

**SYNTHETIC HEXAPLOID WHEAT AS A SOURCE OF IMPROVEMENT FOR
WINTER WHEAT (*Triticum aestivum* L.) IN TEXAS**

A Thesis

by

JESSICA KAY COOPER

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

MASTER OF SCIENCE

December 2010

Major Subject: Plant Breeding

Synthetic Hexaploid Wheat as a Source of Improvement for
Winter Wheat (*Triticum aestivum* L.) in Texas
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Approved by:

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ABSTRACT

Synthetic Hexaploid Wheat as a Source of Improvement for Winter
Wheat (*Triticum aestivum* L.) in Texas. (December 2010)

Jessica Kay Cooper, Texas A&M University

Chair of Advisory Committee: Dr. Amir M.H. Ibrahim

Synthetic hexaploid wheats, created from a durum (*Triticum durum*) cross to *Aegilops tauschii* Coss. (McFadden and Sears, 1946), proved to be an efficient and beneficial source of new genes for common bread wheat (*Triticum aestivum* L.).

The purpose of this research was to evaluate the potential and performance of synthetic wheat in Texas. Ten elite primary synthetics from the International Maize and Wheat Improvement Center (CIMMYT), screened for desirable traits, were backcrossed to two Texas cultivars, TAM 111 and TAM 112. Populations were bulked and modified bulked to advance generations. Agronomic traits related to yield were determined on the F₄ and F₅ populations across five Texas locations.

Improvement was observed in South Texas and the Blacklands, which have more disease pressure and fewer intermittent dry spells than another two locations at Chillicothe and Bushland in Texas Rolling and High Plains, respectively. Selected bulks were not superior to non-selected bulks. Head number per unit area had the highest correlation with yield and seed weight was the most heritable trait. Synthetic lines combined better with TAM 111 than TAM 112 in high yielding environments.

Similar to crosses with spring wheat, synthetics contributed to yield through an increase in seed weight. Synthetic populations that produced higher grain yield than both TAM 111 and TAM 112 were able to maintain their large seed size and weight while improving their seed per head and head number traits. Poorer performance in environments with harsh winters could be due to a lack of winter-hardiness in the primary synthetics. This clearly demonstrates that improving yield, through utilization of common wheat by synthetic crosses, could result from selecting for larger seed per head and heads per unit area in lines driven from these populations.

Introgression of new genes through synthetic backcrosses could contribute to the improvement of wheat in particular regions of Texas. Primary synthetics and recurrent parents combining for superior hybrids were identified.

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NOMENCLATURE

BD	Bushland, TX
BH	Bulk hybrid method of breeding
CH	Chillicothe, TX
CIMMYT	International Maize and Wheat Improvement Center
CS	College Station, TX
Len	Leonard, TX
Mc	McGregor, TX
MB	Modified bulk method of breeding
Plains	Great Plains and Rolling Plains
RCBD	Randomized complete block design
SBC	Synthetic backcross
Stxbl	South Texas and the Blacklands
Syn	Primary synthetic hexaploid wheat

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CHAPTER I

INTRODUCTION

With a global yearly production of more than 620 million tons, wheat (*Triticum aestivum* L.) has become the world's greatest and most significant food crop for direct consumption (Williams, 1993). High nutritional value, good storing ability, and simple transporting ability make cereal crops an important food source. Cereal crops like wheat have provided mankind with its primary source of calories since the beginning of agriculture (Feuillet et al., 2008). Wheat is the most broadly grown cereal crop as it is currently produced in over 40 nations as far north as Norway and Russia and as far south as Argentina (Williams, 1993). The US ranks third in global wheat productions and exports 55 to 60 million tons of wheat a year, making up 40% of world wheat exports (www.fao.org). Winter wheat makes up about 70% of US wheat production and Texas is ranked third in harvested acres of winter wheat (www.nass.usda.gov). Some suggest the global demand of wheat to increase to 720 million tons by 2020 (Rajaram, 2001) while other estimates predict the demand to be as high as one billion (Rosegrant et al., 2007). To provide for these demands, advances must be made in the improvement of wheat to increase production. While wheat can be produced in many locations around the world, its productivity is severely limited by pathogens, insects and abiotic stresses.

This thesis follows the style of Crop Science.

To combat these destructive forces, breeders are looking for new sources of genetic variation in wheat. Genetic variability has been exhausted in wheat due to genetic bottlenecks wheat passed through in the process of evolution and domestication (Appels and Lagudah, 1990). Traditional breeding of crossing elite lines with one another has also lead to a smaller genetic pool (Appelsand Lagudah, 1990; Feuillet et al., 2008; Hajjarand Hodgkin, 2007; Valkoun, 2001). Fortunately, these lost genes can be restored and exploited for the improvement of wheat through crosses with wild ancestors. Breeding programs are beginning to see the benefits of incorporating wild genes into their adapted lines (Ortiz et al., 2008; Warburton et al., 2006).

One way of incorporating wild genes into modern wheat is through synthetic hexaploid wheat. This wheat is produced through the cross of durum wheat to one of the ancestors of wheat, *Aegilops tauschii* Coss. (Trethowanand van Ginkel, 2009). These synthetics can then be backcrossed to modern, adapted wheat lines resulting in adapted varieties with new genes for wheat improvement (Trethowanand Mujeeb-Kazi, 2008). Studies proved synthetic backcrosses to spring wheats show improvement over recurrent parents (del Blanco et al., 2000; Lage et al., 2004a; Mujeeb-Kazi et al., 2008; Villareal et al., 1994) but evidence of the benefits of synthetic backcrosses to winter wheat is meager (Narasimhamoorthy et al., 2006). Therefore, the goal of this study was to determine if synthetic wheat could improve yield of winter wheat, particularly in Texas. In this study, 10 primary synthetics were crossed and backcrossed to adapted Texas wheat lines, and measurements of yield and yield components in F₄ and F₅ populations were analyzed.

The objective of this research is to explore the potential and performance of synthetic wheat in Texas. The specific objectives are to: 1) Evaluate synthetic wheat in five Texas environments, 2) Compare the bulk hybrid versus modified bulk methods in advancing early bulks prior to line derivation, 3) Identify components that contribute to grain yield in synthetic wheat, and 4) Determine the heritability and combining ability of yield and its components in synthetic wheat.

CHAPTER II

REVIEW OF LITERATURE

Origin and domestication of common wheat (*Triticum aestivum* L.)

Cultivated wheat is made up of three ploidy levels; diploid, tetraploid, and hexaploid. Diploid species contains 14 chromosomes and are made up of the A genome. Tetraploid species, such as durum or emmer wheat, are made up of the A and B genome and contain 28 chromosomes. Common bread wheat (*Triticum aestivum* L.) is a hexaploid consisting of the two genomes A and B as well as a third D genome giving it a total of 42 chromosomes. Each genome of the *Triticeae* tribe contributes seven pairs of chromosomes (Gustafson et al., 2009b; Sears, 1952). Over the years, scientists have attempted to locate the origins of these genomes.

The diploid ancestor of wheat is commonly referred to as wild einkorn. About 10,000 years ago wild einkorn was domesticated near southeast Turkey in the Karacadag Mountains (Al Hakimi et al., 1998; Feuillet et al., 2008; Heun et al., 1997; Nesbitt and Samuel, 1998). Wild einkorn consist of two species: *T. monococcum* and *T. urartu* (Feldman, 2001). Studies have lead to the current conclusion that the species *T. urartu* is most likely the A-genome donor to hexaploid wheat as both species' A genomes are homologous and identical in some areas (Feuillet et al., 2008; Gustafson et al., 2009a). Identifying the B genome donor of hexaploid wheat has proven to be a difficult task. Due to the large size and extensive DNA change following ancestor divergence and formation of tetraploid species, the true donor of the B genome to hexaploid wheat has yet to be accredited (Gustafson et al., 2009a). The B genome is believed to be a

modified S genome from the Sitopsis section (Feuillet et al., 2008; Gustafson et al., 2009a; Kerby et al., 1988). Further conclusions have been difficult due to the close taxonomy of the Sitopsis section (Kerby et al., 1990). A 1956 study proved the donor to be an ancestor of *Ae. speltoides* Tausch and a later study suggested *Ae. speltoides* to be the maternal donor of tetraploid and hexaploid wheat (Sarkar and Stebbins, 1956; Wang et al., 1997). Despite evidence supporting *Ae. speltoides* as the origin of the B genome, other species of the Sitopsis section have also been identified as possible donors suggesting more research is needed to be sure of the B genome donor (Daud and Gustafson, 1996; Johnson, 1975; Kerby et al., 1990).

The donor of the D genome has been identified as *Aegilops tauschii* (Kihara, 1944). *Ae. tauschii* is composed of two subspecies; ssp. *strangulata* and ssp. *tauschii*. Many similarities may be seen from ancestors of these subspecies as gene flow is suggested to exist between them (Dvorak et al., 1998). The subspecies *strangulata* has been identified as the D genome donor to the main line of hexaploid wheat (Bushuk and Kerber, 1978; Nishikawa et al., 1992).

Feuillet describes the origin of hexaploid wheat to be the result of two main evolutionary events (Feuillet et al., 2008). In the first event, the diploid A genome donor hybridized with the unknown B genome donor to form a tetraploid wild emmer wheat (Gustafson et al., 2009a). Wild einkorn wheat and wild emmer wheat are both important in the history and origin of bread wheat but no evidence has been given proving one to be domesticated before the other (Nesbitt and Samuel, 1998). It has been suggested that einkorn was the first wheat species to be widely cultivated about 10,000 years ago

(Feuillet et al., 2008). Other reports identify emmer wheat to be the principle wheat in the Near East at that time (Gustafson et al., 2009a). Wild emmer is divided into a southern and northern population, both of which are genetically distinct (Luo et al., 2007). Most likely, the emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) was first domesticated in the Diyarbakir region in Southeast Turkey followed by another hybridization and introgression from wild to domesticated emmer wheat in southern Levant (Luo et al., 2007). These hybridization events eventually lead to the tetraploid *T. turgidum* ssp. *dicoccum* (Feuillet et al., 2008; Gustafson et al., 2009a; Gustafson et al., 2009b). In 2004, a study was conducted to determine a likely candidate for the female progenitor of bread wheat (Matsuoka and Nasuda). In this study, hybrids were produced under natural conditions between *Ae. tauschii* accessions and a durum wheat cultivar. Matsuoka and Nasuda concluded durum wheat to be a likely prospect for the unknown female progenitor of bread wheat (2004). Others give evidence for a younger species, *T. carthlicum*, as a possible AB genome donor but more proof is still needed to establish the tetraploid donor to hexaploid wheat (Bushuk and Kerber, 1978; Fukuda and Sakamoto, 1992; Kerber and Bendelow, 1977).

The second main evolution event was the hybridization of tetraploid wheat with the D genome donor *Ae. tauschii* (Feuillet et al., 2008). About 7,000 to 8,000 years ago, this hybridization of *T. turgidum* ssp. *dicoccum* and *Aegilops tauschii* gave rise to hexaploid wheat with three genomes (AABBDD) (McFadden and Sears, 1946; Zohary and Feldman, 1962). Most likely, this event took place in the southern Caspian Sea region (Nishikawa et al., 1992).

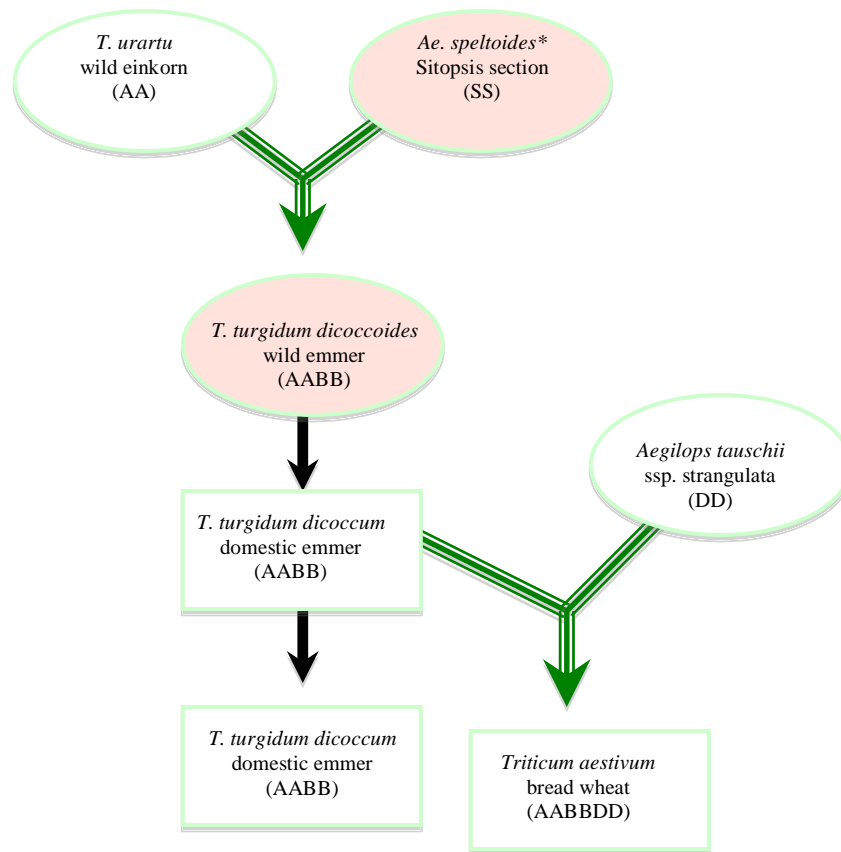


Figure 2.1 Proposed evolution of modern wheat. Wild ancestral species are circled, while domesticated species are in rectangles. Main hybridization events denoted by green triple line. Female progenitors are highlighted in pink. *True donor of B genome is unknown but thought to be ancestor of *Aegilops speltoides*.

Figure 2.1 shows the hybridization events in the evolution of wheat. In both occurrences of these hybridizations, doubling of the chromosomes allowed for fertile F_1 hybrids to develop and reproduce (Feuillet et al., 2008). Naturally occurring hybridizations have been occasionally found between *Ae. tauschii* and durum wheat with the complete 42 chromosomes and seed set suggesting hexaploid wheat was probably

formed recurrently by several hybridizations over time (Feldman, 2001; Fukuda and Sakamoto, 1992).

Need for genetic diversity in wheat

Over the past years, successful improvements in wheat and other cereals through extensive breeding programs have led to a narrowing of genetic diversity. This concerns breeders as the potential of genetic gain becomes more limited with a smaller genetic pool from which to choose beneficial genes (Feuillet et al., 2008). The hybridization events leading to modern hexaploid wheat caused a genetic drift because of partial isolation from the original parents (Feldman, 2001). This partial isolation existed due to barriers preventing gene flow from wild ancestors to their domesticated derivatives (Ladizinsky, 1985). Although it is still unclear if many or few initial hybridization events occurred in the evolution of wheat, the process of domestication caused many genes to be selected against and essentially narrowed the gene pool (Feldman, 1965; Fukuda and Sakamoto, 1992; Ladizinsky, 1985; Mujeeb-Kazi et al., 2008). Plucknett et al. observed a decrease in genetic diversity as high yielding varieties with exceptional adapting abilities were grown in lieu of original landraces (1983). This observation was also seen at the International Maize and Wheat Improvement Center (CIMMYT) with the release of high yielding varieties during the green revolution (Warburton et al., 2006). The authors give a precise account of the decrease in genetic variation of CIMMYT wheat from 1944 to 1982 and conclude the decrease was due to the high selection pressure as CIMMYT produced high yielding and highly adaptable wheat lines. Although these lines proved to be extremely beneficial,

worry began to spread about the fear of genetic uniformity and its associated threat of epidemics. Cox makes a valid point that while uniformity does not indefinitely lead to catastrophic epidemics worldwide and while diversity does not necessarily prevent such events from occurring, the benefits of diversity do provide some defense against new pathogen types (Cox et al., 1986).

Scientists are looking towards wild ancestors of wheat as a solution to a narrowing gene pool. In 1994, the International Center for Agriculture Research in Dry Areas (ICARDA) began a pre-breeding activity based on wild wheat relatives to help in the availability of genetically diverse collections (Valkoun, 2001). Valkoun suggested that wild species genes could be introgressed into cultivated wheats through homologous or homoeologous chromosome recombination (2001b). This is important in wheat as the three genomes of the hexaploid wheat contain chromosome pairs that are homoeologous to one another or share a similar genetic constitution (Sears, 1952). Hajjar and Hodgkin reviewed the use of wild relatives for production of new cultivars over the past twenty years and found nine new traits in wheat that have been contributed by wild relatives (2007). Many breeding strategies have utilized introgression of genes from wild relatives for crop improvement, specifically aimed at resistance (Feuillet et al., 2008; Trethowan and Mujeeb-Kazi, 2008). In 1958, Riley et al. suggested the use of *Aegilops* as a source of variation in wheat “since there are already two doses of this genus in the common wheat of our fields” (1958). Evidence has shown accessions of the D genome progeny, *Ae. tauschii*, to carry a wide range of disease resistance which will be beneficial to add to the current gene pool (Appels and Lagudah, 1990).

Synthetic wheat defined

Synthetic hexaploid wheat is an artificial hybridization between tetraploid wheat and an accession of *Aegilops tauschii*. The possibility of making synthetic hybrids was made feasible due to the invention of the colchicine technique. Colchicine is a poisonous alkaloid that inhibits chromosome segregation in mitosis. Therefore, applying it to haploid plants induces chromosomal doubling (Blakeslee and Avery, 1937). The first primary synthetic between a tetraploid wheat and *Aegilops tauschii* occurred in 1946 (Mc Fadden and Sears). It wasn't until many years later that wheat breeders began to see the benefits of utilizing these synthetics in their programs. The D genome donor, *Ae. tauschii*, is supported as a valuable parent to cross with tetraploid wheat because of its resistance to stresses and its efficiency in incorporating alien genes into wheat (Mujeeb-Kazi et al., 2008). Generally, the diploid parent will be crossed with durum as the tetraploid parent.

Although emmer wheats have more genetic diversity, durum has better agronomic type, which is why it is usually selected as the tetraploid parent (Luo et al., 2007; Trethowan and van Ginkel, 2009). Usually the tetraploid will be the female parent and the *Ae.* accession the male parent. If the reciprocal cross is made in which the *Ae.* accession is the female, the embryo is more difficult to work with and requires special media culturing (Valkoun, 2001). When making crosses it is usually necessary to treat triploid F₁ progeny with colchicine to double the chromosome number although some F₁ plants may originate spontaneously without such treatment (Valkoun, 2001). A primary synthetic will have low yield and poor quality traits (Trethowan and van Ginkel 2009).

When using the synthetics in breeding programs, it is desirable to have one or two backcrosses to the adapted parent in order to rid the progeny of unwanted genes (Trethowan and van Ginkel, 2009; Trethowan and Mujeeb-Kazi, 2008). In the case of using emmer wheat or another less adaptive tetraploid as a parent to the primary synthetic, a larger backcross population must be grown to allow for greater selection pressure to rid the population of negative genes (Trethowan and van Ginkel, 2009).

History and production of synthetic wheat at CIMMYT

Much of the current work and utilization of synthetic hexaploid wheats originated at CIMMYT in the 1980's (Ortiz et al., 2008). In response to the fear of uniformity at CIMMYT, breeders began looking for new sources to bring in resistance genes (Warburton et al., 2006). The first attempt at CIMMYT to use synthetics was brought about by a desire to breed for resistance to Karnal bunt. Soon after this success, more crosses were made as breeders realized the diversity and genetic potential of this source. CIMMYT was able to make over 1000 synthetic lines by the most widely used approach of crossing tetraploid durum to diploid *Ae. tauschii* (Ortiz et al., 2008). To develop these lines, *Ae. tauschii* accessions were first screened and identified according to desired breeding goals before random hybridization with *T. turgidum* cultivars took place (Mujeeb-Kazi et al., 2001). Over 500 synthetic hexaploids were grown in both Obregon and El Batan centers. After scoring the lines for morphological, growth, abiotic, and biotic characteristics, 95 elite hexaploids were chosen as the elite set I (Mujeeb-Kazi et al. 2000). These selected lines were distributed among breeding programs worldwide (Mujeeb-Kazi et al., 2008). In 2002, a second elite set of 33

synthetic hexaploids was characterized and shown to possess resistance to leaf, stem, and stripe rust along with other diseases (Mujeeb-Kazi and Delgado, 2001). After synthetics were introduced to CIMMYT programs, the genetic diversity measured was comparable to the original landraces used before the green revolution (Warburton et al., 2006) but with the added benefits of higher yields, host plant resistance, abiotic stress tolerance and sometimes better end-use quality (Ortiz et al., 2008).

Benefits of synthetic wheat

From the early beginnings of synthetic wheat utilization at CIMMYT and in other programs, many benefits have been observed in the field and lab. Gene introgression from wild ancestors was thought to be beneficial to modern cultivars by bringing in tough genes of defense against stresses of the surrounding environment.

This new genetic variability from the synthetic wheat has proven tolerant or resistant to biotic stresses. Major gene resistance for leaf rust and stem rust, a common problem in Texas, has been found in synthetic wheat (Innes and Kerber, 1994; Kerber and Dyck, 1969). Friesen et al. observed seedling resistance to stem rust in all 46 synthetic lines tested (2008). Other studies have found resistance to stripe rust in the D genome parent as well as the tetraploid parent (Assefa and Fehrman, 2004; Ma et al., 1995a). In some crosses, parents with high resistance to rust produced synthetic hexaploids with no resistance or much lower resistance (Assefa and Fehrman, 2004; Kema et al., 1995; Ma et al., 1995b). Kema et al. and Ma et al. both suggest the presence of suppressor genes in one parent corresponding to the lack of expression from the other parent (1995; 1995a). More research is needed to fully understand the suppression in these

primary synthetics. Despite these observations of suppression, synthetic wheat is still a potential source for more resistance to rust as novel genes in these crosses have yet to be exploited (Trethowan and van Ginkel, 2009). Tadesse et al. reported resistance genes to tan spot in synthetic wheat lines (2006; 2007). Immunity to Karnal bunt was reported in 49 percent of synthetics evaluated (Villareal et al., 1994). Cox et al. studied *Ae. tauschii* accessions for resistance to leaf rust, stem rust, tan spot, and powdery mildew. Among the accessions, 30 percent were resistant to two or more of the diseases while 12 percent were resistant to at least three of the four diseases (Cox et al., 1992). Pests can be a large problem in the fields as they may reduce the quantity and quality of the grain. Resistance to pests such as Russian wheat aphid (Lage et al., 2004a; Lage et al., 2004b), greenbug (Lage et al., 2003) and Hessian fly (Cox and Hatchett, 1994; Friesen et al., 2008; Sardesai et al., 2005), all common biotic stress problems in Texas, has been identified in synthetic wheat lines. Ogbonnaya et al. studied 253 synthetic hexaploid wheats produced from 192 *Ae. tauschii* accessions and 39 durum cultivars to screen for resistance to a number of diseases. Among the diverse collection, resistance of some kind was found for cereal cyst nematode, root lesion nematode, *Stagonospora nodorum* blotch, *Septoria tritici* blotch, and leaf, stem and stripe rusts (Ogbonnaya et al., 2008). Resistance has been summarized in the following table showing sources of resistance found in the *Ae. tauschii* parent, both parents, or the synthetic lines (Table 2.1).

Table 2.1 Biotic resistance in synthetic hexaploid wheat.

Biotic Stress	Disease or Pest	Reference	Source of Resistance
Rust	Leaf Rust	Innes & Kerber 1994	Ae. tauschii
		Kerber & Dyck 1969	Synthetic Hexaploid
		Cox et al. 1992	Ae. tauschii
		Ogbonnaya et al. 2008	Synthetic Hexaploid
	Stem Rust	Innes & Kerber 1994	Ae. tauschii
		Assefa & Fehrman 2004	Synthetic Hexaploid
		Cox et al. 1992	Ae. tauschii
		Friesen et al. 2008	Synthetic Hexaploid
		Ogbonnaya et al. 2008	Synthetic Hexaploid
	Stripe Rust	Ma et al. 1995 Ogbonnaya et al. 2008	Both parents of SH Synthetic Hexaploid
Nematodes	Cereal Cyst Nematode	Ogbonnaya et al. 2008	Synthetic Hexaploid
	Root Lesion	Ogbonnaya et al. 2008	Synthetic Hexaploid
Virus	Barley Yellow Dwarf	Saffdar et. al 2009	Synthetic Hexaploid
	Soil-borne Wheat Mosaic	Hall et al. 2009	Ae. tauschii
Leaf Spot Diseases	Spot Blotch	Mujeeb-Kazi et al. 2007	Ae. tauschii
	Stagonospora Nodorum	Friesen et al. 2008	Synthetic Hexaploid
		Ogbonnaya et al. 2008	Synthetic Hexaploid
	Septoria Tritici blotch	Ogbonnaya et al. 2008	Synthetic Hexaploid
	Tan Spot	Cox et al. 1992 Friesen et al. 2008 Tadesse et al. 2006,2007	Ae. tauschii Synthetic Hexaploid Synthetic Hexaploid
Other Fungal Diseases	Powdery Mildew	Cox et al. 1992	Ae. tauschii
	Karnal Bunt	Mujeeb-Kazi et al. 2006 Villareal et al. 1994	Synthetic Hexaploid Synthetic Hexaploid
Insects	Russian White Aphid	Lage et al. 2004	Synthetic Hexaploid
	Hessian Fly	Friesen et al. 2008 Cox et al. 1994	Synthetic Hexaploid Ae. tauschii
	Greenbug	Lage et al. 2003	Synthetic Hexaploid

Along with biotic stress tolerance and resistance, the utilization of synthetic hexaploid wheat brings more genes of abiotic stress defense into the gene pool. Studies have shown synthetic derived lines to perform better than recurrent parents under drought stress, a common problem in Texas High Plains, as well as heat stress, a common problem in South Texas (del Blanco et al., 2000; Reynolds et al., 2007; Trethowan and Mujeeb-Kazi, 2008). Reynolds et al. attributed synthetic lines to be better adapted to drought because of increased partitioning of root mass to deeper soil profiles allowing for more water extraction from greater depths (2007). Trethowan and Mujeeb-Kazi also attributed better performance of synthetics to be a result of deeper roots (2008). A study of 30 synthetic lines showed synthetic derivatives to be useful for improving wheat in areas of frequently occurring heat stress (Yang et al., 2002). Yang et al. concluded synthetics could be useful in regions with repeatedly high temperatures as the study proved that grain yield, chlorophyll content, and kernel weight of synthetic lines were negatively correlated with heat-susceptibility index under high temperature conditions (2002). Synthetic-derived lines in a study by del Blanco et al. had higher maximum photosynthetic rates than their respective recurrent parents (2000). In a study of synthetic derivatives across various environments, Gororo et al. found relatively higher yields than the recurrent parents when grown in the lowest yielding environments (2002). The reason for this higher performance was due to increased rates of grain filling and larger grains. These studies suggest synthetic wheat to have great potential for improving wheat yield in low yielding, drought stressed and or heat stressed environments.

Yield and yield components

Numerous physiological, morphological, and phenological traits have been identified to be associated with grain yield. Most of the work in improving yield potential has been focused on increasing both source and sink of the plant. To improve source breeders focus on physiological traits such as photosynthetic rate, leaf conductance, and transpiration efficiency. Focus on morphological traits of wheat provide for improvement in sink, or grain number (Reynolds et al., 1999). Many studies have evaluated yield components and their correlation with yield in synthetic and other wheats (Bhatt, 1973; Calderini and Ortiz-Monasterio, 2003; del Blanco et al., 2001; Narasimhamoorthy et al., 2006; Sayre et al., 1997; Slafer and Araus, 2007).

It has been reported that genetic gain in yield potential of wheat has been a result of increase in number of grain, while grain weight hasn't changed significantly (Slafer et al., 1994). In a study of short bread wheat lines, Sayre et al. (1997) found higher yield to be correlated with seed per unit area. Calderini et al. reported similar findings in a study of wheat cultivars representing different eras of breeding, in which improvement was generally attributed to seed per unit area (1995). However, the study showed most recent cultivars to have an increase in yield due to increases in kernel weight. Synthetics generally have greater kernel weights than conventional cultivars (Reynolds et al., 2007). Del Blanco et al. (2001) studied 282 lines from synthetic backcrosses to spring wheat and found over 80 percent had significantly greater kernel weights than recurrent parents. It was suggested that synthetics might be a source of alleles for increased kernel weight leading to a possible increase in yield. In a study of a hard red winter wheat

'Karl 92' backcrossed twice to a primary synthetic, Narasimhamoorthy et al. found means to be greater than the recurrent parent for yield and tiller number but lower for kernel weight (2006). Yield components are important for improving yield but Reynolds suggests all traits associated with yield must be taken into consideration when aiming to improve yield potential and production of wheat (1999).

Path coefficient analysis

As yield is influenced by a number of independent variables, it is assumed that interdependence among such variables exists (Ofori, 1996). For this reason, simple correlation coefficients will not suffice in providing accurate information regarding selection strategies.

Another statistical method of analyzing the effects of independent variables on a dependent variable is path coefficient analysis. Path coefficient analysis separates the correlation coefficient into components of direct and indirect effects (Dewey and Lu, 1959). From this analysis, conclusions can be made regarding the relative importance of such effects.

Bhatt showed the importance of using path coefficient analysis to accurately view character associations and their effects on the primary character (1973). In this study, simple correlation gave a misleading view of plant height having an insignificant effect on yield. Path coefficient analysis proved height to be an important variable due to negative associations with other traits. Other studies have used path coefficient analysis to accurately view associations between yield and yield components (Akanda and Mundt, 1996; Cramer and Wehner, 1998; Mohsin et al., 2009; Ofori, 1996).

Ofori used path coefficient analysis to determine the direct and indirect effects of yield components on seed yield of Bambara groundnut (*Vigna subterranea* L.). Path coefficient analysis showed seed weight to have a positive direct effect on yield but indirect negative effects via other yield components caused the total correlation to be negative. Akunda and Mundt studied the effect of stripe rust on yield of winter wheat cultivars using path coefficient analysis (1996). Results indicated the total negative correlation between rust and yield to be the result of indirect effects through yield components, while the direct effect of rust was insignificant. Studies such as these show the benefit of path coefficient analysis in determining how traits influence other traits through direct and indirect pathways.

