B1b / D1a		TX12A001621	B1b / D1a
LCS Mint	B1b / D1a		TX12A001638	B1b / D1a
LCS PISTOL	B1b / D1a		TX12V7220	B1b / D1a
Progeny PGX 16-21	B1a / D1b		TX12V7229	B1b / D1a
SY Drifter	B1a / D1b		TX12V7415	B1b / D1a
SY Flint	B1b / D1a		TX12V7606	B1b / D1a
SY Grit	B1b / D1a		TX13A001069	B1b / D1a
SY Llano	B1b / D1a		TX13A001169	B1b / D1a
SY RAZOR	B1a / D1a		TX13A001561	B1b / D1a
SY Southwind	B1b / D1a		TX13M5580	B1b / D1a
T158	B1b / D1a		TX13M5625	B1b / D1a
TAM 114	B1b / D1a		TX13V7725	B1b / D1a
TAM 204	B1b / D1a		TX13V7913	B1b / D1a
TAM 304	B1b / D1a		TX14A001035	B1b / D1a
TAM 305	B1b / D1a		TX14A001112	B1b / D1a
TAM 401	B1b / D1a		TX14A001113	B1b / D1a
TAM W-101	B1a / D1b		TX14A001154	B1b / D1a
TX11A001295	B1b / D1a		TX14A001185	B1b / D1a
TX12M4068	B1b / D1a		TX14A001215	B1b / D1a
Underwood	B1b / D1a		TX14A001234	B1b / D1a
WB 4269	B1b / D1a		TX14A001249	B1b / D1a
WB 4303	B1b / D1a		TX14M7051	B1b / D1a
WB 4458	B1b / D1a		TX14M7061	B1b / D1a
WB 4515	B1b / D1a		TX14M7088	B1b / D1a
WB Cedar	B1a / D1b		TX14M7177	B1b / D1a
WB Grainfield	B1b / D1a		TX14V70086	B1b / D1a
Zenda	B1a / D1b		TX14V70088	B1b / D1a

Rht1: B1a = wild allele, B1b = dwarf allele; Rht2: D1a = wild allele, D1b = dwarf allele.

Table 21. Means of the height reduction (Rht) genotypes for each trait for the Uniform Variety Trial (UVT) and the Texas Elite (TXE) trial over 2 years and locations for the floral traits.

Source	Rht1		Rht2		Wild Type
	UVT	TXE	UVT	TXE	UVT
Days to Heading	88.24	89.08	92.0	98.92	85.6
Days to Anthesis	89.23	89.96	92.99	100.25	86.42
Anther Extrusion	44.34	34.78	43.35	33.79	53.50
Anther Score	4.39	3.27	3.89	2.92	5.44
Stigma Exsertion	2.01	1.80	1.67	1.50	2.10
Gape	2.80	2.26	2.52	2.67	2.30
Plant Height	79.01	77.91	76.70	77.33	84.91

Rht1: B1a = wild type, B1b = dwarfing; Rht2: D1a = wild type, D1b = dwarfing
TXE trial do not have any wild type lines.

5. SUMMARY

The success of hybrid wheat production highly depends on justifying the cost of hybrid seed production for farmers. There are several requirements that justify hybrid wheat production. First, a minimum of 21% heterosis is a prerequisite to cover the expenses of hybrid seed production and make it profitable to seed producers. Additionally, wheat is an autogamous self-pollinated crop; therefore, maintaining an efficient male sterility system is crucial for establishing hybrid wheat programs. Finally, the redesign of floral characteristics is a prerequisite for hybrid wheat breeding efforts intended to achieve high outcrossing ability.

Enhancement of fundamental traits such as high seed set in female parents and high tiller production in male parents, facilitated by lower seeding rate to lengthen the period of pollen shed, could increase the economic viability of seed production. Anthers remain viable for one to three days and stigmas remain receptive for pollens for four to thirteen days. Therefore, the first goal of successful hybrid seed production is synchronizing the flowering period of male and female parents. Moreover, to maximize the chances of cross-pollination, the female parents should be shorter than their male pollinators. Finally, the female parents must have open florets and extruding stigma feathers, while male parent plants must have viable extruded anthers and shed pollen outside the florets.

The data from the UVT and TXE trials was used to screen lines for desirable floral characteristics and to characterize the best male and female candidates for inclusion in the hybrid wheat crossing blocks. These floral traits included stigma

exsertion and gape for female traits, anther extrusion and anther score for males, in addition to heading date, anthesis date, and plant height for non-gender traits. The male and female traits were used for selecting lines whose performance was equal to or above the average for successful hybrid seed production.

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