

**FLORAL CHARACTERISTICS AND HYBRID PERFORMANCE OF
POTENTIAL CANDIDATES OF A HYBRID WHEAT (*TRITICUM AESTIVUM*
L.) PROGRAM IN TEXAS**

Thesis

by

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ABSTRACT

Higher wheat prices, performance potential of hybrids and the availability of new next generation sequencing have sparked a renewed interest in the development of hybrid wheat. Floral characteristics and heterosis are an integral part of hybrid wheat studies for discovering compatible parents with desirable traits for hybrid wheat production. The objectives of this study were to 1) screen TAM germplasm for desirable floral characteristics and characterize the best male and female candidates for the beginning of a hybrid wheat program, and 2) to estimate heterosis in F₂ generations as a proxy to F₁.

Advanced breeding lines (1,770) from TAM germplasm, such as Amarillo Preliminary (AP1-AP10), South Texas Preliminary (STP1-STP4), South Texas Observations (SOBS), and Amarillo Observations (AOBS) were screened for floral characteristics to select parents for hybrid wheat crossing. The observations included studying the key male and female floral traits that will enhance the magnitude of cross-pollination. The male characteristics measured were anther exertion, length and width, and female characteristics were glume angle and stigma size, featheriness duration and exertion. Heading date, anthesis, and plant height were also measured. The study was conducted in two years: 2014 and 2015. Initial screening on 1,770 lines was performed during 2014 on a single replication. About 6% of the lines (97 out of 1,770) were selected from the 2014 floral screening and tested for repeatability in 2015. The 97 lines

were grown in two replicates, and out of 97 lines, 17 (18%) were selected for hybrid wheat crossing.

Heterosis in TAM F₂ populations College Station F₂ (CF₂) and Amarillo F₂ (AF₂) for yield and its components were studied as a proxy to the F₁. Results showed that most of the F₂ populations tend to have a higher yield and yield components than the inbred line checks. Though some heterosis is lost in the F₂ due to segregation and inbreeding, the presence of superiority is a good sign of vigor in the previous generation.

DEDICATION

To my supportive family and friends, my wonderful mentor, and fellow students who supported me throughout this journey

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CHAPTER I

INTRODUCTION

Yield increase has always, and continues to be, the specific focus of many plant-breeding programs. As the world population grows, there is increasing pressure on plant breeders to find novel ways to achieve faster yield increase with diminishing land resources and potentially harsher environments. New next generation sequencing technologies yielding faster and cheaper genotyping have emerged, shortening the time cycle for the selection of potential material (Reynolds et al., 1996). As a result, a spark of renewed interest in hybrid wheat (*Triticum aestivum* L.) has grown among large industries and the public sector in the U.S.

Previous studies have shown that hybrids typically perform better than inbred lines in aspects of biomass and yield, as well as other factors such as drought tolerance and nutrient use efficiency (Longin et al., 2013; Singh et al., 2010). Despite this, in most instances, the cost to produce a hybrid wheat cultivar and sell it to growers has not matched the financial returns from harvest (Singh et al., 2010). Therefore, incentives to producers to purchase hybrid seeds were almost nonexistent. With new technologies and methods rising in the plant breeding industry, there is a great opportunity to capture wheat heterosis at such a rate that yield would increase to a profitable threshold

(Reynolds et al., 1996), which will be more appealing to growers and aid in the mission of necessary yield increase to meet population demands.

As hybrids gain more interest, more studies are seeking to prove the role of heterosis in hybrid wheat progeny. Many studies from the U.S. (Koemel, Jr et al., 2004; Martin et al., 1995; Bruns and Peterson, 1998) and Europe (Wilson and Droscholl, 1983; Ebmeyer et al., 2013) on wheat have served to aid in proving this in a number of germplasm produced from hybrid crosses. In order to provide rationale for a hybrid program at Texas A&M University (TAMU), it must be shown with hard evidence that there is potential for increased yields in a hybrid wheat breeding program. This includes proving the existence of sufficient heterosis within the TAM germplasm.

In addition to the agronomic performance, grain quality, and biotic and abiotic stress tolerance, there must be sufficient diversity in the flowering traits of the germplasm to choose the best male and female parents to use in the crossing blocks (Whitford et al., 2013). Screening for the above-mentioned characteristics is the first step toward the creation of a hybrid program at TAMU.

As the private industry invests more effort in cultivation of hybrid wheat, there has also been an interest in collaboration with TAMU in the endeavor. Such partnerships could increase funding and available technology to ensure an efficient and accurate process, as well as additional, trained personnel. In anticipation of the creation of a hybrid wheat program at TAMU and any collaborating public institutions and companies, the TAM Wheat Program has initiated preliminary tests and observations to search for potential parental lines that are necessary for a successful hybrid wheat program.

CHAPTER II

REVIEW OF LITERATURE

Modern Wheat and Its Origins

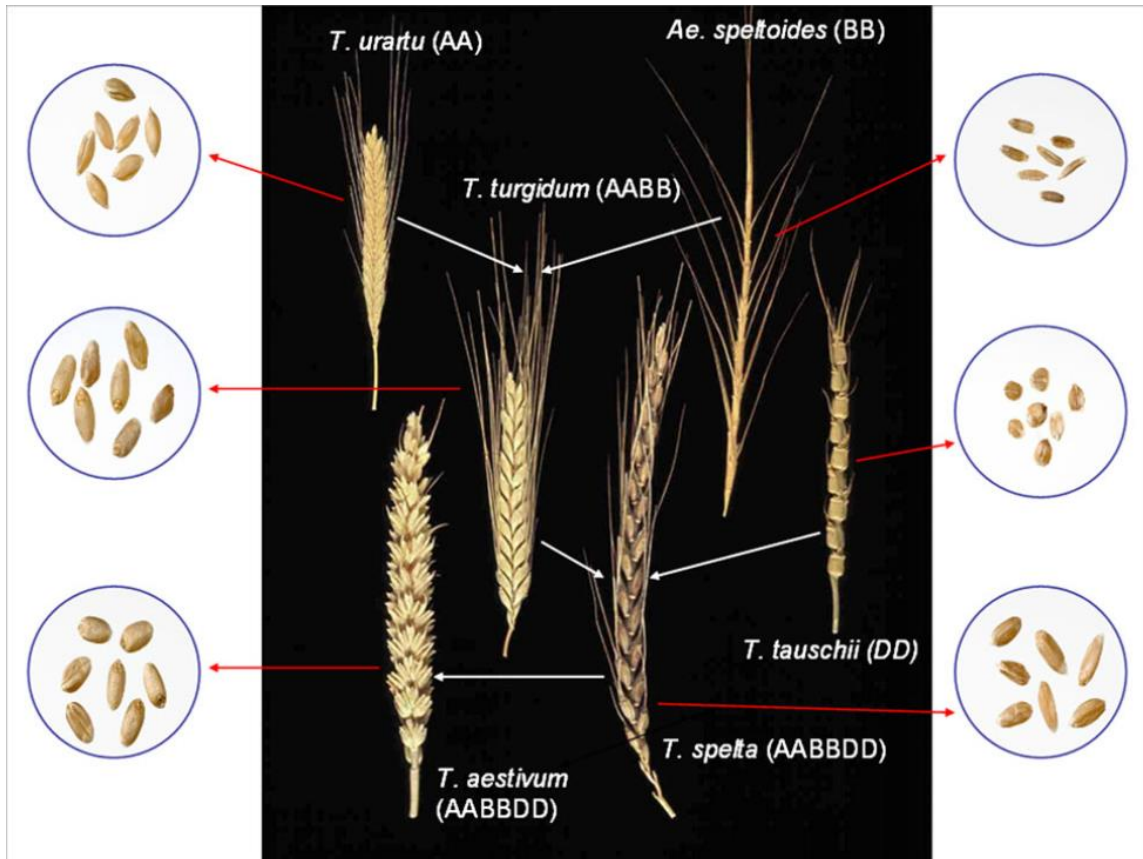
The genetic and geographical origin of modern wheat (*Triticum aestivum*, L.), has long been debated due to its complexity. According to research in evolutionary biology and archaeological excavations, the primary area of the spontaneous hybridizations that led to the creation of the differing genomes in the *Triticum* species occurred in the Fertile Crescent (Gustafson et al., 2009). This area spans through the Mediterranean, Middle East, and Southern part of China, encompassing a vast portion of land where diversity is still abundant even today.

Approximately 500,000 years ago, wild diploid wheat (*Triticum urartu*) hybridized with an ancestor of goatgrass (*Aegilops speltoides*), creating the wild emmer wheat (*Triticum dicoccoides*) (Sun et al., 2011). This hybridization combined the two genomes of the Poaceae species AA and BB from *T. urartu* and *A. speltoides*, respectively, yielding fertile tetraploid offspring. Another form of this tetraploid is commonly called einkorn (*Triticum monococcum*), which was one of the forms that first showed a variety for a non-brittle rachis (Lupton, 1987). Hunter-gatherers of this time likely utilized this as a food source, and there exists evidence that cultivation of this particular species first occurred in Galilee, Israel (Sun et al., 2011).

The allohexaploid nature of the wheat makes it the species with the largest genome among cereals (William et al, 2007). About 9,000 years ago (Sun et al., 2011), the cultivated durum wheat outcrossed to a species of goat grass (*Aegilops tauschii*), adding the DD genome and creating a hexaploid species *Triticum spelta* (AABBDD; $2n = 6x = 42$); Lupton, 1987) (Figure 1.1). This spelt wheat evolved over time into a more cultivated form known as *Triticum aestivum*, common wheat still used today (Shewry, 2009).

Wild emmer bore a gene that aided in seed survival called 'Brittle rachis' (Br). This gene allowed for the shattering of ears at maturity, breaking apart the head for a more efficient dehiscence. Though the non-brittle rachis is controlled by a single gene and has eventually become the dominant phenotype in cultivation by subconscious selection, the process was still slow (Charmet, 2011). The mutation and the brittle rachis remained within the domesticated portion of wild emmer and its descendants, harvested through cultivation. Emmer also contained a gene for a hulled grain tied to longer dormancy and requirement of drying before the hull released the wheat berry (Charmet et al., 2011). A mutation that occurred further into the evolution of emmer toward the common durum wheat was the free-threshing, naked-grain trait (Lupton, 1987). The trait provided a more advantageous plant, whose hull-free grains could allow for quick germination and growth in favorable conditions. The hulled and free threshing form eliminated a step in the processing of the wheat kernels, and over time dominated the fields as the more useful form (Gustafson et al., 2009).

Figure 1.1 Evolution of hexaploid wheat (*Triticum aestivum* L). Reprinted from Shewry, 2009.



Triticum with brittle rachis were long within the domesticated gene pool due to the theoretical factor that early harvest was often practiced that would include those germplasm lines before the head could shatter (Peng et al., 2011). Even if this trait was unintentionally selected for, oftentimes harvests would fail, and early farmers would go to wild sources for seed to start again. This slowed the process of artificial selection by

man, which would have otherwise sped up domestication at a much faster rate (Peng et al., 2011). Hulled traits also long dominated the fields along with its mutated form of naked-grain plants, which were seen to be fit for survival. This is attributed to the fact that there is no evidence showing that hulled and naked grains were separated from each other after harvest (Charmet, 2011).

Though the domestication process was slow, as civilization progressed, and wheat was transported across regions and used more extensively, homogeneity within fields and traits grew more widespread. This started what has become known as the bottleneck of triticum genetic diversity (Peng et al., 2011). When traits that are more desirable for cultivation are selected, much diversity is lost in the process. As genes are lost and defeated, performance potential, especially yield, begin to level off despite newer breeding techniques (Ray et al., 2012). Despite this, wheat today still has an extensive amount of diversity within cultivated and wild species. Wheat continues to be under scrutiny for utilization of these resources (Charmet, 2011). Wheat cultivation expanded throughout the centuries across civilizations and has become one of the most-grown crops in the world today (Singh et al., 2014).

Hybrid Wheat, Past and Present

The majority of ongoing and past studies of hybrid varieties in small grains crops showed a high level of heterosis (Bailey et al., 1980; Boland and Walcott, 1985). Optimistic researchers used these results as an inspiration to test for the same hybrid superiority in wheat (Lucken et al., 1986). An immense amount of publications arose

from the 1960s and onward, focused towards hybrids, particularly in wheat (Patterson, 1966; Wilson and Driscoll, 1983; Bruns and Peterson, 1998). This has continued in recent hybrid wheat studies, which continue to prove that the vast majority of hybrids tend to have higher vigor and yield than their inbred parental counterparts (Kempe et al., 2014).

However, such results were not often observed in early research trials, due to unrefined methods in research of hybrids (Patterson, 1966). Hybrid trials were often quite small, resulting in large experimental error and misrepresentative plot designs (Knott, 1965). The initial attempts in hybrid wheat research were to prove that there was sufficient heterosis to justify the laborious cost of hybrid seed production. Patterson (1966) reported that there was no heterosis in his study. On the other hand, a different study reported an advantage up to 33% over established cultivars and 37% over parents (Wilson, 1983). The difference in hybrid performance in these studies could be due to better experimental design and improved lines.

Although wheat hybrids performed well with significant heterosis, high labor costs, time, and unavailability of trained personnel did not justify hybrid wheat production, thus reducing the interest in commercial hybrid wheat (Singh et al., 2015). Hybrids showed an advantage of a 106% over the check cultivars (or varieties) for a flour yield study, when levels of 115-120% were considered to have potential for commercial success (Boland and Walcott, 1985). These quality parameters were thought to be correlated with yield potential (Boland and Walcott, 1985). Improvements in breeding methods were necessary in order to increase the accuracy of research studies.

Despite this, work progressed around the idea of capturing efficient methods of conducting hybrid crosses. Several discoveries continued scientific ventures into the creation of a commercially justifiable hybrid wheat-breeding program. These included the discovery of the male sterile systems, cytoplasmic male sterile (CMS) gene in 1962, *Triticum timopheevi* (Lucken, 1986), which held potential to increase the efficiency of mass cross pollination in wheat lines. Another was the creation of chemical hybridizing agents (CHA), which could sterilize a selected population to use as female parents in hybrid crossing, thus reducing labor costs. Genesis was developed by Monsanto in the late 1980s, and Croisor 100® was created by Dupont in 1993. Numerous other CHAs exist throughout the world (Adugna et al., 2004), under development and testing against each other and the traditional male sterility system (Singh et al., 2014). Another method visited several times by different sets of researchers is called the “split-gene” system, or “Barnase method” (Kempe et al., 2014), which can shorten the cycle of the traditional male sterility system. These breeding strategies hold potential to reduce costs and time for hybrid production.

Male Sterility Systems

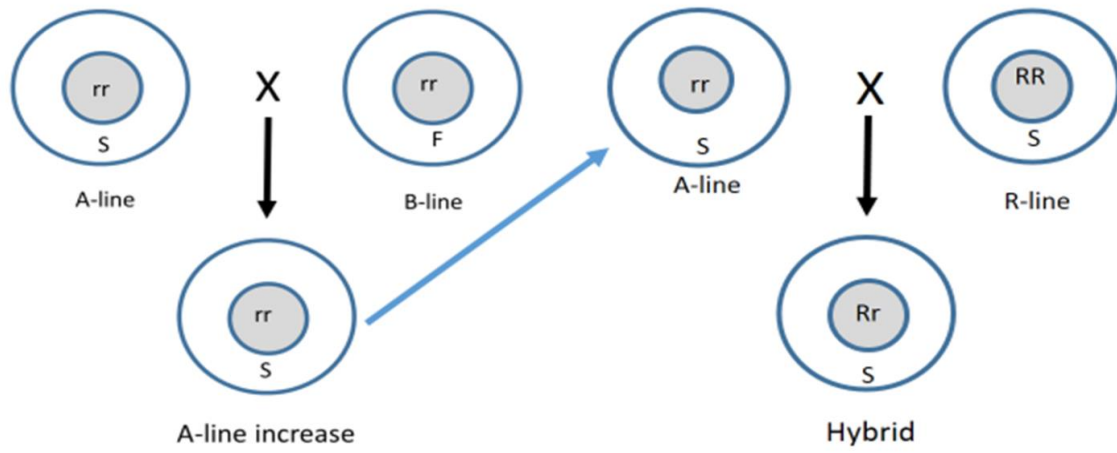
Wheat is a naturally self-pollinating grass species, producing flowers in a cleistogamy type formation (Whitford et al., 2013), with an outcrossing rate of up to 6% in some cases (Hucl, 1996). The glumes generally remain closed, and fertilization occurs within itself, producing stable inbred lines. This makes cross hybridization very difficult and time consuming, contributing to the high costs and time required (Singh et al., 2014). In order to facilitate a crossing block, researchers originally had to emasculate all

chosen female parents manually to ensure accuracy (Driscoll et al., 1983). While this was one of the main driving factors toward disinterest in the costly method, this also drove research into more efficient techniques for conducting hybrid research. Male sterility can be caused by several environmental factors, such as copper deficiency, temperature, and humidity levels, though genetic factors also exist (Athwal et al. 1967; Murai et al. 1993).

Cytoplasmic Male Sterility

In 1951, a male sterile genetic mutant was discovered by Kihara (Adugna, 2004) growing in a population in Japan. Collection of seed and growth in the next season showed that segregations occurred in this novel genetic deformity. Subsequent testing and research diverged into the idea that male sterile plants could still function as female parents in the crossing procedure, thus eliminating the need to hand emasculate (Streiff et al., 1997). Generations following male sterile populations frequently showed at least partial fertility in the progeny, giving scientists a clue that there was some sort of mechanism in the genome that ensured fertile progeny following sterile parents (Maan and Lucken, 1972). As a result, the cytoplasmic and genetic processes were under a greater deal of scrutiny (Murai and Tsunewaki, 1993). In later genetic analysis of this phenomenon, three main lines with varying effects were confirmed in this process (Prakash et al., 2012); the A line, B line, and R line (Figure 1.2).

Figure 1.2 Hybrid wheat production using a three-line system. Figure reprinted from Dr. P. Stephen Baenziger, University of Nebraska.



A sterile A-line is crossed to a maintainer B-line, to increase A-line for hybrid production. The B-line has fertile cytoplasm, and thus when B-line and A-lines are crossed, the resultant progeny essentially resembles the A-line. This expanded population of male-sterile seed is then crossed to a restorer I line, which contains dominant restorer genes. The resulting hybrid progeny are then heterozygous and fertile.

The A line is the male sterile subject, commonly derived from *Triticum timopheevi*, which was the origin of most hybrid wheat research (Maan and Lucken, 1972). Though numerous different sources of male sterile cytoplasm exist, this particular species was deemed most useful for hybrid wheat commercialization due to improvement of the sterile and its restorers over time, such as the use of double cross-hybrids (Maan and Lucken, 1972). A critical amount of time has already been invested into this sterile system, and has been refined to the point that changing to an alternative

source would be a hindrance unless the new system outperformed the *T. timopheevi* system. At this time, no such sources of male sterility exist that exhibit a great advantage (Adugna, 2004). The B lines are the maintainers of sterility, commonly derived from *Triticum aestivum*, which produce male sterile progeny when crossed to male sterile lines, though being fertile themselves. This is due to difference between the two in the cytoplasm; though both retain the recessive, sterile favorable genes, the maintainer line actually retains fertility, as decreed by the dominant allele for fertility (Prakash et al., 2012)

The R line is named so because of its restoration ability on the fertility of the crossed male sterile line, due to the genetic dominance in the cytoplasm (Maan and Lucken, 1972). This dominance can bring a portion of restoration in the progeny but was shown that there is a more complete fertility restoration if there are more than two genes in the genome of the restorer parent (Chen, 2003).

As introgression of the male sterile system into desired lines began to be tested, noticeably lower seed set was seen in male sterile lines (Imrie, 1966). Several explanations existed about the reasons for this, including seeding rates, environmental effects, flowering characteristics, and planting dates (Wilson and Ross, 1962). Some research even suggests that the restorer lines (R-line) did not provide complete restoration. In later studies, seed set was shown to be closer to 75.27% (Adugna, 2004), which could be explained by more precise selection and improvement of CMS lines, and better designed studies encompassing all possible factors, including germplasm, sterile and restorer genes, and environmental effects (Chen, 2003; Wilson and Driscoll, 1983).

Studies on male sterility genes and their impact on end use and reproduction quality has gathered sufficient data to prove that quality of the wheat is not reduced when implementing this system (Driscoll et al., 1983). This information has given scientists an edge when integrating recent developments in technologies into furthering hybrid studies. Better understanding of the genes, due to far more precise technologies than before, has allowed for isolation and recognition of sterility and fertility restoration genes. The compatibility and effectiveness of these have been demonstrated repeatedly in studies over the years (Mukai and Tsunewaki, 1979; Chen, 2003). Linkage maps have been established, and several genes tagged specifically to better understand male sterility, and thus hybrid wheat production (Song et al., 2014; Xing et al., 2003).

More than 70 wheat lines containing the male sterile phenomenon have been discovered, yet none has proven groundbreaking for usage of this method commercially (Guo et al., 2006). Other genetic sources for use in a sterility system have been investigated, like *Aegilops crassa*, which appears to exhibit sterility in long-day conditions and fertility in short days (Murai and Tsunewaki, 1993), and others in the *Triticum* and *Aegilops* genus.

Problems commonly associated with any type of male sterility include low fertility rates, maturity rates of chosen parents, and some degree of segregation into fertility where plants should be completely infertile, causing contamination of hybrids with selfed seed (Mukai and Tsunewaki, 1979). Fertility rates have been recorded often throughout development, ranging from 0 to 87% (Imrie, 1966) to 18.4 to 75.27% (Adugna, 2004).

Despite this, CMS usage still prevails as the most efficient method for the creation of hybrids known today (Adugna et al., 2004), even though there still exists a time commitment of integrating the male sterility system into the desired hybrid crossing block. Work continues to improve the prospect of utilizing more efficient methods for hybrid production, and CHAs are becoming a point of focus due to the potential advantage over CMS systems traditionally used in hybrid operations. One recently released CHA called Croisor100®, manufactured by Saaten-Union shows promise in just that (Longin et al., 2012).

Chemical Hybridizing Agents

CHAs have been under development and study as early as the 1950s (Singh et al., 2014), and first began commercial testing in the 1970s (Nesvadba and Vyhnánek, 2001). These varying chemicals are applied during growth at the three spike length stage (Iskra et al., 2013), upon the desired female parent. When heads form, they will mature devoid of functional pollen, though ideally retain the receptivity of their female organs (Castillo et al., 2014). This method greatly reduces the time necessary for sterilizing the female parent when compared to CMS methods. One CHA known as Genesis©, produced by Monsanto, was reported to have positive results (Miskin et al., 1998), though was removed from production due to environmental hazards (Iskra et al., 2013). Another of the more publicly known commercially released CHA is Croisor100©, owned by the Saaten-Union in France. The early form of this chemical, stintofen, was purchased from Hybrinova, owned by DuPont at that time, in 2005, and released in 2011

under license in France (Longin et al., 2012). Literature on this chemical is not abundant, but indicate the product shows promising results (Nesvadba and Vyhnanek, 2001).

Older research suggested that temperature and humidity greatly affected stigma receptivity in CHA treated lines (Imrie, 1966) as well as CMS lines (Jan and Qualset, 1977), which could be a factor when calculating stigma fertility of male sterile plants. In some studies, it was shown that CHA induced sterility using CH9832 tended to have a lower seed set, as shown by Adugna et al. (2004) where it ranged between 6.3 to 40.40%, and in SC2053 it was seen to be anywhere between 11 and 97% (Streiff et al., 1997), displaying the diversity of different CHAs. Another common issue is incomplete male sterility, which could lead to a seed population contaminated with selfed seeds that skew results (Mukai and Tsunewaki, 1979). This is commonly blamed on the production of tillers sometime after the CHA has already been applied. This is considered a small factor, and studies show most CHAs sterilize upwards of 95% of the population (Tschabold et al., 1988), namely the commercially used Croisor® (Nesvadba and Vyhnanek, 2001). Implementation of this into breeding programs has been slow, because of the cost and other problems commonly associated with it.

Barnase Method-a Transgenic Male Sterility System

The Barnase (bacterial ribonuclease) inserted into wheat activates at translation, producing a phytotoxin that destroys the tapetum, thus eliminating the opportunity to form viable pollen (Block et al., 1997). This involves vectoring non-overlapping Barnase genes into the desired wheat lines. These fragments are found on chromosomally

identical positions, yet on differing homologous chromosomes. This ensures that during meiosis, the two separate and the progeny become heterozygous, therefore with full fertility (Kempe et al., 2014). This process has a self-implemented restoration system, and would eliminate the need for a restoration line. Maintenance of the male sterile lines can be obtained by backcrossing the sterile lines, thus receiving a population of 50% sterile lines (Kempe et al., 2014). There has been no actual implementation of this system into breeding programs. Considering the trends of the public leaning toward non-transgenic, or non-GMO products, including bans of them entirely in some European countries, could be one of the limiting factors thus far.

Justification of Hybrid Wheat Production

With global populations rising, projected at close to 10 billion by 2050 (Cohen, 2003), along with increasing concern about future climate change (Parry et al., 1994; Richter and Semenov, 2005), new diseases developing on the horizon, and several other threats (Shiferaw et al., 2013), scientists are searching thoroughly for a long-term solution to meeting the world demand of food consumption. Among the most important food crops is wheat, contributing to around 20% of calories to the human diet (Shiferaw et al., 2013), needs to be projected to a comfortable level of 1.7% increase per year, but is only currently at 1% (Shiferaw et al., 2013). Some studies find that yields are stagnating (Ray et al., 2012; Matuschke et al., 2007), ranging up to 37% in the world, while varying improvements are left in the remaining 63% (Ray et al., 2012).

Wheat kernels contain 6-16% protein (Evans and Peacock, 1981), and have versatile uses across the human and livestock diet. Wheat provides a stable livelihood and a self-sufficient food source for small farmers in developing and developed countries (Matuschke et al., 2007). Variations in breeding method focuses range from gluten content to protein percentage, as well as bread making qualities. Although these breeding programs are quality-directed, yield and hardiness of the crop remains the most important contributing factor of all.