Gene action and combining ability

General and specific combining ability were established by Sprague and Tatum (1942). General combining ability (GCA) describes the average performance of a line and is measured as the deviation of its progeny mean from the mean of all lines used in the trial. Specific combining ability (SCA) describes how a cross performs relatively better or worse than the expected outcome based on the average performance of the lines involved. GCA is associated with additive gene action while SCA is associated with non-additive gene action or gene effects of dominance and epistasis. Combining ability allows for breeders to identify the best parents or parental combinations for hybridization. It is also a good technique for understanding the nature of quantitatively inherited traits such as yield (Kronstad and Foote, 1964).

Several authors have investigated combining ability for different traits in wheat (Dagustu, 2008; Kronstad and Foote, 1964; Murphy et al., 2008; Widner and Leebsock, 1973; Zwart et al., 2004). Kronstad and Foote (1964) reported positive GCA effects for yield components in a study of 10 winter wheat lines and concluded much of the genetic variability for yield and yield components to be due to additive gene action. Zwart et al. (2004) compared five synthetic wheats showing high resistance to root-lesion nematode resistance to susceptible wheat cultivars. They found GCA was more important than SCA and reported resistance to be inherited through additive gene action. Murphy et al. (2008) studied seven winter wheats for coleoptiles length and found a decrease in SCA/GCA ratio with each generation (0.15, 0.11, 0.06, and 0.04 in F_1 through F_4 , respectively), indicating additive effects increased with homozygosity. Widner and Leebsock (1973) studied F_1 and F_2 populations from a diallel cross among 10 durum varieties. They found GCA significance for all traits measured and SCA significance for kernel weight, test weight, and seedling vigor. They concluded that maximum yields could be attained only through exploitation of both additive and non-additive genetic effects. Dagustu (2008) also concluded both gene actions to be important. In this study of agronomic traits of 42 hybrid wheat lines, genetic variation was reported to be due primarily to additive gene effects along with some non-additive effects in height, grain yield per spike, and thousand kernel weight.

CHAPTER III

EVALUATION OF SYNTHETIC BACKCROSS POPULATIONS IN TEXAS

Introduction

Wheat (*Triticum aestivum* Desf.) is the most broadly grown cereal crop in the world and provides a necessary source of calories for human consumption (Feuillet et al., 2008; Williams, 1993). In order to produce yield in such a broad array of climates, wheat cultivars must be adapted to their environments. In Texas, winter wheat is the predominant wheat crop. Heat stress, drought stress, disease, and pests limit the yield of wheats in Texas. Cultivar performance varies throughout the state because some stresses are more common in certain regions of the state than in others. Breeders are constantly seeking resistance to these stresses through genetic improvements.

Synthetic hexaploid wheats have recently been used in breeding programs as a source of genetic improvement. Studies have shown benefits of synthetics through disease resistance (Cox et al., 1992), pest resistance (Cox and Hatchett, 1994; Lage et al., 2003), and drought and heat tolerance (del Blanco et al., 2000; Reynolds et al., 2007; Trethowan and Mujeeb-Kazi, 2008). Studies have also shown the importance of backcrossing at least once to adapted parents to allow for undesired genes to be discarded (Trethowan and Mujeeb-Kazi, 2008).

The main objective in this study was to evaluate the performance of synthetic wheat in Texas environments. Two breeding methods were compared: modified bulk and bulk hybrid. Synthetics were backcrossed to elite Texas lines which were planted as checks in all environments.

Materials and methods

Plant material- primary synthetics

Ten primary synthetic lines were selected as the donor parents for this study. These lines were chosen from elite sets produce by CIMMYT. Elite set I consisted of 95 synthetic lines selected from primary synthetics grown in El Baton and Obregon, Mexico beginning in 1995. These lines were chosen based upon morphological, growth, abiotic, and biotic tolerance characteristics (Mujeeb-Kazi et al., 2000). The second elite set consisted of 33 synthetic hexaploids shown to possess resistance to leaf, stem, and stripe rust along with other diseases (Mujeeb-Kazi and Delgado, 2001). In this study, 8 synthetic lines were chosen from CIMMYT's elite set I and 2 synthetic lines were chosen from elite set II (Table 3.1).

Table 3.1 Pedigrees of synthetic hexaploid wheats from CIMMYT elite sets.

Syn	Syn- code	Pedigree
S1	4152-5	ALTAR 84/ <i>Ae. tauschii</i> (198)
S2	4152-7	ALTAR 84/ <i>Ae. tauschii</i> (205)
S3	4152-16	ALTAR 84/ <i>Ae. tauschii</i> (219)
S4	4152-37	68.111/RGB-U//WARD/3/FGO/4/RABI/5/ <i>Ae. tauschii</i> (629)
S5	4152-51	PBW114/ <i>Ae. tauschii</i>
S6	4152-61	GAN/ <i>Ae. tauschii</i> (408)
S7	4152-77	RASCON/ <i>Ae. tauschii</i> (312)
S8	4152-78	SCOT/MEXI 1// <i>Ae. tauschii</i> (314)
S9	4153-3	Dverd 2/ <i>Ae. tauschii</i> (214)
S10	4153-31	CETA/ <i>Ae. tauschii</i> (417)

Code and pedigrees according to Mujeeb-Kazi et al. (2000) and Mujeeb-Kazi and Delgado (2001). *Ae. tauschii* accession number from CIMMYT's wide crosses working collection is in parentheses.

Plant material- recurrent parents

‘TAM 111’ is a medium maturing, awned white chaffed, semi-dwarf hard red winter wheat (HRW). It was released in April of 2002 with resistance for stripe rust and stem rust (Lazar et al., 2004). ‘TAM 112’ HRW is adapted to the south and central Great Plains and was released in 2005. It has the *Lr41* gene for leaf rust resistance and has greenbug resistance based on *Gb3* (Rudd et al., 2004).

Synthetic backcross and breeding methods

Ten primary synthetic lines from CIMMYT (Table 3.1) were crossed to TAM 111 and TAM 112 in 2004. These lines were backcrossed to their respective recurrent parents, TAM 111 or TAM 112. The BCF₂ populations were grown in Chillicothe, TX. From the BCF₂ populations, heads were selected based on best plant type and grown as head- rows in the BCF₃ generation using the Modified Bulk (MB) breeding method. Remaining F₂ heads of each population were bulked and advanced to the BCF₃ and BCF₄ generations using the Bulk Hybrid (BH) breeding method. Head- rows of good plant type from BCF₃-MB populations were combined and advanced to BCF₄-MB. The F₄ populations of both breeding methods were bulked to F₅ populations with no selection. Table 3.2 gives an account of the recurrent and donor parents used in each synthetic backcross line.

Table 3.2 Parents of synthetic backcross wheat lines.

Entry	Line	Donor Parent	Recurrent parent
3	SBC01	S1	TAM 111
4	SBC02	S2	TAM 111
5	SBC07	S3	TAM 111
6	SBC17	S4	TAM 111
7	SBC24	S5	TAM 111
8	SBC31	S6	TAM 111
9	SBC34	S7	TAM 111
10	SBC35	S8	TAM 111
11	SBC38	S9	TAM 111
12	SBC46	S10	TAM 111
13	SBC49	S1	TAM112
14	SBC50	S2	TAM112
15	SBC51	S3	TAM112
16	SBC57	S4	TAM112
17	SBC59	S5	TAM112
18	SBC60	S6	TAM112
19	SBC64	S7	TAM112
20	SBC65	S8	TAM112
21	SBC67	S9	TAM112
22	SBC71	S10	TAM112
23	SBC01MB	S1	TAM 111
24	SBC02MB	S2	TAM 111
25	SBC07MB	S3	TAM 111
26	SBC17MB	S4	TAM 111
27	SBC24MB	S5	TAM 111
28	SBC31MB	S6	TAM 111
29	SBC34MB	S7	TAM 111
30	SBC35MB	S8	TAM 111
31	SBC38MB	S9	TAM 111
32	SBC46MB	S10	TAM 111
33	SBC49MB	S1	TAM112
34	SBC50MB	S2	TAM112
35	SBC51MB	S3	TAM112
36	SBC57MB	S4	TAM112
37	SBC59MB	S5	TAM112
38	SBC60MB	S6	TAM112
39	SBC64MB	S7	TAM112
40	SBC65MB	S8	TAM112
41	SBC67MB	S9	TAM112
42	SBC71MB	S10	TAM112

Layout and experimental design

Populations originating using either MB or BH methods were termed SBCF₄ (BCF₄ and BCF₄-MB) and SBCF₅ (BCF₅ and BCF₅-MB), and were both grown in the field at Bushland (latitude = 35.2°N, longitude = 102.1°W), Chillicothe (latitude = 34.2°N, longitude = 99.5°W), College Station (latitude = 30.5°N, longitude = 96.4°W), McGregor (latitude = 31.4°N, longitude = 97.4°W), and Leonard (latitude = 33.4°N, longitude = 96.2°W), TX. Seeds were planted at a rate of 60 pounds per acre in seven rows with a plot size of 10.8 feet by 4 feet. Entries were laid out in a randomized complete block design (RCBD) with two replications. Experiments were planted in October or November and combine harvested from Late May to June. All SBCF₄ and SBCF₅ locations contained a total of 84 plots according to the calculation below:

$$(10 \text{ synthetics}) \times (2 \text{ TAM lines}) \times (2 \text{ reps}) \times (2 \text{ breeding methods}) + (2 \text{ checks}) = 84.$$

Measurements- yield and test weight

Grain yield (GY) and test weight (TW) of all populations were recorded. In locations in which samples were taken, the sample weight (SW) was added to the gram yield to get total grain yield (TGY). Total gram yields were multiplied by factor 0.0369 to convert grams per plot to bushels per acre (Yield).

Measurements- heading date

Heading date notes were taken in rep one of McGregor and College Station populations. Heading date was recorded as days from January 1 when the head on 50 percent of the wheat plants had completely emerged from the boot.

Measurements- height

Average heights in inches were taken on the first rep at College Station and McGregor. Measurements were taken from soil surface to spike tips, excluding awns.

Measurements- leaf rust

Leaf rust notes were taken in early April of 2010 at College Station and in late April of 2010 at McGregor. Measurements were assigned according to average observations of flag leaf. A scale of 0-9 was used at College Station, with 0 being fully resistant and 9 being fully susceptible. At McGregor, disease severity and host response were combined into a coefficient of infection and calculated according to Roelfs et al. (1992).

Measurements- yield components from sample heads

Random samples of 100 heads were collected from each plot one week before harvest in College Station, McGregor, and Leonard. Samples from each plot were collected in labeled bags and recounted before thrashed. Each head was thrashed using a 110 volt Wheat Head Thrasher (Precision Machine Inc; Paducah, Kentucky, USA). Samples were then cleaned by hand and weighed. If samples contained less than 100 heads, it was noted for later calculations. No samples contained more than 100 heads. Five hundred kernels were randomly counted from each thrashed sample using a model

750-2 Totalize Unit seed counter. Weights were doubled to produce thousand kernel weight (TKW). The following calculations were accomplished using thousand kernel weight, sample weight, number of tillers per sample (T), and total gram yield.

$$\text{Seed Weight (Seed wt)} = \text{TKW} / 1000$$

$$\text{Seed per head (Seed/head)} = \text{SW} / (\text{KW} \times \text{T})$$

$$\text{Heads per plot (Head no)} = \text{TGY} \times (\text{T}/\text{SW})$$

Statistical analysis

Measurements were managed and analyzed in AGROBASE II (Agronomix Software Inc.). The data was also analyzed using Microsoft Excel and SAS version 9.2 (SAS Institute Inc., 2008). Individual and combined locations were analyzed as randomized complete block design with PROC GLM in SAS. Using AGROBASE, nearest-neighbor adjusted means were calculated for the recurrent parents and all populations according to Wilkinson et al. to adjust for variability within environments (1983).

Results and discussion

Environments combined and analyzed

The trial consisted of 40 synthetic backcross lines across five locations and two years. Gomez and Gomez (1984) described testing homogeneity of error variance between years and locations before combining data. Hartley's test for homogeneity of variance was performed across years and locations (Peterson, 2004). Results showed

significance when all locations and years were combined indicating data could not be combined across all environments for analysis.

Bushland and Chillicothe are located in the High and Rolling Plains of Texas, respectively, and are classified as having a semi-arid climate. Compared to other regions of Texas, the northern plains have colder winters and are more prone to drought. Average monthly temperatures and total precipitation of Bushland and Chillicothe during 2009 and 2010 proved this to be true. Bushland and Chillicothe had the least amount of rain compared to other locations in the study and temperatures were generally lower (A-1,2).

College Station, McGregor, and Leonard are located in South Texas and the Blacklands regions. These regions are classified as having a humid, subtropical climate. Compared to the High and Rolling Plains, these regions have warmer temperatures and more moisture. The average rainfall per month in each location was greater than Bushland or Chillicothe for both years (A-2). Average monthly temperatures of these locations were generally higher than Bushland and Chillicothe locations (A-1). In 2009, temperatures in Chillicothe were similar to College Station, McGregor, and Leonard, but precipitation was much lower.

Due to climate similarities, Bushland and Chillicothe were grouped to represent the High and Rolling Plains regions of Texas (Plains), and College Station, McGregor, and Leonard were grouped to represent South Texas and the Blacklands (Stxbl). These environments were analyzed according to the Hartley's test and variances were not

significantly different within groups. Normality tests of each location by year proved data to be normal.

Breeding methods analyzed

Split plot analysis of variance mean was performed to determine if breeding method was significant. In the Plains region, results showed the main effect of breeding method was not significant ($P = 0.5$) but lines were significant ($P < 0.0001$) for yield (Table 3.3). Similar results were observed for yield and yield components in the Stxbl region (Tables 3.4 – 3.7). Because lines were derived according to separate breeding methods and interaction between line and breeding method was significant in most traits, breeding methods were not combined for analysis.

Reasons for this outcome may be due to the environment in which selections were made. All selections were made in Chillicothe, TX. At the time of selecting, Chillicothe had very low disease pressures causing selections for resistance to be near impossible. Also, Chillicothe was the only location used for these early generations and did not represent all environments later used in the study. If early generation selections were made in an environment with high disease pressure, results may have shown a significant difference.

Table 3.3 Split plot analysis of variance of mean grain yield of synthetic backcross wheat lines in Bushland and Chillicothe during 2009 and 2010.

Source	df	SS	MS	F value	P value
Year	1	33288.72	33288.72**	2841.20	<.0001
Loc	1	11589.71	11589.71**	989.18	<.0001
rep(year*loc)	5	8690.44	1738.09**	148.35	<.0001
Bmethod [¶]	1	15.75	15.75	0.94	0.5098
rep*Bmethod	1	16.74	16.74	1.43	0.2329
Line	7	365.76	52.25**	4.46	<.0001
Bmethod*Line	7	268.79	38.40**	3.28	0.0023
R²	0.94				
CV	13.10				
Root MSE	3.42				
Grand mean	26.13				

[¶]Bmethod = breeding method.

** Significant at the 0.01 probability level

Table 3.4 Split plot analysis of variance of mean grain yield of synthetic backcross wheat lines in College Station, McGregor, and Leonard during 2009 and 2010.

Source	df	SS	MS	F value	P value
Year	1	166.15	166.15	3.58	0.059
loc	2	24757.46	12378.73**	266.94	<.0001
rep(year*loc)	8	13829.74	1728.72**	37.28	<.0001
Bmethod [†]	1	13.07	13.07	0.65	0.5685
rep*Bmethod	1	20.17	20.17	0.43	0.5099
Line	7	2434.06	347.72**	7.50	<.0001
Bmethod*Line	7	300.23	42.89	0.92	0.4867
R²	0.66				
CV	18.62				
Root MSE	6.81				
Grand mean	36.57				

[†]Bmethod = breeding method.

** Significance at the 0.01 probability level

Table 3.5 Split plot analysis of variance of seed weight (g) of synthetic backcross wheat lines in College Station, McGregor, and Leonard during 2009 and 2010.

Source	df	SS	MS	F value	P
year	1	0.0074466	0.0074466**	1234.67	<.0001
loc	2	0.00104968	0.00052484**	87.02	<.0001
rep(year*loc)	8	0.00156511	0.00019564**	32.44	<.0001
Bmethod [†]	1	2.61E-06	2.61E-06	0.23	0.715
rep*Bmethod	1	0.00001129	0.00001129	1.87	0.172
Line	7	0.00036864	0.00005266**	8.73	<.0001
Bmethod*Line	7	0.00015105	0.00002158**	3.58	0.0009
R²	0.795326				
CV	8.206733				
Root MSE	0.002456				
Grand Mean	0.029925				

[†]Bmethod = breeding method.

** Significance at the 0.01 probability level

Table 3.6 Split plot analysis of variance of mean head number of synthetic backcross wheat lines in College Station, McGregor, and Leonard during 2009 and 2010.

Source	df	SS	MS	F value	P value
year	1	14299426.7	14299426.7**	249.96	<.0001
loc	2	35787079.7	17893539.9**	312.79	<.0001
rep(year*loc)	7	4223661.22	603380.17**	10.55	<.0001
Bmethod [†]	1	175648.84	175648.84	8.19	0.214
rep*Bmethod	1	21437.46	21437.46	0.37	0.541
Line	7	1862452.82	266064.69**	4.65	<.0001
Bmethod*Line	7	812622.94	116088.99*	2.03	0.050
R²	0.69				
CV	19.11				
Root MSE	239.18				
Grand Mean	1251.37				

[†]Bmethod = breeding method.

* Significance at the 0.05 probability level

** Significance at the 0.01 probability level

Table 3.7 Split plot analysis of variance of mean seed per head of synthetic backcross wheat lines in College Station, McGregor, and Leonard during 2009 and 2010.

Source	df	SS	MS	F value	P value
year	1	44.35	44.35	3.27	0.0714
loc	2	2860.40	1430.20**	105.31	<.0001
rep(year*loc)	8	5222.76	652.84**	48.07	<.0001
Bmethod [†]	1	155.61	155.61	9.24	0.2023
rep*Bmethod	1	16.84	16.84	1.24	0.2661
Line	7	1774.30	253.47**	18.66	<.0001
Bmethod*Line	7	315.80	45.11**	3.32	0.0018
R²	0.63				
CV	13.08				
Root MSE	3.69				
Grand Mean	28.17				

[†]Bmethod = breeding method.

** Significance at the 0.01 probability level

Significance of environments

Analysis of variance of mean grain yield was performed across years and locations of the Plains region. Tests were repeated for yield and its components across years and locations of the Stxbl region. All results showed years and locations to be significant (Tables 3.8 - 3.12). For this reason, data is presented within each location by year as well as across years and locations of the Plains and Stxbl regions.

Table 3.8 Analysis of variance of mean grain yield for synthetic backcross wheat lines in Bushland and Chillicothe, TX during 2009 and 2010.

Source of variation	df	MS	σ^2
Locations	1	12445.29**	
Years	1	35417.95**	
Replications in years and locations	1	581.09**	
Year x Locations	1	8551.68**	
Lines	41	49.61**	4.28
Lines x Years	41	12.3**	
Lines x locations	41	18.64**	
Lines x years x locations	41	15.59*	
Error	167	8.39	
Phenotypic variance			12.67
$h^2=0.338$			

** Significant at the 0.01 probability level

* Significance at the 0.05 probability level

Table 3.9 Analysis of variance of mean grain yield for synthetic backcross wheat lines in College Station, McGregor and Leonard, TX in 2009 and 2010.

Source of Variation	df	MS	σ^2
Locations	2	12963.95**	
Years	1	247.1**	
Replications in years and locations	2	917.46**	
Year x Locations	2	6573.41**	
Lines	41	147.46**	-4.17
Lines x Years	41	198.82**	
Lines x locations	82	32.43*	
Lines x years x locations	82	33.77*	
Error	250	23.83	
Phenotypic variance			19.66
$h^2 = -0.212$			

** Significant at the 0.01 probability level

* Significance at the 0.05 probability level

Table 3.10 Analysis of variance of mean head number for synthetic backcross wheat lines in College Station, McGregor and Leonard, TX in 2009 and 2010.

Source of Variation	df	MS	σ^2
Locations	2	19528946.2**	
Years	1	14250275.3**	
Replications in years and locations	2	226705.7**	
Year x Locations	2	2211790.8**	
Lines	41	188094.5**	6939.0
Lines x Years	41	124044.3**	
Lines x locations	82	49460.3 ^{NS}	
Lines x years x locations	82	68677.5**	
Error	250	38577.7	
Phenotypic variance			45516.6
$h^2 = 0.152$			

** Significant at the 0.01 probability level

Table 3.11 Analysis of variance of mean seed per head for synthetic backcross wheat Lines in College Station, McGregor and Leonard, TX in 2009 and 2010.

Source of Variation	df	MS	σ^2
Locations	2	1600.64**	
Years	1	51.69*	
Replications in years and locations	2	137.05**	
Year x Locations	2	2635.86**	
Lines	41	63.3**	3.52
Lines x Years	41	24.98**	
Lines x locations	82	13.05 ^{NS}	
Lines x years x locations	82	16.92**	
Error	250	10.54	
Phenotypic variance			14.06
$h^2=.25$			

** Significant at the 0.01 probability level

* Significance at the 0.05 probability level

Table 3.12 Analysis of variance of mean seed weight (g) for synthetic backcross wheat Lines in College Station, McGregor and Leonard, TX in 2009 and 2010.

Source of Variation	df	MS	σ^2
Locations	2	0.5443**	
Years	1	7.50232**	
Replications in years and locations	2	0.20289**	
Year x Locations	2	0.67037**	
Lines	41	0.0369**	0.002388
Lines x Years	41	0.00904**	
Lines x locations	82	0.00414 ^{NS}	
Lines x years x locations	82	0.00494 ^{NS}	
Error	250	0.00486	
Phenotypic variance			0.007248
$h^2=.329$			

** Significant at the 0.01 probability level

Mean square and variance values are 10^{-3}

Table 3.13 Grain yield mean (bu/ac) of synthetic backcross wheat lines in Bushland and Chillicothe, TX during 2009 and 2010.

Entry	Line	Mean yield	Bushland		Mean	Chillicothe		
			2009	2010		2009	2010	Mean
1	TAM 111	33.5	19.5	34.5	27	27.4	53.5	40.5
2	TAM 112	34.4	24.6	33.6	29.1	26.6	51.8	39.2
3	SBC01	24	16.6	22.6	19.6	13.4	41	27.2
4	SBC02	25.1	14.9	25.3	20.1	16.1	44.6	30.4
5	SBC07	25	13.5	30.4	22.0	19.1	36.6	27.9
6	SBC17	27.3	16.4	28.1	22.3	19.8	49.5	34.7
7	SBC24	24.6	12.9	25.4	19.2	16.4	46.5	31.5
8	SBC31	25.7	14.6	27.9	21.3	15.5	41.5	28.5
9	SBC34	22.6	12	25.8	18.9	11.7	40.4	26.1
10	SBC35	24.7	13.4	24.1	18.8	14.6	48.8	31.7
11	SBC38	25.4	11.5	24.9	18.2	16.1	50.3	33.2
12	SBC46	24.4	16.2	21	18.6	17.2	50.6	33.9
13	SBC49	25.6	19.4	19.8	19.6	14.5	50.3	32.4
14	SBC50	26.8	17.9	24.2	21.1	16.3	54.5	35.4
15	SBC51	28.3	15.4	27	21.2	15.1	49.7	32.4
16	SBC57	28.5	16.3	24.3	20.3	20.3	51.7	36
17	SBC59	28.5	14.4	25.5	20.0	16.9	54.3	35.6
18	SBC60	24	14.3	21.8	18.1	16.4	38.9	27.7
19	SBC64	27.9	16.1	25.3	20.7	16.8	49	32.9
20	SBC65	30.7	15.3	29.8	22.6	24.3	52.7	38.5
21	SBC67	26.1	13	21.9	17.5	17.6	52.8	35.2
22	SBC71	27	13	21.2	17.1	15.8	51.3	33.6
23	SBC01MB	24	14.2	17.3	15.8	15.5	49.5	32.5
24	SBC02MB	24.4	14.7	20.2	17.5	16	44.1	30.1
25	SBC07MB	24.3	15.4	26.3	20.9	12.8	45.1	29.0
26	SBC17MB	30.5	19.7	31	25.4	18.9	53.6	36.3
27	SBC24MB	26.6	14.9	27.2	21.1	16.2	50.1	33.2
28	SBC31MB	26.5	14.5	26	20.3	15	49.7	32.4
29	SBC34MB	24.9	14.9	27.3	21.1	11.1	46.6	28.9
30	SBC35MB	24.4	12.8	28.6	20.7	9.5	45.8	27.7
31	SBC38MB	29.3	12.1	27.6	19.9	20.8	51	35.9
32	SBC46MB	28.1	13.6	28.6	21.1	16.8	49.6	33.2
33	SBC49MB	27.5	15.2	26.7	21.0	19.3	47.8	33.6
34	SBC50MB	25.7	15.4	25	20.2	17.2	48.9	33.1
35	SBC51MB	26	14.6	27.4	21	16.5	44.8	30.7
36	SBC57MB	24.8	13	27.1	20.1	19.7	43.1	31.4
37	SBC59MB	28.6	12.9	26.9	19.9	20.9	52.3	36.6
38	SBC60MB	25.2	15.2	24.3	19.8	21.2	42.2	31.7
39	SBC64MB	24.9	15.2	23.3	19.3	16.9	46.5	31.7
40	SBC65MB	26.3	18.5	23.8	21.2	18.2	46.4	32.3
41	SBC67MB	25.6	15.6	23.1	19.4	20.9	44.8	32.9
42	SBC71MB	25.5	14.3	24.6	19.5	14.2	49.7	32.0
Alpha level		0.1	0.1	0.1		0.1	0.1	
CV		11.03	11.07	9.01		10.10	6.37	
Grand Mean		26.50	15.19	25.64	20.414	17.27	47.90	32.586
LSD		2.417	2.831	3.891		2.938	5.141	
R²		0.978	0.810	0.785		0.897	0.791	

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of original values. Means in bold are significantly higher than one or more check lines, TAM111 or TAM112.

Synthetic performance in Plains region

Significance between means was calculated using the least significance difference (LSD) of each location and of combined locations. No synthetic backcross lines from Bushland or Chillicothe performed significantly higher than TAM 111 or TAM 112 (Table 3.13). CH10 contained six populations with mean yields greater than the recurrent parent. Compared to other environments in the Plains region, synthetics performed the best in this environment, which may be due to good late rains and only minor freeze damage. Overall, synthetics performed the worst in the same location of Chillicothe a year earlier. Two late freezes and very little rain may have caused such poor performance. Of synthetic populations, 26 (SBC17MB) had the highest mean yield (30.8 bu/ac) with a range 18.9 – 53.6 bu/ac across environments. Entry 20 (SBC65) had the second highest mean yield (30.5) with a range 15.3 – 52.7 bu/ac across environments. Entry 9 (SBC34) had the lowest mean yield (22.5 bu/ac) with a range 12 – 40.4 bu/ac, and entry 18 (SBC60) had the next lowest mean yield (22.9 bu/ac) with a range 14.3 – 38.9 bu/ac. Both of these entries were significantly lower than the two checks.

No significant improvement was observed in any population within or across environments. A likely reason for this result is due to the cold temperatures and drought common to these locations. The primary synthetics used in this study were spring wheats adapted to environments in Mexico. Spring wheats have better adaptation to warmer temperatures and more moisture than is seen in Bushland or Chillicothe. The Plains region is a better environment for wheat adapted to drier climates and colder

Table 3.14 Grain yield means and yield component means of synthetic backcross wheat lines in College Station, McGregor, and Leonard, TX during 2009 and 2010.

Entry	Line	Grain yield (bu/ac)	Seed weight (g)	Head number (no)	Seed/head (no)
1	TAM 111	33.9	0.0223	1363.1	31.8
2	TAM 112	39.6	0.0246	1632.8	27.8
3	SBC01	34.0	0.0284	1026.9	32.5
4	SBC02	37.1	0.0259	1382.4	30.2
5	SBC07	40.0	0.0283	1378.5	29.4
6	SBC17	34.8	0.0311	1105.3	29.0
7	SBC24	38.8	0.0301	1257.2	29.8
8	SBC31	36.6	0.0316	1156.6	27.8
9	SBC34	34.8	0.0304	1177.1	28.1
10	SBC35	40.6	0.0301	1333.6	29.2
11	SBC38	41.9	0.0293	1405.4	29.3
12	SBC46	39.9	0.0287	1342.4	30.0
13	SBC49	33.9	0.0323	1065.8	28.4
14	SBC50	35.2	0.0314	1126.3	28.2
15	SBC51	37.8	0.0324	1310.5	26.2
16	SBC57	37.2	0.0300	1371.7	25.9
17	SBC59	37.1	0.0302	1315.6	26.9
18	SBC60	32.0	0.0297	1207.0	25.8
19	SBC64	32.7	0.0300	1268.2	24.5
20	SBC65	36.6	0.0285	1314.0	28.3
21	SBC67	35.1	0.0293	1323.4	25.7
22	SBC71	38.5	0.0312	1336.6	26.6
23	SBC01MB	34.3	0.0295	1023.0	31.9
24	SBC02MB	33.5	0.0283	1152.2	28.9
25	SBC07MB	42.5	0.0288	1340.7	30.8
26	SBC17MB	39.8	0.0324	1149.7	31.3
27	SBC24MB	43.6	0.0283	1350.1	32.3
28	SBC31MB	36.9	0.0304	1263.5	28.4
29	SBC34MB	40.2	0.0294	1351.9	29.6
30	SBC35MB	44.2	0.0316	1324.4	30.7
31	SBC38MB	41.4	0.0299	1271.5	30.2
32	SBC46MB	36.9	0.0297	1063.8	32.5
33	SBC49MB	33.8	0.0327	1062.4	27.8
34	SBC50MB	28.4	0.0263	1161.8	26.4
35	SBC51MB	33.4	0.0308	1208.6	25.6
36	SBC57MB	37.4	0.0305	1397.2	25.5
37	SBC59MB	41.3	0.0310	1506.1	25.5
38	SBC60MB	35.4	0.0319	1307.1	24.6
39	SBC64MB	30.5	0.0301	1223.3	25.2
40	SBC65MB	29.9	0.0292	1297.8	22.9
41	SBC67MB	33.4	0.0295	1271.8	25.5
42	SBC71MB	36.2	0.0321	1180.3	27.8
Alpha level		0.1	0.1	0.1	0.1
CV		13.3	7.3	15.5	11.5
Grand Mean		36.678	0.02971	1264.460	28.206
LSD		3.3	0.0015	132.4	2.2
R²		0.911	0.916	0.893	0.850

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of original values. Means in bold are significantly higher than one or more check lines, TAM111 or TAM112.

Table 3.15 Means of synthetic backcross lines in College Station during 2009.

Entry	Line	Grain yield (bu/ac)	Seed weight (g)	Head number (no)	Seed/head (no)
1	TAM 111	18.4	0.0159	856.1	40.8
2	TAM 112	28.6	0.0196	1168.1	35.2
3	SBC01	18.6	0.0212	758.7	36.5
4	SBC02	24.9	0.0181	1159.1	34.2
5	SBC07	29.8	0.023	1474.8	26.6
6	SBC17	28.5	0.0278	1013.3	30
7	SBC24	21.9	0.0252	706.1	39.4
8	SBC31	22.6	0.0283	820.4	28
9	SBC34	34.4	0.0277	1124.8	32.5
10	SBC35	32.9	0.0284	1199	27.1
11	SBC38	31.1	0.0267	1005.4	33.4
12	SBC46	32.6	0.0265	1001.9	36
13	SBC49	26.3	0.029	819.7	31.8
14	SBC50	37.5	0.0298	1163.9	32
15	SBC51	39.3	0.0262	1386.1	32.2
16	SBC57	38.7	0.0222	1494.7	34.3
17	SBC59	34.9	0.0268	1247.1	30.7
18	SBC60	30.5	0.0245	1174.8	30.3
19	SBC64	28.1	0.0231	1167.8	30.7
20	SBC65	27.6	0.0245	1010.4	33.9
21	SBC67	28.1	0.0247	1095.7	30.6
22	SBC71	31	0.0263	961	36.7
23	SBC01MB	20.1	0.0252	649.4	38
24	SBC02MB	19.5	0.0215	828	34.5
25	SBC07MB	25	0.024	848.9	38.1
26	SBC17MB	32.1	0.0263	883	41.5
27	SBC24MB	28.8	0.0232	977.1	39.5
28	SBC31MB	19.6	0.0234	701	38.6
29	SBC34MB	32.1	0.0249	1036.6	37.4
30	SBC35MB	29.9	0.0278	1085.5	31.8
31	SBC38MB	37.7	0.0269	1107.8	35.8
32	SBC46MB	32.4	0.0246	957.7	40.4
33	SBC49MB	27.2	0.0281	743.8	39.2
34	SBC50MB	22.2	0.0203	948.8	35.3
35	SBC51MB	33.6	0.0251	1167.9	34.4
36	SBC57MB	38.2	0.0264	1424.6	29.9
37	SBC59MB	39.2	0.0253	1310.2	35.1
38	SBC60MB	32.6	0.026	1235.7	29.3
39	SBC64MB	28.8	0.0264	1013.2	30.3
40	SBC65MB	29.6	0.0251	1178.7	28
41	SBC67MB	28.8	0.0243	1165.1	30.7
42	SBC71MB	29.9	0.028	876.1	37.8
Alpha level		0.1	0.1	0.1	0.1
CV		13.3	8.2	12.9	8.2
Grand Mean		29.371	0.02496	1046.378	34.016
LSD		6.6	0.0034	227.6	4.7
R²		0.8	0.7	0.8	0.8

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of adjusted values. Means in bold are significantly higher than respective recurrent parent, TAM111 or TAM112.

Table 3.16 Means of synthetic backcross lines in McGregor during 2009.

Entry	Line	Grain yield (bu/ac)	Seed weight (g)	Head number (no)	Seed/head (no)
1	TAM 111	45	0.0234	1937.1	28
2	TAM 112	55.3	0.0264	2214.8	26.6
3	SBC01	47.1	0.0304	1503.6	30.2
4	SBC02	54.3	0.0279	2052.8	27.3
5	SBC07	49.9	0.0292	1726.5	27.5
6	SBC17	51.5	0.0287	1794.8	29.2
7	SBC24	55	0.0301	1855.7	28.6
8	SBC31	55.5	0.0322	1822.6	28.5
9	SBC34	44.6	0.0304	1604.6	27.8
10	SBC35	50.8	0.0288	1872.9	28
11	SBC38	55	0.026	2187.6	26.4
12	SBC46	52.3	0.0264	1995.8	27.3
13	SBC49	51.3	0.0302	1689.7	28
14	SBC50	53.2	0.0302	1803.5	26.4
15	SBC51	52.3	0.0312	1948.7	24.3
16	SBC57	54	0.0287	2089.1	25.5
17	SBC59	58.6	0.0258	2339.6	26.5
18	SBC60	45.5	0.0311	1602.5	25.8
19	SBC64	47.4	0.0301	1719.7	25.8
20	SBC65	39.8	0.0256	1541.3	28.3
21	SBC67	55.4	0.0295	2139.7	24.6
22	SBC71	59.7	0.0325	1976.3	26.2
23	SBC01MB	52.3	0.0297	1565.6	32.6
24	SBC02MB	50.4	0.0276	1741.1	30.5
25	SBC07MB	59.9	0.028	2052.4	30
26	SBC17MB	54.3	0.0312	1640.2	32
27	SBC24MB	63.7	0.0276	2062.7	33.1
28	SBC31MB	54.4	0.0305	1754.7	31.5
29	SBC34MB	59.5	0.028	2207.4	28.2
30	SBC35MB	63.3	0.0295	2201	27.8
31	SBC38MB	53.3	0.0285	1984.6	27.6
32	SBC46MB	53.1	0.0286	1703.7	30.8
33	SBC49MB	54.1	0.0336	1602.5	27.1
34	SBC50MB	42.7	0.0288	1596.6	25.2
35	SBC51MB	50.6	0.0314	1746.7	24.5
36	SBC57MB	54.5	0.0302	2145	23.5
37	SBC59MB	65.1	0.0279	2584.2	24.2
38	SBC60MB	56.7	0.0278	2181.8	25.5
39	SBC64MB	53.1	0.0293	1938.8	25.3
40	SBC65MB	49.7	0.029	2115.3	22.1
41	SBC67MB	49	0.0284	2029.5	23.7
42	SBC71MB	58	0.0319	1831.8	28.2
Alpha level		0.1	0.1	0.1	0.1
CV		6.9	5.6	8.4	6.4
Grand Mean		53.116	0.02909	1907.251	27.354
LSD		6.2	0.0027	269.7	2.9
R ²		0.8	0.8	0.8	0.8

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of adjusted values. Means in bold are significantly higher than respective recurrent parent, TAM111 or TAM112.

Table 3.17 Means of synthetic backcross lines in Leonard during 2009.

Entry	Line	Grain yield (bu/ac)	Seed weight (g)	Head number (no)	Seed/head (no)
1	TAM 111	18	0.0163	1666.4	17.7
2	TAM 112	37.8	0.0204	1977.5	23.7
3	SBC01	20.2	0.0231	1073.3	23.5
4	SBC02	29.1	0.0203	1733.4	21.3
5	SBC07	33	0.0215	1503.2	28.1
6	SBC17	21.5	0.0249	923.8	25.7
7	SBC24	21.2	0.0237	1543.8	16
8	SBC31	19.9	0.0269	1195.8	16.5
9	SBC34	17.7	0.0207	1317.4	18.6
10	SBC35	27.1	0.0214	1783.9	20.6
11	SBC38	24.3	0.0222	1426.5	22.9
12	SBC46	27.2	0.0192	1464.5	25.9
13	SBC49	31.1	0.0233	1271.3	27.8
14	SBC50	31	0.0235	1202	27.2
15	SBC51	30.4	0.026	1374.6	23
16	SBC57	23.5	0.025	1187.3	20.9
17	SBC59	32.3	0.026	1420.9	23.5
18	SBC60	26.7	0.0259	1478.4	20.8
19	SBC64	22.4	0.0264	1299.2	18.3
20	SBC65	17	0.0245	1599	13.5
21	SBC67	30.5	0.0236	1322.4	26.9
22	SBC71	26.3	0.0252	1235.8	23.8
23	SBC01MB	17.8	0.0233	767	26.2
24	SBC02MB	19.7	0.0241	1089.1	19
25	SBC07MB	23.5	0.0206	1208	24
26	SBC17MB	24.8	0.0208	1330	23.1
27	SBC24MB	28.1	0.0205	1459.5	23.4
28	SBC31MB	21.8	0.0238	1418.5	16
29	SBC34MB	23.1	0.0213	1441.6	22.1
30	SBC35MB	27.3	0.0228	1264.9	28
31	SBC38MB	18.7	0.025	1047	19.3
32	SBC46MB	27.4	0.0251	786.5	32
33	SBC49MB	25.3	0.0241	1072.6	25.3
34	SBC50MB	22.2	0.0174	1439.5	20.8
35	SBC51MB	27.1	0.0245	1343.8	22.8
36	SBC57MB	27	0.0252	1306.7	25.3
37	SBC59MB	37.6	0.0293	1726.6	18
38	SBC60MB	25.4	0.0266	1294.2	19.8
39	SBC64MB	25	0.0237	1660.5	18.3
40	SBC65MB	21.4	0.0259	1378.1	17.3
41	SBC67MB	27.8	0.0238	1163.2	25.6
42	SBC71MB	29.6	0.028	1258.6	23
Alpha level		0.1	0.1	0.1	0.1
CV		12.1	11.0	19.2	15.5
Grand Mean		25.446	0.02346	1344.198	22.273
LSD		5.17	0.0044	435.6	5.8
R²		0.8	0.7	0.6	0.7

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of adjusted values. Means in bold are significantly higher than respective recurrent parent, TAM111 or TAM112.

Table 3.18 Means of synthetic backcross lines in College Station during 2010.

Entry	Line	Grain yield (bu/ac)	Seed weight (g)	Head number (no)	Seed/head (no)
1	TAM 111	37.3	0.0233	839.1	44.1
2	TAM 112	40.9	0.026	1280.3	31.7
3	SBC01	35.2	0.0326	612.6	39.7
4	SBC02	33.8	0.0285	703.5	41.1
5	SBC07	38.5	0.0349	1027.3	30.1
6	SBC17	31.4	0.0355	862.6	28.3
7	SBC24	45.7	0.0378	1059.9	31.1
8	SBC31	42.1	0.0376	1018.2	30.1
9	SBC34	37.5	0.0383	932.4	28.8
10	SBC35	45.4	0.0382	1109.5	29
11	SBC38	50.1	0.0375	1152.4	32.2
12	SBC46	43.2	0.0366	997.4	32.8
13	SBC49	33.6	0.0404	794.9	28.6
14	SBC50	26.6	0.0353	668.2	30.5
15	SBC51	36	0.0403	907.1	27.3
16	SBC57	31.5	0.0368	986.3	22.7
17	SBC59	34.7	0.0385	897.4	28
18	SBC60	33.2	0.0365	951.5	25
19	SBC64	35.5	0.0378	1013.9	24.6
20	SBC65	51.9	0.0364	1239.8	32.1
21	SBC67	30	0.037	780.6	26.9
22	SBC71	38.8	0.0377	1335.6	21.6
23	SBC01MB	38	0.0372	811.5	34.6
24	SBC02MB	40.6	0.0354	1050.7	31
25	SBC07MB	52.9	0.0377	1189.6	32.1
26	SBC17MB	46.1	0.042	1080.7	27.3
27	SBC24MB	51.4	0.0372	1184.1	32.2
28	SBC31MB	41.3	0.0394	990.9	29
29	SBC34MB	40.1	0.0365	978.2	31.2
30	SBC35MB	52.9	0.0407	1139.4	31.8
31	SBC38MB	49.3	0.0355	1201.7	31.4
32	SBC46MB	30.6	0.0331	793.4	31.4
33	SBC49MB	26.7	0.0387	861.4	22.1
34	SBC50MB	29.5	0.0312	901.8	28.2
35	SBC51MB	28.2	0.036	927.9	23.4
36	SBC57MB	33.9	0.0373	892.8	27.2
37	SBC59MB	36.2	0.0372	1019.6	25.8
38	SBC60MB	32.6	0.0394	891	26
39	SBC64MB	24.2	0.0345	598	31.5
40	SBC65MB	29.2	0.0344	1130.9	22.2
41	SBC67MB	34.3	0.0388	998.8	23.5
42	SBC71MB	35	0.0409	918	24.1
Alpha level		0.1	0.1	0.1	0.1
CV		11.5	4.5	12.3	9.1
Grand Mean		37.760	0.03635	969.783	29.339
LSD		7.3	0.0028	200.5	4.5
R²		0.9	0.9	0.8	0.8

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of adjusted values. Means in bold are significantly higher than respective recurrent parent, TAM111 or TAM112.

Table 3.19 Means of synthetic backcross lines in McGregor during 2010.

Entry	Line	Grain yield	Seed weight	Head number	Seed/head
		(bu/ac)	(g)	(no)	(no)
1	TAM 111	46.3	0.0288	1809.2	23.8
2	TAM 112	33.3	0.0285	1857.8	17.2
3	SBC01	48.3	0.0315	1383.6	29.3
4	SBC02	45.9	0.0307	1662	24.7
5	SBC07	51.9	0.031	1592.2	28.5
6	SBC17	44.4	0.0354	1345	25.3
7	SBC24	46.4	0.032	1353.3	28.8
8	SBC31	41.9	0.0314	1164.2	30
9	SBC34	39.3	0.032	1257.5	26.4
10	SBC35	48.3	0.0328	1151.9	31.8
11	SBC38	52.4	0.0325	1666.8	27.4
12	SBC46	47.1	0.032	1631.9	25.5
13	SBC49	35.4	0.0357	1213.2	22.6
14	SBC50	32.3	0.0349	1175.1	20.9
15	SBC51	39.4	0.0355	1500.6	20.1
16	SBC57	41.9	0.0353	1543	20.8
17	SBC59	28.9	0.0322	1096.9	21.6
18	SBC60	31	0.0298	1351.7	20.9
19	SBC64	32.7	0.0307	1522.2	18.5
20	SBC65	42.7	0.0306	1446.6	26
21	SBC67	30.9	0.0302	1398.6	19.8
22	SBC71	38.4	0.0328	1422.9	22.7
23	SBC01MB	39.7	0.0319	1102.3	31.3
24	SBC02MB	41.4	0.032	1329.4	26.3
25	SBC07MB	48.3	0.032	1550.6	26.7
26	SBC17MB	43.9	0.0367	1179.6	28.5
27	SBC24MB	49.7	0.032	1375.9	30.3
28	SBC31MB	47.4	0.0344	1768.2	21.2
29	SBC34MB	46.9	0.0354	1414.5	24.6
30	SBC35MB	50.6	0.0363	1254.4	30
31	SBC38MB	47.5	0.0315	1222.5	34
32	SBC46MB	46.4	0.0346	1359.6	27
33	SBC49MB	37.5	0.0362	1339.3	21.2
34	SBC50MB	25	0.0294	1196.5	19.7
35	SBC51MB	28.8	0.0335	1166.3	20.5
36	SBC57MB	38.1	0.0322	1390.9	23.3
37	SBC59MB	34.5	0.0329	1406.1	21
38	SBC60MB	37.4	0.0359	1455.5	19.9
39	SBC64MB	28.7	0.0332	1451	16.5
40	SBC65MB	24.1	0.0287	1243.1	19
41	SBC67MB	31.8	0.029	1400.8	21.5
42	SBC71MB	36.1	0.0319	1459.2	21.5
Alpha level		0.1	0.1	0.1	0.1
CV		7.2	4.8	10.1	8.3
Grand Mean		40.073	0.03252	1395.526	24.208
LSD		4.8	0.0026	237.9	3.4
R ²		0.9	0.8	0.8	0.9

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of adjusted values. Means in bold are significantly higher than respective recurrent parent, TAM111 or TAM112.

Table 3.20 Means of synthetic backcross lines in Leonard during 2010.

Entry	Line	Grain yield	Seed weight	Head number	Seed/ head
		(bu/ac)	(g)	(no)	(no)
1	TAM 111	38.2	0.0261	1070.9	36.5
2	TAM 112	41.4	0.0265	1298.3	32.2
3	SBC01	34.5	0.0314	829.5	35.8
4	SBC02	34.5	0.0296	983.4	32.3
5	SBC07	36.9	0.0299	946.8	35.3
6	SBC17	31.2	0.0345	692.2	35.3
7	SBC24	42.4	0.0318	1024.4	35.1
8	SBC31	37.3	0.033	918.2	33.5
9	SBC34	35.1	0.0334	825.7	34.6
10	SBC35	38.8	0.0308	884.2	38.8
11	SBC38	38.4	0.0311	993.8	33.5
12	SBC46	37	0.0317	963	32.6
13	SBC49	25.6	0.035	606.1	31.5
14	SBC50	30.3	0.0344	745.1	32
15	SBC51	29.3	0.035	745.8	30.3
16	SBC57	33.5	0.032	929.5	31
17	SBC59	33	0.032	891.9	31.3
18	SBC60	25.1	0.0303	683	32.2
19	SBC64	30.3	0.0316	886.6	29.2
20	SBC65	40.5	0.0291	1046.8	35.8
21	SBC67	35.5	0.0309	1203.2	25.6
22	SBC71	36.8	0.0324	1088	28.6
23	SBC01MB	37.9	0.0295	1242.2	28.7
24	SBC02MB	29.3	0.0292	875	32.2
25	SBC07MB	45.2	0.0305	1194.5	33.9
26	SBC17MB	37.4	0.0373	784.6	35.2
27	SBC24MB	40.1	0.0295	1041.5	35.5
28	SBC31MB	37	0.0308	947.4	34.3
29	SBC34MB	39.5	0.0304	1033	34
30	SBC35MB	41.3	0.0322	1001	34.6
31	SBC38MB	42.1	0.0318	1065.6	33.1
32	SBC46MB	31.4	0.0319	781.7	33.6
33	SBC49MB	31.7	0.0356	755	31.6
34	SBC50MB	28.9	0.0307	887.6	29.2
35	SBC51MB	32.1	0.0344	899.1	28.1
36	SBC57MB	32.8	0.0316	1223.1	23.7
37	SBC59MB	35.1	0.0332	990	29
38	SBC60MB	27.8	0.0357	784.2	27.3
39	SBC64MB	23.3	0.0336	678.1	29
40	SBC65MB	25.1	0.0323	740.9	29
41	SBC67MB	28.6	0.0324	873.1	27.7
42	SBC71MB	28.3	0.0321	738.2	32.2
Alpha level		0.1	0.1	0.1	0.1
CV		7.2	2.8	9.1	6.9
Grand Mean		34.301	0.03183	923.620	32.019
LSD		4.2	0.0015	141.6	3.7
R²		0.9	0.9	0.9	0.8

Mean values are from Nearest-neighbor adjusted means. Statistics are from ANOVA of adjusted values. Means in bold are significantly higher than respective recurrent parent, TAM111 or TAM112.

winters, such as TAM 111 and TAM 112. For this reason, the checks ranked higher than any synthetic backcrosses across Plains environments.

Synthetic performance in Stxbl region

Mean grain yields of synthetic populations were compared to recurrent parent means in each environment. Superior populations were identified in all environments of the Stxbl region (Tables 3.14 – 3.20). Also, a percent increase or decrease was determined to compare how synthetics generally performed at each environment. In CS09, synthetics performed the best with an overall average increase in yield of 30.6 % (Table 3.21). This environment had warmer temperatures and timely rains. An overall average increase was seen in CS09, Mc09, Len09, and Mc10. Synthetics performed the worst in Len10 with a negative overall percentage of 14%. Colder temperatures could be the reason for this low percentage. These percentages give a general idea of how synthetic backcrosses performed in comparison to recurrent parents, but specific population means should be looked at for accurate conclusions regarding the potential of synthetic crosses. Because primary synthetics are spring wheats and adapted to South Texas regions, these synthetic populations were expected to perform better in the Stxbl region than the Plains region.

Table 3.21 Percent improvement of grain yield in Stxbl environments.

Environment	CS09	Mc09	Len09	CS10	Mc10	Len10
Mean Yield	29.7	53.3	25.3	37.7	40.1	34.0
Overall % increase	30.6	7.5	1.4	-2.9	0.8	-14.0
% increase of TAM111 crosses	50.7	20.0	31.5	13.4	0.2	-2.2
% increase of TAM 112 crosses	10.5	-5.0	-28.6	-19.1	1.4	-25.9
No. superior populations [†]	17	16	10	9	6	1

[†]Superior populations had significantly higher mean yield than recurrent parent

Across years and locations of the Stxbl region, 11 synthetic-derived populations with significantly higher grain yield than their recurrent parent were observed (Table 3.14). All synthetic lines had superior seed weight to recurrent parents. No lines had significantly higher means for seed per head or head number than the recurrent parents. Of the 11 superior lines, ten had head number means and eight had seed per head means with no significant difference from recurrent parent means. Therefore, superior lines were superior due to an increase in seed weight while maintaining adequate tillering and kernel number. Across environments, synthetics contributed to yield through increasing seed weight. Del Blanco et al. made the same conclusions in a study of 47 synthetics backcrossed to spring wheat in Mexico (2001).

Across locations of the Stxbl region, entry 30 (SBC35MB) had the best mean yield (44.22 bu/ac; Table 3.14). This population had high yield (27.3 – 63.3 bu/ac) due to high seed weight (0.0228 – 0.0407 grams). Entry 27 (SBC24MB) had the second highest mean yield across environments (43.63 bu/ac; Table 3.12). High yield (28.1 – 63.7 bu/ac) was due to high seed weight (0.0205 – 0.0372). Both lines 30 and 27 were backcrossed to TAM111 and had significantly higher yields than TAM 111 and TAM112 across environments.

Entry 34 (SBC50MB) held the lowest mean yield across environments (28.42 bu/ac; Table 3.14). Low yield (22.2 – 42.7 bu/ac) was most likely due to low head number (887.6 – 1596.6) as well as seed per head (19.7 – 35.3). Entry 34 was backcrossed to TAM112. Of backcrosses with recurrent parent TAM 111, entry 24 (SBC02MB) had the lowest mean yield across environments (33.48 bu/ac; Table 3.14).

This low yield was most likely due to lower head number (828 – 1741.1) and seed per head (19 – 34.5).

Yield means of entries within each environment allow for comparisons between populations (Tables 3.15 – 3.20). Entries 25, 27, and 30 all ranked high for yield in Mc09, CS10, Mc10, and Len10 (Tables 3.16, 3.18, 3.19, 3.20). Entry 31 ranked among the highest in CS09, CS10, Mc10, and Len10, but ranked among the lowest in Len09, which was the poorest environment for improvement (Tables 3.15, 3.17 - 3.20). Entry 37 ranked among the highest at all 2009 locations while entry 11 ranked among the highest at all 2010 locations. Entry 34 was among the lowest mean yields in all environments except Len09. Entry 40 had lower yield in all environments except CS09. Entry 3 performed poorly in all 2009 locations while entry 39 performed poorly in all 2010 locations. Interestingly, entries 7 and 20 performed poorly in some locations of 2009 but ranked high in 2010. On the other hand, entry 14 ranked high in CS09 and Len09 but much lower in CS10 and Mc10. From this information we can conclude performance among synthetic backcrosses varies between environments.

Table 3.22 Agronomic trait and rust score means of synthetic backcross lines in Texas.

Entry	Line	Heading (day)				Height (inch)				Yrust score [¶]	
		CS09 [†]	CS10	Mc09	Mc10	CS09	CS10	Mc09	Mc10	CS10	Mc10
1	TAM 111	97	98	95	102	33	42	29	42	2	0
2	TAM 112	86	91	87	101	35	39	35	38	16.5	3
3	SBC01	95	85	86	96	36	44	30	42	5	3
4	SBC02	81	88	87	95	32	42	28	41	5.5	7
5	SBC07	81	87	87	97	31	45	31	42	2.5	0
6	SBC17	81	88	86	99	38	47	33	44	16.5	7
7	SBC24	84	86	86	98	34	46	31	39	3.5	6
8	SBC31	86	86	86	96	35	45	35	47	8.5	8
9	SBC34	82	85	86	97	33	47	34	43	14	8
10	SBC35	81	86	86	95	35	46	32	43	8.5	8
11	SBC38	81	85	87	96	33	44	33	44	3.5	9
12	SBC46	81	82	87	96	35	47	33	41	8	9
13	SBC49	87	85	86	99	36	49	32	48	17.5	8
14	SBC50	81	84	86	99	34	47	37	48	42	4
15	SBC51	81	83	86	98	35	48	35	41	21	8
16	SBC57	81	84	87	98	37	48	30	47	37	8
17	SBC59	82	84	87	97	35	44	35	42	27.5	8
18	SBC60	81	86	87	98	35	43	32	40	28	8
19	SBC64	81	85	89	96	35	45	33	39	24	8
20	SBC65	86	87	91	99	36	48	34	45	5	2
21	SBC67	81	85	90	97	35	44	33	41	24.5	8
22	SBC71	81	85	90	97	34	47	32	47	20.5	7
23	SBC01MB	80	84	93	96	38	47	31	45	7.5	5
24	SBC02MB	82	86	95	97	37	45	32	41	2	4
25	SBC07MB	81	86	92	97	35	43	30	38	2	4
26	SBC17MB	82	90	97	100	40	51	37	45	5.5	2
27	SBC24MB	83	85	89	97	38	45	32	41	2	4
28	SBC31MB	87	87	91	98	34	46	33	46	5.5	5
29	SBC34MB	82	87	90	99	33	44	32	43	19.5	5
30	SBC35MB	81	82	88	96	31	44	33	44	1	4
31	SBC38MB	81	87	88	99	34	45	33	43	3.5	8
32	SBC46MB	80	88	88	97	37	46	31	41	21	8
33	SBC49MB	83	92	90	99	43	53	31	47	21	5
34	SBC50MB	85	90	91	99	36	42	33	38	23	9
35	SBC51MB	83	87	90	96	36	51	34	44	24	6
36	SBC57MB	82	87	89	100	39	52	36	45	19.5	5
37	SBC59MB	83	87	91	97	37	45	33	41	25.5	8
38	SBC60MB	83	90	92	98	39	47	33	43	25.5	7
39	SBC64MB	82	89	92	99	38	43	31	41	25.5	8
40	SBC65MB	83	90	93	99	37	44	34	48	24	8
41	SBC67MB	85	88	97	98	37	nd	33	42	14	8
42	SBC71MB	81	81	92	96	37	nd	34	45	23	7
Grand mean		83.0	86.7	89.4	97.8	35.6	43.5	32.7	43.0	15.1	6.1

[†]CS=College Station, TX; Mc= McGregor, TX; nd=no data available;

[¶]Stripe rust score calculated according to disease severity and percentage coefficient at CS10; Stripe rust scores calculated on 0-9 scale at McGregor, TX. Values in bold are associated with superior yielding lines within environments. For example, line SBC07 in CS09 has superior mean grain yield to recurrent parent.

Table 3.23 Correlation coefficients for traits of synthetic back cross wheat lines in McGregor and College Station, TX during 2009 and 2010.

Trait	Seed wt.	Head no.	Seed/Head	Yield
<i>College Station 2009</i>				
Height	-0.05	-0.05	-0.06	-0.21
Heading	0.63**	-0.75**	-0.55**	-0.65**
<i>McGregor 2009</i>				
Height	0.11	0.19	-0.35*	-0.01
Heading	-0.38*	-0.17	0.04	-0.54**
<i>College Station 2010</i>				
Height	0.48**	-0.20	-0.33*	-0.23
Heading	-0.28**	-0.01	-0.06	-0.18
Yrust	0.04	-0.27*	-0.36**	-0.47**
<i>McGregor 2010</i>				
Height	0.17	-0.01	0.00	0.03
Heading	-0.18	-0.10	-0.13	-0.25*
Yrust	-0.17	-0.05	-0.42**	-0.40**

* Significant at the 0.05 probability level

** Significance at the 0.01 probability level

Heading

In CS09, CS10, and Mc10, almost all synthetic populations had earlier heading dates than their respective recurrent parents (Table 3.22). In Mc09, most synthetic populations with TAM 111 as their recurrent parent had earlier heading dates than the check; however, most populations with TAM 112 as the parent were later maturing than their check. Besides two entries from Mc09, all superior entries from within environments had earlier heading dates than their respective recurrent parents. These results are different from a previous study of winter wheat backcrossed to a synthetic in which heading dates were the same or later than the recurrent parent (Narasimhamoorthy et al., 2006).

For further analysis, simple correlations between heading date and yield were determined (Table 3.23). Days to heading had a significant and negative correlation with yield in three of the four environments measured. This means earlier maturing plants were associated with higher yields in these environments. Similar findings have been found in studies of synthetic wheat backcrosses (del Blanco et al., 2001; Narasimhamoorthy et al., 2006). Results in this study indicate synthetics may contribute to yield through earlier maturity in these environments.

Stripe rust

At the time of this study, TAM 111 was resistant to stripe rust and susceptible to leaf rust while TAM 112 was susceptible to both diseases. It was suggested these primary synthetics could improve rust resistance in Texas wheat due to extensive screening for such diseases at CIMMYT locations (Mujeeb-Kazi et al., 2000; Mujeeb-

Kazi and Delgado, 2001). Leaf rust and stripe rust pressures were severe in McGregor and College Station in 2010, allowing for comparisons of disease scores between synthetic entries and checks.

According to Mc10 measurements, one population had a lower mean stripe rust score than recurrent parent TAM 112 (Table 3.22). As TAM 111 was completely resistant, no synthetics outperformed this line with regard to stripe rust resistance, but one superior yielding population received an equal score of zero.

In CS10, one superior yielding population had a lower score than recurrent parent TAM 111 and two populations had equivalent scores for stripe rust. Two populations from crosses to TAM 112 had lower scores than the check.

Table 3.23 shows stripe rust correlations with yield and seed per head to be negative and highly significant in both environments. This was expected, as rust can be very detrimental to wheat production in these areas of Texas.