Hybrids have shown superiority in yield (Matuschke et al., 2007; Martin et al., 1995) as well as yield stability (Bruns and Peterson, 1998; Koemel, Jr et al., 2004; Muhleisen et al., 2013), bread making ability (Borghini and Perenzin, 1994), and other superior physiological factors (Kindred and Gooding, 2005; Singh et al., 2010). This superiority has continuously held interest in discovering a method to make hybrid wheat a commercially suitable investment; assuming that cost would be justified by the returns at harvest. Yield factors have shown to be affected by low yielding parents (Boland and Walcott, 1985), and thus calls for scrutiny when choosing the parents for a hybrid program. Characteristics such as yield and hardiness, as well as superior flowering habits have been recommended for observation when searching for suitable parents (Kempe et al., 2014).

In order to justify costs of production of hybrid wheat, a threshold is set at 20% heterosis, though generally only about 5-10% is seen in normal planting conditions (Singh et al., 2010). This is important because of the lack of potential in hybrids during the mid-1900s, when heterosis simply could not provide enough means of income to

cover the cost of seed (Singh et al, 2010). Farmers that have been using elite inbred lines will need extraordinary results and assurance that a change to having to buy seed yearly would be worth the investment.

Floral characteristics and heterosis are an integral part of hybrid wheat studies for discovering compatible parents with desirable traits for hybrid wheat production. To study floral characteristics it is important to understand the anatomy of wheat flower and is discussed in detail in the following section.

Anatomy of the Wheat Flower

The wheat flower is formed typically like most members of the *Poaceae* family. Winter wheat in particular, requires a vernalization period of two to eight weeks (Yong et al., 2002) in order to ensure plants will become reproductive. Without this chilling period, wheat will remain vegetative. Spikelets grow in an alternating pattern upon a central rachis, collectively forming a spike. There can be a wide variation of spike numbers in a single wheat plant, dependent upon tillering ability, weather, soil fertility, and other factors (Thiry et al., 2002). Though tillering ability has shown to be linked to higher seed production (Thiry et al., 2002; Marija, 1986), when comparing the spikes of later tillers to early central spikes, tiller heads are often smaller.

Anthers are green during development, and turn yellow when mature. Fully mature anthers swell and split along the sides, dehiscing pollen from the cavity within the anthers, which is dropped within the closed glumes, or moved by wind if the anther has protruded outside of the floret (personal observation). After the shed of pollen, the

anthers then fade to white and shrivel in as little as hours, to as long as a few days. The pollen can lose its viability within a few hours (Fritz and Lukaszewski, 1989), and thus could account for the evolutionary biology of a higher production of pollen when compared to female organs. The male portion of the wheat flower is the short-lived gender, most likely because of its closed-flower structure.

The female portion of the plant consists of a single ovary per floret, with two stigmas that sprout from the tip of the ovary (De Vries, 1971). These often mature and dry, becoming feathery almost always before the anthers are ready. These stigmas will remain feathery during pollination by the anthers, and could remain feathery for many days afterwards (De Vries, 1971). If no pollination occurs, the stigma and ovary will shrivel and decay within the floret. If pollination occurs, the stigmas will dissipate and the ovary will swell, remaining green until the seed is fully formed. The plants will then begin to die, and the seed will harden and turn brown, signaling full maturity of the seed (Hanft and Wych, 1982).

The maturity of a spike is unique in the *Triticum* species. The earliest signs of maturity show in the central spikelet of the ear, often the largest. Fertility then transitions up and down at once, until the entire spike shows anthesis (De Vries, 1971). Within the spikelet, anthesis will start from the base to the top florets of the spikelet (Bonnett, 1936). Typically, the lowest few spikelets, and occasionally the tip, will show sterility or malformation. Some lower spikelets will form completely devoid of sex organs. Therefore, the most representative and fertile section tends to be the large, central spikelet (Evans and Peacock, 1981).

A spikelet forms in a fan-like shape, made up of two to six florets (Bonnett, 1936). Each floret contains one stigma and three anthers, which shift at maturity and sometimes protrude to the outside on the ends of lengthy filaments (De Vries, 1971). Anthers will shed pollen within the floret before it extrudes, and can still facilitate the possibility of natural cross pollination if there is an unfertilized, receptive female in range (Whitford et al., 2013). Anthers extrude between the palea and lemma of the floret. The palea is the softer, more transparent inner piece that closes against the stiffer lemma, and together they encase the female and male parts of the flower entirely (De Vries, 1971). Though wheat is self-pollinating and rarely outcrosses, there has often been observation of palea and lemma separation, often along with extrusion of anthers and stigma branches outside of the floret, which increases the chances of foreign pollen reception (Whitford et al., 2013).

Self-pollination is common in most small grain crops, though outcrossing has been seen to occur at about 1% (Singh et al., 2010) and up to 6% of the time (Hucl, 1996). This form of reproduction appears to be sort of evolutionary advantage. This ensures the survival of that particular plant, which produces fertile progeny from self-fertilization. It appears that unfertilized ovaries tend to receive a higher rate of disease and fungal problems, so the self-pollinating mechanism seems to be a useful trait in survival. This is supported by increases in disease when male sterility systems are implemented into hybrid programs (Calder, 1930).

In an ideal environment, the reproductive organs of the wheat flower usually have no issues. However, harsher environments influence the floral characteristics. High

temperatures reaching can decrease grain set due to abnormalities in both pollen and stigmas, thus decreasing seed production (Saini et al., 1983). High temperatures, drought, and unusually cool and rainy conditions can contribute to cleistogamous flowering (pollination in unopened flowers) (De Vries, 1971). Low temperatures during pollen development were reported to cause lower pollen production and shedding due to stress during the meiotic phase, though the female fertility appeared unaffected (Demotes-Mainard, 1996). These stresses cause lower seed production, which could be a major hindrance to hybrid programs during the crossing block attempt. However, major reductions in receptivity and production tend to only be seen during abnormally severe environments (Dawson, 1989), and pose little threat.

Though unique and considered stable as a self-pollinating crop (De Vries, 1971), this natural reproduction system has proven to be an enormous obstacle in breeding efforts to outcross these self-fertilizing plants. Most efforts of creating hybrid programs have circulated around finding the most efficient way to ensure non-contaminated crosses, with little input as possible (Lucken, 1986). However, thus far it has been proven to be a daunting task even with the most advanced technology. Scientists are still determined to make this concept a reality, and are growing closer with every trial.

Previous work on floral characteristics concluded that these are highly heritable traits, and can be improved by direct selection (Singh and Joshi, 2003). Heritability for anther length was 97.9%, stigma length was 98.3%, and anther extrusion and openness of floret both displayed a 99.9% heritability (Singh and Joshi, 2003). Most floral traits see a positive correlation with the other, including anther extrusion and flower opening;

an association which would ideally allow the anthers a wider gap to protrude from the interior of the spikelet. (Singh and Joshi, 2003). When choosing parental candidates, it is important to choose a combination of superior floral characteristics, more ideally for those that associate positively with each other. In addition to floral characteristics, it is also important to choose these candidates from a pool germplasm with good agronomic characteristics, which increases the chance of progeny showing high levels of heterosis.

High Parent Heterosis

The performance of the progeny that is greater than that of the two parents is often referred to as heterosis (Stuber, 1994). Heterosis is often interchanged with 'hybrid vigor', and is used across a broad spectrum of studied traits, the most common being yield.

High parent heterosis can be defined as the yield of the hybrid progeny yielding higher than the highest yielding or superior parent (Barbosa-Neto et al., 2012). High parent heterosis is often the point of focus for yield characteristics for its practicality, due to the desire for the progeny to out-yield even the highest standard. Heterosis can also be sought by calculating mid-parent heterosis. This is the determination that the hybrid progeny yields better than the average of the two parents (Barbosa-Neto et al., 2012). The value derived from this can be used as an additional comparison alongside high parent heterosis and performance of the progeny, in case a population does not show high parent heterosis, but still shows potential by mid-parent calculation. This is often used when studying the quantitative traits inherited from the parents.

Heterosis is extremely important in hybrid studies, because this in itself can justify the necessity of a hybrid program and its efforts. Without heterosis, there would be no reason to spend time and labor on a project that would yield no better than those varieties that are already established. Despite decades of research, questions about the true cause of heterosis still circulate across all crop species. Some believe that this is caused by the interaction of inherited loci, which were previously in separate genomes and thus unable to interact until entering the hybrid progeny (Stuber, 1994), or even dominance of favorable genes in inherited linkage groups (Jones, 1917).

Other more common theories exist, one simply called dominance. This is one of the most popular concepts, which denotes that each parent contains genes that are missing from the other, becoming complimentary in the progeny. This is theorized to be the reason for progeny showing superiority (Birchler et al., 2010). The overdominance model denotes that alleles that were present in each parent, became positioned within the same genome in the progeny, thus able to begin interacting, and exhibiting hybrid vigor (Birchler et al., 2010). An examination at the cellular level suggests that heterosis could also be caused by suppression of genes with negative influences, or an increase in cell production to accumulate larger biomass (Birchler et al., 2010).

Studies have shown that heterosis can be partially predicted by observing the strength of ancestral or genetic relationship between wheat lines (Martin et al., 1995). It is believed that higher heterosis can be achieved by increasing the genetic diversity and dissimilarity between the two parents. In other crops such as maize (*Zea mays*), these heterotic pools have been created and utilized, showing excellent results in progeny

(Smith et al., 1990). For wheat, these heterotic pools have only recently become a focus, and thus are undeveloped (Barbosa-Neto et al., 2012). Because of generations of strict inbreeding for a handful of traits, there has been fear that genetic diversity may have been long lost (Gustafson et al., 2009). Some researchers are turning to repeating the original cross that created modern wheat in order to re-introduce lost genetic material back into the population, often referred to as synthetic wheat (Charmet, 2011). Collaboration between separate wheat breeding programs may help to introduce more diversity in crosses (Cox and Murphy, 1990).

Despite the lack of established heterotic pools, several studies still show at least moderate levels of hybrid vigor from most hybrid wheat programs that have published results (Kindred and Gooding, 2005), giving hope that necessary levels of heterosis can be reached with proper development. Varying levels have been achieved, many with the realization that these are not quite reaching the desired gains. In comparison to other crops, refinement of wheat is in its preliminary stage, and still has a great potential left for improvement (Whitford et al., 2013).

Established hybrid crops, particularly maize, find the importance of heterotic pools to be at an increasing level. The fear losing genetic diversity has driven researchers to test for breeding potential in other established programs in vastly different regions. Though this concept is to increase genetic diversity and increase hybrid vigor, this could cause an issue for regional adaptation (Reif et al., 2010). Investigations among genetic distances and relationships are commonly conducted using RFLP (restriction fragment length polymorphism), thus allowing for easy separation of heterotic groups and

selection of a prominent hybrid cross (Livini et al., 1992). The same process has potential use for wheat. Similar research on rice and wheat using SSR markers showed an excellent ability in predicting heterosis by examining genetic distances (Ahmad, 2002). Wheat itself contains a complex genome, though with restricted diversity due to the long breeding practice of self-pollination for certain end-use characteristics (Ahmad, 2002). This narrowed set of genes could prove to be a hindrance, but using cultivars from different regions established for alternative situations could allow for re-introduction of genetic material and increased heterosis (Reif et al., 2010).

Heterosis is often captured in the F_1 , when the generation is at its most uniform and homozygous. However, studies have shown that F_1 heterosis can be easily predicted using data from parents and F_2 generation yield data (Bailey et al., 1980). The greatest amount of segregation exists in the F_2 generations, following the F_1 that remains uniform due to principle fact that the hybrid resulting from the initial cross will be heterozygous at most, if not all, loci (Jones, 1917). The F_2 follows the rule of Hardy-Weinburg, and the equilibrium will eventually balance out over the generations if no selections take place. The F_2 generation is seemingly the best generation to estimate heterosis due to seed numbers. In F_2 , there is still at least a 50% portion of heterozygous progeny, and a sufficient amount of seed to test all traits and properties in order to estimate true heterosis (Krystkowiak et al., 2009). Aside from using F_2 as a proxy to the F_1 , parental performance can also be a good predictor of hybrid performance, with some allowances given to genetic distance between parents and genotype-by-environmental factors (Cox

and Murphy, 1990). This could allow for efficient parental selection based on superior traits and yield performance, thus saving time and money for hybrid programs.

Biplots and Statistical Analysis for Screening Candidates

Data collected during research is only the first phase of the screening and selection process. Environmental and parental effects, experimental design, and several other factors must be carefully taken into consideration (Dehgani et al., 2006) This information can only be determined as important data after a statistical test for significance. If this test shows no significance, then the hypothesis that was being tested would be considered invalid (Yan and Tinker, 2006). Statistical analysis is important for verifying that the conducted research has worth, and is considered important and worth being followed up on. Several analyses are available for utilization in research, and there are several common biplots that almost always appear in scientific papers to serve as visuals to these data analyses.

Biplot analysis is commonly used for multi-environment trials, in order to compare multiple candidates across several different environments, and study those interactions (Dehgani et al., 2006). A biplot is a very simple and easy tool to use to see correlations across genotypes, environments, and between genotypes and environments (Yang et al., 2006). An environment is defined as a location*year interaction. It can also be used to determine relationships between genotypes and traits being studied, such as yield. Two matrices containing research values are plotted together, creating a biplot that allows for the easy comparison of genotype and subjective data (Yan and Hunt, 2002).

The positions of these data points can explain certain interactions very quickly by a single glance from the researcher, such as a genotype superior across all environments causing all environment data points to gather around the specific genotype (Yan et al., 2007). This can allow for an easy estimation of possible significances within the study that could be tested in further analyses. Several different types of biplot visuals exist, each one arranging data in appropriate graphs in order to clarify the best subject across all tests.

The ‘which-won-where’ biplot graphs data in order to explain which genotype performed the best in each environment or trait studied (Yan and Hunt, 2002). This biplot is very simple to read, and its output is very easily summarized. A similar biplot, ‘comparison among all genotypes’, takes an average of the genotypes evaluated and plots the subjects against this line. It easily allows a statistician to see which genotypes fall above the average, or below (Yan and Hunt, 2002). Another common biplot that exists is utilized mainly to determine the dependability of the data that was gathered. This can plot genotypes across all environments against an axis that represents stability upon the X-axis (Yan and Hunt, 2002). A set of concentric circles are plotted in the same plane as the axis, representing the ideal genotype, or highest mean average, in the innermost circle. Those genotypes that fall closest to the X-axis are the most stable across environments, and those that fall within the inner circle are deemed the most desirable of those genotypes participating in the study (Yan and Tinker, 2006). The most sought after result is a balance between high mean average and stability.

Environments and their effects on the given genotypes are important in discriminating between the best and worst participants. An environment that is best able to separate the tested genotypes into easily seen categories is considered very discriminating (Yan and Tinker, 2006). The more discriminating the environment is, the more informative it is. Without this attribute, it would be impossible to distinguish between superior genotypes and poor ones. Despite this, stability in environments is highly desirable, for the sake of reliable data. If genotypes perform similarly year after year in the same location, it is a good sign the location is highly stable (Yan and Tinker, 2006). Stability is one of the key factors for separating cultivars and determining which cultivar grows best within a given environment (Yan and Hunt, 2002). This can pose a challenge, considering environments can change drastically year to year, and cause genotypes to react differently (Dehghani et al., 2006).

Hybrid trials often utilize biplot analysis as the primary method for determining specific interactions and their significances, though a conventional statistical analysis should always accompany these visuals, to confirm and explain the results given in the biplots (Yan and Hunt, 2002). These biplots are generally conducted with genotype yields compared against environments, though genotypes can be plotted against a biplot of traits if these exist in a single environment. The strengths of these correlations can also be tested by using a Pearson's correlation test alongside the biplot visual, though sometimes the biplot itself can sufficiently explain the differences between variables (Yan and Hunt, 2002). If multiple environments exist, three-way biplots are used (Yan and Tinker, 2006). In short-term data collection, especially in heterosis studies, this is a

very simple method of obtaining visuals of significant discrimination between genotypes (Yan et al., 2007).

Because of the simplicity of the biplot analysis, there have been debates over whether the results from this are adequate enough to display the complexity of such interconnected reactions, or if the biplots are being used to interpret more than what they can realistically compute (Yang et al., 2009). The unpredictability of each year in a single location can make it difficult to determine the best cultivar for a single, changing environment (Dehghani et al., 2006). This genotype-by-environment interaction can be hindering to hybrid programs attempting to show data to prove any single cultivar is suited to a certain environment. The confidence levels in biplots, more specifically the ‘which-won-where’, are also another cause for concern when deciding the usefulness and accuracy of these analyses. This can be overcome if the dataset is extensive enough to lower the error and determine the stability of the data points across the biplot (Yang et al., 2006). Biplots are simple visuals, and accurate when the dataset itself is simple. When the data becomes more complicated, biplots must be interpreted very carefully, and always supported by supplemental significances obtained from data analysis.

Path Coefficient Analysis

When studying multiple characteristics that contribute to yield, it becomes necessary to determine the significance of each characteristic to the yield overall and their interactions with each other. This concept was created by a geneticist named Sewall Wright in 1921, and further enhanced over the decades (Land, 1969). Essentially, path

coefficient analysis allows for the determination of a linear, positive or negative relationship, or even no correlation at all. These relationships of the traits analyzed are described as direct or indirect effects. Direct effects are significant and have an effect on the performance of the other subject trait, and indirect effects cause no apparent disturbance. This analysis provides a more confident conclusion to research in quantitative traits, and often accompanies biplots to confirm the visual with confidence.

To perform path coefficients, each variable in question is tested as a dependent to the rest of the traits. Path coefficient is a multi-variate analysis that works with closed systems of variables, where all are assumed to be linear (Land, 1969). Those that fail to show any reaction may be transformed in some cases (Li, 1956). This analysis is one of the more reliable tests, which can be used to confirm or denounce results from other more simplistic analyses.

Path coefficient analysis has been used over the years in countless studies to discover the importance of certain traits contributing to yield. One study in 1982, Gebeyehou et al. challenged a previous study claiming that longer vegetative periods contribute to higher yield, and performed their own with path coefficient analysis, discovering that it was a more complex mix of several traits all contributing to each other and the vegetative period. Others proved to have simpler results, like confirming the relationship between plant height and yield (Khan et al., 2005) with the simple assumption that it negatively affects all other characteristics that contribute to yield. Regardless of the characteristics involved, all combinations and effects are tested, giving a thorough and accurate conclusion to the interactions of what is being studied.

CHAPTER III

EVALUATION OF FLORAL CHARACTERISTICS OF TEXAS A&M (TAM) GERMPLASM

Introduction

Floral characteristics are an integral part of hybrid wheat (*Triticum aestivum* L.) studies, for discovering compatible parents for hybrid seed production. Open florets, extruded anthers, and synchronous flowering are among the most desired aspects of normally self-pollinating species, including wheat (Giles et al., 2014). Although wheat is a self-pollinating species, outcrossing rate of up to 6% was observed (Hucl, 1996). The importance of studying and refining floral characteristics were realized when work on hybrid wheat began in the mid-1960's (De Vries, 1971).

For developing hybrid wheat, adequate cross-pollination attributes are necessary. Outcrossing in wheat is influenced by floral traits such as stigma size, anther size, anther extrusion, pollen number and pollen viability (Singh et al., 2010). Therefore, selection of male floral traits such as duration of flower opening and high anther extrusion, and female floral traits such as openness of florets and stigma receptivity will enhance the magnitude of out-crossing in wheat.

The selection of genotypes for cross-pollination ability is important for hybrid wheat production. The wheat flower can be observed by the naked eye, though sometimes magnification is necessary to see fine details. A wide array of floral traits is easily perceived without any complications, from one wheat spike during the length of

the flower's life span. However, because of the self-pollinating tendencies of the wheat plant, female and male observations should be taken on separate spikes, with appropriate accommodations taken into consideration. For studying male floral traits, the wheat spike can remain untouched, while female spikes need to be emasculated to prevent pollination that could interrupt floral observations. Hindrances in these methods, including pollen contamination, damage from emasculation equipment, and other errors call for an innovative approach to capture all necessary notes at the time of flowering. Therefore, extensive and tedious efforts in floral observations should be made to ensure the most accurate data compilation.

The purpose of this study is to screen a large set of TAM germplasm, including 1,770 advanced breeding lines for superior floral characteristics, and narrow those to approximately 15-20 lines to use in the hybrid wheat crossing block. Two years of observations were grown, the second year comprising of narrowed, replicated observations, to compare repeatability across environments and make final selections for the parental candidates in confidence.

Materials and Methods

Table 2.1 explains the wheat breeding pipeline at Texas A&M University with timing of selection years and duration. Advanced breeding lines were used in this study, and measurements were taken for two years. In both study years, the lines were planted as head-rows, with one and two replications in 2014 and 2015, respectively. In November 2013, 625 head-rows of advanced breeding lines in Amarillo Observation

(AOBS) and 655 head-rows of advanced breeding lines in South Texas Observation (SOBS) nurseries were planted in Castroville, TX [29.348340, -98.797738], and grown out in 2014. Checks of 'TAM 305' were planted every 10 head-rows for SOBS. Four checks of 'TAM 109', 'TAM 111', 'TAM 112', and 'TAM 113' were planted together every 100 head-rows in AOBS. All head-rows were seeded at three linear feet, spaced 12 inches between rows, in sets of four per pass. Fertilizer in the field was applied at a rate of 108lbs nitrogen per acre (N/A).

In the same growing season, in January 2014, 140 breeding lines in South Texas Preliminary (STP1-STP4) and 350 breeding lines in Amarillo Preliminary (AP1-AP10) nurseries were planted in pots and grown in a greenhouse at College Station, TX [30.615825, -96.354355], at a density of three plants per pot. Two checks, TAM 111 and 'TAM 401' were grown for each nursery, on opposite sides of the greenhouse for good measure. Pots measured 14cm tall, 15.3cm wide at the top, 10.7cm at the base, and were filled with potting soil to approximately 11.5cm. Medium consisted of a sandy loam and mulch mixture. When plants reached the tillering stage, a 10-10-10 NPK slow release fertilizer was applied to each pot at a rate of 14.3 grams, then covered with 1 inch of MetroMix potting soil. Each pot was then watered in with 24-8-16 NPK fertilizer to maximize tillering. The field and greenhouse were both irrigated when necessary through a linear irrigation system for the former.

Table 2.1 The Texas A&M 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
10-12	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.

maximize tillering. The field and greenhouse were both irrigated when necessary through a linear irrigation system for the former.

During November 2014, a narrowed set of 97 observational lines were planted in College Station [30.615825, -96.354355]. Checks of TAM 305 were grown at every 10 head-rows. These head-rows measured the same as the observations in Castroville, TX, at three linear feet spaced 12 inches apart, and four rows per block. No irrigation was necessary due to sufficient rainfall during the 2015 growing season. Fertilizer was applied at a rate of 53lbs nitrogen per acre (N/A).

Weather conditions in Castroville, TX in 2014 were average, with adequate rainfall and average temperatures ranging from the 60s to high 90s. This was a high contrast to weather in College Station, TX in 2015. Heavy rainfall and less sunlight were some of the largest differences from 2014. Temperatures in College Station, TX ranged from the 60s to the high 80s, slightly lower than Castroville in the previous year.

Personnel were present at all locations both years once the initial floral observations began. Daily notes were taken to ensure the best accuracy of floral traits.

Emasculation of Wheat Spike

For observing female traits, an entire spike was emasculated, leaving only the stigmas intact. Initial 2014 observation of emasculated spikes (with the top of the florets removed) showed that the stigmas were damaged due to drying and heat. For more accurate observations in 2015, the spikes were emasculated with two florets at the center of the spike retaining intact palea and lemmas, though anthers were still removed to avoid pollen contamination (Figure 2.1). This allowed for natural protection against the elements, and a test for far more accurate reading for female traits. The stigmas within the intact florets were used for observing featheriness, size and extrusion, in order to best mimic the normal circumstances in which a crossing block would be conducted. Observation of the male floral traits required no alteration to the spike, and thus were only tagged.

All floral observations were taken at the central glumes of the spikelet, with consideration to the natural sequence of floral development that most often causes the

lowest and uppermost spikelets to be sterile or malformed, while the upper central are the largest and most representative of the head itself (Evans and Peacock, 1981).

Figure 2.1 Emasculated wheat spike with central spikelets (circled in red) retaining intact palea and lemmas.



Table 2.2 Guidelines for measuring floral characteristics of common wheat.*

Floral characteristics	Scoring scale				
	1	2	3	4	5
Angle of glume separation (°)	0-5°	6-10°	11-15°	16-20°	≥21°
Stigma size (length, mm)	0-0.5	0.6-1.09	1.1-2.09	2.1-3.09	≥3.11
Duration of stigma featheriness (days)	0-2	3-4	5-8	9-10	≥11
Anther size- length (mm)	0-1.09	1.10-2.09	2.10-3.09	3.10-4.09	≥4.10
Anther size- width (mm)	0-0.25	0.26-0.5	0.51-0.75	0.76-1	≥1.01
Anther extrusion (%)	0-15	16-25	26-50	51-75	≥76
Awn length (cm)	0-0.5	0.51-2	2.01-5	5.01-6	≥6.01
Spikelet tightness	Very tight; no space between spikelets	Tight; little space between spikelets	Moderately tight; some space between spikelets	Loose; significant space between spikelets	Very loose; exorbitant space between spikelets
Stigma excscertion	No apparent movement	Reaching toward top	Tips breach glume	Branches visible outside glume	Branches very visible outside glume

*The guidelines from P. H. DeVries (1971) were followed in this study with some modifications to encompass all possible occurrences in floral diversity.