It should be noted that rust measurements are subjective and can differ greatly depending on the environment, pathogen type, growth stage of the host, neighboring plots, and number of readings (Roelfs et al., 1992). Notes in College Station were taken twice by a collective group of three observers while measurements in McGregor were taken once by a group of two observers. Two methods of scoring rust were used among the environments. The calculated coefficient method used at College Station was most likely the better of the two as it incorporated disease severity and host response. Scores in McGregor mostly reflected infection type. Because measurements were taken on segregating populations, finding the average rust score also proved to be challenging as

different infection types were observed within the same population. Despite these difficulties in determining stripe rust resistance and susceptibility, the results give a general idea of the potential for rust resistance among synthetic wheat. If selection pressures were applied effectively, lines may prove to have more resistance than recurrent parents, which would be beneficial in environments where this disease is yield inhibiting. More research is needed to determine rust resistance in synthetic backcrosses to winter wheat.

Conclusions

By comparing synthetic backcross populations to elite Texas lines in varied environments of Texas, conclusions can be made regarding the use of synthetic wheat as a source of improvement in Texas winter wheats. Also, a comparison of breeding methods was of interest in evaluation of the populations.

In this study, there was no significant difference between modified bulk and bulk hybrid breeding methods for yield or yield components across environments. Therefore, selecting for desired traits in early generations did not prove to be advantageous to natural selection in bulked populations.

Significance between years and locations for yield and yield components of synthetic lines highlights the complicated role of environment on yield and yield components of synthetic wheat. Therefore, multiple years and locations are needed in the evaluation of synthetic wheat in Texas.

Superior populations in the Stxbl environments show that synthetic wheat provides a source of improvement for winter wheat grown in South Texas and the Blacklands.

Across environments, all synthetic populations had significantly higher seed weight than the recurrent parents indicating synthetic wheats improve yield of Texas winter wheat by increasing seed size. Other studies have shown this contribution to be true in crosses to spring wheats (del Blanco et al., 2001) but no conclusions regarding winter wheat have been made prior. Synthetic populations that produced higher grain yield than both TAM 111 and TAM 112 were able to maintain their large seed size and weight while improving their seed per head and head number traits. This clearly demonstrates that improving yield, through utilization of common wheat by synthetic crosses, could result from selecting for larger seed per head and heads per unit area in lines driven from these populations. Synthetics may also contribute to yield through other components such as early heading and rust resistance. No improvement was seen in the High and Rolling Plains of Texas but potential for improvement may still be possible through later selections as no selections were made in the F_4 and F_5 generations in this study.

CHAPTER IV

INFLUENCE OF YIELD COMPONENTS ON YIELD OF SYNTHETIC POPULATIONS

Introduction

Many biotic, abiotic, and agronomic factors influence grain yield production of wheat (*Triticum aestivum* Desf.). Yield is generally thought to be a product of kernel weight by kernel number per spike by number of spikes. Yield components give a measure of theoretical yield and some suggest them to be a better indicator of yield than actual yield itself (Johnson et al., 1966b). If one of these yield components is increased while keeping other components stable, then yield should automatically increase; however, yield component compensation will often take place in which one or more of the other components decreases to compensate for the increase (Adams, 1967).

Del Blanco et al. measured the effects of yield components on yield of six synthetic-derived populations from backcrosses to spring wheat cultivars (2001). In all populations, head number was significantly and positively correlated with yield despite negative indirect effects via seed per head or seed weight. All yield components had positive direct effects on yield but total correlations were significantly lower in some populations due to indirect effects.

The objective of this study was to determine yield components that contribute to yielding ability in synthetic lines backcrossed to Texas wheats. Methods of analyzing yield component effects are discussed.

Materials and methods

Plant material- primary synthetics

Ten primary synthetic lines were selected as the donor parents for this study. These lines were chosen from elite sets produce by CIMMYT. Elite set I consisted of 95 synthetic lines selected from primary synthetics grown in El Baton and Obregon, Mexico beginning in 1995. These lines were chosen based upon morphological, growth, abiotic, and biotic tolerance characteristics (Mujeeb-Kazi et al., 2000). The second elite set consisted of 33 synthetic hexaploids shown to possess resistance to leaf, stem, and stripe rust along with other diseases (Mujeeb-Kazi and Delgado, 2001). In this study, 8 synthetic lines were chosen from CIMMYT's elite set I and 2 synthetic lines were chosen from elite set II.

Plant material- recurrent parents

'TAM 111' is a medium maturing, awned white chaffed, semi-dwarf hard red winter wheat (HRW). It was released in April of 2002 with resistance for stripe rust and stem rust (Lazar et al., 2004). 'TAM 112' HRW is adapted to the south and central Great Plains and was released in 2005. It has the *Lr41* gene for leaf rust resistance and has greenbug resistance based on *Gb3* (Rudd et al., 2004).

Synthetic backcross and breeding methods

Ten primary synthetic lines from CIMMYT were crossed to TAM 111 and TAM 112 in 2004. These lines were backcrossed to their respective recurrent parents, TAM 111 or TAM 112. The BCF₂ populations were grown in Chillicothe, TX. From the BCF₂ populations, heads were selected based on best plant type and grown as head-

rows in the BCF₃ generation using the Modified Bulk (MB) breeding method. Remaining F₂ heads of each population were bulked and advanced to the BCF₃ and BCF₄ generations using the Bulk Hybrid (BH) breeding method. Head- rows of good plant type from BCF₃-MB populations were combined and advanced to BCF₄-MB. The F₄ populations of both breeding methods were bulked to F₅ populations with no selection.

Layout and experimental design

Populations originating using either MB or BH methods were termed SBCF₄ (BCF₄ and BCF₄-MB) and SBCF₅ (BCF₅ and BCF₅-MB), and were both grown in the field at College Station (latitude = 30.5°N, longitude = 96.4°W), McGregor (latitude = 31.4°N, longitude = 97.4°W), and Leonard (latitude = 33.4°N, longitude = 96.2°W), TX. Seeds were planted at a rate of 60 pounds per acre in seven rows with a plot size of 10.8 feet by 4 feet. Entries were laid out in a randomized complete block design (RCBD) with two replications. Experiments were planted in October or November and combine harvested from Late May to June. All SBCF₄ and SBCF₅ locations contained a total of 84 plots according to the calculation below.

$$(10 \text{ synthetics}) \times (2 \text{ TAM lines}) \times (2 \text{ reps}) \times (2 \text{ breeding methods}) + (2 \text{ checks}) = 84.$$

Measurements- yield and test weight

Grain yield (GY) and test weight (TW) of all populations were recorded. The sample weight from 100 random heads selected before harvest (SW) was added to the

gram yield to get total grain yield (TGY). Total gram yields were multiplied by factor 0.0369 to convert grams per plot to bushels per acre (Yield).

Measurements- yield components from sample heads

Random samples of 100 heads were collected from each plot one week before harvest. Samples from each plot were collected in labeled bags and recounted before thrashed. Each head was thrashed using a 110 volt Wheat Head Thrasher (Precision Machine Inc; Paducah, Kentucky, USA). Samples were then cleaned by hand and weighed. If samples contained less than 100 heads, it was noted for later calculations. No samples contained more than 100 heads. Five hundred kernels were randomly counted from each thrashed sample using a model 750-2 Totalize Unit seed counter. Weights were doubled to produce thousand kernel weight (TKW). The following calculations were accomplished using thousand kernel weight, sample weight, number of tillers per sample (T), and total gram yield.

$$\text{Seed Weight (Seed wt)} = \text{TKW} / 1000$$

$$\text{Seed per head (Seed/head)} = \text{SW} / (\text{KW} \times \text{T})$$

$$\text{Heads per plot (Head no)} = \text{TGY} \times (\text{T} / \text{SW})$$

SAS procedures

Correlations of data were calculated through SAS (SAS Inc., 2008). Cramer et al. (1999) developed a SAS program for path coefficient analysis of quantitative data. Pathsas calculates path coefficients and simple correlations. A bootstrap analysis may

also be performed to calculate a total correlation estimate and confidence intervals for each estimate. Macros `pathsas.sas` and `bootstrap.sas` were performed in SAS (A-8,9).

Biplot analysis

To generate genotype-by-trait biplots, GGE biplot software was used according to Yan and Kang (2003). A two-way matrix of genotypes as entries and traits as testers was generated from mean values for genotypes. Rows and columns were treated as entries and testers, respectively. The biplot model was as follows:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

where Y_{ij} = expected value of entry i and tester j , μ = grand mean, β_j = mean of all crosses to j , λ_1 = PC1, ξ_{i1} = PC1 eigenvector of entry i , η_{j1} = PC1 eigenvector of tester j , λ_2 = PC2, ξ_{i2} = PC2 eigenvector of entry i , η_{j2} = PC2 eigenvector of tester j , and ϵ_{ij} = residual of model associated with combinations of entry i and tester j .

Biplots were interpreted according to Yan and Tinker (2006). Traits with acute angles were positively associated, while obtuse angles indicated a negative association. Traits with near right angles were independent. Entries close to one another signify similar trait profiles and entries opposite one another relative to the origin signify opposite trait profiles. Performance of an entry with regard to a trait is better than average if the angle between its vector and the trait's vector is less than 90°; lower than average if greater than 90°; and near average if the angle is near 90°.

Results and discussion

Environments analyzed

College Station, McGregor, and Leonard locations of 2009 and 2010 were analyzed according to the Hartley's test and variances were not significantly different among environments. Normality tests of each location by year proved data to be normal.

Pearson correlations in combined and individual environments

Correlations between yield and its components were calculated over two years. Across locations grain yield was significantly ($P < .01$) and positively correlated with head number and seed per head (.54 and .53, respectively; Table 4.1). No significant negative correlations between yield components were observed in the combined analysis.

Analysis within locations proved significant negative correlations existed between components. In College Station, seed per head was negatively correlated with seed weight and head number. In Leonard, head number was negatively correlated with seed weight and seed per head. No significant correlations existed between yield components in McGregor. In all locations no significant positive correlation existed

between yield components, which was expected as similar results have been found (Narasimhamoorthy et al., 2006). Negative correlations between yield components in Leonard and College Station indicate yield component compensation.

Significant positive correlations between yield and its components varied within locations. In College Station, a positive correlation existed between seed weight and yield. All locations showed a positive correlation between head number and yield. Leonard and McGregor illustrated a positive correlation between seed per head and yield. Positive but not necessarily significant correlations coefficients with yield were found in all locations except in Leonard, which had a negative but insignificant correlation with seed weight.

In previous studies of synthetic wheats, head number and seed per head were positively correlated with grain yield and negatively correlated with seed weight (del Blanco 2001; Mohsin et al., 2009). In a study of 190 lines derived from a synthetic cross to Hard Red Winter Wheat, yield was only significantly and positively correlated with seed weight (Narasimhamoorthy et al., 2006).

Table 4.1 Correlation coefficients for yield and its components of synthetic backcross wheat lines in Texas during 2009 and 2010.

Trait	Seed wt.	Head number	Seed/head	Yield
<i>College Station, McGregor, and Leonard</i>				
Seed wt.	1.00	-0.22	-0.21	0.08
Head number	-	1.00	-0.28	0.54**
Seed/head	-	-	1.00	0.53**
Yield	-	-	-	1.00
<i>College Station</i>				
Seed wt.	1.00	0.09	-0.34*	0.38*
Head number	-	1.00	-0.51**	0.64**
Seed/head	-	-	1.00	0.10
Yield	-	-	-	1.00
<i>McGregor</i>				
Seed wt.	1.00	-0.24	0.01	0.17
Head number	-	1.00	-0.30	0.33*
Seed/head	-	-	1.00	0.50**
Yield	-	-	-	1.00
<i>Leonard</i>				
Seed wt.	1.00	-0.43**	-0.28	-0.20
Head number	-	1.00	-0.31*	0.54**
Seed/head	-	-	1.00	0.41**
Yield	-	-	-	1.00

* Significant at the 0.05 probability level

** Significance at the 0.01 probability level

Table 4.2 Direct^a and indirect effects and total correlation with grain yield of yield components of synthetic backcross wheat lines in Texas during 2009 and 2010.

Component	Seed wt.	Head number	Seed/head	Nobs	Total
<i>College Station, McGregor, and Leonard</i>					
Seed wt.	<u>0.46</u>	-0.19	-0.18	40	0.08
Head number	-0.10	<u>0.88</u>	-0.25	40	0.54
Seed/head	-0.09	-0.25	<u>0.87</u>	40	0.53
<i>College Station</i>					
Seed wt.	<u>0.57</u>	0.09	-0.28	40	0.38
Head number	0.05	<u>1.01</u>	-0.42	40	0.64
Seed/head	-0.19	-0.52	<u>0.81</u>	40	0.10
<i>McGregor</i>					
Seed wt.	<u>0.31</u>	-0.14	0.01	40	0.17
Head number	-0.07	<u>0.60</u>	-0.20	40	0.33
Seed/head	0.00	-0.18	<u>0.68</u>	40	0.50
<i>Leonard</i>					
Seed wt.	<u>0.47</u>	-0.43	-0.24	40	-0.20
Head number	-0.20	<u>1.01</u>	-0.26	40	0.54
Seed/head	-0.13	-0.31	<u>0.85</u>	40	0.41

^adirect effects underlined

Path coefficient analysis

Table 4.2 shows the direct and indirect effects of yield components on grain yield. Across locations, seed weight had a positive direct effect on yield but this was removed by a similarly strong, indirect negative effect of head number and seed per head. Head number had a strong positive influence on yield that was brought down slightly by indirect effects from seed per head and seed weight. Likewise, seed per head had a high direct effect on yield that was lowered by seed weight and head number. In both of these instances seed weight was the lesser of the opposing effects. These indirect negative effects were expected because yield components are competitive sinks and as one component increases usually another decreases.

Similar to the combined analysis, individual locations showed indirect, opposing effects of either head number or seed per head removed direct effects of seed weight.

In College Station, head number had the highest direct effect and total correlation. A negative indirect effect of seed per head was not strong enough to significantly lower the total correlation. Seed per head had a high direct effect but was significantly lowered due mostly to the opposing indirect effect of head number. Seed weight had a positive total correlation due to a high direct effect despite a negative indirect effect of seed per head. Interestingly, seed weight and head number both had small but positive indirect effects on one another with regards to yield.

In McGregor, seed per head had the highest total correlation with yield followed by head number. Both traits had similar direct effects on yield with insignificant indirect effects.

Leonard was the only location from the Pearson correlations to show a negative correlation between a yield and a yield component, seed weight (Table 4.1). Path coefficient analysis shows the component to have a positive direct effect but opposing indirect effects of head number and seed per head cancelled the direct effect (Table 4.2). Head number and seed per head had high positive direct effects. Negative indirect effects from other components were insignificant for total correlation.

Direct effects of yield components to yield were similar for all locations. Most discrepancies between locations were due to indirect opposing effects. This is similar to findings by Akanda and Mundt (1996).

Table 4.3 Bootstrap 95% confidence intervals of yield component direct effects on grain yield of synthetic back cross wheat lines in locations of Texas during 2009 and 2010.

Components	Lower ^a	Observed ^b	Upper ^c
<i>College Station, McGregor, and Leonard</i>			
Seed wt.	0.32	0.46	0.66
Head number	0.63	0.88	1.16
Seed/head	0.69	0.87	1.07
<i>College Station</i>			
Seed wt.	0.38	0.57	0.79
Head number	0.82	1.01	1.26
Seed/head	0.64	0.81	1.01
<i>McGregor</i>			
Seed wt.	0.08	0.31	0.52
Head number	0.38	0.60	0.83
Seed/head	0.48	0.68	0.88
<i>Leonard</i>			
Seed wt.	0.27	0.47	0.66
Head number	0.72	1.01	1.38
Seed/head	0.65	0.85	1.11

^aapproximate lower confidence limit

^bobserved statistic

^capproximate upper confidence limit

Re-sampling techniques, such as bootstrap, provide estimates of standard error, confidence intervals, and distribution of any statistic (Efron and Tibshirani, 1993).

Direct effects were estimated from a set of 1000 samples obtained through random re-sampling with replacement. Observed direct effects were in agreement with calculated confidence intervals indicating the robustness of the path sequential model (Table 4.3). Confidence intervals show all yield components to have positive direct effects on yield.

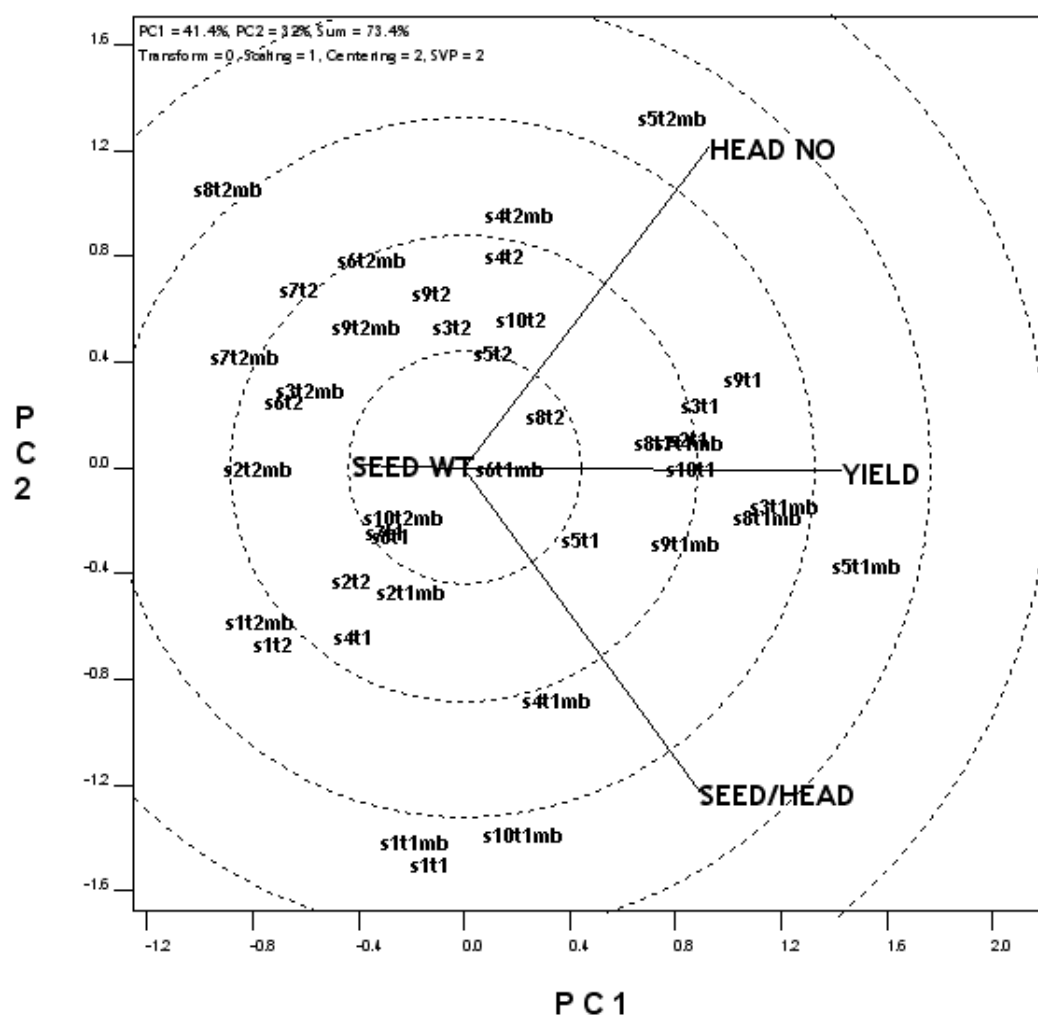


Figure 4.1 GGE biplot based on trait means of 40 synthetic backcross wheat lines at College Station, McGregor, and Leonard, TX during 2009 and 2010. Codes of traits are: YIELD = grain yield; SEED WT = individual seed weight; SEED/HEAD = number of seeds per head; HEAD NO = number of heads per unit area. Lines are labeled by synthetic parent first and recurrent parent second. Codes of synthetic parent: s1 = E95Syn4152-5, s2 = E95Syn4152-7, s3 = E95Syn4152-16, s4 = E95Syn4152-37, s5 = E95Syn4152-51, s6 = E95Syn4152-61, s7 = E95Syn4152-77, s8 = E95Syn4152-78, s9 = E2Syn4153-3, s10 = E2Syn4153-31; Codes of recurrent parent: t1 = TAM111; t2 = TAM112. Lines derived from modified bulk breeding method are labeled 'mb'.

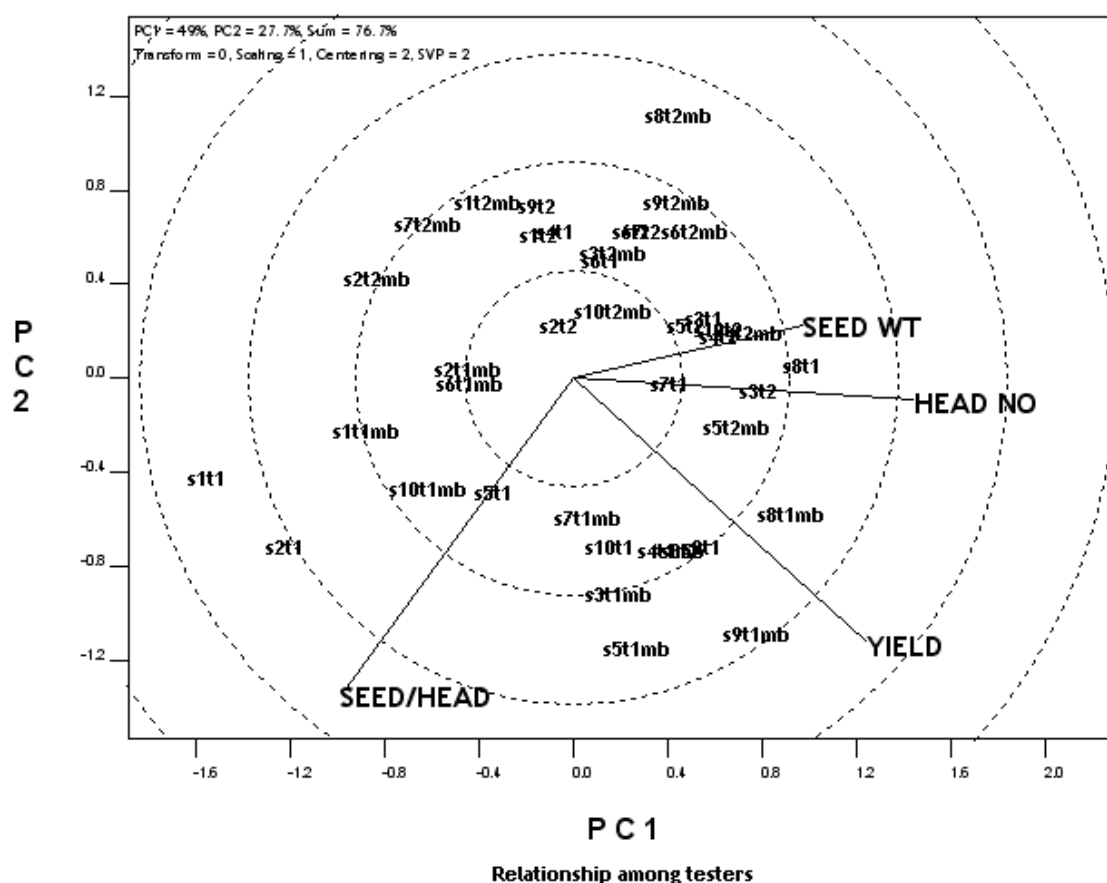


Figure 4.2 GGE biplot based on trait means of 40 synthetic backcross wheat lines at College Station, TX during 2009 and 2010. Codes of traits are: YIELD = grain yield; SEED WT= individual seed weight; SEED/HEAD = number of seeds per head; HEAD NO = number of heads per unit area. Lines are labeled by synthetic parent first and recurrent parent second. Codes of synthetic parent: s1 = E95Syn4152-5, s2 = E95Syn4152-7, s3 = E95Syn4152-16, s4 = E95Syn4152-37, s5 = E95Syn4152-51, s6 = E95Syn4152-61, s7 = E95Syn4152-77, s8 = E95Syn4152-78, s9 = E2Syn4153-3, s10 = E2Syn4153-31; Codes of recurrent parent: t1 = TAM111; t2 = TAM112. Lines derived from modified bulk breeding method are labeled 'mb'.

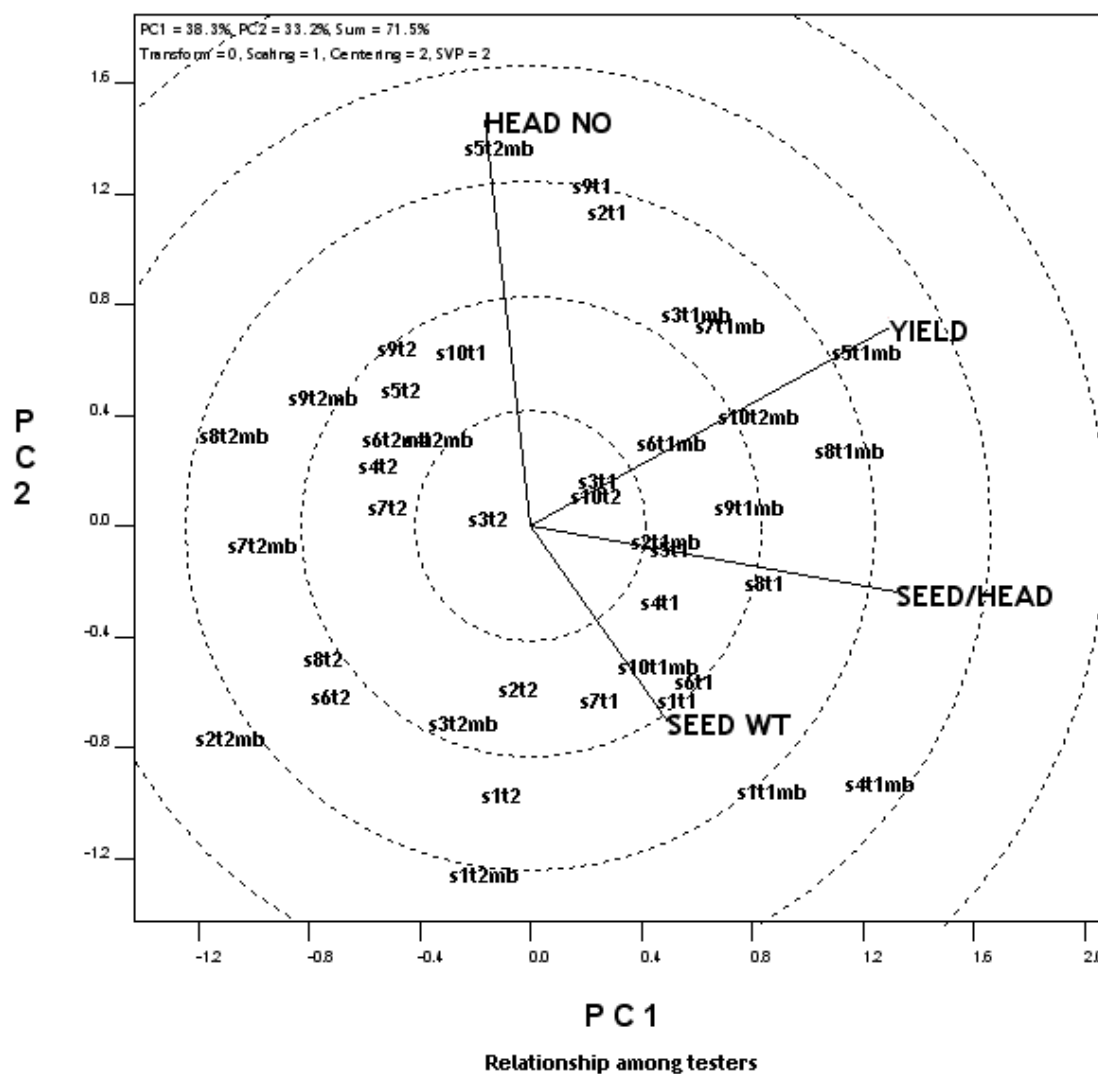


Figure 4.3 GGE biplot based on trait means of 40 synthetic backcross wheat lines at McGregor, TX during 2009 and 2010. Codes of traits are: YIELD = grain yield; SEED WT = individual seed weight; SEED/HEAD = number of seeds per head; HEAD NO = number of heads per unit area. Lines are labeled by synthetic parent first and recurrent parent second. Codes of synthetic parent: s1 = E95Syn4152-5, s2 = E95Syn4152-7, s3 = E95Syn4152-16, s4 = E95Syn4152-37, s5 = E95Syn4152-51, s6 = E95Syn4152-61, s7 = E95Syn4152-77, s8 = E95Syn4152-78, s9 = E2Syn4153-3, s10 = E2Syn4153-31; Codes of recurrent parent: t1 = TAM111; t2 = TAM112. Lines derived from modified bulk breeding method are labeled 'mb'.

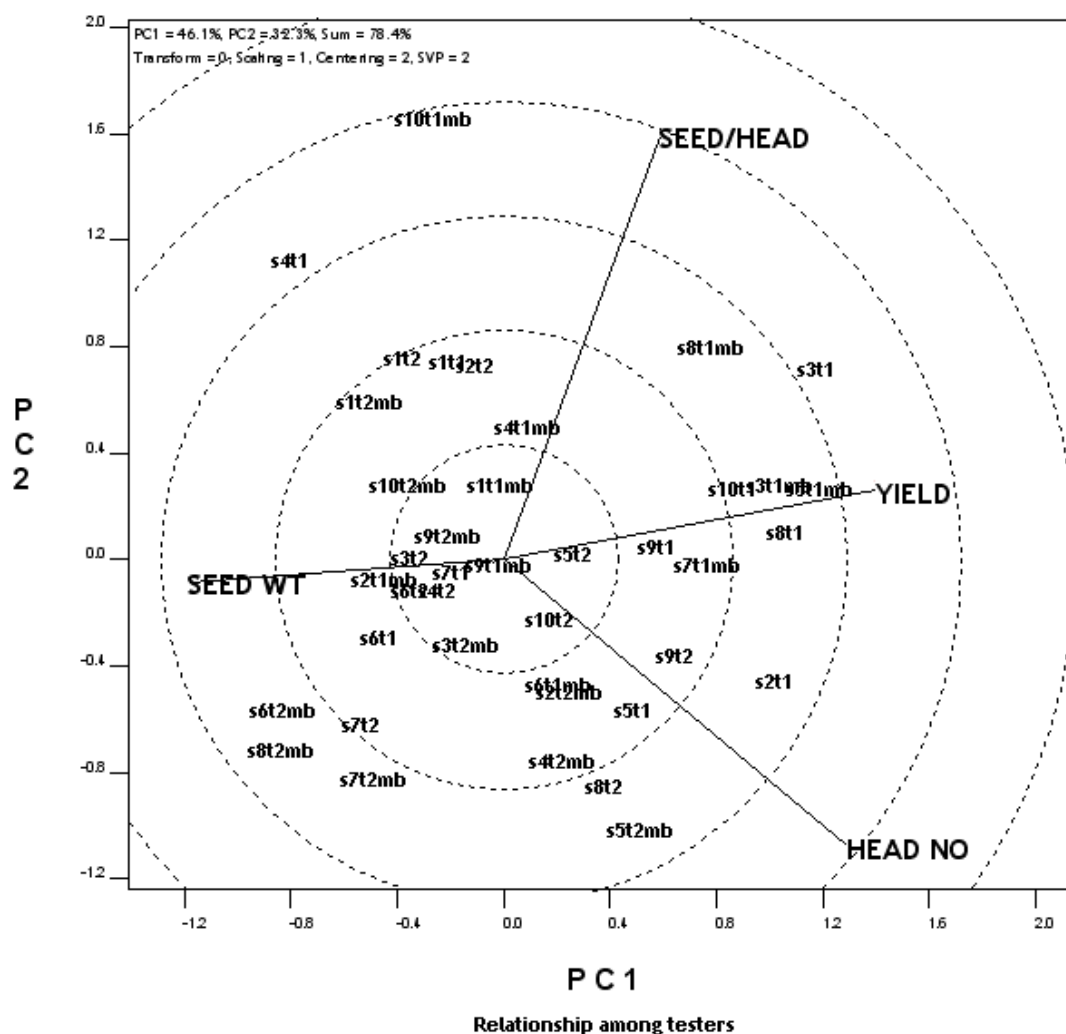


Figure 4.4 GGE biplot based on trait means of 40 synthetic backcross wheat lines at Leonard, TX during 2009 and 2010. Codes of traits are: YIELD = grain yield; SEED WT= individual seed weight; SEED/HEAD = number of seeds per head; HEAD NO = number of heads per unit area. Lines are labeled by synthetic parent first and recurrent parent second. Codes of synthetic parent: s1 = E95Syn4152-5, s2 = E95Syn4152-7, s3 = E95Syn4152-16, s4 = E95Syn4152-37, s5 = E95Syn4152-51, s6 = E95Syn4152-61, s7 = E95Syn4152-77, s8 = E95Syn4152-78, s9 = E2Syn4153-3, s10 = E2Syn4153-31; Codes of recurrent parent: t1 = TAM111; t2 = TAM112. Lines derived from modified bulk breeding method are labeled 'mb'.

Genotype-by-trait biplot analysis

Another procedure used to view the influence of yield components on yield was genotype-by-trait biplot. Biplot analysis has not been used prior to illustrate yield components of synthetic wheat. GGE biplots of traits of synthetic entries were developed for combined and individual locations (Figures 4.1 – 4.4). These biplots show the similar trait profiles of genotypes and help to identify traits that can be used in indirect selection (Yan and Tinker 2006).

Across 40 synthetic lines in Stxbl environments, head number and seed per head were positively associated with yield as noted by acute angles (Figure 4.1). Angles were similar to one another, indicating similar correlations with yield. Because traits were on opposite sides of the yield vector, components had indirect negative effects on yield via one another. Because seed weight had negative correlations with seed per head and head number and had the lowest total correlation with yield, its vector is in the opposite direction. In this case, this does not necessarily mean seed weight is negatively correlated with yield but that its correlation was the lowest of the three. From angles between trait vectors, one can see head number and seed per head have similar positive correlations with yield and similar negative correlations with seed weight. Vector length is indicative of discriminating ability of the trait. Seed weight had the lowest discriminating ability, as variation among populations was minimal. Entries closer to discriminating vectors, such as head number, seed per head, or yield have high values for respective traits and vice versa. For example, the entry s10t1mb (SBC46MB) had the highest mean for seed per head and falls close to the vector, while s8t2mb (SBC65MB)

had the lowest mean for seed per head and was opposite the trait in respect to the origin. Therefore, the GGE biplot provides a visual of which populations are similar to one another according to yield and yield components while also displaying which traits are of most interest for increasing yield. In one view, a breeder can decide what component to select for while also deciding which population to choose from.

Figure 4.2 shows correlations and trait profiles of synthetic backcrossed populations in College Station. According to angles with the yield vector, head number had the highest positive total correlation with yield followed by seed weight and seed per head. Seed per head has negative correlations with head number and seed weight and therefore negative indirect effects exist between the traits. Seed weight and head number have positive correlations with one another and therefore positive indirect effects exist between the two. Because head number is closer to yield, the indirect positive effect via head number will be greater than the indirect positive effect via seed weight. From this visual one can see that head number would be the most valuable trait to select for in College Station as it has the highest positive correlation with yield and positive correlations with seed weight.

McGregor correlations between traits and trait profiles are displayed by the GGE biplot (Figure 4.3). Seed per head had the highest positive correlation with yield followed by head number and seed weight. According to the graph, seed per head and seed weight have negative correlations with head number and therefore negative indirect effects exist between them. Because seed weight and seed per head are on similar sides of the yield vector, they have positive correlations with one another. Similar to the

concept from the College Station biplot, the indirect effect via seed per head should be greater than the indirect effect via seed weight. This is relatively true as path coefficient analysis shows the indirect effect via seed per head (0.01) to be greater than the indirect effect via seed weight (0.00) despite both values being insignificant (Table 4.2). Therefore, the visual is a good comparison but path coefficient values should be determined as well for more precise results. Again, in McGregor, seed weight is the least discriminating trait (Figure 4.3).

Similar to the combined environments, all yield components of synthetics backcrosses from Leonard have negative correlations with one another as indicated by obtuse angles (Figure 4.4). From the biplot, one can see head number to have the highest correlation with yield followed by seed per head and seed weight. Negative indirect effects on yield exist between all components. Because head number is closest to yield, negative indirect effects will be greatest via head number, followed by seed per head. This can be verified in the path coefficient analysis as seed weight has an indirect negative effect via head number (-0.43) that is greater than the negative indirect effect via seed per head (-0.24; Table 4.2). According to the graph, selections should be made for head number or seed per head as these components have the highest correlations with yield and negative indirect effects via seed weight are minimal.

Biplot and path coefficient analysis comparison

According to the results, all biplots were accurate in signifying positive or negative relationships between yield components, which is important in understanding the indirect and direct effects of each trait. Although the GGE biplot is not completely

accurate in showing positive or negative total correlations with yield, it does display how total correlations rank among one another, which is an important factor in deciding which component or components to select for. Another benefit of the biplot was its correct display of trait profiles among the synthetic populations, allowing for populations of particular interest to be identified. This is an advantage over the use of path coefficient tables as no information is given regarding entries. In one view, a breeder can determine what component to select for while also deciding which population to choose from.

For these reasons, it may be concluded that GGE biplot analysis enhances path coefficient analysis by providing a graphical display of the data. In a study of interrelationships among traits of white lupin (*Lupinus albus* L.), Rubio et al. made similar conclusions on the benefits of using GGE biplot analysis to visually display path coefficient results (Rubio et al., 2004). However, path coefficient values should be observed as well to determine precise values of direct effects, indirect effects, and total correlation. The use of both methods is beneficial to the observer.

Conclusions

Direct selections of yield are usually unreliable as yield varies greatly among environments due to poor heritability. Furthermore, yield is difficult to measure in the early generations, but visual estimation of head and seed number can be practiced by the experienced breeder. Therefore, selecting a high yielding plant in one location does not guarantee seeds from the plant will produce high yields in another location or

generation. Instead, it is desirable to identify traits that permit efficient indirect selection for yield (Fehr, 1993).

In these environments of College Station, McGregor, and Leonard, TX, selection for high grain yield through direct selection of seed weight would generally be ineffective because of the restrictions imposed by head number and seed per head. This means if seed weight is increased then seed per head and head number would decrease substantially. Although it is assumed some compensation effects will take place under any selection process, the goal is to minimize the effect by choosing the right yield component. It was noted that synthetics generally maintained their large seed weight across years and locations; therefore, higher gain from selection is expected when other components are selected for.

In this study, head number proved to be the most beneficial trait to select for in synthetic backcrosses, as its total correlation was positive and significant for yield in all locations. There were consistent compensatory effects in environments, but they were not large enough to completely offset the positive effect on yield of head number. Because seed per head had a high total correlation with yield in two of the three locations, it may be beneficial to select for as well. However, a significant negative correlation was common between head number and seed per head. Similar findings have been reported in synthetic wheat crosses (Narasimhamoorthy et al., 2006). Therefore, selecting for high tillering and high seed per head may prove to be difficult. Fortunately, selection for either trait will not sacrifice seed size as indirect effects were negligible.

Genotype-by-trait biplots generally produced similar results to Pearson correlations. The biplot is useful for providing a visual of yield component association with yield but should be accompanied by path coefficient analysis for accurate and precise results.

CHAPTER V

HERITABILITY AND COMBINING ABILITY OF SYNTHETIC POPULATIONS

Introduction

Synthetic hexaploid wheats are a promising source of improvement for quantitative traits in wheat (*Triticum aestivum* Desf.) (del Blanco et al., 2001). Heritability and combining ability play a major role in predicting the outcome of further generations. Heritability is the measure of genetic variability based on phenotypic variability and allows for the breeder to see which traits are more likely to be passed on to progeny (Fehr, 1993). Heritability estimates of yield and yield components are useful to the breeder when attempting to increase yield. Because yield usually has low heritability, it has been suggested that selecting for one or more yield components, a method of indirect selection, could be more effective in increasing the genetic potential for grain (Johnson et al., 1966a; Smith, 1976). Studies in wheat have shown indirect selection to be advantageous (Ketata et al., 1976; Sharma and Knott, 1964; Sidwell et al., 1976), but in some cases direct selection was just as valuable (Alexander et al., 1984).

Combining ability is important for hybrid crosses. If the superiority of the hybrid is great, then the parents are most likely more genetically diverse than parents producing little or no heterosis (Hallauer & Miranda, 1998).

The main objective of this study was to determine the heritability and combining ability in synthetic lines backcrossed to Texas wheats. Four methods of heritability were compared: variance component heritability (h^2_{vc}), parent-offspring regression (b) parent-

offspring correlation (r), and realized heritability. The last three methods are usually used in estimating heritability in bi-parental populations. Their use in this study is solely for comparison to variance component heritability. The use of GGE biplot analysis for evaluating combining ability will also be discussed.

Materials and methods

Plant material

Forty synthetic backcross lines were planted in a randomized complete block design with two replications in the field at Bushland, Chillicothe, College Station, McGregor, and Leonard, TX as described in chapter III. SBCF₄ and SBCF₅ lines were harvested in 2009 and 2010, respectively. Description of location information and trial management is outlined in chapter III.

Measurements

Grain yield of all locations was measured according to chapter III. Yield component traits of seed weight, head number, and seed per head were obtained in College Station, McGregor, and Leonard as described in chapter III.

Heritability estimates

Heritability of yield and its components was estimated using variance component heritability (h^2_{vc}), parent-offspring regression (b) parent-offspring correlation (r), and realized heritability. Parent-offspring regression heritability values were adjusted for degree of inbreeding as suggested by Smith and Kinman (1965).

Variance component heritability

Variance component heritability (h^2_{vc}) was calculated from mean squares as described by Fehr (1993).

Genotypic variance was calculated as:

$$\sigma^2_g = [(MS1 + MS4) - (MS2 + MS3)]/rly$$

where MS1 = mean squares of lines, MS2 = mean squares of lines-by-years interaction, MS3 = mean squares of lines-by-locations interaction, MS4 = mean squares of lines-by-years-by-locations interaction, r = number of replications, l = number of locations, and y = number of years.

Phenotypic variance was calculated as:

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Broad-sense heritability was then calculated as:

$$h^2 = \sigma^2_g / \sigma^2_p$$

Parent-offspring regression

Linear regression coefficients (b) were calculated by regressing F_5 progeny means (Y_i) on F_4 parental means (X_i) using SAS proc reg (SAS Institute Inc., 2008). Because parents in F_4 are selfed lines, an adjustment factor of 8/15 was applied to the heritability estimate according to Smith and Kinman (1965).

Parent offspring correlation

To find the parent-offspring correlation (r), simple linear correlation of genotype means between years was calculated using SAS proc CORR (SAS Institute Inc., 2008).

Realized heritability

Estimates of realized heritability were calculated using the following formula (Guthrie et al., 1984):

$$H_R^2 = \frac{\overline{F_5H} - \overline{F_5L}}{\overline{F_4H} - \overline{F_4L}}$$

where $\overline{F_5H}$ = mean of high F_5 lines, $\overline{F_5L}$ = mean of low F_5 lines, $\overline{F_4H}$ = mean of high F_4 selections, $\overline{F_4L}$ = mean of low F_4 selections, based on 10% selection intensity.

Biplot analysis

To generate biplots for yield and yield components, GGEbiplot software was used according to Yan and Kang (2003). Because an atypical diallel was used in this study, all genotypes were used as entries and only recurrent parents were used as testers. A two-way matrix of entries and testers was generated from mean values for hybrids. Rows were regarded as entries and columns as testers. The biplot model used was as follows:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

where Y_{ij} = expected value of entry i and tester j , μ = grand mean, β_j = mean of all crosses to j , λ_1 = PC1, ξ_{i1} = PC1 eigenvector of entry i , η_{j1} = PC1 eigenvector of tester j , λ_2 = PC2, ξ_{i2} = PC2 eigenvector of entry i , η_{j2} = PC2 eigenvector of tester j , and ϵ_{ij} = residual of model associated with combinations of entry i and tester j .

The GGEbiplot software generated average tester coordinate view and polygon view of the data. Biplots were interpreted according to Yan and Hunt (2002) and Yan and Kang (2003). General combining ability (GCA) effects were approximated by

projections of the entries onto the average tester coordinate (ATC) abscissa, which is the vector of the average tester. Specific combining ability (SCA) effects of entries were approximated by their projections from the biplot origin onto the ATC ordinate.

Polygon views of the biplots displayed interactions between testers and entries. Connecting the outermost entries, a.k.a. vertex entries, from the origin created the polygon. It was then divided into sectors by perpendicular lines from each polygon side to the origin. A tester would form a superior hybrid with the vertex entry of the sector it was located in. If a tester and entry of the same genotype fell in the same sector, no hybrids would be superior to the pure line.

Results and discussion

Environments analyzed

Due to climate similarities, Bushland and Chillicothe were grouped to represent the High and Rolling Plains regions of Texas (Plains), and College Station, McGregor, and Leonard were grouped to represent South Texas and the Blacklands (Stxbl). These environments were analyzed according to the Hartley's test and variances were not significantly different within groups. Normality tests of each location by year proved data to be normal.

Comparison of heritability estimates

Among the Stxbl region, variance component and parent-offspring regression gave similar heritability estimates (Table 5.1). Realized heritability and parent offspring correlation estimates were similar to one another and higher than the other methods. Estimations in these two methods were expected to be less conservative as they did not

account for inbreeding depression in the selfed lines (Fehr, 1993; Smith and Kinman, 1965). Because populations of different backcross combinations were used in this study, variance component heritability is the most reliable method of the four estimates. Other methods used are designed for related lines derived from the same set of parents (Fehr, 1993). However, it is interesting that heritability estimates across methods agree with one another in this study.

Table 5.1 Estimates of heritability for yield and its components in synthetic backcross lines, using variance component heritability (h^2_{VC}), parent offspring regression (b), parent offspring correlation (r), and realized heritability (Rh^2) among F_4 plants and their F_5 progenies.

Trait	n	h^2_{VC}	b	r	h^2_R
<i>College Station, McGregor, and Leonard</i>					
Yield	40	-0.212	-0.0121	-0.014	-0.313
Seed weight	40	0.329	0.368	0.608	0.598
Head Number	40	0.152	0.096	0.283	0.177
Seeds/head	40	0.250	0.291	0.406	0.594
<i>Bushland and Chillicothe</i>					
Yield	40	0.338	0.211	0.281	0.455

Heritability among yield components

Heritability estimates for yield were very poor (-0.313 to -0.012) in the Stxbl region (Table 5.1). Negative heritability was assumed as zero (Robinson et al., 1955). Low values were expected, as yield is a complex trait with low heritability in wheat. All yield components of the synthetic populations had higher heritability than yield. This is important because the effectiveness of indirect selection is made better when the secondary variable has a higher heritability than the variable of ultimate importance (Fehr, 1993). Therefore, selection for any of the three yield components would be better than direct selection of yield. Head number had lower estimates and seed per head and

seed weight had intermediate to high estimates. Seed weight had the highest heritability (0.329 – 0.608). Heritability values in synthetic populations were similar to generally accepted relative magnitudes in wheat, with seed weight having the highest heritability followed by seed per head, head number, and grain yield (Johnson et al., 1966a; Kronstad and Foote, 1964; Smith, 1976). In the Plains region, heritability of yield was positive (0.211 to 0.455). Heritability estimates of this region were not important in this study, as no synthetics were superior to recurrent parents in Bushland and Chillicothe and no measurements of yield components were taken.

Results indicate good gain from selection of seed weight and seed per head can be expected. Even fair gain from selection is expected from using head number due to the relatively higher heritability compared to yield. Because seed weight is highly heritable in these synthetics and because all populations had superior seed weights across environments, breeders may focus their attention on other desired traits. This would be beneficial as the previously calculated correlations are not significantly high for yield and seed weight (Table 4.1). Because head number has a relatively low heritability, selections for this trait should be made repeatedly as it is highly influenced by the environment.

Table 5.2 Combining ability means of synthetic lines in Bushland and Chillicothe, TX during 2009 and 2010.

Entry	Line	Bushland		Chillicothe		Total Mean
		2009	2010	2009	2010	
s1	E95Syn4152-5	16.4 ¹	21.6 ¹⁰	15.7 ⁹	47.2 ⁷	25.3 ⁹
s2	E95Syn4152-7	15.7 ³	23.7 ⁹	16.4 ⁶	48.0 ⁶	25.5 ⁷
s3	E95Syn4152-16	14.7 ⁵	27.8 ¹	15.9 ⁸	44.1 ⁹	25.9 ⁶
s4	E95Syn4152-37	16.4 ²	27.6 ²	19.7 ¹	49.5 ⁴	27.8 ¹
s5	E95Syn4152-51	13.8 ⁹	26.3 ⁴	17.6 ³	50.8 ¹	27.1 ²
s6	E95Syn4152-61	14.7 ⁶	25.0 ⁶	17.0 ⁴	43.1 ¹⁰	25.4 ⁸
s7	E95Syn4152-77	14.6 ⁷	25.4 ⁵	14.1 ¹⁰	45.6 ⁸	25.1 ¹⁰
s8	E95Syn4152-78	15.0 ⁴	26.6 ³	16.7 ⁵	48.4 ⁵	26.5 ⁴
s9	E2Syn4153-3	13.1 ¹⁰	24.4 ⁷	18.9 ²	49.7 ³	26.6 ³
s10	E2Syn4153-31	14.3 ⁸	23.9 ⁸	16.0 ⁷	50.3 ²	26.3 ⁵
t1	TAM 111	14.4	25.4	16.0	46.5	25.6
t2	TAM 112	15.5	25.1	17.8	48.2	26.7

*Rank among synthetic lines is noted to right of mean values;

Table 5.3 Combining ability means of synthetic lines across College Station, McGregor, and Leonard, TX during 2009 and 2010.

Entry	Line	Yield	Seed wt.	Head number	Seed/head
		(bu/ac)	(g)	(no)	(no)
s1	E95Syn4152-5	34.0 ⁹	0.0307 ³	1044.5 ¹⁰	28.1 ¹
s2	E95Syn4152-7	33.5 ¹⁰	0.0280 ¹⁰	1205.7 ⁹	27.3 ²
s3	E95Syn4152-16	38.4 ²	0.0301 ⁵	1309.6 ⁴	25.9 ⁵
s4	E95Syn4152-37	37.3 ⁶	0.0310 ¹	1256.0 ⁵	25.7 ⁶
s5	E95Syn4152-51	40.2 ¹	0.0299 ⁷	1357.3 ¹	26.2 ⁴
s6	E95Syn4152-61	35.2 ⁷	0.0309 ²	1233.5 ⁷	25.2 ⁹
s7	E95Syn4152-77	34.6 ⁸	0.0300 ⁶	1255.1 ⁶	24.8 ¹⁰
s8	E95Syn4152-78	37.8 ⁵	0.0298 ⁸	1317.4 ³	25.6 ⁷
s9	E2Syn4153-3	37.9 ³	0.0295 ⁹	1318.0 ²	25.6 ⁸
s10	E2Syn4153-31	37.9 ⁴	0.0304 ⁴	1230.8 ⁸	27.2 ³
t1	TAM111	38.6	.0296	1242.8	30.1
t2	TAM112	34.8	.0304	1262.8	26.2
Grand mean		36.7	0.0299	1264.5	28.2

*Rank among synthetic lines is noted to right of mean values.

Table 5.4 Combining ability means of synthetic lines in College Station, TX during 2009.

Entry	Line	Yield (bu/ac)	Seed wt. (g)	Head number (no)	Seed/head (no)
s1	E95Syn4152-5	23.1 ¹⁰	0.0259 ³	743 ¹⁰	36.4 ²
s2	E95Syn4152-7	26.0 ⁹	0.0224 ¹⁰	1025 ⁷	34.0 ⁴
s3	E95Syn4152-16	31.9 ²	0.0246 ⁹	1219 ¹	32.8 ⁶
s4	E95Syn4152-37	34.4 ¹	0.0257 ⁴	1204 ²	33.9 ⁵
s5	E95Syn4152-51	31.2 ⁵	0.0251 ⁸	1060 ⁶	36.2 ³
s6	E95Syn4152-61	26.3 ⁸	0.0256 ⁶	983 ⁸	31.6 ⁹
s7	E95Syn4152-77	30.9 ⁶	0.0255 ⁷	1086 ⁵	32.7 ⁷
s8	E95Syn4152-78	30.0 ⁷	0.0265 ¹	1118 ³	30.2 ¹⁰
s9	E2Syn4153-3	31.4 ⁴	0.0257 ⁵	1094 ⁴	32.6 ⁸
s10	E2Syn4153-31	31.5 ³	0.0264 ²	949 ⁹	37.7 ¹
t1	TAM111	28.7	0.0247	1013	35.0
t2	TAM112	30.6	0.0256	1091	32.8

*Rank among synthetic lines is noted to right of mean values;

Table 5.5 Combining ability means of synthetic lines in College Station, TX during 2010.

Entry	Line	Yield (bu/ac)	Seed wt. (g)	Head number (no)	Seed/head (no)
s1	E95Syn4152-5	33.4 ⁹	0.0372 ⁶	770 ¹⁰	31.3 ²
s2	E95Syn4152-7	32.6 ¹⁰	0.0326 ¹⁰	831 ⁹	32.7 ¹
s3	E95Syn4152-16	38.9 ⁴	0.0372 ⁵	1013 ⁴	28.2 ⁷
s4	E95Syn4152-37	35.7 ⁷	0.0379 ²	956 ⁷	26.4 ¹⁰
s5	E95Syn4152-51	42.0 ²	0.0377 ³	1040 ²	29.3 ³
s6	E95Syn4152-61	37.3 ⁵	0.0382 ¹	963 ⁶	27.5 ⁸
s7	E95Syn4152-77	34.3 ⁸	0.0368 ⁹	881 ⁸	29.0 ⁴
s8	E95Syn4152-78	44.9 ¹	0.0374 ⁴	1155 ¹	28.8 ⁵
s9	E2Syn4153-3	40.9 ³	0.0372 ⁷	1033 ³	28.5 ⁶
s10	E2Syn4153-31	36.9 ⁶	0.0371 ⁸	1011 ⁵	27.5 ⁹
t1	TAM111	43.3	0.0366	1010	32.0
t2	TAM112	31.5	0.0368	896.4	26.3

*Rank among synthetic lines is noted to right of mean values;

Table 5.6 Combining ability means of synthetic lines in McGregor, TX during 2009.

Entry	Line	Yield (bu/ac)	Seed wt. (g)	Head number (no)	Seed/head (no)
s1	E95Syn4152-5	51.2 ⁷	0.0310 ¹	1590 ¹⁰	29.5 ¹
s2	E95Syn4152-7	50.2 ¹⁰	0.0286 ⁷	1799 ⁹	27.4 ⁶
s3	E95Syn4152-16	53.2 ⁴	0.0300 ³	1869 ⁶	26.6 ⁸
s4	E95Syn4152-37	53.6 ³	0.0297 ⁵	1917 ⁴	27.6 ⁵
s5	E95Syn4152-51	60.6 ¹	0.0279 ¹⁰	2211 ¹	28.1 ³
s6	E95Syn4152-61	53.0 ⁶	0.0304 ²	1840 ⁸	27.8 ⁴
s7	E95Syn4152-77	51.2 ⁸	0.0295 ⁶	1868 ⁷	26.8 ⁷
s8	E95Syn4152-78	50.9 ⁹	0.0282 ⁸	1933 ³	26.6 ⁹
s9	E2Syn4153-3	53.2 ⁵	0.0281 ⁹	2085 ²	25.6 ¹⁰
s10	E2Syn4153-31	55.8 ²	0.0299 ⁴	1877 ⁵	28.1 ²
t1	TAM111	52.0	0.0289	1767	29.2
t2	TAM112	54.1	0.0297	2026	25.4

*Rank among synthetic lines is noted to right of mean values;

Table 5.7 Combining ability means of synthetic lines in McGregor, TX during 2010.

Entry	Line	Yield (bu/ac)	Seed wt. (g)	Head number (no)	Seed/head (no)
s1	E95Syn4152-5	40.2 ⁶	0.0338 ²	1260 ¹⁰	26.1 ²
s2	E95Syn4152-7	36.2 ¹⁰	0.0318 ⁹	1341 ⁷	22.9 ⁹
s3	E95Syn4152-16	42.1 ¹	0.0330 ³	1452 ²	24.0 ⁷
s4	E95Syn4152-37	42.1 ²	0.0349 ¹	1365 ⁶	24.5 ⁵
s5	E95Syn4152-51	39.9 ⁷	0.0323 ⁷	1308 ⁸	25.4 ⁴
s6	E95Syn4152-61	39.4 ⁸	0.0329 ⁴	1435 ³	23.0 ⁸
s7	E95Syn4152-77	36.9 ⁹	0.0328 ⁵	1411 ⁵	21.5 ¹⁰
s8	E95Syn4152-78	41.4 ⁴	0.0321 ⁸	1274 ⁹	26.7 ¹
s9	E2Syn4153-3	40.7 ⁵	0.0308 ¹⁰	1422 ⁴	25.7 ³
s10	E2Syn4153-31	42.0 ³	0.0328 ⁶	1468 ¹	24.2 ⁶
t1	TAM111	46.5	0.0330	1459	26.8
t2	TAM112	33.4	0.0325	1283	21.8

*Rank among synthetic lines is noted to right of mean values;

Table 5.8 Combining ability means of synthetic lines in Leonard, TX during 2009.

Entry	Line	Yield (bu/ac)	Seed wt. (g)	Head number (no)	Seed/head (no)
s1	E95Syn4152-5	23.6 ⁷	0.0235 ⁷	1046 ¹⁰	25.7 ²
s2	E95Syn4152-7	25.5 ⁴	0.0213 ¹⁰	1366 ⁴	22.1 ⁶
s3	E95Syn4152-16	28.5 ²	0.0232 ⁸	1357 ⁵	24.5 ³
s4	E95Syn4152-37	24.2 ⁶	0.0240 ⁴	1187 ⁸	23.8 ⁴
s5	E95Syn4152-51	29.8 ¹	0.0249 ²	1538 ¹	20.2 ⁷
s6	E95Syn4152-61	23.5 ⁸	0.0258 ¹	1347 ⁶	18.3 ¹⁰
s7	E95Syn4152-77	22.1 ¹⁰	0.0230 ⁹	1430 ³	19.3 ⁹
s8	E95Syn4152-78	23.2 ⁹	0.0237 ⁶	1506 ²	19.9 ⁸
s9	E2Syn4153-3	25.3 ⁵	0.0237 ⁵	1240 ⁷	23.7 ⁵
s10	E2Syn4153-31	27.6 ³	0.0244 ³	1186 ⁹	26.2 ¹
t1	TAM111	22.7	0.0231	1227	22.7
t2	TAM112	27.8	0.0240	1429	21.9

*Rank among synthetic lines is noted to right of mean values;

Table 5.9 Combining ability means of synthetic lines in Leonard, TX during 2010.

Entry	Line	Yield (bu/ac)	Seed wt. (g)	Head number (no)	Seed/head (no)
s1	E95Syn4152-5	32.4 ⁷	0.0329 ²	858 ⁸	31.9 ⁴
s2	E95Syn4152-7	30.8 ¹⁰	0.0310 ¹⁰	873 ⁷	31.4 ⁸
s3	E95Syn4152-16	35.9 ⁴	0.0325 ³	947 ³	31.9 ³
s4	E95Syn4152-37	33.7 ⁵	0.0339 ¹	907 ⁵	31.3 ⁹
s5	E95Syn4152-51	37.7 ¹	0.0316 ⁷	987 ²	32.7 ²
s6	E95Syn4152-61	31.8 ⁹	0.0325 ⁴	833 ¹⁰	31.8 ⁵
s7	E95Syn4152-77	32.1 ⁸	0.0323 ⁵	856 ⁹	31.7 ⁷
s8	E95Syn4152-78	36.4 ²	0.0311 ⁹	918 ⁴	34.6 ¹
s9	E2Syn4153-3	36.2 ³	0.0316 ⁸	1034 ¹	30.0 ¹⁰
s10	E2Syn4153-31	33.4 ⁶	0.0320 ⁶	893 ⁶	31.8 ⁶
t1	TAM111	36.9	0.0314	935	34.4
t2	TAM112	31.4	0.0329	890	29.6

*Rank among synthetic lines is noted to right of mean values;

Combining ability means across environments

Combining ability means were calculated by averaging trait means of populations with the same synthetic parent. Rankings of combining abilities allowed for comparisons to be made between traits and environments. In the Plains region, combining ability rankings for yield varied among years and locations (Table 5.2). Across environments of the Stxbl region, rankings of combining ability means for yield were similar to rankings concerning head number (Table 5.3).