Guidelines for Measuring Floral Characteristics

Particular ranges were set up to help categorize the non-uniform floral data and compare them against each other (Table 2.2). Previous research on floral traits aided in the creation of these ranges (De Vries, 1971) beforehand, so that thresholds for the best performers could be established, and poor performers easily removed from the program.

For each trait observation, specific sets of guidelines existed to ensure the most accurate and uniform results were gathered. These can be separated into non-gender specific and gender specific guidelines.

Non-Gender Specific Categories

Heading Date: Heading date was recorded when at least 50% of the heads in a plot had emerged from the boots.

Anthesis Date: Anthesis date was recorded when at least 50% of the spikes in the plot had yellow anthers, either outside or inside of the florets. In some lines the anthers would be trapped inside the floret, therefore the florets were opened to check if anthers turned yellow from their original green color. Additionally, each head observed must have at least 50% of anthers within the spikelets showing yellow and viable pollen production to be counted as reaching anthesis. This was checked by carefully pulling the palea and lemma apart and looking inside of the floret at the anthers within. This could be done using needlepoint tweezers to grasp the palea and lemma, and gently pulling the two apart. The lodicule would naturally separate these at maturity, giving anthers a chance to extrude (De Vries, 1971). So it was important not to damage the palea and lemma, otherwise this would have skewed the later observation of anther extrusion. A sufficient amount of glumes were checked for anthesis, in order to assure that anthesis was confirmed.

Spikelet Tightness: This is a measure of how tightly together the floret tends to hold itself. As the maturing and swelling of the wheat kernel could alter the appearance

of spikelet tightness (personal observation), observations were made during the growth period and viability, before pollination and enlargement of ovaries. A scale of 1-5 (1= very tight and immobile; 5= very loose and easily moveable) was used (Table 2.2) to determine the closeness of the spikelets that formed together on the central rachis of the wheat head. The observation must be taken by one researcher alone, to avoid error due to bias. A visual guide to this characteristic is shown in Figure 2.2.

Figure 2.2 Comparison of spikelet tightness (scale of 1-5).



The numbers (1-3) indicate the score for spikelet tightness. This characteristic was judged visually and the largest spacing observed, according to pre-ordained guidelines was a scale of 3.

Plant Height: Plant height was measured at the end of the growing season when plants reached physiological maturity (loss of green color in the last internode below the spike) (Hanft and Wych, 1982). Measurements were recorded on representative plants in the center of the head-row by measuring height from soil surface to the tip of the spike excluding awns.

Gender Specific Categories

Anther Size: The length and width of anthers (in mm) were measured using a high precision digital caliper during the viable period. Taking measurements during the viable period is important due to the shriveling of the anthers after they passed maturity. Measurements were taken from anthers in the central area of the spike, where the most prominent spikelets exist. Most of the measurements were taken from anthers that were extruded out of the floret, with an exception to some lines that did not have anther extrusion. These measurements were taken from viable anthers inside the spikelet.

Anther Extrusion: Extrusion of anthers outside of the floret during the viable period is important to pollen dispersal to other plants. Ideally, a genotype showing a high rate of extrusion would be an excellent male parent in a crossing block during hybrid wheat production. Often, the viable period would span over 1-3 days, with a few spikelets becoming viable at a time, and losing viability within the day. Therefore, extrusion percentages were calculated (Table 2.2) after the three day period when extrusion was finished, and all possible anthers were outside of the floret in an attempt to

disperse pollen. All spikelets with pollen dispersal were counted and divided against the number of spikelets on the head, and this yielded a percentage used in later selection.

Angle of Glume Separation During Viability: After anthesis is reached, on some genotypes, the palea and lemma separate due to the swelling of the lodicule (De Vries, 1971). This aids in anther extrusion by allowing space for the anthers to push outside of the floret. This can also facilitate the movement of the feathery stigma branches, which can also extrude outside the floret during the viable period of the female flower. The timespan of glume separation was not measured in this study though the observable gape may allow the foreign pollen to enter this normally self-pollinating crop and allow cross pollination (Whitford et al., 2013). The angle of separation was measured between the separation of the palea and lemma, where the flower is exposed.

Stigma Exsertion: This is a visual estimate of measuring the extent to which the stigma extrudes from the floret. A scale of 1-5 was used for measuring the stigma exsertion (Table 2.2, and Figure 2.3). High exsertion increases the chance of capturing foreign pollen, which in turn enhances the cross-pollinating ability for hybrid wheat production.

Stigma Size: The length of the stigma was measured from the base of the stigma where the branches meet the ovary to the tip of the feathery branches. The measurements were taken in mm using a caliper during the viable period, when the stigma still shows sufficient featheriness.

Duration of Stigma Featheriness: This trait was measured by emasculating the wheat spike before pollination and observing the length in days (Table 2.2) that the flower remains feathery and sustainable for reception of pollen.

Selection Criteria

After all results were gathered, populations were screened for superiority. Poor performing candidates were discarded, and the population narrowed. The best performing males and females were selected based on the criteria shown in Table 2.3. Those performing well in female traits could be chosen as a female candidate, even if male traits were poor. It was vice versa for male traits, though this was not always the case. It was possible for some to perform well in both areas, and could be advanced as a dual-purpose line.

Anthesis date and plant height were the main factors used in selecting the lines as male or female. Shorter, earlier flowering lines were selected as females, whereas taller, later flowering lines were selected as males (Table 2.3), to facilitate timely flowering and pollen shedding for successful crossing.

Featheriness of the stigma is a good indicator of pollen receptivity during the viable period. Duration of this viability increases the window for cross pollination to occur. This is important because anthers are viable only for a very short period of time. A female can be chosen as a cross to a male parent, where the flower will be receptive at a period before and during the time the pollen becomes viable and available for a crosspollination attempt. Research has reported stigmas remaining receptive for up to

eight days under normal conditions before flowers dissipate (De Vries, 1971), but there was no fertility testing done in this study.

The mean value of the trait was used as a threshold for selecting non-gender specific characteristics, where females and males were chosen if the trait value was less than or equal to the mean, and greater than or equal to the mean, respectively (Table 2.3). For gender specific traits, lines that performed above the mean value in combination of traits were chosen. Lines could be chosen as dual-purpose candidates if they overlapped on the separation threshold, (84cm in height and 89 days of anthesis for 2014, for example) with combined good male and female floral traits. Due to missing data in some female floral traits in 2014 data (Table 2.4), selections for female were made with less stringency than those in 2015.

Pearson's correlation was performed on floral traits for 2015 using PROC-CORR (SAS v9). This test excluded 2014 data due to large amounts of missing data. Previous work on floral traits also utilized this tool to test for relationships among studied floral habits (Singh and Joshi, 2003). These show trends between two traits, but do not account for actual interactions between them.

Results and Discussion

The observation of floral traits in 97 selected TAM germplasm in 2014 (Table 2.4) and 2015 (Table 2.5) showed that a vast amount of genetic diversity exists within the germplasm. The selection criteria was very stringent and approximately 6% of the lines (97 out of 1,770) were selected from 2014 floral screening. In 2015, another

selection of approximately 18% (17 out of 97) was made for moving on into the next research process, including seed increase and hybrid crossing.

The pedigrees of the selected lines were examined and shared similar ancestors, though much of this similarity was divided between nursery originations. Many AOBS selection pedigrees contained similar parental origins, though these pedigrees were similar throughout the entire nursery. The same held true for the SOBS and AP lines, whose pedigrees did not hold stand-out similarities for the selections, nor discriminate between male and female candidates. The only similarity between these three nurseries was the appearance of the 'Jagger' (Kansas origin) parental background, though this pedigree appeared the most in the AOBS lines. For the STP lines, 'Halberd' and 'Cutter' appeared in nearly every selection's background, though did not hold any similarities to any other nursery. The differences in environments for both observation years show a contrast between the pattern of selections for male and female candidates, which makes it impossible to tie pedigrees to certain floral traits. In case of possible influence, future observation of Jagger, Halberd, and Cutter in floral traits would be beneficial to these studies.

The majority of the floral characteristics showed a reliable CV in the 2015 replicated study (Table 2.5), providing confidence for future screening attempts. The female traits with the best CVs (2015 study) were stigma size at 18.86%, stigma featheriness duration at 8.5%, and stigma exertion at 31.72%. For males, it appeared to be anther length at 17.58%, anther width at 14.85%, and anther extrusion at 37.52%

Figure 2.3 Visual estimation of stigma exertion rates (scale 1-5).



1 indicates no exertion and 5 indicates high stigma exertion. Exsertion rates varied across genotypes and were not affected by glume angle.

Table 2.3 Selection criteria for floral traits

	HD	A	GA	SZ	SFD	SE	ANL	AW	AE	ST	AWL	HT
2014												
Mean (M)	86	89	8	2.63	7	3	3.16	0.92	73	2	4	84
Male		<u>>M</u>					^		^			<u>>M</u>
Female		<u><M</u>		^	^	^						<u><M</u>
2015												
Mean (M)	96	96	9	2.62	13	3	3.16	0.92	49	2	4	77
Male		<u>>M</u>					^		^			<u>>M</u>
Female		<u><M</u>		^	^	^						<u><M</u>

HD = heading date; A = Anthesis date; GA = glume angle; SZ = Stigma size; SFD = stigma featheriness duration; SE = Stigma exertion; ANL = Anther length; AW = Anther width; AE = Anther extrusion; ST = Spikelet tightness; AWL = Awn length; HT = Plant height in cm; Units for the measured floral traits were as shown in Table 2.2. Average: Average of the measured traits. >A or <A: For non-gender specific traits, lines greater than or equal to the average were selected as male and lines less than or equal to the average as female; ^For gender specific traits, selections were based on equal to or above the average value of the measured traits.

Table 2.4 Floral characteristics of advanced breeding lines from Amarillo Observations (AOBS) and South Texas Observations (SOBS) in Castroville, TX, and South Texas Preliminary (STP)^ and Amarillo Primary (AP)^ in College Station, TX in 2014

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ ^s	SFD ^s	SE ^s	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
STP3	1	HT201-01	X		82	86	10	2.89	9	3	3.68	0.89	10	2	5	76
STP3	2	HT202-08			81	84	5	2.3	10	2	2.94	1	10	2	5	68
STP3	3	HT202-24			85	89	10	3.33	4	3	3.43	0.72	90	2	5	62
STP3	4	HT205-03			91	95	5	1.59	14	1	3.44	1.1	50	1	5	57
STP3	5	HT207-13	X		84	87	10	3.31	9	3	3.16	0.71	10	2	5	61
STP3	6	HT207-31	X		86	89	5	3.49	9	3	3.49	0.89	40	1	5	61
STP3	7	HT209-01	X		79	82	5	3.17	15	3	4.04	0.77	90	2	5	65
STP4	8	HT210-04			81	84		3.34	6	4	3.49	1.06	80	2	5	66
STP4	9	HT210-05			77	81		2.71	6	2	2.94	0.83	90	2	5	62
STP4	10	HT215-11	X		79	84	5	3.16	10	3	3.12	1.1	50	2	5	67
STP4	11	HT238-14			80	85		2.21	11	2	3.4	0.7	100	2	5	66
AOBS	12	N14A685			90	93	10	1.97			2.91	0.9	80	1	5	87
AOBS	13	TAM 109			93	96	5	1.88			2.65	0.89	10	2	1	90
CHECK	14	TAM305			96	96	7	2.90	12	3	3.2	0.80	36	2	5	72
AP1	15	TX10A001006-AZ152			80	85	25	2.94	3	5	2.58	0.76	80	2	5	55
AP1	16	TX10A001018-AZ246			80	82	15	1.49		5	2.28	0.72	85	1	5	62
AP2	17	TX12A001173		X	86	90	5	2.62	4	2	3.61	0.77	90	3	1	86
AP2	18	TX12A001420			85	86	10	2.64		2	3.24	0.78	90	2	5	90
AP2	19	TX12A001517			88	91	5	1.93		2	2.35	0.86	80	2	5	81
AP3	20	TX13A001080			84	88	5	1.91		3	3.85	0.56	80	3	5	76
AP9	21	TX13A001194			94	95	30	2.83	4	2	2.94	0.68	90	2	5	61
AP9	22	TX13A001300			85	87		2.39		3	2.74	1.24	90	2	5	68
AP7	23	TX13A001347			83	87	10	3.44	5	4	3.33	0.94	80	2	5	62
AP7	24	TX13A001392			87	91	15	2.37	11	3	3.81	0.76	20	1	5	68

Table 2.4 Continued

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ [§]	SFD [§]	SE [§]	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
AP10	25	TX13A001431			85	87	5	2.42		3	3.15	0.89	90	1	5	63
AP8	26	TX13A001433			91	93	5	1.9		1	3.17	0.94	90	2	5	71
AP8	27	TX13A001443			83	86	5	2.35	5	3	3.21	0.89	80	2	5	69
AP9	28	TX13A001495			77	81		3.56	6	4	3.64	1.05	100	2	5	68
AP8	29	TX13A001554	X		81	83		3.55	13	5	2.89	1.19	60	2	5	69
STP2	30	TX13D5445	X		83	85		3.38	14	3	2.78	0.88	50	2	5	64
STP2	31	TX13M5579	X		83	86		2.8	14	3	2.46	0.81	100	3	5	68
STP2	32	TX13M5724	X		78	81		4.12	13	4	3.21	0.55	100	2	5	68
STP1	33	TX13M5739			82	85		2.5		2	3.32	0.82	100	2	5	66
AOBS	34	TX14A001085			84	87	10	2.49	5		2.97	1.11	80	2	5	93
AOBS	35	TX14A001158		X	88	91	5	2.31			3.49	1.14	80	2	5	106
AOBS	36	TX14A001165		X	89	92	5	2.38			3.41	0.9	80	1	3	111
AOBS	37	TX14A001195			89	92	5	2.54			3.53	0.93	70	1	4	89
AOBS	38	TX14A001247			88	91	15	2.5			3.06	0.81	80	1	5	103
AOBS	39	TX14A001259		X	88	91	5	2.51			3.17	1.09	80	2	5	98
AOBS	40	TX14A001266		X	90	93	5	1.99			3.55	1.07	80	1		98
AOBS	41	TX14A001271		X	88	91	5	2.01			3.42	1.06	90	1	5	97
AOBS	42	TX14A001285			85	88	10	2.04			3.23	0.89	80	1	5	96
AOBS	43	TX14A001293			94	97	20	2.18			2.86	0.87	50	1	4	89
AOBS	44	TX14A001306		X	89	92	5	2.26			3.29	1.08	80	2	5	94
AOBS	45	TX14A001317		X	88	91	5	2.51			3.49	1.03	80	2	5	100
AOBS	46	TX14A001320		X	94	94	5	2.26			3.5	1.01	80	1	5	101
AOBS	47	TX14A001324		X	87	90	10	2.48			3.19	0.98	80	3	4	106
AOBS	48	TX14A001336			88	91		2.27			3.13	1.16	80	2	4	91
AOBS	49	TX14A001349			86	89	5	2.35			3.23	1.01	70	3	5	96
AOBS	50	TX14A001364		X	87	90	10	2.32			3.16	0.68	80	2	5	92

Table 2.4 Continued

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ [§]	SFD [§]	SE [§]	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
AOBS	51	TX14A001374			73	79	10	1.68	8	2	2.17	0.82	60	2	4	78
AOBS	52	TX14A001387			89	92	5	2.6			2.97	1.01	40	2	4	77
AOBS	53	TX14A001388			87	90		2.15			2.85	0.95	90	2	5	98
AOBS	54	TX14A001396		X	88	91	10	2.39			3.49	0.89	80	2	4	89
AOBS	55	TX14A001398		X	88	91	5	2.2			3.41	0.99	90	2	3	105
AOBS	56	TX14A001410			88	91	5	2.03			3.09	0.91	80	3	3	100
AOBS	57	TX14A001412		X	90	93	10	2.38			3.29	1.13	80	2	4	102
AOBS	58	TX14A001413		X	90	93	5	2.66			3.5	1	80	2	5	95
AOBS	59	TX14A001489			91	94	5	2.86			3.11	1.07	80	1	1	85
AOBS	60	TX14A001564			85	88	5	2.18			3.17	0.81	80	2	3	88
AOBS	61	TX14A001588			89	93	5	2.09			3.05	0.81	80	2	5	93
AOBS	62	TX14A001598			91	94	20	2.3			2.92	0.9	40	2	2	86
SOBS	63	TX14M7005			87	91	5	2.8	5		4.29		50	1	5	80
SOBS	64	TX14M7008			83	89	5	2.89	7	2	3.56		60	1	5	82
SOBS	65	TX14M7010		X	89	91	5	3.19	7	3	3.54	0.77	100	2	5	84
SOBS	66	TX14M7022		X	87	91		3.48	5	3	3.24	1.05	80	1	1	91
SOBS	67	TX14M7023			88	91	5	3.31	5	3	3.12	1.12	90	1	5	91
SOBS	68	TX14M7025			89	91	5	2.3	6	2	3.07	0.99	90	1	5	93
SOBS	69	TX14M7026		X	88	90		3.46	5	3	3.41	1.02	90	1	1	93
SOBS	70	TX14M7029			88	90	5	2.39	6	1	2.92	0.76	60	1	5	95
SOBS	71	TX14M7031			89	90	10	2.81	5	2	3.09	0.91	80	2	5	98
SOBS	72	TX14M7044			82	85		2.93	5	2	2.76	0.83	60	2	5	65
SOBS	73	TX14M7045			81	86		3.25	5	2	2.34	0.56	75	1	5	69
SOBS	74	TX14M7061			87	89	5	3.72	5	3	3.73	1.24	50	3	5	76
SOBS	75	TX14M7092			87	88	10	3.18	5	2	3.17	0.87	80	2	5	80
SOBS	76	TX14M7135			90	91	5	2.53	2	2	3.14	0.82	80	2	4	84

Table 2.4 Continued

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ [§]	SFD [§]	SE [§]	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
SOBS	77	TX14M7147			90	91	5	3.41	5	3	3.06	0.81	75	2	5	85
SOBS	78	TX14M7155			81	85		2.64	5	2	2.89	0.85	60	3	5	85
SOBS	79	TX14M7191			86	89	5	2.72	5	2	2.12	0.86	50	2	4	86
SOBS	80	TX14M7210			88	90	5	2.72	6	2	3.15	0.87	80	1	5	88
SOBS	81	TX14M7214			88	91	5	3.75	4	3	3.08	0.96	80	3	4	88
SOBS	82	TX14M7304		X	88	90	5	2.29	4		3.6	1.14	90	2	4	92
SOBS	83	TX14M7329			88	90		2.74	3		2.66	0.88	100	2	5	95
SOBS	84	TX14M7334			88	92	5	2.21			2.81	0.87	90	1	2	95
SOBS	85	TX14M7337			88	90		2.92			2.73	0.88	90	2	5	96
SOBS	86	TX14M7344			81	85		2.83	5	3	2.93	0.87	50	1	5	75
SOBS	87	TX14M7374			89	91	10	2.18			2.22	1.06	75	2	5	83
SOBS	88	TX14M7393			87	89	15	2.29			3.12	0.76	80	1	5	86
SOBS	89	TX14M7408		X	87	90					3.22	0.8	90	2	5	88
SOBS	90	TX14M7442			73	83	10	1.48	5	2	2.99	0.74	30	2	5	90
SOBS	91	TX14M7523			79	82	10	2.65	6	2	3.75	1.86	100	2	5	95
SOBS	92	TX14M7538		X	92	94	5				3.68	1.16	90	2	5	96
SOBS	93	TX14M7545			76	82	10	3.03	5	2	3.35	0.95	30	3	1	97
SOBS	94	TX14M7566			81	84	10	3.21	5	2	2.96	0.95	50	1	5	98
SOBS	95	TX14M7570			81	82	5	2.51	7	2	3.38	0.67	50	3	5	98
SOBS	96	TX14M7603			91	93	5				3.14	0.81	90	2	5	100
SOBS	97	TX14M7631			81	84	5	3.11	5		2.76	1.05	50	1	1	105
Means					86	89	8.0	2.63	7	3	3.16	0.92	73	2	4	84
Range					73-96	79-97	5-30	1.48-4.12	2-15	1-5	2.12-4.29	0.55-1.86	10-100	1-3	1-5	55-111

[#]Grown in greenhouse; The selected male or female lines are indicated by 'X'; Based on averages of traits, gender-specific characteristics ([#]Male and female; [§]Female; [&]Male) were observed for choosing lines that showed performance superior to the averages of the population as a whole. HD = heading date; A = Anthesis date; GA = glume angle; SZ = Stigma size; SFD = stigma featheriness duration; SE = Stigma exsertion; ANL = Anther length; AW = Anther width; AE = Anther extrusion; ST = Spikelet tightness; AWL = Awn length; HT = Plant height; Blank spaces indicate missing data. Units for the measured floral traits were as shown in Table 2.2.

Table 2.5 Floral characteristics of selected advanced breeding lines from Amarillo Observations (AOBS), South Texas Observations (SOBS), South Texas Preliminary (STP) and Amarillo Primary (AP) in College Station, TX in 2015, and selections based on CV and averages of two replications.

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ ^{\$}	SFD ^{\$}	SE ^{\$}	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
STP3	1	HT201-01			97	96	5	2.1	13	3	2.86	1.10	30	2	5	74
STP3	2	HT202-08			94	94	8	2.5	12	3	2.51	1.07	63	2	5	67
STP3	3	HT202-24			92	92	5	2.7	13	3	2.93	1.03	63	2	5	77
STP3	4	HT205-03			97	97	15	1.6	14	2	2.64	1.04	35	2	5	70
STP3	5	HT207-13			98	98	5	2.8	14	3	3.32	0.74	38	2	5	66
STP3	6	HT207-31			95	95	3	2.0	12	3	3.00	1.01	10	2	4	71
STP3	7	HT209-01	X		94	94	5	3.2	14	4	3.64	1.04	18	2	4	75
STP4	8	HT210-04			94	94	8	2.1	13	3	2.53	0.83	85	2	5	72
STP4	9	HT210-05			93	94	5	2.5	13	3	3.00	1.12	63	2	4	64
STP4	10	HT215-11			96	96	5	2.4	13	2	2.93	0.97	10	2	5	72
STP4	11	HT238-14			93	94	3	3.0	12	4	2.71	0.89	63	2	4	72
AOBS	12	N14A685			99	98	5	2.6	12	3	3.10	0.85	63	2	5	67
AOBS	13	TAM 109			107	104	8	2.1	9	2	3.36	0.78	28	2	1	71
CHECK	14	TAM305	X		96	96	8	2.8	13	3	3.25	0.85	47	2	5	70
AP1	15	TX10A001006-AZ152			92	93	3	2.5	13	3	3.11	0.91	38	2	5	72
AP1	16	TX10A001018-AZ246	X		94	94	18	2.7	13	3	3.21	1.01	83	2	5	69
AP2	17	TX12A001173			101	101	15	1.4	14	2	2.70	1.02	45	2	1	93
AP2	18	TX12A001420			93	93	13	3.4	14	3	3.15	1.07	90	2	5	80
AP2	19	TX12A001517			98	97	3	2.8	12	3	3.00	0.86	15	1	5	84
AP3	20	TX13A001080			97	98	3	2.5	14	3	2.97	0.87	5	2	5	81
AP9	21	TX13A001194			101	99	8	2.8	13	3	3.20	1.02	53	2	4	70
AP9	22	TX13A001300			98	97	3	2.7	12	3	2.84	0.84	20	2	5	64
AP7	23	TX13A001347			93	94	8	3.1	12	4	3.31	0.89	25	2	5	83

Table 2.5 Continued

Nursery	Entry	ID	F	M	HD	A#	GA	SZ ^{\$}	SFD ^{\$}	SE ^{\$}	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
AP7	24	TX13A001392			99	98	5	2.8	13	4	3.89	1.06	18	2	5	79
AP10	25	TX13A001431			97	97	5	2.6	13	2	3.21	0.75	38	2	5	80
AP8	26	TX13A001433			106	101	8	2.2	13	2	2.83	0.89	60	2	5	74
AP8	27	TX13A001443			97	97	10	3.0	14	3	5.09	0.87	30	2	5	72
AP9	28	TX13A001495			95	95	10	2.0	12	3	3.39	1.06	40	2	5	69
AP8	29	TX13A001554			95	97	5	3.4	14	4	3.20	0.86	3	3	5	70
STP2	30	TX13D5445			93	93	3	2.6	12	3	2.96	0.89	38	2	5	76
STP2	31	TX13M5579			94	94	13	1.9	11	2	3.27	0.99	63	2	5	76
STP2	32	TX13M5724			93	94	10	2.6	12	3	1.67	0.70	50	3	5	80
STP1	33	TX13M5739	X		97	96	5	3.2	13	3	3.37	0.87	38	1	5	69
AOBS	34	TX14A001085	X		94	95	13	2.7	13	4	3.27	0.95	63	2	5	75
AOBS	35	TX14A001158			103	100	5	2.8	13	4	2.74	0.99	33	2	5	77
AOBS	36	TX14A001165			96	98	8	2.8	13	3	3.28	0.96	38	2	5	75
AOBS	37	TX14A001195			99	98	5	2.9	13	3	3.06	1.01	28	2	5	74
AOBS	38	TX14A001247			101	101	5	3.0	13	4	3.23	0.91	40	2	5	72
AOBS	39	TX14A001259			100	100	5	3.1	13	3	3.34	0.92	75	1	5	71
AOBS	40	TX14A001266			98	98	3	3.6	12	4	3.10	0.88	3	2	2	76
AOBS	41	TX14A001271		X	100	99	5	3.0	14	4	3.30	0.98	68	2	5	80
AOBS	42	TX14A001285		X	97	97	10	3.5	14	4	3.19	0.94	55	2	5	79
AOBS	43	TX14A001293			101	98	5	2.5	12	3	2.72	1.03	55	2	5	77
AOBS	44	TX14A001306			104	104	10	3.0	14	4	3.30	0.94	45	3	5	67
AOBS	45	TX14A001317			98	96	5	2.5	13	3	3.24	0.90	30	3	5	75
AOBS	46	TX14A001320			101	98	3	2.3	11	2	4.21	1.09	0	2	5	71
AOBS	47	TX14A001324			95	95	5	2.0	13	2	3.37	0.95	63	3	4	81
AOBS	48	TX14A001336			97	96	5	2.4	13	3	2.42	0.82	25	2	5	74
AOBS	49	TX14A001349			98	98	3	1.9	13	2	3.23	0.86	15	3	5	62

Table 2.5 Continued

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ ^{\$}	SFD ^{\$}	SE ^{\$}	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
AOBS	50	TX14A001364			99	98	13	2.0	14	2	3.21	0.89	38	2	5	70
AOBS	51	TX14A001374			89	90	13	2.5	14	4	3.69	0.92	75	3	5	70
AOBS	52	TX14A001387			95	96	10	2.3	14	3	3.17	0.94	63	2	5	74
AOBS	53	TX14A001388			93	94	5	3.7	12	3	3.23	1.10	70	3	5	74
AOBS	54	TX14A001396			98	98	5	2.4	12	2	3.63	0.91	90	2	5	74
AOBS	55	TX14A001398			102	100	8	3.2	11	3	3.01	0.91	63	2	5	74
AOBS	56	TX14A001410			102	102	5	2.6	11	3	3.13	0.84	18	2	5	80
AOBS	57	TX14A001412		X	100	98	13	2.5	13	2	3.21	0.81	53	2	4	83
AOBS	58	TX14A001413		X	103	102	15	2.6	14	3	3.53	1.07	78	3	5	77
AOBS	59	TX14A001489		X	98	97	5	4.0	13	5	3.55	0.89	63	2	1	80
AOBS	60	TX14A001564			98	97	5	3.0	13	3	2.99	0.78	18	1	2	71
AOBS	61	TX14A001588			99	98	5	2.3	13	2	2.79	0.89	25	2	4	65
AOBS	62	TX14A001598			103	103	25	3.1	8	4	3.76	0.76	83	3	2	74
SOBS	63	TX14M7005			98	97	5	2.5	13	3	3.24	0.76	55	2	5	71
SOBS	64	TX14M7008			97	97	5	2.1	14	2	2.74	0.80	30	2	5	76
SOBS	65	TX14M7010			93	93	13	2.8	14	2	3.47	0.95	75	1	5	74
SOBS	66	TX14M7022			93	93	3	2.4	12	3	2.54	0.98	58	2	5	76
SOBS	67	TX14M7023			93	93	18	2.8	12	3	3.63	0.96	50	3	5	74
SOBS	68	TX14M7025		X	96	96	10	2.5	14	3	3.19	0.88	88	1	5	84
SOBS	69	TX14M7026			94	94	13	2.5	13	3	3.23	0.88	83	2	5	70
SOBS	70	TX14M7029			96	97	8	2.3	14	2	3.32	0.97	30	2	5	69
SOBS	71	TX14M7031			99	98	13	2.2	13	2	3.20	0.95	30	2	5	76
SOBS	72	TX14M7044			93	93	10	2.1	14	3	2.57	0.82	50	2	5	90
SOBS	73	TX14M7045			92	94	5	2.4	13	2	3.58	0.92	38	2	5	81
SOBS	74	TX14M7061			95	95	3	1.9	12	2	3.47	0.81	25	2	5	75
SOBS	75	TX14M7092			98	98	3	2.6	13	3	2.82	0.92	38	2	1	74

Table 2.5 Continued

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ ^{\$}	SFD ^{\$}	SE ^{\$}	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
SOBS	76	TX14M7135			102	102	8	2.5	11	4	3.08	0.85	38	2	5	66
SOBS	77	TX14M7147			97	96	20	3.2	12	4	3.06	0.85	75	2	5	81
SOBS	78	TX14M7155	X		90	91	5	3.3	15	4	2.83	0.78	90	2	5	74
SOBS	79	TX14M7191			100	102	8	2.0	12	2	2.44	0.81	25	2	5	76
SOBS	80	TX14M7210			93	93	13	2.5	13	3	3.53	0.95	75	2	5	79
SOBS	81	TX14M7214			98	97	3	3.2	14	2	3.46	0.97	18	3	1	93
SOBS	82	TX14M7304			95	95	5	3.0	13	3	3.29	1.02	30	3	5	84
SOBS	83	TX14M7329	X		94	95	15	2.7	13	3	3.61	0.99	90	2	3	70
SOBS	84	TX14M7334			93	94	8	2.8	12	4	3.04	0.79	78	2	2	74
SOBS	85	TX14M7337			95	96	8	2.6	13	2	2.85	0.97	90	1	5	69
SOBS	86	TX14M7344			92	93	20	2.3	14	3	3.40	1.05	70	2	5	70
SOBS	87	TX14M7374			96	97	20	2.3	13	2	2.27	0.81	63	2	5	83
SOBS	88	TX14M7393			95	95	5	2.5	14	3	3.40	0.89	50	2	5	74
SOBS	89	TX14M7408			98	97	5	2.9	14	3	2.42	1.00	30	2	5	74
SOBS	90	TX14M7442			89	90	5	2.3	13	3	3.21	0.78	63	2	4	67
SOBS	91	TX14M7523	X		87	88	20	3.2	16	4	3.35	1.13	75	2	5	76
SOBS	92	TX14M7538			107	104	25	2.1	11	3	3.38	0.86	30	1	4	71
SOBS	93	TX14M7545	X		89	90	15	2.7	15	3	3.12	0.98	95	2	4	70
SOBS	94	TX14M7566			90	91	5	2.6	14	2	2.95	0.77	75	2	5	77
SOBS	95	TX14M7570	X		94	94	30	2.8	13	4	3.79	1.11	88	3	5	77
SOBS	96	TX14M7603			95	96	10	2.1	13	2	2.93	0.90	63	3	5	67
SOBS	97	TX14M7631	X		93	94	10	3.0	14	3	3.42	0.98	30	2	1	72
		Means			96	96	8.5	2.62	13	3	3.16	0.92	49	2	4	77
		Range			87-107	88-104	3-30	1.4-4	8-16	2-5	1.67-5.09	0.7-1.1	0-95	1-3	1-5	62-93
		CV			2.24	2.33	77.45	18.86	8.5	31.72	17.58	14.85	37.52	23.82	15.66	8.68
		LSD (0.05)			4.27	4.25	12.84	0.98	2.14	1.73	1.98	0.27	36.15	0.9	1.35	12.81

Table 2.5 Continued

Nursery	Entry	ID	F	M	HD	A [#]	GA	SZ [§]	SFD [§]	SE [§]	ANL ^{&}	AW ^{&}	AE	ST	AWL	HT [#]
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The selected male or female lines are indicated by 'X'; Based on averages of traits showing good CV levels, gender-specific traits ([#]Male and female; [§]Female; [&]Male) were observed for choosing lines that showed performance superior to the averages of the population as a whole: HD = heading date; A = Anthesis date; GA = glume angle; SZ = Stigma size; SFD = stigma featheriness duration; SE = Stigma exertion; ANL = Anther length; AW = Anther width; AE = Anther extrusion; ST = Spikelet tightness; AWL = Awn length; HT = Plant height; Blank space indicate missing data: CV: Coefficient of Variance; LSD: Least Significant Difference. Units for the measured floral traits were as shown in Table 2.2.

(Table 2.5). The non-gender specific categories were all at excellent CV levels, though only those that were determined to be directly tied to the selection process were anthesis, heading date, and height. The CVs for these were 2.33%, 2.24%, and 8.68%, respectively. Anthesis was the most important factor as far as viability times for males and females, so heading date was not used during the selection process (Table 2.3). Variation among the lines for anther width was very small, so anther length was focused on instead while selecting male traits.

After the traits with reliable CVs were discovered, the averages of these traits were then used to separate proficient and poor performers. In order to be chosen as a parental candidate, ideally the floral traits must be in combination above the average. In 2015, a female candidate must be equal to or before the anthesis date average of 96, and at or below the height average of 77cm. For floral characteristics, the female was required to be at or above 2.62mm in stigma size, 13 days of stigma featheriness duration, and at or above a scale of three in stigma exertion. For a male to be chosen, anthesis must be at 96 days or later, and at 77cm in height or taller. For floral traits, the male must have an anther extrusion rate of 49% or higher, and an anther length of 3.16mm or longer. A candidate could theoretically be chosen as a dual-purpose line if it was superior in both genders, and met at the separation threshold of height and anthesis dates for males and females.

Because the 2014 screenings had missing data and un-replicated plots, no CV values were captured in 2014. The selection process in 2014 was based only on choosing the best candidates in combination of traits. After gathering results from the 2015 data,

the same process was then used on the 97 selections and their performances in the 2014 year, for comparison purposes. The female candidates must have an anthesis date of 89 or earlier, and be 84 cm or shorter. Female candidates would perform at or higher than 2.63mm in stigma size, seven days of stigma featheriness duration, and a scale of three or higher in stigma exertion. For males, anther length would be 3.16mm or higher, and have an extrusion rate of 73% or higher.

Comparing these selections from 2014 and 2015, it's clear to see that performance in male candidates was more prominent in 2014. There were 20 males in 2014, and six males in the 2015 data that were chosen using the same exact criteria. Nine females were chosen in the 2014 data, and 11 in the 2015 data. Of these selections from 2014 and 2015, only four candidates (HT209-01, TX14A001271, TX14A001412, and TX14A001413) were selected in both generations, in the same gender. These low amount of repeatability is possible evidence of different environmental influences on gender specific traits.

The 97 lines that were advanced to 2015 compared their performance in 2014 for floral data. Although the lines seemed to have similar scores as that of 2014 scores, the repeatability was not high, quite possibly due to vast weather differences. Compared to the 2014 data, the heading dates and anthesis in 2015 were later by 10 and seven days, respectively. Furthermore, reductions in anther extrusion (24.45%) and plant height (6.6cm) were observed in 2015 data. This difference could be due to different environmental conditions and better observation techniques in 2015.

In March 2014, Castroville, TX experienced 10 sunny days, seven partly cloudy days, seven overcast days, and six days with precipitation. In College Station in March of 2015, there were four sunny days, 11 partly cloudy, seven overcast days, and eight days that experienced precipitation. April 2014 in Castroville saw nine sunny days, 13 partly cloudy, four overcast, and four days with rain. For 2015 in College Station, there were two sunny days, nine partly cloudy, six overcast days, and 13 days that experienced precipitation. Temperatures for Castroville, TX in 2014 ranged from 8 to 34 Celsius and 17 to 37 Celsius for March and April, respectively. 2015 in College Station, TX ranged from 7 to 28 Celsius, and 18 to 32 Celsius for March and April, respectively. These months were during peak observation periods, when flowering was at its most active. Weather data was taken from Weather Underground weather history section, for both locations to compare environmental conditions. In observing the ranges, College Station, TX in 2015 experienced lower day temperatures, as well as fewer sunny days and a larger portion of rainy days.

Lower temperatures favor the longevity of wheat flower, late heading and anthesis dates, and lower anther extrusion rates (Saini et al., 1983; Bagga et al., 1979). This reinforces that flowering characteristics of wheat are influenced by environmental conditions, which can be seen by the contrasting differences in the floral results for each year. Furthermore, the difference could be due to the better observation techniques used during 2015 such as leaving the lemma and palea intact, as well as using protective coverings for emasculated heads and working with a smaller set of lines. This indicates that uniform, superior techniques are needed when planning and executing experiments

on floral traits. It must also be inferred that optimal conditions are desired when taking observations on floral characteristics. The sensitivity of the traits to environmental conditions and the unpredictability of weather conditions could lead to lower repeatability.

Previous research on floral characteristics studied and analyzed certain traits and their possible ties to each other. In Singh et al.'s study (2003), it was determined by a correlation coefficient analysis that some traits were correlated. Anther length (size in mm) appeared to be significantly and positively related to stigma length (size in mm), anther extrusion, and openness of floret (glume angle in degrees). Anther extrusion was positively and significantly correlated with openness of floret. There has also been research that states differing spikelet tightness levels could affect glume separation angle (De Vries, 1971), and thus looser heads are theoretically desired for a better flower opening. This would then ideally show an increase in gape of the glumes as looser spikelet tightness characteristics were observed. Correlation of the stigma size could theoretically be tied to stigma exertion, though after meticulous observations, it appears that even large stigmas occasionally will curl or grow upwards rather than to the side, where they become trapped inside the floret (De Vries, 1971). In some cases, very small stigma sizes still extruded outside the floret, possibly because of the stigma growth habit. Table 2.6 is a Pearson's correlation tested across the 2015 data, in order to test for these associations mentioned in earlier text, and to discover any new correlations not mentioned before. In 2015, anther length was positively correlated at 0.23 with weak significance (<0.05) with stigma size. Anther length had a weak positive correlation at

$r=0.005$ with anther extrusion, though there was no significance. Anther length was also positively correlated with glume angle at 0.18, though there was no significance in that relationship either, which disagrees with Singh et al. (2003). Anther extrusion in the Pearson's correlation was positively correlated with glume angle at $r=0.47$, with a high degree of significance (<0001). This trend was also seen in previous tests (Singh and Joshi, 2003). The relationship between these two is most likely explained by the opening of the flower and its size allowing the anthers more space to push free of the floret and extrude. In contrast to previous research, trends were only slightly similar. This could be because of many different factors including a more stable environment, a larger workforce with better access to specialized equipment, and differences in genetic material in contrast to this study.

De Vries (1971) mentioned that there was a possibility of spikelet tightness being positively correlated to the angle of separation for the glumes (glume angle), and though there was a positive correlation of 0.11 in the 2015 data, there was no significance of this relationship. Another correlation focused on that was mentioned earlier was the possibility of stigma sizes contributing to exertion out of the glumes. These could also be dependent on growth habits, but the correlation was still very important to this research. There was a high and positive correlation between these two traits ($r=0.66$; $P < 0.001$).

Heading date and anthesis were strongly and positively correlated ($r=0.96$; $P < 0.001$). Heading date and anthesis are often very closely related phenological traits. Anthesis date was negatively associated with stigma featheriness duration ($r=-0.40$; $P <$

Table 2.6 Pearson's correlation for 2015 floral characteristics.

	A	GA	SZ	SFD	SE	ANL	AW	AE	ST	AWL	HT
HD	0.96***	-0.037 ^{NS}	-0.096 ^{NS}	-0.42 ^{NS}	-0.096 ^{NS}	0.036 ^{NS}	-0.13 ^{NS}	-0.34***	-0.073 ^{NS}	-0.17	-0.007 ^{NS}
A		-0.025 ^{NS}	-0.089 ^{NS}	-0.40***	-0.080 ^{NS}	0.028 ^{NS}	-0.18 ^{NS}	-0.35***	-0.035 ^{NS}	-0.18 ^{NS}	-0.020 ^{NS}
GA			-0.076 ^{NS}	-0.009 ^{NS}	0.086 ^{NS}	0.18 ^{NS}	0.16 ^{NS}	0.47***	0.11 ^{NS}	-0.003 ^{NS}	0.065 ^{NS}
SZ				0.094 ^{NS}	0.66***	0.23*	0.043 ^{NS}	0.12 ^{NS}	0.034 ^{NS}	-0.14 ^{NS}	0.090 ^{NS}
SFD					0.021 ^{NS}	-0.003 ^{NS}	0.22 ^{NS}	0.13 ^{NS}	-0.027 ^{NS}	0.18 ^{NS}	0.11 ^{NS}
SE						0.13 ^{NS}	0.076 ^{NS}	0.14 ^{NS}	0.098 ^{NS}	-0.077 ^{NS}	-0.009 ^{NS}
ANL							0.21*	0.005 ^{NS}	0.083 ^{NS}	-0.07 ^{NS}	-0.079 ^{NS}
AW								0.094 ^{NS}	0.10 ^{NS}	0.091 ^{NS}	-0.005 ^{NS}
AE									-0.008 ^{NS}	0.090 ^{NS}	-0.012 ^{NS}
ST										-0.009 ^{NS}	0.042 ^{NS}
AWL											-0.16 ^{NS}

HD = heading date; A = Anthesis date; GA = glume angle; SZ = Stigma size; SFD = stigma featheriness duration; SE = Stigma exertion; ANL = Anther length; AW = Anther width; AE = Anther extrusion; ST = Spikelet tightness; AWL = Awn length; HT = Plant height in cm; NS- non-significant; *P<0.05; **P<0.01; ***P<0.001; Bold font are those with some degree of significance.

0.001). This can possibly be explained by the timing of planting and the resulting weather patterns. Wheat generally begins flowering during March-April from a November planting in South Texas, thus temperatures are rising higher. The later a wheat heads, the higher the temperature would be, thus resulting in a shorter flowering duration. The wheat flower favors lower temperatures (Saini et al., 1983). This same principle can be applied to the negative and strongly significant correlations between heading date and anther extrusion ($r=-0.34$; $P < 0.001$) and between anthesis and anther extrusion ($r=-0.35$; $P < 0.001$). Though the wheat plant favors warmer temperatures for heavier anther extrusion, temperatures that become too hot can actually lower extrusion rates in some lines (Dawson and Wardlaw, 1989). The final barely significant correlation was between anther length and anther width ($r=0.21$; $P < 0.05$). This could theoretically be caused by relationships in growth habits of the anther. Some longer anthers would often have a wider size correlated with it, as observed during the study. All other correlations in this Pearson's analysis were not significant.

Factors Affecting Floral Measurements

Emasculation and usage of protective cover: female characteristics tend to be more laborious and time-sensitive than male observations, and methods in order to obtain this data must be continuously refined via improved methods or possibly implementing CHAs. Careful removal of anthers and covering the emasculated spike with a protective cover is the key to undamaged, fully functional stigmas for observations. Stigmas that were protected from sunlight by a protective cover on the emasculated spike in 2015 had a more natural and profound exertion than uncovered

spikes in 2014. The unprotected flowers would prematurely shrivel and skew the observations. Moisture became a concern with the covered heads during the unusually rainy year 2015, though intermittent sunny days were enough to dry the paper covers and prevent them from mildewing. Because flowering lasts approximately two weeks, it was not necessary to change the covers during the observation period.

Labor intensity: Because of the time constraints on measuring floral characteristics, these screenings are very labor intensive and often requires several workers in order to emasculate all flowering female heads and obtain observations in a timely manner. Observations upon all actively flowering lines are necessary on a daily basis, sometimes twice daily during peak flowering times.

Repeatability: The chances for repeatability in floral observations are possible, if done under controlled growth chamber conditions or in locations with more predictable climates. Future efforts to capture floral characteristics while screening for parents should focus on finding lines that show a good level of stability, to ensure those parents will be truly compatible when crossing occurs (Lucken, 1986; Yan and Hunt, 2002). Timing is key when crossing of two different lines is attempted, and it's necessary to have accurate data for these expectations for hybrid seed production.

Conclusions

The self-pollinating nature of wheat is one of the most important hindrances for hybrid wheat development. Synchronous flowering and outcrossing improvement in wheat are the important aspects for hybrid wheat that must be researched and improved

(Giles et al., 2014; Wilson and Driscoll, 1983). Without compatible parents, there is little chance of cross pollination occurring. Therefore, selections in this study consisted of balanced characteristics, often encompassing only one gender because of height and anthesis restrictions. Both optimum and poor floral characteristics were seen, varying between superior male or female characteristics.

The diversity within the screened TAM germplasm is adequate, and allowed for selection of compatible lines to be moved into a crossing block. Methods for accurate selection have been tested and refined in this study for use in future screenings if needed. Criteria for selection, specifically based on averages and CV levels appear to be the most efficient in this task. Though collection of data is intensive and tedious, this is only the preliminary step toward the development of a hybrid wheat program.

CHAPTER IV

ESTIMATING HETEROSIS IN TAM F₂ HYBRIDS

Introduction

Hybrids crops including wheat (*Triticum aestivum* L.) have a tendency to show a desirable amount of heterosis in progeny that scientists are continuously attempting to capture (Longin et al., 2012). Finding the appropriate parents and combination of traits is the key to obtaining progeny that exhibits high-parent heterosis (Ebmeyer et al., 2013).

F₁ hybrids following a cross between two genetically diverse parents will be 100% heterozygous and uniform, displaying the highest degree of hybrid vigor. However, heterosis will be reduced in the F₂ and subsequent generations, due to segregation and reduction in heterozygosity caused by inbreeding. Although the F₁ hybrids display high heterosis, it is sometimes not used because of the lack of sufficient seed and fear of a large error due to the small amount of plots utilized (Bailey et al., 1980). In some cases, the F₁ has been used to show an excellent amount of hybrid vigor (Wilson and Driscoll, 1983). Studies that have used F₂ instead, predict that if there is sufficient heterosis in that generation, it can be estimated that the F₁ parents can be chosen for superior hybrid performance with confidence (Bailey et al., 1980).

In this study, heterosis was estimated in the F₂ generations as a proxy to the F₁. This test would also determine if TAM wheat germplasm have superior progeny derived from high performing parents. This would reinforce the confidence in producing a hybrid program from the current TAM germplasm.

Methods and Materials

In 2013, 146 F₂ from Amarillo (AF₂) (Table 3.1) and 304 from College Station (CF₂) (Table 3.2), with five checks (cultivars- TAM 113, 'TAM W-101', TAM 111, TAM 112 and TAM 305) were grown in Castroville, TX field plots at 25 foot lengths, and five feet wide. Each consisted of seven rows, spaced seven inches apart. Planting was done in November 2013, and the fields were artificially watered from a linear irrigation system throughout the season to ensure maximum potential. Fertilizer was applied at a rate of 108lbs nitrogen per acre (N/A).

At the end of the growing season, a representative sample of 20 heads from each plot were randomly picked from Castroville, and transported back to College Station for processing. The heads were re-counted and bulk threshed using a Precision, Co. wheat head thresher, and weighed. Seed from these sample heads were counted using an International Marketing & Design, Co. Model U seed counter, and weighed using a scientific scale. Single seed weight was calculated by dividing sample seed weight by seed count.

Whole plot was bulk harvested using a Wintersteiger combine harvester. Total harvested grain weight was determined by adding the 20 head sample weight and yield plot weight. Grain yield in bushels per acre (GY (bu/ac)) was calculated using the formula given below, where dimensions for square feet of an acre (43,560 feet) and the row dimensions (125 square feet) were used:

$$GY (bu/ac) = \frac{\text{Total plot weight} * 43560}{454\left(\frac{g}{lb}\right) * 125 * 60\left(\frac{lb}{bu}\right)}$$

Table 3.1 Pedigree of 2014 Amarillo F₂ (AF₂) populations.