Combining ability means within environments

Combining ability means were calculated within environments, allowing for comparisons (Tables 5.4 – 5.9). Synthetic entry 5 (E95Syn4152-51) ranked among the top two for yield combining ability in four of the six environments. Synthetic entry 3 (4152-16) ranked among the top two for yield in three of the environments. Synthetic entry 8 (4152-78) ranked high in yield combining ability in CS10 and Len10 but low in Len09 and Mc09. In all environments except Len09, synthetic entry 2 (4152-7) had a low combining ability for yield, seed weight, and head number. In four of the environments, rankings of yield combining abilities among synthetics were similar to head number rankings. Therefore, a synthetic with good combining ability for head number will have good combining ability for yield in these environments.

Table 5.10 Combining ability means with TAM 111 and TAM 112 of synthetic lines across Plains.

Syn	TAM 111	TAM 112	Mean
1	22.5 ⁷	25.1⁴	23.8 ⁷
2	22.7 ⁵	25.5³	24.1 ⁴
3	21.6 ⁸	23.4 ⁹	22.5 ⁹
4	26.9 ¹	24.8 ⁵	25.9 ¹
5	23.4 ⁴	25.5 ²	24.5 ²
6	22.6 ⁶	22.7 ¹⁰	22.6 ⁸
7	20.2 ¹⁰	24.1⁷	22.2 ¹⁰
8	21.3 ⁹	26.7¹	24.0 ⁵
9	24.0 ³	24.8 ⁶	24.4 ³
10	24.5 ²	23.4 ⁸	23.9 ⁶

Bolded means are significantly different from other TAM parent, based on LSD values.

Table 5.11 Combining ability means with TAM 111 and TAM 112 of synthetic lines across Stxbl.

Syn	Grain Yield			Seed weight			Head number			Seed per head		
	TAM 111	TAM 112	Mean	TAM 111	TAM 112	Mean	TAM 111	TAM 112	Mean	TAM 111	TAM 112	Mean
s1	34.1 ¹⁰	33.8 ⁶	34.0 ⁹	0.0289 ⁸	0.0325¹	0.0307 ³	1025 ¹⁰	1064 ¹⁰	1045 ¹⁰	32.2¹	28.1 ¹	30.1 ¹
s2	35.3⁹	31.8 ⁹	33.5 ¹⁰	0.0271 ¹⁰	0.0288 ¹⁰	0.0280 ¹⁰	1267⁵	1144 ⁹	1206 ⁹	29.5⁸	27.3 ²	28.4 ⁴
s3	41.2³	35.6 ⁴	38.4 ²	0.0285 ⁹	0.0316³	0.0301 ⁵	1360 ¹	1260 ⁵	1310 ⁴	30.1⁵	25.9 ⁵	28.0 ⁵
s4	37.3 ⁷	37.3 ³	37.3 ⁶	0.0318 ¹	0.0302 ⁶	0.0310 ¹	1128 ⁹	1384²	1256 ⁵	30.1⁴	25.7 ⁶	27.9 ⁶
s5	41.2 ⁴	39.2 ¹	40.2 ¹	0.0292 ⁶	0.0306 ⁵	0.0299 ⁷	1304 ⁴	1411 ¹	1357 ¹	31.1³	26.2 ⁴	28.7 ³
s6	36.7 ⁸	33.7 ⁷	35.2 ⁷	0.0310 ²	0.0308 ⁴	0.0309 ²	1210 ⁷	1257 ⁷	1234 ⁷	28.1¹⁰	25.2 ⁹	26.7 ¹⁰
s7	37.5⁶	31.6 ¹⁰	34.6 ⁸	0.0299 ⁴	0.0300 ⁷	0.0300 ⁶	1265 ⁶	1246 ⁸	1255 ⁶	28.9⁹	24.8 ¹⁰	26.8 ⁹
s8	42.4¹	33.2 ⁸	37.8 ⁵	0.0308 ³	0.0288 ⁹	0.0298 ⁸	1329 ³	1306 ³	1317 ³	29.9⁶	25.6 ⁷	27.8 ⁷
s9	41.7²	34.2 ⁵	37.9 ³	0.0296 ⁵	0.0294 ⁸	0.0295 ⁹	1339 ²	1298 ⁴	1318 ²	29.8⁷	25.6 ⁸	27.7 ⁸
s10	38.4 ⁵	37.3 ²	37.9 ⁴	0.0292 ⁷	0.0316²	0.0304 ⁴	1203 ⁸	1259 ⁶	1231 ⁸	31.3²	27.2 ³	29.2 ²

Bolded means are significantly different from other TAM parent, based on LSD values.

Combining ability means by recurrent parent

To determine the specific combining ability of crosses, combining ability means were calculated according to recurrent parents (Table 5.10, 3.11). According to the results, TAM 112 produced better progeny with synthetics than TAM 111 in the Plains region (Table 5.10). Four hybrids of a synthetic by TAM 112 produced mean yields superior to the same synthetic backcrossed to TAM 111. However, mean yields show

two synthetics to produce higher mean yields with TAM 111 than TAM 112. Therefore, we cannot conclude a better parent overall for synthetic lines in the Plains region.

Previous analysis showed no significantly higher mean yields in crosses to TAM 112 across Stxbl environments. A lack of superior means to TAM 112 may be due to poor combining ability or due to high yields in the check, in which there is no room for improvement in TAM 112. Indeed, TAM 112 performed higher than TAM 111 in most environments. Therefore, the hypothesis is made that superior means were not as abundant in crosses to TAM 112 simply because the yield of TAM 112 was too high to beat. Combining ability results between recurrent parents shows this statement to be false.

According to combining ability means across environments of the Stxbl region, TAM 111 had better combining ability for yield than TAM 112 (Table 5.11). This was mostly due to good combining ability for seed per head. Every synthetic cross to TAM 111 was significantly higher than the same synthetic cross to TAM 112 with regards to seed per head means. Therefore, TAM 111 contributed higher seed per head than TAM 112. All ten synthetic mean yields were higher for crosses to TAM 111 than TAM 112 and five synthetic mean yields were significantly higher for crosses to TAM 111 than TAM 112. Therefore, when choosing recurrent parents for synthetic backcrosses in the Stxbl region, TAM 111 would be the better choice of the two.

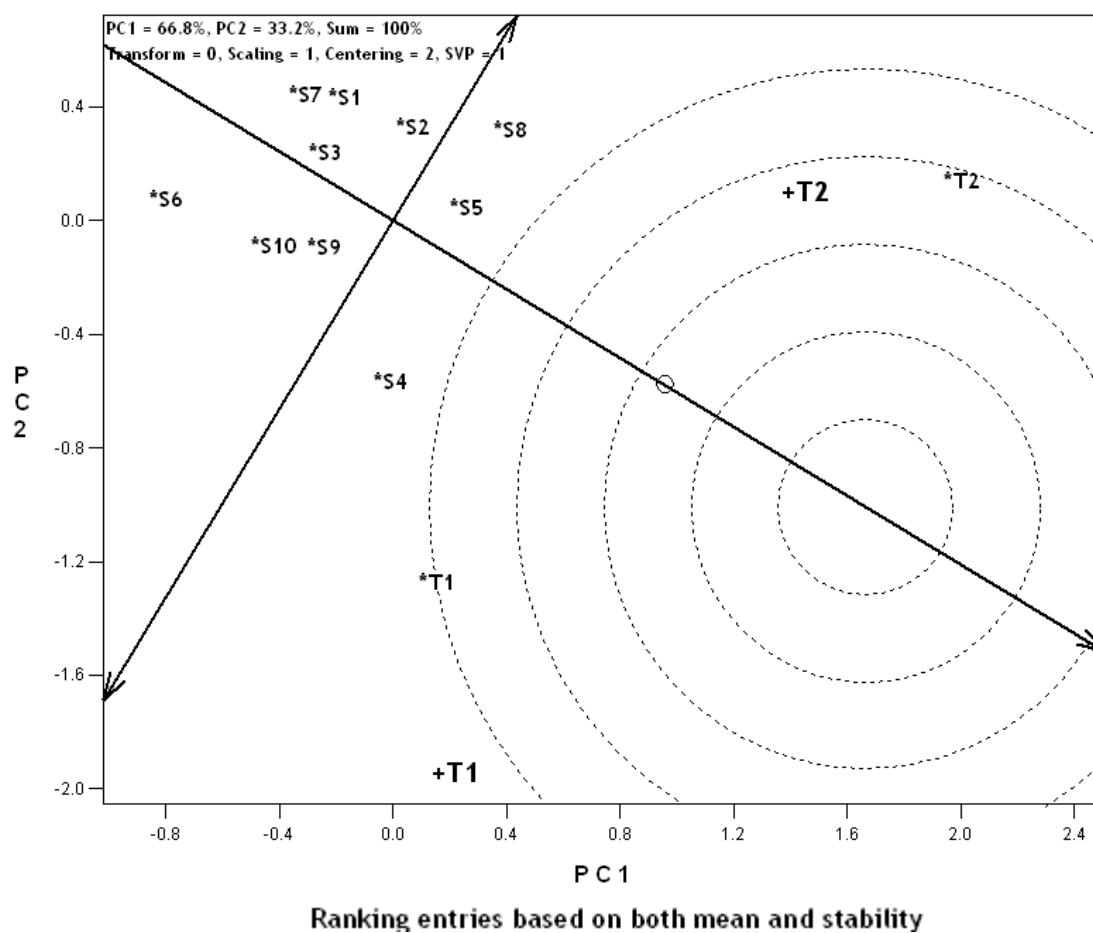
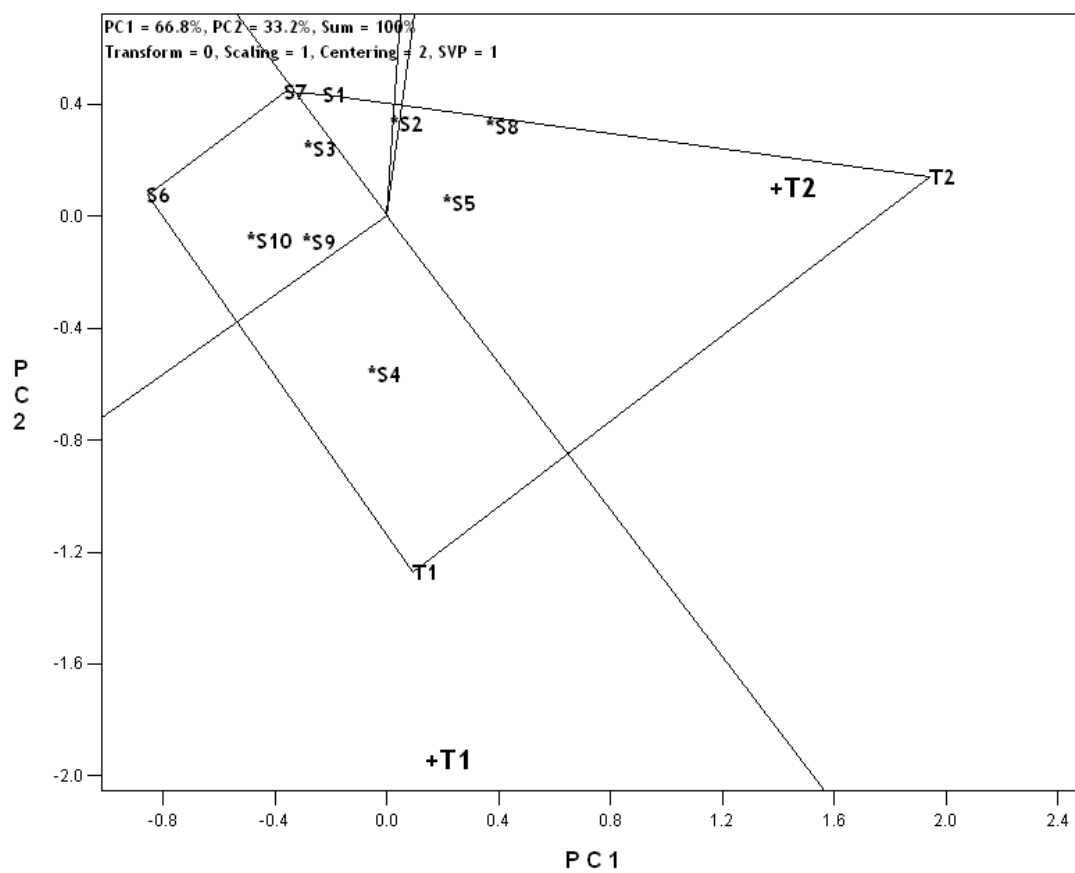


Figure 5.1 Biplot views based on mean yield of 10 synthetic wheat lines and 2 Texas lines tested in Bushland and Chillicothe, TX during 2009 and 2010. (A) average tester coordination view, (B) polygon view. Codes of lines are: T1 = TAM111, T2 = TAM112, S1 = E95Syn4152-5, S2 = E95Syn4152-7, S3 = E95Syn4152-16, S4 = E95Syn4152-37, S5 = E95Syn4152-51, S6 = E95Syn4152-61, S7 = E95Syn4152-77, S8 = E95Syn4152-78, S9 = E2Syn4153-3, S10 = E2Syn4153-31. The circle indicates the average tester; * lines as entries; + lines as testers.



Which wins where or which is best for what

B

Figure 5.1 continued.

Plains biplots

The biplot for the mean yield data of Bushland and Chillicothe explained 100% of the total variation with 66.8% by PC1 and 33.2% by PC2 (Figure 5.1). With breeding methods combined, synthetic entries S4 (E95Syn4152-37), S5 (E95Syn4152-51), and S8 (E95Syn4152-78) had positive GCA effects as they were on the positive end of the ATC abscissa. These entries contributed to high yield in their offspring. Entries S1 (E95Syn4152-5), S2 (E95Syn4152-7), S3 (E95Syn4152-16), S6 (E95Syn4152-61), S7 (E95Syn4152-77), S9 (E2Syn4153-3), and S10 (E2Syn4153-31) had negative GCA effects. The ranking of entries based on combining ability means ($S4 < S5 < S9 \approx S8 < S10 < S3 < S2 \approx S6 \approx S1 < S7$; Table 5.2) was consistent with the ranking suggested by the biplot with the exception of S2 (E95Syn4152-7 ; Figure 5.1A). An ideal entry would be located at the center of the concentric ring in Figure 5.1A. The entry closest to the ideal would be the best. According to the graph, entry T2 was closest to the ideal. The closest synthetic entries were S4 (4152-37) and S5 (E95Syn4152-51).

The ATC ordinate discriminated the entries based on SCA effects, therefore, an entry with a high SCA effect would project farthest from the biplot origin. According to the figure, S6 (E95Syn4152-61) had the highest SCA effect compared to the other synthetic entries (Figure 5.1A). In the polygon view, no tester falls into the sector S6, which means it was not the best parent for any of the crosses (Figure 5.1B). The polygon view shows testers T1 and T2 to fall into their respective entry's sector,

meaning no synthetic crosses were better than purelines of recurrent parents. According to grain yield means previously calculated, no synthetic populations were found to be significantly higher than parent lines TAM111 or TAM112 at Bushland and Chillicothe (Table 5.11). Despite the absence of superior crosses, the entries s4 (E95Syn4152-37) and s8 (E95Syn4152-78) appear to have positive GCA and good SCA as they are both projected farther from the origin than other synthetic entries and lie closer to the testers. Mean yields show the top ranked synthetic lines to be SBC17MB and SBC65 which involve crosses with S4 and S8, respectively (Table 5.11). Therefore, the biplot agrees with yield means.

Stxbl biplots

Figure 5.2 shows the polygon biplot for mean yield of synthetic backcross lines in College Station, McGregor, and Leonard. The biplot explained 100% of the total variation of yield with 69.5% by PC1 and 30.5% by PC2. Entries s2m and s5m had the highest SCA effects with the highest projections from the origin of the biplot. Because no testers fell in the s2m sector, this synthetic line did not have good combining ability with T1 or T2. In fact, entry s2m is expected to produce the worst hybrid as it is farthest from T2 and T1. This holds true according to means from chapter one. The cross s2m/t2 (SBC50MB) has the lowest grain yield average of all lines (28.4 bu/ac) and the

cross s2m/t1 (SBC02MB) has the lowest grain yield of all T1 crosses (33.48 bu/ac; Table 3.12). Tester T2 falls in sector s5m but because entry t2 also falls in this sector, no positive transgressive segregation can be declared by any synthetic cross with T2. Tester T1 falls in sector s8m indicating the best hybrid combination to be s8m/T1. Because the tester T1 is close to the perpendicular line separating sectors s8m and s5m, crosses of T1 with either entry should be equally good. Based on the polygon view, crosses s8m/T1 and s5m/T1 should produce superior hybrids. Indeed, previously calculated yield means show the top line to be the cross s8mb/t1 (SBC24MB, 44.2 bu/ac) and the second ranked to be s5mb/t1 (SBC35MB, 43.6 bu/ac; Table 3.12). All other lines with means significantly higher than TAM111 were from crosses with entries s3m, s9, s9m, s8, s7m, s3, s10, s4m, and s5 (Table 5.12). These entries all appear in the sectors s8m and s5m, in which T1 lies close to the perpendicular line between the two (Figure 5.2).

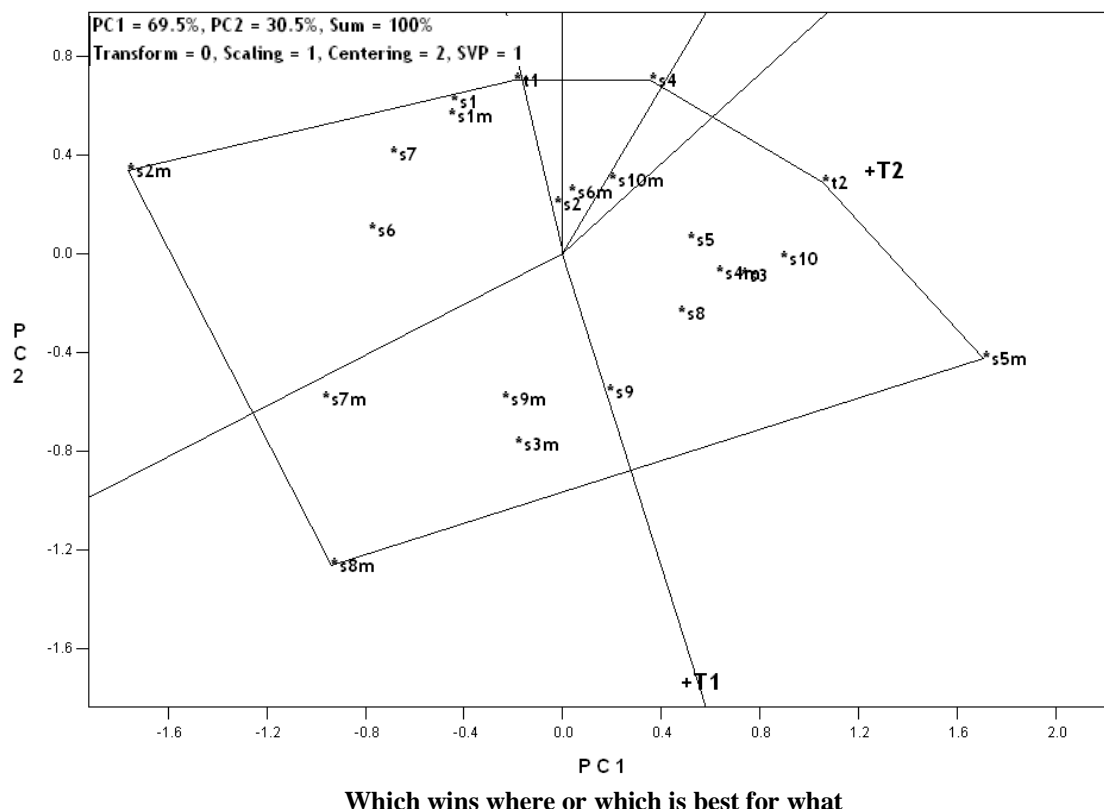
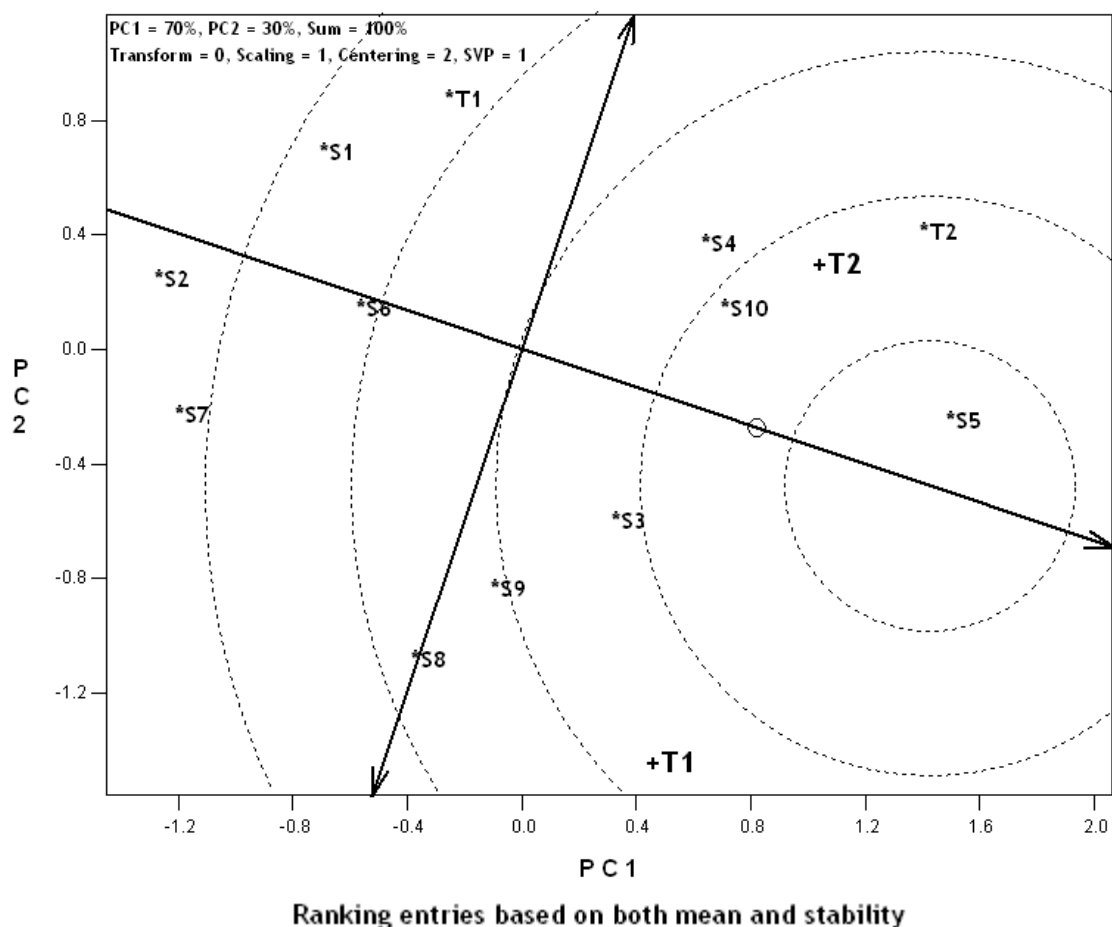
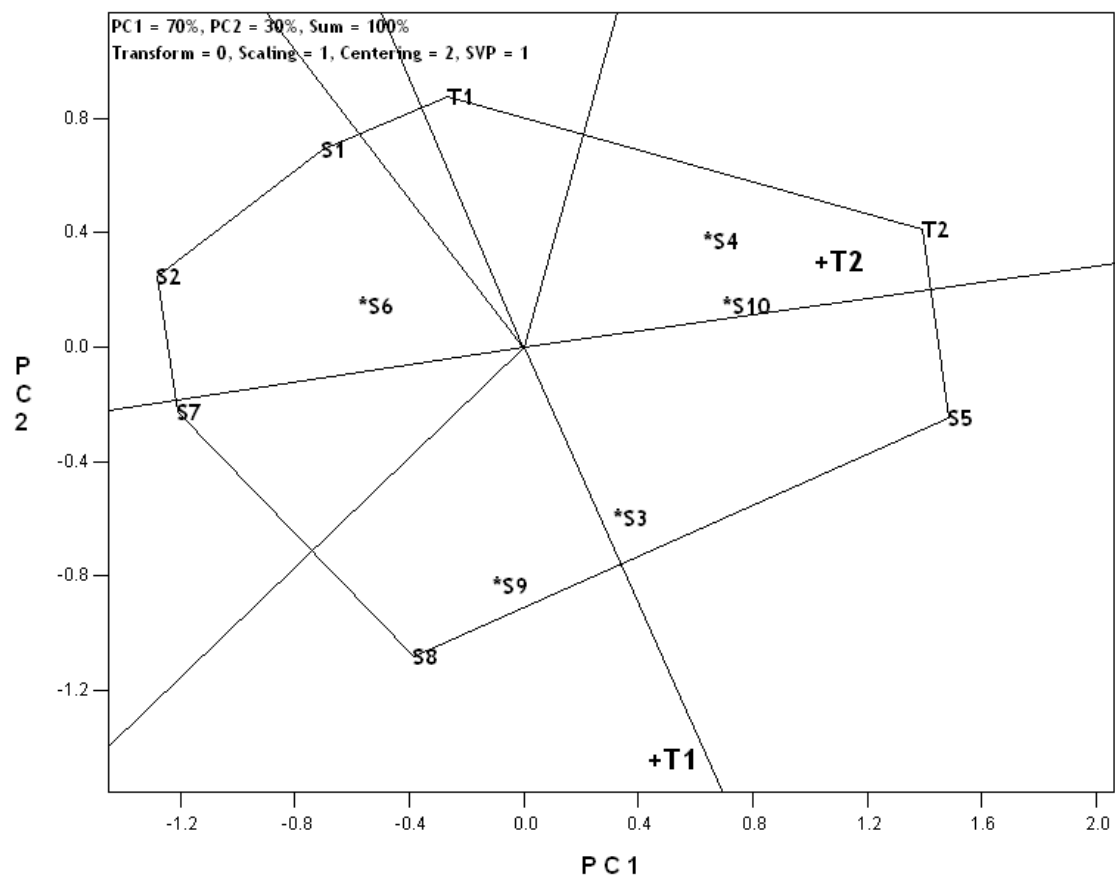


Figure 5.2 Polygon view of biplot based on mean grain yield of 10 synthetic wheat lines and 2 Texas wheat lines tested in College Station, McGregor, and Leonard, TX during 2009 and 2010. Codes of lines are: T1 = TAM111, T2 = TAM112, S1 = E95Syn4152-5, S2 = E95Syn4152-7, S3 = E95Syn4152-16, S4 = E95Syn4152-37, S5 = E95Syn4152-51, S6 = E95Syn4152-61, S7 = E95Syn4152-77, S8 = E95Syn4152-78, S9 = E2Syn4153-3, S10 = E2Syn4153-31; * denotes lines as entries; + denotes lines as testers; synthetic lines followed by “m” were derived through modified bulk breeding method while other synthetic entries were derived through bulk hybrid method.



A

Figure 5.3 Biplot views based on mean yield of 10 synthetic wheat lines and 2 Texas lines tested in College Station, McGregor, and Leonard, TX during 2009 and 2010. (A) Average Tester Coordinate view, (B) Polygon view. Codes of lines are: T1 = TAM111, T2 = TAM112, S1 = E95Syn4152-5, S2 = E95Syn4152-7, S3 = E95Syn4152-16, S4 = E95Syn4152-37, S5 = E95Syn4152-51, S6 = E95Syn4152-61, S7 = E95Syn4152-77, S8 = E95Syn4152-78, S9 = E2Syn4153-3, S10 = E2Syn4153-31. The circle indicates the average tester; * lines as entries; + lines as testers.



B

Figure 5.3 continued.