Population Name	Population No.	Pedigree
X12A307 T	1	X11A524S [=AK11WWCB-2237 (=ID800994.W/KAUZ// GEREK 79 (OCW00S366S-1B-6,8,9,10))/Greer (=AP06T3832=HBK0935-29-15/KS90W077-2-2/VBF0589-1)]/TX06V7266 (=TX99U8617/TX97U2001)
X12A168 S	2	Hatcher (=CO980607=Yuma/PI 372129//TAM 200/3/4*Yuma/4/KS91H184/Vista)/TAM 305 (=TX06A001263=TX97V3006/TX98V6239)
X12A013 S	3	TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A041 S	4	TX08A001249 (=TAM 112/TX98D1158)/TX07A001418-YRR Resel#2 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)
X12A073 S	5	TX10A001018 (=Doans (=AP02T4342=Coronado//1174-27-46/X960210.)/TX01M5009-28 (=MASON/JAGGER//PECOS))/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A376 T	6	X11A596S [=AK11SPWCB-3021 (=URES/BOW//OPATA/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/TILHI)/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)]/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A379 T	7	X11A599S [=AK11SPWCB-3024 (=WBLL1*2/KIRITATI)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)]/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A074 S	8	TX08V7675 (=KS940786-6-7/TX01M5009)/TAM 401 (=TX03M1096=MASON/JAGGER)
X12A340 T	9	X11A558S [=AK11WWCB-2367 (=U1254-1-5-1-1/TX89V4212//WEEBILL 1/3/OK91P609/CRR//2174 (OK99219)(OCW01M696T-9))/TX09A001186 (=TX99U8618/TX95V4339)]/TX07A001418-YRR Resel#2 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)
X12A378 T	1	X11A598S [=AK11SPWCB-3023 (=WBLL1*2/BRAMBLING)/Greer (=AP06T3832=HBK0935-29-15/KS90W077-2-2/VBF0589-1)]/TAM 401 (=TX03M1096=MASON/JAGGER)
X12A020 S	1	TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)/TX08V7675 (=KS940786-6-7/TX01M5009)
X12A237 T	1	X11A452S [=TX08A001342-HFR2 (=SHAAN 213/ TAM 400/3/2180/OK88803//ABI (OK96705-6745))/TX06V7266 (=TX99U8617/TX97U2001)]/TX08A001128 (=TAM 112/TX01U2685)
X12A362 T	1	X11A582S [=X05VSBC23-0CH (=TAM 111*2/CIMMYT E95Syn4152-49)/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)]/TX07V7327 (=TAM 111/Yumar)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A243 T	14	X11A458S [=TX08V7133-HFR1 (=CUTTER/TAM 400Resel)/TAM 111 (=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233)]/TAM 305 (=TX06A001263=TX97V3006/TX98V6239)
X12A164 S	15	CJ (=W99-188\$-1/BC950814-1-1)/TAM 401 (=TX03M1096=MASON/JAGGER)
X12A254 T	16	X11A469S [=OK07214 (=OK93P656-(RMH 3299)/OK99711 F4:10)/TX10A001016 (=Doans (=AP02T4342=Coronado//1174-27-46/X960210.)/TX01M5009-28 (=MASON/JAGGER//PECOS))]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A372 T	17	X11A592S [=AK11SPWCB-3012 (=TAM200/TUI/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1)/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)]/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A004 S	18	TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)/OK07214 (=OK93P656-RMH3299/OK99711 F4:11)
X12A021 S	19	TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A142 S	20	TX08V7753 (=TAM 303/TAM 112//Cutter)/TX07A001418-YRR Resel#2 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)
X12A265 T	21	X11A480S [=09AYT SIR-5080 (=NESSER/OK81306//55.1744/MEX67.1/3/NO57/NAC)/CO050337-2 (=OK93P656-(RMH 3299)/OK99621 F4:10)]/TX06V7266 (=TX99U8617/TX97U2001)
X12A224 T	22	X11A439S [=TX07A001422-YRR Resel#1 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)/TX08V7313 (=TX97V5300/TAM 111)]/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A297 T	23	X11A512S [=AK11WWCB-2210 (=SKAUZ/PARUS//PARUS/3/2180/OK88803//ABI (OK96705-6745)/4/TX89D9537/KARL (OCW02S089T-4))/TX05V7269 (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)]/TX08A001249 (=TAM 112/TX98D1158)
X12A050 S	24	TX08V7313 (=TX97V5300/TAM 111)/TAM 305 (=TX06A001263=TX97V3006/TX98V6239)
X12A392 T	25	X11A613S [=AK11SPWCB-3050 (=CMH82A.1294/CMH84.3621//CMH81.749/3/ELVIRA)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)]/TX06V7266 (=TX99U8617/TX97U2001)
X12A030 S	26	TX06V7266 (=TX99U8617/TX97U2001)/TX08A001249 (=TAM 112/TX98D1158)
X12A009 S	27	TAM 401 (=TX03M1096=MASON/JAGGER)/OK07214 (=OK93P656-RMH3299/OK99711 F4:11)
X12A001 S	28	TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A228 T	29	X11A443S [=TX07A001534-YRR Resel#1 (=L92283C64-1/JAGGER//OGALLALA)/TX08V7647 (=TX99A0155/2145)]/TX08A001249 (=TAM 112/TX98D1158)
X12A369 T	30	X11A589S [=AK11SPWCB-3007 (=WBLL1*2/BRAMBLING)/TX05A001188 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)]/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)
X12A394 T	31	X11A615S [=AK11SPWCB-3052 (=BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47)/TX05A001822 (=2145/X940786-6-7)]/TX09A001251 (=Tam 111/Yumar)
X12A062 S	32	TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A368 T	33	X11A588S [=AK11SPWCB-3006 (=WBLL1*2/TUKURU)/TX06A001281 (=TX98VR8422/U3704A-7-7)]/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A312 T	34	X11A530S [=AK11WWCB-2254 (=WEEBILL 1(B)/2*2174 (OCW03S667T-1))/CJ (=CJ)]/TAM 305 (=TX06A001263=TX97V3006/TX98V6239)
X12A231 T	35	X11A446S [=TX07V7458-YRR Resel#2 (=RWA177-B2-4/TX95A3091//Dumas)/TX07V7327 (=TAM 111/Yumar)]/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A126 S	36	TX09A001205 (=TAM 303/TX99U8618)/TX08V7313 (=TX97V5300/TAM 111)
X12A399 T	37	X11A620S [=AK11SPWCB-3060 (=PBW343*2/KUKUNA)/TX08A001111 (=TX99U8618/TX01U2699)]/TX08A001249 (=TAM 112/TX98D1158)
X12A178 S	38	Hitch (=HV9W02-942R=53/3/ABL/1113//K92/4/JAG/5/KS89180B)/TX08V7313 (=TX97V5300/TAM 111)
X12A032 S	39	TX06V7266 (=TX99U8617/TX97U2001)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A008 S	40	TAM 401 (=TX03M1096=MASON/JAGGER)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
TAM 113	41	TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A138 S	42	TX08V7579 (=TAM 303/TX95V4339)/TX08V7313 (=TX97V5300/TAM 111)
X12A344 T	43	X11A562S [=AK11WWCB-2375 (=DELIVER/FRET 2//LUT12688/KARL92 (OK99602)(OCW01M742T-5))/TX05V7259 (=T107//TX78V3620/Ctk78/3/TX87V1233/4/Arap//TX86V1540/T200)]/TX08V7313 (=TX97V5300/TAM 111)
X12A034 S	44	TX08A001128 (=TAM 112/TX01U2685)/TX06V7266 (=TX99U8617/TX97U2001)
X12A343 T	45	X11A561S [=AK11WWCB-2370 (=FRET 2//KARL/2*OK91724 (OK99221)/3/DUSTER (OCW01M760T-2))/CO08RWA028 (=94M370/6*Yuma)]/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A384 T	46	X11A604S [=AK11SPWCB-3032 (=PASTOR//HXL7573/2*BAU)/Deliver (=OK98690=OK91724/Karl)]/TX08V7313 (=TX97V5300/TAM 111)
X12A151 S	47	TX10VS7876 (=TAM 111*2/CIMMYT E95Syn4152-46)/Hatcher (=CO980607=Yuma/PI 372129//TAM 200/3/4*Yuma/4/KS91H184/Vista)
X12A259 T	48	X11A474S [=TX09D1028 (=TX98V9628/TX01M5008)/TX09A001286 (=Unknown)]/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A006 S	49	TAM 401 (=TX03M1096=MASON/JAGGER)/TX08V7313 (=TX97V5300/TAM 111)
X12A014 S	50	TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)/OK07214 (=OK93P656-RMH3299/OK99711 F4:11)
X12A213 T	51	X11A428S [=TX06V7324-YRR Resel#3 (=Hickok//TX84V1317/TX85V1326)/TX06V7266 (=TX99U8617/TX97U2001)]/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)
X12A083 S	52	TX07A001418-YRR Resel#2 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)/TX08V7706 (=TX99A0383-2/TX97V5300)
X12A141 S	53	TX08V7753 (=TAM 303/TAM 112//Cutter)/TX08A001249 (=TAM 112/TX98D1158)
X12A127 S	54	TX09A001205 (=TAM 303/TX99U8618)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A407 T	55	X11A628S [=AK11SPWCB-3080 (=OASIS/SKAUZ//4*BCN/3/2*PASTOR)/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)]/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A355 T	56	X11A574S [=KS99WGRC42 (= Karl 92/PI 94641//Jagger *2/Karl 92)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A070 S	57	TX09A001251 (=Tam 111/Yumar)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A260 T	58	X11A475S [=TX09D1028 (=TX98V9628/TX01M5008)/TX09A001307 (=Thunderbolt/TX97V5300//TX01M5008)]/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A087 S	59	TX09D1037 (=TX00A0580/TX99D4151)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A387 T	60	X11A607S [=AK11SPWCB-3036 (=ALTAR 84/AE.SQ.(TAUS)//OCI/3/VEE/MJI//2*TUI)/Art (=98x0338-13=Jagger/W94-244-132)]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A350 T	61	X11A568S [=AK11WWCB-2404 (=78014.40/ATTLA/3/SWM17702-5YC- 3YC/HKK//OK97G611 (99x175)/4/G223W/ABI (OCW01M856T-2))/TX07V7571 (=Unknown)]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A061 S	62	TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)/TX09D1037 (=TX00A0580/TX99D4151)
X12A390 T	63	X11A610S [=AK11SPWCB-3045 (=CROC_1/AE.SQ.(205)//KAUZ)/Everest (=KS970093-8-9- #1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)]/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A238 T	64	X11A453S [=TX08A001342-HFR2 (=SHAAN 213/ TAM 400/3/2180/OK88803//ABI (OK96705-6745))/TAM 111 (=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233)]/Duster (=OK93P656H3299- 2C04=WO405D/HGF112//W7469C/HCF012)
X12A189 S	65	CO05W111 (=CO980829/TAM 111)/TAM 305 (=TX06A001263=TX97V3006/TX98V6239)
X12A080 S	66	TX08V7706 (=TX99A0383-2/TX97V5300)/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A304 T	67	X11A521S [=AK11WWCB-2231 (=KS93U69/KS92WGRC16/6/CNDO/R143//ENTE/MEXI_2/3/AE.SQ.(TAUS)/4/WEAVER/5/2 *KAUZ/7/Ok 102 (OCW02S160T-3))/TAM 112 (=TX98V9628=U1254-7-9-2- 1/TXGH10440)]/TX06V7266 (=TX99U8617/TX97U2001)
X12A097 S	68	Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)/TX09A001235 (=TTAM 112//Trego/TX99A0155)
X12A251 T	69	X11A466S [=KS09HW120 (=KS02HW35-5TR)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1- 1/TX86V1405)]/TX08V7675 (=KS940786-6-7/TX01M5009)
X12A248 T	70	X11A463S [=TX08A001133 (=TAM 303/TX99U8618)/TX08V7173 (=Abilene/TX99U8611)]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A363 T	71	X11A583S [=AK11SPWCB-3001 (=SERI.1B//KAUZ/HEVO/3/AMAD)/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)]/Duster (=OK93P656H3299- 2C04=WO405D/HGF112//W7469C/HCF012)
X12A222 T	72	X11A437S [=TX07A001422-YRR Resel#1 (=U1254-1-5-2- 1/TX81V6582//DESCONOCIDO)/TAM 112 (=TX98V9628=U1254-7-9-2- 1/TXGH10440)]/TX09A001235 (=TTAM 112//Trego/TX99A0155)
X12A095 S	73	Garrison (=OK05212=OK95616-1/Hickok//Betty F4:12)/TAM 401 (=TX03M1096=MASON/JAGGER)
X12A022 S	74	TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)
X12A113 S	75	TAM 111 (=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233)/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A042 S	76	TX08A001249 (=TAM 112/TX98D1158)/Billings (=OK03522=N566/OK94P597 F4:14)
X12A112 S	77	TAM 111 (=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233)/TX09D1037 (=TX00A0580/TX99D4151)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A341 T	78	X11A559S [=AK11WWCB-2367 (=U1254-1-5-1-1/TX89V4212//WEEBILL 1/3/OK91P609/CRR//2174 (OK99219)(OCW01M696T-9))/T167 (=T81/T137)]/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A374 T	79	X11A594S [=AK11SPWCB-3018 (=D67.2/P66.270//AE.SQUARROSA (320)/3/CUNNINGHAM)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405))/TX09A001235 (=TTAM 112//Trego/TX99A0155)
X12A373 T	80	X11A593S [=AK11SPWCB-3017 (=BRBT1*2/KIRITATI)/TAM 401 (=TX03M1096=MASON/JAGGER)]/TX09A001235 (=TTAM 112//Trego/TX99A0155)
X12A165 S	81	CJ (=W99-188\$-1/BC950814-1-1)/TX07A001418-YRR Resel#2 (=U1254-1-5-2- 1/TX81V6582//DESCONOCIDO)
X12A257 T	82	X11A472S [=KS020635-M-2 (=KS920709-B-5-2- 2/TX00C5008//OVERLEY)/TX08V7313 (=TX97V5300/TAM 111)]/OK07214 (=OK93P656-RMH3299/OK99711 F4:11)
X12A400 T	83	X11A621S [=AK11SPWCB-3061 (=ND643/2*WBLL1)/CJ (=CJ)]/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)
TAM W- 101	84	Norin 10/3/Nebraska 60//Mediterranean/Hope/4/Bison (=TX65A1682) (CI 15324)
TAM 111	85	TAM 111 (=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233)
X12A005 S	86	TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1- 1/TX86V1405)/KS08HW35-1 (=KS03HW154/KS03HW1)
X12A134 S	87	TX08V7140 (=TX00V1131/TX96D1073)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A405 T	88	X11A626S [=AK11SPWCB-3072 (=EMB16/CBRD//CBRD)/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)]/TX09A001172 (=TX98A5424/TX99A0136)
X12A402 T	89	X11A623S [=AK11SPWCB-3064 (=WHEAR/KUKUNA//WHEAR)/TX05A001822 (=2145/X940786-6-7)]/Duster (=OK93P656H3299- 2C04=WO405D/HGF112//W7469C/HCF012)
X12A398 T	90	X11A619S [=AK11SPWCB-3059 (=WBLL1*2/BRAMBLING)/TX05V7269 (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)]/Everest (=KS970093-8-9-#1- 1=HBK1064-3/KS84063-9-39-3-4W//X960103)
X12A261 T	91	X11A476S [=09AYT SIR-5031 (=GANSU-1//VORONA/HD2402)/TX08A001117 (=TX99U8618/TX01U2735)]/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A108 S	92	OK07214 (=OK93P656-RMH3299/OK99711 F4:11)/TX09A001172 (=TX98A5424/TX99A0136)
X12A298 T	93	X11A514S [=AK11WWCB-2217 (=BAU/MILAN//ENDURANCE 'S' (OK94P549- 6621)(OCW00S013S-2-3,4,8,9,12))/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)]/TX08A0012 49 (=TAM 112/TX98D1158)
X12A018	94	TAM 305 (=TX06A001263=TX97V3006/TX98V6239)/Garrison (=OK05212=OK95616- 1/Hickok//Betty F4:12)
X12A322 T	95	X11A540S [=AK11WWCB-2291 (=TX94V3718/TX92V4536/4/W8427/2157 'S'//W2440/3/HBK0075 (95x27a)(OCW03S572S-1))/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A031 S	96	TX06V7266 (=TX99U8617/TX97U2001)/TX09D1037 (=TX00A0580/TX99D4151)
X12A023 S	97	TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)/OK08328 (=GK Keve/Ok101//OK93P656-RMH3299 F4:10)
X12A181 S	98	OK07209 (=OK93P656-(RMH 3299)/OK99621 F4:10)/TX03A0563-07AZHR247 (=X96V107/OGALLALA)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A082 S	99	TX08V7706 (=TX99A0383-2/TX97V5300)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A314 T	100	X11A532S [=AK11WWCB-2266 (=WEEBILL1//2163/2174 (OK02321)(OCW03S426S-7))/TX09A001186 (=TX99U8618/TX95V4339)]/TX08V7313 (=TX97V5300/TAM 111)
X12A233 T	101	X11A448S [=TX04M410164-08AZHR207-HFR1 (=MIT/TX93V5722//W95-301)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)]/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A188 S	102	OK07231 (=OK92P577-(RMH 3099)/OK93P656-(RMH 3299) F4:10)/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A388 T	103	X11A608S [=AK11SPWCB-3040 (=ALTAR 84/AE.SQ.(J BANGOR)/ESDA)/Deliver (=OK98690=OK91724/Karl)]/TX03A0563-07AZHR247 (=X96V107/OGALLALA)
X12A167 S	104	Hatcher (=CO980607=Yuma/PI 372129//TAM 200/3/4*Yuma/4/KS91H184/Vista)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A029 S	105	TX06V7266 (=TX99U8617/TX97U2001)/TX03A0563-07AZHR247 (=X96V107/OGALLALA)
X12A386 T	106	X11A606S [=AK11SPWCB-3035 (=RL6043/4*NAC//PASTOR/3/BABAX)/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)]/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A364 T	107	X11A584S [=AK11SPWCB-3002 (=SERI.1B//KAUZ/GEN/3/AMAD)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)]/TX09A001172 (=TX98A5424/TX99A0136)
X12A028 S	108	TX03A0563-07AZHR247 (=X96V107/OGALLALA)/OK07231 (=OK92P577-(RMH 3099)/OK93P656-(RMH 3299) F4:10)
X12A336 T	109	X11A554S [=AK11WWCB-2304 (=KASORO 3/CSM//TXGH13622/2180 (OK95616-6756)(OCW03S112T-2))/TX03A0563-07AZHR247 (=X96V107/OGALLALA)]/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A051 S	110	TX08V7313 (=TX97V5300/TAM 111)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A278 T	111	X11A493S [=AK11WWCB-2185 (=ID800994.W//KAUZ// GEREK 79 (OCW00S366S))/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)]/TX03A0563-07AZHR247 (=X96V107/OGALLALA)
X12A283 T	112	X11A498S [=AK11WWCB-2193 (=KAUZ/STAR//U1254-1-5-1-1/TX89V4213 (OCW00S063S-1B-3,6,11))/TX05V7269 (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)]/TX08V7313 (=TX97V5300/TAM 111)
X12A037 S	113	TX08A001128 (=TAM 112/TX01U2685)/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)
X12A120 S	114	TAM 304 (=TX01D3232=TX92U3060/TX91D6564 (=X95U104-P66))/Ruby Lee (=OK05526=KS94U275/OK94P549 F4:12)
X12A102 S	115	Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A084 S	116	TX07A001418-YRR Resel#2 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)/Hatcher (=CO980607=Yuma/PI 372129//TAM 200/3/4*Yuma/4/KS91H184/Vista)
X12A121 S	117	TAM 304 (=TX01D3232=TX92U3060/TX91D6564 (=X95U104-P66))/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)
X12A019 S	118	TAM 305 (=TX06A001263=TX97V3006/TX98V6239)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)
X12A192 S	119	CO06052 (=Teal 11A/Above//CO99314)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A136 S	120	TX08V7579 (=TAM 303/TX95V4339)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A060 S	121	TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)/TAM 203 (=TX01V5314=TX89V4132/704 L I-2221)
X12A125 S	122	TX09A001205 (=TAM 303/TX99U8618)/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A199 T	123	X11A413S [=Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)]/TX08A001128 (=TAM 112/TX01U2685)
X12A027 S	124	TX03A0563-07AZHR247 (=X96V107/OGALLALA)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A033 S	125	TX06V7266 (=TX99U8617/TX97U2001)/OK07209 (=OK93P656-(RMH 3299)/OK99621 F4:10)
X12A190 S	126	CO05W111 (=CO980829/TAM 111)/TX08A001249 (=TAM 112/TX98D1158)
X12A153 S	127	TX10VS7976 (=TAM 111*2/CIMMYT E95Syn4152-83)/TX10A001016 (=Doans (=AP02T4342=Coronado//1174-27-46/X960210.)/TX01M5009-28 (=MASON/JAGGER//PECOS))
X12A117 S	128	TAM 112 (=TX98V9628=U1254-7-9-2-1/TXGH10440)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)
X12A115 S	129	TAM 112 (=TX98V9628=U1254-7-9-2-1/TXGH10440)/TX08V7313 (=TX97V5300/TAM 111)
X12A130 S	130	TX09A001343 (=TX97V2836/KS015538)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)
X12A123 S	131	TX09A001197 (=TAM 112/TX01U2527)/Everest (=KS970093-8-9-#1-1=HBK1064-3/KS84063-9-39-3-4W//X960103)
X12A360 T	132	X11A580S [=X05VSBC04 (=TAM 111*2/CIMMYT E95Syn4152-11)/TX08V7313 (=TX97V5300/TAM 111)]/OK07214 (=OK93P656-RMH3299/OK99711 F4:11)
TAM 112	133	TX98V9628=U1254-7-9-2-1/TXGH10440
X12A152 S	134	TX10VS7976 (=TAM 111*2/CIMMYT E95Syn4152-83)/TX08A001128 (=TAM 112/TX01U2685)
X12A239 T	135	X11A454S [=TX09A001239-HFR2 (=TX98V9628/TAM 400//TX01M5009)/Deliver (=OK98690=OK91724/Karl)]/TX09A001172 (=TX98A5424/TX99A0136)
X12A002 S	136	TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)/TX09D1193 (=TAM200/TAM 303)
X12A140 S	137	TX08V7753 (=TAM 303/TAM 112//Cutter)/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A067 S	138	TX09A001251 (=Tam 111/Yumar)/TAM 113 (=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)
X12A131 S	139	TX09A001343 (=TX97V2836/KS015538)/OK07214 (=OK93P656-RMH3299/OK99711 F4:11)
X12A218 T	140	X11A433S [=TX07A001418-YRR Resel#2 (=U1254-1-5-2-1/TX81V6582//DESCONOCIDO)/TX05A001822 (=2145/X940786-6-7)]/TX09A001235 (=TTAM 112//Trego/TX99A0155)
X12A313 T	141	X11A531S [=AK11WWCB-2254 (=WEEBILL 1(B)/2*2174 (OCW03S667T-1))/TAM 304 (=TX01D3232=TX92U3060/TX91D6564 (=X95U104-P66))]/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)
X12A114 S	142	TAM 111 (=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233)/Tiger (=KS05HW133=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)

Table 3.1 Continued

Population Name	Population No.	Pedigree
X12A171 S	143	Danby (=KS02HW34=TREGO/JGR 8W)/TX06A001132-Resel (=HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233)
X12A054 S	144	TX09A001172 (=TX98A5424/TX99A0136)/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)
X12A066 S	145	TX09A001235 (=TTAM 112//Trego/TX99A0155)/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)
TAM 305	146	TX97V3006/TX98V6239
X12A186 S	147	OK07231 (=OK92P577-(RMH 3099)/OK93P656-(RMH 3299) F4:10)/TX07A001505 (=T107//TX98V3620/Ctk78/3/TX87V1233/4/N87V106//TX86V1540/T200)
X12A143 S	148	TX08V7753 (=TAM 303/TAM 112//Cutter)/Tiger (=KS05HW136-3=KS98HW518(93HW91/93HW255)//KS98H245(IKE/TA2460//*3T200)/TREGO)
X12A124 S	149	TX09A001197 (=TAM 112/TX01U2527)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A055 S	150	TX09A001172 (=TX98A5424/TX99A0136)/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)
X12A291 T	151	X11A506S [=AK11WWCB-2200 (=2145/OK98G507W/3/ID#840335//PIN39/PEW (OCW00M749T-4-5,8))/Danby (=KS02HW34=TREGO/JGR 8W)]/TX08A001249 (=TAM 112/TX98D1158)

Table 3.2 Pedigree of 2014 Castroville F₂ (CF₂) populations.

Population Name	Population No.	Pedigree
12WXCS331	1	TX08A001128/TX09D1119
12WXCS372	2	TX09A001343/H101-4
12WXCS388	3	TX09D1172/TX09D1193
12WXCS383	4	TX09D1163/TX06V7266
12WXCS376	5	TX09D1127/TAM 401
12WXCS381	6	TX09D1163/TX06A001263
12WXCS313	7	TAM 401/TX06V7266
12WXCS117	8	TAM 304//TX99U8544/Ogallala/3/TAM 203/4/Seri82/Cutter//TX99U8544/Ogallala/3/Armour
12WXCS358	9	TX08V7313/TX09D1172
12WXCS337	10	TX08A001249/TX09A001197
12WXCS145	11	LA03217D-P2/3/TX06A001822//Seri82/5009/4/U5954-1-5/Billings
12WXCS339	12	TX08A001249/TX09D1193
12WXCS285	13	CJ/TX08V7173
12WXCS382	14	TX09D1163/TX06A001263
12WXCS314	15	TAM 401/TX08V7140
12WXCS342	16	TX08V7140/TX07V7327
12WXCS379	17	TX09D1127/TX04CS00230
12WXCS343	18	TX08V7140/TX08V7313
12WXCS235	19	U5954-1-5/LA03217D-P2//U5942-10-1/TAM 203
12WXCS439	20	U5954-1-5/U5928-1-5
12WXCS284	21	Billings/T78-34
12WXCS378	22	TX09D1127/TX09D1193
12WXCS320	23	TX06A001263/TX08V7579
12WXCS116	24	TAM 112/Fuller//TAM 203/4/RonL//Seri82/5009/3/TAM 203
12WXCS364	25	TX09A001197/H124-2
12WXCS157	26	U5930-11-3/U5928-1-5//U5954-1-5
12WXCS159	27	U5930-11-3/U5938-10-5//U5941-1-6
12WXCS387	28	TX09D1172/TX08V7140
12WXCS344	29	TX08V7140/TX09A001205
12WXCS391	30	TX09D1193/H124-2
12WXCS361	31	TX09A001197/TX06A001263
12WXCS340	32	TX08A001249/WB-Cedar
12WXCS312	33	TAM 304/H124-2
12WXCS281	34	LA03217D-P2/TX06A001281/4/TAM 203//FM6/OGALLALA/3/TX06A001822
12WXCS349	35	TX08V7140/T68-21
12WXCS233	36	U5954-1-5/TX05A001188//TAM 111/TX06A001822

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS375	37	TX09D1036/TX09D1163
12WXCS413	38	U5931-3-1/U5928-1-5
12WXCS253	39	U5942-10-1/TX06A001263//TAM 304/U5930-13-5
12WXCS447	40	T74-13X/TX10A001006
12WXCS288	41	Everest/TAM 113
12WXCS221	42	U5924-10-1/TAM 401//TAM 401/U5926-3-4
12WXCS275	43	TAM 401/U5926-3-4//TAM 203/U5924-10-1
12WXCS356	44	TX08V7313/TX08V7579
12WXCS335	45	TX08A001249/TX08V7173
12WXCS188	46	U5937-4-2/TAM 401//TAM 203/CJ
12WXCS135	47	8618/FANG//unknown/3/H117-1/4/TAM 203/TX01V5134RC-3//U5926-2-8
12WXCS324	48	TX06V7266/TX07V7327
12WXCS430	49	U5941-1-6/U5930-11-3
12WXCS319	50	TX06A001263/TX07A001505
12WXCS118	51	RonL//Seri82/5009/3/TAM 203/4/TAM 111//FM3/OGALLALA/3/U5930-13-5
12WXCS350	52	TX08V7140/TX04CS00232
12WXCS438	53	U5954-1-5/U5926-2-8
12WXCS279	54	TX09D1007/TX09D1127//TAM 203/CJ
12WXCS282	55	Armour/CJ
12WXCS440	56	U5954-1-5/U5931-3-1
12WXCS143	57	TAM 111/3/TX99U8544/Ogallala//TX02A0252/4/TAM 203/TX01V5134RC-3//U5926-2-8
12WXCS396	58	U5924-10-1//U5947-1-3/U5938-10-5
12WXCS389	59	TX09D1172/TX04CS00237
12WXCS196	60	U5947-1-3/U5938-10-5//U5928-1-5
12WXCS280	61	TX04CS00244/LA01110D-150/3/TAM 112/TX03A0148 //Fuller
12WXCS386	62	TX09D1172/Hitch
12WXCS374	63	TX09D1036/TX09D1119
12WXCS345	64	TX08V7140/TX09D1127
12WXCS317	65	TAMsoft 700/TX08V7579
12WXCS274	66	TAM 401/U5926-3-4//U5935-2-3/TAM 401
12WXCS405	67	U5928-1-5//U5947-1-3/U5938-10-5
12WXCS384	68	TX09D1163/T68-21
12WXCS307	69	TAM 304/OK07231
12WXCS467	70	XT04CS00231/H124-2
12WXCS355	71	TX08V7173/H117-3
12WXCS278	72	TX06A001281/TAM 401/4/TX03A0148//Seri82/5009/3/TX04CS00244
TAM 113	73	(=TX02A0252=TX90V6313//TX94V3724(TAM-200 BC41254-1-8-1-1/TX86V1405)/