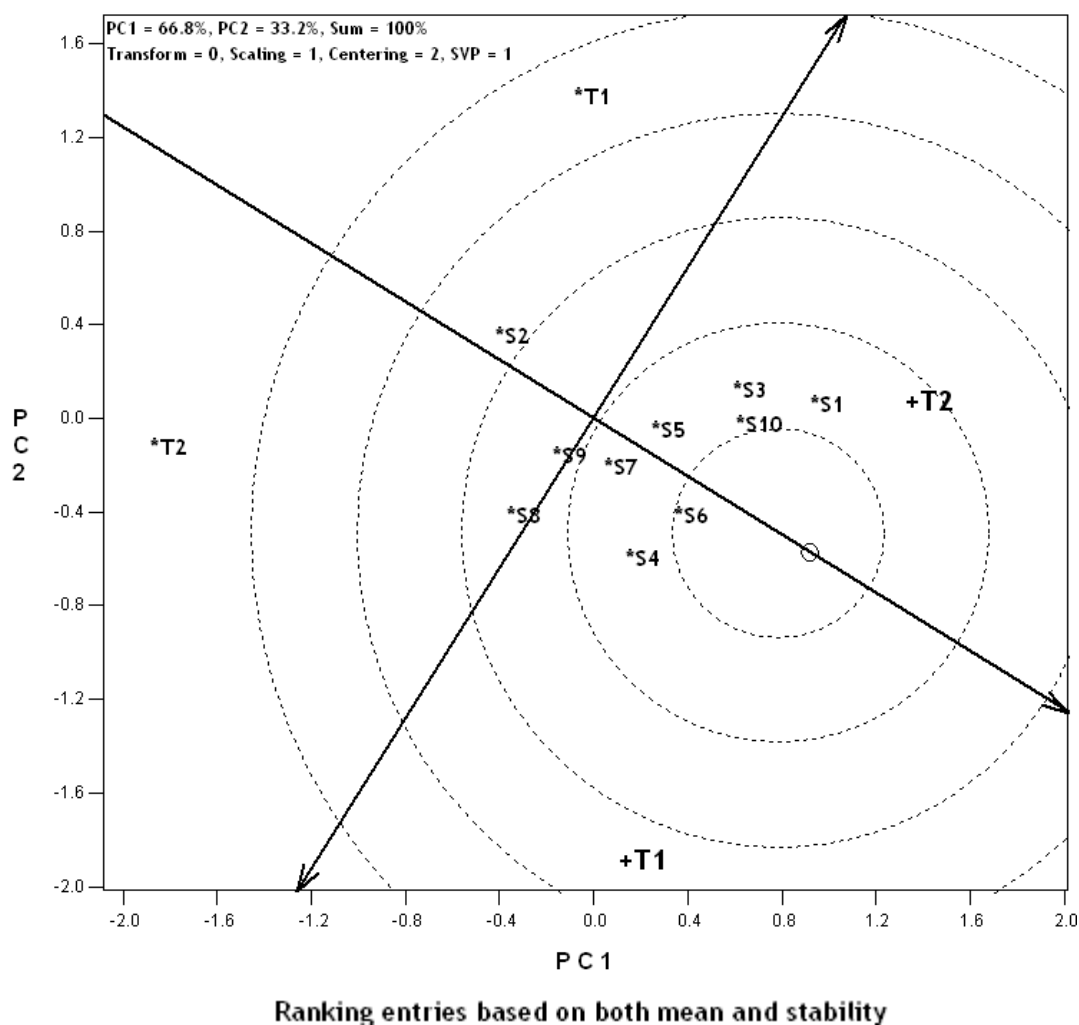
The biplot for the mean yield data in College Station, McGregor, and Leonard locations explained 100% (70% and 30% by PC1 and PC2, respectively) of the total variation (Figure 5.3). This figure and the ones to follow show combined breeding methods. Synthetic entries S3 (E95Syn4152-16), S4 (E95Syn4152-37), S5 (E95Syn4152-51), S9 (E92Syn4153-3), and S10 (E2Syn4153-31) had positive GCA effects as they were on the positive end of the ATC abscissa, whereas entries S1 (E95Syn4152-5), S2 (E95Syn4152-7), S6 (E95Syn4152-61), and S7 (E95Syn4152-77) were on the negative side and had negative GCA effects. The entries with the highest and lowest GCA effects were S5 (E95Syn4152-51) and S2 (E95Syn4152-7), respectively. Rankings of entries based on entry means ($S5 > S3 > S9 > S10 > S8 > S4 > S6 > S7 > S1 > S2$; Table 5.3) were roughly consistent with the order suggested by the biplot analysis ($S5 > S10 > S3 \approx S4 > S9 > S8 > S6 > S1 \approx S7 > S2$; Figure 5.3A).

The polygon view showed sectors T1, T2, S1, S2, S5, S7, and S8 (Figure 5.3B). Neither testers T1 nor T2 fell in or close to sectors S1, S2, or S7 indicating that these synthetics did not produce good hybrids with either TAM line. Entry S7 (E95Syn4152-77) was expected to produce the worst hybrid with tester T2 as the entry fell far from the tester in the opposite sector. According to previously calculated means, the average yield of populations involving the cross S7/T2 (SBC64 and SBC64MB) was not significantly different from the lowest yielding population (Table 3.12). Entry S2

(E95Syn4152-7) was expected to have the lowest combining ability with testers as it was located far from both testers. This holds true according to combining ability means in Table 5.3 as S2 ranked the lowest for yield.

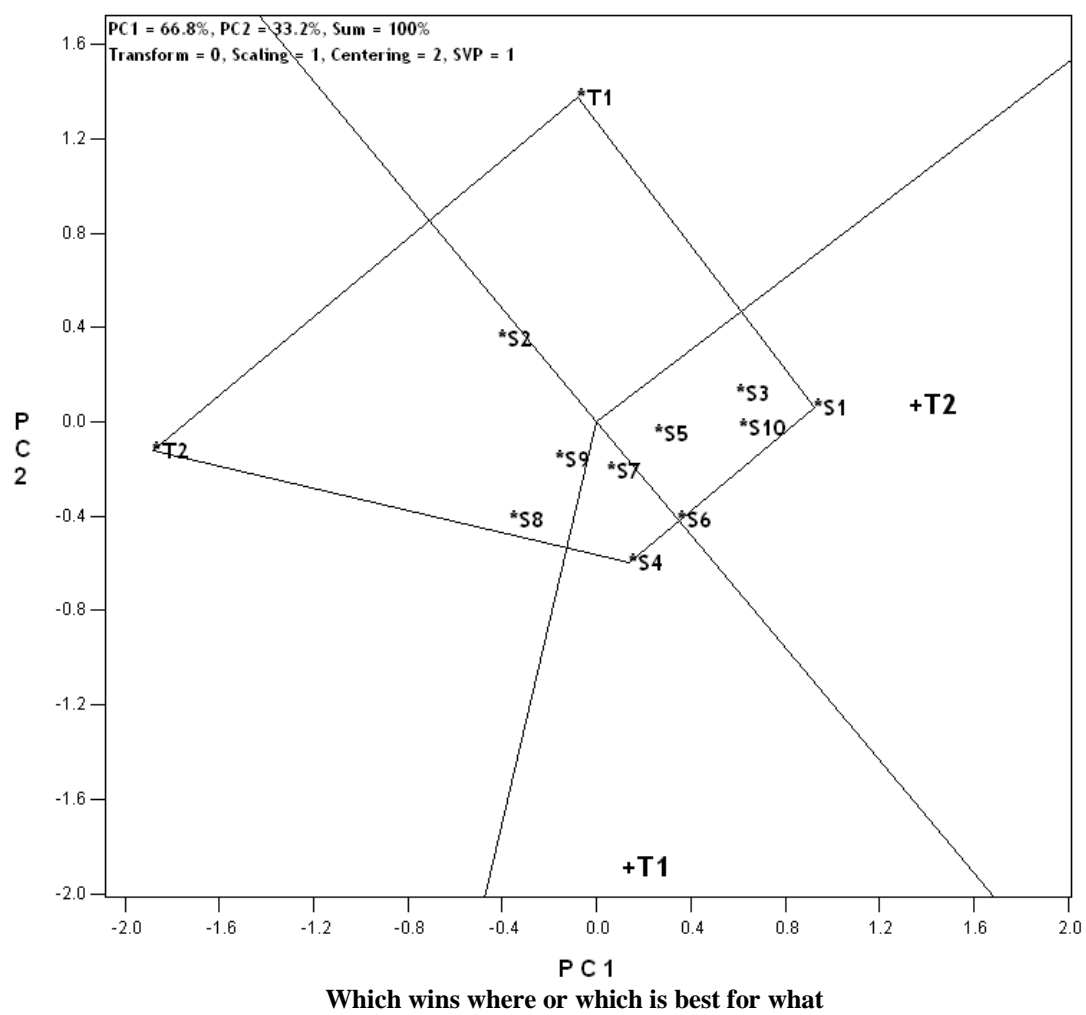
The ATC ordinate discriminated entries based on SCA effects. Entry S5 (E95Syn4152-51) projected high on the ATC ordinate from the biplot origin, so it had large SCA effects compared to other entries and was also closest to the ideal entry (Figure 5.3A). In the polygon view (Figure 5.3B), no testers fell inside sector S5 but T1 was close to the perpendicular line separating sectors S5 and S8 indicating T1 could be equally good with either entry.

According to the graph, crosses S8/T1 and S5/T1 produced superior hybrids. As tester T1 was not in either sector, the hybrid crosses would be better than purelines and expected to show positive transgressive segregation. Indeed, SBC35MB and SBC24MB were the best two lines among all combinations, with the highest yields of 44.2 bu/ac and 43.6 bu/ac, respectively (Table 3.12). As tester T2 fell in sector T2, no synthetic crosses were expected to perform better than the parent line TAM112.



A

Figure 5.4 Biplot views based on mean seed weight of 10 synthetic wheat lines and 2 Texas lines tested in College Station, McGregor, and Leonard, TX during 2009 and 2010. (A) average tester coordination view, (B) polygon view. Codes of lines are: T1 = TAM111, T2 = TAM112, S1 = E95Syn4152-5, S2 = E95Syn4152-7, S3 = E95Syn4152-16, S4 = E95Syn4152-37, S5 = E95Syn4152-51, S6 = E95Syn4152-61, S7 = E95Syn4152-77, S8 = E95Syn4152-78, S9 = E2Syn4153-3, S10 = E2Syn4153-31. The circle indicates the average tester; * lines as entries; + lines as testers.

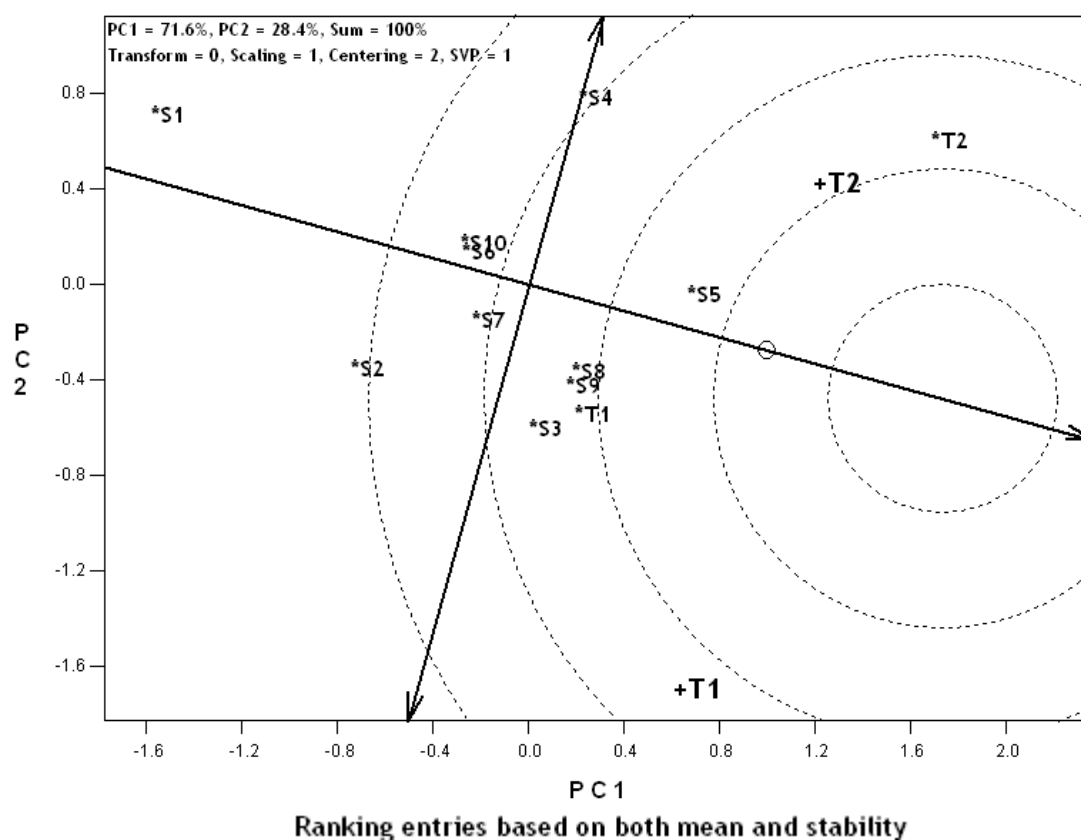


B

Figure 5.4 continued.

Seed weight in Stxbl

The biplot analysis of mean seed weight explained 100% (66.8% and 33.2% by PC1 and PC2, respectively) of the total variation (Figure 5.4). Synthetic entries with positive GCA effects were S1 (E95Syn4152-5), S3 (E95Syn4152-16), S4 (E95Syn4152-37), S5 (E95Syn4152-51), S6 (E95Syn4152-61), S7 (E95Syn4152-77), and S10 (E2Syn4153-31). Those with negative GCA effects were S2 (E95Syn4152-7), S8 (E95Syn4152-78), and S9 (E2Syn4153-3). Entries S6 (E95Syn4152- 61) and S10 (E2Syn4153-31) were closest to the ideal entry and therefore considered the best. The order of GCA effect according to entry means ($S4 \approx S6 > S1 > S10 > S3 > S7 > S5 > S8 > S9 > S2$) was similar to the biplot ranking (Table 5.3). Entry S1 (E95Syn4152- 5) projected high on the ATC ordinate from the biplot origin and had large SCA effects compared to other synthetic entries (Figure 5.4A). Testers T1 and T2 fell into sectors S4 and S1, respectively. Also, entries T1 and T2 were not located in these sectors leading to the conclusion that crosses S1/T2 and S4/T1 produced superior hybrids with better performance than parent lines. Indeed, SBC49MB and SBC17MB were the highest ranked lines for seed weight (Table 3.12). Entry S2 (E95Syn4152-7) was expected to produce the worst hybrid with either testers, T1 or T2. Table 5.3 shows this to be true as S2 had the lowest combining ability mean for seed weight. However, all synthetic backcrosses proved to have superior seed weight to respective recurrent parents, TAM 111 and TAM112. This can be seen in the polygon view as all synthetic entries fell much closer to testers than entries T1 and T2 (Figure 5.4B).



A

Figure 5.5 Biplot views based on mean head number of 10 synthetic wheat lines and 2 Texas lines tested in College Station, McGregor, and Leonard, TX during 2009 and 2010. (A) average tester coordination view, (B) polygon view. Codes of lines are: T1 = TAM111, T2 = TAM112, S1 = E95Syn4152-5, S2 = E95Syn4152-7, S3 = E95Syn4152-16, S4 = E95Syn4152-37, S5 = E95Syn4152-51, S6 = E95Syn4152-61, S7 = E95Syn4152-77, S8 = E95Syn4152-78, S9 = E2Syn4153-3, S10 = E2Syn4153-31. The circle indicates the average tester; * lines as entries; + lines as testers.

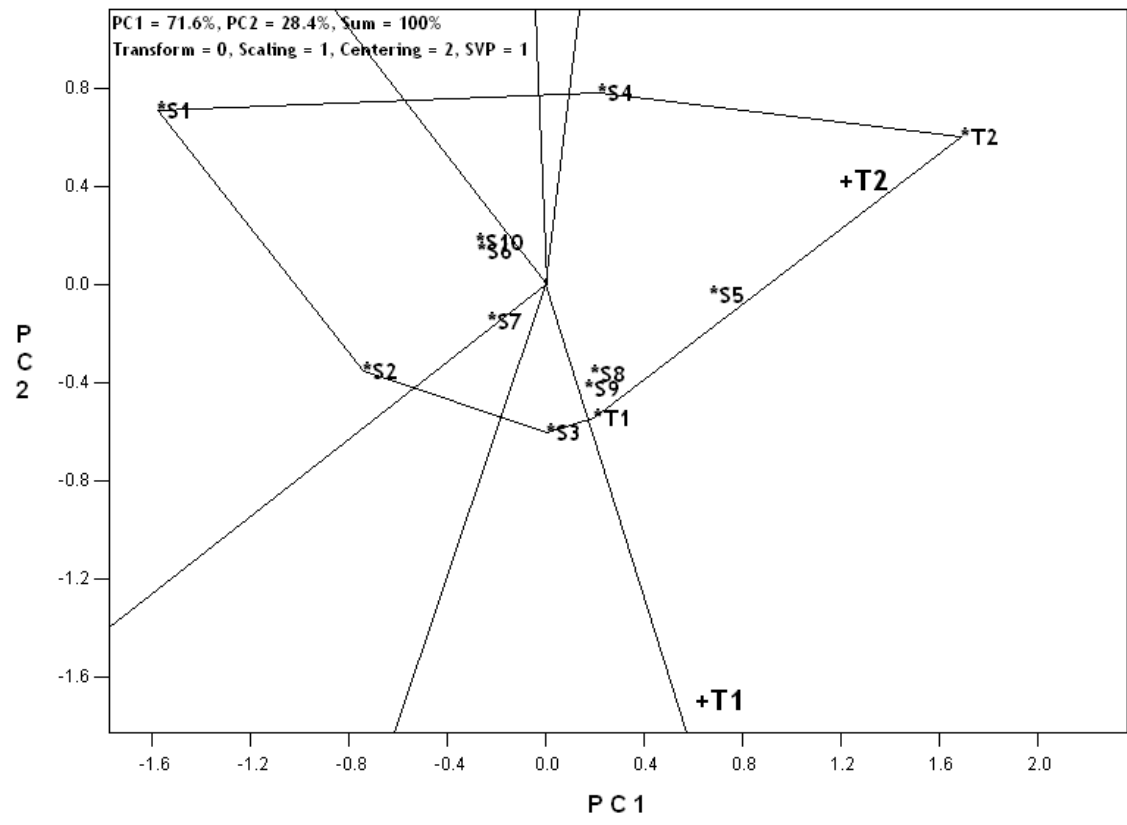
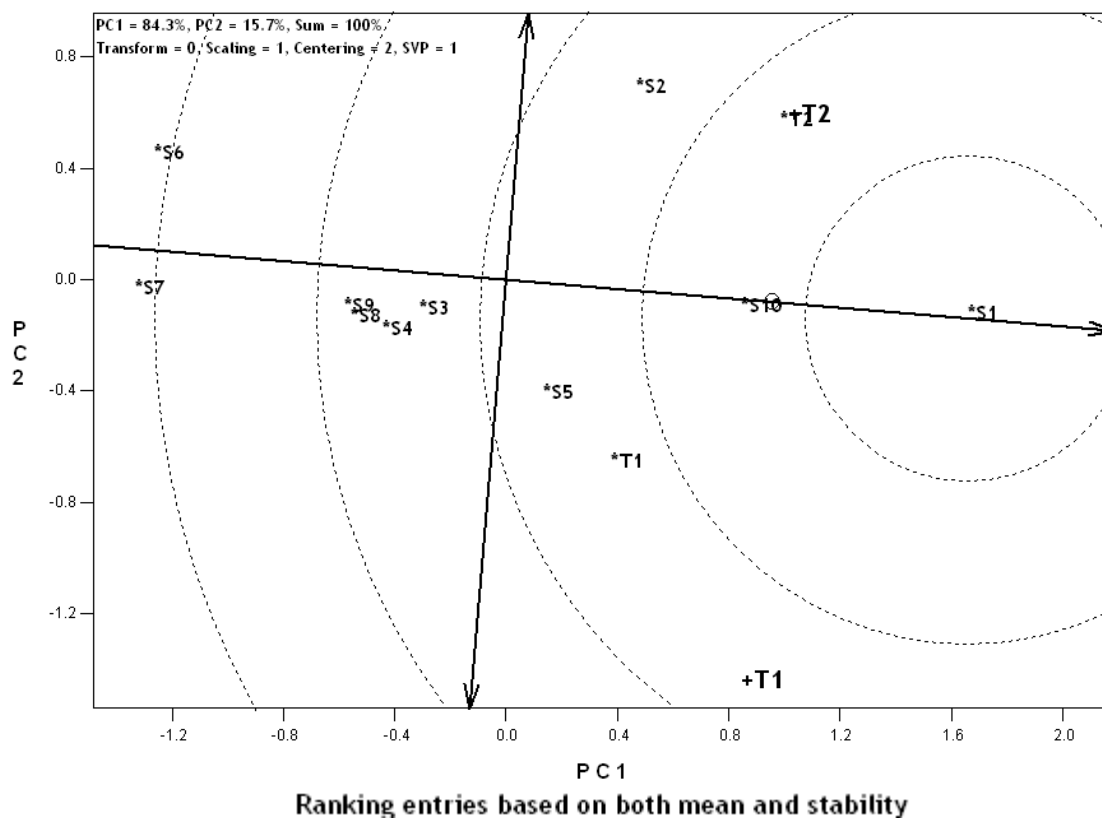


Figure 5.5 continued.

Head number in Stxbl

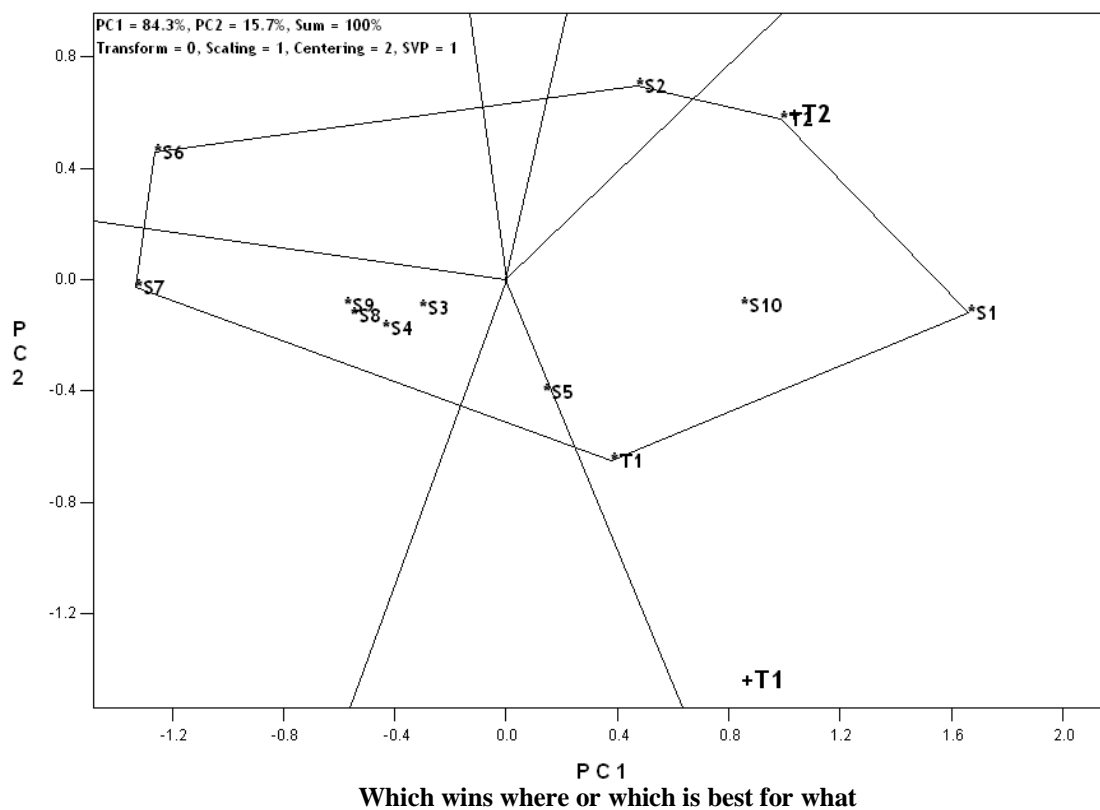
The biplot for head number data also explained 100% of total variation with PC1 and PC2 explaining 71.6 and 28.4%, respectively (Figure 5.5). Positive GCA entries were S3, S4, S5, S8, and S9 (Figure 5.5A). Entries with negative GCA effects were S1, S2, S6, S7, and S10. The order of GCA rankings is similar to combining ability means ($S5 > S9 > S8 > S3 > S4 > S7 > S6 > S10 > S2 > S1$; Table 5.3). Both identify S5 (E95Syn4152-51) to have the best GCA effects and S1 (E95Syn4152-5) to have the lowest GCA effects. S5 was the closest synthetic entry to the ideal entry.

Entry S1 (E95Syn4152- 5) projected high on the ATC ordinate from the biplot origin but because no testers fell in the S1 sector, it was not the best mating partner with either TAM 111 or TAM 112 (Figure 5.5B). In fact, S1 was expected to produce the worst hybrids with T1 and T2, which were the furthest in the opposite sector, and therefore had negative SCA effect. According to yield means, all lines involving crosses with S1 (SBC01, SBC49, SBC01MB, and SBC49MB; Table 3.12) ranked in the bottom five with regard to head number. The polygon view shows both testers to be in their respective entry's sector (Figure 5.5B). Therefore, no hybrid crosses were better than TAM 111 and TAM 112 for head number, as previously shown by population means (Table 3.12).



A

Figure 5.6 Biplot views based on mean seed per head of 10 synthetic wheat lines and 2 Texas lines tested in College Station, McGregor, and Leonard, TX during 2009 and 2010. (A) average tester coordination view, (B) polygon view. Codes of lines are: T1 = TAM111, T2 = TAM112, S1 = E95Syn4152-5, S2 = E95Syn4152-7, S3 = E95Syn4152-16, S4 = E95Syn4152-37, S5 = E95Syn4152-51, S6 = E95Syn4152-61, S7 = E95Syn4152-77, S8 = E95Syn4152-78, S9 = E2Syn4153-3, S10 = E2Syn4153-31. The circle indicates the average tester; * lines as entries; + lines as testers.



B

Figure 5.6 continued.

Seed per head in Stxbl

Biplots for seed per head data explained 100% of total variation with 84.3% by PC1 and 15.7% by PC2 (Figure 5.6). Entries S1, S2, S5, and S10 had positive GCA effects while entries S3, S4, S6, S7, S8, and S9 had negative effects (Figure 5.6A). Rankings of GCA effects were similar to combining ability means ($S1 > S2 > S10 > S5 > S3 > S4 > S8 > S9 > S6 > S7$; Table 5.3). Entry S1 (E95Syn4152-5) was the best and had the highest SCA effect. Combining ability means also showed S1 to have the

highest rank with regard to seed per head (Table 5.3). The polygon view shows both testers to fall in sector S1, but entries T1 and T2 also fall into this sector (Figure 5.6B). The results were similar to biplots for head number as no hybrid was proved to be better than the parental lines. Entry means agreed with this as no synthetic backcrosses had significantly higher head number than respective recurrent parent (Table 3.12).

Conclusions

Poor heritability values for yield in this study were expected, and indicate that direct selection for this trait in early generations is not recommended. Instead indirect selection for yield via seed weight and seed per head would provide better gain from selection, especially if selections were made in more advanced generations (F_4 to F_6). Selection for head number would also be advantageous to that for yield but repeated selections in subsequent generations are necessary as this trait has lower heritability compared to the other two components.

In this study, GGE biplots gave an accurate visual display of GCA and SCA effects of synthetic entries and Texas wheat lines. Together, combining ability from entry means and GGE biplots would provide the breeder with useful information for selection of potential parents and populations.

It is difficult to determine a synthetic that has good GCA with Texas wheat as only two recurrent parents were used in this study. However, S5 (E95Syn4152-51) ranked consistently high for GCA in yield and head number. Negative or lower GCA in seed weight and seed per head did not seem to affect the yield performance of this synthetic. The synthetic S4 (E95Syn4152-37) had a negative GCA for yield and the

worst GCA for head number but ranked high with regard to seed weight and seed per head combining abilities. Therefore, synthetics with high GCA for head number were desirable, as this trait seemed to have the greatest effect on yield. Generally synthetics with a high GCA for yield had either a high combining ability for head number or in some cases seed per head but results varied among environments.

Overall, the primary synthetics combined better with TAM 111 than with TAM 112 in South Texas and the Blacklands, possibly due to stripe rust resistance that was prevalent in 2010. Interestingly, the reverse was true in the High and Rolling Plains. Because yield components were not measured in these locations, it is difficult to conclude why TAM 112 crosses performed better in this region. These results indicate recurrent parents and environment are important factors to consider in making crosses between synthetics and hard winter wheat.

In the Stxbl region, synthetic parents with high SCA for head number also had high SCA for yield. TAM 111 was the better recurrent parent of the two Texas lines because of higher SCA for seed per head. All synthetic lines had positive combining ability effects for seed weight. Therefore, synthetics with the highest SCA for head number (S8, S9, S3, S5) crossed to the recurrent parent with the highest combining ability for seed per head (TAM 111) produced the highest yielding populations. Consequently, it may be concluded the primary synthetics contributed higher seed weight as well as head number to the cross while TAM 111 contributed to seed per head.

CHAPTER VI

SUMMARY

Synthetic hexaploid wheat proves to be an efficient method of gene introgression from wild ancestors for the improvement of modern wheat cultivars. Evidence has shown the benefits of incorporating synthetic wheat into breeding programs worldwide (Mujeeb-Kazi et al., 2008; Warburton et al., 2006). However, most evidence of wheat improvement through crosses to synthetics has been in spring wheats (del Blanco et al., 2001; Reynolds et al., 2007). Therefore, it is of interest to explore the potential of synthetic hexaploids for the improvement of winter wheat.

In this study, populations derived from synthetic hexaploid backcrosses to Texas top ranking hard winter wheat cultivars, TAM 111 and TAM 112, were studied and observed for yield potential, yield component association, heritability, and combining ability. Observations were made in the F_4 and F_5 generations across five locations and two years.

Two breeding methods were used to advance populations. Modified bulk consisted of selections in early generations while bulk hybrid involved no intentional selection. Results showed no significant difference between the two methods.

Synthetic performance was greatest in environments of mild winters and high rainfall. Superior yielding populations were observed in South Texas and the Blacklands, while no improvement was observed in the High and Rolling Plains. Yield component measurements showed improvement to be attributed to an increase in seed weight. Similar results have been found in synthetic crosses to spring wheat (del Blanco

et al., 2001). All synthetic populations had significantly higher seed weight than the recurrent parents and superior yielding lines had equal or increased head number or seed per head.

Yield component compensation was present in synthetic populations. According to path coefficient analysis, head number had the strongest influence on yield of synthetic populations through direct and indirect effects. Seed per head also had a significant influence on yield. A negative correlation between the two components suggests difficulty in selecting for high tillering ability and high seed per head, simultaneously.

Although head number had a high correlation with yield, lower heritability than the other two components was observed. Therefore, selection for this trait will need to be repeated in subsequent generations if desired. Seed weight had the highest heritability but indirect effects from other components suggest this trait should not be selected for, as negative effects on seed per head and head number would significantly lower yield. Because yield had a heritability estimate of zero, direct selection of yield per se would be ineffective in the early generations in synthetic lines.

Synthetics with the highest combining ability for head number (S8, S9, S3, S5) crossed to the recurrent parent with the highest combining ability for seed per head (TAM 111) produced the highest yielding populations across environments in South Texas and the Blacklands.

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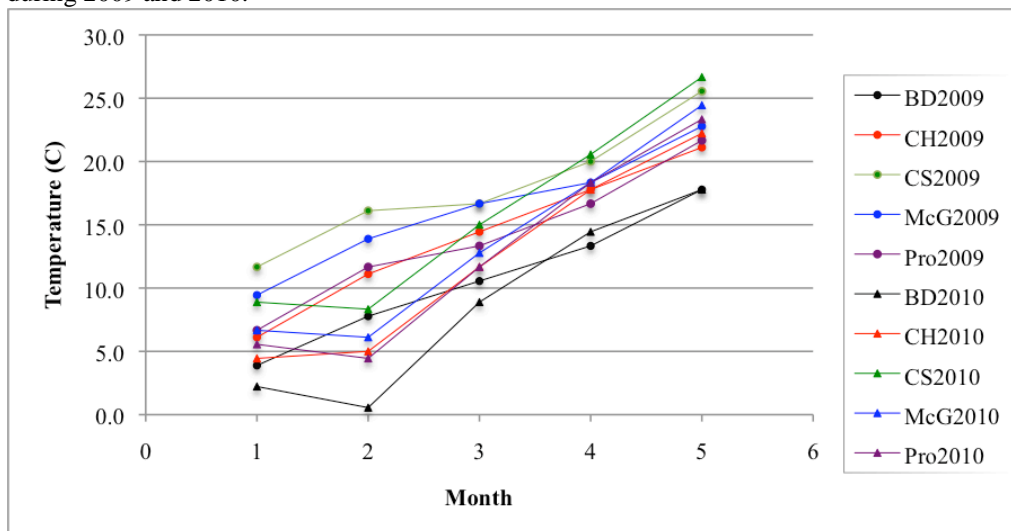
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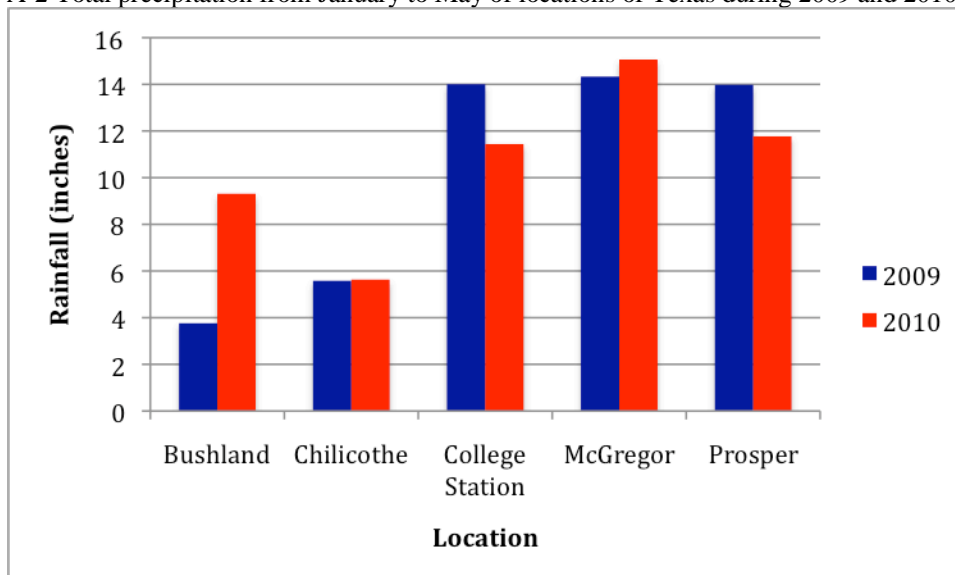
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APPENDIX A

A-1 Average monthly temperature for Bushland, Chillicothe, College Station, McGregor, and Prosper, TX during 2009 and 2010.



A-2 Total precipitation from January to May of locations of Texas during 2009 and 2010.



A-3 Normality testing of data of yield of synthetic wheat lines grown at five locations in Texas during 2009 and 2010.

Location	Mean	Median	W* value	(Pr<W)
2009				
Bushland	15.19	15.25	0.933	(0.0003)
Chillicothe	17.27	16.85	0.992	(0.891)
College Station	29.5	29.8	0.993	(0.928)
McGregor	53.12	51.8	0.984	(0.361)
Leonard	25.45	25.65	0.981	(0.256)
2010				
Bushland	25.6	25.2	0.975	(0.099)
Chillicothe	47.9	48	0.989	(0.699)
College Station	37.8	36.9	0.987	(0.591)
McGregor	40.1	40.6	0.975	(0.095)
Leonard	34.3	33.5	0.971	(0.055)

*According to Shapiro-Wilk test for normality

A-4 Normality testing of data for yield components of synthetic wheat lines grown at three locations in Texas during 2009 and 2010.

Location	Seed weight		Head number		Seed/head	
2009	W* value	(Pr<W)	W* value	(Pr<W)	W* value	(Pr<W)
College Station	0.99	(0.786)	0.961	(0.013)	0.976	(0.119)
McGregor	0.985	(0.467)	0.995	(0.985)	0.968	(0.034)
Leonard	0.945	(0.001)	0.988	(0.643)	0.973	(0.073)
2010						
College Station	0.967	(0.030)	0.977	(0.129)	0.979	(0.174)
McGregor	0.967	(0.029)	0.955	(0.005)	0.966	(0.026)
Leonard	0.99	(0.739)	0.979	(0.193)	0.96	(0.011)

*According to Shapiro-Wilk test for normality

A-5 Error mean squares of yield of synthetic wheat at five locations in Texas during 2009 and 2010.

Location	Error MS	CV%
2009		
Bushland	6.537	16.83
Chillicothe	6.897	15.30
McGregor	33.329	10.87
College Station	18.374	14.59
Leonard	16.753	16.08
2010		
6.411	9.88	6.411
14.225	7.87	14.23
41.852	17.13	41.85
20.08	11.18	20.08
15.37	11.43	15.37

A-6 Homogeneity of variance for yield of synthetic wheat in Texas during 2009 and 2010.

Environments*	Max	Min	F calc	F tab	Conclusion
All locations	41.852	6.411	6.528	3.18	Fcal > Ftab heterogeneous variances
Bushland and Chillicothe	14.225	6.411	2.219	8.81	Fcal < Ftab homogeneous variances
College Station, McGregor, and Leonard	41.852	15.37	2.72	5.05	Fcal < Ftab homogeneous variances

*Environments included are across years 2009 and 2010; Max and Min values are maximum and minimum of error mean squares from previous table; Conclusions according to Hartley's test of homogeneity of variance as described by Peterson (1944).

A-7 Broad-sense heritability estimates of yield and its components of synthetic backcross wheat lines across five locations in Texas during 2009 and 2010.

Trait	$\sigma_g^{2§}$	σ_p^2	h^2
Stxbl Region^a			
Yield	-4.17	19.66	-0.212
Seed wt.	2.866×10^{-5}	3.352×10^{-5}	0.329
Head number	6939	45517	0.152
Seed/head	3.52	14.06	0.25
Plains Region^b			
Yield	4.28	12.67	0.338

^aincludes College Station, McGregor and Leonard

^bincludes Bushland and Chillicothe

§ σ_g^2 = Genotypic variance; σ_p^2 = phenotypic variance; h^2 = broad-sense heritability

A-8 The startup.sas file used for PATHSAS analysis.

/* This program was pasted into SAS Program editor and has used a data file, pathsas.sas, and jackboot.sas files stored in a specified directory for analysis to be conducted */

Title1 'testpathsas';

options nodate;

Data test;

infile 'orig.data';

input name \$ loc gy kw tp seed_t;

run;

%inc 'pathsas.sas';

%inc 'jackboot.sas';

%pathsas (data=test,

indep=kw tp seed_t,

dep0=gy,

bylist=loc,

printreg=no,

printout=yes,

corrind=yes,

corrdep=yes,

boot=yes,

random=4578091,

samples=1000);

run;

A-9 The pathsas.sas macro used for PATHSAS analysis.

/* This file was included in a specified directory that startup.sas was able to recognize */

%macro analyze(data=, out=);

data data1; set &data;

proc standard data=data1 mean=0 std=1 out=_sdata2;

by &bylist; var &indep &dep0 &dep;

proc reg data=_sdata2 noprint

outest=_estdep(drop=_model_ _type_ _rmse_ intercept);

```

    by &bylist; model &dep0=&indep;
%if &dep ne %then %do;
proc reg data=_sdata2 noprint
    outest=estindep(drop=_model_ _type_ _rmse_ intercept);
    by &bylist;
    model &dep=&dep0;
data _estind2; set estindep end=eof;
    by &bylist;
    array _r regc1-regc&nodep;
    retain regc1-regc&nodep;
    * if first.&bylast then _i_=0; _i_+1; _r=&dep0;
    if eof then output; drop &dep0 &dep_depvar_; run; %end;
proc corr data=data1 outp=_corr noprint;
    by &bylist; var &indep; run;
data _corr; set _corr;
    if _type_='CORR';
    drop _type_; run;
data _estdep; set _estdep;
    array _reg &indep;
    array _r2 reg1-reg&noind;
    do over _reg; _r2=_reg; end;
    drop &indep; run;
data _tog;
    if _n_=1 then set _estdep; set _corr; by &bylist;
    array _dir &indep;
    array _corr &indep;
    array _r2 reg1-reg&noind;
    _n+1; &dep0=0; do over _dir;
        if _n=_i_ then _dir=_r2; else _dir=_r2*corr; &dep0 + _dir; end;
    drop _n;
    * keep &bylist--_name_ &indep &dep0_depvar_;
    drop reg1-reg&noind ; format &indep &dep0 5.2; run;
data _tog2; set _tog;
    * drop &indep; drop _depvar_;
%if &dep ne %then %do;
data _tog2;
    if _n_=1 then set _estind2;
    set _tog; by &bylist;
    array _r regc1-regc&nodep;
    array _t &dep;
    do over _r; _t=&dep0 * _r; end;
    format &dep &dep0 5.2;
    format regc1-regc&nodep 5.2;
    drop regc1-regc&nodep;
    * drop &indep; drop _depvar_; run; %end;
data &out; set _tog2;
    rename _name_= indep; run;
%mend analyze;

%macro pathsas(data,indep,dep0,dep,bylist,printreg,printout,corrind,
    corrdep,boot,random=1234501,samples=1000);

%local word printr;
%global noind nodep noby bylast;
%let noind=0; %if &indep ne %then %do;
    %let word=%scan(&indep,1); %do %while (&word ne );
    %let noind=%eval(&noind+1);
    %let word=%scan(&indep,&noind+1);%end;%end;

%let nodep=0;
%if &dep ne %then %do;
    %let word=%scan(&dep,1);
    %do %while (&word ne );
        %let nodep=%eval(&nodep+1);
        %let word=%scan(&dep,&nodep+1);
    %end;

```

```

    %end;
%let noby=0;
%if &bylist ne %then %do;
    %let word=%scan(&bylist,1);
    %do %while (&word ne );
        %let noby=%eval(&noby+1);
        %let by&noby=%scan(&bylist,&noby);
        %let word=%scan(&bylist,&noby+1); %end;
    %let bylast=%scan(&bylist,&noby); %end;
%if %upcase(&printreg)=YES %then %let printr=;
    %else %let printr=noprint;
%if &bylist eq %then %do;
    %let bylist=_dummy; %let noby=%eval(1);
    %let by&noby=%scan(&bylist,&noby);
    %let bylast=%scan(&bylist,&noby); %end;
data _data1; set &data;
    %if &bylist eq _dummy %then _dummy=1;;
    keep &bylist &dep0 &dep &indep; run;
proc sort data=_data1;
    by &bylist;
proc standard data=_data1 mean=0 std=1 out=_sdata2;
    by &bylist;
    var &indep &dep0 &dep; run;
proc reg data=_sdata2 &printr
    outsscp=_sscp(keep=&bylist intercept _type_)
    outest=_estdep(drop=_model_ _type_ _rmse_ intercept);
    by &bylist;
    model &dep0=&indep; run;
data _sscp; set _sscp;
    if _type_='N';
    rename intercept=nobs;
    drop _type_;
data _estdep; merge _sscp _estdep;
    by &bylist; array _v &indep; _look='no ';
    if nobs<=&noinid then do; _look='yes'; do over _v; _v=.; end; end;run;
proc print data=_estdep;
    where _look='yes'; var &bylist nobs;
title3 'The following identification levels do not have enough obs. for
analysis';
title4 ' ' and the regression coefficients were set to missing ' ';run;
title3 ' ';
title3 'Correlation coefficients for Independent variables';
%if %upcase(&corrind)=YES %then %do;
    %if &bylist eq _dummy %then
        %str(proc print data=_corr(drop=&bylist); format &indep 5.2;
            run;);
    %else %str(proc print data=_corr; format &indep 5.2; run;);
%end;
%if %upcase(&corrdep)=YES and &nodedep>0 %then %do;
    title3 'Correlation coefficients for dependent variables';
    proc corr data=_data1 outp=_corrdep noprint;
        by &bylist; var &dep0 &dep;
    data _corrdep; set _corrdep;
        if _type_='CORR'; drop _type_;
    %if &bylist eq _dummy %then %str(
proc print data=_corrdep(drop=&bylist);
format &dep0 &dep 5.2; run;);
%else %str( proc print data=_corrdep; format &dep0 &dep 5.2; run;);
title3 ' ';%end;
data _estdep; set _estdep;
    array _reg &indep; array _r2 reg1-reg&noinid;
    do over _reg; _r2=_reg; end; drop &indep; run;
data _tog;
    merge _corr _estdep; by &bylist;
    array _dir &indep;
    array _corr &indep;

```



```

array _r2 reg1-reg&noind;
if first.&bylast then do; _totc=0; _n=0; end;
_n+1; &dep0=.; do over _dir; if _n=_i_ then _dir= _r2; else _dir= _r2* _corr;
&dep0 + _dir; end; drop _n; keep &bylist--_name_ &indep &dep0 _depvar_ nob;
format &indep &dep0 5.2; run;
data _tog2; set _tog;
drop _depvar_;

title3 'Direct Effects, Indirect Effects and Total Correlations';
%if %upcase(&printout)=YES %then %do;
%if &bylist eq _dummy %then %str(proc print data=_tog2(drop=&bylist);run;);
%else %str(proc print data=_tog2; run;); %end;
title3 ' ';
%if %upcase(&boot)=YES %then %do;
* %inc 'jackboot.sas';
proc freq data=_data1;
tables %do i=1 %to &noby; &&by&i
%if &i lt &noby %then *; %end;
/ noprint out=_levels; run;
data _null_;
if 0 then set _levels nob;total;
call symput('nlevel',left(put(total,8.)));
stop; run;
data _out; delete; run;
%do i=1 %to &nlevel; title3 "&i";
data _one; set _levels;
if _n_=&i;
drop count percent; run;
data _sub;
merge _data1 _one(in=yes);
by &bylist; if yes;
%boot(data=_sub, samples=&samples,id=indep, chart=0,
print=0, random=&random,stat=&dep0 &dep);
%bootci(bc, id=indep, print=0 , stat=&dep0 &dep); run;
data _ci;
set bootci;
data _ci;
if _n_=1 then set _one;
set _ci(keep=indep name value alcl aucl confid method n); method=scan(method,2);
if not(alcl<=value<=aucl) then check='*'; else check=' ';
if (alcl<-1) or (aucl>1) then check='*'; data _out; set _out _ci; run; %end;
title3 'Bootstrap 95% confidence intervals - using BC method';
title4 "Random Seed= &random";
title5 "Number of Resamples=&samples";
proc print data=_out label split='*';
%if &bylist eq _dummy %then %str(var indep name alcl value aucl );
%else %str(var &bylist indep name alcl value aucl );
label indep='Independent*Variables';

format alcl aucl 6.2; run;
title3 ' '; %end;
proc datasets library=work memtype=data;
delete
_CI_CORR_CORRDEP_DATA1_ESTDEP_ESTINDEP_ESTIND2_LEVELS_ONE
_SDATA2_SSCP

_SUB_TOG_TOG2; run;quit;

%mend pathsas;

```

A-10. Example of jackboot.sas macro used for bootstrap analysis.

```

/* This file was included in a specified directory that startup.sas was able to recognize */
%macro boot(data=,samples=200,residual=,equation size=,balanced random=0,stat=_numeric_,id=,biascorr=1,alpha=.05,
print=1,chart=1);

```

```

%if %bquote(&data)= %then %do;
  %put ERROR in BOOT: The DATA= argument must be specified.;
  %goto exit; %end; %global _bootdat; %let _bootdat=&data;
%local by useby; %let useby=0; %global usevardf vardef; %let usevardf=0;
*** compute the actual values of the statistics;
%let vardef=DF; %let by=; %analyze(data=&data,out=_ACTUAL_);
%if &syserr>4 %then %goto exit;
*** compute plug-in estimates;
%if &usevardf %then %do;
  %let vardef=N;
  %analyze(data=&data,out=_PLUGIN_);
  %let vardef=DF;
  %if &syserr>4 %then %goto exit;%end;
%if &useby=0 %then %let balanced=0;
%if %bquote(&size)^= %then %do;
  %if %bquote(&balanced)= %then %let balanced=0;
  %else %if &balanced %then %do;
    %put %cmpres(ERROR in BOOT: The SIZE= argument may not be used
      with BALANCED=1.);%goto exit;%end;
  %if %bquote(&residual)^= %then %do;
    %put %cmpres;%goto exit;%end;%end;
  %else %if %bquote(&balanced)= %then %let balanced=1;
  *** find number of observations in the input data set;
%global _nobs; data _null_; call symput(' _nobs',trim(left(put(_nobs,12.))));
  if 0 then set &data nobs=_nobs; stop; run;
%if &syserr>4 %then %goto exit;
%if &balanced %then %bootbal(data=&data,samples=&samples,random=&random,print=0);
%else %if &useby %then %bootby(data=&data,samples=&samples,random=&random,size=&size,print=0);
%if &syserr>4 %then %goto exit;%if &balanced | &useby %then %do;
  %let by=_sample_; %analyze(data=BOOTDATA,out=BOOTDIST);
%end; %else %bootslow(data=&data,samples=&samples,random=&random,size=&size);
%if &syserr>4 %then %goto exit;%if &chart %then %do;
  %if %bquote(&id)^= %then %do;
    proc sort data=BOOTDIST; by &id; run;
    proc chart data=BOOTDIST(drop=_sample_);
      vbar &stat;by &id;run; %end; %else %do;
proc chart data=BOOTDIST(drop=_sample_);vbar &stat; run;%end;%end;
%bootse(stat=&stat,id=&id,alpha=&alpha,biacorr=&biacorr,print=&print)
%exit;%mend boot;%macro bootbal(data=&_bootdat,samples=200,random=0,print=0);
data BOOTDATA/view=BOOTDATA;
%bootin; drop _a _cbig _ii _j _jbig _k _s; array _c(&_nobs) _temporary_;
array _p(&_nobs) _temporary_;do _j=1 to &_nobs;_c(_j)=&samples;end;
do _j=1 to &_nobs;_p(_j)=_j;end; _k=&_nobs; _jbig=_k;
_cbig=&samples;do _sample=1 to &samples;do _i=1 to &_nobs;do until(_s<=_c(_j));
_j=ceil(ranuni(&random)*_k); _s=ceil(ranuni(&random)*_cbig);end;
_l=_p(_j);_obs=_l;_c(_j)+1;
* put _sample=_i _k=_l @30 %do i=1 %to &_nobs; _c(&i) %end;;
if _j=_jbig then do;
  _a=floor((&samples-_sample-_k)/_k); if _cbig-_c(_j)>_a then do;
do _ii=1 to _k; if _c(_ii)>_c(_jbig) then _jbig=_ii;end; _
cbig=_c(_jbig); end; end;
if _c(_j)=0 then do; if _jbig=_k then _jbig=_j; _p(_j)=_p(_k); _c(_j)=_c(_k); _k+1; end;
%bootout(_l);end;end;stop;run;%if &syserr>4 %then %goto exit;
%if &print %then %do; proc print data=BOOTDATA; id _sample _obs; run; %end;%exit;;
%mend bootbal;
%macro bootby(data=&_bootdat,samples=200,random=0,size=,print=0);
%if %bquote(&size)= %then %let size=&_nobs;
data BOOTDATA/view=BOOTDATA;
%bootin; do _sample=1 to &samples; do _i=1 to &size;
_p=ceil(ranuni(&random)*&_nobs); _obs=_p; %bootout(_p); end; end; stop; run;
%if &syserr>4 %then %goto exit;
%if &print %then %do; proc print data=BOOTDATA; id _sample _obs; run;
%end;%exit;; %mend bootby;
%macro bootslow(data=&_bootdat,samples=20,random=0,size=);
%put %cmpres; %if %bquote(&size)= %then %let size=&_nobs;
data BOOTDIST; set _ACTUAL_ _sample_=0; delete; run; options nonotes;

```

```

%local sample; %do sample=1 %to &samples; %put Bootstrap sample &sample;
data _TMPD_; %bootin; do _i=1 to &size; _p=ceil(ranuni(%eval(&random+&sample))*&_nobs);
  %bootout(_p); end; stop; run;
%if &syserr>4 %then %goto exit; %analyze(data=_TMPD_,out=_TMPS_);
%if &syserr>4 %then %goto exit; data _TMPS_; set _TMPS_; _sample_=&sample; run;
%if &syserr>4 %then %goto exit; proc append data=_TMPS_ base=BOOTDIST; run;
%if &syserr>4 %then %goto exit; %end; %exit;; options notes;
%mend bootslow;
%macro bootci(method, stat=, student=, id=, alpha=.05, print=1); %global _bootdat;
%if %bquote(&_bootdat)= %then %do; %put ERROR in BOOTCI: You must run BOOT before BOOTCI; %goto exit;%end;
data _null_; length method $10; method=upcase(symget('method'));
  if method=' ' then do; put 'ERROR in BOOTCI: You must specify one of the methods '
'PCTL, HYBRID, T, BC or BCA'; abort; end;
  else if method='PERCENTILE' then method='PCTL';
  else if method not in ('PCTL' 'HYBRID' 'BC' 'BCA' 'T')
then do; put "ERROR in BOOTCI: Unrecognized method '" method "'"; abort; end;
  call symput('qmethod',method); run;
%if &syserr>4 %then %goto exit; %if &qmethod=T %then %do;
  %if %bquote(&stat)= | %bquote(&student)= %then %do;
data _null_; put 'ERROR: VAR= and STUDENT= must be specified with the T method'; run;
%goto exit; %end; %end;
%if %bquote(&id)^= %then %do; proc sort data=BOOTDIST; by &id _sample_; run;
  %if &syserr>4 %then %goto exit; %end;
proc transpose data=BOOTDIST prefix=col out=BOOTTRAN(rename=(col1=value _name_=name));
  %if %bquote(&stat)^= %then %do; var &stat; %end;
  by %if %bquote(&id)^= %then &id; _sample_; run;
%if &syserr>4 %then %goto exit; %if &qmethod=T %then %do;
proc transpose data=BOOTDIST prefix=col
out=BOOTSTUD(rename=(col1=student _name_=studname)); var &student;
  by %if %bquote(&id)^= %then &id; _sample_; run;
%if &syserr>4 %then %goto exit;
data BOOTTRAN; merge BOOTTRAN BOOTSTUD;
  label student='Value of Studentizing Statistic'
  studname='Name of Studentizing Statistic'; run;
%if &syserr>4 %then %goto exit; %end;
proc sort data=BOOTTRAN;
  by %if %bquote(&id)^= %then &id; name
  %if &qmethod=BC | &qmethod=BCA %then value;
  %else %if &qmethod=T %then _sample_; run;
%if &syserr>4 %then %goto exit; %if &qmethod=T %then %do;
  proc transpose data=_ACTUAL_ out=_ACTTR_ prefix=value;
%if %bquote(&stat)^= %then %do; var &stat; %end;
  %if %bquote(&id)^= %then %do; by &id; %end; run;
  %if &syserr>4 %then %goto exit;
proc transpose data=_ACTUAL_ prefix=col
out=_ACTSTUD(rename=( _name_=studname col1=student)); var &student;
  %if %bquote(&id)^= %then %do; by &id; %end; run;
%if &syserr>4 %then %goto exit;
data _ACT_T_; merge _ACTTR_ _ACTSTUD;
  label student='Value of Studentizing Statistic'
  studname='Name of Studentizing Statistic'; run;
%if &syserr>4 %then %goto exit;
proc sort data=_ACT_T_;
  by %if %bquote(&id)^= %then &id; _name_ ; run;
%if &syserr>4 %then %goto exit;
data BOOTTRAN;
  merge BOOTTRAN _ACT_T_(rename=( _name_=name));
  by %if %bquote(&id)^= %then &id; name; value=(value-value1)/student;
run; %if &syserr>4 %then %goto exit; %end;
%if &qmethod=BC | &qmethod=BCA %then %do;
%if &qmethod=BCA %then %do;
  %global _jackdat;
  %if %bquote(&_jackdat)^=%bquote(&_bootdat) %then %do;
    %jack(data=&_bootdat,stat=&stat,id=&id,alpha=&alpha,
      chart=0,print=&print); %if &syserr>4 %then %goto exit; %end;
  proc means data=JACKDIST noprint vardef=df;

```

```

    %if %bquote(&stat)^= %then %do; var &stat;%end;
    output out=JACKSKEW(drop=_type_ _freq_ _sample_) skewness=;
    %if %bquote(&id)^= %then %do; by &id; %end; run;
    %if &syserr>4 %then %goto exit;
    proc transpose data=JACKSKEW prefix=col
        out=_ACCEL_(rename=(col1=skewness _name_=name));
        %if %bquote(&stat)^= %then %do; var &stat; %end;
        %if %bquote(&id)^= %then %do; by &id; %end; run;
    %if &syserr>4 %then %goto exit;
    proc sort data=_ACCEL_;
        by %if %bquote(&id)^= %then &id; name ; run;
    %if &syserr>4 %then %goto exit;
    %end;
    data _BC_; retain _alpha _conf; drop value value1; if _n_=1 then do; _alpha=&alpha;
    _conf=100*(1-_alpha); call symput('conf',trim(left(put(_conf,best8.)))); end;
    merge _ACTTR_(rename=( _name_=name)) BOOTTRAN;
    by %if %bquote(&id)^= %then &id; name; if first.name then do; n=0; _z0=0; end;
    n+1; _z0+(value<value1)+.5*(value=value1);
    if last.name then do; _z0=probit(_z0/n); output; end; run;
    %if &syserr>4 %then %goto exit;
    data BOOTPCTL;
        retain _i _lo _up _nplo _jlo _glo _npup _jup _aup _auc;
        drop _alpha _sample_ _conf _i _nplo _jlo _glo _npup _jup _aup _auc;
        merge BOOTTRAN _BC_ %if &qmethod=BCA %then _ACCEL_;
        by %if %bquote(&id)^= %then &id; name;
        label _lo='Lower Percentile Point'
            _up='Upper Percentile Point'
            _z0='Bias Correction (Z0)';
        if first.name then do;%if &qmethod=BC %then %do;
            _lo=probnorm(_z0+(_z0+probit(_alpha/2)));
            _up=probnorm(_z0+(_z0+probit(1-_alpha/2))); %end;
            %else %if &qmethod=BCA %then %do;
drop skewness; retain _accel; label _accel='Acceleration';
        _accel=skewness/(-6*sqrt(&nobs))*(&nobs-2)/&nobs/sqrt((&nobs-1)/&nobs); _i=_z0+probit(_alpha/2);
        _lo=probnorm(_z0+_i/(1-_i*_accel)); _i=_z0+probit(1-_alpha/2);
        _up=probnorm(_z0+_i/(1-_i*_accel)); %end;
        _nplo=min(n-.5,max(.5,fuzz(n*_lo))); _jlo=floor(_nplo); _glo=_nplo-_jlo;
        _npup=min(n-.5,max(.5,fuzz(n*_up))); _jup=floor(_npup); _gup=_npup-_jup; _i=0; end; _i+1; if _glo then do; if _i=_jlo+1 then
        alcl=value; end;
        else do; if _i=_jlo then alcl=value; else if _i=_jlo+1 then alcl=(alcl+value)/2; end;
            if _gup then do; if _i=_jup+1 then auc=value; end;
        else do; if _i=_jup then auc=value; else if _i=_jup+1 then auc=(auc+value)/2; end;
            if last.name then do; output; end; run;
    %if &syserr>4 %then %goto exit;%end;
    %else %do; %local conf pctlpts pctlpre pctlname; %let pctlpre=a; %let pctlname=lcl ucl;
        data _null_; _alpha=&alpha; _conf=100*(1-_alpha);
        call symput('conf',trim(left(put(_conf,best8.))));
        %if &qmethod=PCTL %then %do; _lo=_alpha/2; _up=1-_lo;
        %end; %else %if &qmethod=HYBRID | &qmethod=T %then %do;
            _up=_alpha/2; _lo=1-_up; %end; _lo=100*_lo; _up=100*_up;
        call symput('pctlpts',trim(left(put(_lo,best8.))||" "||
            trim(left(put(_up,best8.))));run; %if &syserr>4 %then %goto exit;
        proc univariate data=BOOTTRAN noprint pctldef=5;
            var value; output out=BOOTPCTL n=n
pctlpts=&pctlpts pctlpre=&pctlpre pctlname=&pctlname;
        by %if %bquote(&id)^= %then &id; name; run;%if &syserr>4 %then %goto exit;%end;
    data BOOTCI; retain &id name value alcl auc confid method n;
    merge %if &qmethod=T %then _ACT_T_(rename=( _name_=name value1=value));
        %else _ACTTR_(rename=( _name_=name value1=value));
        BOOTPCTL; by %if %bquote(&id)^= %then &id; name; %if &qmethod=HYBRID %then %do;
            auc=2*value-auc; alcl=2*value-alcl;%end;
        %else %if &qmethod=T %then %do;
            auc=value-auc*student;alcl=value-alcl*student;%end;
        confid=&conf; length method $20; method='Bootstrap' ||symget('method');
        label name ='Name'
            value ='Observed Statistic'

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```

    alcl ='Approximate Lower Confidence Limit'
    aucl ='Approximate Upper Confidence Limit'
    confid='Confidence Level (%)'
    method='Method for Confidence Interval'
    n      ='Number of Resamples';run;
%if &syserr>4 %then %goto exit; %if &print %then %do; proc print data=BOOTCI label;
    id %if %bquote(&id)^= %then &id; name; run; %end;
%exit:%mend bootci;

```

VITA

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