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS454	74	T82-1/TX09D1193
12WXCS351	75	TX08V7173/TX08V7313
12WXCS357	76	TX08V7313/TX09A001197
12WXCS423	77	U5938-10-5/TX08V7579
12WXCS160	78	U5930-11-3/U5924-10-1//U5947-1-3/U5926-2-8
12WXCS363	79	TX09A001197/T78-34
12WXCS232	80	U5954-1-5/TAM 203//TAM 203/U5924-10-1
12WXCS286	81	Deliver/TX08V7173
12WXCS380	82	TX09D1127/H124-2
12WXCS412	83	U5931-3-1/U5926-2-8
12WXCS390	84	TX09D1193/TX06A001263
12WXCS134	85	TX99U8544/Halberd//8618/FANG/3/TAM 112/4/TX06A001132/Fannin
12WXCS332	86	TX08A001128/TX09D1193
12WXCS193	87	U5947-1-3/U5938-10-5//U5930-11-3/U5924-10-1
12WXCS322	88	TX06A001263//U5954-1-5/TAM 203
12WXCS197	89	U5947-1-3/U5938-10-5//U5928-1-5/U5924-10-1
12WXCS424	90	U5938-10-5/U5926-2-8
12WXCS136	91	8618/FANG//unknown/3/H117-1/4/TX06A001263/Jackpot/3/TX06A001822
12WXCS441	92	U5954-1-5//U5930-11-3/U5924-10-1
12WXCS289	93	Everest/TX06A001263
12WXCS409	94	U5930-11-3/U5941-1-6
12WXCS227	95	U5924-10-6/U5928-1-5//U5947-1-3/U5938-10-5
12WXCS393	96	TX10A001006/T68-21
12WXCS187	97	U5937-4-2/TAM 401//TAM 203/U5924-10-1
12WXCS366	98	TX09A001205/TX09D1172
12WXCS299	99	OK07231/TX09D1172
12WXCS165	100	U5930-11-3/TX02CS001//U5930-11-3/U5938-10-5
12WXCS248	101	U5942-10-1/U5928-1-5//TAM 401
12WXCS369	102	TX09A001343/T68-21
12WXCS444	103	T68-21/TX10A001006
12WXCS295	104	Hitch/TX06A001263
12WXCS198	105	U5947-1-3/U5938-10-5//U5924-10-6
12WXCS170	106	U5930-11-3/TAM 203//TAM 203/CJ
12WXCS422	107	U5938-10-5/TAM 203
12WXCS113	108	TAM 111//FM3/OGALLALA/3/U5930-13-5/4/U5930-11-3/U5924-10-6
12WXCS108	109	Jackpot/TX03A0148 //VA08W-295/4/TX01M5009/Halberd//FM6/JAGGER/3/TX09D1181
12WXCS346	110	TX08V7140/TX09D1127

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS365	111	TX09A001205/TX08V7173
12WXCS352	112	TX08V7173/TX08V7313
12WXCS392	113	TX10A001006/TX06A001263
12WXCS359	114	TX08V7579/T82-1
12WXCS400	115	U5926-2-8/U5924-10-6
12WXCS121	116	TAMsoft 700/TAM 112//Armour/4/TX99U8544/Halberd//RonL/3/TAM 112
12WXCS304	117	TAM 113/TX07V7327
12WXCS112	118	TAM 111//FM3/OGALLALA/3/NC08-23323/4/TX06A001263*2/Jackpot
12WXCS437	119	U5954-1-5/U5924-10-6
12WXCS425	120	U5938-10-5//U5930-13-5/U5924-10-1
12WXCS321	121	TX06A001263/TX04CS00237
12WXCS443	122	T68-21/TX07V7327
12WXCS178	123	U5937-4-2/U5947-1-3//U5924-10-1/TAM 401
12WXCS246	124	U5942-10-1/U5928-1-5//U5930-11-3/U5937-4-2
12WXCS315	125	TAM 401/TX09D1193
12WXCS385	126	TX09D1172/Hitch
12WXCS398	127	U5924-10-6/U5947-1-3
12WXCS183	128	U5937-4-2/2*TAM 203
12WXCS459	129	TX04CS00230/TX06A001263
12WXCS464	130	TX04CS00232/TX09A001197
12WXCS309	131	TAM 304/TX09D1119
12WXCS267	132	TX06A001263/U5930-11-3//TX06A001263/U5926-2-8
12WXCS250	133	U5942-10-1/U5928-1-5//U5954-1-5
12WXCS182	134	U5937-4-2/TAM 203//TX05V7259/TX06A001263
12WXCS234	135	U5954-1-5/TX05A001188//TAM 304/H117-4
12WXCS428	136	U5941-1-6/U5924-10-1
12WXCS166	137	U5930-11-3/TX02CS001//U5928-1-5/TX06A001822
12WXCS436	138	U5947-1-3//U5924-10-6/U5928-1-5
12WXCS290	139	Everest/TX08A001128
12WXCS404	140	U5926-3-4//U5947-1-3/U5938-10-5
12WXCS155	141	U5930-11-3/U5947-1-3//U5924-10-6
12WXCS427	142	U5938-10-5//KS980512-2-2/TAM 401
12WXCS341	143	TX08A001249/TX04CS00230
12WXCS181	144	U5937-4-2/U5931-3-1//U5924-10-6/U5928-1-5
12WXCS151	145	U5930-11-3/U5937-4-2//U5941-1-6
12WXCS252	146	U5942-10-1/TX06A001263//U5935-2-3/U5926-2-8
12WXCS176	147	U5930-13-5/U5935-2-3//TAM 111/TAM 401

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS362	148	TX09A001197/TX09D1193
TAM W-101	149	Norin 10/3/Nebraska 60//Mediterranean/Hope/4/Bison (=TX65A1682) (CI 15324)
12WXCS348	150	TX08V7140/U5931-3-1
TAM 111	151	(=TX95A3091=TAM 107//TX78V3620/CTK78/3/TX87V1233
12WXCS153	152	U5930-11-3/U5947-1-3//U5938-10-5/U5924-10-6
12WXCS146	153	U5926-2-8/U5930-11-3//U5954-1-5/TAM 203
12WXCS394	154	TX10A001006/TX04CS00237
12WXCS139	155	TX01M5009/Halberd//FM6/JAGGER/3/TX04CS00239/4/Seri82/5009//Jackpot/3/TX06A001281
12WXCS426	156	U5938-10-5//U5924-10-6/U5928-1-5
12WXCS442	157	WB-Cedar/T68-21
12WXCS266	158	TAM 203/TAM 112/4/TAM 304//8618/FANG/3/Duster
12WXCS208	159	U5928-1-5/TX06A001822//U5935-2-3/TX06A001822
12WXCS415	160	U5931-3-1//U5942-10-1/U5928-1-5
12WXCS204	161	U5928-1-5/U5924-10-1/3/TAM 203/TX01V5134RC-3//U5926-2-8
12WXCS247	162	U5942-10-1/U5928-1-5//U5930-11-3/U5924-10-1
12WXCS462	163	TX04CS00232/TX07V7327
12WXCS158	164	U5930-11-3/U5938-10-5//U5926-2-8
12WXCS429	165	U5941-1-6/U5924-10-6
12WXCS180	166	U5937-4-2/U5931-3-1//U5924-10-6/U5926-2-8
12WXCS406	167	U5930-11-3/U5926-2-8
12WXCS271	168	TAM 304/U5926-2-8//U5930-11-3/TAM 401
12WXCS161	169	U5930-11-3/U5924-10-1//U5947-1-3/U5938-10-5
12WXCS408	170	U5930-11-3/U5937-4-2
12WXCS460	171	TX04CS00230/TX10A001006
12WXCS205	172	U5928-1-5/Fuller/3/Jackpot/TX06A001822//U5930-13-5
12WXCS210	173	U5928-1-5/TAMsoft 700//TX06A001263/U5930-11-3
12WXCS194	174	U5947-1-3/U5938-10-5//TAM 401/U5926-3-4
12WXCS416	175	U5931-3-1//TAM 203/U5924-10-1
12WXCS120	176	TAMsoft 700/TAM 112//Armour/4/Seri82/Cutter//TX06A001263/3/NC08-23323
12WXCS230	177	U5924-10-6/TAM 203//TAM 203/U5924-10-1
12WXCS305	178	TAM 113//U5930-13-5/U5935-2-3
12WXCS263	179	TAM 203/U5941-1-6//Armour/OK05526
12WXCS347	180	TX08V7140/TX10A001006
12WXCS127	181	Seri82/Cutter//TX06A001263/3/NC08-23323/4/Jackpot/TX03A0148 //VA08W-295
12WXCS167	182	U5930-11-3/TX02CS001//U5942-10-1/U5928-1-5
12WXCS471	183	H101-4/TX09D1163
12WXCS474	184	H100/TX08V7140

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS326	185	TX07A001505/T76-11
12WXCS207	186	U5928-1-5/TX02A0252/3/Jackpot/TX03A0148 //NC08-23323
12WXCS445	187	T74-13X/TAM 401
12WXCS448	188	T78-34/TX06A001263
12WXCS293	189	Hitch/OK07231
12WXCS162	190	U5930-11-3/U5924-10-1//U5926-2-8
12WXCS407	191	U5930-11-3/U5926-3-4
12WXCS330	192	TX07V7327/TX04CS00232
12WXCS222	193	U5924-10-1/2*TAM 401
12WXCS131	194	TX99U8544/Halberd//RonL/3/TAM 112/4/U5947-1-3/U5926-2-8
12WXCS129	195	Seri82/Cutter//FM6/OGALLALA/3/NC08-23323/4/Jackpot/TX03A0148 //VA08W-295
12WXCS226	196	U5924-10-6/U5928-1-5//U5937-4-2/TAM 401
12WXCS122	197	TAMsoft 700/TAM 112//Armour/4/TX99U8544/Halberd//8618/FANG/3/TAM 112
12WXCS173	198	U5930-11-3/TAM 401//U5926-3-4
12WXCS190	199	U5947-1-3/U5926-2-8//U5930-11-3
12WXCS219	200	U5924-10-1/TAM 401//U5930-11-3/TAM 401
12WXCS353	201	TX08V7173/TX09D1127
12WXCS149	202	U5930-11-3/U5937-4-2/4/TX03A0148//Seri82/5009/3/TX04CS00244
12WXCS283	203	Billings/U5931-3-1
12WXCS291	204	Everest/TX09A001205
12WXCS325	205	TX06V7266/TX09D1163
12WXCS249	206	U5942-10-1/U5928-1-5//U5924-10-6
12WXCS463	207	TX04CS00232/TX08V7579
12WXCS140	208	Seri82/5009//Jackpot/3/TX06A001281/4/Seri82/5009//Seri82/Cutter/3/Fuller
12WXCS402	209	U5926-2-8/U5954-1-5
12WXCS329	210	TX07V7327/TX08V7313
12WXCS308	211	TAM 304/TX07A001505
12WXCS130	212	TX99U8544/Ogallala//TAM 111/3/TAM 112/4/U5954-1-5/TAM 203
12WXCS154	213	U5930-11-3/U5947-1-3//U5924-10-6/U5928-1-5
12WXCS338	214	TX08A001249/TX09D1163
12WXCS333	215	TX08A001128/WB-Cedar
12WXCS433	216	U5941-1-6//U5928-1-5/U5924-10-1
12WXCS418	217	U5935-2-3//TAM 203/U5924-10-1
12WXCS142	218	U5954-1-5//TX06A001263/TX01V5134RC-3 /3/U5930-13-5/TX02A0252
12WXCS410	219	U5930-13-5/U5924-10-6
12WXCS141	220	U5941-1-6//TX04V075080/TX02A0252/3/TAM 203/TX01V5134RC-3//U5926-2-8
12WXCS455	221	T82-37/TX09D1163

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS421	222	U5937-4-2//U5924-10-6/U5928-1-5
12WXCS244	223	U5942-10-1/U5930-13-5//U5942-10-1/TAM 203
12WXCS449	224	T78-34/TX09A001197
12WXCS126	225	Seri82/Cutter//TX06A001263/3/NC08-23323/4/TX03A0148//Seri82/5009/3/TX09D1181
12WXCS152	226	U5930-11-3/U5947-1-3//U5937-4-2/TAM 401
12WXCS373	227	TX09D1036/TX09D1119
12WXCS109	228	Jackpot/TX03A0148 //NC08-23323/3/H117-4/TX09D1181
12WXCS465	229	TX04CS00232/WB-Cedar
12WXCS132	230	TX99U8544/Halberd//RonL/3/TAM 112/4/TX06A001132/Fannin
12WXCS411	231	U5930-13-5/U5926-3-4
12WXCS327	232	TX07V7327/OK07231
12WXCS228	233	U5924-10-6/U5928-1-5//U5947-1-3/U5938-10-5
12WXCS195	234	U5947-1-3/U5938-10-5//U5926-2-8
12WXCS287	235	Everest/Hitch
12WXCS334	236	TX08A001128/T74-13X
12WXCS156	237	U5930-11-3/U5947-1-3//U5954-1-5
12WXCS399	238	U5924-10-6//U5947-1-3/U5938-10-5
12WXCS164	239	U5930-11-3/U5924-10-1//U5954-1-5
12WXCS185	240	U5937-4-2/TAM 401//U5930-13-5/U5924-10-1
12WXCS223	241	U5924-10-6/U5926-2-8/4/TX03A0148//Seri82/5009/3/TX09D1181
12WXCS468	242	H117-3/TX08V7140
12WXCS110	243	Jackpot/Fuller //NC08-23323/3/U5928-1-5/TX02A0252
12WXCS328	244	TX07V7327/TX08A001128
12WXCS125	245	TX99U8544/Ogallala//TAM 111/3/CJ/4/TAM 304/U5930-13-5
12WXCS216	246	U5924-10-1/TX06A001263//U5937-4-2
12WXCS245	247	U5942-10-1/U5928-1-5//U5930-11-3/U5937-4-2
12WXCS403	248	U5926-3-4/U5938-10-5
12WXCS336	249	TX08A001249/TX09A001197
12WXCS294	250	Hitch/TAMsoft 700
12WXCS200	251	U5947-1-3/TX06A001822//U5928-1-5/TAMsoft 700
12WXCS192	252	U5947-1-3/U5926-2-8//U5937-4-2
12WXCS106	253	TX03A0148//Seri82/5009/3/TX09D1181/4/U5935-2-3/TX06A001822
12WXCS148	254	U5930-11-3/U5937-4-2//U5928-1-5
12WXCS214	255	U5924-10-1/TX06A001263/4/TAM 111//FM3/OGALLALA/3/NC08-23323
12WXCS297	256	Hitch/H117-3
12WXCS268	257	TX06A001822/U5948-11-1//U5950-11-2/KS980512-2-2
12WXCS300	258	OK08328/TX04CS00230

Table 3.2 Continued

Population Name	Population No.	Pedigree
TAM 112	259	TX98V9628=U1254-7-9-2-1/TXGH10440
12WXCS123	260	TAMsoft 700//FM3/OGALLALA/3/TX06A001263/4/TAMsoft 700/TAM 112//Armour
12WXCS119	261	TAMsoft 700/Jackpot//Armour/4/HV9W96-1271R-1//TX01M5009/Halberd/3/TAM 401
12WXCS242	262	U5942-10-1/U5930-11-3//U5924-10-6
12WXCS472	263	H101-4/U5926-2-8
12WXCS318	264	TX03A0563-07AZHR247/TAM 304
12WXCS458	265	TX04CS00230/OK07231
12WXCS302	266	TAM 112/TX08V7579
12WXCS115	267	TAM 112/Fuller//TAM 203/3/KS980512-2-2/unknown//U5931-3-1
12WXCS401	268	U5926-2-8/U5930-13-5
12WXCS225	269	U5924-10-6/U5926-2-8//TAM 401
12WXCS128	270	Seri82/Cutter//TX06A001263/3/NC08-23323/4/8618/FANG//Jackpot/3/TX05V7259
12WXCS144	271	TX06A001263//TAM 203/TX03A0148 /3/U5935-2-3/TAM 401
12WXCS414	272	U5931-3-1//U5924-10-6/U5926-2-8
12WXCS453	273	T82-1/TX09D1163
12WXCS420	274	U5937-4-2/U5926-2-8
12WXCS432	275	U5941-1-6//U5930-11-3/U5924-10-1
12WXCS276	276	CJ/Duster/4/TAMsoft 700//FM6/JAGGER/3/TAM 203
12WXCS277	277	OK07209/TX05V7269/3/Jackpot/TX03A0148 //VA08W-295
12WXCS218	278	U5924-10-1/TX06A001822//TAM 304/U5926-2-8
12WXCS452	279	T82-1/TX08V7579
12WXCS435	280	U5947-1-3/U5924-10-6
12WXCS469	281	H117-3/TX09D1163
12WXCS397	282	U5924-10-6/U5937-4-2
12WXCS272	283	TAM 304/U5930-13-5//U5942-10-1/U5938-10-5
12WXCS457	284	T82-37/H124-2
12WXCS431	285	U5941-1-6/U5931-3-1
12WXCS303	286	TAM 112/TX04CS00232
12WXCS296	287	Hitch/TX07A001505
12WXCS174	288	U5930-13-5/U5924-10-1//U5947-1-3/U5926-2-8
12WXCS241	289	U5942-10-1/U5930-11-3//U5924-10-6/U5928-1-5
12WXCS211	290	U5928-1-5/Duster/3/Fuller/TX01V5134RC-3//TAM 203
12WXCS124	291	TX99U8544/Ogallala/TAM 111/3/CJ/4/NC08-23323//TX03A0148/TAM 401
12WXCS133	292	TX99U8544/Halberd//8618/FANG/3/TAM 112/4/KS980512-2-2/unknown//U5931-3-1
12WXCS434	293	U5942-10-1//TX06A001822/U5954-1-5
12WXCS217	294	U5924-10-1/TX06A001263//U5937-4-2
12WXCS179	295	U5937-4-2/U5931-3-1//U5947-1-3/TX06A001822

Table 3.2 Continued

Population Name	Population No.	Pedigree
12WXCS147	296	U5926-2-8/U5930-11-3//TAM 203/U5926-2-8
12WXCS419	297	U5937-4-2/U5924-10-6
TAM 305	298	TX97V3006/TX98V6239
12WXCS220	299	U5924-10-1/TAM 401//U5954-1-5/TAM 203
12WXCS111	300	TAM 111//FM3/OGALLALA/3/NC08-23323/4/Seri82/Cutter//FM6/OGALLALA/3/NC08-23323
12WXCS107	301	Jackpot/TX06A001822//U5930-13-5/3/U5935-2-3/U5926-2-8
12WXCS269	302	TX06A001822/U5948-11-1//U5937-4-2
12WXCS360	303	TX08V7753/TX09A001205
12WXCS273	304	TAM 304/U5941-1-6//TAM 304
12WXCS191	305	U5947-1-3/U5926-2-8//U5931-3-1
12WXCS213	306	U5938-10-5/U5930-13-5//U5924-10-6/TAM 203
12WXCS367	307	TX09A001343/TAM 304
12WXCS237	308	U5935-2-3/U5926-2-8//TAM 203/U5926-2-8
12WXCS186	309	U5937-4-2/TAM 401//U5924-10-1/TAM 401

Heads per square foot (heads/sq.ft) was estimated using the following formula.

$$Heads/sq. ft = \frac{((Total\ plot\ weight\ (g)/Single\ head\ wt\ (g))}{125\ (sq.\ ft/plot)}$$

All components were first calculated in imperial format, then converted to the metric output, using a conversion factor of (0.0929) for heads/ft² to heads/m⁻², and (67.25) for GY (bu ac⁻¹) to GY (kg/ha⁻¹). This was necessary to compare these results with the existing data of other lines and other published studies.

Values from these initial calculations were used to determine means and ranges for each population. Checks were included in these calculations, and the averages were used to determine the level of advantage each population held over these checks.

Statistical Analysis

The data from AF₂ and CF₂ populations were subjected to biplot, correlation, and path-coefficient methods. Data analysis was performed using SAS v9.3 (SAS Institute Inc., 2008). GGE biplot was used to find which F₂ population performed best in each trait category, as well as relationship among testers and their yield components. Path coefficients and Pearson's correlations were conducted to discern the relationships among yield and its components.

The AF₂ and CF₂ results were compared to the checks in order to gain a representation of heterosis and the ability to use these populations as a proxy to predicting heterosis in the F₁ generation. The yield and its components of the F₂ were compared for each populations and check cultivars to obtain a rough estimate of heterosis levels.

Results and Discussion

Results from sampled heads and plot weights were used in preliminary calculations to estimate yield and its components. These values were then used to gain mean, ranges, and percentage of advantage for each population over the five check averages (Yield (% of Ch Avg)) as well as advantage over the high check (Yield (% of High Ch)).

AF₂ (Table 3.3) populations averaged 3,600 kilograms per hectare (kg/ha⁻¹), and ranged between 1,445 and 5,267 (kg/ha⁻¹). When compared against the check average of 3,111 (kg/ha⁻¹), 106 of the 146 (73%) of the AF₂ populations surpassed the checks averages in terms of yield itself. Single seed weight mean for the AF₂ was 0.036, with a range of 0.030 to 0.045 grams (g). The checks averaged 0.036 as well, though 63 of the 146 (43%) AF₂ populations exceeded this average. Seeds per head averaged 43.9 for the AF₂s, with a range of 32.3 to 56.5. Checks for this trait averaged 39.5, which 123 of 146 (84%) of AF₂ populations surpassed. The average of heads per square meter (head m²) was 226, with a range of 100 to 421. The check average was also 226, which was outperformed by 73 of 146 (50%) AF₂ populations.

For CF₂ populations (Table 3.4), yield averaged 3,433 kg/ha⁻¹, and ranged between 213 and 5,441 kg/ha⁻¹. For yield, 192 of 304 (63%) CF₂ populations outperformed the check average of 3,111 kg/ha⁻¹. Single seed weight was averaged at 0.035 g with a range of 0.028 to 0.048 g. This average was slightly less than the checks at 0.036 g, though 117 of 304 (38%) appeared to perform better than the check average. Seeds per head in the CF₂ populations averaged at 44 seed per head, and ranged between 29 and 68 seed per head. The check average was 39.5 seed per head, which was surpassed by 239 of the 304 (79%) CF₂ populations. Heads per square meter held an average of 277, with a range of 16 to 416. Checks averaged at 266, which was outperformed by only 82 of the 304 (27%) populations.

Table 3.3 Yield and its components for Amarillo F₂ (AF₂) population

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
1	X12A307T	5267	169	128	0.034	56.5
2	X12A168S	5211	167	126	0.038	32.3
3	X12A013S	5119	165	124	0.037	40.2
4	X12A041S	5011	161	121	0.037	46.9
5	X12A073S	4933	159	119	0.036	45
6	X12A376T	4865	156	118	0.036	45.4
7	X12A379T	4863	156	118	0.044	38.8
8	X12A074S	4825	155	117	0.038	47.5
9	X12A340T	4790	154	116	0.038	52.6
10	X12A378T	4732	152	115	0.04	45.2
11	X12A020S	4677	150	113	0.034	51.7
12	X12A237T	4672	150	113	0.039	41.1
13	X12A362T	4665	150	113	0.038	44.5
14	X12A243T	4650	149	113	0.036	51.2
15	X12A164S	4634	149	112	0.035	51.8
16	X12A254T	4619	148	112	0.035	44.6
17	X12A372T	4602	148	111	0.042	47.8
18	X12A004S	4589	147	111	0.036	42.7
19	X12A021S	4560	147	110	0.033	39
20	X12A142S	4531	146	110	0.038	46.2
21	X12A265T	4506	145	109	0.035	46
22	X12A224T	4500	145	109	0.039	48.3
23	X12A297T	4495	144	109	0.038	47.6
24	X12A050S	4493	144	109	0.035	42.5
25	X12A392T	4491	144	109	0.038	47.3
26	X12A030S	4459	143	108	0.034	42.1
27	X12A009S	4458	143	108	0.038	49
28	X12A001S	4432	142	107	0.034	47.4
29	X12A228T	4424	142	107	0.037	44.2
30	X12A369T	4419	142	107	0.041	43
31	X12A394T	4404	142	107	0.039	43
32	X12A062S	4398	141	106	0.039	42.9
33	X12A368T	4392	141	106	0.043	36.2
34	X12A312T	4364	140	106	0.034	42
35	X12A231T	4271	137	103	0.039	45.7
36	X12A126S	4242	136	103	0.036	47.4
37	X12A399T	4227	136	102	0.041	46.3

Table 3.3 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
38	X12A178S	4226	136	102	0.03	41.7
39	X12A032S	4166	134	101	0.033	49.7
40	X12A008S	4148	133	100	0.035	48.4
41	TAM 113 (Ch)	4130	133	100	0.035	43.1
42	X12A138S	4126	133	100	0.038	45.3
43	X12A344T	4104	132	99	0.036	37.7
44	X12A034S	4079	131	99	0.036	42.8
45	X12A343T	4063	131	98	0.037	44.5
46	X12A384T	4030	130	98	0.04	46.4
47	X12A151S	4006	129	97	0.042	39.7
48	X12A259T	3982	128	96	0.034	43.3
49	X12A006S	3975	128	96	0.036	46.2
50	X12A014S	3974	128	96	0.036	45.6
51	X12A213T	3955	127	96	0.035	42.2
52	X12A083S	3948	127	96	0.04	44
53	X12A141S	3945	127	96	0.037	51
54	X12A127S	3923	126	95	0.035	43.7
55	X12A407T	3909	126	95	0.042	44.4
56	X12A355T	3889	125	94	0.038	46.1
57	X12A070S	3872	124	94	0.036	44.2
58	X12A260T	3867	124	94	0.034	40.7
59	X12A087S	3858	124	93	0.039	40.6
60	X12A387T	3848	124	93	0.038	43.5
61	X12A350T	3848	124	93	0.037	52.2
62	X12A061S	3844	124	93	0.039	39
63	X12A390T	3844	124	93	0.04	40.3
64	X12A238T	3818	123	92	0.035	42.7
65	X12A189S	3796	122	92	0.034	44.8
66	X12A080S	3792	122	92	0.041	45.7
67	X12A304T	3790	122	92	0.033	41.2
68	X12A097S	3779	121	92	0.035	37.1
69	X12A251T	3763	121	91	0.038	45.7
70	X12A248T	3753	121	91	0.037	41.1
71	X12A363T	3715	119	90	0.036	38
72	X12A222T	3701	119	90	0.035	48.4
73	X12A095S	3677	118	89	0.033	45.3
74	X12A022S	3676	118	89	0.035	39
75	X12A113S	3674	118	89	0.036	46.7

Table 3.3 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
76	X12A042S	3668	118	89	0.041	49.4
77	X12A112S	3665	118	89	0.037	34.8
78	X12A341T	3622	116	88	0.039	46.6
79	X12A374T	3602	116	87	0.039	43.4
80	X12A373T	3590	115	87	0.04	44.3
81	X12A165S	3571	115	86	0.036	49.2
82	X12A257T	3550	114	86	0.035	40.9
83	X12A400T	3523	113	85	0.041	45.3
84	TAM W-101 (Ch)	3522	113	85	0.042	26.7
85	TAM 111 (Ch)	3503	113	85	0.035	45
86	X12A005S	3502	113	85	0.035	41.3
87	X12A134S	3468	111	84	0.036	43.9
88	X12A405T	3464	111	84	0.043	50.8
89	X12A402T	3429	110	83	0.038	38.7
90	X12A398T	3399	109	82	0.045	42.5
91	X12A261T	3383	109	82	0.041	46.4
92	X12A108S	3350	108	81	0.036	53.7
93	X12A298T	3339	107	81	0.033	41.8
94	X12A018S	3337	107	81	0.033	44.7
95	X12A322T	3336	107	81	0.036	46.4
96	X12A031S	3310	106	80	0.035	38
97	X12A023S	3310	106	80	0.035	47.7
98	X12A181S	3307	106	80	0.034	42.6
99	X12A082S	3269	105	79	0.035	40.9
100	X12A314T	3246	104	79	0.036	41.8
101	X12A233T	3243	104	79	0.033	43.6
102	X12A188S	3234	104	78	0.033	46.8
103	X12A388T	3220	104	78	0.044	38.6
104	X12A167S	3205	103	78	0.038	45.5
105	X12A029S	3188	102	77	0.034	44
106	X12A386T	3173	102	77	0.041	45.1
107	X12A364T	3172	102	77	0.041	45.5
108	X12A028S	3161	102	77	0.032	34.3
109	X12A336T	3134	101	76	0.035	35.8
110	X12A051S	3096	100	75	0.032	42.9
111	X12A278T	3089	99	75	0.032	43.4
112	X12A283T	3063	98	74	0.038	48.4
113	X12A037S	3038	98	74	0.036	36.4

Table 3.3 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
114	X12A120S	3020	97	73	0.036	46.1
115	X12A102S	2987	96	72	0.037	43.1
116	X12A084S	2978	96	72	0.035	40.4
117	X12A121S	2958	95	72	0.033	40.5
118	X12A019S	2954	95	72	0.035	38.2
119	X12A192S	2948	95	71	0.033	50
120	X12A136S	2941	95	71	0.037	42.1
121	X12A060S	2935	94	71	0.038	41.9
122	X12A125S	2931	94	71	0.033	50.1
123	X12A199T	2925	94	71	0.036	42.3
124	X12A027S	2912	94	71	0.032	41.3
125	X12A033S	2908	93	70	0.034	44.9
126	X12A190S	2889	93	70	0.033	43.7
127	X12A153S	2859	92	69	0.037	54.4
128	X12A117S	2835	91	69	0.04	41.7
129	X12A115S	2806	90	68	0.035	42.7
130	X12A130S	2745	88	66	0.038	45.3
131	X12A123S	2724	88	66	0.04	43.5
132	X12A360T	2721	87	66	0.038	48.3
133	TAM 112 (Ch)	2665	86	65	0.035	41.1
134	X12A152S	2655	85	64	0.036	44.3
135	X12A239T	2613	84	63	0.035	37.6
136	X12A002S	2556	82	62	0.033	34.6
137	X12A140S	2516	81	61	0.034	48.2
138	X12A067S	2442	79	59	0.032	47.2
139	X12A131S	2413	78	58	0.036	44.7
140	X12A218T	2277	73	55	0.033	44.8
141	X12A313T	2162	69	52	0.032	36.8
142	X12A114S	2113	68	51	0.036	40.3
143	X12A171S	1985	64	48	0.037	48.9
144	X12A054S	1805	58	44	0.032	44.6
145	X12A066S	1781	57	43	0.034	37.5
146	TAM 305 (Ch)	1736	56	42	0.031	41.8
147	X12A186S	1688	54	41	0.032	47.6
148	X12A143S	1667	54	40	0.038	43.7
149	X12A124S	1661	53	40	0.033	41.4
150	X12A055S	1464	47	35	0.035	37.9
151	X12A291T	1445	46	35	0.033	39.5

Table 3.3 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
	Mean	3600			0.036	43.9
	Range	1445-5267			0.030-0.045	32.3-56.5
	Ch Avg	3111			0.036	39.5
	High Ch	4130				

Seed wt= weight of individual seeds in g; Seed/head= number of seeds per individual head; Heads/sqft= number of heads per unit area; Yield (% of check average)= comparison of AF2 populations against the checks by weighing the yield of each population against the average of all checks and obtaining a percentage.

Table 3.4 Yield and its components for College Station F₂ (CF₂) populations

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
1	12WXCS331	5441	175	132	0.037	39.5
2	12WXCS372	5277	170	128	0.037	39.1
3	12WXCS388	5062	163	123	0.034	36
4	12WXCS383	5042	162	122	0.035	39.6
5	12WXCS376	5022	161	122	0.035	42.3
6	12WXCS381	5020	161	122	0.035	43.6
7	12WXCS313	4999	161	121	0.035	47.8
8	12WXCS117	4933	159	119	0.034	49.1
9	12WXCS358	4888	157	118	0.034	38.2
10	12WXCS337	4888	157	118	0.039	39.6
11	12WXCS145	4856	156	118	0.033	50.8
12	12WXCS339	4849	156	117	0.034	47.2
13	12WXCS285	4815	155	117	0.035	52.4
14	12WXCS382	4792	154	116	0.036	43.4
15	12WXCS314	4775	153	116	0.035	46.9
16	12WXCS342	4736	152	115	0.038	36.5
17	12WXCS379	4734	152	115	0.032	39.2
18	12WXCS343	4699	151	114	0.035	46.4
19	12WXCS235	4691	151	114	0.035	45.6
20	12WXCS439	4691	151	114	0.037	47
21	12WXCS284	4680	150	113	0.044	46.2
22	12WXCS378	4652	150	113	0.032	43.2
23	12WXCS320	4631	149	112	0.038	42.1
24	12WXCS116	4631	149	112	0.037	42.6
25	12WXCS364	4628	149	112	0.037	40.1
26	12WXCS157	4587	147	111	0.039	37.6
27	12WXCS159	4558	146	110	0.035	46.7
28	12WXCS387	4554	146	110	0.034	43
29	12WXCS344	4553	146	110	0.035	37.3
30	12WXCS391	4505	145	109	0.035	39.3
31	12WXCS361	4501	145	109	0.034	42.1
32	12WXCS340	4467	144	108	0.039	34.6
33	12WXCS312	4464	143	108	0.035	43.1
34	12WXCS281	4455	143	108	0.033	35.7
35	12WXCS349	4449	143	108	0.04	42.1
36	12WXCS233	4439	143	107	0.034	39.6
37	12WXCS375	4436	143	107	0.039	41.6

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
38	12WXCS413	4427	142	107	0.032	52
39	12WXCS253	4427	142	107	0.034	40.8
40	12WXCS447	4416	142	107	0.038	46.4
41	12WXCS288	4394	141	106	0.037	38.6
42	12WXCS221	4384	141	106	0.033	46.2
43	12WXCS275	4382	141	106	0.034	48.1
44	12WXCS356	4373	141	106	0.037	38.1
45	12WXCS335	4360	140	106	0.034	41
46	12WXCS188	4355	140	105	0.038	40.4
47	12WXCS135	4353	140	105	0.038	44
48	12WXCS324	4323	139	105	0.035	44.5
49	12WXCS430	4304	138	104	0.035	48.2
50	12WXCS319	4301	138	104	0.033	48.5
51	12WXCS118	4292	138	104	0.036	41.4
52	12WXCS350	4289	138	104	0.04	38.4
53	12WXCS438	4270	137	103	0.039	46.6
54	12WXCS279	4266	137	103	0.035	50
55	12WXCS282	4265	137	103	0.037	48.9
56	12WXCS440	4251	137	103	0.038	48.8
57	12WXCS143	4248	137	103	0.036	49.9
58	12WXCS396	4238	136	103	0.033	38.7
59	12WXCS389	4234	136	103	0.037	32.1
60	12WXCS196	4226	136	102	0.035	44.5
61	12WXCS280	4224	136	102	0.043	35
62	12WXCS386	4209	135	102	0.033	41.2
63	12WXCS374	4201	135	102	0.038	41.9
64	12WXCS345	4200	135	102	0.035	47.4
65	12WXCS317	4195	135	102	0.039	38.9
66	12WXCS274	4182	134	101	0.037	45.8
67	12WXCS405	4174	134	101	0.031	48.9
68	12WXCS384	4162	134	101	0.042	35.5
69	12WXCS307	4161	134	101	0.034	46.2
70	12WXCS467	4159	134	101	0.039	33.5
71	12WXCS355	4151	133	101	0.034	50.5
72	12WXCS278	4132	133	100	0.035	46.2
73	TAM 113 (Ch)	4130	133	100	0.0351	43.1
74	12WXCS454	4117	132	100	0.036	39
75	12WXCS351	4055	130	98	0.034	35.9

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
76	12WXCS357	4051	130	98	0.033	41
77	12WXCS423	4047	130	98	0.035	48.3
78	12WXCS160	4046	130	98	0.031	38.1
79	12WXCS363	3999	129	97	0.034	44.8
80	12WXCS232	3999	129	97	0.035	48.1
81	12WXCS286	3998	129	97	0.037	48.3
82	12WXCS380	3995	128	97	0.038	41
83	12WXCS412	3991	128	97	0.034	49.8
84	12WXCS390	3987	128	97	0.035	44.3
85	12WXCS134	3966	127	96	0.038	47.3
86	12WXCS332	3950	127	96	0.037	43.9
87	12WXCS193	3949	127	96	0.034	48.6
88	12WXCS322	3944	127	95	0.036	45.6
89	12WXCS197	3936	127	95	0.034	52.7
90	12WXCS424	3932	126	95	0.037	41.6
91	12WXCS136	3918	126	95	0.036	58
92	12WXCS441	3910	126	95	0.035	46.7
93	12WXCS289	3908	126	95	0.038	45.6
94	12WXCS409	3907	126	95	0.032	46.1
95	12WXCS227	3902	125	94	0.032	40.7
96	12WXCS393	3894	125	94	0.039	50.5
97	12WXCS187	3885	125	94	0.034	37.2
98	12WXCS366	3884	125	94	0.034	47.1
99	12WXCS299	3881	125	94	0.034	37.6
100	12WXCS165	3880	125	94	0.034	40.2
101	12WXCS248	3864	124	94	0.034	43.5
102	12WXCS369	3846	124	93	0.048	29.5
103	12WXCS444	3844	124	93	0.041	45.5
104	12WXCS295	3837	123	93	0.034	54.8
105	12WXCS198	3831	123	93	0.034	50.4
106	12WXCS170	3827	123	93	0.033	44.6
107	12WXCS422	3806	122	92	0.036	43.8
108	12WXCS113	3795	122	92	0.04	44.5
109	12WXCS108	3783	122	92	0.042	42.6
110	12WXCS346	3782	122	92	0.037	43.8
111	12WXCS365	3779	121	92	0.032	37.6
112	12WXCS352	3775	121	91	0.033	42.2
113	12WXCS392	3775	121	91	0.038	51.2

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
114	12WXCS359	3774	121	91	0.03	31.9
115	12WXCS400	3764	121	91	0.036	46.9
116	12WXCS121	3746	120	91	0.034	42.2
117	12WXCS304	3738	120	91	0.036	50.2
118	12WXCS112	3732	120	90	0.04	36.3
119	12WXCS437	3716	119	90	0.036	45.3
120	12WXCS425	3707	119	90	0.035	45.2
121	12WXCS321	3693	119	89	0.038	44.2
122	12WXCS443	3690	119	89	0.042	42.6
123	12WXCS178	3683	118	89	0.038	36.2
124	12WXCS246	3677	118	89	0.033	42.7
125	12WXCS315	3675	118	89	0.034	43.7
126	12WXCS385	3673	118	89	0.032	40.5
127	12WXCS398	3672	118	89	0.037	31
128	12WXCS183	3670	118	89	0.036	37.9
129	12WXCS459	3668	118	89	0.034	35
130	12WXCS464	3667	118	89	0.039	43.2
131	12WXCS309	3646	117	88	0.032	52.7
132	12WXCS267	3638	117	88	0.032	39.9
133	12WXCS250	3638	117	88	0.032	46.1
134	12WXCS182	3626	117	88	0.035	38.2
135	12WXCS234	3623	116	88	0.038	47.4
136	12WXCS428	3620	116	88	0.034	50
137	12WXCS166	3613	116	87	0.033	46.1
138	12WXCS436	3611	116	87	0.034	34.3
139	12WXCS290	3589	115	87	0.04	40.2
140	12WXCS404	3588	115	87	0.033	47.8
141	12WXCS155	3585	115	87	0.032	30.4
142	12WXCS427	3550	114	86	0.037	46.4
143	12WXCS341	3543	114	86	0.038	35.9
144	12WXCS181	3543	114	86	0.033	39.8
145	12WXCS151	3537	114	86	0.036	41.3
146	12WXCS252	3531	113	85	0.03	43.9
147	12WXCS176	3529	113	85	0.034	43.8
148	12WXCS362	3528	113	85	0.033	42.9
149	TAM W-101 (Ch)	3522	113	85	0.042	26.7
150	12WXCS348	3512	113	85	0.033	48

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
151	TAM 111 (Ch)	3503	113	85	0.0345	45
152	12WXCS153	3501	113	85	0.032	40.9
153	12WXCS146	3500	112	85	0.039	51.8
154	12WXCS394	3497	112	85	0.038	40.7
155	12WXCS139	3493	112	85	0.034	46.9
156	12WXCS426	3492	112	85	0.031	38
157	12WXCS442	3485	112	84	0.033	50.9
158	12WXCS266	3471	112	84	0.034	41.7
159	12WXCS208	3470	112	84	0.033	47.6
160	12WXCS415	3452	111	84	0.029	49.2
161	12WXCS204	3440	111	83	0.037	53.1
162	12WXCS247	3439	111	83	0.032	40.7
163	12WXCS462	3437	110	83	0.036	41
164	12WXCS158	3408	110	83	0.032	41.9
165	12WXCS429	3408	110	83	0.032	38.4
166	12WXCS180	3407	109	82	0.036	37.3
167	12WXCS406	3401	109	82	0.034	46.6
168	12WXCS271	3397	109	82	0.034	45.8
169	12WXCS161	3390	109	82	0.032	40.6
170	12WXCS408	3386	109	82	0.036	46.6
171	12WXCS460	3383	109	82	0.033	42.4
172	12WXCS205	3369	108	82	0.037	49.4
173	12WXCS210	3365	108	81	0.036	48.8
174	12WXCS194	3352	108	81	0.035	53.8
175	12WXCS416	3344	107	81	0.033	45.2
176	12WXCS120	3342	107	81	0.032	41.6
177	12WXCS230	3315	107	80	0.032	46.1
178	12WXCS305	3314	107	80	0.035	43.2
179	12WXCS263	3314	107	80	0.04	44.9
180	12WXCS347	3313	106	80	0.037	44
181	12WXCS127	3300	106	80	0.037	35.2
182	12WXCS167	3294	106	80	0.033	42
183	12WXCS471	3292	106	80	0.039	40.6
184	12WXCS474	3281	105	79	0.036	40.9
185	12WXCS326	3281	105	79	0.036	46.4
186	12WXCS207	3269	105	79	0.036	46.6
187	12WXCS445	3235	104	78	0.038	52.4
188	12WXCS448	3209	103	78	0.04	38.2

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
189	12WXCS293	3204	103	78	0.037	47.6
190	12WXCS162	3200	103	77	0.035	42.8
191	12WXCS407	3185	102	77	0.031	38.1
192	12WXCS330	3174	102	77	0.037	53.6
193	12WXCS222	3172	102	77	0.032	49.2
194	12WXCS131	3161	102	77	0.034	47.4
195	12WXCS129	3126	100	76	0.042	41.1
196	12WXCS226	3110	100	75	0.033	35.6
197	12WXCS122	3104	100	75	0.035	44.1
198	12WXCS173	3087	99	75	0.032	47.4
199	12WXCS190	3084	99	75	0.032	38.5
200	12WXCS219	3080	99	75	0.034	51.2
201	12WXCS353	3077	99	75	0.031	44
202	12WXCS149	3073	99	74	0.037	38.3
203	12WXCS283	3070	99	74	0.04	51.1
204	12WXCS291	3070	99	74	0.041	42.2
205	12WXCS325	3068	99	74	0.041	37.5
206	12WXCS249	3065	99	74	0.031	38.6
207	12WXCS463	3061	98	74	0.037	38
208	12WXCS140	3050	98	74	0.035	39.9
209	12WXCS402	3048	98	74	0.036	52.2
210	12WXCS329	3029	97	73	0.034	42.7
211	12WXCS308	3028	97	73	0.034	47.9
212	12WXCS130	3027	97	73	0.034	39.9
213	12WXCS154	3025	97	73	0.034	36.5
214	12WXCS338	3023	97	73	0.034	44.4
215	12WXCS333	3008	97	73	0.039	46.7
216	12WXCS433	3004	97	73	0.031	39
217	12WXCS418	3003	97	73	0.036	45.8
218	12WXCS142	2981	96	72	0.034	36.1
219	12WXCS410	2981	96	72	0.032	43.9
220	12WXCS141	2977	96	72	0.034	34.8
221	12WXCS455	2976	96	72	0.039	39.8
222	12WXCS421	2949	95	71	0.035	43.4
223	12WXCS244	2945	95	71	0.032	47
224	12WXCS449	2939	94	71	0.04	49.9
225	12WXCS126	2929	94	71	0.038	43.8
226	12WXCS152	2919	94	71	0.035	35.3

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
227	12WXCS373	2918	94	71	0.035	47.9
228	12WXCS109	2914	94	71	0.039	42.6
229	12WXCS465	2913	94	71	0.039	38.4
230	12WXCS132	2912	94	71	0.037	49.1
231	12WXCS411	2905	93	70	0.03	39.9
232	12WXCS327	2892	93	70	0.035	52.1
233	12WXCS228	2870	92	69	0.032	40.7
234	12WXCS195	2868	92	69	0.033	47.3
235	12WXCS287	2860	92	69	0.035	51.3
236	12WXCS334	2854	92	69	0.04	49
237	12WXCS156	2847	91	69	0.036	34.1
238	12WXCS399	2846	91	69	0.036	43.5
239	12WXCS164	2842	91	69	0.034	41.8
240	12WXCS185	2842	91	69	0.035	42.9
241	12WXCS223	2827	91	68	0.032	49.6
242	12WXCS468	2816	91	68	0.035	49.1
243	12WXCS110	2797	90	68	0.036	52.2
244	12WXCS328	2794	90	68	0.039	48.5
245	12WXCS125	2778	89	67	0.037	45.4
246	12WXCS216	2769	89	67	0.034	38.7
247	12WXCS245	2766	89	67	0.033	49.3
248	12WXCS403	2761	89	67	0.034	43.6
249	12WXCS336	2761	89	67	0.037	49.3
250	12WXCS294	2744	88	66	0.033	53.8
251	12WXCS200	2743	88	66	0.034	48.4
252	12WXCS192	2735	88	66	0.035	38.6
253	12WXCS106	2729	88	66	0.035	43.7
254	12WXCS148	2693	87	65	0.036	39.3
255	12WXCS214	2693	87	65	0.034	56.3
256	12WXCS297	2684	86	65	0.036	49.6
257	12WXCS268	2679	86	65	0.032	51
258	12WXCS300	2676	86	65	0.033	42.1
259	TAM 112 (Ch)	2665	86	65	0.035	41.1
260	12WXCS123	2660	86	64	0.03	52.1
261	12WXCS119	2660	85	64	0.033	39.8
262	12WXCS242	2651	85	64	0.032	35.2
263	12WXCS472	2618	84	63	0.038	51.6
264	12WXCS318	2610	84	63	0.034	48.1

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
265	12WXCS458	2606	84	63	0.034	42.9
266	12WXCS302	2596	83	63	0.036	41
267	12WXCS115	2590	83	63	0.034	45.6
268	12WXCS401	2579	83	62	0.034	40.6
269	12WXCS225	2576	83	62	0.033	49
270	12WXCS128	2555	82	62	0.033	37.9
271	12WXCS144	2480	80	60	0.035	53.7
272	12WXCS414	2480	80	60	0.031	47.8
273	12WXCS453	2465	79	60	0.036	36.4
274	12WXCS420	2431	78	59	0.037	47.7
275	12WXCS432	2412	78	58	0.03	42.4
276	12WXCS276	2411	77	58	0.039	44.5
277	12WXCS277	2405	77	58	0.034	48.5
278	12WXCS218	2381	77	58	0.032	55.5
279	12WXCS452	2329	75	56	0.036	43.8
280	12WXCS435	2325	75	56	0.034	37.6
281	12WXCS469	2270	73	55	0.037	45.4
282	12WXCS397	2252	72	55	0.035	44
283	12WXCS272	2241	72	54	0.034	50
284	12WXCS457	2182	70	53	0.034	41.5
285	12WXCS431	2178	70	53	0.031	41.8
286	12WXCS303	2161	69	52	0.037	41.9
287	12WXCS296	2150	69	52	0.032	57.1
288	12WXCS174	2111	68	51	0.031	42.2
289	12WXCS241	2101	68	51	0.033	43
290	12WXCS211	2096	67	51	0.034	55
291	12WXCS124	2076	67	50	0.034	52.8
292	12WXCS133	2047	66	50	0.033	57.2
293	12WXCS434	1956	63	47	0.032	43.6
294	12WXCS217	1952	63	47	0.033	55
295	12WXCS179	1902	61	46	0.035	35.7
296	12WXCS147	1890	61	46	0.041	45.2
297	12WXCS419	1871	60	45	0.035	44
298	TAM 305 (Ch)	1736	56	42	0.0314	41.8
299	12WXCS220	1610	52	39	0.031	47.9
300	12WXCS111	1492	48	36	0.028	44.8
301	12WXCS107	1431	46	35	0.037	47.3
302	12WXCS269	1410	45	34	0.032	38.8

Table 3.4 Continued

No.	Population	Yield (kg/ha)	Yield (% of Ch Avg)	Yield (% of High Ch)	Seed wt (g)	Seed/head
303	12WXCS360	1347	43	33	0.035	44.6
304	12WXCS273	1245	40	30	0.033	68
305	12WXCS191	1178	38	29	0.031	49.5
306	12WXCS213	976	31	24	0.032	60.9
307	12WXCS367	665	21	16	0.034	53.5
308	12WXCS237	569	18	14	0.035	57.5
309	12WXCS186	213	7	5	0.032	41.2
	Mean	3433			0.035	44
	Range	213-5441			0.028-0.048	29-68
	Ch Avg	3111			0.036	39.5
	High Ch	4130				

Seed wt= weight of individual seeds in g; Seed/head= number of seeds per individual head; Heads/sqft= number of heads per unit area; Yield (% of check average)= comparison of CF₂ populations against the checks by weighing the yield of each population against the average of all checks and obtaining a percentage.

When observing the differences between the AF₂ and CF₂ populations, it appears that the AF₂ had a slightly better performance in terms of averaging higher in yield and its components when compared to the high check. Reasons for this difference could be caused by field gradients or pedigree differences between nurseries.

Advantages of yield over the high check, TAM 113 (Yield High Ch %) were calculated for each set of populations. Of the AF₂ populations, 41 of 146 (28%) scored at least a 100% advantage (equal to or higher than the check). The highest performing AF₂ population was X12A307T (pedigree: X11A524S [=AK11WWCB-2237 (=ID800994.W/KAUZ// GEREK 79 (OCW00S366S-1B-6,8,9,10))/Greer

(=AP06T3832=HBK0935-29-15/KS90W077-2-2/VBF0589-1)]/TX06V7266
(=TX99U8617/TX97U2001)) with a 28% advantage over the high check.

For CF₂s, 73 of 304 (24%) scored at least a 100% advantage over the high check. The highest performing CF₂, 12WXCS331 (pedigree: TX08A001128/TX09D1119) scored a 32% of advantage over the high check.

The percentage of yield advantage of each AF₂ and CF₂ populations over the high check showed that a good portion of the F₂ populations performed well and were superior to the inbred line checks as a whole. This is an expected outcome of hybrid vigor, seen in many studies (Knott, 1965; Brunes et al, 1998).

Previous work by Boland and Walcott (1985) compared an F₁ hybrid to the mean of the checks and showed a 114% advantage, which bore a similar result as when the hybrid was compared to mid-parent heterosis (113.9%). Another study showed hybrid F₁ having an advantage of 1.86 Mg ha⁻¹ over the highest yielding line varieties (Longin et al, 2013). Because parents of these F₂s were not included in this study, it was not possible to determine mid-parent or high-parent heterosis. Only advantages over check averages could be determined in this study.

GGE Biplot Analyses

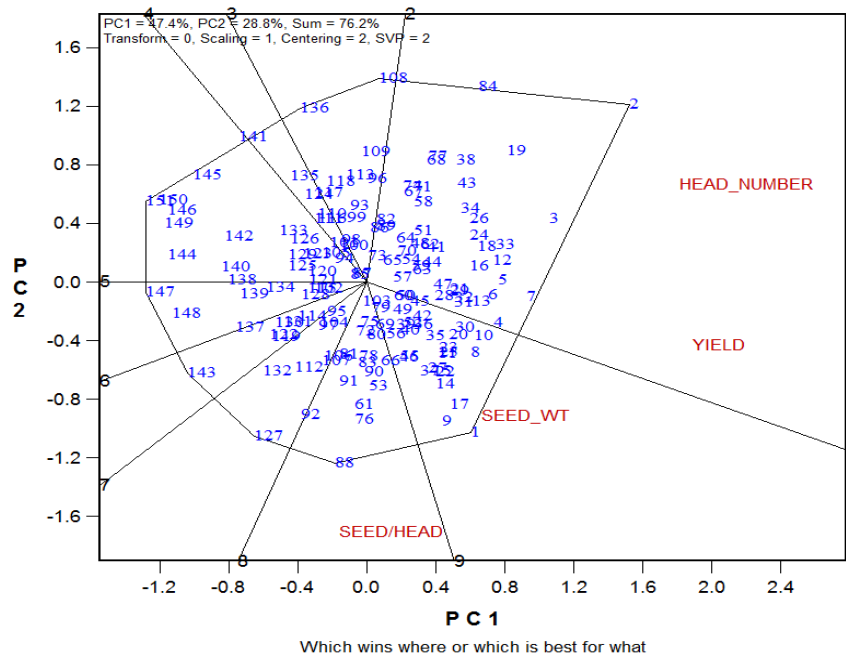
The GGE biplot (Figures 3.1 and 3.2) shows the performance of F₂ populations yield and its components for AF₂ and CF₂ respectively.

In AF₂ population, the head number and yield fall between two vertices (Figure 3.1). According to guidelines by Yan et al. (2007), the genotypes that performed the best in combination between head number and yield fall within the vertices encompassing these

two traits. The best performer in combination of these two traits is population 2 (X12A168S; pedigree: Hatcher (=CO980607=Yuma/PI 372129//TAM 200/3/4*Yuma/4/KS91H184/Vista)/TAM 305 (=TX06A001263=TX97V3006/TX98V6239)) as seen by the number furthest out within this category on the biplot. Best performer of seed weight appears to be population 1 (X12A307T; pedigree: X11A524S [=AK11WWCB-2237 (=ID800994.W/KAUZ//GEREK 79 (OCW00S366S-1B-6,8,9,10))/Greer (=AP06T3832=HBK0935-29-15/KS90W077-2-2/VBF0589-1)]/TX06V7266 (=TX99U8617/TX97U2001)). In the seeds per head trait, population 88 (X12A405T; pedigree: X11A623S [=AK11SPWCB-3064 (=WHEAR/KUKUNA//WHEAR)/TX05A001822 (=2145/X940786-6-7)]/Duster (=OK93P656H3299-2C04=WO405D/HGF112//W7469C/HCF012)) appears to be the superior performer. The biplot itself depicts that it explains 76.2% of the data. Table 3.5 provides the data of these best performing AF₂ populations. The CF₂ generation was tested in the same way using biplot analysis.

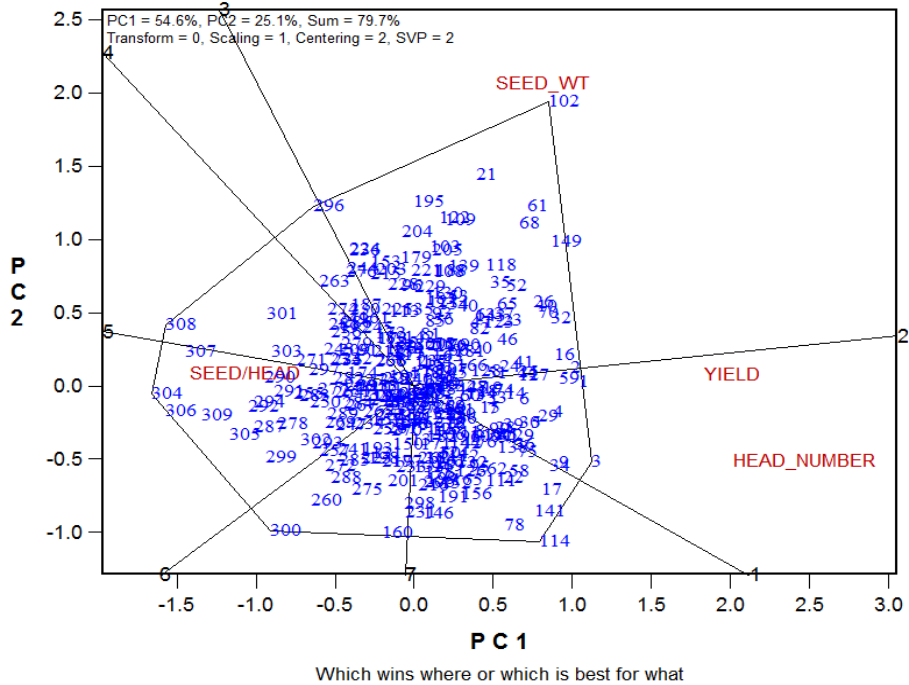
In CF₂ populations, population 3 (12WXCS388; pedigree: TX09D1172/TX09D1193) performed best for the combined yield and head number traits (Figure 3.2.) Population 102 (12WXCS369; pedigree: TX09A001343/T68-21) performed best for seed weight, with a median level of yield superiority. Population 304 (12WXCS273; pedigree: TAM 304/U5941-1-6//TAM 304) was the best for seeds/head, though was one of the worst populations overall. The CF₂ biplot explains 79.7% of the data, which is slightly higher than that of the AF₂. Table 3.6 provides the data of these best performing CF₂ populations.

Figure 3.1 The which-won-where view of the GGE biplot of 2014 Amarillo F₂ (AF₂) populations.



This figure shows the best performing populations in each characteristic category. Population 2 (X12A168S) performed best for combined head number and yield. Population 1 (X12A307T) performed best for seed weight. Population 88 (X12A405T) performed best for seeds/head, yet proved to be a less appealing population overall. Population 2 appears to be the most desirable overall across all germplasm tested. Details on the best performing F₂ populations were presented in Table 3.4.

Figure. 3.2 The which-won-where view of the GGE biplot of 2014 College Station F₂ (CF₂) populations.



This figure shows the best performing populations in each characteristic category. In this particular set of populations, 3 [12WXCS388] stands out as the most superior overall, as well as the best performing for both yield and head number. Population 102 [12WXCS369] performed best for seed weight. Population 304 [12WXCS273] was the best performer for seeds/head.

Table 3.5 Biplot results showing the best performers of Amarillo F₂ (AF₂) populations based on yield and its components in 2014.

Population No.	Population name	Seed wt. (g)	Yield (bu/a)	Head number (number)	Seeds/head (number)
1	X12A307T	0.03	78.3	25.2	56.5
2	X12A168S	0.04	77.5	39.1	39.1
3	X12AO13S	0.04	76.1	32.1	32.1
9	X12A340T	0.04	71.2	22.4	52.6
17	X12A372T	0.04	67.8	32.9	47.8
19	X12A021S	0.03	64.5	32.8	39.0
76	X12A042S	0.04	54.5	16.8	49.4
88	X12A405T	0.04	51.5	14.7	50.8
92	X12A108S	0.04	49.8	16.3	53.7
Check	TAM 113	0.04	61.4	25.4	43.1
Check	TAM W-101	0.04	52.4	29.1	26.7
Check	TAM 111	0.03	52.1	20.1	45
Check	TAM 112	0.04	39.6	17.3	41.1
Check	TAM 305	0.03	25.8	12.3	41.1

Table 3.6 Biplot results showing the best performers of College Station F₂ (CF₂) populations based on yield and its components in 2014.

Population No.	Population name	Seed wt. (g)	Yield (bu/a)	Head number (number)	Seeds/head (number)
1	12WXCS331	0.04	80.9	34.9	39.5
3	12WXCS388	0.03	75.3	38.6	36.0
9	12WXCS358	0.03	72.7	35.5	38.2
21	12WXCS284	0.04	69.6	21.6	46.2
61	12WXCS280	0.04	62.8	26.0	35.0
102	12WXCS369	0.05	57.2	25.5	29.5
304	12WXCS273	0.03	18.5	5.2	68.0
306	12WXCS213	0.03	14.5	4.7	60.9
Check	TAM 113	0.04	61.4	25.4	43.1
Check	TAM W-101	0.04	52.4	29.1	26.7
Check	TAM 111	0.03	52.1	20.1	45
Check	TAM 112	0.04	39.6	17.3	41.1
Check	TAM 305	0.03	25.8	12.3	41.1

Pearson's Correlations

Pearson's correlation coefficient analysis was conducted to determine the relationships between yield and its components in the AF₂ and CF₂ populations (Tables 3.7 and 3.8). Head number showed a significant, positive correlation with yield in both the AF₂ ($r = 0.84, P < 0.001$) (Table 3.7) and CF₂ populations ($r = 0.86, P < 0.001$) (Table 3.8). This agrees with Bhatt (1972) who showed that tillering plays a big role in hybrid vigor in wheat. A significant, positive correlation was found between seed weight and yield in both populations (AF₂, $r = 0.31, P < 0.01$) (Table 3.7) and (CF₂, $r = 0.23, P < 0.001$). There was a significant, positive correlation between seeds per head and yield ($r = 0.19, P < 0.01$) (Table 3.7) in the AF₂s but the CF₂s held a negative correlation ($r = -0.23, P < 0.001$). There was a negative correlation ($r = -0.27, P < 0.001$) between seeds per head and head number in the AF₂'s, and ($r = -0.58, P < 0.001$) in the CF₂. Negative and non-significant correlations existed between head number and seed weight, as well as seeds per head and seed weight for the CF₂ populations. Most of the measured yield components in this study were positively related to yield, though not always with each other, which agree with Mohsin et al., (2009) and Aycicek and Yildirim, (2006).

Path Coefficient Analysis

Path coefficient analysis was conducted to determine direct and indirect relationship among the measured traits in both populations (Table 3.9). Grain yield is a product of the yield components, such as head number, seeds per head and seed weight. Combination of direct and indirect effects of yield components results in total effect due

Table 3.7 Pearson correlation coefficient showing the relationship among the yield and its components in the 2014 Amarillo F₂ (AF₂) populations.

	Seed wt.	Seed/head	Head number
Yield	0.310 ***	0.186*	0.836 ***
Seed wt.		0.015 NS	-0.009 NS
Seed/head			-0.274 ***

NS- non-significant; *P<0.05; **P<0.01; ***P<0.001

Table 3.8 Pearson correlation coefficient showing the relationship among yield and its components in the College Station F₂ (CF₂) populations in 2014.

	Seed wt.	Seed/head	Head number
Yield	0.229 ***	-0.234 ***	0.855 ***
Seed wt.		-0.146 NS	-0.007 NS
Seed/head			-0.579 ***

NS- non-significant; *P<0.05; **P<0.01; ***P<0.001

to the trait on the grain yield. Table 3.9 shows that the head number had the strongest direct effects on yield in both populations, followed by seeds per head and seed weight.

In the AF₂s, head number held the strongest direct effect of all yield components, unaffected by seed weight (0.00) and slightly negatively affected by seeds per head (-0.12), bringing the total effect to 0.84. Seed weight was influenced by a negative indirect effect (-0.01) by head number, though was offset by seed weight (0.01), which brought

the total effect of seed weight to 0.31. Seeds per head received a strong indirect effect by head number (-0.26), and remained unaffected by seed weight (0.00), bringing the total effect of seeds per head to 0.19.

Head number held a much stronger direct effect in the CF₂ population, but was more negatively affected by seeds per head (-0.27). However, it still remained unaffected by seed weight (0.00), rendering the total effect of head number to 0.85. Seed weight was negatively affected by seeds per head (-0.07) and slightly by head number (-0.01), leaving the total effect of seed weight at 0.23. Seeds per head held a stronger direct effect than seed weight, though was negatively affected by seed weight (-0.04), and drastically by head number (-0.65), leaving the direct total toward yield at a -0.23.

Previous research reports head number continuously had the strongest direct effect regardless of environment (Akanda and Mundt, 1996; Bhatt, 1972). The negative indirect effects between yield components is expected due to competition for resources in the plant (Thiry et al., 2002). The same is true for other traits; a negative correlation can commonly exist between yield factors, though some consideration must be given to plant-plant interactions for yield loss (Akanda and Mundt, 1996).

Biplot Analyses for Relationship Between Yield and its Components

Figures 3.3 and 3.4 show the relationship between yield and its components, head number, seeds per head and seed weight in the AF₂ and CF₂ populations, respectively. The biplot is a visual representation of relationship between the variables. Head number

Table 3.9 Path coefficient analysis of direct (underlined) and indirect effects for Amarillo F₂ (AF₂) and College Station F₂ (CF₂) populations in 2014.

	Seed wt.	Seed/head	Head number	Nobs*	Total*
<i>*AF₂</i>					
Seed wt.	<u>0.31</u>	0.01	-0.01	151	0.31
Seed/head	0.00	<u>0.44</u>	-0.26	151	0.19
Head number	-0.00	-0.12	<u>0.96</u>	151	0.84
<i>CF₂</i>					
Seed wt.	<u>0.30</u>	-0.07	-0.01	309	0.23
Seed/head	-0.04	<u>0.46</u>	-0.65	309	-0.23
Head number	-0.00	-0.27	<u>1.12</u>	309	0.85

*Nobs = number of observations; Total = total yield

and yield were positively correlated in both populations, in accordance with Thiry et al. (2002), which stated that these two traits are almost always correlated positively with the other.

From observation of the AF₂ biplot, it appears that there is a positive relationship between yield and seed weight, and between seeds per head and seed weight. There also appears to be a very weak positive correlation between yield and seed per head. The wide angle between seeds per head and head number suggest a negative correlation, while seed weight and head number show a much weaker relationship. The CF₂ biplot appears to have a very weak, but positive correlation between seed weight and head number, as well as between seeds per head and seed weight. There seems to be a stronger correlation between seed weight and yield, though the biplot depicts negative

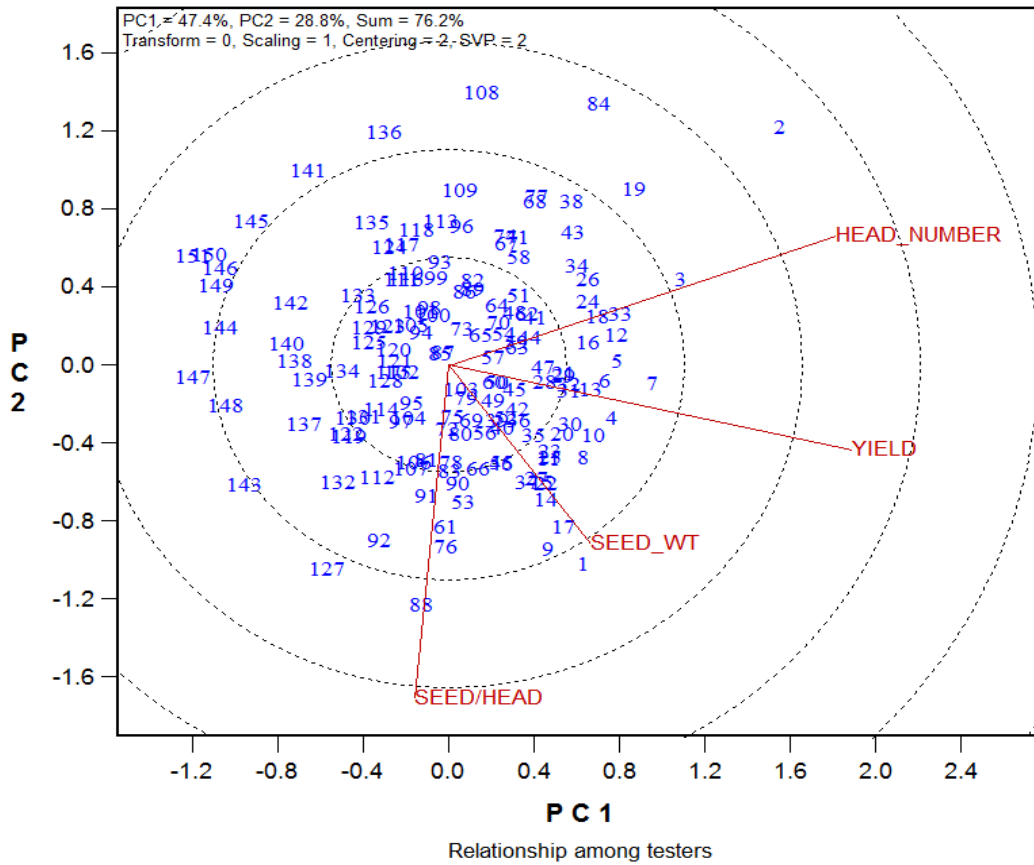
correlations between yield and seeds per head as well as between head number and seeds per head. This can be seen by focusing on the degree of the angle between the two given traits, and by referring to the Pearson's correlations on Tables 3.7 and 3.8 for AF₂ and CF₂ respectively. Obtuse angles denote negative correlation, and acute angles denote strong correlations. Right angles point to the absence of significant correlations, or presence of very weak ones. Though these relationships can be quickly inferred by observing the biplot, a Pearson's correlation accompanying the image will provide a more detailed story of the correlations seen there.

The relationship among testers biplot for AF₂ appears to show that yield and head number are the most discriminating trait among the others, due to the length of the vector. In the CF₂ populations, head number and seed weight appear to be the most discriminating. The further out the vector from the origin, the less stable, yet more discriminating the trait becomes (Yan et al, 2007).

Conclusions

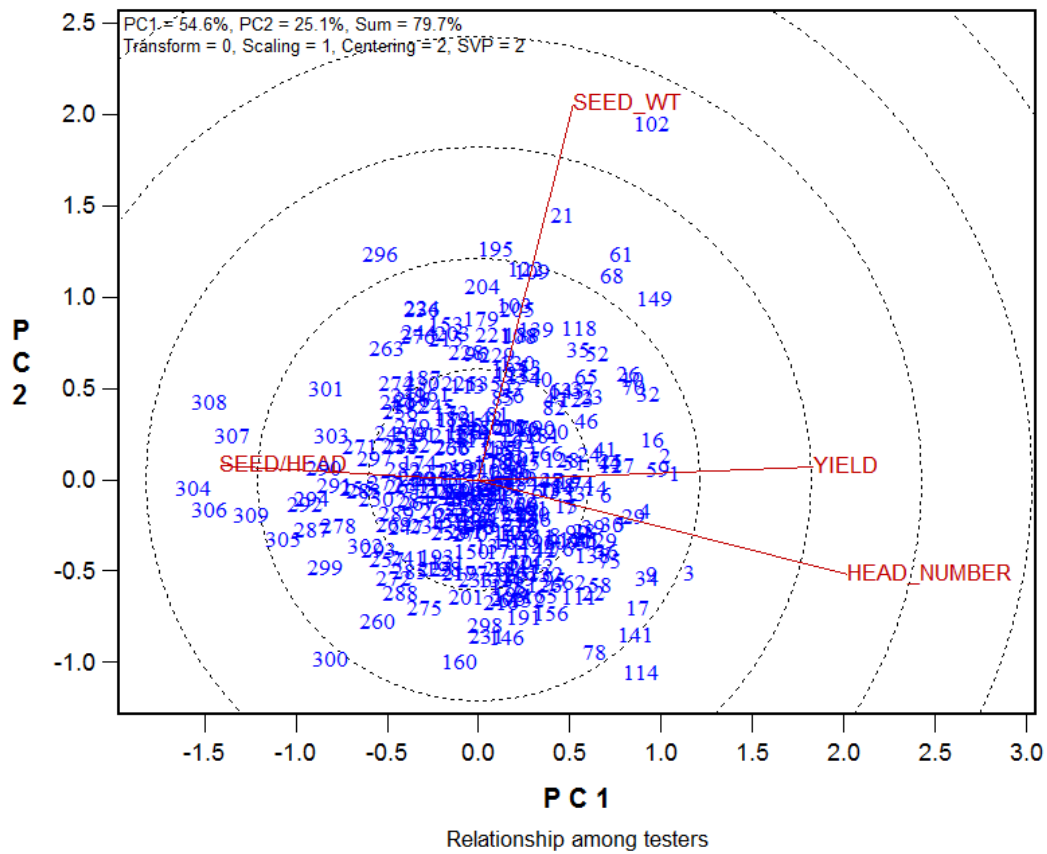
The majority of the F₂ populations tend to have a higher yield and its components than the inbred line checks. The data shows superiority of F₂ populations over the check cultivars. Though some heterosis is lost into the F₂ because of segregation, the presence of superiority is a good sign of vigor in the previous generation. It is very possible to use the F₂ with confidence in estimating heterosis for the F₁, as it is a good predictor as observed in previous studies (Martin et al., 1980).

Figure 3.3 GGE biplot based on trait means for the 2014 Amarillo F₂ (AF₂) populations.



Trait codes: YIELD = grain yield; HEAD_NUMBER = heads per unit area; SEED_WT = weight per individual seed; SEED/HEAD = number of seeds per head.

Figure 3.4 GGE biplot based on trait means for the 2014 College Station F₂ (CF₂) populations.



Trait codes: YIELD = grain yield; HEAD_NUMBER = heads per unit area; SEED_WT = weight per individual seed; SEED/HEAD = number of seeds per head.

CHAPTER V

SUMMARY

Gathering data on floral traits is a daunting and time consuming task, and previous literature upon other undertakings is almost nonexistent. Floral traits are reported to be highly heritable and quantitative, and thus are expected to be capable of improving by crossing superior selections (Singh and Joshi, 2003). These floral traits could become an integral part of the breeding process along with yield, if hybrid wheat becomes a common practice.

Weather influences floral characteristics in a way that researchers must take care in replicating trials each year, and conduct them across several environments. This would allow for the use of coefficient of variance (CV) and lsmeans to make accurate selections. However, the selections made in non-replicated 2014 using only the most superior performers proved to be quite stable in some characteristics when compared to 2015 data. Others were heavily influenced by the drastic weather differences, though as only expected by knowledge of previous research.

The data from the 2015 replicated floral study was used in analysis to determine reliable CV levels in the subject traits. These included stigma size, stigma featheriness duration, and stigma exertion for female traits, anther length, anther width, and anther extrusion for males, and heading date, anthesis date, spikelet tightness, and height for non-gender specific traits. Anther width, heading date, and spikelet tightness were not used during selection. The specified traits were then used for selecting lines whose

performance was equal to or above the averages. The 17 lines selected via traits with significant CVs and averages in the 2015 data will be moved onto seed increase and used for an experimental crossing block.

Early populations used to study heterosis provided excellent results. In both CF_2 and AF_2 , the top performers out-yielded some of TAM's prominent inbred germplasm. After examining the biplot and correlation analyses, it was concluded that there was a strong, positive correlation between head number and yield. Pearson's correlation also revealed that head number had the strongest direct effect on yield components, which agreed with earlier works (Akanda and Mundt, 1996).

Preliminary testing has yielded promising data. As work is conducted parallel to this study by fellow researchers, results only continuously justify focus on the creation of a hybrid wheat program. TAM germplasm possesses vastly diversified floral characteristics as well as prominent heterosis, with the ability to use the diverse F_2 generation for estimating heterosis in the F_1 population. The success of a program stemming from these early tests are very well within reach.

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APPENDIX

SAS code for LSMEANS, LSD, and CV values for 2015 floral data

```
data ;  
data floral15;  
options nodate;  
input Rep entry HD A GA SZ SFD SE ANL AW AE ST AWL HT;  
cards;  
  
proc glm;  
class rep entry;  
model HD A GA SZ SFD SE ANL AW AE ST AWL HT = rep entry;  
means entry/ lsd lines;  
lsmeans entry;  
ODS Graphics off;  
run;
```

SAS code for Pearson's correlation on 2015 floral characteristics

```
data ;  
input HD A GA SZ SFD SE ANL AW AE ST AWL HT;  
cards;  
  
;  
proc corr; var HD A GA SZ SFD SE ANL AW AE ST  
AWL HT;  
run;
```

SAS code for Pearson's correlation between yield components for CF₂ and AF₂ 2014

```
ods listing gpath="c:\temp";  
data CFcorr;  
input Yield Seed_wt Seed_head Headnumber;  
cards;  
  
proc corr; var Yield Seed_wt Seed_head Headnumber;  
run;
```

Startup File used for PathSAS

```
Title1 'testpathsas';
options nodate;
Data test;
Input nur$      number Yield Seed_wt      Seed_head      Head_number;
cards;

;
%inc 'pathsas.sas';
%pathsas (data=test,
indep=Seed_wt      Seed_head      Head_number,
dep0=Yield,
bylist=nur,
printreg=no,
printout=yes,
corrind=yes,
corrdep=yes,
boot=yes,
random=1234501,
samples=200
);
run;
```